User's Guide

PMOD Base Functionality (PBAS)

Version 3.5

PMOD Technologies

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Contents

PMOD Base Functionality Introduction

This guide describes the installation of the PMOD software, the different levels of configuration, and the versatile image analysis tool which belongs to the base installation of PMOD. It supports many operations for image reviewing and scientific data analysis:

- Loading medical images in different formats, including DICOM.
- Viewing the images with different color tables and in different layouts.
- Calculating new slice images in arbitrary new orientations.
- Performing various image processing and manipulation operations.
- Displaying fusion images of matched data sets (image registration is a separate option).
- Performing volume-of-interest analyses and the calculation of time-activity curves from dynamic studies.
- Saving images in different formats, including DICOM, and directly C-STORE them to a DICOM server.

Additionally, this guide explains important notions generally used in PMOD tools such as

- The image data formats, their loading and saving.
- Control of layouts and image display.
- Inter-operation of tools.

For getting started with PMOD we recommend the following approach:

Browse this document as it gives the foundation for all other PMOD tools.

Browse the **PMOD User's Guides** of the other PMOD tools you are interested in.

Perform some practical exercises based on the example data provided with the installation and the step-by-step descriptions in the **PMOD Workbook**.

Attend one of the proven bi-annual **PMOD Trainings** which are announced on ***PMOD's website http://www.***.

For in-depth understanding of PET Kinetic Modeling we strongly recommend the PMOD users to attend one of the excellent yearly *PET Pharmacokinetics Courses.* These courses include theory as well as practical work and are organized by the the top experts in the domain. The 2014 course is scheduled prior to the NeuroReceptor Meeting in Amsterdam (May 21-24, 2014). Two other worthwhile courses are *PET Methodology* (King's College London,) and *Basic Kinetic Modeling in Molecular Imaging* (Copenhagen, March 10-14, 2014).

Chapter 1

PMOD Basics

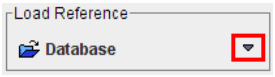
In This Chapter

Basic User Interface Elements

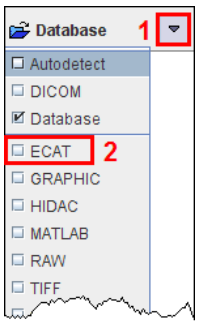
For efficient use of the PMOD programs it will be helpful being aware of the behavior of some user interface elements.

Option Buttons

Frequently used are option buttons. Their appearance is a button with an arrow next to it, for instance the loading button of image data



The arrow ▾ indicates that there is a selection. As soon as it is activated with the left mouse button, the different options appear as a list.



Select the appropriate option with the left mouse button, for example ECAT in the example above. The list closes, the button changes to the new option,

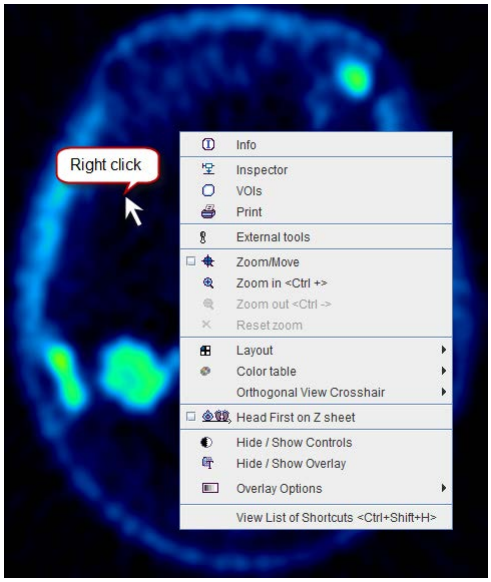
and the button operation is executed.

Option buttons allow organizing related functionality with minimal space requirements, but the hidden functionality might be overlooked. Therefore it is worthwhile to initially check the hidden list wherever you see a ▾.

In some cases option buttons have also left and right arrows to quickly step through the available options, for instance through the color tables.

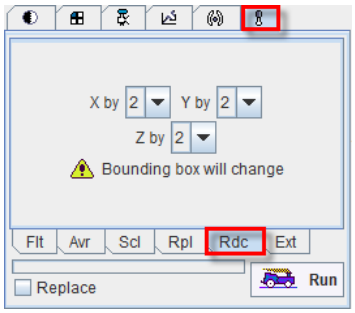
Context Menus

Context menus are another way of collecting function related to a certain element. A context menu is opened by clicking the right mouse button at an element. If available, the menu opens and allows changing configurations or initiating actions. Context menus are available for image display ports (example below), curve areas, and color bars.



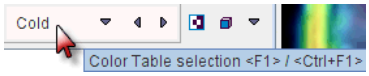
Tabbed Panes

A third way of grouping elements is through tabbed panes. Each tab shows different functions, and may also contain nested tabbed panes. The example below shows the image processing tools pane with the selected reduce **Rdc** sub-pane.



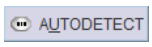
Tooltips

Many elements of the user interface are equipped with an explanatory tooltip. If you move the cursor over the element and wait a while, the explanation pops up and may save you the effort of referring to the reference documentation. From the example below you may learn that you can use the function key `F1` for stepping through the list of color tables in the forward direction, and the combined `Ctrl` and `F1` keys in the backward direction.



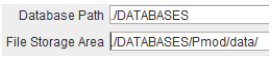
Data Loading, Example Data, Relative Paths

As long as the database functionality is enabled, loading components such as VOIs will always first bring up the database loading interface. If your data resides outside the database, use the button



to start a file-based loader which can be pointed to a particular directory. In some situations the button is abbreviated to ....

In case the user decided to install the example data with PMOD (recommended), there is a database **Pmod** available which contains examples for kinetic modeling (PKIN and PXMOD), cardiac modeling (PCARD) and image fusion (PFUS). This data is installed in a sub-directory data of the PMOD installation directory. The configuration of the database shows the paths



The leading part of the path **./** indicates a path which is relative to the installation directory, currently

Installation-path/Pmod3.5/data

where *Installation-path* might be something like *C:* , */opt*, or */Applications*, depending on the operating system.

The use of relative paths has the consequence that after an upgrade to the next version the data have to be moved to the *data* directory of the new installation.

Accelerator Keys and Mouse Dragging

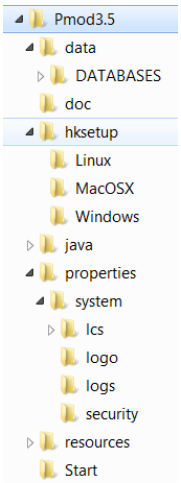
A substantial number of functions can be accessed using keyboard shortcuts. For instance, clicking into an image to activate it and then pressing the "Ctrl" and the "D" keyboard key (`CTRL+D`) will switch the layout to orthogonal planes.

Another sort of shortcuts is using modifier keys and mouse dragging. As an example, the lower and upper color table thresholds can be interactively changed by clicking into the image, then holding down the `SHIFT` key, and dragging the mouse left/right (lower threshold) and up/down (upper threshold) with the left mouse button pressed.

These accelerator capabilities are describe in a separate ***section*** (on page 26).

Directory Tree

The installation of the PMOD software results in directory tree containing the Java classes, configuration information, installers for the USB key driver, and example data for kinetic modeling data and image analysis.



The content of the most important sub-directories is:

data Container for data. **DATABASES** contains the tables and data of JavaDB databases, for instance of the example **Pmod** database.

doc Directory containing the PMOD html documentation as well as the pdf application guides.

hksetup Contains the driver installation files for the USB protection key. Each operating system has a dedicated sub-directory.

java The **ext** sub-directory contains external Java libraries which support specific functions accessed from within PMOD. The **jre** sub-directory contains the Java Runtime Environment for running the PMOD applications. The **jre** is not required for MacOSX.

properties Contains the configuration of PMOD and the different tools.
properties/system: log files
properties/system/lcs: license file pstarter.lcs
properties/system/logo: customer logo
properties/system/logs: log files of PMOD program and the servers
properties/user1, etc: Each PMOD user has a subdirectory containing his configuration of the different tools (*.props), the starting settings (*.ini), and the database queries (*.qry).

Start The PMOD start scripts are located here. They are generated during the installation and take into account the installation directory and the operating system. Therefore, they can not simply be copied to another system or moved to a different directory.

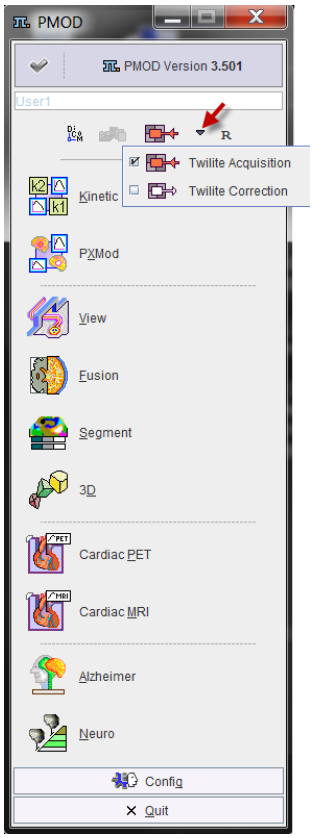
- **RunPmod**: starts the interactive PMOD environment.

- **RunDbSvr**: starts the transaction server for publishing the Pmod database and for license serving. Default port of the transaction server is 5100. Please edit the script for using a different port.
- **RunDcmSvr**: starts the DICOM server for receiving DICOM images and saving them into the **Pmod** database. Default port of the DICOM server is 4030.
- **RunLcsSvr**: starts the transaction server for license serving only.

Starting

Starting the Tools from the ToolBox

PMOD is started using the **RunPmod** script in the Pmod3.5/Start directory. Please refer to the system-specific installation guides if adjustments are needed. After starting, the PMOD ToolBox appears, initially with grayed tool buttons.



If multiple users have been configured, one of them needs to be selected and the **Log In** button activated. Otherwise, the login procedure proceeds automatically. Note the startup window which reminds you that PMOD is research software and shows some license-related information.

After the login, the tool buttons are active and you can start working with PMOD. The ToolBox allows starting the different tools by activating the buttons. Alternatively, you can directly *drag* appropriate files (image files, or .km modeling files) onto the buttons.

The buttons below the login section are related to the different PMOD server functionalities. They are not available for the clients of a network license setup.

Starts the **DICOM server** using the configuration of the current user. If it is already running, the configuration is shown. A blue background color indicates ongoing server activity, e.g. the receiving of images.

Starts the **Transaction Server** for publishing a local JDBC database. If the Transaction Server is already running, an information window is shown which

describes the server status. A blue background color indicates ongoing server activity.

 Access to the PSAMPLE Acquisition and Correction modules used with the Twilite Blood Sampling system

Note: The number of buttons in the ToolBox depends on the configuration you purchased. Only the base functionality **View** is always present.

Starting PMOD Tools from the Command Line with Data

In some situations it is an advantage when a single tool is started rather than first opening the ToolBox. An example is a user program such as IRW which wants to open a PMOD tool with specific data.

This can be done by adding to the system-specific startup script the name of the tool and the file names of the data to be loaded. The Windows example below

```
cd /Pmod3.5
./java/jre/bin/java -Xmx1200M -jar pmod.jar PFUS
C:/DICOM/20060815/38243299/00000210 C:/DICOM/20060815/38243299/00000888
```

starts the fusion tool (PFUS) and loads two DICOM series. The first is loaded as the reference series, the second (and following) as the reslice series. Note that it is sufficient to specify a single file even if a DICOM series consists of multiple files. The loader will find and load all images belonging to the series.

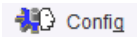
Checking for Updates

The dedicated software update check button  allows comparing whether your PMOD installation corresponds to the latest PMOD software available. Please see the ***Release Notes http://www.pmod.com/technologies/pdf/doc/ReleaseNotes.pdf*** on the PMOD website to find out about the changes occurring in the different versions and builds.

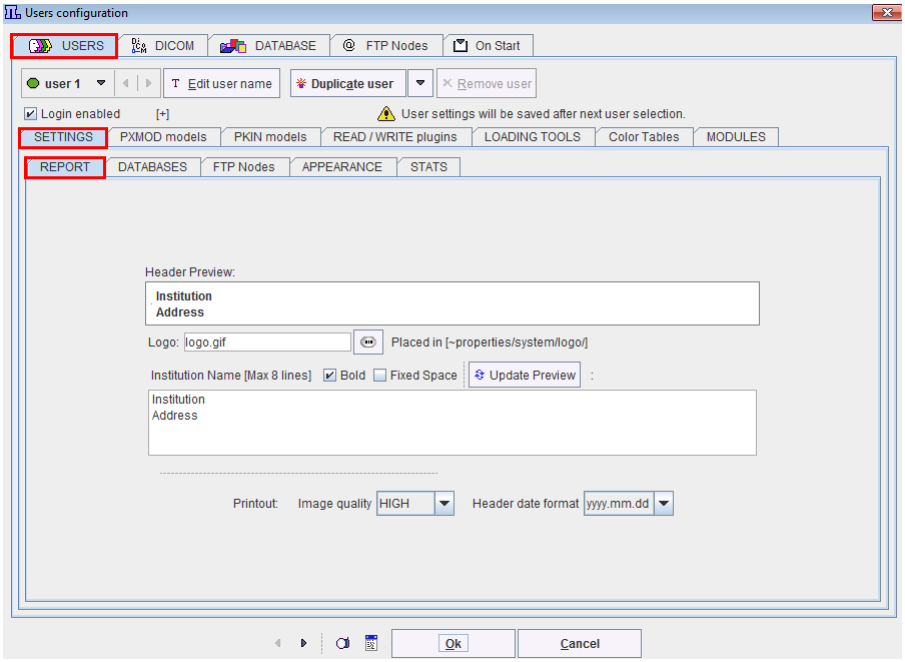
Note: New builds of the current PMOD version are uploaded at irregular intervals, mainly to fix bugs. We therefore recommend using the latest build of a version.

General Configuration

The PMOD configuration utility is started with the **Config** button



at the bottom of the PMOD ToolBox. It appears with four sections accessible by the main tabs.



The **DICOM** and **DATABASE** tabs are described in the ***PMOD DICOM Functionality*** (on page 31) and ***PMOD Database Functionality*** (on page 46) sections, respectively, and the **USERS** ad **On Start** tabs below.

USERS

PMOD supports the concept of different PMOD users. Each user can maintain his own preferences such as the model selection and order, user interface font size, report layout etc, and PMOD maintains for each user independent tool configurations and loading histories. The **USERS** tab of the configuration utility allows creating PMOD user accounts, and configuring their properties.

Note: For all changes of the settings it is important to *first select the affected user*, and then proceed with the configuration.

User Creation

New user accounts are created with the option button:

- **Add new user**: Creates a new user account with the default settings.
- **Duplicate user:** Creates a new user account using the settings of the currently selected user.

The user name needs to be specified during user creation, but can be changed later using the **Edit user name** button. This name will be attached to data saved in a database and can be used in data filtering.

Note that no user passwords are required in the standard PMOD usage, since the accounts are rather aimed at separating the processing environments for different tasks than protecting data access. Only in the case of an ATL version which is aimed at controlled data processing are passwords enforced.

SETTINGS

The **SETTINGS** tab houses the different settings of the currently selected user account. Their configuration panes are accessible by the sub-tabs. Since the majority of the functionality is self-explanatory, only the most important entries are briefly described below.

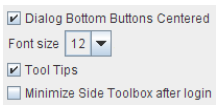
REPORT Configuration of the PMOD report pages. A **Logo** can be specified (a GIF file located in the properties/system/logo sub-directory) as well as the institution address in the **Clinic Name** section. The address can be set to **Bold** and to use **Fixed Space** by checking the corresponding boxes. Please use the **Update Preview** button to inspect the configured layout in the **Header Preview** section.

The **Image quality** selection determines the resolution of the created jpeg pages and should normally be set to **HIGH** to achieve a satisfactory image and text quality. The **Header date format** allows choosing between year first/last variants.

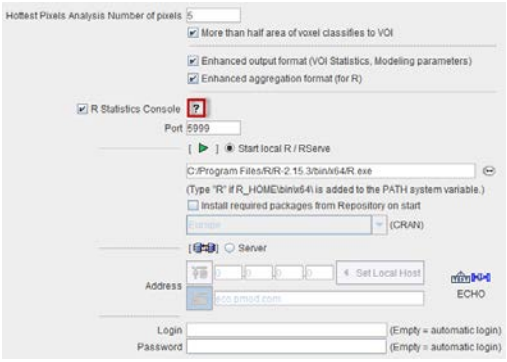
DATABASES Database usage profile. See PMOD ***User-specific Database Configuration*** (on page 57).

FTP nodes FTP nodes usage profile. See PMOD @ FTP Nodes.

APPEARANCE Allows changing the location of the dialog buttons, the font size, whether tooltips should be shown, and whether the ToolBox should be collapsed automatically after login.



STATS



One of the VOI statistics results is the average of the highest pixel values. The **Hottest Pixel Analysis Number of Pixels** specifies the default how many pixels are included in this analysis.

The ***PMOD R console*** (on page 251) provides statistical analyses via the R package. In order to obtain the best results it is recommended to switch on the **Enhance output format (..)** and **Enhanced aggregation format (for R)**. Otherwise the information available in R will be limited.

The functionality is configured by default and should be ***adjusted*** (on page 252). If the user doesn't want to use this functionality, the **R Statistics Console** should be disabled.

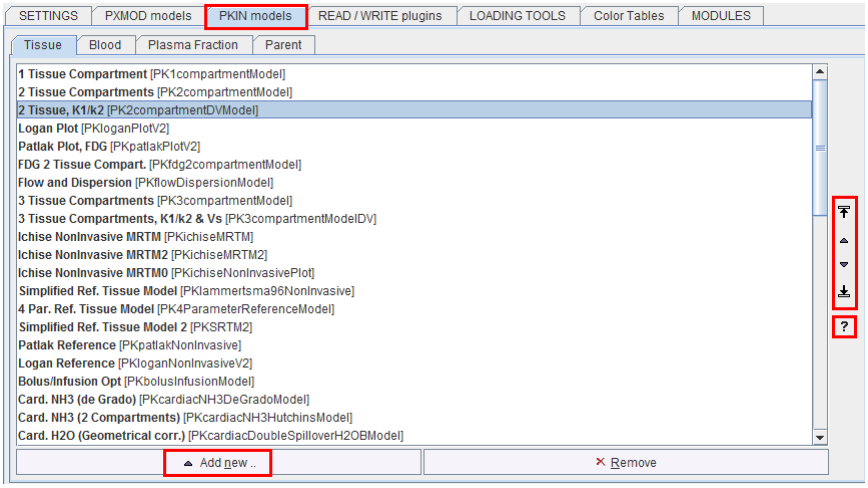
PXMOD, PKIN, READ/WRITE, LOADING, Color Tables Plug-ins

Many PMOD functionalities are programmed as plug-ins. Most of these plug-ins are initially installed, but they can be removed or rearranged for each user account with the different tabs. The procedure is always the same and is explained with the plug-ins (the models) of the kinetic modeling tool PKIN.

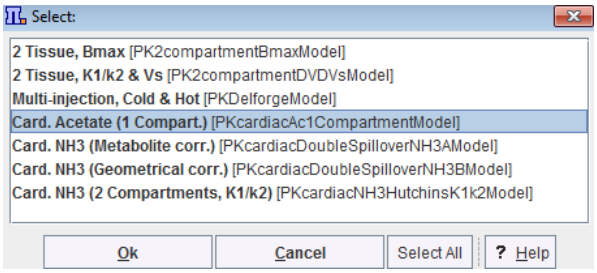
PKIN Models

When the **PKIN models** tab is selected, the list of the currently installed model plug-ins is shown. The entries show the name in the model selection of the PKIN tool as bold and in parentheses the file names of the plug-in.

To modify the order how the models appear in the PKIN application please select an entry and move it up/down using the arrows to the right. The **?** button shows a quick model explanation.



To remove a model from the list just select its list entry and activate **Remove**. To add a model back to the list use the **Add new** button. The appearing dialog window allows selecting one or more plug-in(s) and adding them by the **Ok** button.



Contents of the different Plug-In Tabs

PXMOD models Configuration of the models which appear in the pixel-wise modeling (PXMOD) tool.

PKIN models Configuration of the models which appear in the modeling tool for time-activity curves (PKIN). **Tissue** contains the actual kinetic models for the tissue TACs, **Blood** the models for interpolation of the blood activity, **Plasma fraction** the models for plasma fraction activity and **Parent** the models for metabolite correction.

READ/WRITE plug-ins Configuration of the image data file formats. Note that only a subset ot the formats can be written.

LOADING TOOLS Configuration of image processing filters usable during loading.

Color Tables Configuration of user-defined color tables. These files must be

- located in the resources/colortables sub-directory (see the examples there),
- text files ending in .cltb, and
- contain 3 columns with the RGB values such as

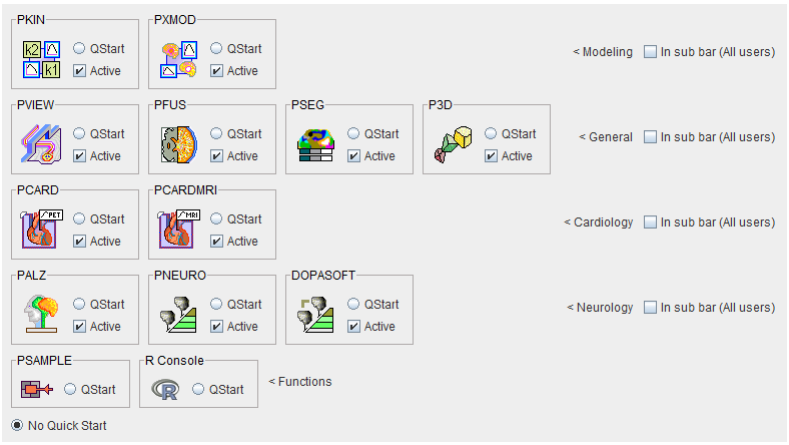
```
# R G B
0 0 0
0 2 2
0 4 4
```

etc.

System color tables cannot be removed or arranged in a different order.

MODULES

The **MODULES** tab shows the PMOD tools available with the installed license file. If needed, tools can be removed from the PMOD toolbar by un-checking the **Active** box. It is also possible to configure a favorite tool which is started as soon as the current user logs in by activating the **QStart** radio button of that tool. By activating the **In sub bar** box, the modules can be grouped together in an additional horizontal bar.



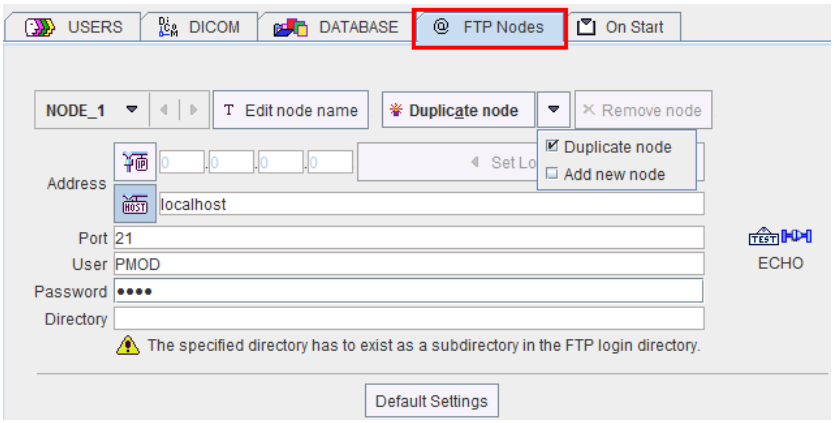
@ FTP Nodes

FTP nodes can be configured and used to remotely connect with external servers. These servers can be used only for sending data.

New nodes are created with the option button:

- **Add new node**: Creates a new node with the default settings.
- **Duplicate node:** Creates a new node using the settings of the currently selected node.

The node name needs to be specified during node creation, but can be changed later using the **Edit node name** button.



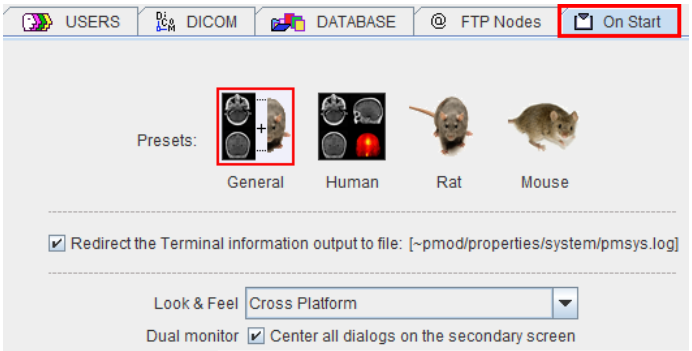
For each of them define the address by IP number or host name. The default port is 21 and supports only unsecured data export. Same port can be used for all nodes. As soon as the remote server has been started, it can be contacted and used for saving images.

The **User** and the **Password** need to be the same as the ones used for the login on the remote server. After configuration has been completed, the **C-ECHO** button can be used to test the connectivity.

In the **Directory** field should be specified a directory name that already exists as a subdirectory in the FTP login directory.

On Start

The **On Start** page contains some global layout options.



Presets

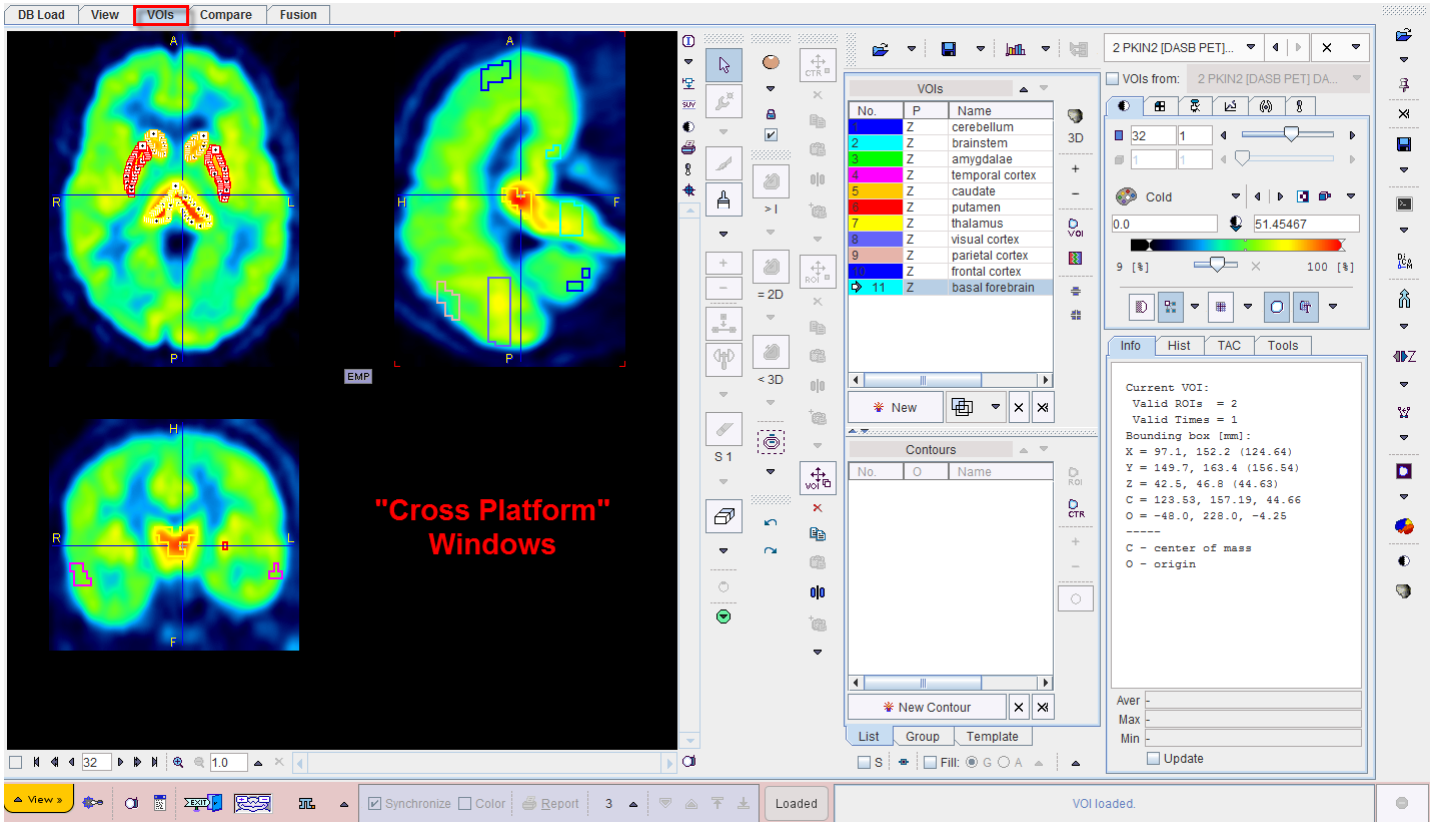
The type of the processed data may matter for some PMOD functions. For instance, animal data with small pixel sizes require also smaller default values for the sampling rates and filter sizes. If the user configures the **Human**, **Rat** or **Mouse** application domain PMOD is able to exploit appropriate presets. Otherwise, with the **General** configuration, the user can choose between the presets during data processing.

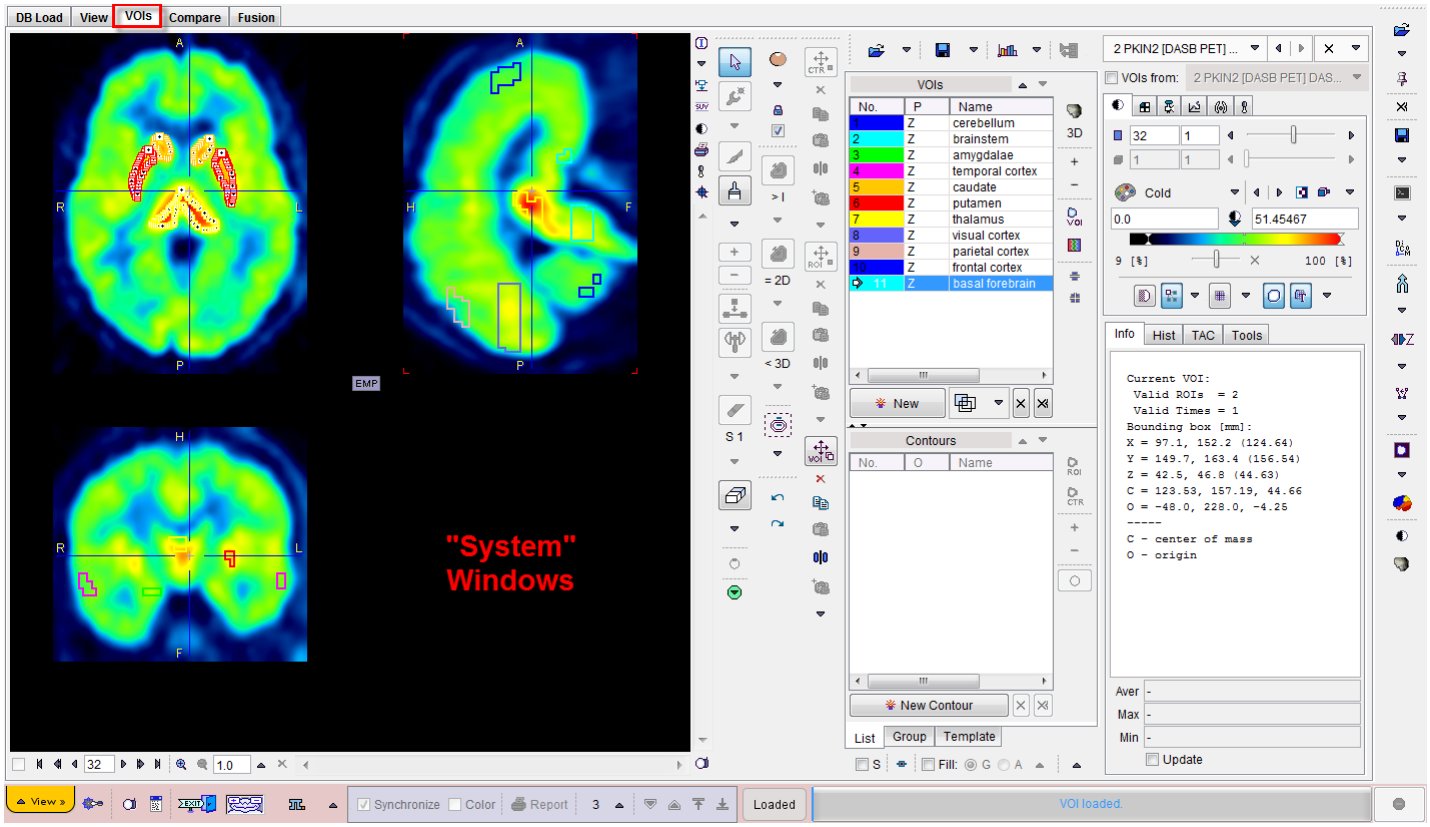
Log File

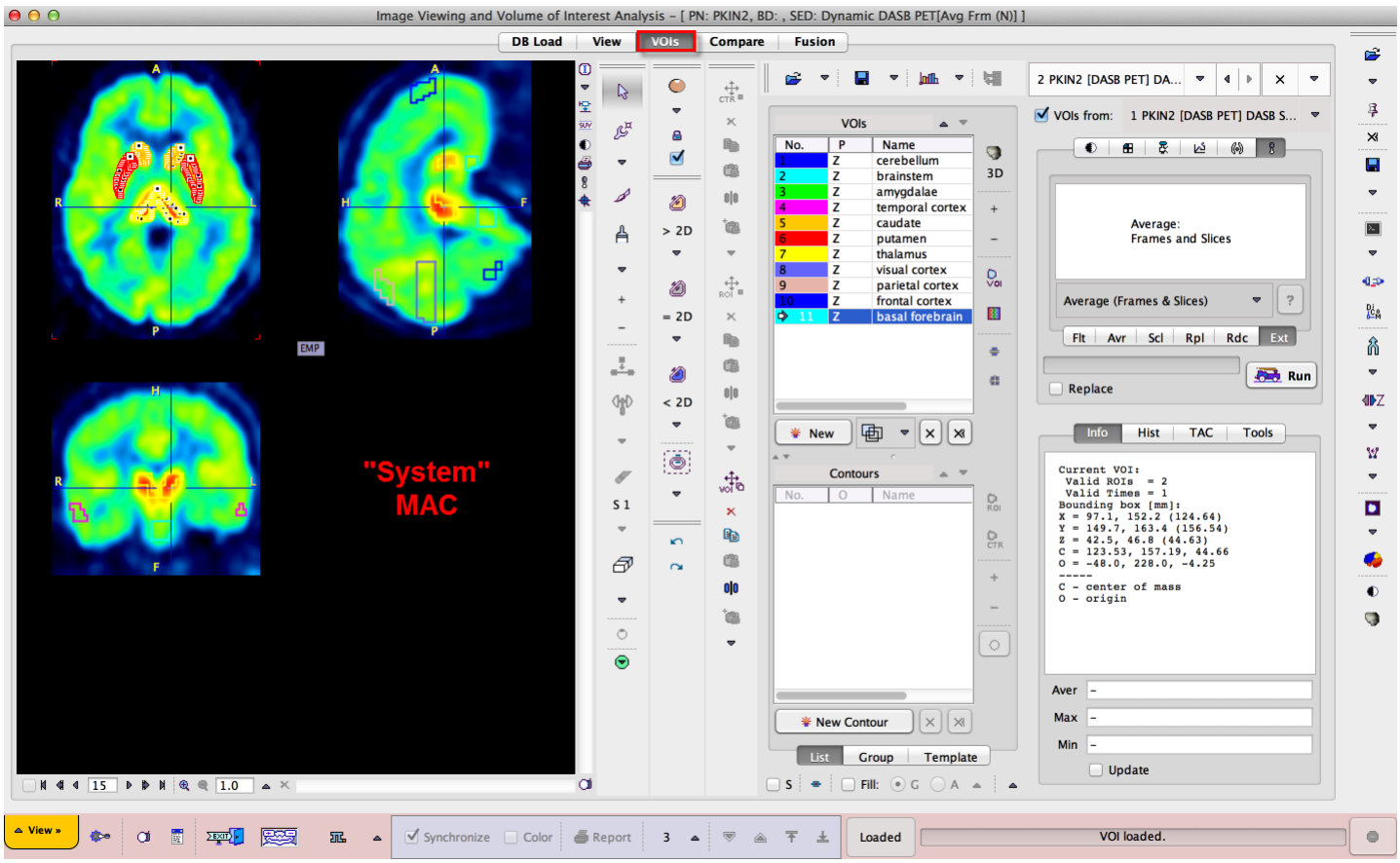
If the box **Redirect the Terminal information outtput to file** is checked, the program messages are saved in the file properties/system/pmsys.log rather than shown in the console window. This is helpful in the case of problems because it can be submitted to the PMOD support as part of an problem report.

Look and Feel

The appearance of the PMOD user interface is dependent on the operating system, and on the selected **Look & Feel**. In principle, the **Cross Platform** and the **System** choices are available. However, on the latest Mac OSX systems, **Cross Platform** is not supported any longer by Java. Below an example of a Cross Platform on Windows system and two examples of System Look & Feel on both Windows and MAC.







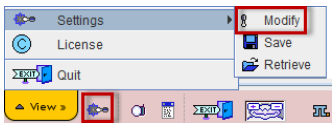
The illustrations in the PMOD User's Guides use the **Cross Platform** look.

Dual Monitor

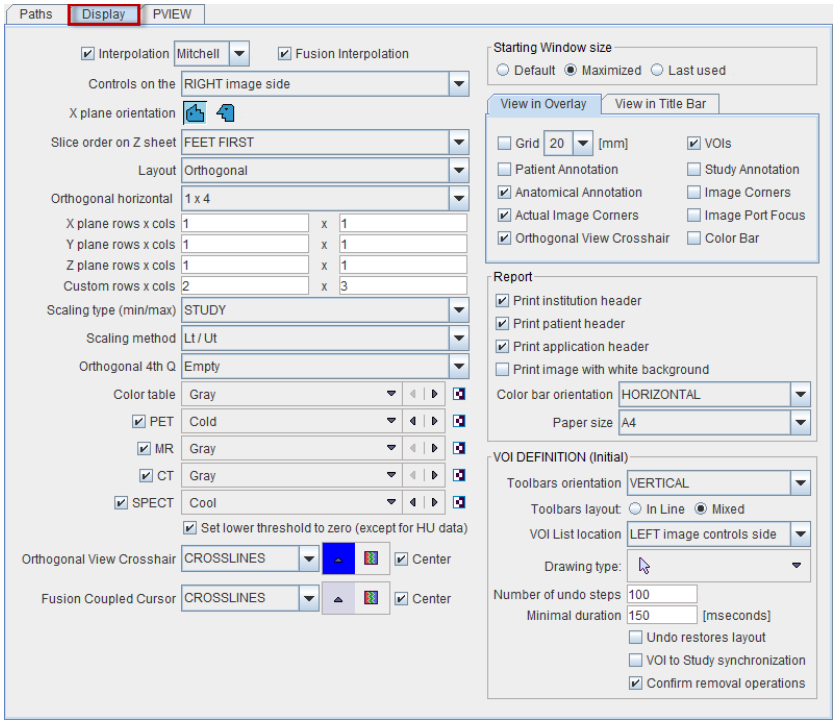
The support for two monitors in an extended screen mode by PMOD is limited. The user needs to arrange the windows himself appropriately. If the **Center dialog windows on the secondary screen** box is enabled, all dialog windows will be shown on the same secondary screen.

Tool Configurations

Each PMOD tool also has individual configuration settings which tailor it to the user's needs. These settings dialogs can be accessed by using the menu **View/Settings/Modify** entry or directly by the button



in the lowest line of the tool. The example below shows the settings dialog window of the viewing tool.



The **Paths** tab contains the default input format definition, the default output format definition, and the data paths.

The **Display** tab depends somewhat on the tool. It is mainly used for

- tailoring the initial appearance such as the size and location of the tool,
- the default image layouts and color table properties. Note that different colortable can be set for different image modalities.
- the organization of the VOI toolbars for optimal arrangement depending on the screen size, and
- configuring the contents of the report page.

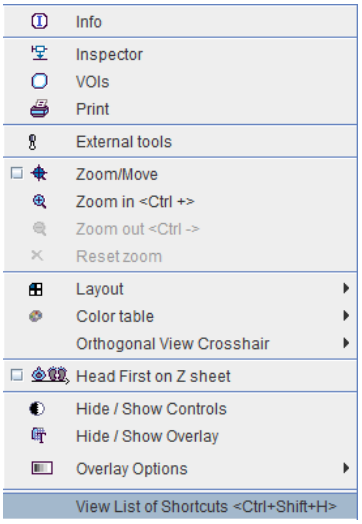
The last tab, in the example above **PVIEW,** is completely tool-specific.

When the **Ok** button is activated the settings are saved and will serve as the starting configuration when the tool is opened the next time.

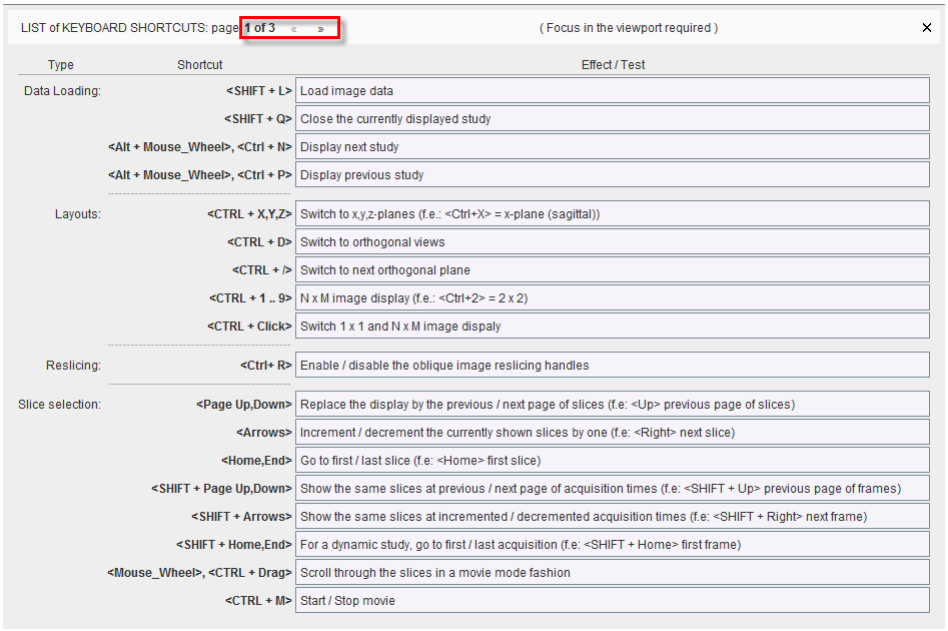
Keyboard Shortcuts

Many of the viewing functions can be activated and are much faster to use by keyboard shortcuts. To direct the keyboard shortcuts to the right images it is essential that they are active, indicated by the *blue color of the activator rectangle* in the upper left corner of the image display. Clicking into the image activates it. To avoid reslicing in the orthogonal viewing mode please hold down the `CTRL` key when clicking.

While working in PMOD the list of keyboard shortcuts can be displayed via the image context menu, which is obtained by clicking with the right mouse button onto an image shown in PMOD.

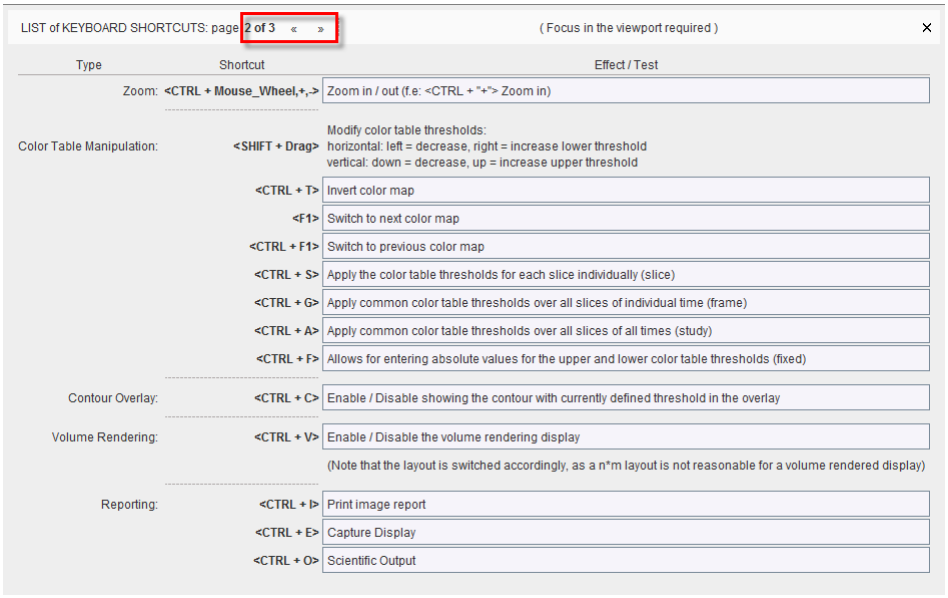


The last entry **View List of Shortcuts <Ctrl+Shift+H>** displays the window reproduced below. Note the arrow buttons to switch between pages.



LIST of KEYBOARD SHORTCUTS: page 1 of 3 « » (Focus in the viewport required) ×

Type	Shortcut	Effect / Test
Data Loading:	<SHIFT + L>	Load image data
	<SHIFT + Q>	Close the currently displayed study
	<Alt + Mouse_Wheel>, <Ctrl + N>	Display next study
	<Alt + Mouse_Wheel>, <Ctrl + P>	Display previous study
Layouts:	<CTRL + X,Y,Z>	Switch to x,y,z-planes (f.e.: <Ctrl+X> = x-plane (sagittal))
	<CTRL + D>	Switch to orthogonal views
	<CTRL + />	Switch to next orthogonal plane
	<CTRL + 1 .. 9>	N x M image display (f.e.: <Ctrl+2> = 2 x 2)
	<CTRL + Click>	Switch 1 x 1 and N x M image dispaly
Reslicing:	<Ctrl+ R>	Enable / disable the oblique image reslicing handles
Slice selection:	<Page Up,Down>	Replace the display by the previous / next page of slices (f.e: <Up> previous page of slices)
	<Arrows>	Increment / decrement the currently shown slices by one (f.e: <Right> next slice)
	<Home,End>	Go to first / last slice (f.e: <Home> first slice)
	<SHIFT + Page Up,Down>	Show the same slices at previous / next page of acquisition times (f.e: <SHIFT + Up> previous page of frames)
	<SHIFT + Arrows>	Show the same slices at incremented / decremented acquisition times (f.e: <SHIFT + Right> next frame)
	<SHIFT + Home,End>	For a dynamic study, go to first / last acquisition (f.e: <SHIFT + Home> first frame)
	<Mouse_Wheel>, <CTRL + Drag>	Scroll through the slices in a movie mode fashion
	<CTRL + M>	Start / Stop movie

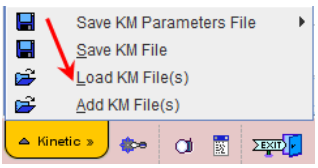


LIST of KEYBOARD SHORTCUTS: page 2 of 3 « » (Focus in the viewport required) ×

Type	Shortcut	Effect / Test
Zoom:	<CTRL + Mouse_Wheel,+,->	Zoom in / out (f.e: <CTRL + "+"> Zoom in)
Color Table Manipulation:	<SHIFT + Drag>	Modify color table thresholds: horizontal: left = decrease, right = increase lower threshold vertical: down = decrease, up = increase upper threshold
	<CTRL + T>	Invert color map
	<F1>	Switch to next color map
	<CTRL + F1>	Switch to previous color map
	<CTRL + S>	Apply the color table thresholds for each slice individually (slice)
	<CTRL + G>	Apply common color table thresholds over all slices of individual time (frame)
	<CTRL + A>	Apply common color table thresholds over all slices of all times (study)
	<CTRL + F>	Allows for entering absolute values for the upper and lower color table thresholds (fixed)
Contour Overlay:	<CTRL + C>	Enable / Disable showing the contour with currently defined threshold in the overlay
Volume Rendering:	<CTRL + V>	Enable / Disable the volume rendering display (Note that the layout is switched accordingly, as a n*m layout is not reasonable for a volume rendered display)
Reporting:	<CTRL + P>	Print image report
	<CTRL + E>	Capture Display
	<CTRL + O>	Scientific Output

Button- and Menu-Related Shortcuts

Functionality implemented as a button or a menu item can often be activated using the keyboard. In these cases, a letter in the item text is underlined. The action item can then be activated by combining the `ALT` key with the underlined letter. In dialog windows, `ALT+C` is typically used for the **Cancel** action.



For instance, when working in PKIN, the menu **Kinetic** can be brought up quickly by `ALT+M`. Once the menu is open, an underlined letter is sufficient to activate a menu item. So `ALT+M` and then an "`L`" will quickly perform the Load KM File(s) action.

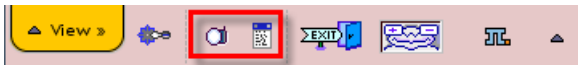
Dialog Default Action

When a dialog window is opened, the button with the most likely action is usually pre-selected. This default button can be activated with the `SPACE` keyboard key (not with the `ENTER` key). This is a Java property.

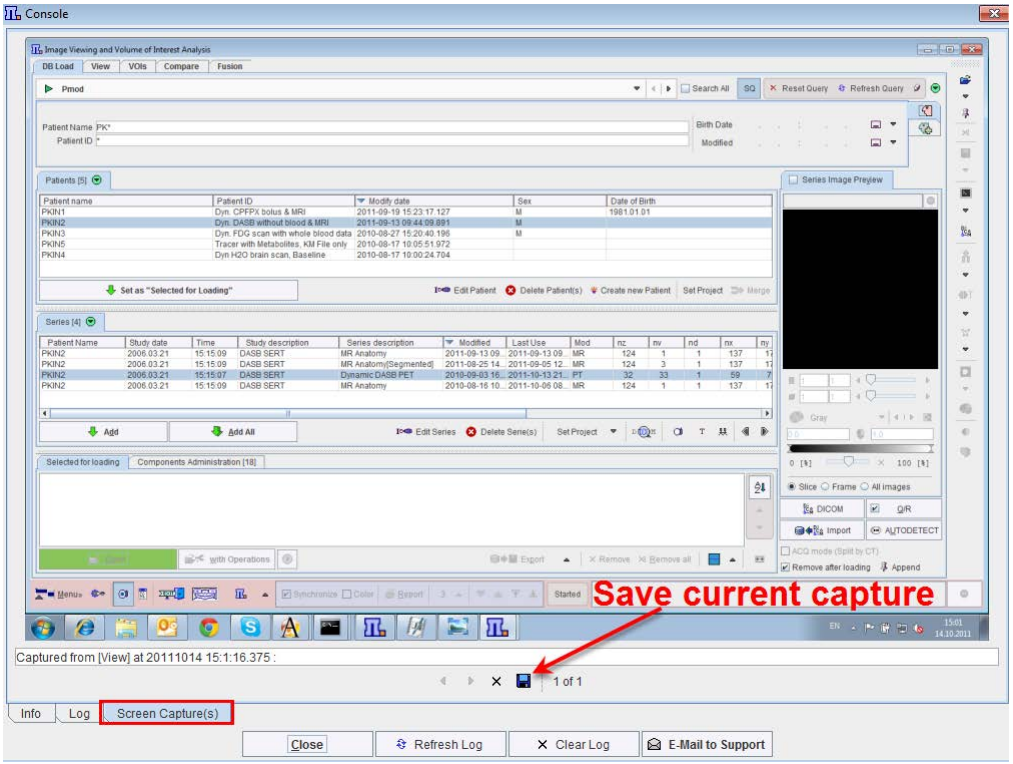
Problem Reporting

PMOD includes a functionality to directly send a problem report to the support staff of PMOD Technologies. This report can include the log output, screen captures and a problem description entered by the user.

Every PMOD tool contains in the lower left bottom line the functions for creating the report.

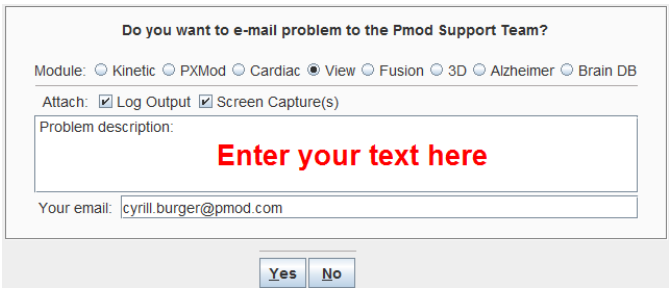


The capture button creates a capture of the entire screen (not only the PMOD window) and adds it to a buffer of up to 20 captures. The console button opens the a **Console** dialog window illustrated below.



The captures can be inspected on the **Screen Capture(s)** pane with the left/right arrow buttons, and the current one saved in JPEG. The **Log** pane contains the log messages, if the terminal output has been configured to be saved in a file on the **On Start** ***tab*** (on page 20) of the **Users Configuration**. Its contents can be updated by the **Refresh Log** button. Once in a while it is recommended to use **Clear Log**, to an avoid excessive length of the log file. The **Info** contains some more general information.

To submit a problem description please activate the **E-mail to Support** button. It opens a dialog window,



wherein the user can select the affected **Module**, and confirm whether the **Log Output** and the **Screen Capture(s)** should be included. The problem description should be typed into the text field, and the user's email address into the **Your email** field. Note that multiple addresses can be specified, separated by the colon character (;). use the **Yes** button to submit the report, or **No** to cancel.

Note: Although the standard mailing port is used, corporate firewalls may prevent PMOD from submitting the e-mail. In this case a notification will be shown, and the user needs to report the problem either through his support login, or by standard e-mail.

Chapter 2
PMOD DICOM Functionality

DICOM

The DICOM standard has been established to facilitate data exchange between medical systems. It defines how the medical data must be encoded, and how they can be sent from an application on one computer to an application on a remote computer. DICOM basically consists of two components:

- **Information Object Definitions** (IOD): For each modality it defines a set of data fields. Some of them are mandatory, others are optional. This approach allows saving demographical and acquisition information together with the actual images.
- **Communication protocol**: DICOM has a client-server architecture. To send data from one host to the other the sender (client) must contact the potential receiver (server) whether it is ready to accept data. The server may reject the request because it has no space left, because the client is not allowed to send data, or because it does not understand the data to be sent. Otherwise it accepts the request and sends back a proposal how the data should be transmitted. The client then sends the data and gets an acknowledgment when the data have been correctly received.

PMOD is able to act both as a DICOM client and a server.

- The PMOD DICOM server allows clients such as a PET system to push images to PMOD. Additionally, it allows a user to query remote DICOM servers (such as imaging modalities or a Picture Archiving System) and fetch studies to process them locally.
- The PMOD DICOM client allows sending image data using the C-STORE communication to any DICOM server which has been entered in the PMOD configuration.

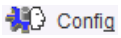
Database for DICOM Data

The DICOM standard includes a description how DICOM data must be organized for off-line media such as CDs or DVDs. Basically, all the DICOM objects are stored in a directory tree, and a description of all stored studies must be written into a file called DICOMDIR at the root level of the directory tree. This approach is not suited for dynamically managed data, because the DICOMDIR file must be updated each time a study is removed or added, and because reading of the DICOMDIR is relatively slow.

To improve the performance when working with DICOM images, PMOD uses SQL databases to organize DICOM data access. The most important attributes of the DICOM objects like patient information, study and image descriptions as well as the file locations are stored in database tables. When the user needs to select image data, he is shown the information from the database tables which can very efficiently be searched and retrieved. After a study is selected, the file access information is immediately available to start the loading process.

DICOM Configuration

The configuration of the PMOD DICOM functionality is a part of the general PMOD configuration. It is opened by calling the

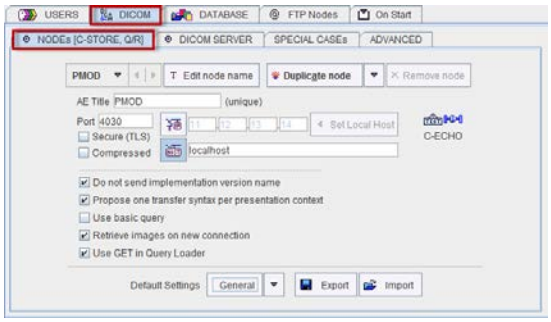


button from the PMOD ToolBox, and selecting the **DICOM** tab in the appearing dialog window.

In This Chapter

DICOM Client Configuration

The **NODEs [C-STORE, Q/R]** tab allows specifying remote DICOM nodes. These nodes include DICOM servers to which PMOD can send images, and DICOM clients which are able to send images to PMOD, but not to receive.



For each of them define its application entity title (**AE Title**), the **Port** number, and **IP** number or **host name**. The example above configures the local PMOD DICOM server as a node. As soon as the server has been started, it can be contacted and used for saving/retrieving images as any other node.

If the remote node is a PMOD DICOM server listening on a secure TLS port, please check the **Secure(TLS)** box. The **Compressed** box is the indication that the given node supports the DICOM deflated transfer syntax (1.2.840.10008.1.2.1.99). If it is checked, PMOD will propose a deflated transfer syntax, and if given a choice in the association acceptance it will choose the deflated transfer syntax with highest priority. Using compressed communication has the advantage of speeding-up communication across slow internet lines.

After configuration has been completed, the **C-ECHO** button can be used to test the connectivity. If a node is a DICOM server and running, verification should return **DICOM Verification successful**. If it is a client which just can send, verification is not applicable.

The lower part of the pane contains a list of configuration details which may need a change for some connections. Shown is the default configuration, which can be recovered by the **General** button. The option button also allows retrieving a configuration which has been proven to work with GE **Xeleris** systems.

Note the **Export** and **Import** facility for the DICOM nodes list which allows a system administrator to easily distribute a master DICOM list among PMOD installations.

DICOM Server Configuration

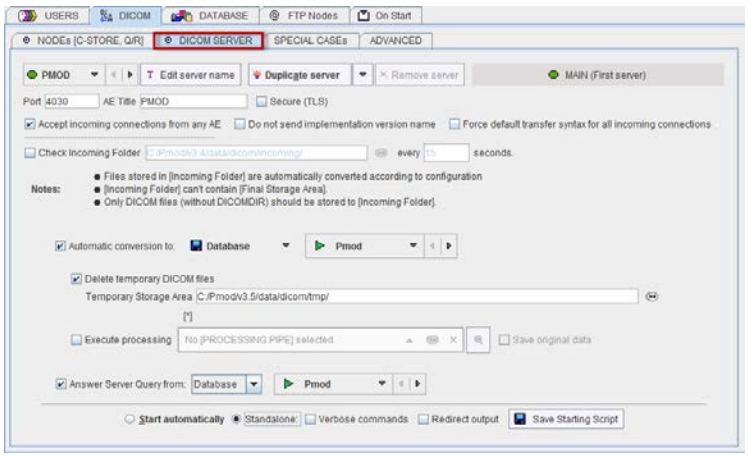
PMOD can run one or multiple DICOM server processs in the background which are able to receive data sent to it from modalities or a picture archiving system.

DICOM Server Properties

In general, a DICOM server is defined by three entities, the:

- **IP-number** (or host name) of the computer on which the DICOM server is running,
- **Port number** on which the server is listening,
- **Application Entity Title** (AET) which has been given to the server.

This information is configured on the **DICOM / DICOM SERVER** pane.



Note: On Linux systems there exist reserved ports which require special permission to allocate. If such a port is defined as the PMOD DICOM server port, the server cannot be started from a user account and issues a message *Permission denied*. Starting as root will normally succeed, but this has the disadvantage that the saved files will all belong to the root. To prevent this situation a higher port number (typically >4000) should be used on Linux, rather than the standard DICOM port 104. PMOD uses 4030 per default.

Besides the basic server information there are three checks relevant for the DICOM server operation:

- **Accept incoming connections from any AE**: If this box is not checked, the DICOM server only accepts remote systems which are configured as remote DICOM clients. If it is checked, any association request will be accepted.
- **Do not sent implementation version name (server)**: Allows switching off sending the implementation version component. This is required if a client does not handle this exchange properly and connection to the PMOD server fails.
- **Force default transfer syntax for all incoming connections**: Transfer syntax negotiation may fail when a client proposes only one transfer syntax which is not the DICOM default and a PMOD server prefers another. In such cases the option forces the PMOD

server to always negotiate the default Little Endian Implicit transfer syntax which all DICOM applications are required to support.

Standard DICOM communication is not secure, and therefore is not recommended over public networks. To overcome this problem, a DICOM supplement has been finalized which allows implementing secure connections. PMOD supports one of the proposed variants called BASIC TLS SECURE TRANSPORT CONNECTION PROFILE. Of the three optional features (entity authentication, encryption, integrity check) encryption is implemented in the current release. As a consequence, the data transferred can only be interpreted by the target DICOM server with which the communication has been established. To enable secure DICOM, check the **Secure (TLS)** box. The corresponding script option is **-tls**.

Multiple DICOM Server Creation

New Dicom servers are created with the option button:

- **Add new server**: Creates a new server with the default settings.
- **Duplicate server:** Creates a new server using the settings of the currently selected server.

The server name needs to be specified during server creation, but can be changed later using the **Edit server name** button.

The default installation creates two Dicom servers: **PMOD** as **MAIN (First server)** and **PMODQ** as **Auxiliary (Second server)**. These servers are internal DICOM server and have as default ports **4030** for **PMOD** and **5003** for **PMODQ**. They cannot be removed from the configuration.

Note that all DICOM (and Transaction) servers need unique port addresses.

What happens with received DICOM Images

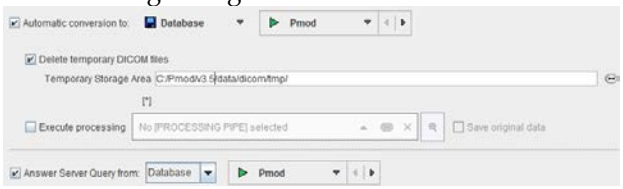
There are different possibilities what the PMOD DICOM server can do with the received images:

- Save them in a directory structure and update the DICOMDIR file (DICOM part 10 conformant).
- Save them in a database as the original DICOM objects.
- Convert them to any of the supported formats and save them as files, eg. as NiFTI files.
- Convert them to a JPEG file, and print a report page.

PMOD has the capability to configure different behaviors of the DICOM server. The configuration is not tied to the PMOD *user* who starts it. Therefore, the saving configuration is performed in the **DICOM** section of the PMOD configuration. So please select the **DICOM** tab and finally the **DICOM SERVER** sub-tab. Example configurations are shown below, but many other conversions are also possible.

Saving the Images in a Database

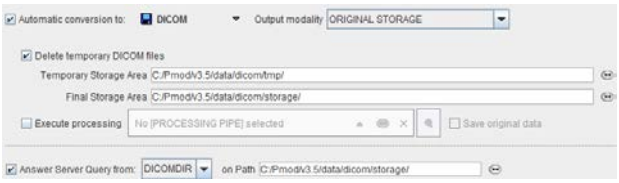
The following configuration is recommended for all users who run a local database.



In the example the DICOM server is receiving the images in the directory *C:/Pmod3.5/data/dicom/tmp*, saves them in the database **Pmod**, and then deletes the images in the temporary directory. When a remote DICOM client queries the PMOD DICOM server for studies, it will list all the studies in the **Pmod** database.

Saving the Images as DICOM Part 10 Offline-Files

Alternatively, the received images can be saved in a DICOM Part 10 compliant manner. This behavior is configured as follows.

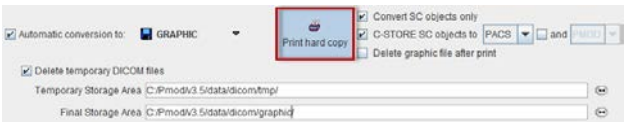


With this configuration, the images are stored in a directory hierarchy starting at *Pmod3.5/data/dicom/storage*. A DICOMDIR file will be maintained in the same root directory, and used to answer queries.

Note that you can use PMOD to create DICOM-compliant CDs. Just burn the DICOMDIR and the directory containing the DICOM files to a CD.

Filtering out Secondary Capture Images and Printing them

The configuration below illustrates another conversion ability.



The images are converted to JPEG (**GRAPHIC**), a report page is prepared (**Print hard copy**) and sent to the system default printer, but only if the incoming object is of type Secondary Capture (**Convert SC objects only**). The original DICOM files are deleted, but the JPEG images are retained in the directory *Pmod3.5/data/dicom/graphic*. The additional checks allow routing the SC DICOM objects to a remote DICOM server such as a PACS, and deleting the JPEG files after printing.

Incoming Folder

Normally the DICOM server is receiving data over the network from DICOM clients. However, it is also possible to have the DICOM server scan a directory and treat found

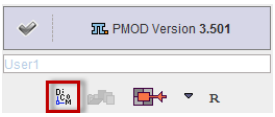
DICOM series in the same way as if they had arrived by the network. This functionality can be configured by the **Check Incoming Folder** box. If it is checked, the directory to be scanned can be entered as well as a scanning interval **every ... seconds**. This import feature can be used to convert from DICOM to any other output format, or to add DICOM images to a PMOD database. Note that after processing the images by the DICOM server they are removed from the incoming folder.

DICOM Server Starting

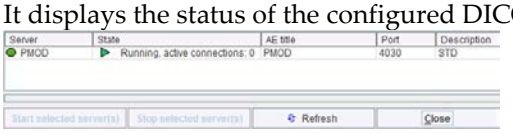
There are two ways of starting the DICOM server, as part of a PMOD processing session, or as a standalone process running independently. The latter has the advantage, that images can be received while PMOD is not in active use.

Interactive Starting

When the starting option is switched to **Start automatically**, the DICOM server is started with PMOD, and also stopped with it. Otherwise, with the **Stand alone** option, the DICOM server has to be started explicitly. With PMOD is running, this can be done with the DICOM button in the ToolBox.



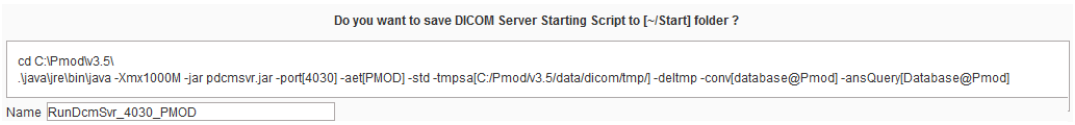
It displays the status of the configured DICOM servers in a dialog window, for example:



Each server can be individually started and stopped by selecting it in the list and using the corresponding buttons.

Script Starting

Alternatively, the *RunDcmSvr* script in the *Start* directory can be started by double-clicking. This script is generated during the installation and represents the default DICOM server configuration. If any DICOM server setting has been changed, a new script should be generated with the **Save Starting Script** button. It shows a dialog window with the contents of the script as illustrated below.



A DICOM server offers the following debug options:

- **Verbose commands**: Serves for generating detailed communication information. While it slows the operation down, it may be helpful to troubleshoot connectivity problems. The corresponding script option is **-d**.
- **Redirect output**: Serves for redirecting the standalone server output to a file in *Pmod3.5/properties/system/logs*.

Operation of DICOM Servers on a Dedicated Machine

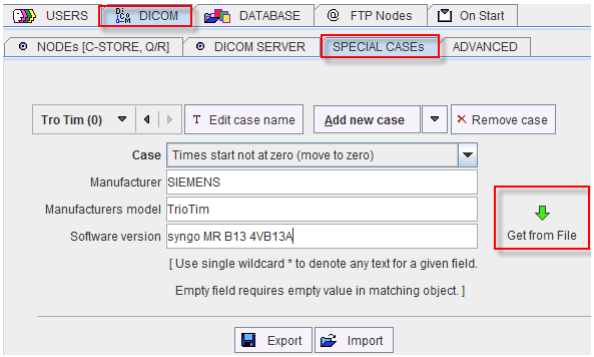
Note that DICOM (and transaction) servers can be operated without a PMOD license. Only their configuration requires a license. Therefore, particularly in a multi-user environment the server processes can be moved to a dedicated machine with fast disks.

To establish such a configuration, perform a standard PMOD installation on a server machine including the USB license protection key. Use the **Config** facility for the database and DICOM server configuration, and generate the server starting scripts. Thereafter, the USB key can be removed and used on client machines. The server processes can be started at any time, only re-configurations will require the USB key again.

DICOM Special Cases

Sometimes the interpretation of DICOM data is unequivocal and PMOD may organize the images in an unexpected manner. To solve this situation **SPECIAL CASEs** can be defined which impose a specific interpretation of data from a certain **Manufacturer model** and **Software version**.

To create a new special case select **Add new case,** specify a name, and then select the appropriate behavior from the **Case** list. The requested information can be entered manually, but it is easier and safer to select **Get from file**, browse to the directory where the data resides, and select the appropriate series. PMOD reads the required information from the DICOM attributes and fills it into the **Manufacturer**, the **Manufacturer model** and **Software version** fields. Note that * can be used to indicate applicability for all possible strings, while an empty field requires that information is also empty in the corresponding DICOM field.



To transfer these definitions between systems there is an **Export** button for saving the special cases, and **Import** button for loading them.

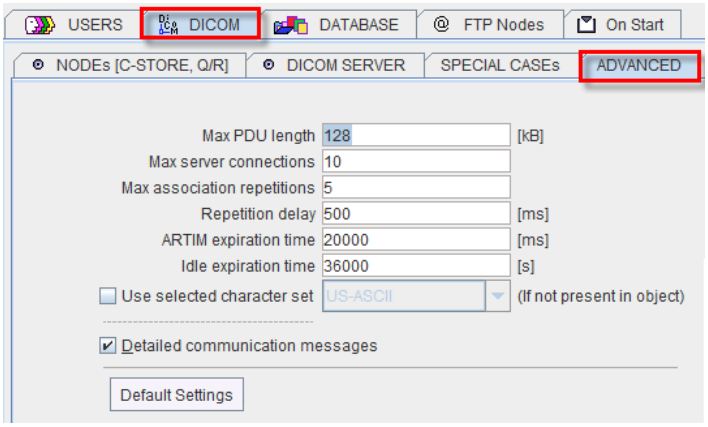
The **Case** selections are listed below with some example systems. However, the need and applicability of these special cases may depend on specific software versions of the originating system.

- **Non identical images times for single volume**: Select this option if the slices of a single volume are interpreted as separate frames in a dynamic series (e.g. series with no positioning information like SC).
- **Multivolume (sort by volume times)**: To be used when the time sorting of a dynamic series is wrong (Siemens Sonata, Siemens Symbia).
- **Multivolume (sort by slice position)**: Another situation where the time sorting of dynamic volume data is wrong (Siemens Evolution EBCT scanner, GE Discovery LS, GE Discovery HR, GE Signa Excite).
- **Multivolume MR (sort by trigger times)**: A third situation with wrong time sorting (GE Signa Genesis).
- **Pet times in sec (instead of ms)**: To be applied if the acquisition times presented in PMOD for PET objects are 1000 times too small.
- **Volume SC**: For situations when a screen capture series representing a volume is displayed as a big number of separate series (GE Advantage Windows, GE Discovery HR, Siemens Somatom Emotion Duo).
- **Wrong slice spacing (use slice thickness)**: Try this case in case the slice thickness presented in PMOD differs from what you expected (some GE Xeleris versions).
- **Wrong Image Index in PET objects**: Some PET/CT systems do not construct the Image Index (0054,1330) as specified in Dicom PS3.3 paragraph C.8.9.4.1.9. As a result PET images may be sorted wrongly (GE Discovery LS via Xeleris).
- **Wrong frame reference time (use acquisition time)**: Instead of the PET specific element 0054,1300 (Frame Reference Time) the general element 0008,0032 (Acquisition Time) is used to determine frame start and end times. If the acquisition time element is present and it is filled with the frame start time this usually solves the problem. (Philips, Protocol Guardian Bod; SUINSA animal PET system).
- **Reference time at frame half (calc from duration)**: The default behavior for PMOD is to calculate frame start and end times based on frame reference time and duration assuming that the reference time points to frame start. This special case uses the assumption that the reference time is at frame mid-time. (Philips)
- **Times start not at zero (move to zero)**: This case was introduced for Philips data that had a substantial offset in the 0054,1300 Frame Reference Time. It just offsets the times so the first frame starts at 0. It does the same as **Set acquisition start time to zero** in the loading parameters dialog.
- **Wrong image class unique id**: This special case is to allow PMOD to read images that have wrong DICOM object class specified in the file.
- **Use acquisition times for frame times**: This special case is instructs PMOD to use the acquisition time instead of the content time when determining the frame times for single slice objects.

Note: The DICOM server will use these case definitions when receiving the images and storing them in the database. So if series are not correctly entered into the database, export the data and define a suitable **Case** using the **Get from file** facility. Then, delete the database entry, restart the DICOM server, and transfer the series again.

DICOM Advanced Options

ADVANCED options allow changing some specific conditions and parameters of the dicom communication. The default settings are illustrated below. Changing these settings means tuning of PMOD to work with systems that are not 100% conformant with Dicom 3.0.



- **Max PDU length** is a PDU (Protocol Data Unit) length that PMOD will propose to other communicating nodes as well as a maximal length PMOD will accept as a PDU. The minimal value for this field is 2. A zero value (that according to the DICOM standard means accept any size) is not allowed because problems may occur with some systems.
- **Max server connections** is the maximal number of open connections handled by the PMOD server.
- **Max association repetitions** instructs PMOD how many times it will attempt an association to an other node before reporting connection failure.
- **Repetition delay** is the waiting time between association retries.
- **ARTIM Expiration Time** is the time PMOD will wait for a reply from a remote DICOM system before it will close connection and report failure.
- **Idle expiration time**: is the time after which the established dicom connection will be closed if there is no activity (message exchange) on the connection.
- **Use selected character set ..**: DICOM allows the specification of character sets in the file. If no character set is specified, PMOD uses the operating system default character set for the interpretation of non-ASCII characters. In case non-ASCII characters are not properly displayed, the user can explicitly define the proper character set. ISO 8859-1 will be appropriate for most western european languages. Please consult the ISO 8859-x standards to choose the right one for other languages.

Note the **Default Settings** button which allows restoring the default state.

DICOM Query/Retrieve

The purpose of the **DICOM Query/Retrieve** is retrieving images from remote DICOM servers in order to store them locally. After the images have been received, they can be loaded and processed independent of the remote server.

Configurations for DICOM Query/Retrieve (Q/R)

There are some prerequisites for using DICOM Q/R with PMOD:

1) Locally in PMOD, the DICOM server must be configured and running because it receives the images sent from the remote system. The PMOD DICOM server configuration is explained ***above*** (on page 34).

Locally in PMOD, the remote DICOM systems from which images should be retrieved must be defined. Because they will send images to the PMOD DICOM server, they are configured as DICOM nodes as described ***above*** (on page 33).

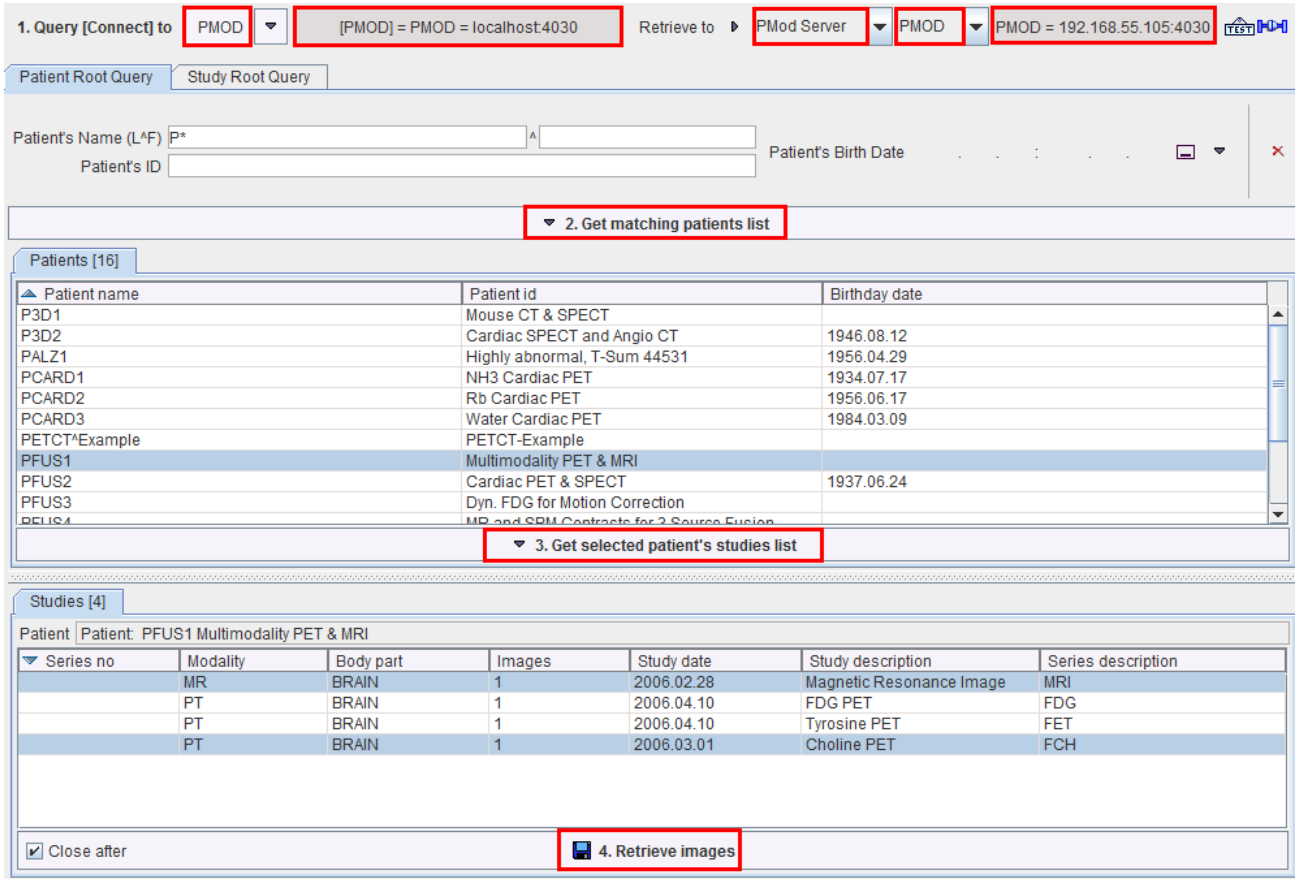
The PMOD DICOM server must be configured on the remote DICOM systems. Otherwise these systems will most likely reject the association request from PMOD, so that no images can be queried.

Retrieving Images per DICOM Query/Retrieve

The DICOM Q/R function can be called from

- the **Menu** in the PVIEW tool, or
- using the **Q/R** button on the **DB Load** page in any of the PMOD tools.

The dialog window shown below appears which allows to query and retrieve studies.



The following steps need to be performed:

1) **Query [Connect] to:** The selection lists all DICOM systems which have been configured as DICOM Clients.

Retrieve to: Typically, one would like to retrieve to the local DICOM server as shown in the example, but with **External node** it is also possible to select any of the configured DICOM clients (which must be a DICOM server) as the destination.

As soon as a system is selected (configure, then activate), the connection can be tested and established, if possible.

Select the query mode, **Patient Root Query** or **Study Root Query** by the tab. Note that some servers may not support both modes. If the query is not supported, **Get matching patients list** remains grey.

Get matching patients list: The purpose of this step is to get a list of studies, from which the ones of interest are retrieved. To avoid excessive numbers of matches some filter fields are available. In the example above, only patients with names starting with "**P**" are queried. When **Get matching patients list** is activated, the query is sent to the remote system, the response is received and the matching patients are listed.

Get selected patients studies list: Only studies from one patient can be retrieved at once. Therefore a patient must be selected in the upper list, and then the **Get selected patient's**

studies list button activated. As a result, the remote system is asked for all studies of the selected patient, and the results listed.

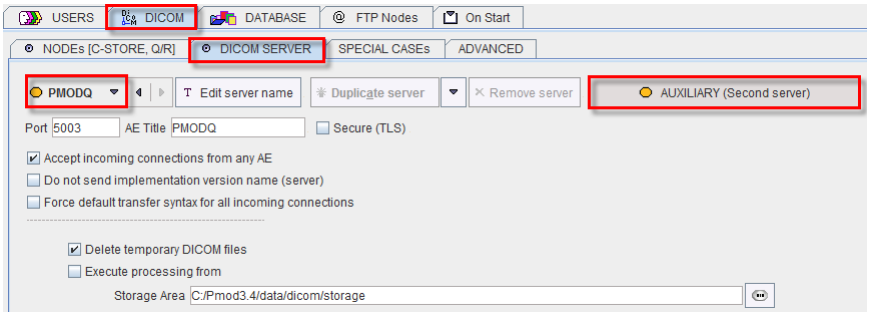
Retrieve images: To retrieve some of the studies select them in the list (`CTRL+Click`), and then activate the **Retrieve images** button. A request is submitted to the remote system, which will send the requested images to the **Retrieve to** DICOM server. If the **Close after** box is checked, the dialog window will be closed while the receive process is going on in the background and will show a notification once the transfer completed. Otherwise, the dialog remains open until the transfer completes.

Note: It depends on the configuration of the receiving DICOM server, where the images are saved, and thus from where they can be loaded. The default of the local PMOD DICOM server is saving the images in the PMOD database.

DICOM Query Loader (Auxiliary Server)

The **Query Loader** function is a simplified **Query/Retrieve** function. Instead of first retrieving images from a remote DICOM server to the local disk and then opening them in a second step, the query loader directly displays the retrieved images. Due to the retrieve time, it may take a while until the images are shown.

A separate auxiliary DICOM server is used for this purpose, which by default is configured in the **DICOM** tab, **DICOM SERVER** sub-tab. The settings are available selecting **PMODQ** Dicom server in the server list. Note that both the application entity title and the IP port must be different from the main DICOM server, and that this definition must also be entered on the remote DICOM servers from which images should be loaded.



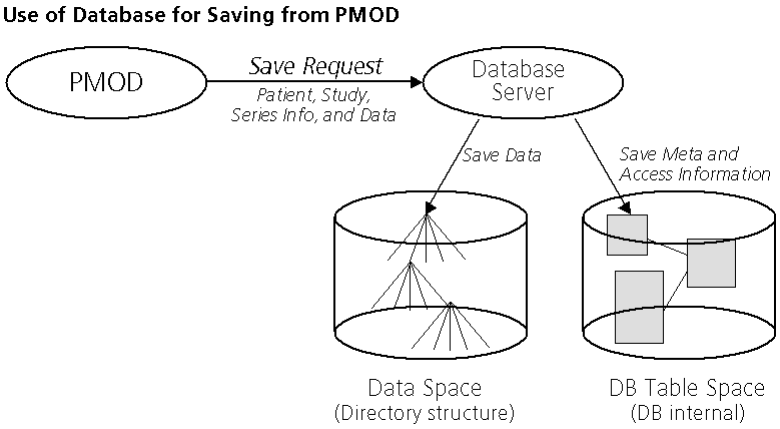
To use the **Query Loader** functionality the data format **Query** must be added to the **READ/WRITE plugins** in the **Users** configuration dialog. Then **Query** will appear as an additional format for all image loading buttons.

Chapter 3
PMOD Database Functionality

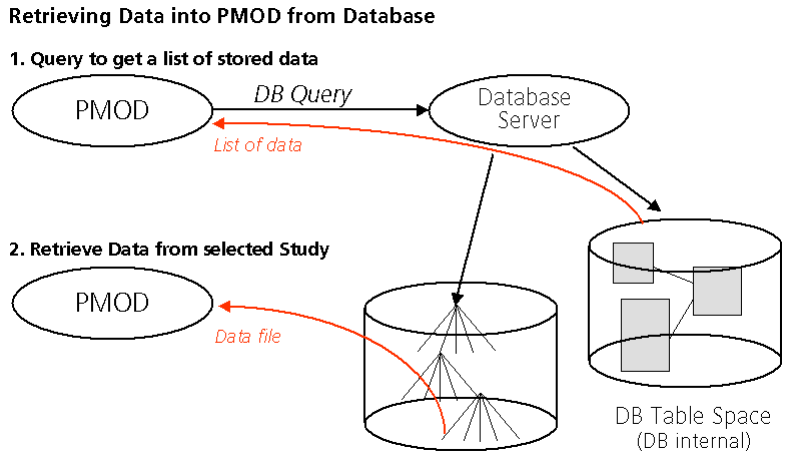
DICOM Operations using a Database

If the database is configured, PMOD can save images and all other information types such as VOIs, transformations, kinetic modeling files etc. in the same manner as described for the DICOM objects:

A **Save** operation sends a request to the database containing all relevant meta-information about the data (patient name, study, series, data type, etc) and the data itself. The database server then saves the data into a directory structure and adds the access information into its tables.



When **Load** operations are performed, this access information is presented to the user in a way which allows to perform database searches, and if a data set is selected, it can be loaded into the PMOD tool using the internal access information.



Benefits of Using the Database

There are several benefits resulting from the use of the PMOD database:

- A unified user interface is shown when loading or saving all types of data.
- The searching process supports many filters and is very fast.
- Loading of the data itself, particularly the DICOM images, is fast.
- The databases can be shared over the network between different PMOD installations.

Database Engines

The PMOD database functionality is based on an external SQL database engine. Two such databases are currently supported:

- **JavaDB http://developers.sun.com/javadb/** (recommended), an embedded database bundled with Java 6 which requires no installation. The use of JavaDB is encouraged, and at some time point support of mySQL might be suspended.
- **mySQL** is a database which runs on different platforms. Note that only mySQL server versions up to 5.0 are supported. Therefore, mySQL is only recommended for continuing legacy databases. In all other cases, JavaDB should be used.

In this section it is assumed that the database engine is working properly.

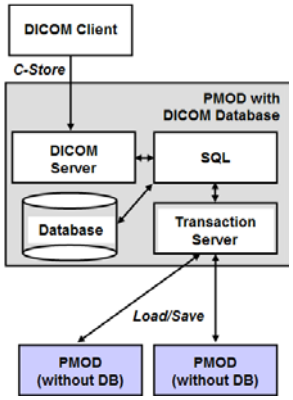
Database Access Types

There are two different types of databases in PMOD:

1) **JDBC Databases**: These are SQL databases to which PMOD communicates using the Java Data Base Connection (JDBC) interface. Typically, the JDBC Databases reside on the local machine. The user can create new JDBC databases from the PMOD configuration utility. If he wants, he can make them available to PMOD installations on different computers by a PMOD protocol called **Transaction Server** (TS, see below).

Remote Transaction Server Databases: These are SQL databases which are not directly accessed, but indirectly through a PMOD installation residing on a different computer. As the transaction server databases are managed by a different PMOD installation, they cannot be created or deleted, but only used for reading and writing.

The transaction server concept is useful in an environment of multiple PMOD installations. On one of the PMOD installations, the PMOD JDBC databases are created. On the same system, the PMOD DICOM server is started, and saves the received images in one of the databases. On all other installations, mySQL need not be installed. Those installations access the databases just through the transaction server as illustrated below.



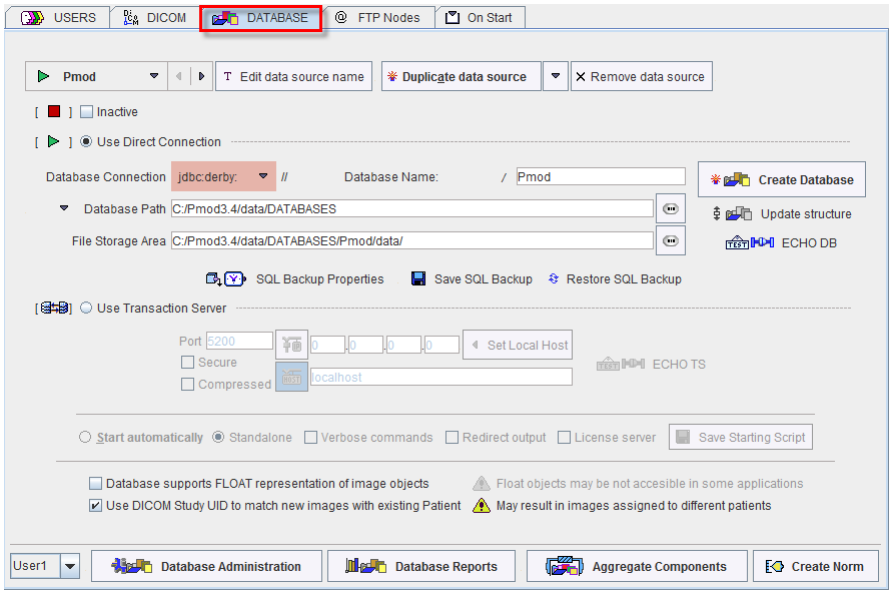
Note: After the installation of Pmod3.5, the **Pmod** database and the **DbSvr** transaction server for publishing this database are available. The **Pmod** database contains various example data if the example database was not selected for installation. This database resides in the PMOD installation directory. Please create a new database for your productive work which resides on a disk which is regularly backed up.

In This Chapter

Creation and Configuration of Databases

The creation of databases and the configuration of remote databases is a part of the general PMOD configuration. It is opened by calling the

button from the PMOD ToolBox, and selecting the **DATABASE** tab in the appearing dialog window.



To create a new database please proceed as follows.

Derby JDBC Database Creation (default)

1) **Add new data source**: Both types of databases are called a *data source*. Activating the **Add new data source** button pops up a dialog window to request a name for the new data source (e.g. **Pmod**). The new data source is added to the list selection and must be configured in the lower section. Please do not change the data source name after the database has been in use.

Use JDBC connection: Only JDBC databases can be created, so this radio button must be selected.

Database Connection: This entry defines the database access. The first part **jdbc:derby:** is the driver specification. The **Database Name** is the name by which the data source is known to the JavaDB. In principle the name can differ from the data source name, but this is not recommended.

Database Path: The directory where JavaDB can save the database tables (in a subdirectory named according the database name). **./DATABASES** represents the DATABASES directory in *Pmod3.5/data.*

File Storage Area Path: This is the path of the root directory in which the data files will be stored. **./DATABASES/Pmod/data/** represents the directory *Pmod3.5/data/DATABASES/Pmod/data/*. In principle, there is no need for creating the data

directory within the database directory, but it makes it is easy to copy or backup all information belonging to the database.

Create Data Base: Activating this button finally creates the JDBC database. Connectivity can be tested with the **Echo** button.

Note: After the installation of Pmod3.5, the **Pmod** database illustrated above is already available and contains different types of example data, unless the example database was not selected for installation.

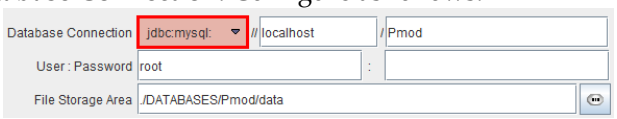
---

mySQL JDBC Database Creation (deprecated)

1) **Add new data source**: Both types of databases are called a *data source*. Activating the **Add new data source** button pops up a dialog to request a name for the new data source (eg. **Pmod**). The new data source is added to the list selection and must be configured in the lower section. Please do not change the data source name after the database has been in use.

Use JDBC connection: Only JDBC databases can be created, so this radio button must be selected.

Database Connection: Configure as follows:



The first part is the driver **jdbc:mysql**. The second part is the host on which the mySQL server is running, in the example above the same machine PMOD is running on, thus **localhost**. The third part is the mySQL database name, **Pmod**. In principle the database name can differ from the data source name, but this is not recommended.

User:Password: Fields to specify a user who has administrator privileges in the addressed mySQL installation and his password. The standard setting of mySQl is **root** and an *empty password*. If mySQL requires to enter a non-empty password for root, please specify it in this password field.

File Storage Area Path: This is the path of the root directory in which the data files will be stored. **./DATABASES/Pmod/data/** represents the directory *Pmod3.5/data/DATABASES/Pmod/data*.

Create Data Base: Activating this button finally creates the JDBC database. Connectivity can be tested with the **Echo** button.

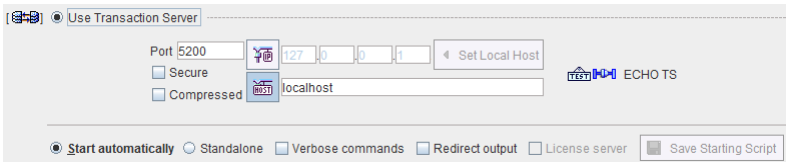
Note: You can create different SQL databases to collect data for different projects. They must, of course, have different names and should most likely save the data files in different directories.

PMOD allows publishing a local data base to other PMOD installations by a server program called **Transaction Server** (see below how to set up the transaction server). To address such a transaction server database, a data source must be defined as follows:

Access to Remote Transaction Server Databases

1) **Add new data source**: Again, a new data source must be created and adequately named.

Use Transaction Server: This radio button must be selected, and the transaction server address and port entered.



In this example, PMOD is installed on a host called *localhost* where a transaction server for a particular JDBC database has been started listening on port 5200. As the database is already existing, the initialization step is not necessary.

Note the two boxes **Secure** and **Compressed**. Please configure the communication with the properties that the transaction server is expecting (see below).

If the transaction server is running, connectivity can be tested with the **ECHO** button.

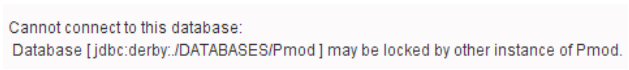
Numerical Accuracy of Images Stored in the Database

Images are stored to the database using Enhanced DICOM IODs which are selected according to the image modality setting. The accuracy of the standard IODs is limited, and if the images have a large dynamic range rounding errors can occur. In these situations PMOD may use a private IOD which supports floating numbers to avoid rounding errors. This behavior is enabled by the **Database supports FLOAT representation of image objects** box.

The float representation is an advantage if the images are used for further processing in PMOD. When such images are exported, PMOD converts the images to the standard IODs, whereby the rounding errors might be introduced.

Multiple Access to Derby JDBC Database

It is the nature of embedded databases as a Derby JDBC database that they can only be accessed by a single process. Therefore, if you start two instances of PMOD, only the first one will be able to access the database directly. The second one will not get access and show an error message



The solution for this case is to publish the database by a transaction server and access the data through it. In this way, an arbitrary number of processes can access the database.

Note: The default configuration of Pmod3.5 already includes a transaction server definition of the **Pmod** database. The transaction server will be automatically started with the first interactive PMOD session. Access to **Pmod** through the transaction server is configured as the **PmodTS** database.

Database De-Activation

Sometimes there is a need to temporarily deactivate a data source, e.g. because a remote system is down. In this case the box **Inactive** can be checked to avoid lengthy timeouts.

Default Database

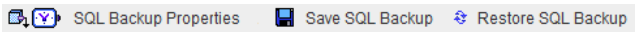
The database which is shown in the data source list when the configuration is saved will serve as the database initially. However, once in use Pmod remembers the least recently used database.

Database Upgrading

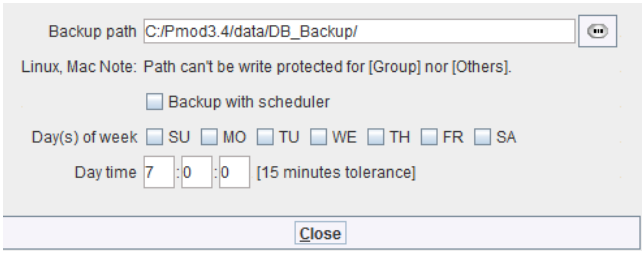
After updating a PMOD installation there might be a need to adjust the data structure of the existing databases for using them further. To do so, select a JDBC data source and activate the **Update structure** button.
Note: Transaction server data sources must be upgraded on the remote installation.

Database Backup

The SQL database tables of a local JDBC data source can be backed up using the buttons shown below.



The **Backup path** can be specified with the **SQL Backup Properties** button.



An interactive backup can then be performed with the **Backup with scheduler** button. It can be restored with the **Restore SQL Backup** button.

Automatic backups based on a scheduling are also supported. Initially the scheduling section is gray. Only when a local transaction server has been defined and started, and the **Backup with scheduler** box is checked, it becomes active. At the scheduled times the database tables are saved to the specified directory, provided that the local transaction server is running.

CAUTION: The database backup described above only saves the SQL database tables to a safe place, not the data files themselves. To backup the data please manually copy all information in the configured **File Storage Area Path** to the backup place.

Setting up a Transaction Server to Publish a Database

If a PMOD installation has a JDBC database running, it can make the data available for other PMOD installations. To this end a server program - the *Transaction Server (TS)* - must be started to run in the background and wait for database access requests.

In PMOD multiple TSs can be started automatically. Therefore memory usage for multiple TS is optimized while providing a better management of the TSs.

Transaction Server Configuration

The transaction server requires several configuration items, which are available on the **DATABASE** panel. Perform the following steps to define the transaction server which is started automatically with PMOD.

1) Switch the radio button from **Use JDBC connection** to **Use Transaction Server**.

1) Configure the properties of the transaction server. The **Secure** box is for enabling secure communication. This mode should be used if the communication is not confined within the institution. Otherwise it will slow down the communication speed unnecessarily. The **Compressed** box allows enabling compressed image transfer which can result in an acceleration across slow connection lines.

An important property is the IP **Port** for the communication. It must be a unique number not used by any other transaction server or other process. In the example above is **5203**.

Another important property is the **IP address**. It must contain the address of the host in which the servers are running, so typically the system on which the configuration is performed. For this system the **HOST** button is enabled and the host system is "localhost". In alternative, the **IP address** can be obtained by activating the **Set Local Host** button.

Check the box **Start automatically** such that the transaction server is started simultaneously with PMOD.

Starting a Transaction Server

The PMOD transaction server is a background process. It can be started in one of the following ways:

1) *Automatically* : If **Start automatically** has been configured in the **DATABASE** configuration page, the transaction server is started as soon as PMOD is started and not after user login.

By running a *command script*: A script for starting a Transaction Server is specific for the operating system platform. A start script *RunDbSvr* with the default configuration is created at installation time in the *Start* directory. Transaction server scripts with a different configuration can easily be generated on the **DATABASE** configuration pane as described below. As an example, the *RunDcmSvr* script for Windows and Derby looks as follows:

```
C:
cd "C:\Pmod3.5"
.\java\jre\bin\java -version
.\java\jre\bin\java -Xmx1200M -jar pmtsvr.jar 5203 JAVA_DB
org.apache.derby.jdbc.EmbeddedDriver jdbc:derby:./DATABASES/Pmod
./DATABASES/Pmod/data -noLS
```

A script for mySQL has a different driver specification

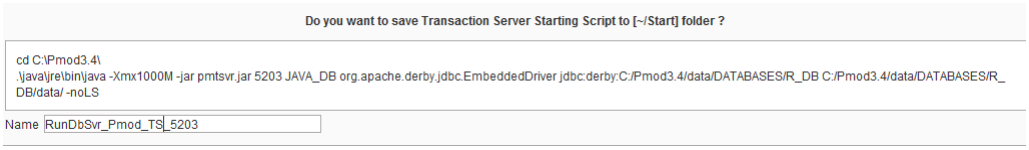
```
C:
cd "C:\Pmod3.5"
.\java\jre\bin\java -version
.\java\jre\bin\java -Xmx1200M -jar pmtsvr.jar 5203 MY_SQL
org.gjt.mm.mysql.Driver jdbc:mysql://localhost/Pmod
./DATABASES/Pmod/data -noLS
```

This mySQL script requires that the *root* user has an empty password. If this is not the case, the user and password must be specified as additional command line arguments:

```
.\java\jre\bin\java -Xmx1200M -jar pmtsvr.jar 5203 MY_SQL
org.gjt.mm.mysql.Driver jdbc:mysql://localhost/Pmod
./DATABASES/Pmod/data -noLS root password
```

Transaction Server Scripts

The **Save Starting Script** button is a facility for generating scripts according to the configured transaction server properties. It becomes active when the **Start automatically** radio button is disabled and **Standalone** option is enabled. The script is dependent on the operating system. The example below is the result for a Windows system.



The **-noLS** text indicates that the TS is not used as license server.

The **License Server** box can be checked if the server is at the same time managing a network license. In this case the **-noLS** flag will disappear. The **Yes** button saves the operating-system specific script illustrated in the **Commands** area to the *Pmod3.5*/*Start* directory using the specified **Name**.

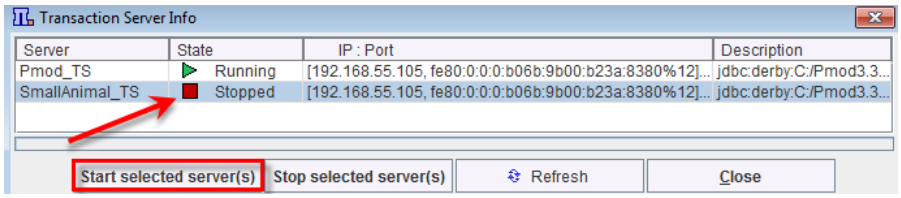
The **Verbose commands** box can be checked to enable verbose output. In this case a **-d** argument will appear. It is only recommended for debugging purposes, because it will slow communication down.

The **Redirect output** box can be enabled to redirect the output to a log file. In this case a **-o** argument will appear.

The database information required in the next section can most easily be completed using the **Get from Data Source** button. See **Creation and Configuration of Databases** (on page 49) for details regarding **Data Base Connection**, **Database Path**, and **File Storage Area Path**

Transaction Server Status Information

All automatically started TSs are available for management. The TS management and status information are available activating the button from PMOD ToolBox:



The current status is displayed in the **State** column. The status of a TS can be easily modified: initially the TS have to be selected in the **Server** list and then, depending on the status, the **Start selected server(s)** or **Stop selected server(s)** button need to be activated.

When the color of the button changes to blue, a transaction server request is being served. The color changes back after all communications have completed.

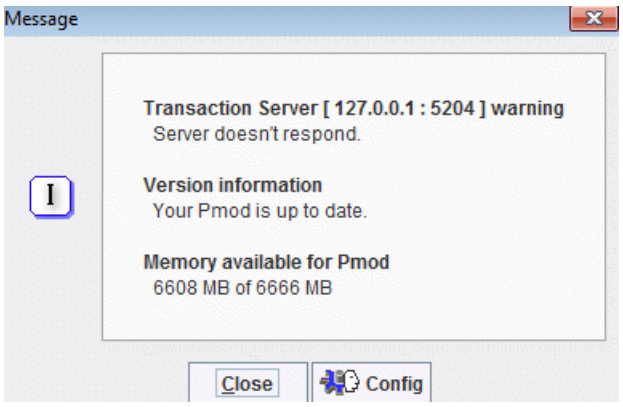
Pmod Status

The PMOD status is extended to provide more information about PMOD environment. The following status information are available:

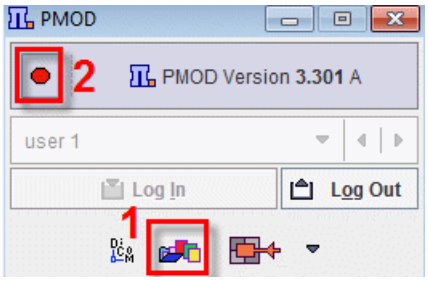
1) reports problems with the TSs configured and enabled in data sources.

informs if new Pmod build or version is available for download from www.pmod.com. Note that this functionality might not be available in tightly secured corporate networks.

displays memory availability.



In case of problems with the TS status the Pmod status button in the toolbox turn into red bullet.



The status is refreshed in the following situations:

1) on Pmod start.

when TS management panel is closed.

when Pmod status dialog is closed.

Recommendations

Methods 1 allows publishing a single database. Method 2 is not limited in this sense. A script can be run for each database in parallel. In this case, the transaction servers must be started using unique port numbers (eg. 5200, 5201, 5202, ...).

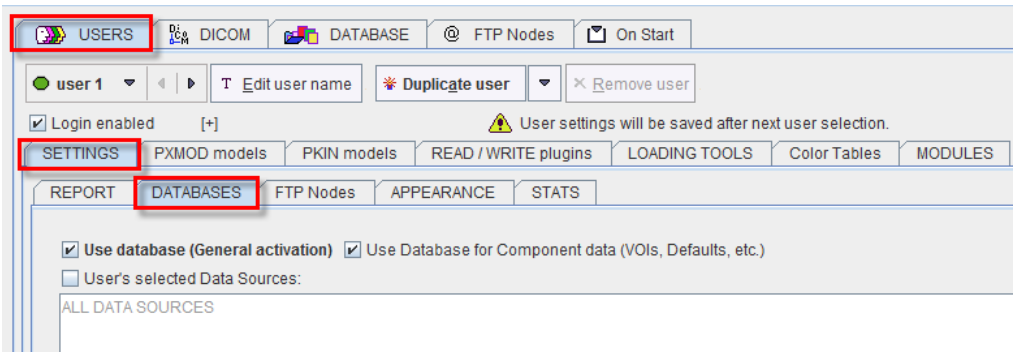
Note that transaction servers can be started and operated without consuming a PMOD license. This allows moving them to a server machine that is continuously operating and has fast disks. On this server machine perform a standard PMOD installation, plug the USB license protection key in, and use the **Config** facility for the database configuration and transaction server script generation. Then start each of the scripts in a separate command window. In the case of a standalone license, the USB key can now be moved to the computer, where the actual data processing is performed. In the case of a network license the USB key should remain, as it is used for license serving.

Depending on the network and server performance the speed of the load/save operations via a transaction server may be slower than with local loading/saving. The benefit, however, is the global availability and centralized maintenance of the data.

CAUTION: Note that the proper interaction between the transaction server and clients requires that all systems run the same PMOD version.

User-Specific Database Preferences

Every user can configure the use of databases individually in the PMOD configuration.



As the behavior can be differently configured for each user, a user must first be selected, **user 1** in the example above. The configuration items are then available on the **SETTINGS** pane, on the **DATABASE** sub-tab:

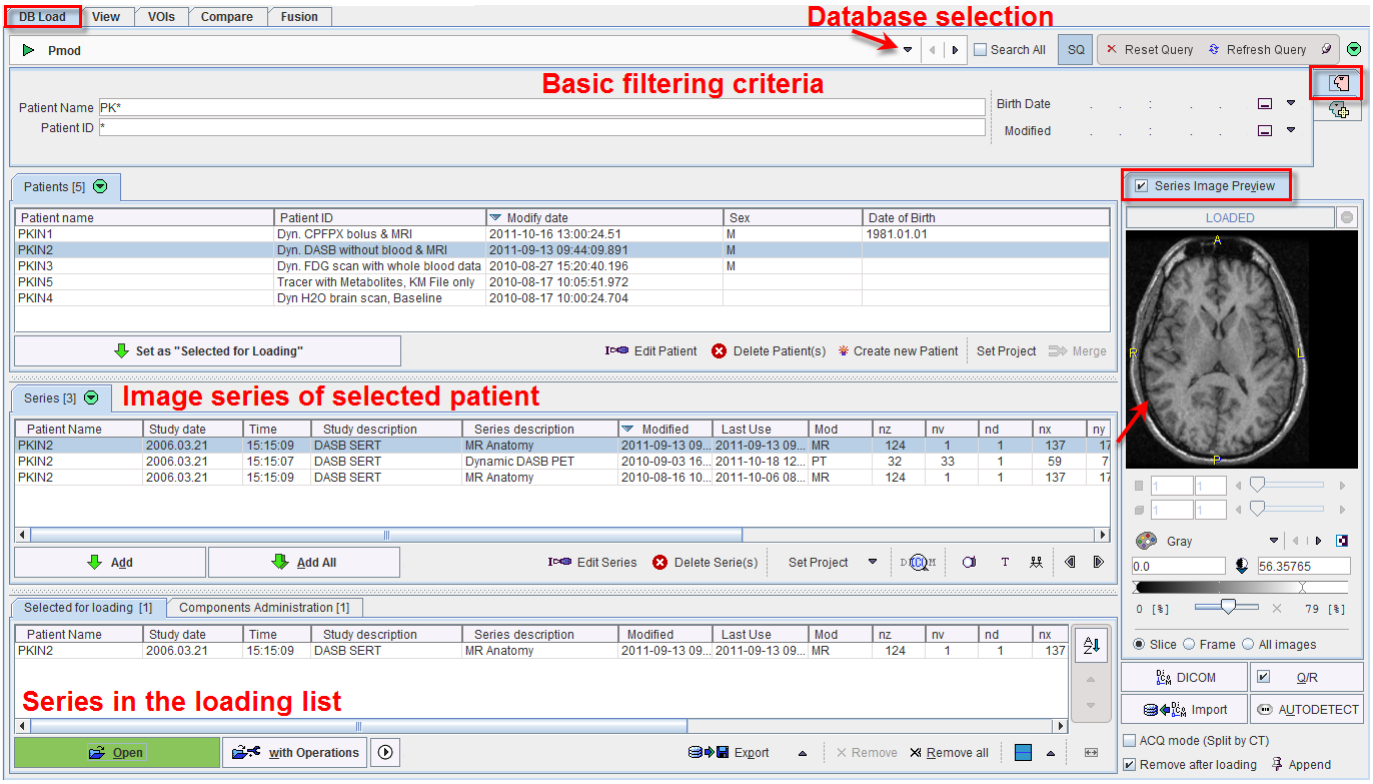
- **Use Database (General activation)**: This is the main switch. If the box is not checked, all databases are invisible for this particular user and all data loading/saving is file-based.
- **Use Database for Component data (VOIs, Defaults, etc.)**: Sometimes it is preferable to use the database only for the image data. In this case, the check can be removed from this box. Using the full database capability has the advantage that TACs and VOIs etc. are related to the image series they are derived from.
- **User's selected Data Sources**: If there is a substantial number of different databases and a user requires only a few he can check this box, and then add the relevant ones with the **Add new** button. An additional advantage is that the user can sort the database list according to his preference.

Loading Data from Databases

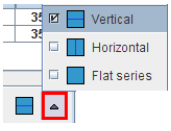
If the database is enabled the **Database** format is available in the list of input formats for image loading.

Image Data Loading

When loading images from the database the interface shown below allows searching for studies according to different criteria such as patient demographics, study date, modality, a project name or diagnosis. There is a basic filtering mode as illustrated bellow, and an advanced filtering mode illustrated later.



The layout can be organized vertically (as illustrated above), or horizontally with the **Series** tab stacked behind the **Patients** tab. This may be an advantage if patients tend to have many image series. The layout is switched by the option button



The **Flat series** is another arrangement which lists all image series in a single list. The **Flat series** DB layout mode allows searching in all active databases if the **Search All** checkbox is enabled.

Loading Overview

The uppermost section represents the filtering options. The use of filtering is recommended in large databases, because it substantially reduces the response time. Below the filters, the list of **Patients** is shown which match the current selection criteria. When one of these patients is selected, his image series available in the database are updated in the **Series** list section.

One or several image series can be selected and brought into the **Selected for loading** area by the **Add** button or by a double-click at the series entry. On the right side there is a preview window to verify the image contents before actually loading the whole data set. If the **Series Image preview** box is checked, an image is displayed as soon as a series is selected.

Finally, by activating the **Open** button, all series in the **Selected for loading** area are loaded into the PMOD tool. **Append** pushpin button is important for the outcome of the loading operation: with the appending setting the images are added, while with the overwriting setting any already loaded images will be discarded.

Note that multi-series selection depends on the context. If only a single series is expected by the program, double-clicking at the series will immediately start image loading.

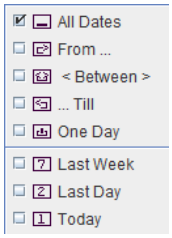
User Interface Elements for Filtering

First of all the database to be searched must be selected with the selection in uppermost section, **Pmod** in the example above. The basic filtering options include the following elements.

Name Patient name, starting with the last name. The wildcard * can be used as a replacement for arbitrary sub-strings.

Patient ID The patient ID filter, also supporting wildcards.

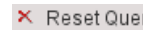
Birth Date The filters for the birth date include an exact date, or a date range available from the selection list.



These specifications apply for all other filter dates.

Modified A date/time is maintained in the database recording when the data of the patients was modified the last time by adding an image series or by changing the patient information. For example, setting the field to **Last Week** only shows patients modified in the last seven days.

SQ Means *Save Query*. If this button is enabled, the same filter settings will be applied when the database window is opened again.

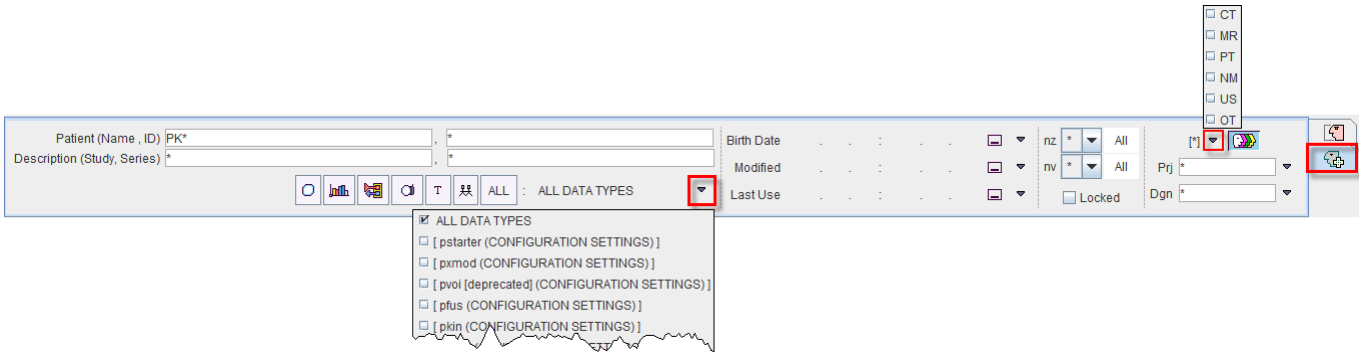


This button resets the filter settings by removing all specifications.

The refresh button to apply the query to the database potentially updated in the meantime, or after changing the filter and disabled automatic refreshing.

Toggle button to enable/disable automatic refreshing after changing a filter element

There is an extended filtering capability available on the second sub-tab which is illustrated below.



It contains several new elements:

Study Description Filtering of text appearing in the study description. The * wildcard is supported.

Series Description Filtering of text appearing in the series description. The * wildcard is supported.

ALL DATA TYPES This selection lists all available data types in PMOD such as images, VOIs, etc. Setting this field to *VOI Templates* for example will only list patients who have a VOI definition attached to one of the image series.

These shortcut buttons allow filtering for frequently used data types such as VOIs, statistics, kinetic modeling files, comment texts, paired series. **ALL** resets all filter setting.

Last Use A date/time is maintained in the database when data of the patients was accessed the last time. This information is listed for each database object. Selecting a date range allows browsing the database content based on a *least recently used* criterion.

nz Filter to search for studies with a certain number of slices, including the criteria

For instance, planar only studies could be looked for by setting nz = 1.

nv Filter to search for studies with a certain number of dynamic frames. For

instance nv > 1 will only list dynamic series.

Locked If the box is checked, only patients who have a *Locked* flag are listed.

Modality A selection to restrict the search to a specific modality, e.g. to *PT* (PET) as in the example. Multiple modalities can be searched for at once.

Prj Patients can be assigned to a **Project**. The selection allows choosing from the list of available project names.

Dgn Similarly, patients can be given a **Diagnosis**. The selection allows choosing from the list of available diagnosis names.

 Every time data is saved in the database, the PMOD name of the user who saved is recorded together with the data. This button allows restricting the search to the PMOD user currently logged in (button out), or to show data of all users (button in).

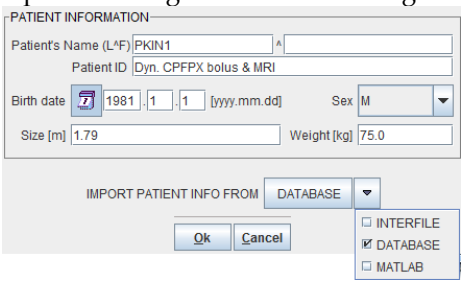
The green button allows hiding the filter section. Upon activation the filter area collapses and the button appearance changes. This new button allows showing the hidden filtering settings.

Patient Operations

When a patient has been selected from the list, a row of buttons becomes active.

Set as "Selected for loading" Moves all series of the patient to the **Selected for loading** area.

Edit Patient Opens a dialog window for editing the patient demographic data.



The **IMPORT PATIENT INFO FROM** button allows importing this information from a file in the Interfile format, from an existing **DATABASE** patient, or from a **MATLAB** file. Note that the information in the DICOM object is not modified, just the database entries. However, when loading the images, the information in the database overrides the DICOM information, and when the data is saved or exported, it will contain the changed information in the file.

Set Project | Locked Allows defining three attributes for a patient:

A **Project** name can be entered, or if it already exists, selected from a list. Similarly, a **Diagnosis** can be specified, and the patient can be **Locked** to

prevent erroneous deleting.

Delete Patient(s) Delete the patients selected in the list.

Create new Patient Create a new patient in the database, to whom information can be attached if there is no image series in the database.

Merge Sometimes several entries are created for a single patient because of a mismatch in the name/ID information. To merge such entries, select all of them in the **Patients** list (with `CTRL+Click`) and activate the **Merge** button. As a result all series end up under a single patient entry.

The / buttons allow hiding/showing the patient list controls.

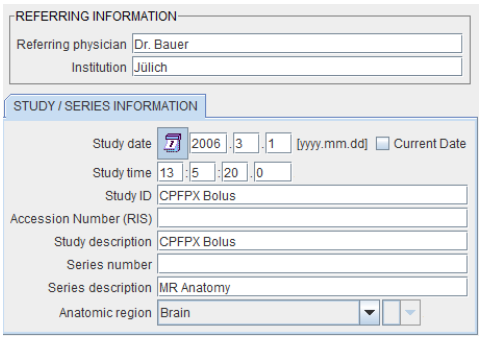
Series Operations

When a series of the current patient is selected, the row of buttons below the list becomes active.

Add Moves the selected series of the patient to the **Selected for loading** area.

Add All Moves all series of the patient to the **Selected for loading** area.

Edit Series Opens a dialog window for editing the series information



Set Project | Locked Brings up the same dialog window as on the patient level to define project, diagnosis and locking on the series level.

Pair Images This option in the selection list serves for associating two (or more) series. This association is used in processing tools which require the information of two image series.

Pair VOIs This option in the selection list allows associating a VOI file to image series.

Delete Serie(s) Delete the series selected in the list.

DICOM Inspect the attributes of the selected series in a DICOM browser.

Search JPEG or TIFF captures stored in the database. They can be opened in a

viewer.

Comment editor. Allows creating a comment for the selected image series. Existing comments can be edited or read.

Search for a study which is associated to the selected series.

Buttons allowing to step from patient to patient

The / buttons allow hiding/showing the series list controls. The / buttons allow hiding/showing the series image preview.

Selected for Loading Area

In most situations more than one series (from the same or different patients) can be added to the loading area, but there are exceptions when only a single series is allowed. The *order* in the list is relevant for the loading order. This is most important for the fusion tool because the first series will serve as the reference. To change the sorting order just click one of the column headers.

As soon as there are series in this area, the row of buttons below the list becomes active.

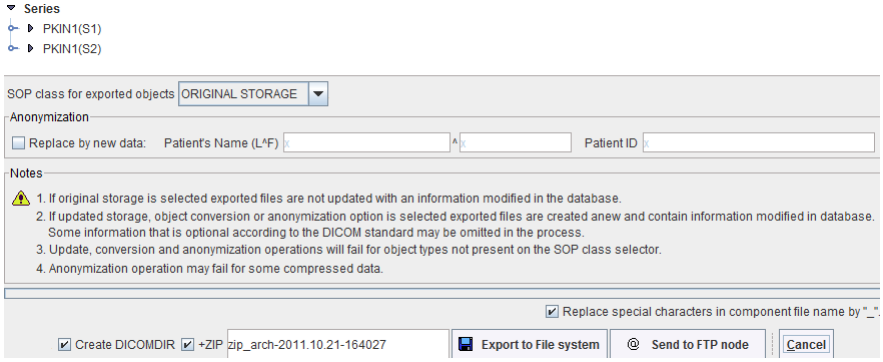
Open Starts loading the image series directly. The images are loaded without intervening dialog, and without any operations. Otherwise the dialog for specifying pre-processing options is shown. If the **Append** flag is on (), the selected series will be loaded as *additional* images to the tool, otherwise the tool will be cleared before loading.

with Operations Starts loading the image series. The dialog for specifying pre-processing options is shown. If the **Append** flag is on (), the selected series will be loaded as *additional* images to the tool, otherwise the tool will be cleared before loading.

This button serves for loading the selected data with a macro.

Replicate Copy the selected series including components to another database which can be selected in the appearing dialog window.

Export Export the series in the list from the database to a directory located on the fyle system or directly to an FTP node. The export dialog window



optionally allows anonymizing the images, generating a **DICOMDIR** file and compressing the whole data into a **ZIP** archive. The action can be aborted with

the **Cancel** button.

C-Store This button allows sending the selected series directly to a DICOM server without first loading them into an image area. This has the advantage that *no modifications are done to the original DICOM objects*. In contrast, when loading the images and sending them to a DICOM server, some changes are applied to the DICOM attributes.

Remove Removes the selected series from the selected for loading area, but does not delete from the database.

Remove All Clears the **Selected for loading** area.

 This button allows setting defaults column order and width.

 This button allows sorting the images **Selected for loading** by the selected column.

 This buttons allow changing the images order in the list.

DICOM Query/Retrieve

Q/R This button underneath the image display area starts the dialog window for the ***DICOM Query/Retrieve*** (on page 42) functionality. If the box left to Q/R is checked the demographic patient information is copied to the Q/R dialog window.

Loading Images from the File System

AUTODETECT This button allows loading image data from outside the database. Basically, it is an **Autodetect** loading, so the user can just browse to any directory and select any type of image file. PMOD will detect its file format and perform the image loading operation, if possible.

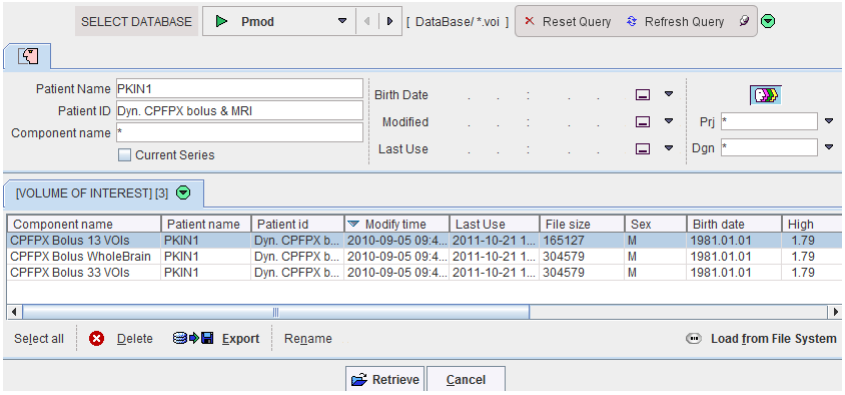
DICOM This button serves ***loading DICOM part 10 images*** (on page 86). The difference with the **Autodetect** loading is that the user has to select a directory, not a file.

Import This buttons allows direct importing of Dicom files to the current database.

Component Data Loading

Access to component data in the database is only available, if the database configuration has been set to **Use Database for Component data**.

The dialog window shown is somewhat different to the dialog window when loading images. The example below shows the dialog which appears after loading images of a patient **PKIN1** into the PVIEW tool and activating the **Load** button on the **VOI** tab.



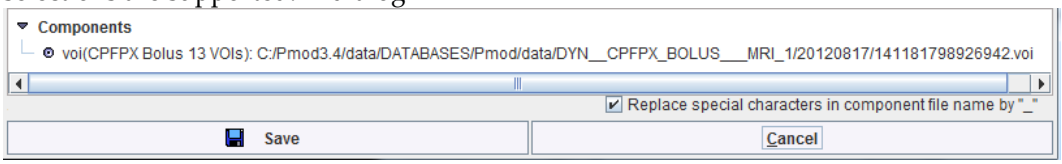
First, the database containing the data, here **Pmod**, must be selected. In the filter section similar options are available as described for image data loading. The **Patient Name** and **Patient ID** fields are normally filled in by the information of the image data which has already been loaded. The component section lists all data of proper type and matching the selection criteria.

The example patient **PKIN1** has three VOIs in the database. When a component in the list is selected, a row of action buttons below the list area become active.

Select all Selects all components of the list (also CTRL+A).

Delete Attention: Deletes the component data from the database and the disk!

Export Exports the selected component data out of the database into a disk file. Multiple selections are supported. A dialog



appears, and after the **Save** button has been activated the user is requested to specify the destination directory for the data export.

Rename For changing the **component name**.

Retrieve Starts loading the selected component.

Cancel Closes dialog without loading.

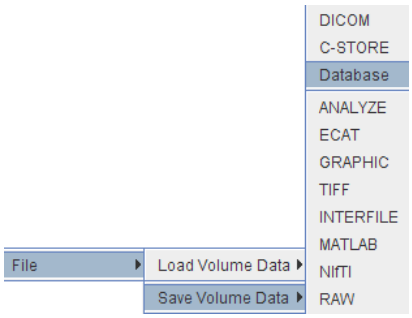
The **Load from File System** button changes to file-based loading directly from the disk.

Saving Data to Databases

Database saving is only possible of if the database functionality is enabled.

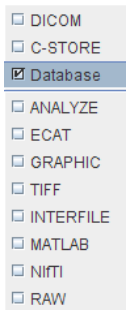
Image Data Saving

If the database has been configured the **Database** entry is available in the list of output image formats. Image saving can be either done from the **Menu** of a PMOD tool,

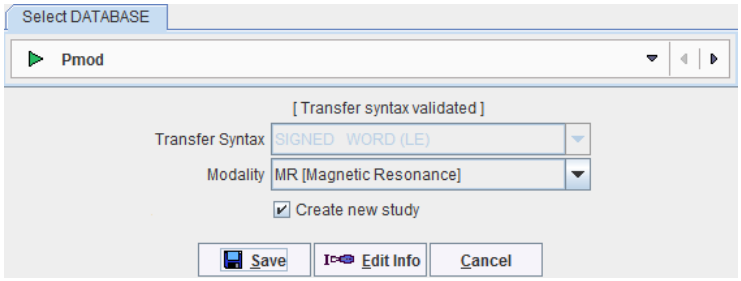


or using a **Save** button.

The **Save** button must be configured to the **Database** format beforehand using the arrow indicated in red.



Saving to the database brings up a dialog window



which is similar to the dialog window for saving images in DICOM part 10 files or C-STORE to a DICOM server.

The images are saved to the database as the following DICOM IODs :

- CT images as Enhanced CT,
- MR images as Enhanced MR,
- all other images otherwise as Enhanced PET.

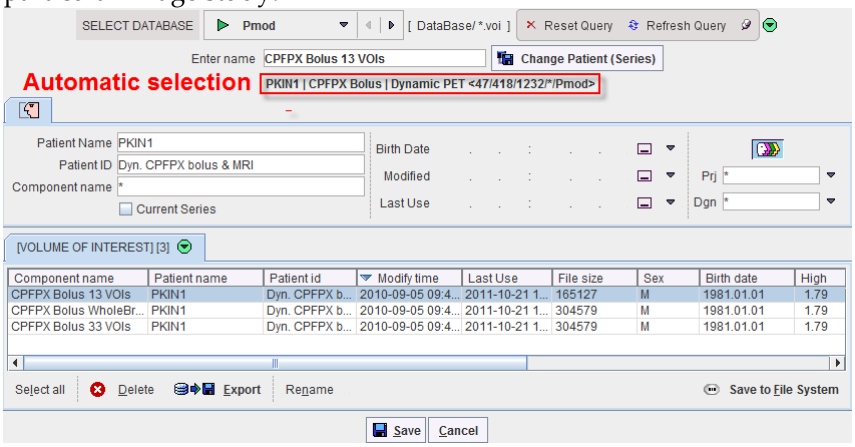
For databases with enabled float storage, images with internal float representation are saved as private enhanced PMOD objects.

The **Edit Info** button can be used for adding/changing descriptive information on the patient and series level.

Component Data Saving

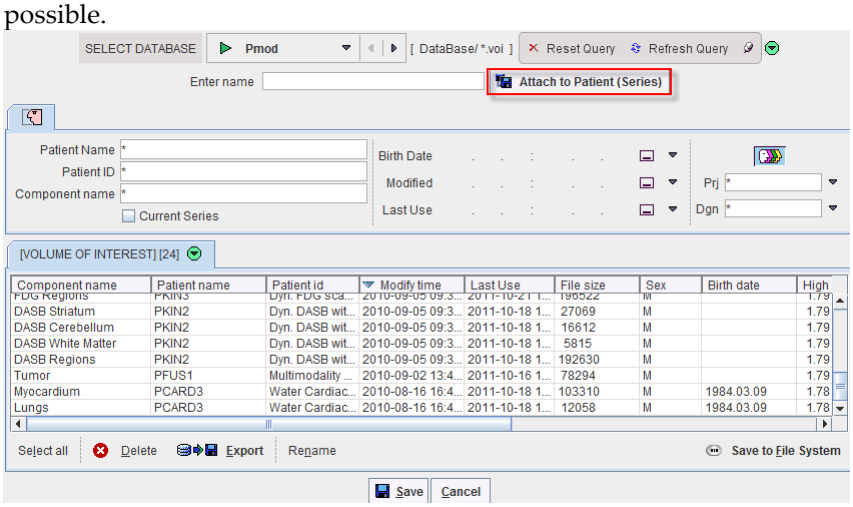
When saving component data to the database, the principle is that it is attached to the image series it was derived from. In practice, there are two situations to consider:

1) The component data was derived from an image series loaded from the database. In this case the patient and the series are already selected in the appearing dialog. After entering a name for the component, the data is saved to the database and attached to the particular image study.



Owing to this mechanism, all derived data ends up as additional components of the images, e.g. the VOIs and the VOI statistics. If needed, the **Change Patient (Series)** button allows attaching the information to a different series.

When the image data was not loaded from the database pre-selection of the series is not possible.

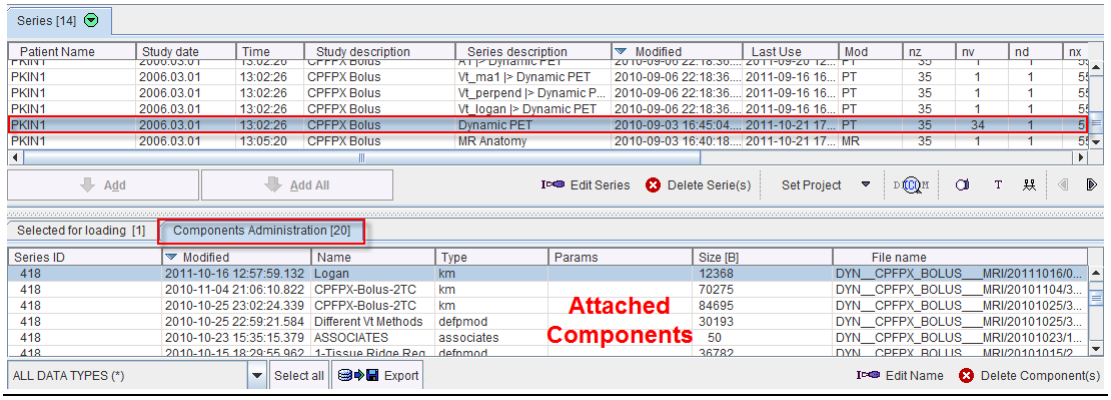


In this case the **Attach to Patient** button must be activated to look for the patient and

selecting one of his image series using the appearing database browser. If the patient is not yet defined in any of the databases, a suitable patient record with a dummy series can be created using the **Create new Patient** button of the database browser.

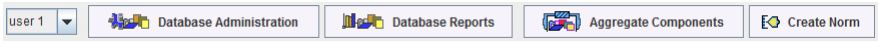
To save the data outside the database as a stand-alone file, activate the **Save to File System** button, browse to a specific directory, and save the component there.

Note: The saved components can be made visible and administered (exported, deleted, renamed) in the database dialog window by selecting the **Components Administration** tab.



Administrative Tools

There are four buttons on the **DATABASE** panel of the PMOD configuration page for performing administrative database tasks.

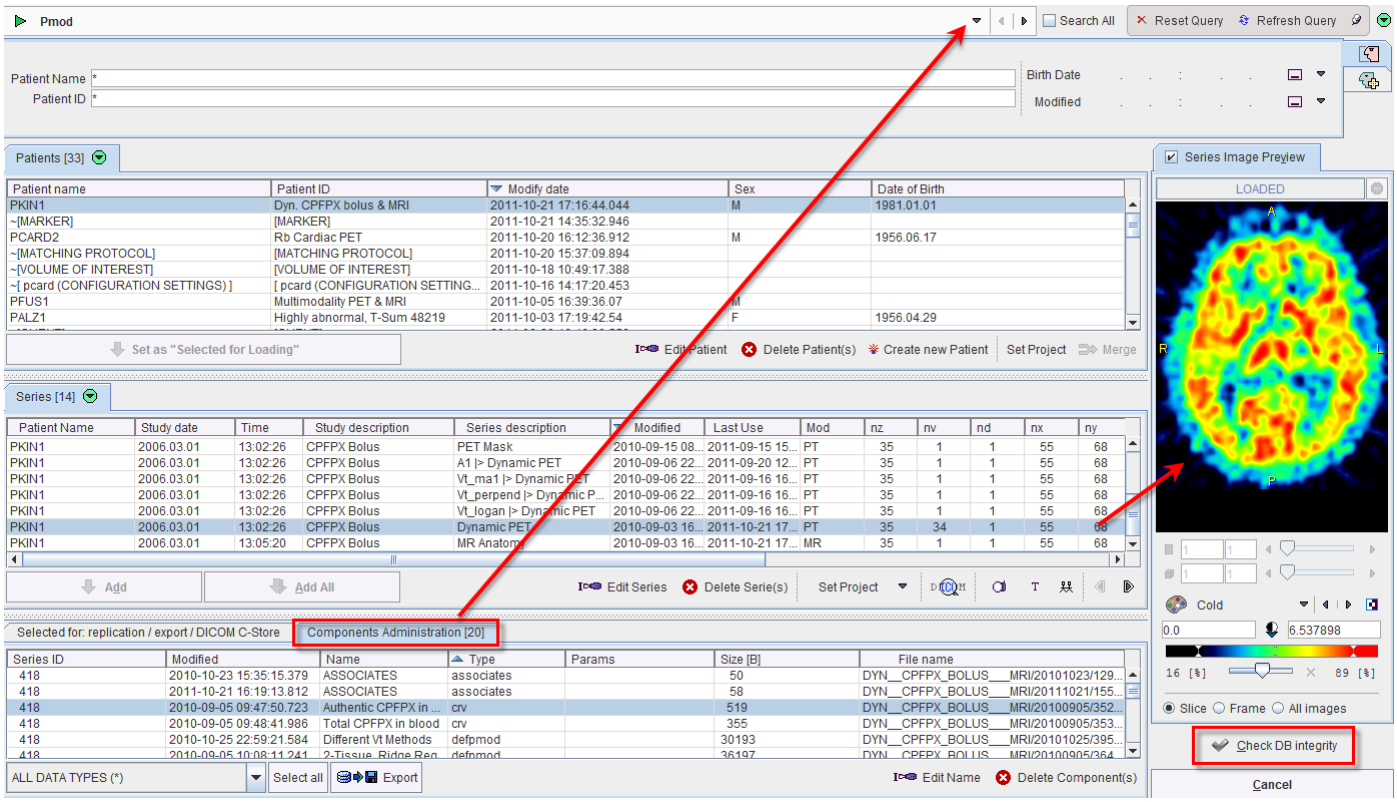


Their function briefly:

- **Data Base Administration**: Check database integrity, export data into an external directory or zip archive, replicate data between databases, modify attributes.
- **Database Reports**: Investigate the database contents, e.g. find out the number of patients, studies, series, and list/print the patients contained in the database, filtered using criteria such as gender, weight, etc.
- **Aggregate Components**: Export the data of certain component types, and generate tables with the VOI statistics or Kinetic Modeling results from multiple studies.
- **Create Norm**: Build normal databases from a number of healthy control subjects. There are two optional tools available, one for brain databases (Brain Tool), the other for cardiac databases (Cariac PET Tool). Their creation is explained in the respective User's Guides.

Database Administration

The interface of the Data Base Administration tool is almost the same as explained in the section *image loading from the database* (on page 58).



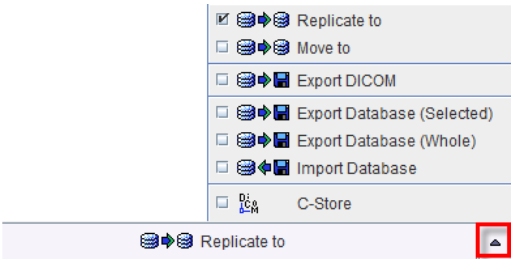
The following elements are additional:

Check DB integrity	When the button is activated the contents of the currently selected database is checked. If integrity constraints are violated, a dialog window is shown which allows fixing the problem.
Selected for: replication / export / DICOM C-Store	This tab is used for the backup of data as described below.
ALL DATA TYPES (*)	Selection to filter specific types of data, e.g. to list only VOI definitions, kinetic modeling files, etc. This element is not visible on the **Selected fo: replication/...** tab.

Note: For switching between databases the **Components Administration** tab must be selected. The reason is that only data from a single database can be used in backup procedures.

Export and Backup of Database Contents

There are different mechanisms for backing up and restoring data maintained by a PMOD database. This functionality is only visible on the **Selected for backup or replication** tab. The options can be found on the configuration button in the lower left bottom.



Replicate to	Copy data from one database to another online database.
Move to	Copy data to another online database and delete the original information.
Export DICOM	Copy data to a directory.
Export Database (Selected)	Export the selected data together with the describing database attributes into a composite backup file (.bkp).
Export Database (Whole)	Export all data of the database into a composite backup file (.bkp).
Import Database	Restore data from a composite backup into an arbitrary database.
C-Store	Sends all selected images to a DICOM server.

Export DICOM

To export images from a database using **Export DICOM** option, the following steps must be performed:

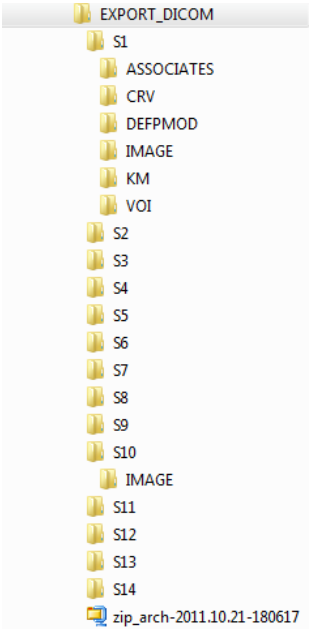
1) Select the source database from which data should be exported. The **Components Administration** tab must be selected for switching databases.

Activate **Selected for: replication/..** tab.

"elect the patient(s) to be backed up, then activate the **Set as "Selected for Loading"** button. To incrementally add more data, select patients/series and then activate the **Add** or **Add all** buttons. Note that image and component data are backed up with this procedure.

Configure the operation selection to **Export DICOM**. A dialog windows appears listing the series selected for export. A DICOMDIR can optionally be created which lists all image data, and the whole information can be packed into a zip archive.

Finally activate the **Export to File system** button. The selected components are exported to the selected output directory and organized in a hierarchical structure, so that all data belonging to a study end up in a common directory tree.



Export/Import with DB Information

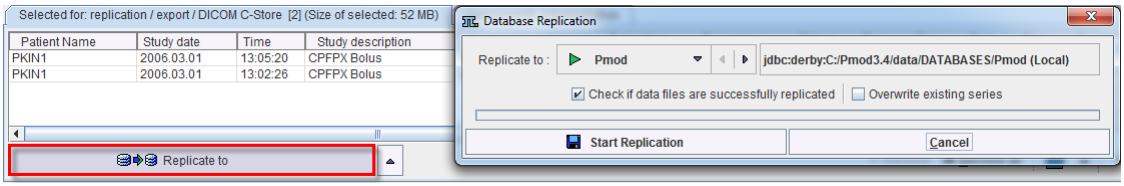
The purpose of this approach is to export data so that they can be re-imported to any other database, which need not be connected. The procedure is similar as described above. However, the result of **Export Database (Selected)** and **Export Database (Whole)** is a single file (.bkp) which contains both the data and the database information.

The information in the .bkp file is only accessible through **Import Database**. When a .bkp file is opened with **Import Database**, data can selectively be imported to any PMOD database.

CAUTION: The .bkp export is limited to a total size of 2GB due to system limitations and thus not intended as a backup facility. It can be used to exchange data within a Pmod version, while compatibility across different versions is limited.

Replication from one Database to Another

Data replication is a method to copy data between two PMOD databases without any interactive loading/saving operations. The preparation steps are the same as for export DICOM data. But instead of selecting the backup option button, the **Replicate to** button is selected and the appropriate target database configured among the available ones.



Activating **Replicate to** will then copy all selected data to the target database. For instance, data related to a single project could be copied to a newly created dedicated database, which will provide a faster response to queries than a big general database.

The **Move to** button also performs a database replication, but additionally deletes the source data after successful replication.

External Backup Procedure

For the purpose of having a backup in the case of a disaster, we propose the following simple and fast procedure:

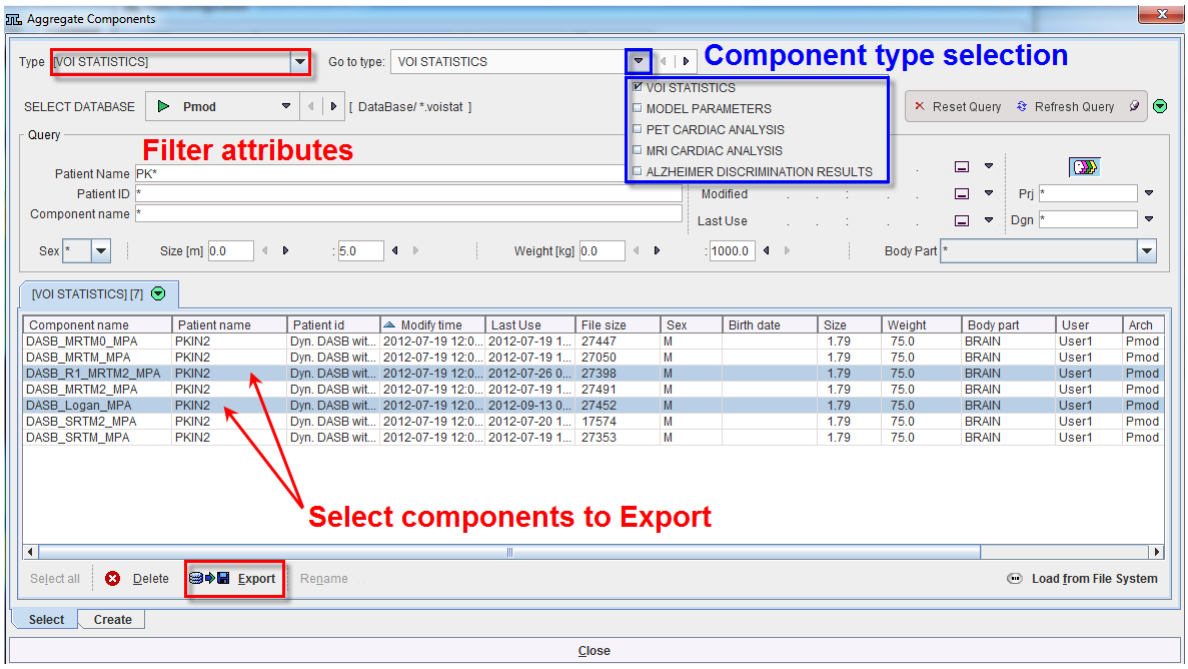
1) **Back up of the database tables.** To this end, automatic backups can be defined in the configuration section of the ***data sources*** (on page 49). Furthermore, the **Save SQL Backup** button allows saving the tables manually.
   Another alternative is to directly backup the relevant SQL database directory, in Windows for example:
   C:\Pmod3.5\data\DATABASES\dbname for JavaDB databases
   C:\Program Files\MySQL\MySQL Server 5.0\data\dbname for mySQL databases.

Back up of the data directory. All data files reside under a common directory. So after the database tables have been saved, copy this directory to a different disk as a data backup.

Aggregate Components such as VOIs and Kinetic Parameters

Over time, the database may collect a large amount of data. The **Aggregate Components** tool allows summarizing and extracting data of a specific component type such as VOI statistics, kinetic modeling parameter files etc.

The example below shows how VOI STATISTICS results can be exported. After selecting the component type **VOI STATISTICS** all corresponding results are listed.



The list can further be filtered using demographic or project attributes. Then select the results to be exported (CTRL+A for *Select all*), right click on the list, and activate the appearing **Export** button. The files are then saved into a directory which can be specified. Similarly, other types of derived component data can be exported.

More sophisticated operations than a mere file export are available for *VOI statistics* (.voistat), *Model Parameters* (.kinpar), *Pet Cardiac Analysis* (.pcardRes), *MR Cardiac Analysis* (.mcardRes) and *Alzheimer Discrimination Results* (.palzRes). If either of these types is selected, the **Create** tab become active. Its purpose is to compile the results contained in multiple files into a comprehensive table (.dbTab), which can be exported for further analyses or loaded and sent directly to Pmod-R interface for statistic analysis. Note that this type of analysis is most effective if consistent naming conventions (same region names) are obeyed.

Chapter 4
Data Loading and Saving

The PMOD tools are able to read and write different types of image data. It is important to understand that *correct data units and acquisition timing information is required* for quantitative processing steps to derive meaningful results. As an example: In quantitative PET studies a tracer is injected at time 0. At the same time a series of image acquisitions is started, and arterial blood samples are withdrawn in certain intervals. The images are needed to monitor the time-course of tracer distribution in tissue. The blood samples are analyzed to determine the unchanged tracer in plasma, the input curve during the acquisition. The tissue response and the input curve are fed into kinetic models to quantify certain properties of the tissue under investigation. For applying the model, the image and blood units must be calibrated and the times must be measured in a common time scale.

In some image formats the data units are saved with the data (eg. DICOM, Ecat). With these formats the units are automatically detected upon loading into PMOD. Otherwise the user must select the correct units for the data and specify the acquisition timing. During loading, PMOD converts activity concentration data to its internal units, ie. kBq/cc and seconds. The appropriate scale factor is derived from the specified input units. As a result, PET images are always displayed in kBq/cc, and images are always saved with the displayed units. This has the consequence that if PET images residing in an Analyze format are loaded with units nCi/cc specified, and then again saved in Analyze, the values in the file are different, namely calibrated in kBq/cc. If this file is loaded, the units must therefore be specified as kBq/cc. These considerations do not apply if the image data are in DICOM. Therefore we highly recommend using the DICOM format, preferably in combination with the PMOD database.

Multiple transformations of the image data are supported during loading. The pre-processing capabilities include re-orientations such as orthogonal reslicing, rotations, mirroring, data processing such as smoothing or averaging over time, as well as the selection of subsets of the available slices and time frames.

Besides actual image data files PMOD is able to read and save a information needed for kinetic modeling from column-delimited text files (component data). These files may hold Volume-of-Interest definitions, kinetic modeling data, the configuration of the PMOD tools etc. They are either directly written as files into a directory, or to the database which saves the actual data into an internal directory and adds access information to the database tables. Component data reading/writing uses a unified interface which looks identical for the different component types.

It is helpful to remember that PMOD maintains three paths which are related to data loading/saving:

- DICOM path: the directory which PMOD scans in order to look for DICOM part 10 data files.
- Data path: the directory to load other image data types.
- Database path: the directory where to look for component data.

PMOD maintains a separate history for each of the three paths to rapidly switch between frequently used locations. If databases are used to manage the data, access to all types of data can be done through the database user interface.

In This Chapter

Image Data Formats

PMOD supports numerous image data formats in reading, and a subset also in writing. As described below the image formats have different properties. Some formats support information in addition to the image pixels such as:

- demographic patient information;
- patient positioning information which allows the derivation of the anatomical orientation in the images (anterior/posterior, left/right, head/feet);
- acquisition parameters such as the timing of a dynamic series which is essential for the modeling of the uptake;
- radiotracer information such as dose and radionuclide;
- image unit information.

Format Overview

The following formats are supported by PMOD. Their properties are summarized in the different columns.

Format	Read	Write	Units	Times	Write Precision	Patient Info	SUV Calculation Info
AFNI	yes	no	no	only identical duration for all frames	-	no	no
ANALYZE	yes	yes	no	only identical duration for all frames	16bit int (scaled), 32bit float	no	no
ANALYZE LPS	no	yes	Compatibility version to write images suitable for older PMOD versions				
ANALYZE SPM	yes	no	Compatibility version for reading SPM-generated images so that they are shown in HFS orientation (however, left and right are dependent on SPM settings)				
AVW	yes	no	no	no	-	no	no
BrainVISA	yes	no					

DICOM	yes	yes	yes	yes	16bit short (scaled), private objects with 32bit float precision	yes	yes, post-injection values only on private GE tags
ECAT 6	yes	no	yes	yes	-	yes	yes
ECAT 7	yes	yes	yes	yes	16bit int (scaled), 32bit float	yes	yes, during save no support for post-injection information
GE Advance	yes	no	yes	yes	-	yes	yes
Graphic	bmp, jpeg, tiff	jpeg	no	no	RGB	no	no
HIDAC	yes	no	no	yes	-	no	no
Interfile	yes	yes	yes	for dynamic study	16bit int (scaled), 32bit float	yes, some information on private tags including patient size, weight, study description, body part	yes, on save only standard elements are populated (no time values or postinjection values)
Matlab	yes	yes	yes	yes	32bit float	patient name, id and study id only	no
MicroPET	yes	no	yes	yes	-	yes	yes
Neurostat	yes	no			-		
NifTI	yes	yes	PMOD Files	PMOD files, otherwise identical duration for all frames	16bit int (scaled), 32bit float	only comments supported as series description	no
MINC 1	yes	no	yes	(yes)	-	yes	yes
Philips ImageIO	yes	no	no	yes	-	yes	yes

Paravision							
Raw	yes	yes	no	no	8bit int (scaled), 16bit int (scaled), 32bit float	no	no
TIFF	yes	yes	no	no	RGB	no	no
Varian FDF	yes	no			-		

Format Descriptions

Autodetect (Read only)

For users working with different image formats it may be cumbersome to remember the data format of the different files, which may have similar suffixes. The **Autodetect** format makes it unnecessary to select a specific format before image loading. The user can just select the file(s) he wants to load, and PMOD will try to find out the appropriate format based on the file contents (not on the suffix) when loading.

DICOM (Read/Write)

Image data according to the ***DICOM standard http://medical.nema.org/dicom/***. As input data, the following Information Objects have been tested: CT, Enhanced CT, MR, Enhanced MR, NM, PET, Enhanced PET, SC, SC multi-frame true color, US.

PMOD's DICOM Conformance Statement describes in detail the DICOM support implemented in PMOD. It can be downloaded from the ***Support http://www.pmod.com/technologies/support/enter-support.php*** page on the PMOD Website.

Database (Read/Write)

Data loading/saving with a PMOD database. Image data are saved based on the modality: CT as Enhanced CT IOD, MR as Enhanced MR IOD, other images as Enhanced PET IOD.

Query (Read only)

This loading "format" is a shortcut for retrieving images from a remote DICOM server and directly loading them to the image display.

Interfile (Read/Write)

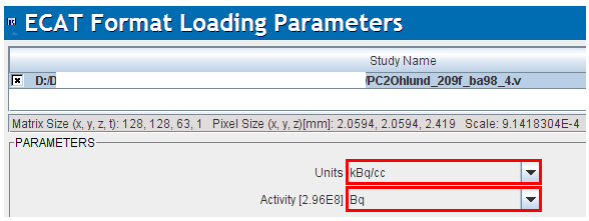
Interfile is a file format developed for data in Nuclear Medicine (Todd-Pokropek A, Cradduck TD, Deconinck F, A file format for the exchange of nuclear medicine image data: a specification of Interfile version 3.3, Nucl Med Commun. 1992 Sep;13(9):673-99).

There are two basic variants of Interfile. One variant has separate header (.hdr) and image (.img) files. This variant has the advantage that the header file can be viewed and edited with a simple text editor. The other variant includes all the information in a single file (.hdr). Both variants are supported in reading and writing, restricted to the subset of data objects which are relevant for PET.

Ecat 6/7 (Read/Write)

Data format of PET data from older CTI/Siemens systems. It is a self-contained format containing all acquisition information.

When loading Ecat data an additional choice appears to explicitly define the units of the patient dose values. This facility was introduced because Ecat files without well-defined units were encountered. Experience has shown that the *Bq* unit should be selected to arrive at the correct doses, but other examples were also encountered. The dose value is important for the SUV calculation and can be checked on the SUV-related panels.



When saving data in the Ecat format, after the specification of the file name, a dialog is presented to the user with a choice of transfer syntaxes. They define the byte ordering used for saving the data. In case you want to read the images using a program other than PMOD, you are recommended to select a *big-endian (BE) encoding*.

MicroPET (Read only)

Data format of the Siemens Inveon and MicroPET ***preclinical systems http://www.medical.siemens.com/webapp/wcs/stores/servlet/CategoryDisplay~q_catalogId~e_-1~a_categoryId~e_1011531~a_catTree~e_100010,1007660,1011525,1011531~a_langId~e_-1~a_storeId~e_10001.htm***. It is used both for PET and CT data.

NifTI (Read/Write)

Extended ***variant http://nifti.nimh.nih.gov/nifti-1*** of the analyze format by the Neuroimaging Informatics Technology Initiative. Both single file (.nii) and double file (.hdr + .img) images are accepted but only in uncompressed form.

PMOD reads the following NIfTI data types:
8-bit unsigned and signed byte (DT_UINT8 and DT_INT8), 16-bit unsigned and signed short (DT_UINT16 and DT_INT16), 32-bit unsigned and signed int (DT_UINT32 and DT_INT32), 32-bit float (DT_FLOAT32), 64-bit double (DT_DOUBLE) and 24-bit RGB (DT_RGB). 64-bit double data are rounded to 32-bit float representation. Up to 4D data is supported, meaning PMOD does not accept files with the 5th dimension greater 1. Only a single value or a single RGB triplet per pixel is supported. If qform_code > 0, PMOD uses qform matrices, otherwise if sform_code > 0 sform matrices will be used. When neither is defined data orientations

remain undefined in PMOD. PMOD does not support any extensions nor NIfTI statistical codes. Gzipped images must be uncompressed prior to their usage with PMOD.

NIfTI images produced by SPM require A/P mirroring (**TOP to BOTTOM** sorting) to get them into HFS position. Other NIfTI images should best be loaded with **Reoriente to Anatomical Position** *enabled* (on page 90).

In writing, PMOD supports the variants with two files (header information in *.hdr, image data in *.img) or a composite file (*.nii). The single file variant is required when preparing atlas template images.

Analyze (Read/Write)

Data in the ***Analyze 7.5 format http://www.mayo.edu/bir/PDF/ANALYZE75.pdf*** consists of two files. The header file (*.hdr) contains information about dimensions, pixel representation (transfer syntax) and value scaling. The data file (*.img) contains the pixel data itself without any header offset. Value units and information about acquisition timing must be manually entered, or can be loaded from definition files.

SPM produced Analyze files are usually L/R mirrored. Such files require a 180◦ rotation about the z-axis s to get them into the radiological head first supine (HFS) position which is the PMOD default.

Note: Analyze has the possibility to include timing information, but only for a single frame. If a timing is specified in the file it will be applied for all frames of a dynamic study, even if a different timing was specified using Edit Times in the user interface. In such cases it is advised to load the image data, change the timing, and save the images again in a format wit better timing support (DICOM, Ecat, Interfile). PMOD writes Analyze files without timing information.

AVW (Read only)

Newer version of the Analyze format.

Raw (Read/Write)

A raw image file which holds only the pixel data. All additional information must be edited manually. Different types of number encoding (byte, signed and unsigned short integer, float) and byte orders (big/little endian) are supported.

Graphic (Read/Write)

Graphic images in **jpg**, **gif** and **bmp** can be read. When writing as a **Graphic** file, the **jpg** format is used.

TIFF (Read/Write)

The graphic tiff format is treated separately and can be read and written.

Matlab (Read/Write)

Image data can be read which has been prepared and saved in Matlab using the `save -V4` command (Note: only Matlab version 4 format is supported, thus the requirement of the `-V4` option). The following Matlab variable names/contents are expected:

- `dim[nx,ny,nz,nTime]` (number of columns, rows, slices, acquisitions)
- `vox[xSize,ySize,zSize]` (voxel sizes in mm in all 3 dimensions)
- `orig[xOrig,yOrig,zOrig]` (position of the origin measured in mm from the top left corner of the first slice)
- `time[1,...nTime]` (times when the acquisitions started)
- `timeEnd[1,...nTime]` (times when the acquisitions ended)
- a series of value vectors named `v1s1` till `v21s35` when `nTime=21` and `nz=35` (`v` denotes acquisition number and `s` slice number)
- `patientName[]` (string with patient name)
- `patientId[]` (string with patient ID)
- `vUnits[]` (string with value unit name)
- `tUnits[]` (string with time unit name)

Note that only the variables `dim` and `v1s1` etc. are mandatory.

Neurostat (Read only)

Neurostat http://128.95.65.28/~Download/ uses the Interfile format (.hdr, .img) to save the 8 surface projections into an image file. Please note, that this is not a volumetric data set, and therefore should be viewed in a *planar layout* such as 2x4.

AFNI (Read only)

AFNI http://afni.nimh.nih.gov/afni/doc/edu/afni01_intro (acronym for Analysis of Functional NeuroImages) creates two-file data (.HEAD, .BRIK).

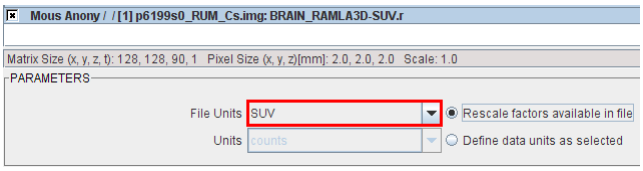
GE Advance (Read only)

Data format of PET data exported from GE PET systems (Advance, Discovery) with the *Investigator* utility. It is a self-contained format with all acquisition information.

Philips (Read only)

Mosaic data format of PET data from Philips PET (Allegro, Gemini) and older GE Quest systems.

When PMOD recognizes more than one unit defined in the file the loading dialog window shows a choice selection for the user to choose which units will be loaded from a file, providing different range of values.



HIDAC (Read only)

Data format of the (historic) animal PET system HIDAC (Oxford Positron Systems). *To be retired.*

BrainVISA (Read only)

Format used by the ***Brainvisa software http://brainvisa.info/***.

Varian FDF (Read only)

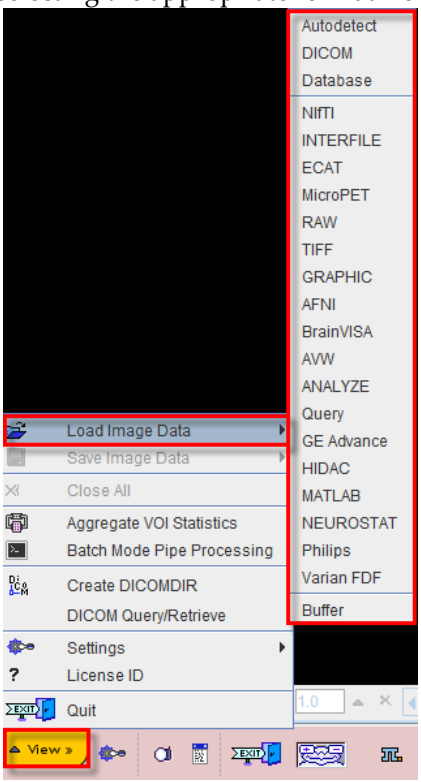
Flexible Image Format of Varian MR systems.

Image Data Loading

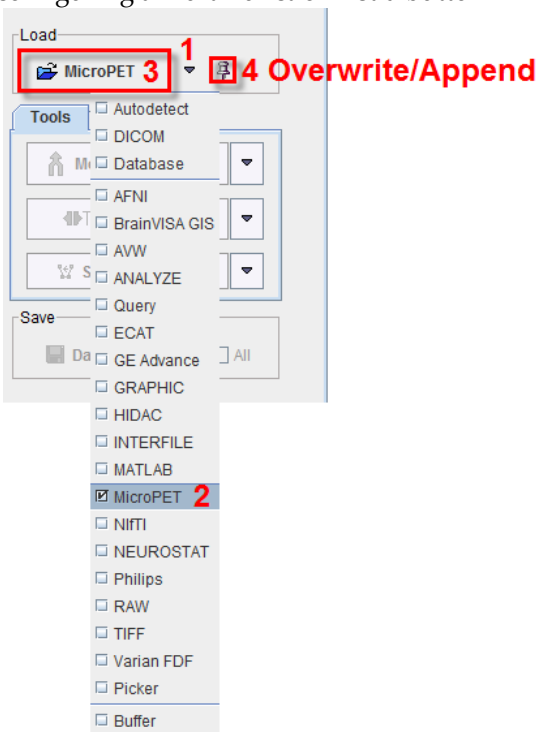
In most tools there are four different ways to load image data:

1) By **dragging** an image file from the desktop onto the title bar of the PMOD tool, or onto a tool button on the PMOD tool bar. PMOD will try to recognize the data type and read the images accordingly. If it is a data format without header information the information from the last successful loading operation will be applied.

By selecting the appropriate format from the menu **View/Load Image Data**, eg

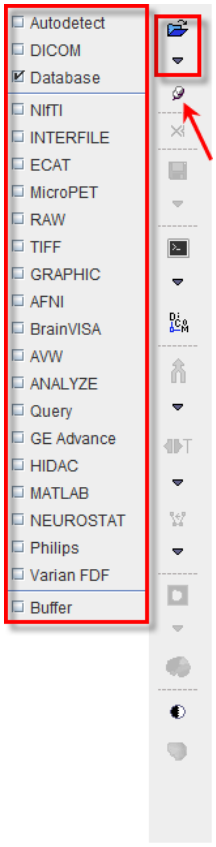


By configuring a multi-function **Load** button



to the correct type. The loading operation will be immediately started.

By selecting and configuring the appropriate format in the lateral taskbar using the **Load**



button

In many situations (indicated by the pin besides the format selector, 4) it is possible to load several files into a tool. In this case multiple file names can be selected in the file selection box, or multiple image series in the database loader. If images have already been loaded and

the pin is fixed , the newly selected studies will be *appended* to the present one(s). Otherwise the prior studies will be overwritten.

Data Units

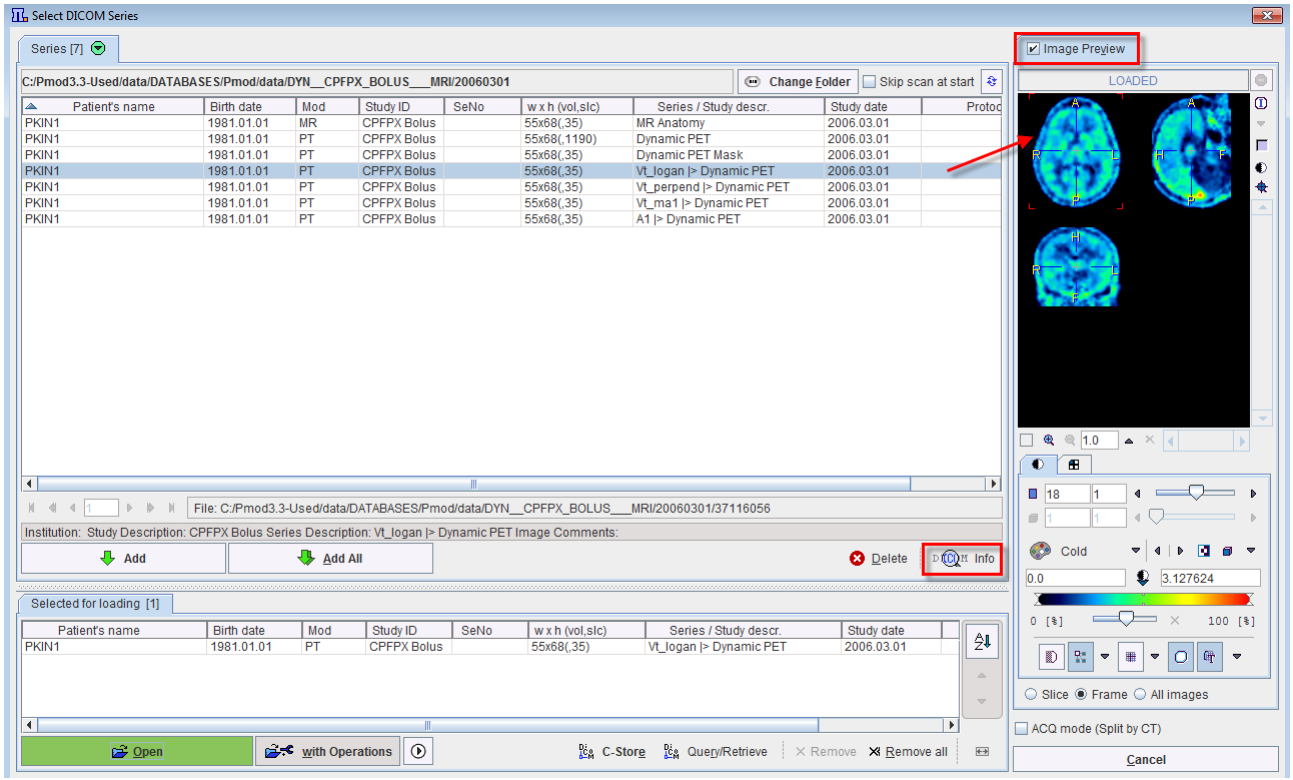
For any quantitative PET work you have to make sure that the right *input data* units are specified if the data is not read from DICOM, ECAT or the database. Activity concentration values are always converted to the internal representation of kBq/cc during a read operation. If the data is saved again, the *values after conversion will be stored.* Additionally, the acquisition times must also be specified. There is a facility for saving/retrieving timing protocols in all tools which load image data.

DICOM Part 10 Data Loading

When loading DICOM data, the directory of the last DICOM loading operation is referred to. If the **Skip scan at start** box is not checked, PMOD searches for DICOM images in the directory when the dialog windows opens. In case there are many files in a directory, the scanning process may take substantial time. This is annoying if the data to be loaded resides somewhere else. To avoid initial file scanning, the **Skip scan at start** box can be checked. The user can then locate the proper directory with the **Change Folder** button and activate the button to initiate scanning for DICOM files. If no DICOMDIR exists, all files of the directory are scanned and all valid DICOM series listed.

If a DICOMDIR file exists in the directory, it is parsed and the registered image series presented for loading. As a consequence, all non-registered DICOM files in the same directory are neglected.

The DICOM loader presents the selection of the available image series in a dialog window as illustrated below.



Select the series to be loaded, **Add**, and activate the **Open** button. Use **Remove** or **Remove all** to remove series from the **Selected for loading** area. Depending on the context, several series can be loaded at once, or the selection is restricted to a single series. Please note the **with Operations** button. If it is activated, the dialog window specifying loading transformations explained below is opened.

Sometimes the information shown in the list may be insufficient to identify a series unambiguously. To find out more about the selected series activate the **DICOM Info** button which opens a full DICOM data inspector. Another alternative is to use the **Image Preview** to the right: if the **Image preview** box is checked, the images are loaded as soon as a series is selected.

The **ACQ mode (Split by CT)** box allows grouping the images in the selected series by the acquisition number, an optional sub-level beneath the series. This is required to properly load some DICOM series, for example with CT studies which contain different reconstructions (different area/pixel) in a single series. With other series, however, acquisitions need to be displayed together, for example with whole body SPECT data covering subsequent bed positions in separate acquisitions. As there is no way for PMOD to determine the right interpretation, the user may choose between the two loading modes to solve unsatisfactory loading results.

DICOM Query/Retrieve starts the dialog window for querying a remote DICOM node and pulling images from it as explained ***above*** (on page 42).

C-Store is a utility for sending selected data sets directly to a remote DICOM server without the need to open it for viewing, and then selecting the **C-Store** saving button. Direct sending

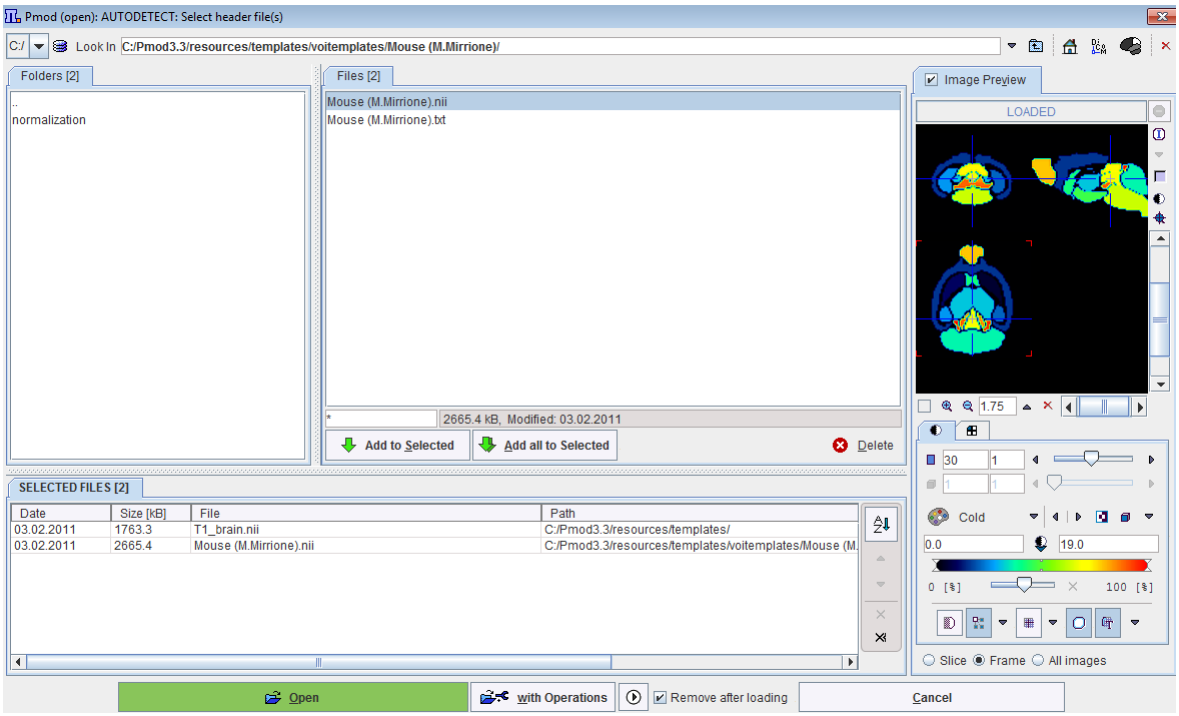
has the advantage that the original DICOM images are transferred. Otherwise, if loaded images are sent, they contain information modified by PMOD.

Use the **Delete** button to remove all files belonging to the currently selected series from the disk.

Note: A new DICOMDIR including all DICOM studies in a directory tree can be generated using the **Create Dicomdir** entry in the menu of the PMOD viewing tool (PVIEW).

File-based loading

For all non-DICOM type of image data the loading dialog looks like this example using the **Autodetect** format.



Use the navigation elements at the top to browse the directory hierarchy. The files to be viewed need to be brought to the **SELECTED FILES** area by double-clicking, or by using the **Add to SELECTED** or the **Add all to SELECTED** button. Note that in some contexts multiple file selection may not be possible. In that case, only one file can be brought to **SELECTED FILES.**

The images will be loaded in the order they appear on the list. This may be relevant in the fusion tool where the first image will serve as the reference, or if multiple static images are to be combined into a dynamic study. To modify the list order use the **Sort by selected column** button or **Up** and **Down** buttons , or **Remove from selected** a file and add it later back to the end of the list. Optionally, **Remove all from selected** using the button allows removing all images available in the **SELECTED FILES** area.

A preview facility allows inspecting images in the **Image Preview** to the right before loading them and continue processing. When the box **Image preview** is checked, the images are shown as soon as an item in the **Files** list is selected.

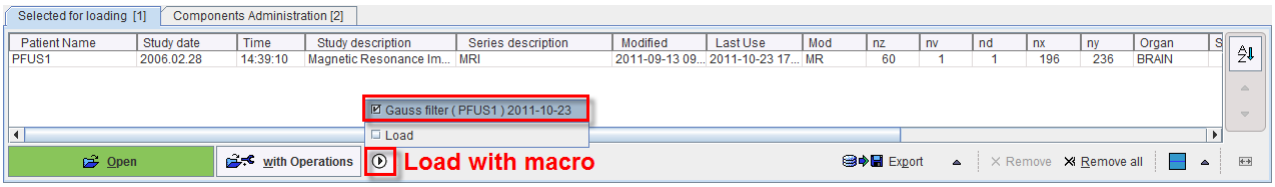
When **Open** is activated, the selected files are loaded directly. If **with Operations** button is activated, a dialog window is opened specifying loading transformations to be applied to the image as explained below.

Database Loading

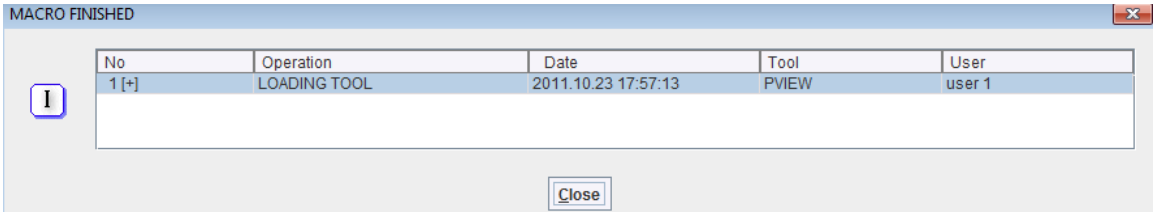
Database loading of images has already been described ***above*** (on page 58).

Loading Macros

Macros are applied as a data transformation during loading. To this end select one or several images for loading. Then, instead of using the **Open** button, use the ⏲ button next to it.



A list opens showing the currently available macros. To load a macro from a different source, use the **Load** entry. As soon as a macro is selected, the data is loaded, the processing steps applied, and finally a confirmation window **MACRO FINISHED** shown as illustrated below.



Macros can be prepared based on the ***image history*** (on page 113) of a representative data processing session.

Buffer Loading

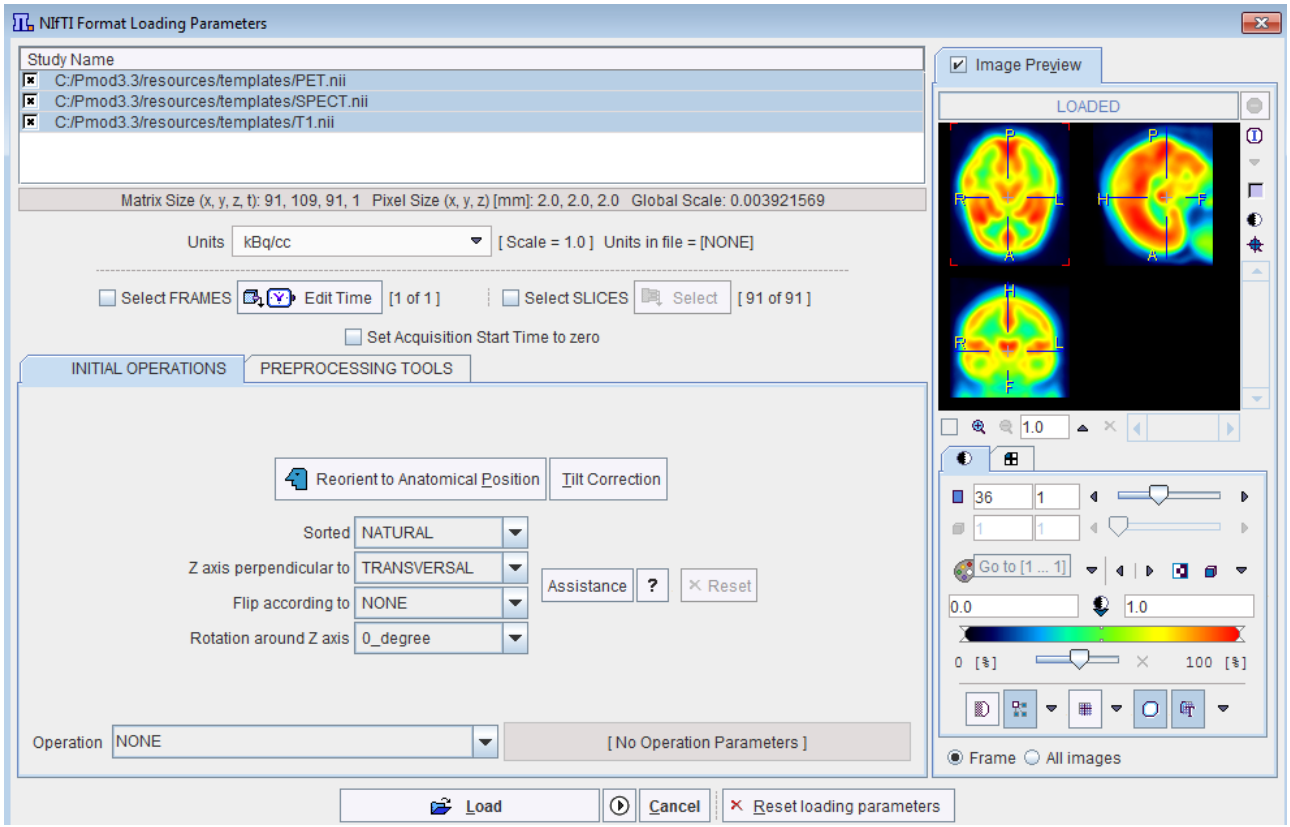
Note that to be able to load from the **Buffer**, the images need to be initially loaded in a PMOD tool and then saved to the **Buffer**. The procedure is described in the ***Buffer Saving*** (on page 102) section.

Image Data Transformations during Loading

There are two basic ways how images are loaded:

1) Direct loading**:** if the **Open** Open button is selected on the image selection dialog; the images are immediately loaded without any data transformations.

If the **with Operations** with Operations button is selected, an intermediate dialog window is shown which allows configuring the image data properties as well as optional pre-processing steps. Initially, the *settings of the last loading* operation are shown.
The example below is an illustration of the loading dialog after three NiFTI files from the templates directory have been selected for loading.

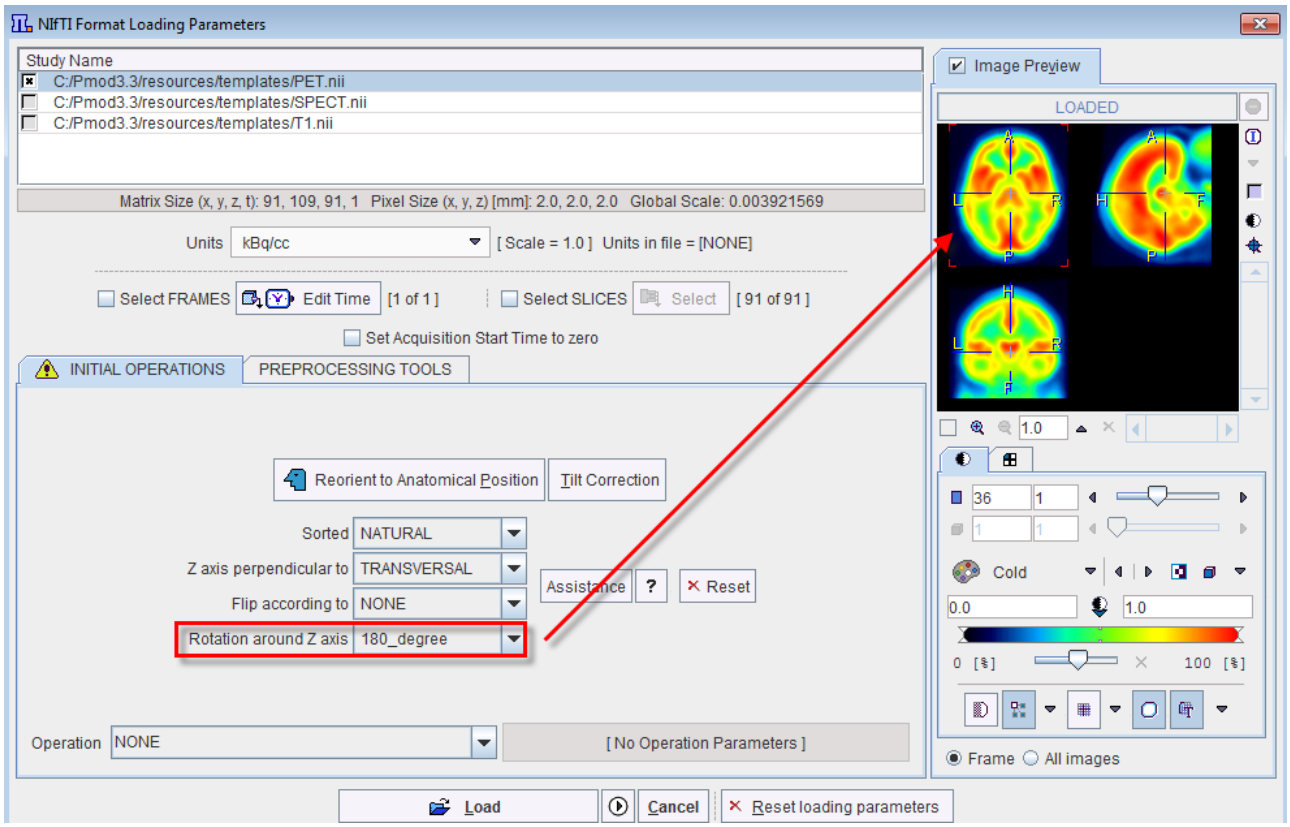


In the upper part the list of images for loading is shown. The rest of the dialog window allows defining the properties of the images and transformations which are to be applied to the selected image during loading.
To apply one or several transformations to an image select it in the list, and then perform the configuration in the lower sections. When **Load** is activated, only the files with a check are loaded.

Changing the Image Orientation

Note that in the above SPM template example the anterior-posterior (AP) direction is opposite to the standard convention, and in fact patient right is on the right image side. To

bring this image set into a radiological convention orientation, a rotation by 180° about the z-axis must be applied as illustrated below



The following image re-orientations are supported

- modification of the sorting order to interchange left-right, top-bottom in the image, and front-back (slice ordering);
- rotation about the z axis;
- orthogonal sections such as coronals or sagittals.

As there are many possible combinations, activating the **Image Preview** function helps verifying how the images will look like after loading.

If data are loaded which contain consistent information about the orientation of the acquired slices (eg. DICOM, NiFTI, Ecat), the following steps allow bringing the image in the correct anatomical orientation:

1) To start activate the **Assistance** button (**1**).

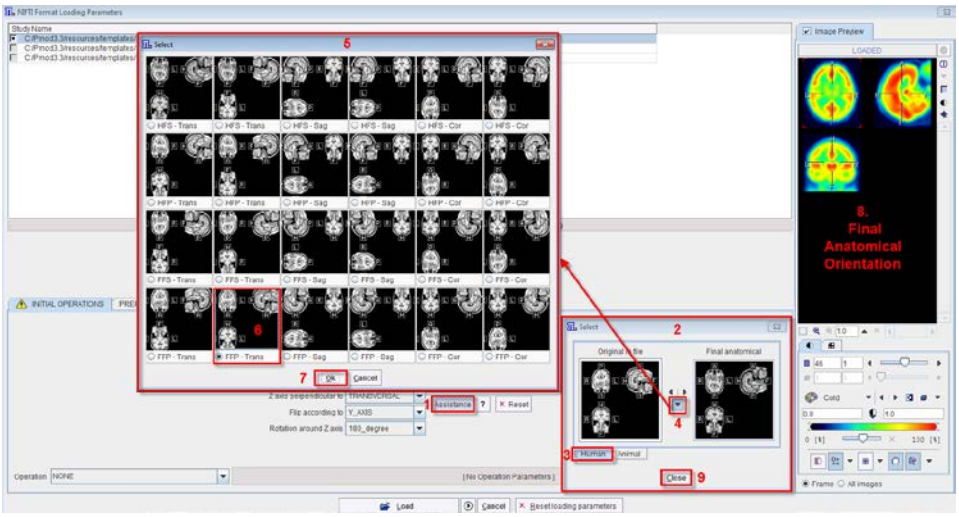
A selection window (**2**) appears allowing to choose the image type to be load: **Human** or **Animal** (**3**).

To select the original orientation in the image file the **Down** arrow (**4**) need to be activated.

A dialog window pops up (**5**) allowing to select the original orientation in the image file (in the example FFP-Trans **6**).

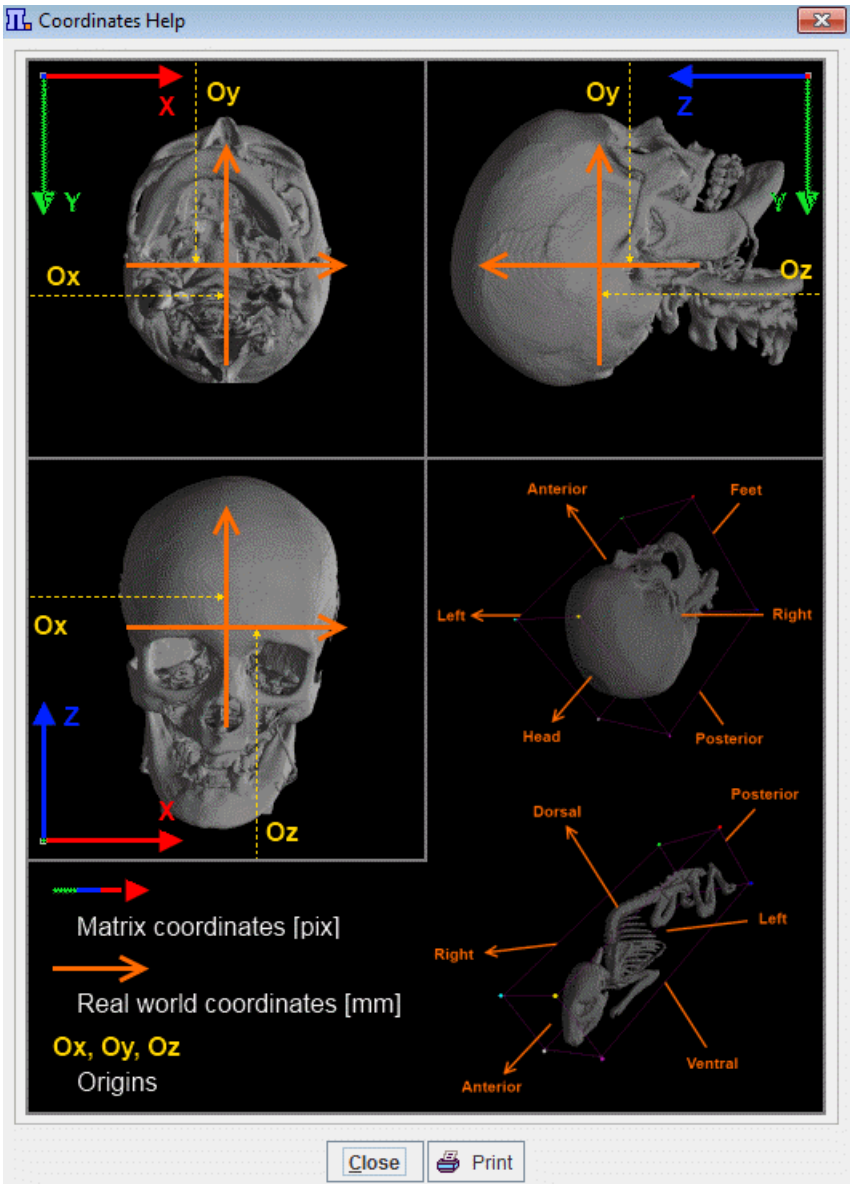
To set the selection for the original orientation in the file, the selection dialog window need to be closed with **OK** (**7**).

The result of re-orientation is immediately reflected in the **Image Preview** section if the coresponding checkbox is enabled (**8**).



Finally, **Close** the orientation selection window and load the image with the **Load** button.

More information and help about human and small animal matrix coordinates and real world coordinates are provided activating the question mark button next to the **Assistance** button.



The re-orientation settings may be easily calcelled activating the **Reset** button next to the **Assistance** button.

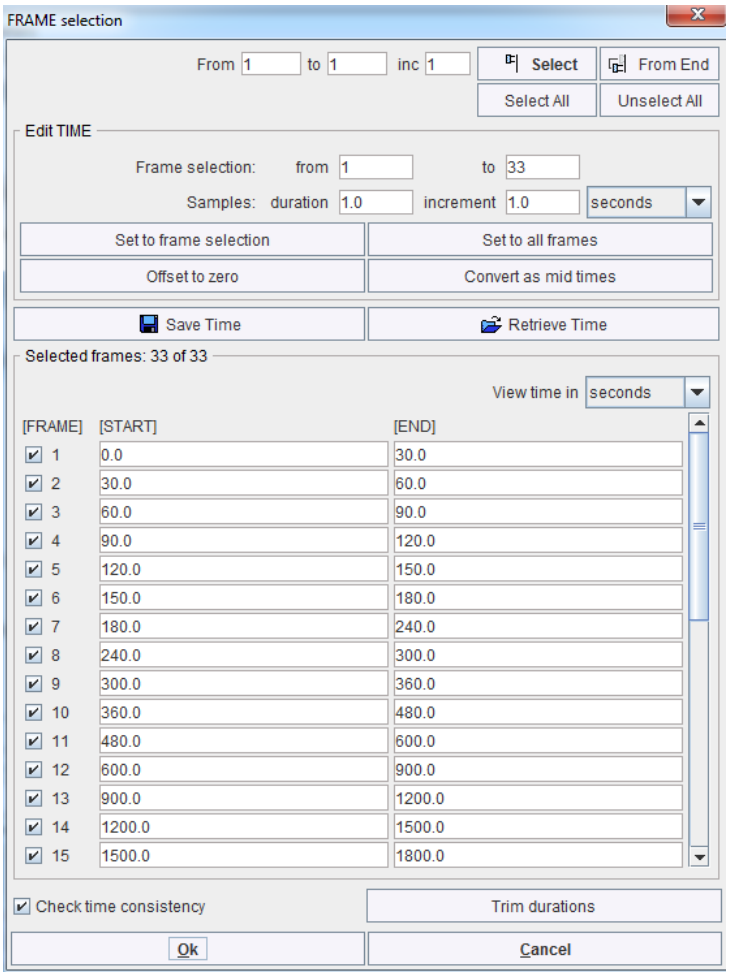
Reorient to Anatomical Position: This option will arrange the data such that the patient position is closest to the head first supine (HFS). The patient's head is directed into the display, looking up the display and left patient hand to the right side of the display. This adjustment is performed without reslicing, using only rotations by 90 degrees or multiplications of this value. It requires that enough patient positioning information is available in the image file.

Tilt Correction: If this option is selected, the corners of the slices are checked whether they are located on a line perpendicular to the slice plane. If this is not the case, as with CT data acquired with a tilted gantry, they will be resliced such that the new top left corner of the

image are aligned. The default reference frame is the frame closest to the origin. If **Reorient to Anatomical Position** is active tilt correction will always be checked and performed prior to data reorientation. As a result of this correction the orthogonal planes will not show displacement artifacts.

Defining the Acquisition Timing

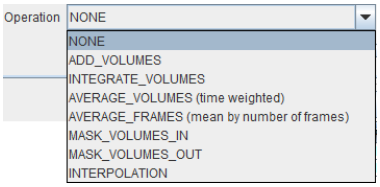
The specification of the acquisition times is important for using dynamic data in a quantification process. The times can be inspected and the definition overwritten using the **Edit Time** button, which shows the following dialog window.



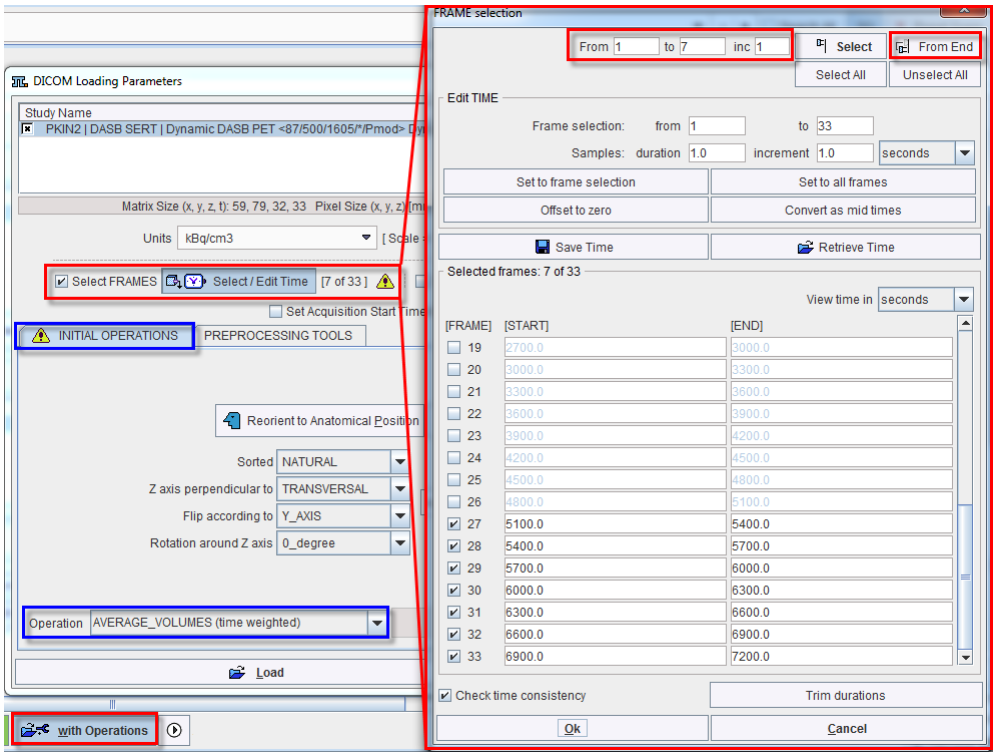
For DICOM, Ecat, MicroPET, Interfile and GE Advance data the times are read from the selected file and shown in the list. Note the **Save Time**/**Retrieve Time** buttons which allow saving/retrieving the timing of the dynamic frames to/from a file. If the **Select FRAMES** box is checked when opening the dialog window, it is additionally possible to arbitrarily select a subset of frames for loading. The **Trim durations** button ensures that the end times are not after the following start times.

Enabling Pre-Processing Operations

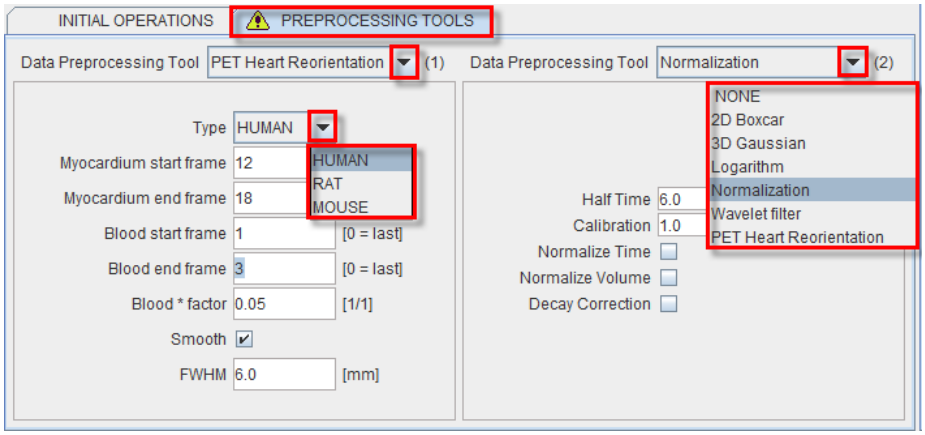
In addition to image reorientations there are several optional preprocessing methods available. On the **INITIAL OPERATIONS** tab the **Operation** selection provides the operations shown below.



The example below illustrates how the last seven acquisitions of a dynamic study can be averaged by selecting the frames sub-range and setting the **Operation** selection from **NONE** to **AVERAGE_VOLUMES (time weighted)**.



The tab **PREPROCESSING TOOLS** makes available two successive filters and a reorientation facility for the heart studies as illustrated below.



The purpose of **Normalization** is to transform reconstructed counts into activity density values calibrated in kBq/cc. The following parameters are needed for the calibration process:

- **Half Time** is used for a correction of the physical decay to the acquisition start. If the SPECT counts are already decay corrected, set **Half Time** to a big value to avoid an additional correction.
- **Calibration** is a factor for the conversion of the measured SPECT counts - which represent only a fraction of the emitted photons - into the true number of physical decays.
  The calibration factor can be determined using a phantom filled with a known, representative activity concentration. Phantom images are acquired, corrected and reconstructed using the same protocol as the research study. Then, the image values are decay corrected, time and volume normalized, resulting in images with SPECT counts per ml per second. As the next step, a homogeneous VOI is outlined and the average pixel value calculated. Finally, the calibration factor is calculated by dividing the known true phantom activity concentration by the VOI average.
- **Normalize Time** is a flag indicating whether the values in the file are already average counts per time (.ie. not total accumulated counts during the acquisition). If your image files just contain counts, check this box, and the image values are divided by the acquisition duration.
- **Normalize Volume** is a flag indicating whether the values are already counts per unit volume. If not, check this box, and the values are divided by the image voxel size (known from the image header).
- Decay Correction: Apply a decay correction to scan start.

Note: The preprocessing tools are plug-ins and must be configured in the main configuration dialog.

The **PET Heart Reorientation** is a facilty that allows heart images re-orientation in short axis during loading. The following parameters need to be defined:

- **Type** is representing the heart model type and can be selected from the available selection list: **HUMAN**, **RAT** or **MOUSE** according to the image to be analyzed.
- **Myocardium start frame** and **Myocardium end frame** are used to define the frames average range for creating the myocarium averaged image.
- **Blood start frame** and **Blood end frame** are used to define the frames average range for creating the blood averaged image.
- **Blood*factor**: as there may exist some activity in the cavities, a fraction of the blood volume image can be subtracted to improve the contrast. In the example above a fraction of 0.05 of the blood averaged image will be subtracted.
- **Smooth** and **FWHM**: optionally, the blood and myocardium averaged image can be smoothed with a 3D Gaussian filter with full-width half maximum value defined in the FWHM text box.

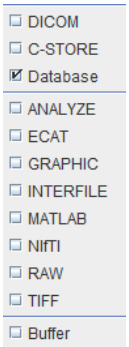
Image Data Saving

There are three types of image saving procedures:

- **File formats**: The user selects a file format and the directory wherein the image files are saved.
- **C-STORE:** The images are directly sent as DICOM objects to a DICOM server.
- **Database:** The images are saved to one of the configured databases (local or remote). To do so, they are converted to DICOM.
- **Buffer**: The images are saved to the buffer and can be loaded in any module with the **Buffer** option for loading.

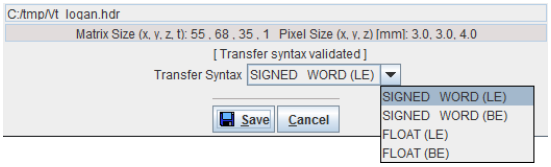
The saving of image data is in analogy to the data loading operation. It can be started from the application **File** menu or from a **Save** multi-function button

with the selections



File-based Saving

Saving as a file involves selecting a destination directory and specifying a file name. In some cases further input is required and an additional dialog box pops up. For the **Analyze** and **Raw** formats a dialog such as



is shown and requests the definition of the number encoding in the **Transfer Syntax** selection.

The accuracy of the data representation - and the disk space requirements - increases from top to bottom. If the dynamic range in the images is large, you are recommended to use a **FLOAT** format. For PMOD the number encoding does not matter. For other programs,

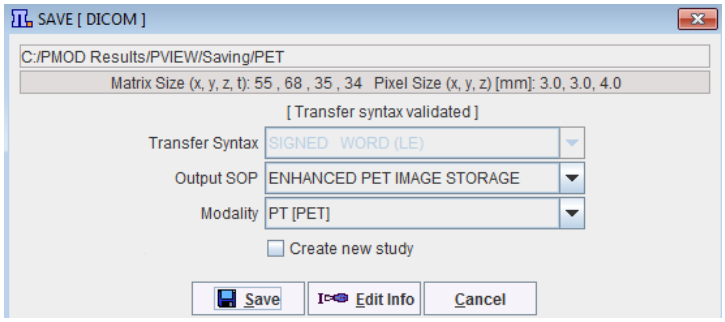
however, there may be preferred formats. **BE** and **LE** are related to the *byte ordering* which is different among processors (LE = little endian, on Intel and DEC Alpha processors; BE = big endian, for most other processors).

The **Transfer syntax validated** string is shown in case there is no precision loss for the selected transfer syntax. Otherwise (for the **Raw** format when saving short to byte or float to short) a warning message **Selected transfer Syntax will cause rounding error** is shown.

DICOM Part 10 Data, C-STORE

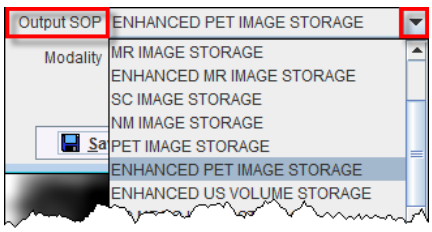
DICOM Part 10 Saving

When storing the data in **DICOM** (part 10) files, a first dialog window appears to select the destination directory and to define the name of the created DICOM file(s). Then, a second window appears.



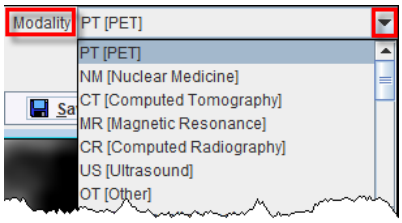
It allows defining the DICOM Image Information Object type into which the data will be stored.

The **Output SOP** determines compatibility with other systems that may not support all types of objects. The list contains all DICOM IODs supported by PMOD. Initially, a suitable definition is proposed, but the user may change the list selection. For RGB image data and screen captures only Secondary Capture (SC) objects are available as an **Output SOP**.



Please see our **DICOM Conformance Statement** for details.

The **Modality** type is just a descriptive string. It can be selected from the long list of modalities that are defined in the DICOM standard:



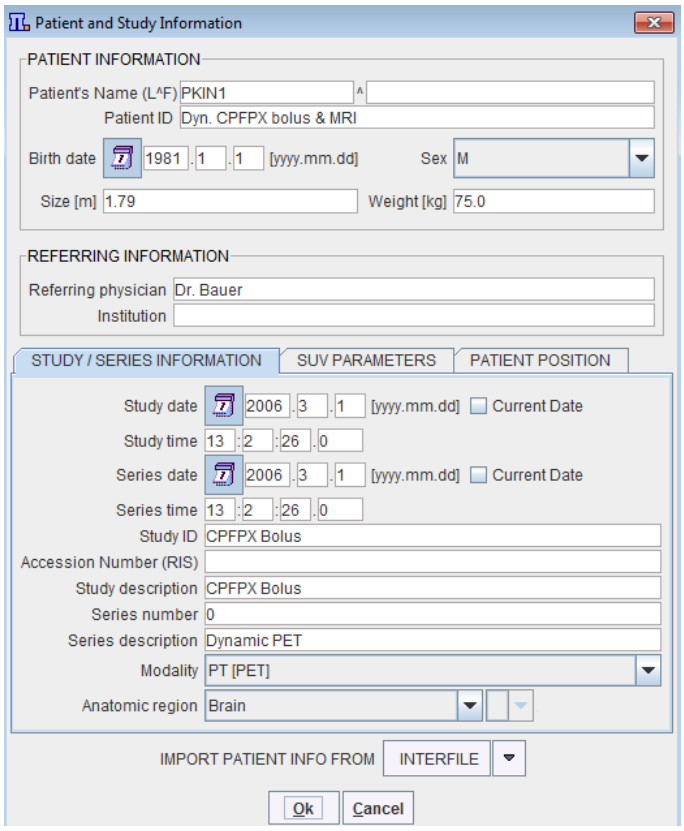
The **Create new study** box is only relevant for data originally loaded in DICOM:

- If the **Create new study** box is checked, PMOD generates new study UIDs when saving the DICOM objects.
- If the **Create new study** box is not checked, PMOD uses the study UIDs of the original data when saving the DICOM objects. In this case please do not change patient or study level information with **Edit Info**. Otherwise the receiving system may create a new study anyway.

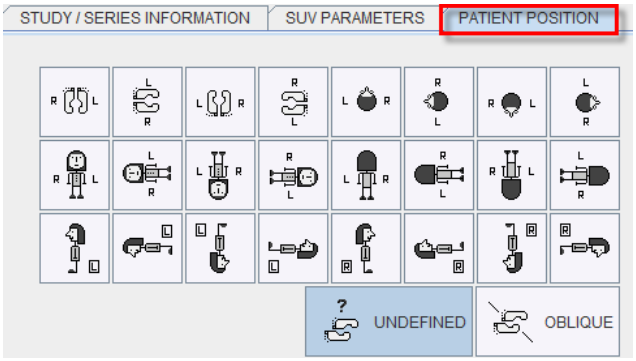
For non-DICOM data PMOD will always generate new study UIDs.

Editing DICOM Information

DICOM has the ability to save administrative information with the image data. By activating the **Edit Info** button some of the important attributes can manually be edited:



The elements on the **SUV PARAMETERS** pane are explained in the SUV section ***below*** (on page 127). The **PATIENT POSITION** panel contains an array of buttons which allow defining (or correcting) the patient orientation.

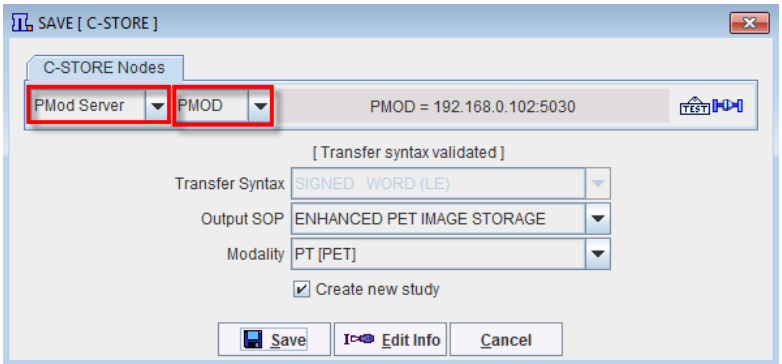


Note that after activating one of the buttons the anatomical annotations in the image overlay are adjusted. Please identify the button which generates an appropriate labeling. This information will then be saved with the data.

The buttons should only be needed for data loaded in other formats than DICOM, or if there was not enough orientation information in the loaded DICOM data. This situation is clearly indicated by the lack of anatomical annotations. If you are not sure about the anatomy, please use the **UNDEFINED Patient Position** button.

C-Store

When storing the data in **C-STORE**, a similar dialog window appears as for DICOM saving, but included is also a list of DICOM servers to which the data can be sent.



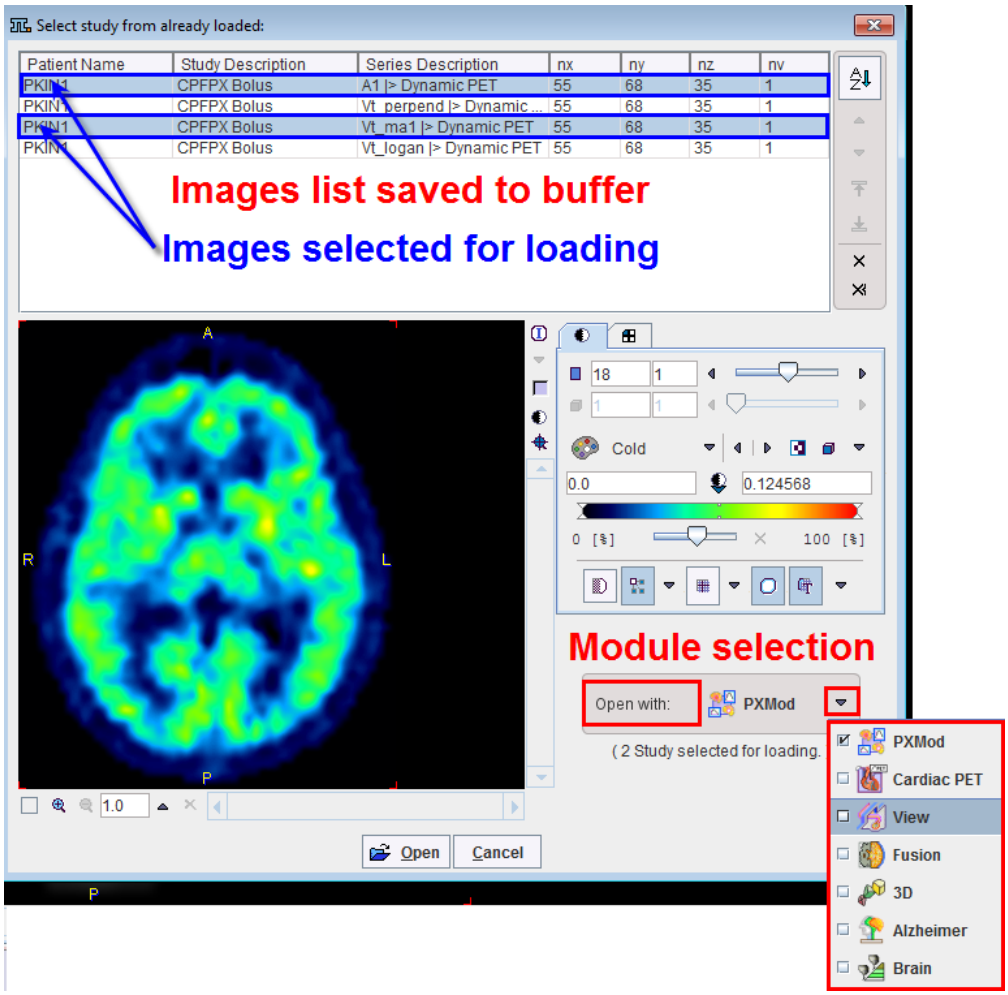
For details regarding DICOM support in PMOD please refer to the PMOD DICOM Conformance Statement.

Database Saving

The saving of images into a PMOD database is described ***above*** (on page 66).

Buffer Saving

Saving to the buffer does not involve selecting a destination directory or specifying a file name. All the images processed in, e.g., the **View** module can be saved to the **Buffer** and then loaded in a different module with **Load** from **Buffer** option. Additionally, a new module can be opened during the loading from buffer procedure as shown below:



When **Load** from **Buffer** is activated a dialog window as above appers. In the uppermost part the images saved to buffer are displayed. More then one image can be selected with CTRL + click. On the right side of the image preview display, an **Open with** button allows choosing the module where the selected images are going to be loaded. Finally, click **Open** to load the images.

Component Data Loading and Saving

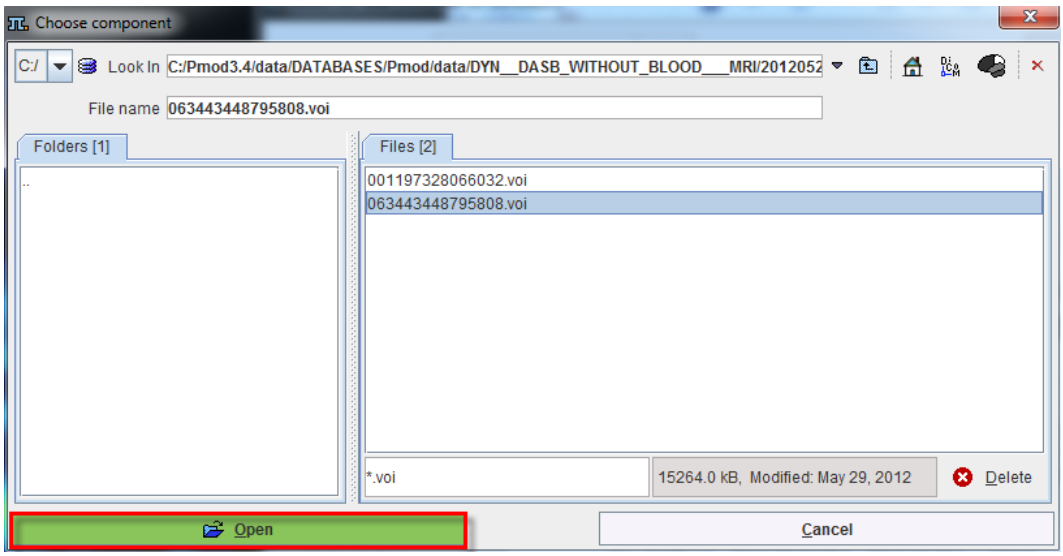
Component data such as pixel-wise modeling protocols (.defpmod), volume-of-interest definitions (.voi), kinetic modeling files (.km), matching transformations (.mat) etc. can be saved as disk files or database data using the component saving buttons in the user interface.

If the database option is active, the database loading/saving dialog always appears first.

Loading/Saving without Database Option

Loading

If there is no database installed or it is not enabled for component data, a dialog of the following type appears when loading component data.

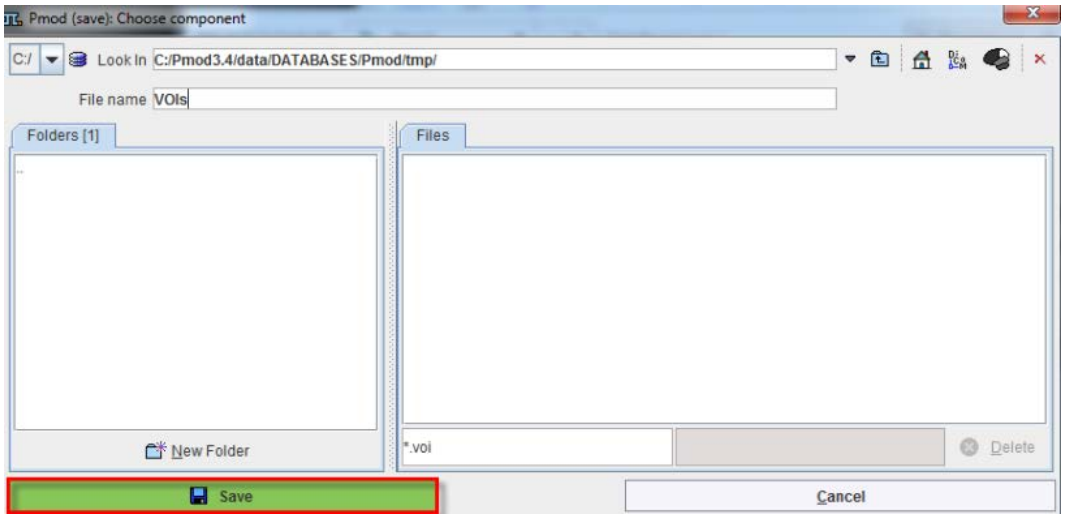


In the upper part the current search directory is indicated. Initially, it points to the directory of the last successful loading operation. To change the search directory, use the navigation buttons in the **Folders** section (**..** indicates up one level).

All files suitable for loading (having the right suffix, such as .voi for VOIs) in the search directory are listed in the **Files** section. The **Open** button starts loading the selected file, **Cancel** quits the operation, and **Delete** erases the file from the disk.

Saving

When a component is saved, a dialog appears which is very similar to the loading dialog.



It has the same elements for changing the directory. The **File name** field allows specifying a name for the new data file, and the **Save** button will start saving.

Loading/Saving with Database Option

Database ***loading*** (on page 64) and ***saving*** (on page 67) of component data is described above.

Loading of Vector Data

The input of vector data is required at different places. The most important example is kinetic modeling where the plasma and the whole blood curves are time vectors. Another example is quantitative autoradiography whereby a vector contains the table to convert from optical image units to radioactivity density. Such data is expected as a two-column text file in the form below.

sample-time[time_unit]	value[value_unit]
0.0	0.0
1.0	27.0
2.0	123.1
...	...

Typical time_units are **seconds**, **minutes**, and **hours**. Typical value units are **kBq/cc** and **uCi/cc**.

Note: The *header line is required* - otherwise the values on the first line will be skipped. If valid units are found in the file header the values are converted to the internal

representation [sec] and [kBq/cc]. If there are no valid units in the header line, the import procedure assumes that the data units are equal to the ones in the configuration settings of the tool.

Tabular data such as the tissue time-activity curves in kinetic modeling can be loaded from a text file with multiple columns in the form below.

start[time_unit]	end**[value_unit]**	frontal	temporal	cerebellum
0.0	10.0	0	0	0
10.0	20.0	12.3	13.5	7.8
20.0	30.0	28.6	31.9	15.5
...	...	...	...	...

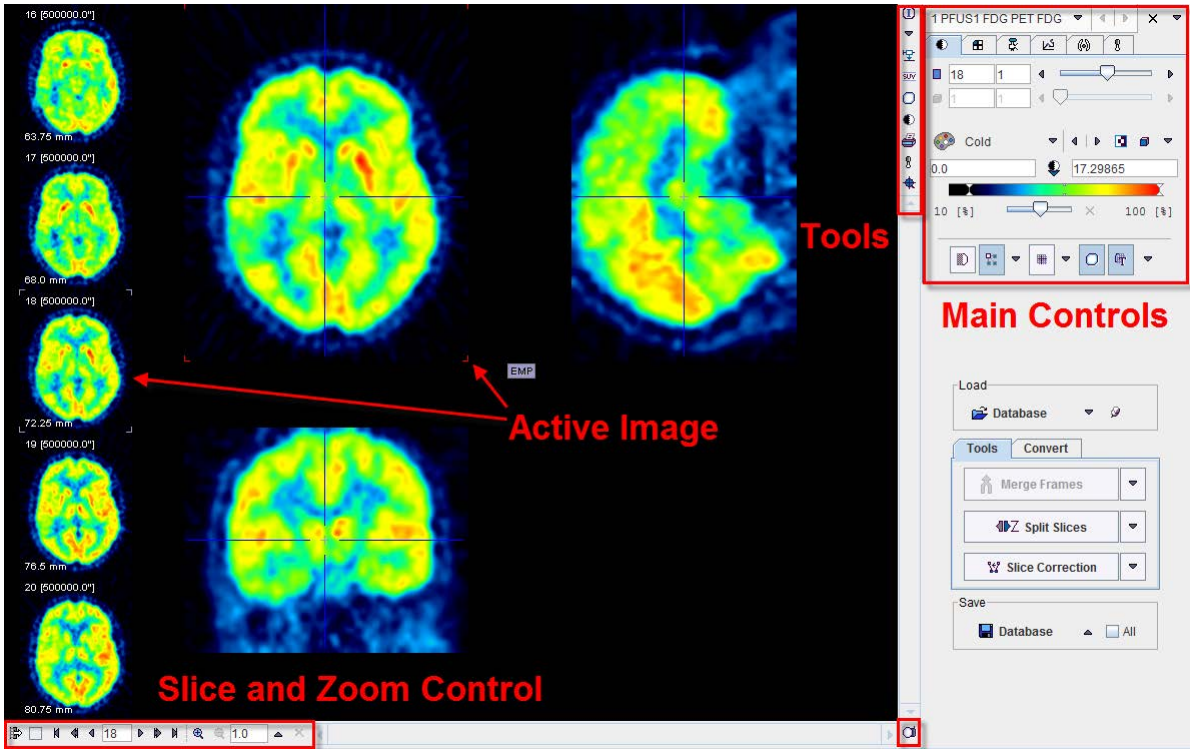
Again the header line is required, and the units are considered if they are recognized. Please note that the activity units are defined *after the header of the second time column*, not after the first value header.

Such files can easily be prepared in text editors, or with MS Excel and saving as a **tab delimited text file**.

Chapter 5

Image Display and Basic Processing

The same image display object is used in all PMOD tools. It consists of an image viewport, ie. the black area for the images, a set of image presentation and layout controls to the upper right of the viewport, and some tools grouped along the image.



The viewport shows one or several images of a series, depending on the image layout which can be modified by use of controls. Most PMOD tools allow for loading more than one image series. The image display may then be switched between the available series with the selection at the top of the controls, eg.

There are two arrays of buttons next to the images themselves. The vertical row in the upper right presents auxiliary tools for inspecting the image data currently displayed. Their functions are:

	Shows information related to the displayed image series and also allows changing timing and patient/study information.
	Selection between the stacked image series.
	Start the **Data Inspector** to examine the pixel values, time vectors of dynamic studies, the acquisition times, standard uptake values (SUV), and the origin.

	Start the **SUV** page of the data inspector directly.
	Start the **Volume-of-Interest** tool to outline VOIs and calculate statistics on the currently shown images.
	Start the **Large View** tool which allows looking at the same images but in a maximized viewport.
	Button to **hide/show** the image controls. Hiding the controls after the images are in a suitable presentation has the advantage of a larger viewing area.
	Generate a **Report** for printing or saving.
	Activate the mouse-operated **zooming** mode.
	Show the external tools list.

The horizontal button row in the lower left embodies the following functions (starting from the left):

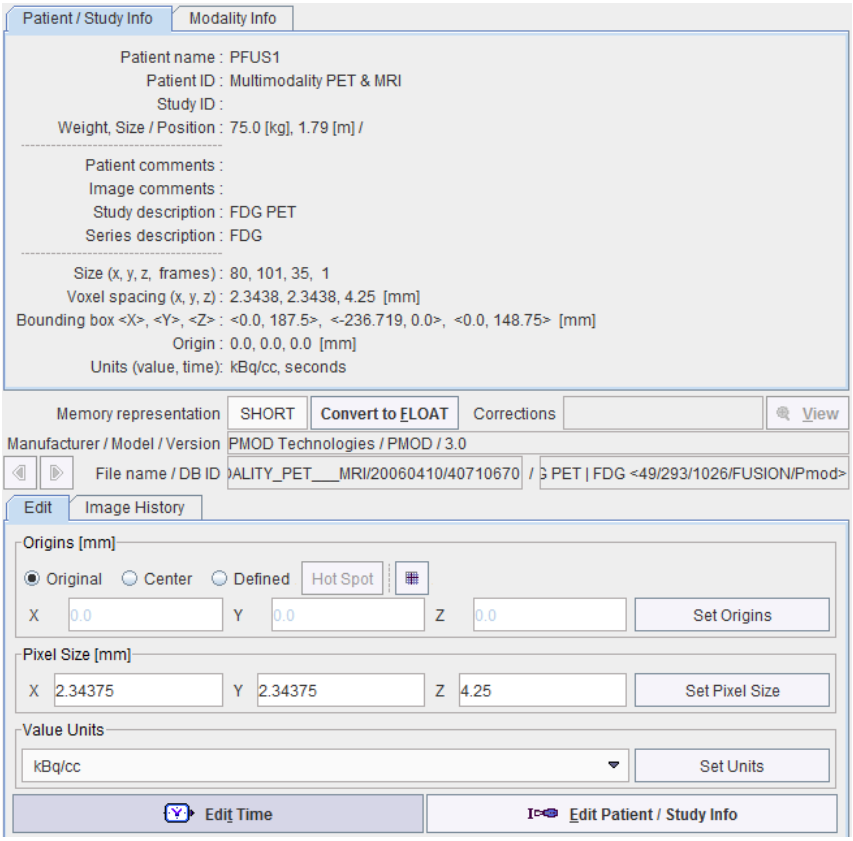
	This toggle button enables/disables the **preview** of slices neighboring the active one along the left side of the image viewport (in 1x1 and orthogonal layouts only).
	This box is only functional for **dynamic** studies. In this case the user can select between stepping through the slices at a certain time (no check), or through the times for a fixed slice (check).
	Buttons to step backward/forward in increments of an slice or a page (for multi-image layouts), or to jump to the begin/end. Entering a number allows positioning the display immediately. Note that slice scrolling can also be done using the mouse wheel.
	Buttons for zooming and resetting the zoom. The sliders appearing in zoom mode below/besides the image allow positioning the zoomed images.

The image presentation can be modified in many ways by means of the control panels, which can be brought forward by clicking on the corresponding tab. Note that depending on the context some of the panels (e.g. oblique reslicing) and buttons may be missing.

In This Chapter

Viewing and Changing Study Information

In PMOD, each loaded image series has a set of attributes. Depending on the loaded image format they may be partly empty. Using the button, the information can be shown in a dialog window as illustrated below, and edited.



Note that after changing information the data set needs to be saved to make the changes permanent.

Modality Info

If information regarding **Tracer activity** and **Dose** are stored in the original image file, these informations are available in the **Modality Info** tab.

Image Properties

Memory Representation

Images with short **Memory representation** can be converted to **float** by the **Convert to Float** button. This requires more RAM, but avoids rounding problems.

Edit the Image Origin

The **Origins** area shows the coordinate of the image origin and allows setting it to a different location. The origin is relevant for the definition of volumes-of-interest, because they are

defined relative to the origin. They are also relevant for image fusion. In hybrid imaging, the origin of the different modalities is set to the same anatomical location, so that the images can be aligned by simply aligning the origins. An origin of (0,0,0) indicates the upper left corner of the first slice.

The **Origins** radio button has three positions with the following meaning.

- **Original**: With this setting the origin obtained with data loading is used. This is the standard setting.
- **Center**: By selecting this button and activating **Sets Origins**, the center coordinate of the data volume is defined as the new coordinate origin.
- **Defined**: When this button is set, the origin coordinate can be entered manually into the **X**, **Y** and **Z** fields, for instance the values from an other study. As an alternative, the triangulation point can be set to the intended location of the origin, and then the button **Get from Hotspot** activated. This will transfer the triangulation coordinate to the origin to the pixel. **Sets Origins** has to be activated for making the coordinates actual.

Edit the Pixel Size

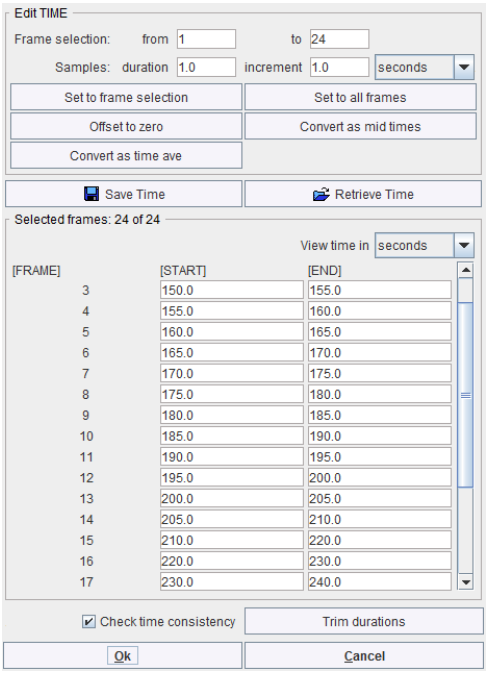
The **X**, **Y** and **Z** fields of **Pixel Size** shows the current pixel size. To change them edit the values and then activate **Set Pixel Size**.

Edit Value Units

The **Value Units** selection contains the list of supported image units. To change the units select the correct unit from the list, and then activate **Set Units**. Note that only the interpretation of the values is changed, but that there no scaling applied to the data values.

Edit Acquisition Times

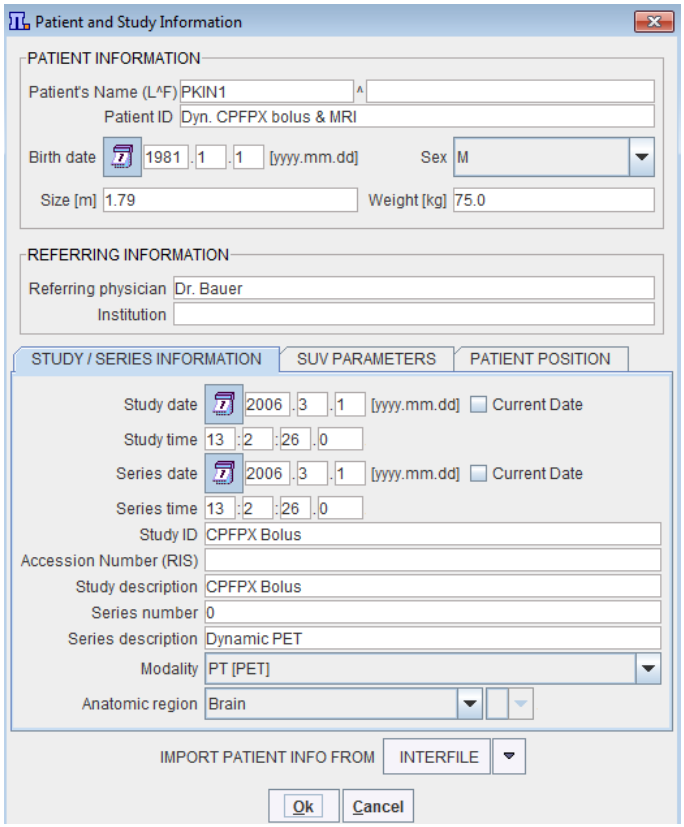
Correct acquisition times are very important for using dynamic data in a quantification process. The times can be inspected and overwritten using the **Edit Time** button, which shows the dialog window below.



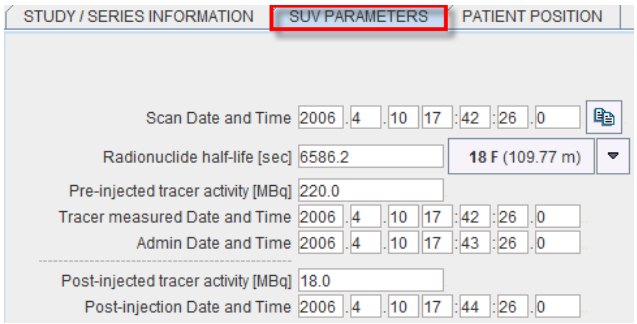
Note the **Save Time/Retrieve Time** buttons which allow saving/retrieving the timing of the dynamic frames to/from a file. If changes are required, the values can be overwritten and then saved with the **Ok** button.

Patient, Study and SUV-related Information

To modify the study information use the **Edit Patient/Study Info** button which displays the following data editor:



Note the **SUV PARAMETERS** tab which houses the information relevant for the SUV calculation. All these fields must be completed. For more information please refer to the section ***Inspecting SUV Values*** (on page 127).



If the anatomical annotations are not correct, for instance because wrong patient positioning information was entered at the acquisition console, the **PATIENT POSITION** tab can be used for correction purposes. The buttons represent the view when looking at the transaxial images. As soon as a button is activated, the annotations in the images are adjusted.

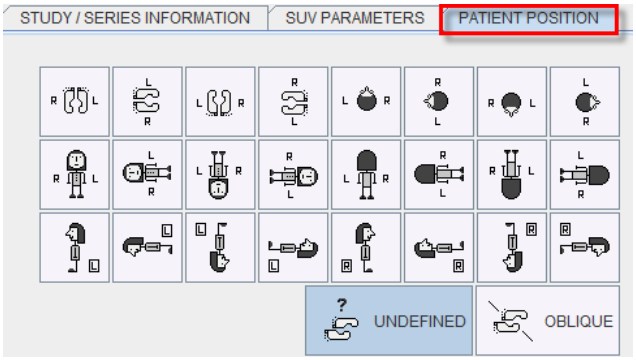
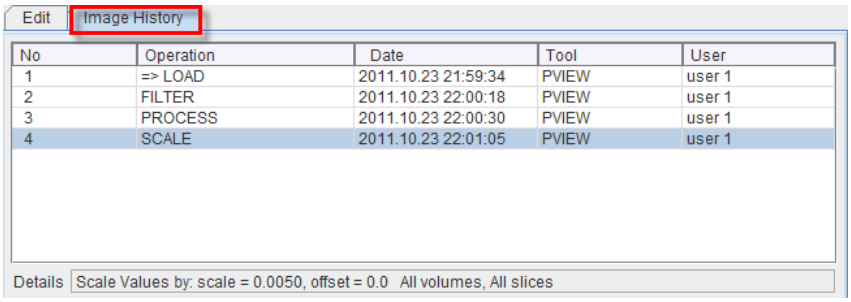


Image History and Macros

PMOD keeps a record for all operations applied to an image in a structure called **Image History**. The history starts with loading the data, and then a sequence of operations for which the following information are recorded:

- The **Operation** name.
- **Date** and time when the operation was applied.
- The PMOD **Tool** in which the operation was performed.
- The PMOD **User** who performed the image analysis.
- The **Details** of the operation such as filter sizes, rotation angles etc.

An example history is shown below.



The information can be printed or saved as an image using the **Print Report** button.

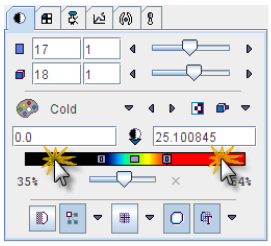
Macros

In some situations, the user may have to repeat the same sequence of image transformations with many data sets. In this case, he can convert the image history of a representative data processing session into a macro by saving it with the **Save Macro** button.

Macros can be applied as a data transformation during ***loading*** (on page 89) or in pipe processing.

Changing the Image Presentation

The first tab in the main controls contains most functions to modify the way how the images and the overlay information look like.



Control of Slice(s)

The slice control section allows scrolling through the images using the increment buttons, the slider, or directly by entering a slice number. The value right to the number of the active slice controls incrementing. This is particularly relevant in multi-image layouts. For example, if the increment value is set to 2, only every second image will be displayed.

Instead of selecting slices using the controls, the user can also scroll slices by dragging the left mouse button over the image holding the `CTRL` key in the `Up/Down` direction (see the summary of shortcuts below), or with the mouse wheel.

The frame control section only becomes active for dynamic studies with multiple time frames and behaves the same way as the slice control. To allow for mouse-operated scrolling over time, the time box on the left side below the image must first be checked.

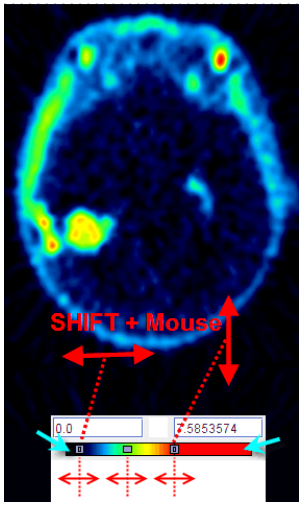
Note: There is a quick way for jumping to the particular slice/frame containing the maximal pixels value: just click the buttons / next to the slice/frame selection.

Color Tables

There is a selection of pre-defined gray and color tables which can be chosen with the list selection.

Note: A new user defined color table can be simply be added. Create a 3-column text file with the RGB values and saving it to the sub-directory *resources/colortables* (see the examples there). They are appended to the lower section of the color table list such as **PETCT** in the example above.

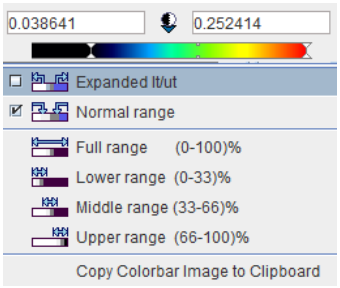
A minimal/maximal threshold value defines the range of displayed values. The thresholds can be entered numerically, or the handles in the color bar can be dragged with the mouse. Additionally, the user can modify them by dragging the left mouse button over the image holding the `SHIFT` key. `Left/Right` movements modify the lower threshold, while `Up/Down` movements modify the upper window.



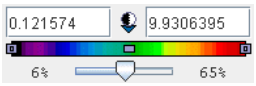
Note: Double-clicking into the lower end of the color bar sets the lower threshold to zero. Double-clicking into the upper end of the color bar sets the upper threshold to the maximum.

Zooming into Color Table

In some cases, the range of image values of interest only covers a small part of the color bar which makes it difficult to adjust the brightness precisely. In this situation, the user can zoom the color bar into the current sub-range of values. Clicking the right mouse button into the color bar pops up the context menu



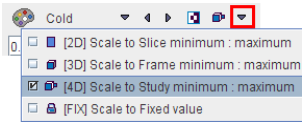
The first menu entry **Expand lt/ut** then performs the desired task and makes the color bar change to



The second entry performs the reverse operation, and the other entries are just shortcuts which may be helpful. The last option in the list allows copying the colorbar image to clipboard.

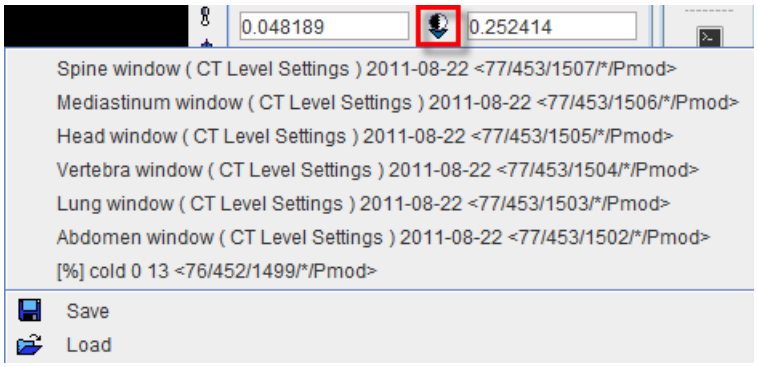
Color Table Modes

Several modes are available for the color table application. They can be selected using the option button



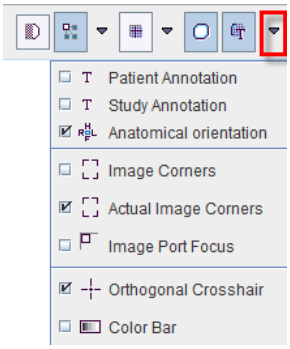
The different modes are:

	**Inversion** of the color table order.
	**Slice mode**: The same % threshold is applied to each individual slice. Hereby the dynamic color range is fully exploited per slice. However, *the same color will represent a different value in different slices*. Therefore, this mode is not recommended in most cases.
	**Frame mode**: With this setting, the minimal/maximal value in an entire frame is determined, and the % threshold applied to them. As a consequence, the colors

	represent fixed values when inspecting the slices of a frame. However, as the absolute minimal/maximal value will vary at different times of a dynamic acquisition, the *same color will most likely represent different values when comparing different frames*. This setting is recommended for static studies.
	**Study mode**: With this setting, the minimal/maximal value in the entire series is determined, and the % threshold applied to them. This setting is recommended for dynamic series and movies because the same color represents the same value at all times and in all slices.
	**Fixed mode**: This setting allows the user entering arbitrary minimal/maximal values which need not belong to the data range.
	This button allows saving or retrieving a color table configuration. During saving a dialog windows appears allowing to choose the thresholding save option: **% Maximum-Minimum** or **Absolute values.** Finally activate **OK** to save the level settings. Different level settings can be define and saved in the database as **Absolute values** for CT images and used for CT image presentations. These settings are available on the list when the button is selected. Alternatively, the predefined color properties can be retreived from the file system selecting the **Load** button. 

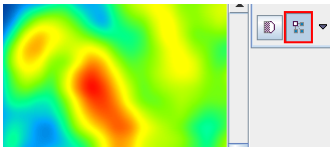
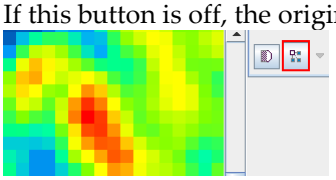
Information Overlays and Image Smoothing

The lowest row contains several control buttons.



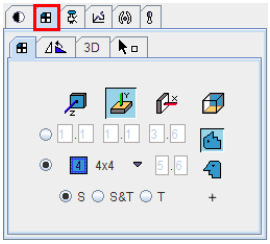
All of the buttons can be on or off, and some might have some configuration options attached. Their functionality is:

	**Smoothing:** Enables a temporary 9-point smoothing filter. The smoothing is only for display

	purposes and does not affect calculations.
	**Interpolation:** Enables image interpolation. Interpolation is needed because in most situations the resolution of the display viewport differs from the original image matrix.  If this button is off, the original rectangular pixels are shown.  The three interpolation options are **Triangle**, **BSpline**, **Mitchell** (Default). **Note:** the smoothing/interpolation functions serve only for image display enhancement. Statistical analyses are always performed with the original pixel values.
	**Grid:** Enables a grid centered at the origin of the data set. Bold lines indicate the location of the image origin. The grid size can be defined by the option (50,20,10,5,1mm or from 1 pixel to 10 pixels with 1 pixel increment).
	**VOIs:** Enables the displays of VOI contours, if there have any been defined for the current series.
	**Overlay:** A toggle to **switch off all overlay information at once**. Its option menu allows defining the level of information included in the overlay display as illustrated above.  : This option enables Display of the anatomical annotations in the images: H - head, F - feet, A - anterior, P - posterior, R - right, L - left For oblique orientations the letters are combined whereby the first letter indicates the direction closest to the current row/column direction. Allows displaying the colorbar selected for the image.

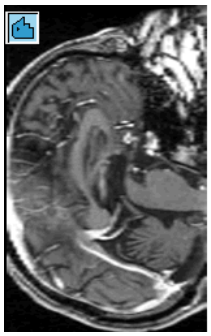
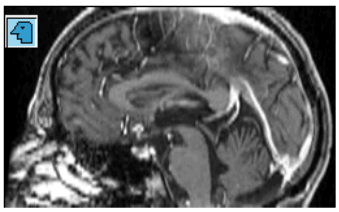
Configuring the Layout

Volumetric images can be displayed in many different ways in the PMOD tools. The layouts are accessible by the second control tab, on the first sub-tab **Layout.**



Slice Orientation

The buttons in the first row allow defining the orientation of the displayed images.

	**z-Plane:** Corresponding to the major slice orientation of the loaded data. Usually *axial* images. Keyboard shortcut: `CTRL+Z`.
	**y-Plane**: Usually the *coronal* images. Keyboard shortcut: `CTRL+Y`.
	**x-Plane**: Usually the *sagittal* images. Keyboard shortcut: `CTRL+X`. The x-plane image can be shown in two different ways depending on the modifier buttons.  
	**Orthogonal Planes:** Layout showing three orthogonal slice images. The intersection point can be moved by clicking into the images.

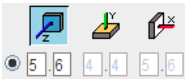
The plane orientation can rapidly be switched by first activating an image (click into image), and then entering the keyboard shortcut.

The direction z, y or x indicates the normal to the shown plane shown. The y-, x- and orthogonal buttons are not active if the study is planar only and can thus not be resliced in an other than the original direction.

Tiling Layouts

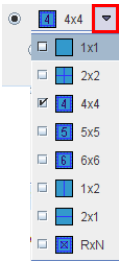
The second and third rows allow configuring the number of images shown concurrently.

If the radio button in the second row is enabled, a dedicated row x column layout is used for the different orientations.



This is particularly helpful for a whole-body study where the coverage in z is much larger than in the other directions. The definition of the layout per plane orientation is done in the particular tool configuration .

Otherwise, if the radio button of the third row is enabled, the same layout is applied for all orientations and the arrangements are accessible through the selection



Keyboard shortcuts allow to quickly switch arrangements. After clicking into an image enter

- `CTRL+1` for 1x1
- `CTRL+2` for 2x2
- `CTRL+3` for 3x3
- etc.

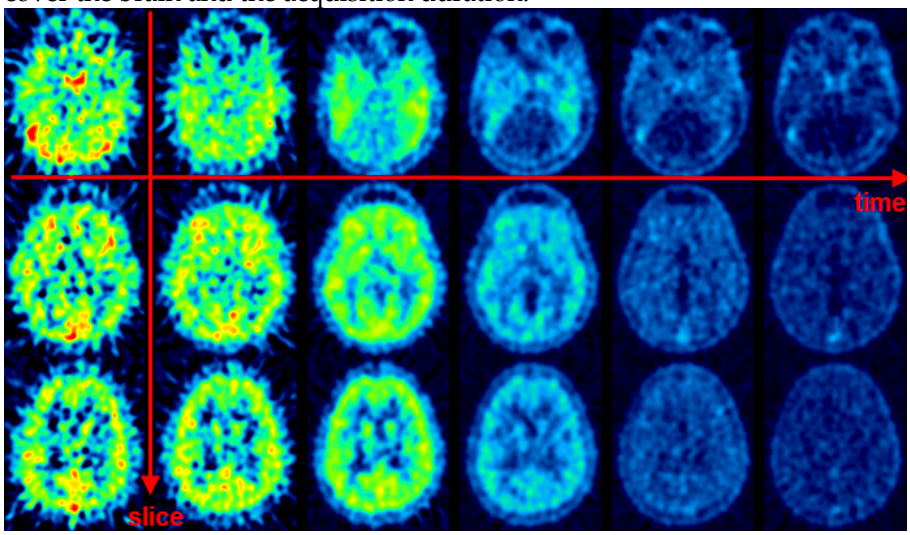
To change from a tiling layout to 1x1 just click on the image to be enlarged holding down the `CTRL` key. To change back to the multi-image layout just `CTRL` and click once more.

The radio button in the fourth row is only applicable for image tiling with dynamic studies.

If the radio button is in the position of

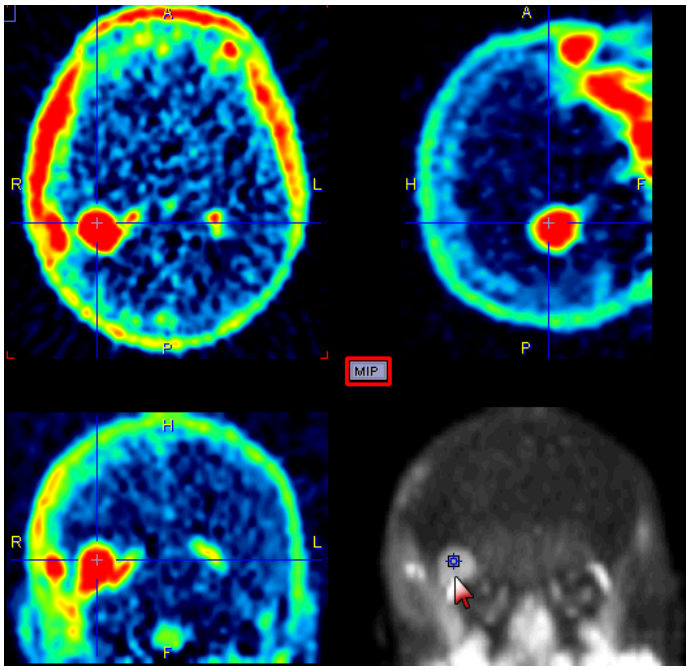
- **S**: only slices acquired in a single time frame are shown in the image window.
- **T**: only the images of a single slice are shown at different acquisition times.
- **S&T**: the images are sorted by slice (vertically) and time (horizontally). Consequently each row corresponds to a slice at different times, and each column to the slices of an acquisition. An example is shown below. Note that increments >>1 have been set to

cover the brain and the acquisition duration.

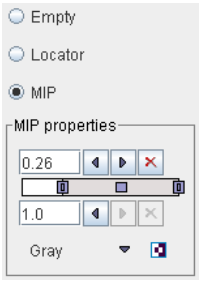


Orthogonal Layout

If the orthogonal layout is selected, three quadrants show the orthogonal slice images intersecting at the point indicated by the cross centered in the blue slice indication lines (triangulation point). As soon as the user clicks into an image, the images are updated by the slices intersecting at that new point.



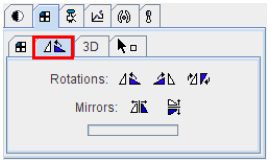
The fourth quadrant is available for different information. It can be configured by activating the button located in the upper left corner of that quadrant, indicated in red in the screen capture above. A dialog appears



which lets choose between an **Empty** quadrant, a **Locator** display showing the slices location schematically, and a **MIP** (Maximum Intensity Projection)**.** Note that there is a marker in the MIP image, which indicates the current slices intersection. It can be moved, and the slice images will follow. This function may be helpful to track vessels showing up highlighted in the MIP.

Rotations and Mirroring

Image reorientation operations such as mirroring and rotations can be done using the buttons in the dedicated pane.



If the display is in the orthogonal viewing mode, first activate the appropriate plane by clicking onto the corresponding image (holding down the `CTRL` key avoids new reslicing), and then activate the appropriate button.

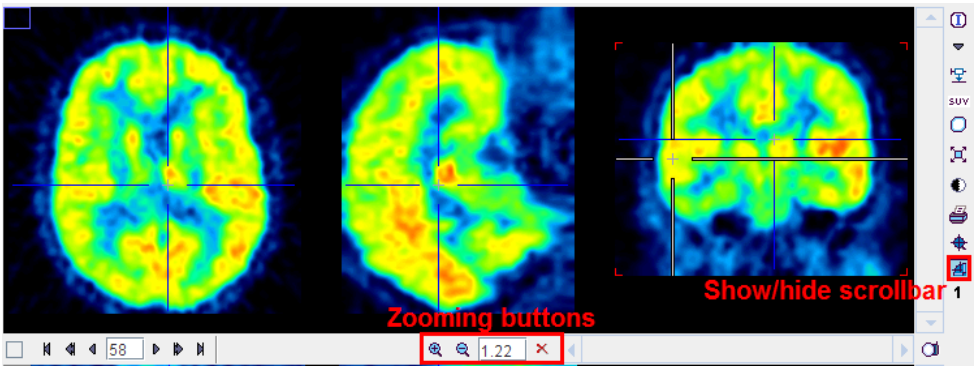
Note: For data with enough information about patient positioning PMOD will keep track of patient orientation and update the annotations accordingly.

Image Zooming

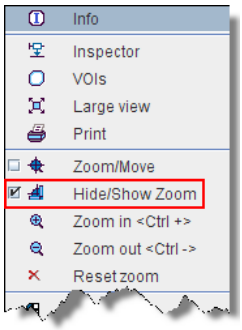
Sometimes it will be helpful to zoom the shown images, for instance during VOI outlining. Image zooming can be operated in different ways

Scrollbar Zooming

Often images ports have a scrollbar area around them. Then the zoom buttons can be used for zooming/shrinking, or a zooming factor can directly be entered. ✕ resets zooming. If the scrollbar is not visible, it can be shown by the indicated button to the image right.



If there is no such button, the image context menu (click right mouse button in image area) can be used instead.



The visible part of the image can be adjusted using the scrollbars around the image which appear as soon as the full image is not visible any more.

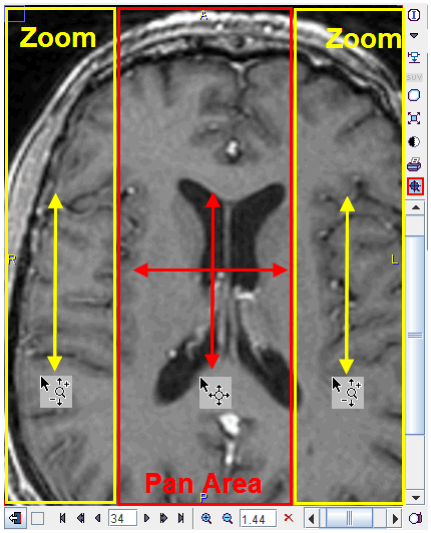
Mouse-driven Zooming

There is also a mode for mouse-driving zooming which can be entered by the button from the image border or the context menu.

When the cursor is moved over the image, it changes its shape:

1) In left and right border area (zooming area) it has a shape. To zoom in/out click the left mouse button and drag up/down.

In the central area (panning area) it has a shape. To adjust the visible part of the image click the left mouse button into the center of the image and drag the image around



After appropriate zooming, the zoom mode should be quit by pressing once more, because some of other mouse-operated functions might not work.

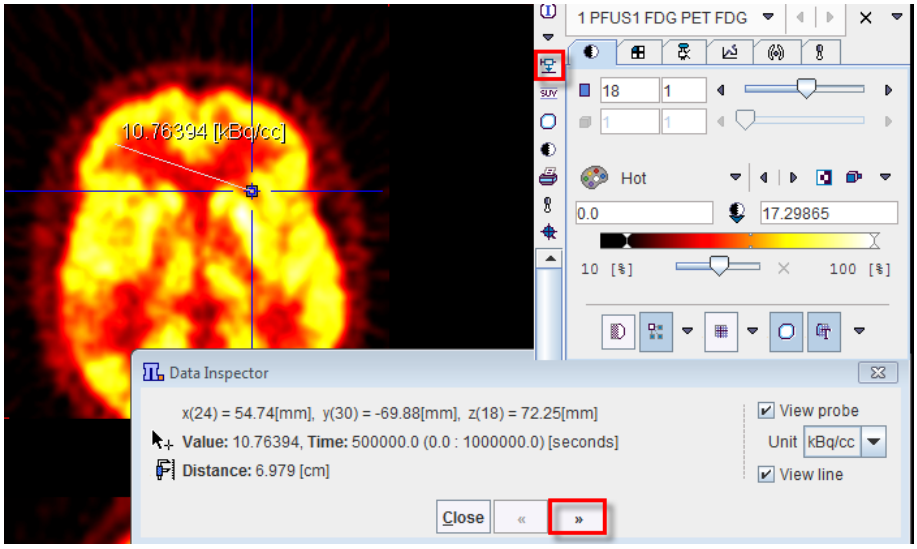
Zooming with Mouse-Wheel

Similar to the zooming mode in other programs PMOD supports zooming with the mouse wheel while holding down the CTRL key. Note that in the orthogonal mode the triangulation point will be kept within the visible area.

Data Inspector

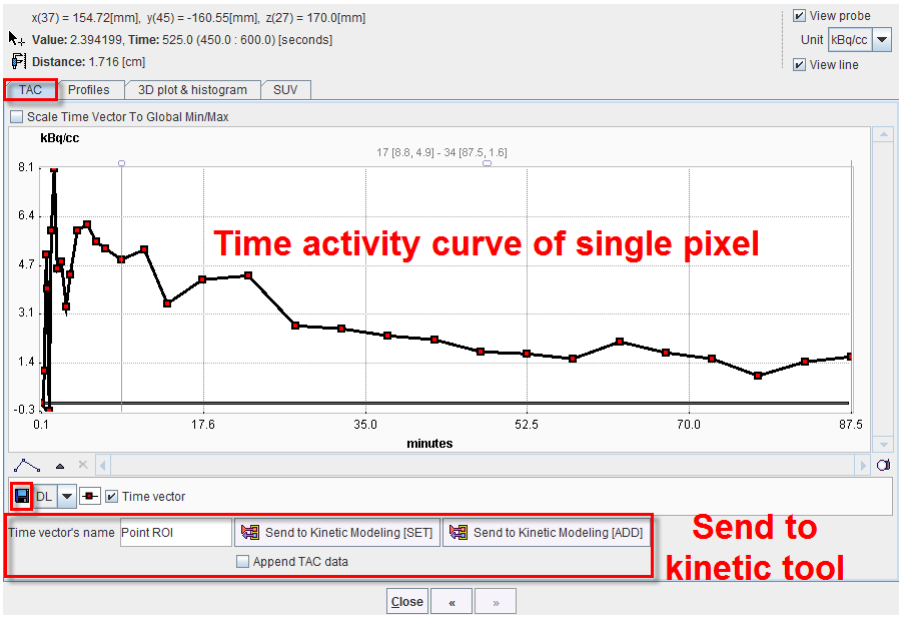
The data inspector tool is opened using the button

and initially shows the dialog window illustrated below.



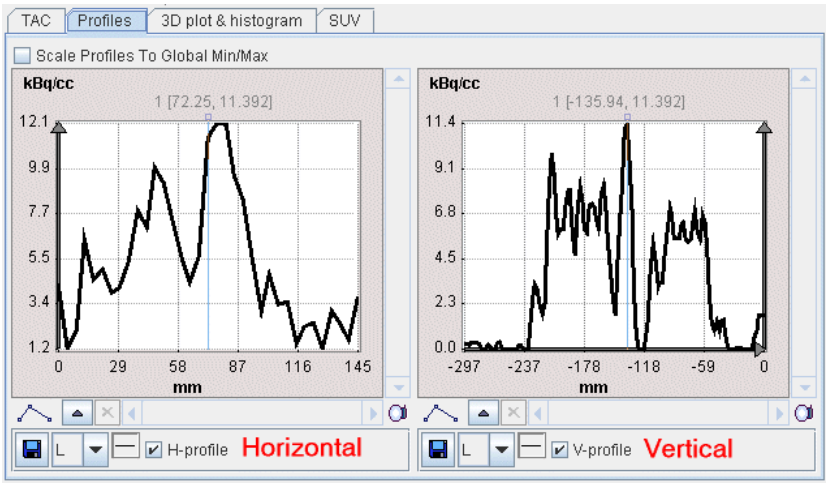
When the cursor is moved over the images, the information about the cursor location (in pixels, and mm from the coordinate system origin) and the pixel value at that location is continuously updated. A locator is shown in the image, marking the last position where the left mouse button was clicked into the image. The distance from the locator to the current cursor position is continuously updated. If the **View line** box is checked, a line indicates the measured distance. If the **View probe** box is checked, the pixel value is also shown close to the cursor and the units displayed. If the **SUV** option is selected in the **Unit** list while **View probe** box is enabled, the **SUV [g/ml]** is automatically calculated and displayed for each pixel. Note that in order to calculated the SUV, the patient weight and size as well as the injected dose are requested.

The >> button extends the dialog window to show more information



Using the **TAC** tab the time-activity curve of single pixels can be inspected (for dynamic studies only) and sent to the kinetic modeling tool. It gets updated as soon as the user clicks at a pixel.

The **Profiles** tab displays the horizontal and vertical profiles at the current location of the locator.



On the **3D plot & histogram** tab a 3D plot and the histogram of the slice values are shown, whereas the **SUV** tab allows to inspect the pixel values in SUV rather than kBq/cc, provided that all activity information is available. The **SUV** tab is explained in the next section.

SUV Value Inspection and Statistics

Standard Uptake Values (SUV)

The information contained in PET and SPECT images is related to the physical concentration of tracer in tissue. If all images distortions are corrected by the reconstruction procedure, the value units are activity concentrations, for instance Bq/ml. The uptake in tissue is dependent on many factors. It is directly proportional to the injected activity, and inversely related to the mass within the tracer can distribute. To calculated a measure of tracer uptake which is better comparable among patients (therefore Standard Uptake Value) the measured activities are therefore divided by the injected dose and multiplied by the (mean) body mass. PMOD supports three variants of this calculation:

1) **SUV Body mass** [g/ml]: Directly uses the patient weight entered in the demographic patient information. This is the mostly used SUV.

SUV Lean Body Mass [g/ml]: First calculates a mean body mass from the patient weight, the height and the gender, which is used in the actual SUV calculation.

SUV Body Surface Area [cm^2/ml]: In this case the uptake is normalized to the body surface area, which is calculated from the weight, the height and the gender.

Additionally, the **Injected dose per cc** [%ID/ml] is available for normalizing the uptake to the injected dose and then multiply with 100.

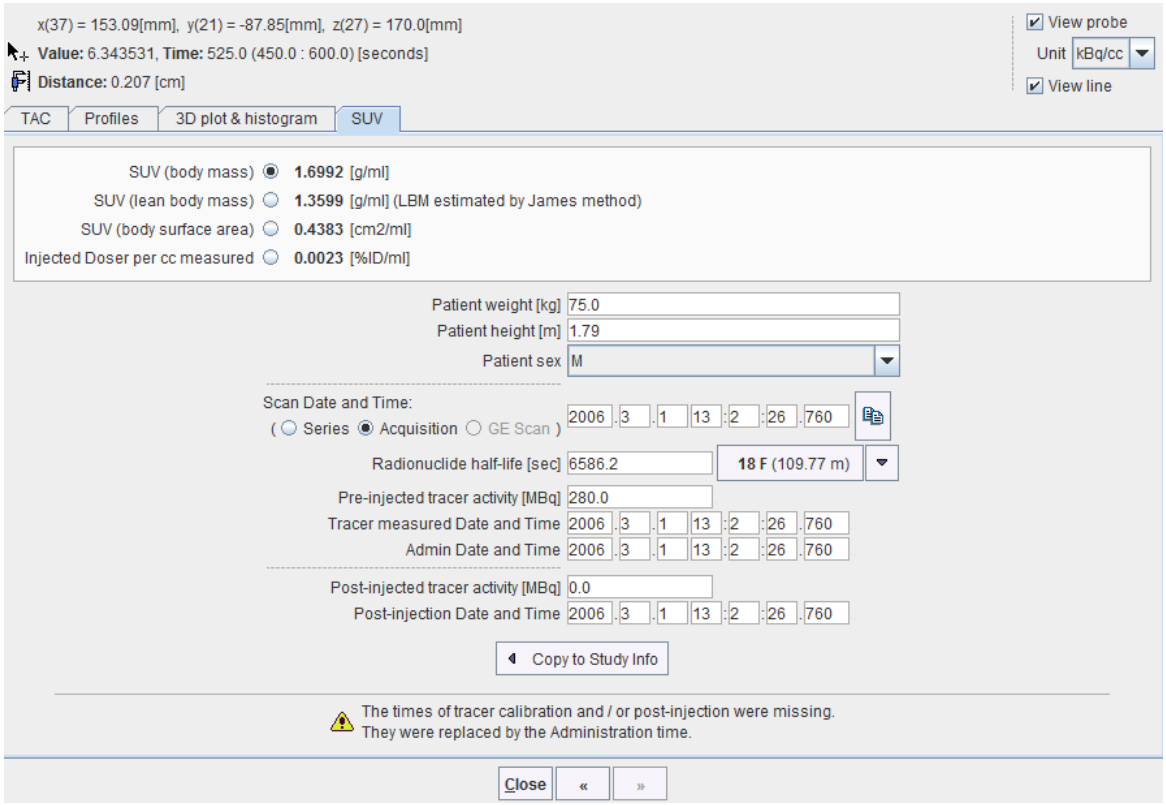
In addition to the patient weight (and size) the SUV calculation has to know the injected dose. For correcting the physical radioactive decay of all activities to the same time the program also requires information about radionuclide, the time of dose calibration, time of injection, the activity remaining in the syringe and when it was measured. Also required is the acquisition start time, because the PET measurements are decay-corrected to the acquisition start.

If all information has been entered by the technicians during the acquisitions, it is directly extracted from the DICOM header. Otherwise, the information has to be completed in a dialog window before the SUV can be calculated.

SUV Value Inspection

The **SUV** (Standard Uptake Value) button

below the data inspector button is a shortcut for opening the data inspector with the SUV tab selected:



The upper part serves for showing the SUVs of the current pixel. The SUV changes when the cursor is moved over the image. Note that the three different types of SUV and the image normalization value respect to the injected dose are displayed simultaneously.

The lower part shows the information which is involved in the calculation of the SUV. It requires that the image units are kBq/cc, and that all information fields in the dialog are filled in. Per default, the scan start time is read from the acquisition time field of DICOM. However, as situations have been met where this information was wrong whereas the series time was correct, the **Scan Date and Time** radio button allows switching to the **Series** time.

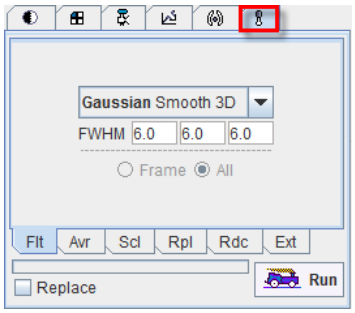
Note that using the **Copy to Study Info** button the information can be saved for later use, and for saving together with the data.

SUV Statistics

The calculation of statistics in SUV units is directly supported on the original image by the ***VOI functionality*** (on page 232), provided that all required information is available. Explicit SUV images can be calculated with the **Calculate SUV Image (on page 132)** external tool.

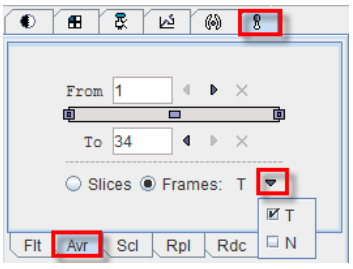
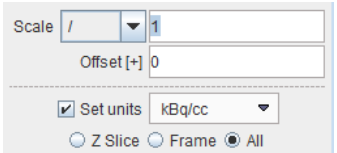
Handy Image Processing Tools

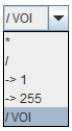
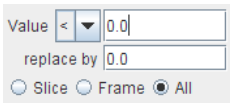
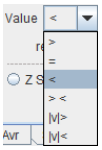
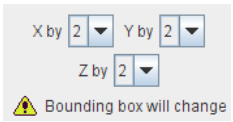
The processing tools pane offers a substantial range of image transformation methods.



The operation principle is that the user selects a particular method by the sub-tab, configures the parameters in the pane, and then activates the **Run** button. In case the replace **Rpl** box is checked, the original data will be overwritten, otherwise a new series is created and added to the list.

Note the button which allows selecting a data format using the arrow down button, and save the image data of the current tab. This save button is missing in the PVIEW tool because the images can be saved using the standard saving button of the tool.

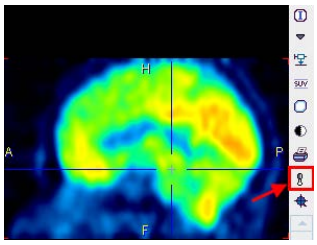
Flt (Filter)	The following image filters are available: ▸▸ **Gaussian smoothing 3D** filter with a full-width at half maximum (**FWHM**) in mm; ▸▸ **Median smoothing 3D** filter with a width in mm; ▸▸ **Canny Deriche 2D** edge enhancing filter; ▸▸ **Median Frames 1D** smoothing filter in the time domain.
Avr (Average)	 There are two variants available: ▸▸ Averaging of a range of **Frames** of a dynamic series.there are two weighting options: divided by time sum **T** (time weighted) or divided by number of frames **N** (means). ▸▸ Averaging of a contiguous range of **Slices**.
Scl (Scale)	

	There are five variants for scaling the pixel values which can be selected from the list  ▸▸ *: multiply with a constant and optionally add an offset; ▸▸ /: divide by a constant and optionally add an offset; ▸▸ **->1**: transform the value range to the interval [0,1]; ▸▸ **->255**: transform the value range to the interval [0,255]; ▸▸ **/VOI**: divide by a VOI average; the VOI has to be saved beforehand and needs to be selected. If **Set units** is enabled, units appropriate for the scaled image can be selected from the units list.
Rpl (Replace)	 This function is for replacing pixel values which satisfy a certain condition by a constant. The available criteria are  larger than (>), equal to (=), smaller than (<) within an interval (> <), absolute value larger than (|**v**|>), absolute value smaller than (|**v**|<), respectively.
Rdc (Reduce)	 Simple function for reducing the number of pixels in each direction. This function is intended for situations where the number of pixels is divisible without remainder by the selected reduction factor. If this is not the case, a warning is shown indicating that the bounding box is changed by the operation, and the **Interpolation (on page 137)** function of the **External** tools should rather be applied.

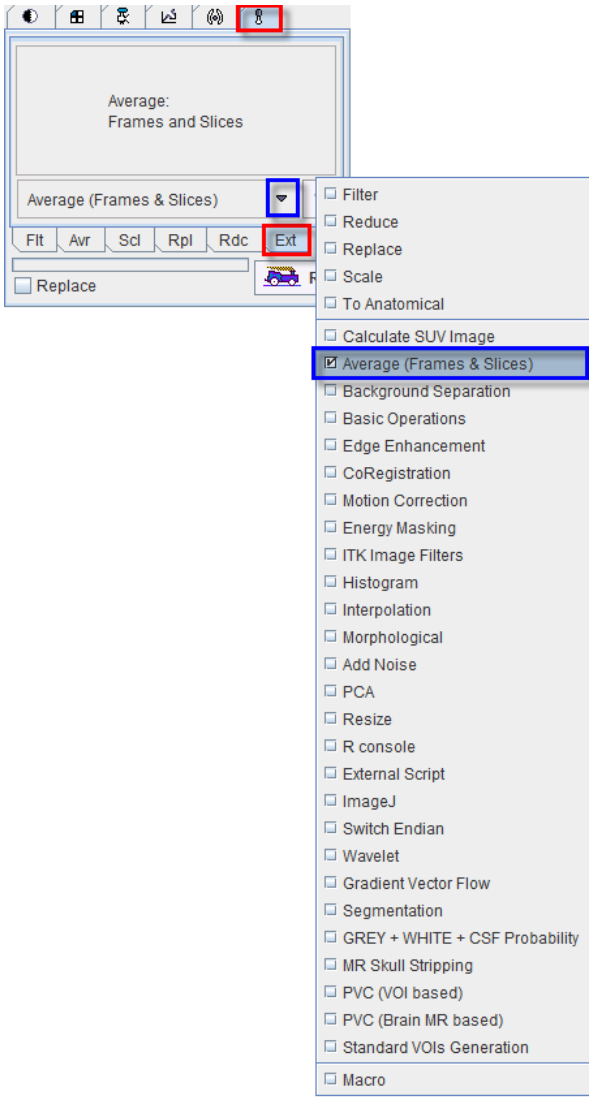
External Tools

External tools are data processing plug-ins which take one or several images as input, and return a result image. The tools can be interactively called on individual data, or they can be changed into a ***processing pipeline*** (on page 338), which can be applied to a whole list of images.

External tools can be called from the image sidebar

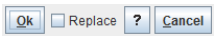


or from the **External** tab in the tools section.



After selecting a function from the list (and activating **Run** in the tool version), a specific dialog window is opened to request the parameters needed for processing.

All tools have the following buttons at the bottom.

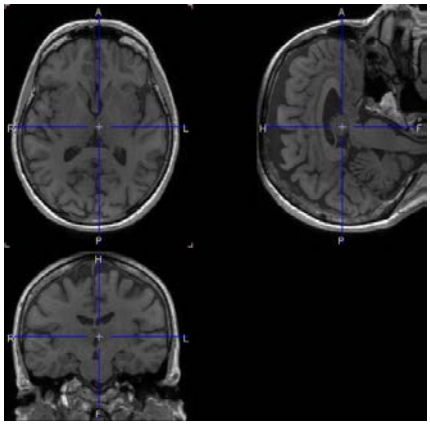


The **Ok** button starts processing. If the **Replace** box is checked, the data are overwritten by the results, otherwise a new image series is created for returning the results. **?** provides a short help text of the functionality.

The external tools are described briefly below, except for the ***SUV*** (on page 127) and ***Partial Volume Correction (PVC)*** (on page 297) tools which are explained separately.

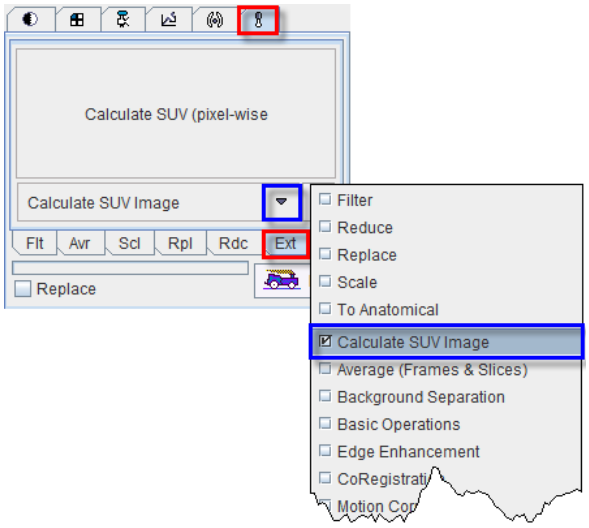
To Anatomical

Reformats the loaded images such that they are displayed in the standard radiological head first supine (HFS) position. This function requires that correct patient positioning information is available in the original data.

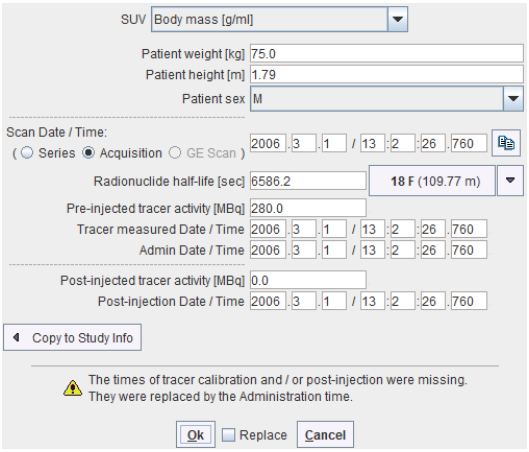


Calculate SUV Image

The calculation of statistics in SUV units is directly supported on the original image by the ***VOI functionality*** (on page 232), provided that all required information is available. Explicit SUV images can be calculated with the **Calculate SUV Image** entry of the external tools as shown below.

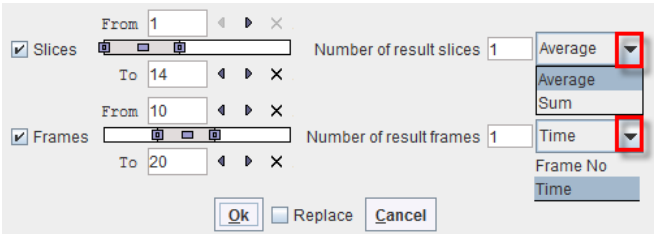


The SUV tool shows a dialog window with the activity-related information.



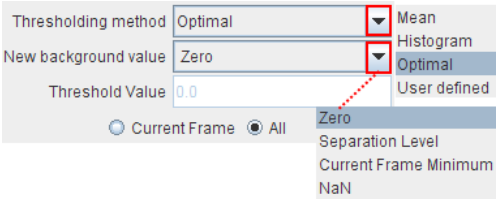
The **SUV** selection determines the SUV type to be calculated as described ***before*** (on page 127). The **Ok** button starts the calculation. A new image series with changed units ([g/ml], [cm²/ml] or [%ID/ml]) is created if the **Replace** box is unchecked, otherwise the original series is overwritten.

Average (Frames & Slices)



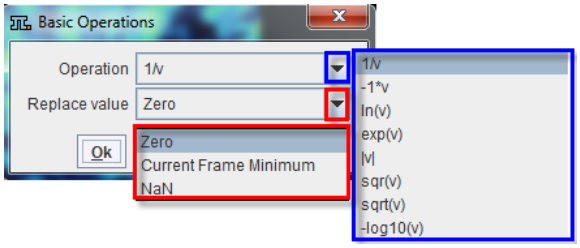
Allows simple averaging within a time range and/or within a slice range. The number of generated slices/frames can be entered numerically.

Background Separation



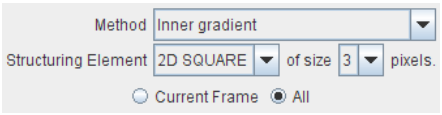
Methods to perform image background subtraction. The **Thresholding** selection contains **Mean**, **Histogram**, **Optimal**, and **User Defined**. The selected method determines a separation value, and all pixels below it will be replaced by the value specified with the **New background value**.

Basic Operations



Applies the numeric function configured as **Operation** to every pixel value, and uses the defined **Replace value** if the operation is mathematically undefined.

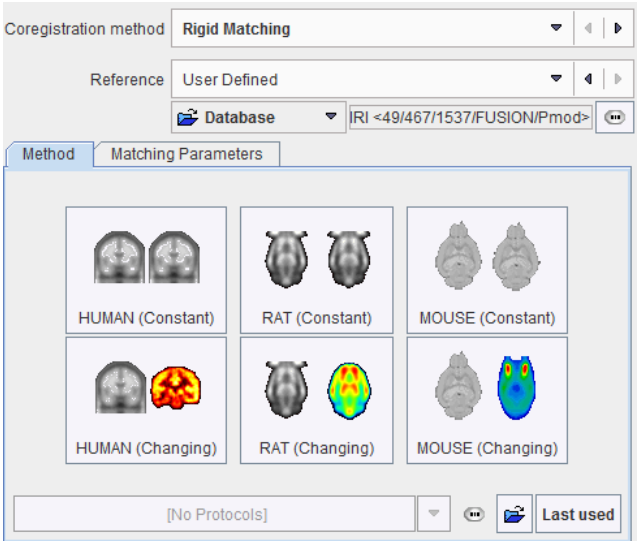
Edge Enhancement



Performs an edge enhancement operation based on different **Methods**: **Inner gradient**, **Outer gradient**, **Gradient (Morphological)** and **Top hat**. **Structuring Elements** of **2D SQUARE**, **3D CUBE** and **3D CROSS** are available at the sizes of **3**, **5**, **7**, and **9** pixels.

CoRegistration (with PFUS Option)

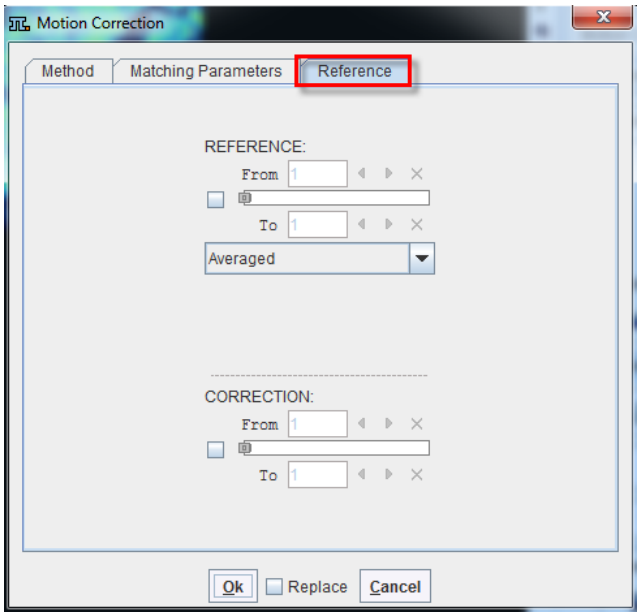
The matching in the external tools is mainly for the use in pipe processing. It is only available if the image fusion option is included in the PMOD license.



Please refer to the *PMOD Image Fusion Guide* for details about the matching options.

Motion Correction (with PFUS option)

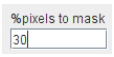
The motion correction in the external tools is mainly for the use in pipe processing. It is only available if the image fusion option is included in the PMOD license.



Please refer to the *PMOD Image Fusion Guide* for details about the matching options.

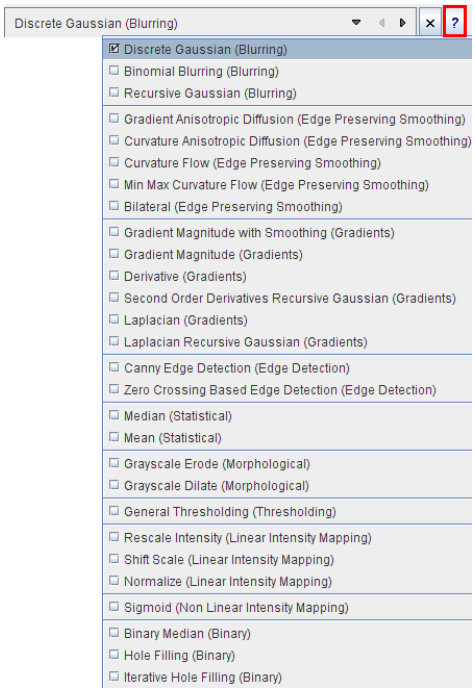
Energy Masking

Performs the masking of an image series based on the signal energy.



The tool calculates the pixel-wise energy (sum of the squared signal values), determines the histogram of this energy map, and masks the specified percentage of pixels with lowest energy values based on a histogram analysis.

ITK Image Filters

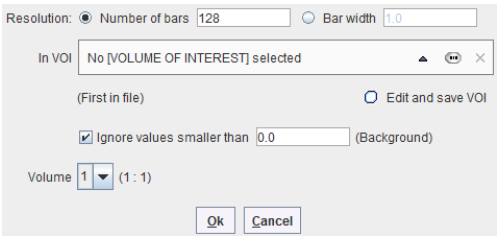


This tool provides an interface to 28 image filters provided by the ITK (Insight Toolkit) libraries. For each filter there is a short description which can be viewed with the **?** button. The ITK is under an open-source BSD license which allows free usage. For more details please refer to the ***The ITK Software Guide*** (***http://www.itk.org/ItkSoftwareGuide.pdf***).

Note: PMOD Technologies can not be held liable for permanent support of the ITK interface, nor for the performance of the provided libraries.

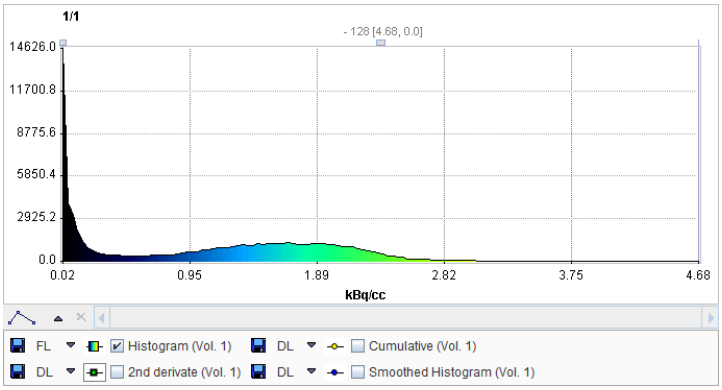
Histogram

Calculates the histogram of the pixel values in the whole **Volume** or within a VOI. An existing VOI can be selected, or created with the **Edit and save VOI** button.



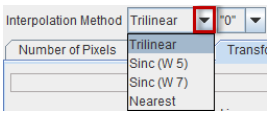
If **Number of bars** is enabled, the value range is divided into the specified number of equal intervals (e.g. 128). With **Bar width**, the interval size is directly specified. Values below a **Background level** can be excluded by checking **Ignore values smaller than** and specifying the **Background** level.

The number of occurrences in each interval are counted and plotted as a curve. Additional curves (**2nd derivative**, **Cumulative**, **Smoothed Histogram**) can be enabled in the control area. Note that the numeric values of the histogram can be exported using the context menu (right mouse button in curve are, then **View Values**).



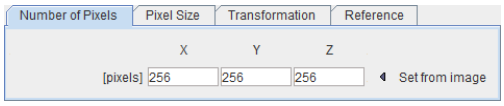
Interpolation

This tool serves for calculating a new image volume by an interpolating values from the current image volume. There are four choices for the **Interpolation Method**

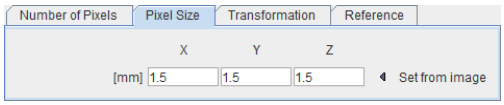


Default is **Trilinear** which is a simple and fast interpolation using all 8 enclosing pixel values. The truncated sinc interpolations **Sinc (Window 5)** and **Sinc (Window 7)** are more accurate, but considerably slower. **Nearest** neighbor interpolation just uses the value of the closest pixel, so it is very fast but in most cases does not provide satisfactory quality. However, it is the method of choice if an object map image containing integer values needs to be resliced.

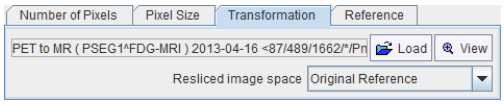
With **Number of Pixels** the image volume is sampled into a new number of pixels in each direction. **Set from image** copies the current numbers into the **pixels** number fields.



With **Pixel Size**, a new size in each direction can be specified. The matrix size results from the division of the volume sizes by the pixel sizes. **Set from image** copies the current numbers into the **mm** number fields.



With **Transformation**, a spatial transformation matrix calculated by the fusion tool can be applied to the image.



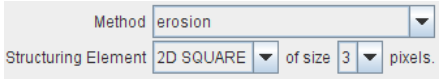
Resliced image space has three different settings:

- **Original Reference:** The transformation is applied with the resolution of the reference image used during matching, and the result is in the bounding box of the original reference image.
- **Preserved Input Dimensions:** The transformation is applied with the current image resolution, and the result is in the bounding box of the original reference image.
- **Preserved Input Space:** The transformation is applied within the bounding box of the input image. Large translations may move the image data completely outside the bounding box.

The **Reference** option allows interpolating the image to the space of the selected reference image assuming identity transformation.

The resulting image will have the dimensions, pixel size, and the origins of the reference image and the pixels at zero of the real coordinates will coincide.

Morphological



Morphological operations process images based on shapes. Therefore **Structuring Elements** are required (**2D SQUARE**, **3D CUBE** and **3D CROSS**) of a certain **size** (**3**,**5**,**7**,**9**).

Erosion removes pixels on object boundaries, darkens small bright areas, and very small bright areas like noise spikes or small spurs might be totally removed.

Dilation adds pixels to the boundaries, brightens small dark areas, and very small dark spots might be totally removed.

Opening (Erosion-Dilation) removes small objects from an image while preserving the shape and size of larger objects in the image. It darkens small bright areas, and may entirely remove very small bright spots like noise spikes.

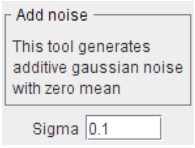
Closing (Dilation-Erosion) brightens small dark areas, and may entirely remove very small dark spots.

Deblurr

Inner gradient

Outer gradient

Add Noise



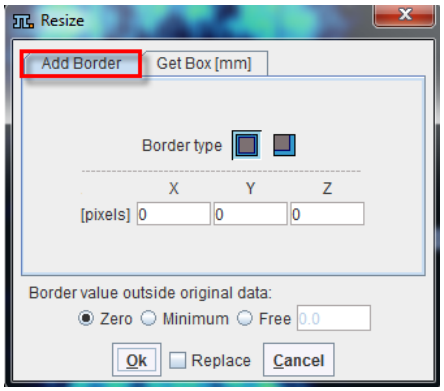
Adds Gaussian noise with zero mean and a standard deviation **Sigma** to the image.

PCA (Principal Component Analysis)

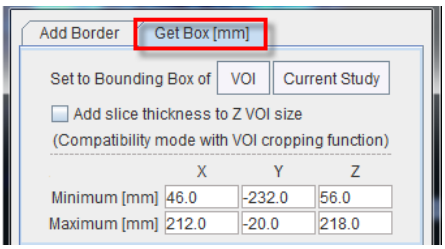
No input is required for this function which is only applicable to *dynamic* series. The PCA performs a principal component analysis in the time domain. The generated series consists of the components sorted according to decreasing eigenvalues. The expectation is, that the PCA groups pixels with a similar uptake pattern over time in different components (representing "frames" in the generated series). The eigenvalues are written to the console.

Resize

Resize has two tabs.



Add Border serves for padding pixels around the current series. There is a symmetrical and an unilateral variant. The number of padded pixels can be specified for each direction separately, and there are different options for the filling value.



Get Box allows extracting a sub-volume of the current series (cropping). To this end, the new bounding box must be specified.

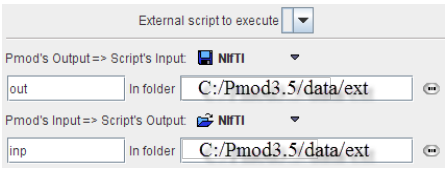
One way is to activate the **Current Study** button, which populates the **Minimum** and **Maximum** coordinates with that of the current study. Then the user can adjust the values appropriately to get a sub-volume.

Ana alternative way is to base the extraction on the bounding box of a suitable VOI, which has been defined beforehand. Using the **VOI** button a VOI can be selected, its bounding box is read from the file and applied for sub-volume extraction. Note that the same functionality is also directly available in the VOI tool. Additionally, the slice thickness can be added to the Z VOI size enabling the **Add slice thickness to Z VOI size** box.

R console

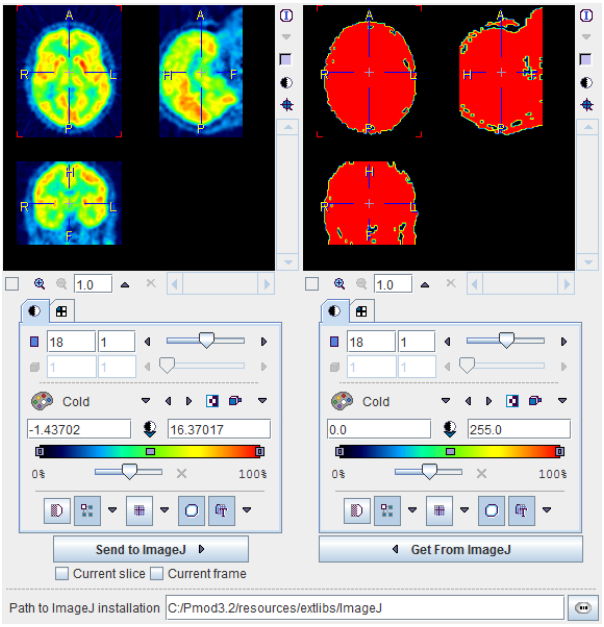
Allows loading the image data displayed in the view port in the PMOD R interface for further statistic analysis.

External Script



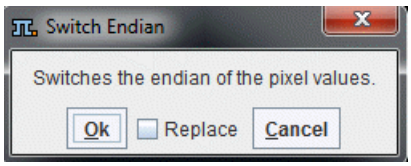
This tool allows running an external program, to which the current image is provided as **Script's Input**. It is expected, that the result is returned as a specific file defined by **Script's Output**, which is loaded after the script completes. The external script should be placed in the *Pmod3.5/resources/extlibs/scripts* folder.

ImageJ



This tool allows transferring image data to ***ImageJ http://rsbweb.nih.gov/ij/*** with the **Send to ImageJ** button, process the images with dedicated procedures in ImageJ, and retrieving the results with the **Get from ImageJ** button back to PMOD. Included in the distribution is a basic ImageJ version. For using a different version with dedicated plug-ins please point to your own installation using **Path to ImageJ installation**.

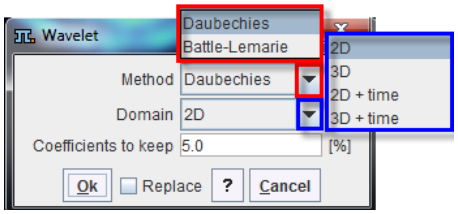
Switch Endian



Allows switching the endian encoding of the pixel values.This can be helpful of the wrong endianness was assumed during image loading.

Wavelet

The **Wavelet** tool performs de-noising of the dynamic data.

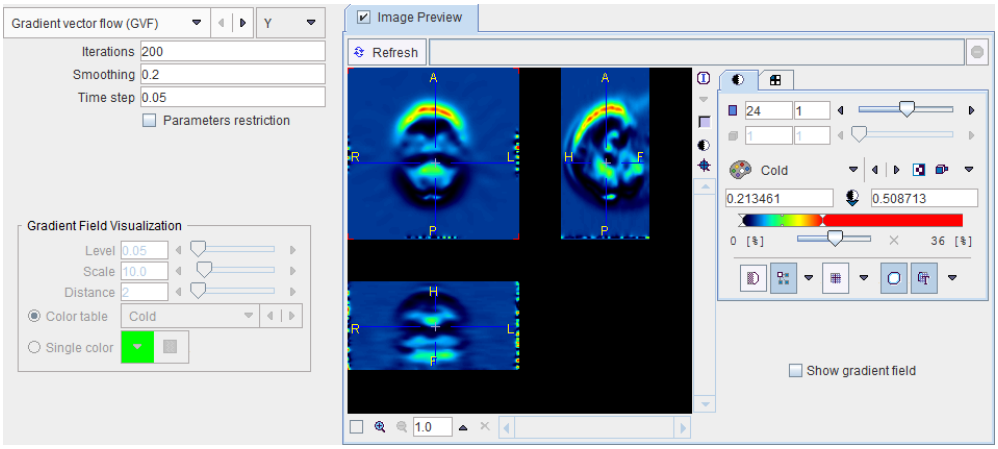


Daubechies or **Battle-Lemarie** wavelets are supported. There are different modes of operation: each plane separately (**2D**), each frame separately (**3D**), each plane over time separately (**2D + time**), or the volume over time (**3D + time**). Image dimensions 2^n are

required. The **coefficients to keep** determine the level of smoothing: the lower the % value entered, the smoother the image.

Gradient Vector Flow

The **Gradient Vector Flow** tool allows calculating the image gradient in a specified direction [1], which is for instance used for active contours algorithms.



Different algorithms are supported:

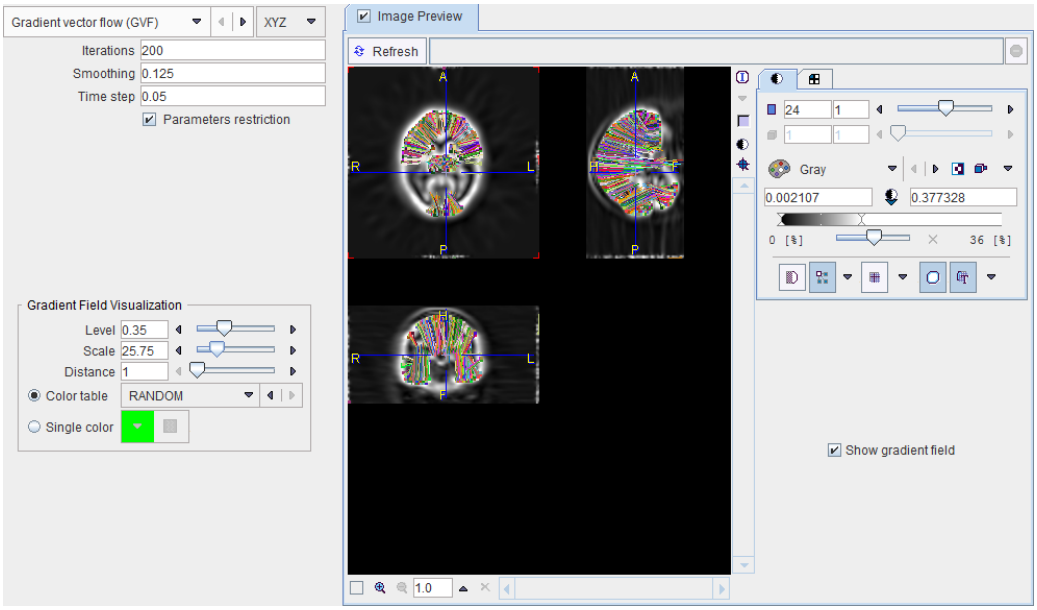
- **GVF**: calculates the gradient using the gradient vector flow algorithm;
- **General GVF**: calculates the gradient using a generalized gradient vector flow algorithm;
- **Differential gradient**: calculates the gradient by subtracting values of neighbouring pixels;
- **Sobel operator**: calculates the gradient by convolving filter mask with matrix consisting of image pixels.

During the estimation procedure the following parameters can be set:

- **Gradient width**: distance (in pixels) between two points, the intensity difference which defines the gradient value;
- **Iterations**: number of iterations performed during **GVF** and **GGVF** calculation;
- Smoothing parameter (μ): regularization parameter governing the trade-off between the first and the second integral term. Smoothing parameters should be set according to the amount of noise present in the image: the higher the noise the bigger the value.
- Time step (Δ): is representing the time length for each iteration.

In order to guarantee algorithm convergence, the smoothing parameter and the time step should satisfy the following expression: $\mu<-1.36*\Delta t+0.22$. Therefore, the **Parameters restriction** box should be enabled.

By enabling **Image Preview** and the **Show gradient field**, the gradient vectors can be visualized.

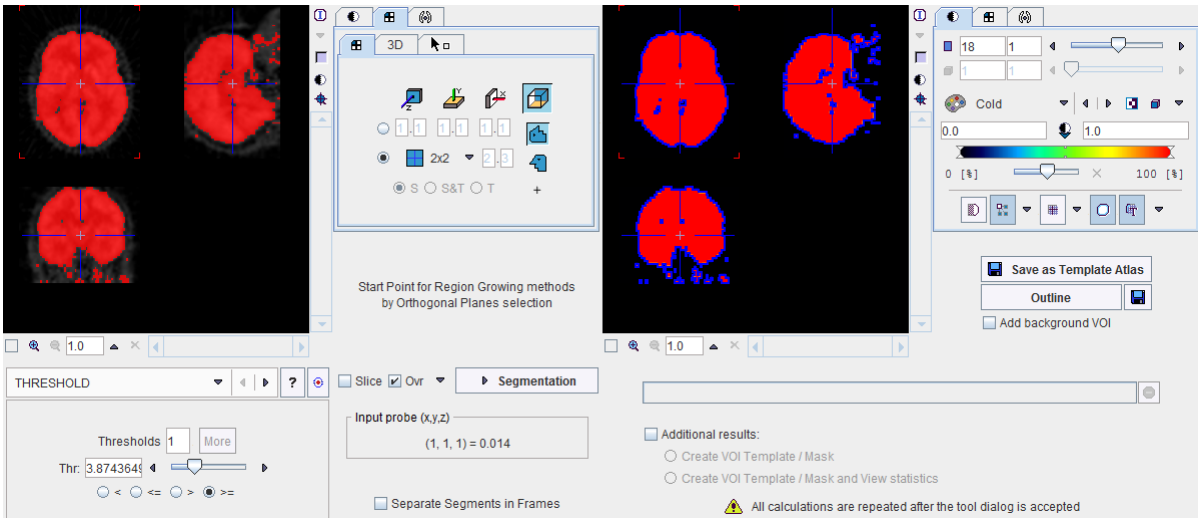


Reference

[1] Chenyang Xu, Jerry L. Prince. Snakes, Shapes and Gradient Vector Flow, Transactions on Image Processing, March 1998, p. 359-369.

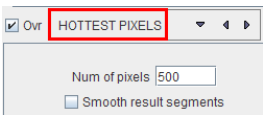
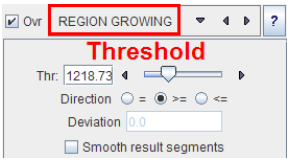
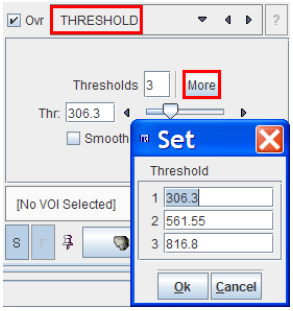
Segmentation

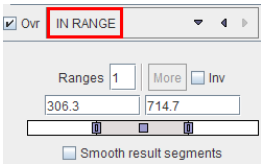
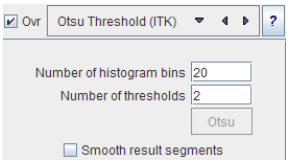
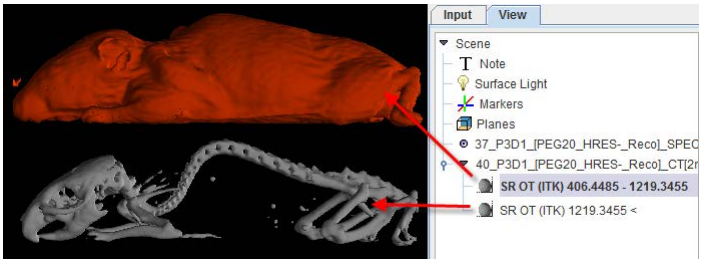
The **Segmentation** tool is a method for simple mask creation similar to the segmentation in the 3D tool. It opens the following dialog window.

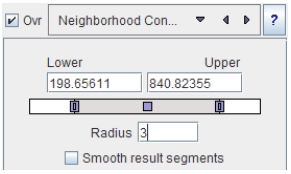


The following segmentation methods are available.

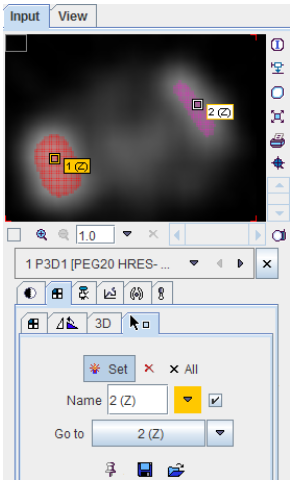
HOTTEST PIXELS	The **HOTTEST PIXELS** segmentation allows obtaining a 3D object of the (potentially disconnected) pixels with the highest values. The

	number of included pixels can be specified in the **Num of pixels** field. 
REGION GROWING	Region growing is a method by which the user defines a starting point (*seed*) within the object of interest, and the algorithm tries to find all connected pixels which fulfill a certain criterion. After selecting **REGION GROWING** the following control elements appear.  The slider and the number field serve for defining the pixel value. Together with the **Direction** radio button the criterion for pixel inclusion is formed. ▸▸ = include all connected pixels with a value threshold ± **Deviation**; ▸▸ >= include all connected pixels above the defined threshold value; ▸▸ <= include all connected pixels below the defined threshold value. A preview of the result is shown in the **Input** display if the **Ovr** (Overlay) box is checked, for example after clicking into a hot spot. To start the segmentation, navigate to a slice (in any direction) which shows the tissue of interest and click with the left mouse button onto a central point. Then adjust the criterion until the overlay indicates a promising segmentation.
THRESHOLD	The **THRESHOLD** segmentation is conceptually simple. All pixels above the threshold are included in the segment. Sometimes it is helpful to segment at several threshold levels at once. This can easily be realized by setting the number in the **Thresholds** field accordingly, select **More**, and enter the threshold values in the appearing **Set** dialog. In the example below, three segments of decreasing volume will be generated at thresholds 306.3, 561.55 and 816.8. During visualization, the user can show or hide each of the segments separately. 

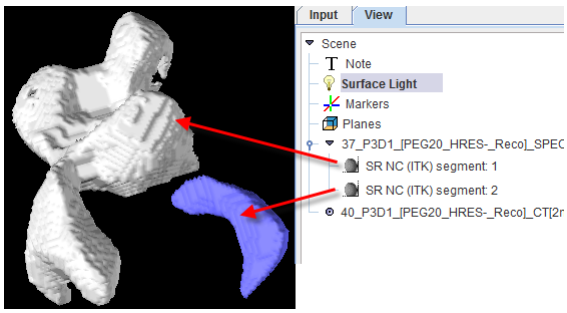
IN RANGE	The **IN RANGE** segmentation is similar to the **THRESHOLD** method, except that an upper limit is also defined. This can be helpful to find objects with intermediate intensities. The complementary pixels which are outside the specified range can be obtained by checking the **Inv** box. Similar to the **THRESHOLD** segmentation, multiple **Ranges** can be defined and segmented at once 
Otsu Threshold (ITK)	"Another criterion for classifying pixels is to minimize the error of misclassification. The goal is to find a threshold that classifies the image into two clusters such that we minimize the area under the histogram for one cluster that lies on the other cluster's side of the threshold. This is equivalent to minimizing the within class variance or equivalently maximizing the between class variance." ***The ITK Software Guide.*** (***http://www.itk.org/ItkSoftwareGuide.pdf***)  With the mouse CT, Otsu with the settings above finds appropriate thresholds for the skeleton object and the soft tissue, as illustrated below. 
Neighborhood Connected (ITK)	**Neighborhood Connected** is a region growing method with two criteria: **1)** The included pixels must have values between a **Lower** and **Upper** threshold. All pixels in the neighborhood (within a specified pixel radius) must also be within the value range. By the combination of these criteria small structures are less likely to be accepted in the region.

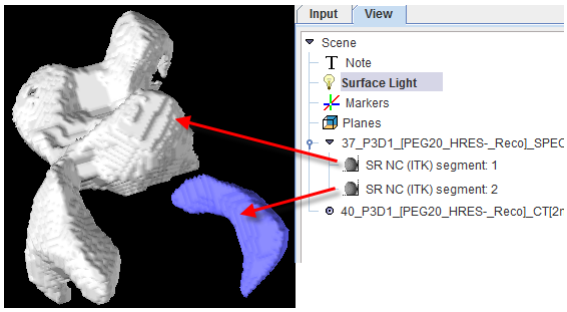


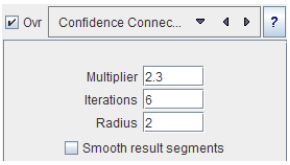
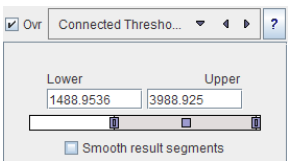
Multiple seed points can be specified by the use of markers.

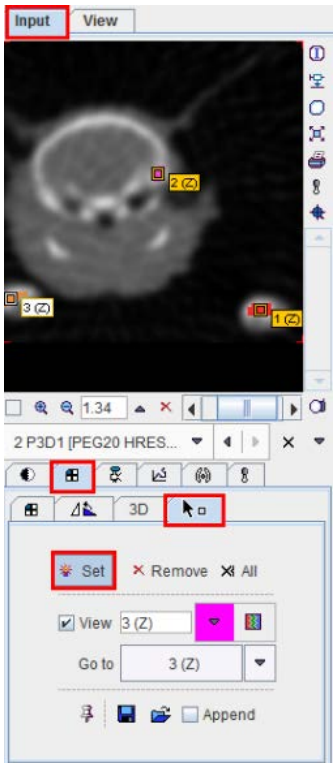
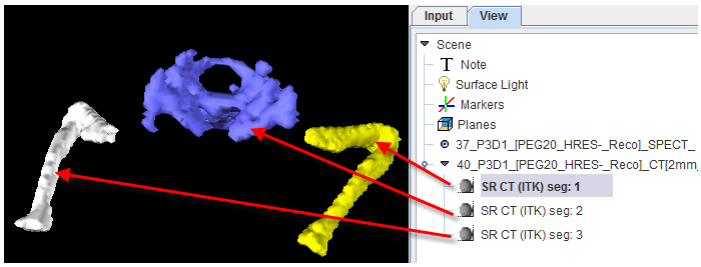


and correspondingly multiple structures can be found at once.





Confidence Connected (ITK)	"The criterion used by the **Confidence Connected** method is based on simple statistics of the current region. First, the algorithm computes the mean and standard deviation of intensity values for all the pixels currently included in the region. A user-provided factor is used to multiply the standard deviation and define a range around the mean. Neighbor pixels whose intensity values fall inside the range are accepted and included in the region. When no more neighbor pixels are found that satisfy the criterion, the algorithm is considered to have finished its first iteration. At that point, the mean and standard deviation of the intensity levels are recomputed using all the pixels currently included in the region. This mean and standard deviation defines a new intensity range that is used to visit current region neighbors and evaluate whether their intensity falls inside the range. This iterative process is repeated until no more pixels are added or the maximum number of iterations is reached." The number of iterations is specified based on the homogeneity of the intensities of the anatomical structure to be segmented. Highly homogeneous regions may only require a couple of iterations. Regions with ramp effects, like MRI images with inhomogeneous fields, may require more iterations. In practice, it seems to be more important to carefully select the multiplier factor than the number of iterations. However, keep in mind that there is no reason to assume that this algorithm should converge to a stable region. It is possible that by letting the algorithm run for more iterations the region will end up engulfing the entire image. The initialization of the algorithm requires the user to provide a seed point. It is convenient to select this point to be placed in a typical region of the anatomical structure to be segmented. A small neighborhood around the seed point will be used to compute the initial mean and standard deviation for the inclusion criterion." ***The ITK Software Guide.*** (***http://www.itk.org/ItkSoftwareGuide.pdf***) 
Connected Threshold (ITK)	**Connected Threshold** is a region growing method with the criterion that (similar to the **IN RANGE** method) the included pixels must have values between a **Lower** and **Upper** threshold.  As usual with region growing methods, the user has to specify a seed point by clicking into the image. The ITK region growing methods are

	particular in that multiple seed points can be specified at once by the use of markers as illustrated below.  Once the markers tab has been activated and the **Set** button enabled, a marker is created as a seed point for each clicking into the image. When the segmentation is started, the region growing with the specified value range is performed from each marker. 
SCATTER in VOI	This particular method for localizing pixels from 2D scatter plots is described in a separate ***section*** (on page 149).

After specification of the segmentation method and its parameters, the segmentation can be started with the **Segmentation** button. The result is shown in the right image display port. Note that if the study is dynamic, an additional box **All Frames** appears. If it is checked, segmentation will be performed for all frames separately, otherwise with the frame which is currently shown.

The segmentation result can be used in different ways:

- **Save as Template Atlas** directly saves the segmented series in an atlas format in the directory Pmod3.5/resources/templates/voitemplates. Subsequently, it can be used for statistics using the **Atlas** tab of the **Templates** pane in the VOI definition function.
- The **Outline** button allows creating VOIs for each generated segment. Optionally, the background can be added as a VOI by enabling the **Add background VOI** box. The outlined VOIs can be saved as files and later used for statistics by the **Save** icon next to the **Outline** button.

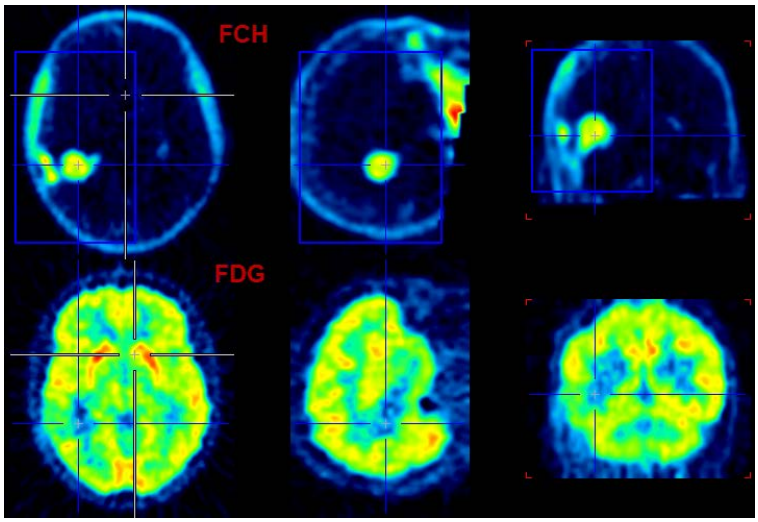
With the **Ok** button the segmentation is performed again and the resulting segment returned as an image series which is binary for a simple segmentation and an object map in the case of a clustering method. The following **Additional results** can be returned.

1) **Create VOI Template/Mask:** With this setting, the segments are also returned as a VOI template which can be activated by the **Mask** tab of the VOI **Template** function.

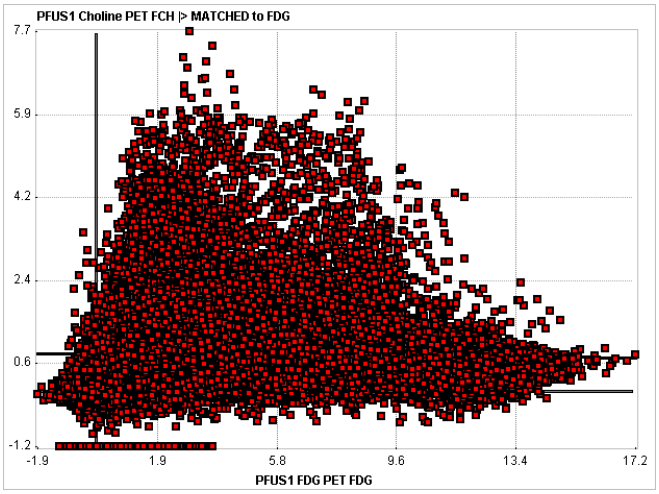
Create VOI Template/Mask and View Statistics: As 1), but the statistics on the current image are additionally calculated.

Mapping of Pixels from Scatter Plots

Scatter plots are a convenient method for exploring tissue function, if matched image series are available. With the brain PET example illustrated below,



we get the following scatter plot of the pixel values in the blue VOI box.



The FDG uptake of a pixel is plotted on the x-axis, and the corresponding PCH uptake on the y-axis. The **Segmentation** tool allows defining areas of interest in the scatter plot plane and mapping the enclosed pixels back to the image. The procedure converts the scatter plot to an image, in order to apply the standard PMOD VOI functionality for the area definition.

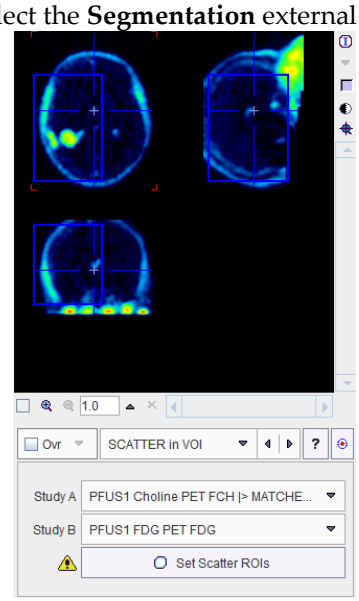
Segmentation Procedure

Please proceed as follows:

1) Load the two matched image series.

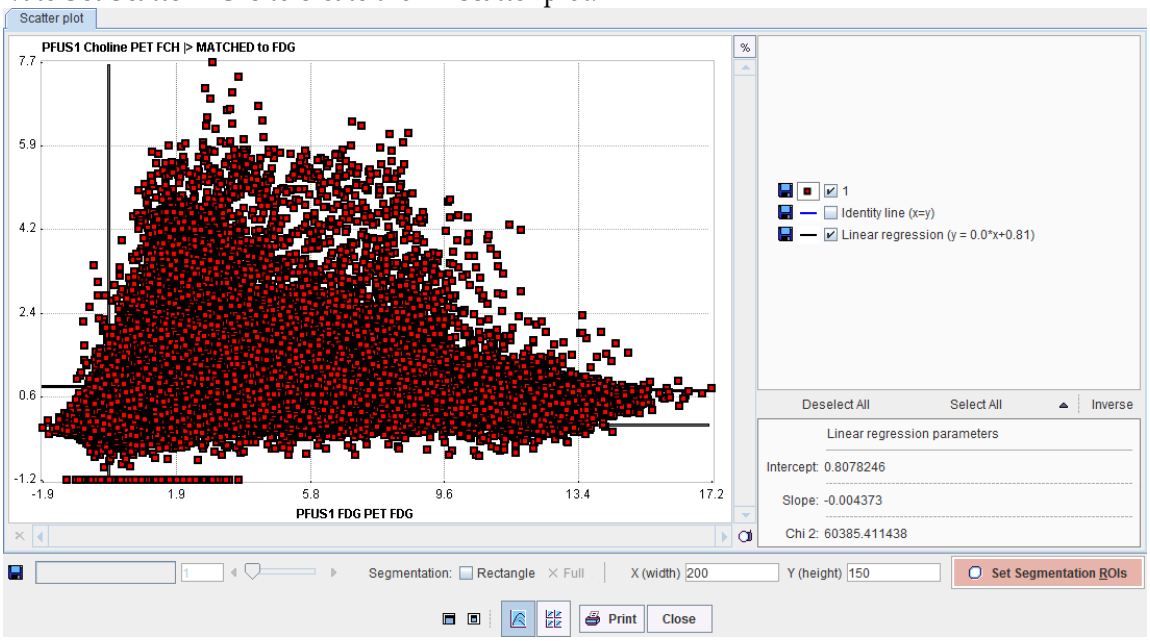
Define one or multiple VOIs on the first image series which enclose the tissue of interest, if needed the whole volume.

Select the **Segmentation** external tool, and chose the **SCATTER in VOI** method.



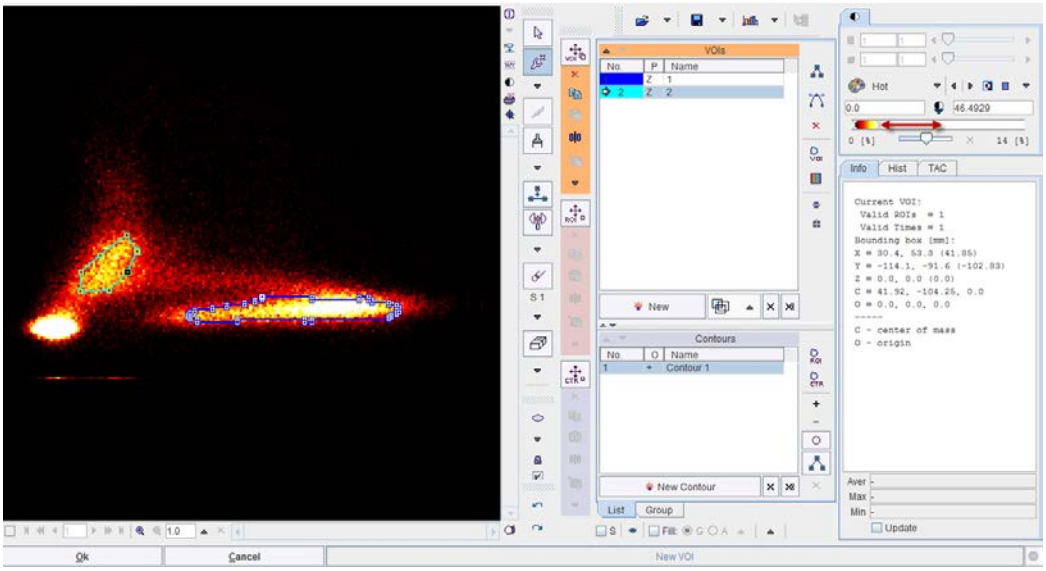
Using the list selection arrow, define the series with the defined VOI as **Study A**, and the other series as **Study B**.

Activate **Set Scatter ROIs** to create the 2D scatter plot.

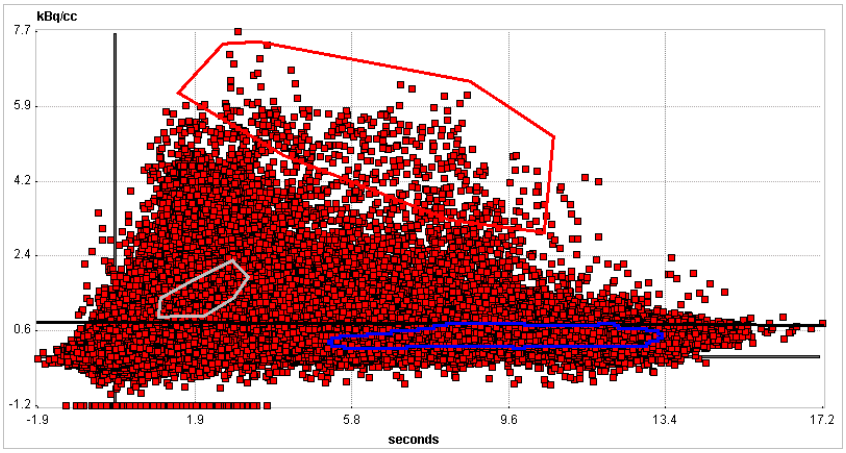


Convert the plot into an image by **Set Segmentation ROIs**. The **X(width)** and **Y(height)** define the number of image pixels in the two dimensions. The image value is given by the number of scatter points in the area of each image pixel.

A window appears showing the generated image together with the VOI definition interface. Adjust the color thresholds for localizing pixels with a specific uptake pattern and draw the ROIs.

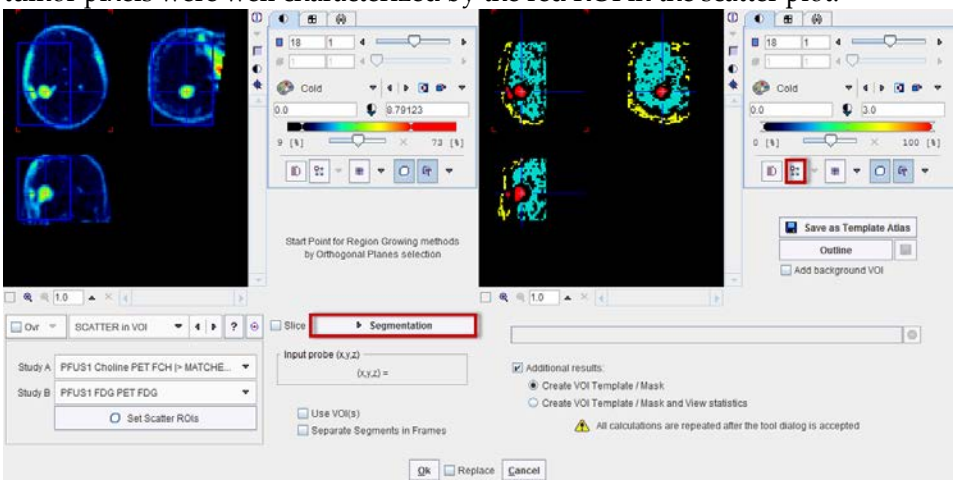


Closing of the VOI interface with **OK** returns to the scatter plot which now also displays the ROIs.



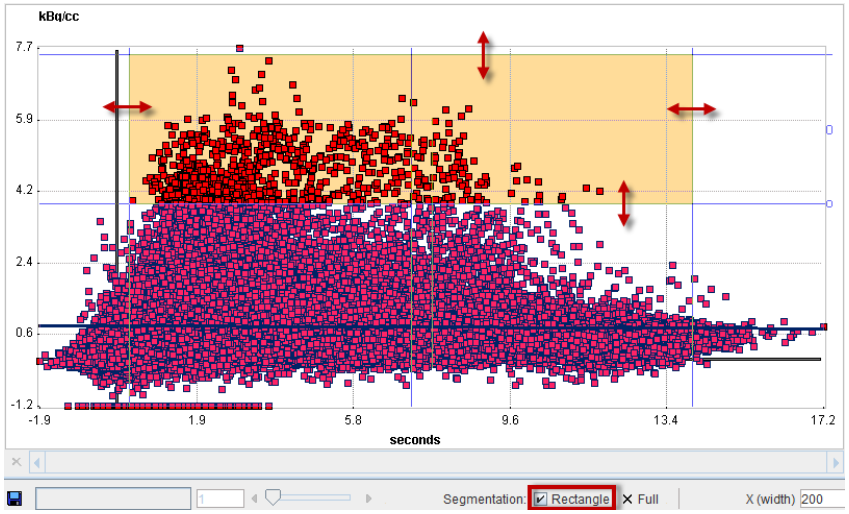
Complete the definition by the **Close** button to return to the **Segmentation** tool.

Now the the scatter pixels can be mapped with the **Segmentation** button. The interpolation should be disabled to better see the generated segments. The result indicates that the tumor pixels were well characterized by the red ROI in the scatter plot.

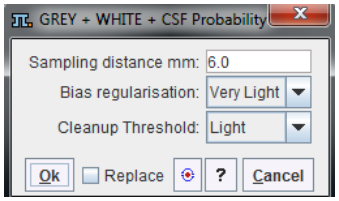


Rectangle ROI

An quick alternative to going through scatter plot rasterization and ROI outlining is to use a simple rectangular ROI. This functionality is enabled by the **Rectangle** box. A red-shaded area appears, which can be adjusted by dragging the edges. **Segmentation** will map the pixels in the defined rectangle.



GREY + WHITE + CSF Probability

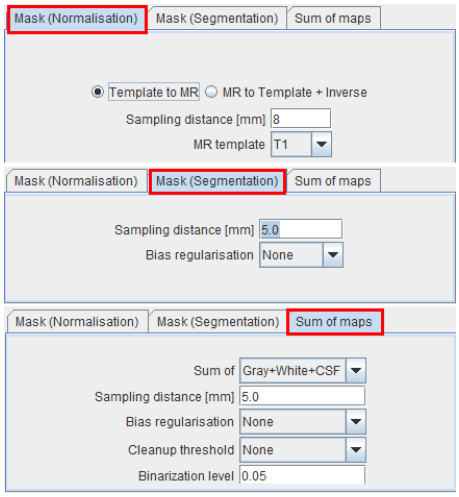


This tool calculates the grey matter (GM), white matter (WM) and cerebrospinal fluid (CSF) probability maps from a T_1-MRI of a human brain. The procedure has three parameters: **Sampling distance** determines the density of pixels considered in the calculation. **Bias Regularisation** serves for compensating modulations of the image intensity across the field-of-view. Depending on the degree of the artifact, a corresponding setting can be selected from the list. **Cleanup** is a procedure for rectifying the segmentation along the boundaries. It is recommended to use the default settings and only experiment with other parameter values if the segmentation fails. The default settings are available by activating the default settings button .

The results are the three probability maps of GM, WM and CSF which are arranged in this order as the frames in a "dynamic" series.

MR Skull Stripping

This tool serves for extracting the brain part from human anatomical MR images which need to be provided in HFS orientation.



There are three processing variants available:

1) **Mask (Normalization):** This procedure is based on the **Brain Normalization** method implemented in the fusion tool. Depending on the setting **Template to MR** or **MR to Template + Inverse**, the normalization between the MR and the MR MNI template is calculated, and then applied to transform the standard MNI brain mask to the MRI space.

Mask (Segmentation): The normalization between the MR and the MR MNI template is calculated based on the GREY + WHITE + CSF segmentation method. It is then applied to transform the standard MNI brain mask to the MRI space.

Sum of maps: The MRI images is segmented using the GREY + WHITE + CSF method. The mask is created by applying a threshold to the summed segments.

Finally, the mask is inverted and applied to the MR image for removing all non-brain pixels.

PVC (VOI based)

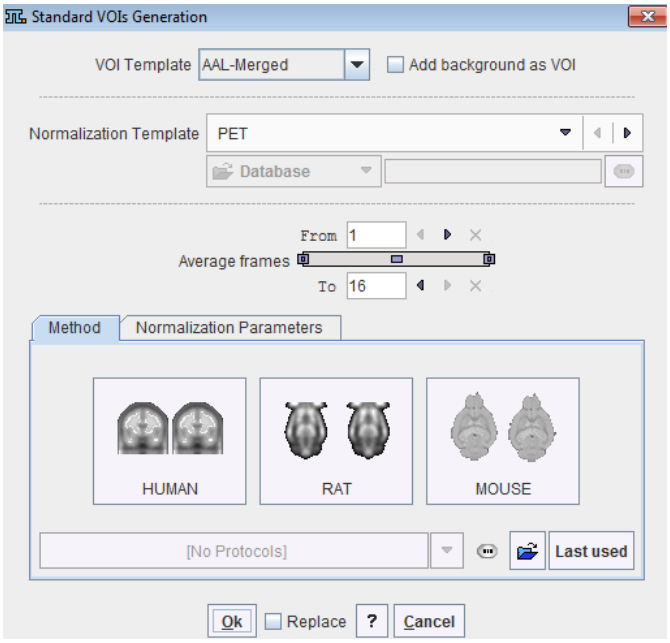
General tool for partial-volume effect correction based on VOIs as explained in detail in a separate ***section*** (on page 297).

PVC (Brain MR based)

Tool for the partial-volume effect correction of a human brain PET based on the Muller-Gartner method as described in a separate ***section*** (on page 297).

Standard VOIs Generation

The tool allows generating contours VOIs in the input space according to the selected **VOI template**. If the tools is called from pipe processing, the VOI statistics will also be evaluated and can be saved.



The **Method** is available for **HUMAN**, **RAT** and **MOUSE** studies. The **Input** study is normalized to the chosen normalization template. The algorithm applied is *Brain Normalization* and the inverse transformation is calculated. In case the input study is dynamic, an averaged input is created for the selected frame range **Average frames**. The selected template VOIs is transformed to the input space using the inverse transformation calculated during the normalization procedure. Finally the transformed VOI template is outlined automatically.

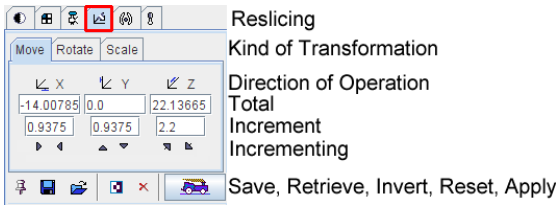
Notes: This procedure is crucially dependent on a successful normalization.

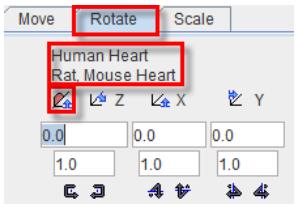
Macro

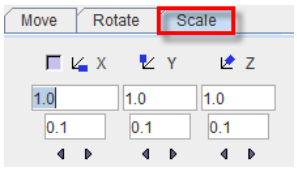
This tool allows applying an image ***macro*** (on page 113) which is most useful in the context of ***Pipe processing*** (on page 338).

Reslicing of the Images at Oblique Orientations

To calculate slices at oblique orientations or rotate images the reslicing pane must be activated. Reslicing is defined by a transformation consisting of translations in all directions, rotations about all axes, and potentially scaling along the axes. Each of these transformation components has its own sub-pane.







Note that **Scale** values of 1 indicate that the pixels sizes read from the image header are correct. Any other number will scale the pixel size accordingly.

The transformation parameters can be specified in different ways, on the corresponding sub-panes **Move, Rotate, Scale:**

- by entering values for the shifts or rotations in the number fields, or
- by clicking on one of the arrows to increase/decrease the values by the shown increments.

In the **Rotate** tab a help re-orientation button is available for heart studies . This option button allows re-orienting the heart data such that is closest to the short axis orientation (SA).The heart type can be selected when the button is activated. Two options are available: **Human Heart** and **Rat Mouse Heart**.

After changing the transformation, new slice images are immediately calculated and shown. However, the entire data set is only generated when needed, for instance to save the images. The button serves for enforcing the reslicing process for the whole data volume.

The button resets the transformation parameters. A transformation can be saved to disk using , and later retrieved with if needed.

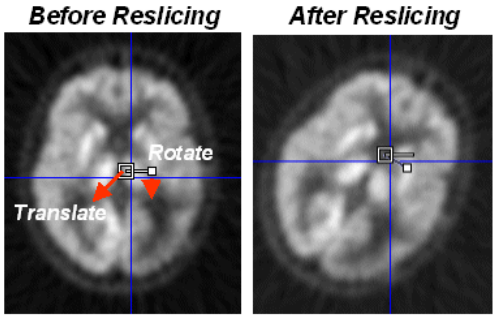
Important Notes:

1. The facility buttons in the reslicing panel for **Save**, **Retrieve** and **Apply** transformation are not always available.

2. The manual transformations are not fully equivalent with the automatic rigid matching transforms of the fusion tool. Manual transformation can be used in PFUS activating the **Load Transformation** button in the **Auto** panel available on the **Initialize/Match** page. In PFUS, the **Inverse** transformation is possible to calculate for any type of transformation activating the dedicated button Inverse .

Mouse-driven Reslicing

As soon as the reslicing pane is activated, handles appear in the image overlay. They allow for interactive, mouse-driven reslicing.



Symbols alwas stay in image center

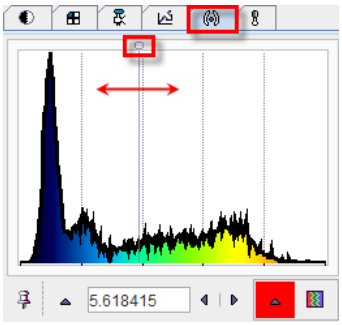
Translation: Move the mouse pointer to the open white rectangle. The cursor changes to . Click the left mouse button down, and then drag along the direction you want to move the image to.

Rotation: Move the mouse pointer to the filled small white rectangle. The cursor changes to . Click the left mouse button down, and then drag while the image gets rotated. To get finer control of rotation, the rectangle can first be dragged radially outward, so that the handle distance from center increases.

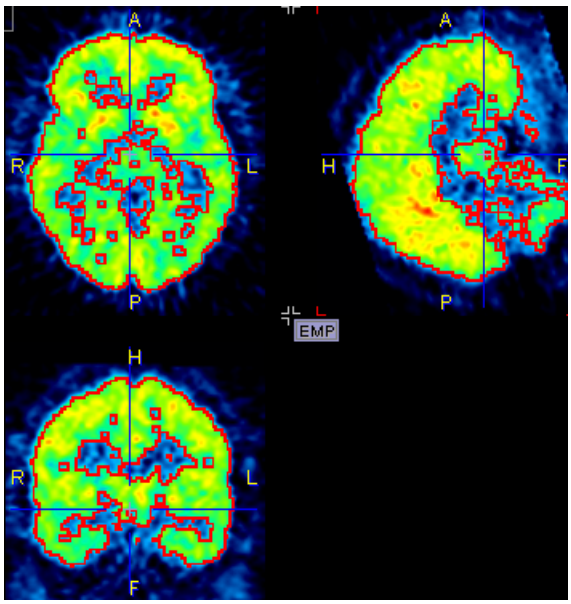
Per default, the reslicing handles are shown as long as the reslicing tab is selected. If another tab is selected, they disappear. To make them appear permanently in the images and enable mouse-driven reslicing at all times, the pin button can be fixed to . A quick alternative to show/hide the reslicing controls in the active image is the CTRL+R shortcut.

Adding Iso-Contour Lines to Images

The fourth tab



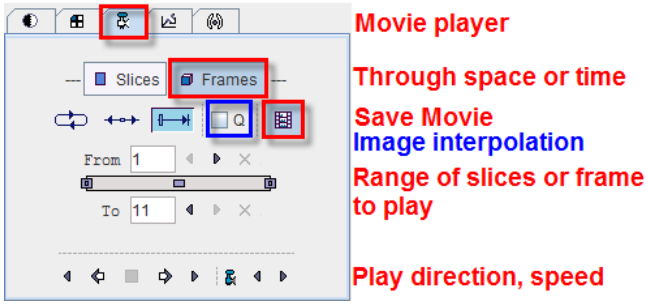
is used to overlay iso-contour lines onto the images. A histogram of the pixel values is shown, and the value at which the iso-contour lines are drawn can be adjusted by entering a numerical value, or by dragging the marker highlighted in the graphics above. The selection on the right allows to choose among several colors for the contour lines.



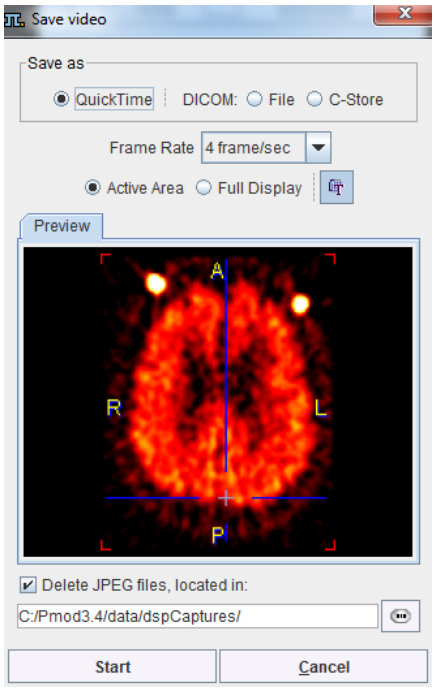
Per default, the iso-contour lines are shown as long as the iso-contour tab is selected. If another tab is selected, they disappear. To make them appear permanently in the images the pin button can be fixed to .

Showing and Saving Movies

The movie player allows showing movies of slice images through the volume or through time (dynamic studies only), as well as rotating MIPs if the 3D button was selected in the layout.



Please use the **Q** box to enable image interpolation when working with low-resolution images. If the save movie button is activated at the time the user hits the start button, a dialog window appears requesting information for movie generation.



The movie formats include Quicktime or DICOM, and the active image or the entire image viewport can be captured. The movies are generated from intermediate JPEG files, which can optionally be kept for other uses.

A movie of the active image can also be started/stopped with the `CTRL+M` shortcut without the need to open the movie tab.

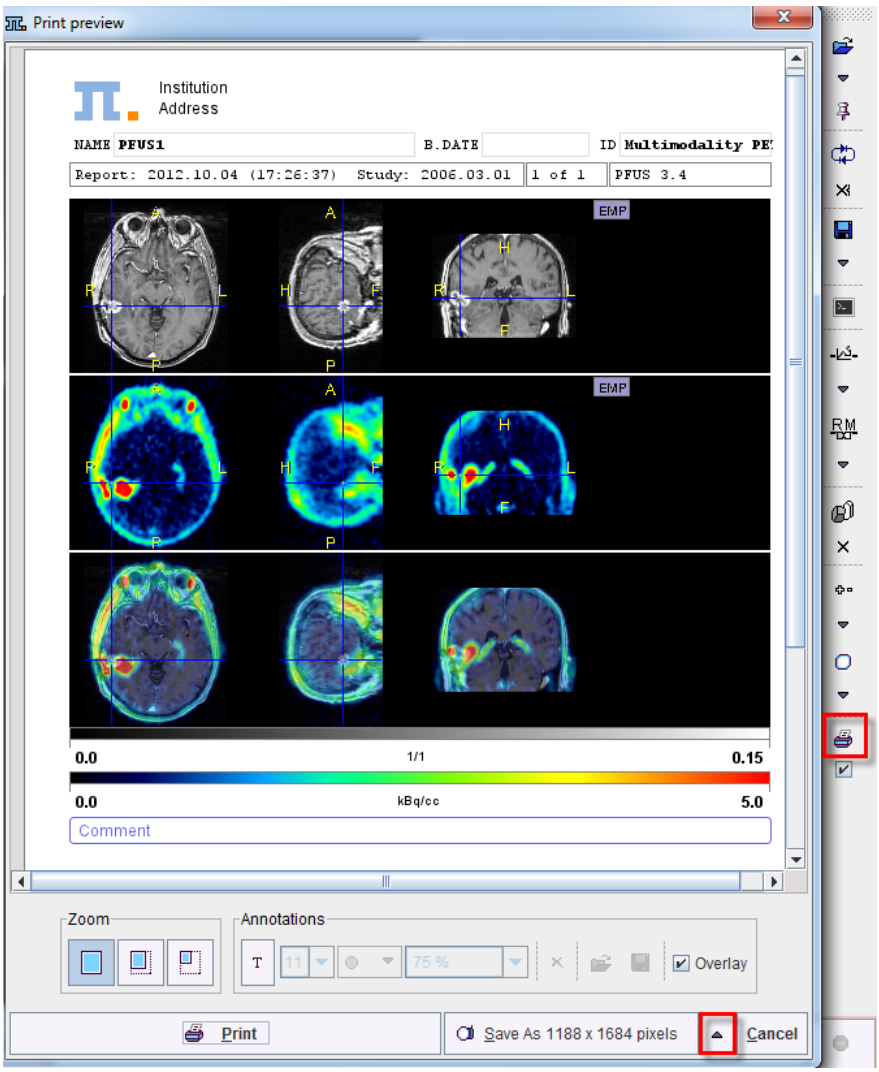
Reports

Reports of the current configuration in a single image display can always be generated using the report button next to the image. In more complex configurations such as image fusion (PFUS) or image comparison (PVIEW) a dedicated report button is available which creates a composite report.

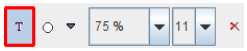
The report button opens a dialog window consisting of a header part, the image area, a comment field, and control buttons for adding annotations, saving and printing.

The logo and the institution address of the header can be configured using the Config button in the PMOD ToolBox. The patient demographic information is extracted from the image header. It can only be changed by changing the image information itself with the **Edit Patient/Study Info** function.

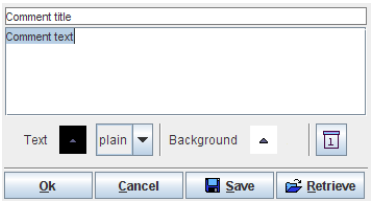
The central part contains the image(s) in the layout and color as on the image viewing port(s). As long as the presentation is not fully satisfactory, the user can change it in the application and then activating the button again.



In addition to the provided content the user may add annotations. This can be achieved by enabling the T toggle button in the **Annotations** area



and then clicking into the report. A dialog window opens for entering a comment title and body.

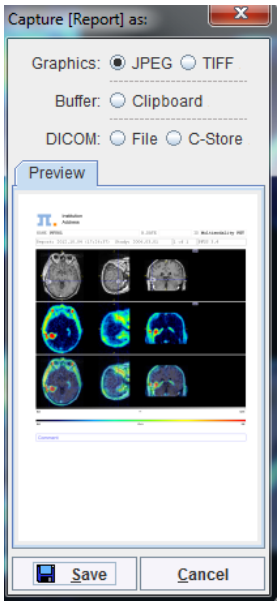


After closing with **Ok**, the comment text is shown together with a circular marker, connected by a line.

Both the text and the marker can be dragged around so as to properly label a point of interest without obstructing the view on relevant information. By changing the opacity and font size in the **Annotations** area, the comment appearance can be adjusted appropriately. To stop adding annotations, the T toggle button must be set to off by clicking it again.

When the report contents is satisfactory, the page can be sent to a printer using the **Print** button. Alternatively it can be saved in different graphic formats using the **Save as** option button. Note that there are two resolutions available: **1188x1684** and **594x842**. With **1188x1684**, the generated graphic files have notable better quality (particularly the text), but are considerably larger in size.

Several saving formats are available in the appearing dialog:



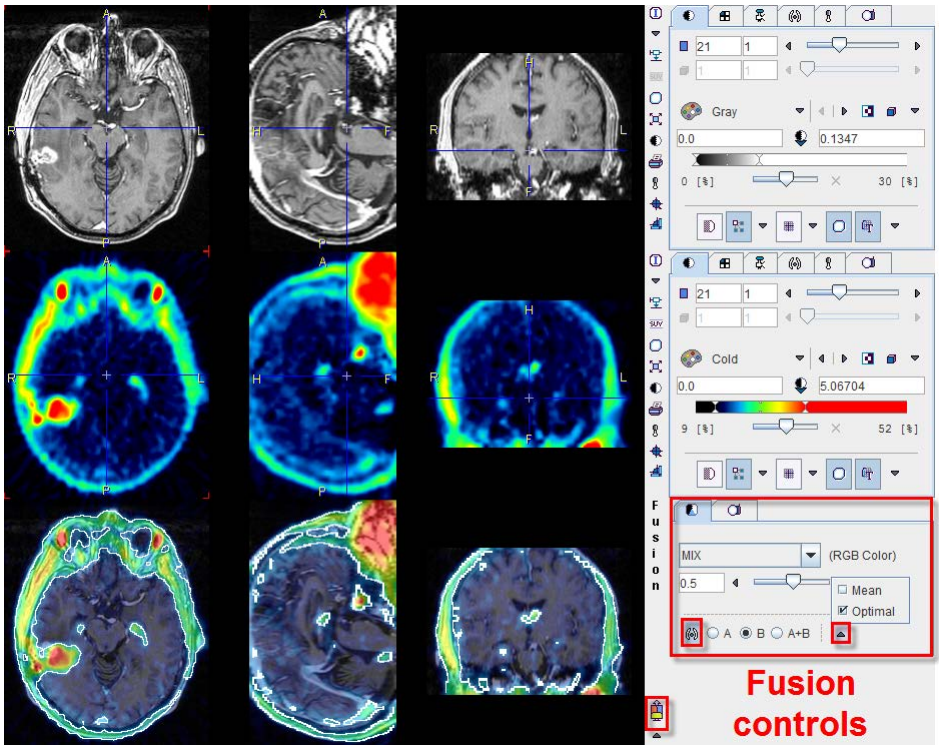
The report page can be saved as a graphic file **(JPEG** or **TIFF**) or copied to the **Clipboard** (for pasting it into a different application). Another alternative is to create a DICOM Secondary Capture object which can be can be saved to disk (**DICOM File**) or directly sent to a DICOM server (**DICOM C-Store**).

Presentation of Fused Images

There are multiple places in PMOD where two different image sets can be combined into a fused image. Depending on the context, there are two arrangements for performing the image fusion.

Separate Source and Fusion Images

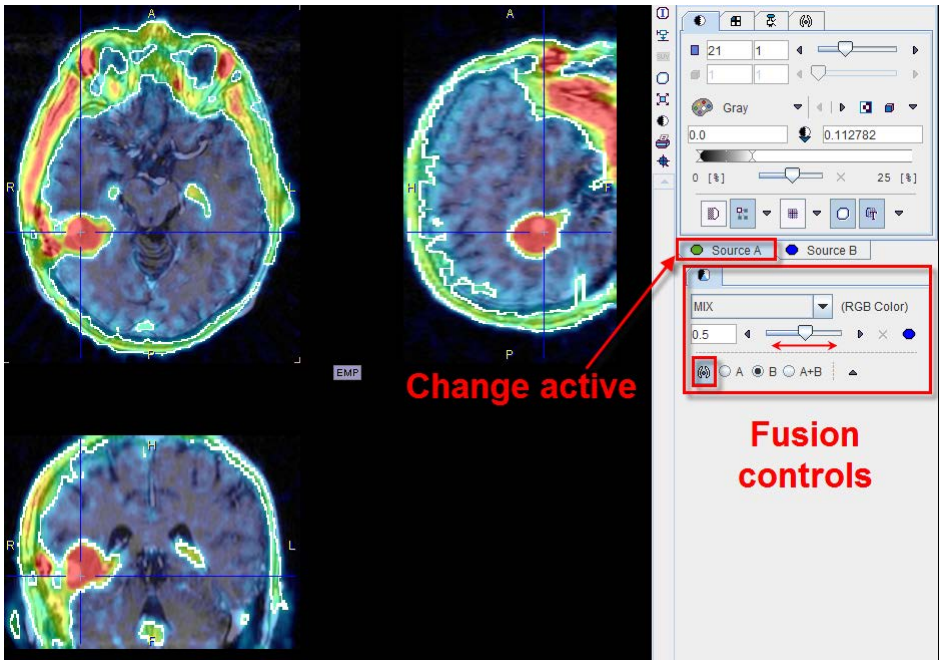
In this layout both the input images and the fusion images are visible at the same time, as in the example shown below.



In this example the first row shows a T_1-weighted MR image, and the second a matched ^{18}F-Choline PET image with a highlighted tumor. To the right of the images the controls are available for changing the way how the images are displayed such as the color table, the thresholds, and the layouts. The third row shows the result of the fusion, depending both on the renderings of the source images, and on choice of the fusion controls located to the right.

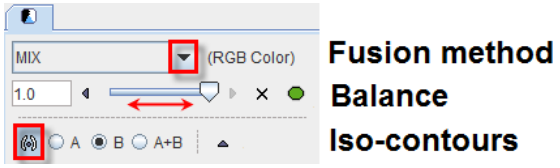
Fusion Images not Visible at the same Time as the Source Images

In this layout only the fusion of two source series is shown.



To adjust the presentation of either source image, select the appropriate tab **Source A** or **Source B**, and use the image controls. During such adjustments it will sometimes be helpful to only see the image you are working on, not the fusion. This can easily be achieved by moving the balance slider to one of the end positions left or right.

The image fusion control



consists of three rows. The first row contains the selection(s) for choosing between the different fusion renderings, the second row allows enabling the balance to blend the contributions of the two images in the fusionthe, and the third row allows enabling the iso-contour overlays.

Image Fusion Methods

The fusion methods available are:

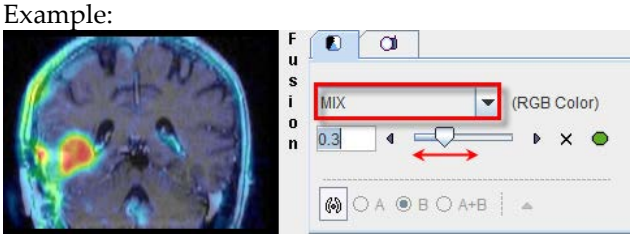
MIX Alpha Blending: weighted addition of the RGB values of both source images according to

$R_{fusion} = R_A*x + R_b*(1-x)$

$G_{fusion} = G_A*x + G_b*(1-x)$

$B_{fusion} = B_A*x + B_b*(1-x)$

Example:



The slider allows defining the relative contributions of the source images. In the example shown image A contributes 30%, and image B 70%.

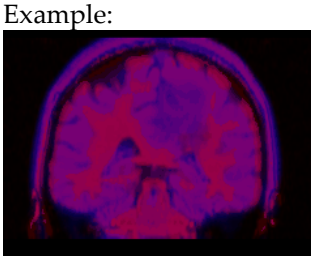
MERGE RGB merging uses the maximal RGB value of both source images according to

$R_{fusion} = Max(R_A, R_b)$

$G_{fusion} = Max(G_A, G_b)$

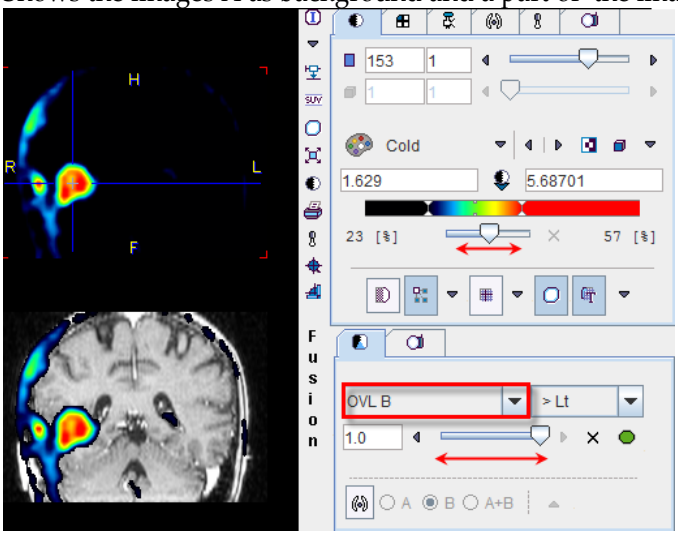
$B_{fusion} = Max(B_A, B_b)$

Example:



This fusion mode is most adequate for data arising form RGB sources, or when encoding the images with the [R]ed, [G]reen, [B]lue color tables.

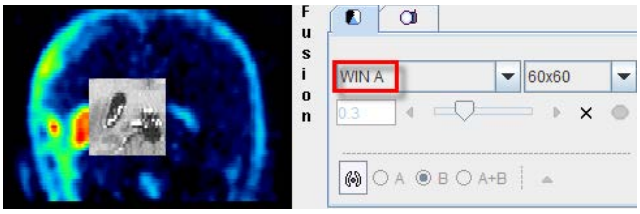
OVL B Shows the images A as background and a part of the images B as the overlay.



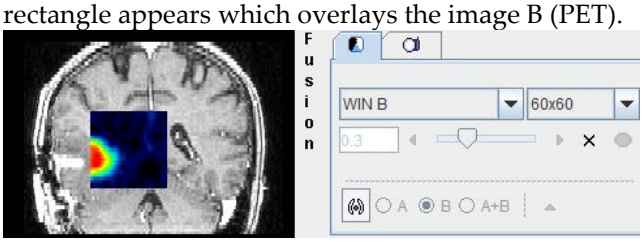
With the **>Lt** setting, all pixels in the PET image (B) below the lower threshold of the color table are replaced by the MR (A) values. Additionally, some transparency is added in the lesion by the balance slider. See below the description of the different threshold options.

OVL A Is equivalent to **OVL B** except that the role of the images is reversed.

WIN A Shows the images B (PET) as the background. When clicking into an image a rectangle appears which overlays the image A (MR).



WIN B Shows the images A (MR) as the background. When clicking into an image a rectangle appears which overlays the image B (PET).



When the **OVL A** or **OVL B** methods are selected, different threshold settings are available in the selection to the right:

> Lt Only the pixels (in A for **OVL A** , in B for **OVL B**) with values *above* the lower threshold are displayed. This is the most useful setting when a hot lesion is to be blended into an anatomical image (see example for **OVL B** above).

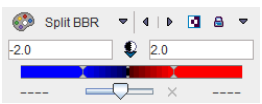
< Ut Only the pixels (in A for **OVL A** , in B for **OVL B**) with values *below* the upper threshold are displayed.

>Lt Ut< Only the pixels (in A for **OVL A** , in B for **OVL B**) with values *between* the lower and upper threshold are displayed.

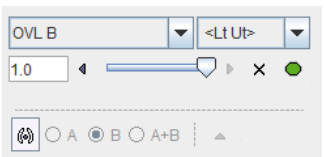
<Lt Ut> Only the pixels (in A for **OVL A** , in B for **OVL B**) with values *outside* the lower and upper threshold are displayed. Note that only the first and last color of the selected color table are applied in this setting. A suitable selection in this configuration is the **Split** color table.

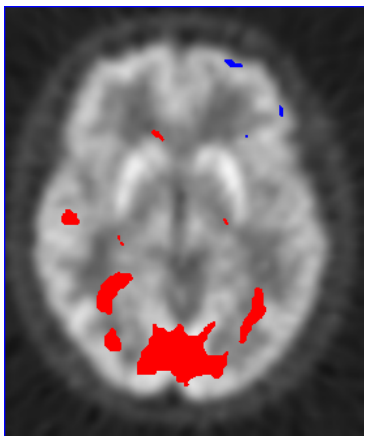
An example of the **<Lt Ut>** method is shown below.

Image A represents normalized patient images, and image B the deviation from the normal pattern expressed as z-score values. The color table configuration of image B is



and the fusion settings



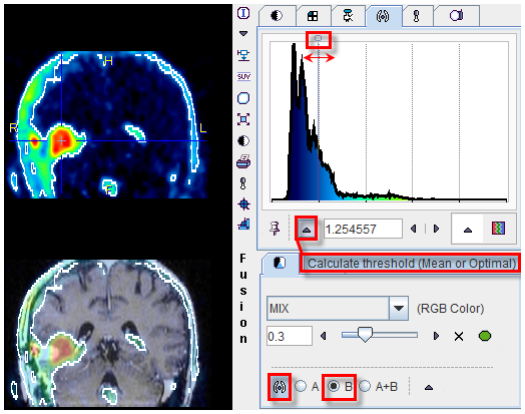


Only z-score values < -2 and > 2 are shown, without transparency. Because only the minimal and the maximal

colors are use, the result has a binary character. Red are all pixels with an activation of more than two standard deviations, and blue all the pixels with the uptake reduced by at least two standard deviations. This is probably the most useful configuration for exploring the deviations from the standard pattern.

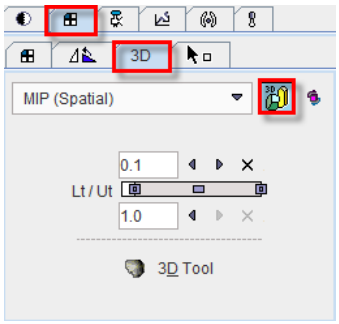
Iso-contours in Image Fusion

The contours radio box allows overlaying iso-contours derived from the source images **A** or **B** or both onto the fusion result. In the example below an iso-contour circumscribes the lesion clearly delineated in the FCH PET image. The iso-contour for the image **B** can be generated automatically selecting the **Optimal** option in the list in the **Contouring** tab. Setting the radio box **B** displays this contour in the fusion, which has been set to show mainly the MR image (A) by moving the balance slider to the left end. Another helpful application of the contours is in image matching.



3D Volume Rendering, Rotating MIP Images

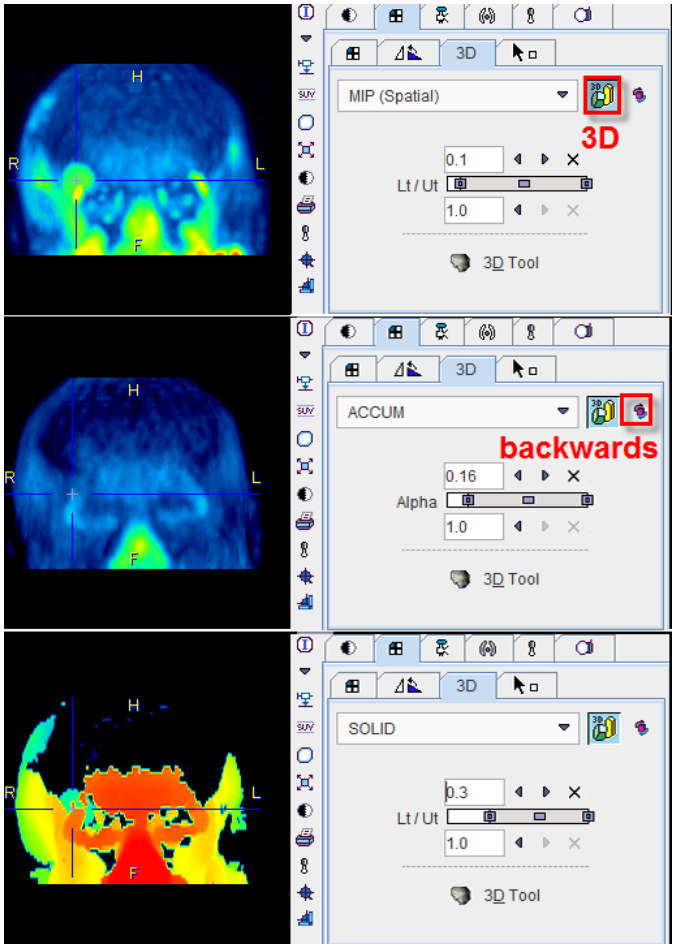
Instead of showing individual slice images, a volumetric data set can be volume rendered. Simple volume rendering can be enabled in the **3D** sub-pane



There are four methods to choose from the selection

- **MIP** (Maximum Intensity Projection) being the most known one
- **MinIP** (Minimal Intensity Projection)
- **ACCUM** (Accumulation of color and opacity)
- **SOLID**

As soon as the rendering button indicated in red is activated (or `CTRL+V` on the image) the image display switches from slice display to volumetric display, with the projection direction orthogonal to the image plane. Three renderings of an example PET using the same color table are shown below. Note that the value range considered in the renderings is somewhat different.



The button to the right of the 3D selection is a toggle to perform the 3D operation from backwards, which will result in a different image in the case of a depth-dependent weighting function.

Note that image scrolling is still enabled in 3D mode. When `CTRL+Drag` the left mouse button over the image, the 3D rendering disappears and the slice images are shown until the mouse button is released.

Rotating MIP

To create a rotating coronal MIP movie please proceed as follows:

- In the **Layout** pane select the **Coronal** orientation (or CTRL+Y in the image).
- In the **3D** pane enable MIP and 3D, then adjust the upper/lower thresholds.
- In the **Movie** pane the number of slices has been replaced by the number of projections with a default value of 40 angles. Increase the number to get smoother rotations. Start playing.

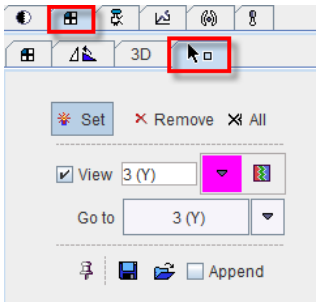
MIP images will be calculated from different viewpoints and displayed as a rotating cine. If you would like to save a movie, enable the saving button as explained in ***Showing and Saving Movies*** (on page 159).

Transfer to Full 3D Rendering

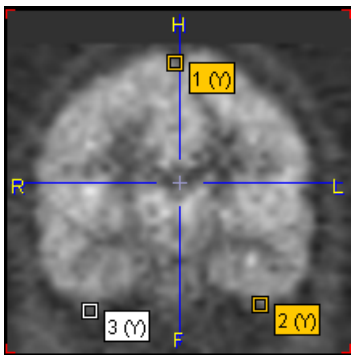
The  button in the 3D pane is only functional if the PMOD 3D option is installed. When this button is activated, the current data set is loaded into the full 3D rendering tool for advanced processing.

Markers

The **Markers** sub-pane



is used in combination with landmark-based image matching.The best way to define landmarks is to operate in the orthogonal layout.

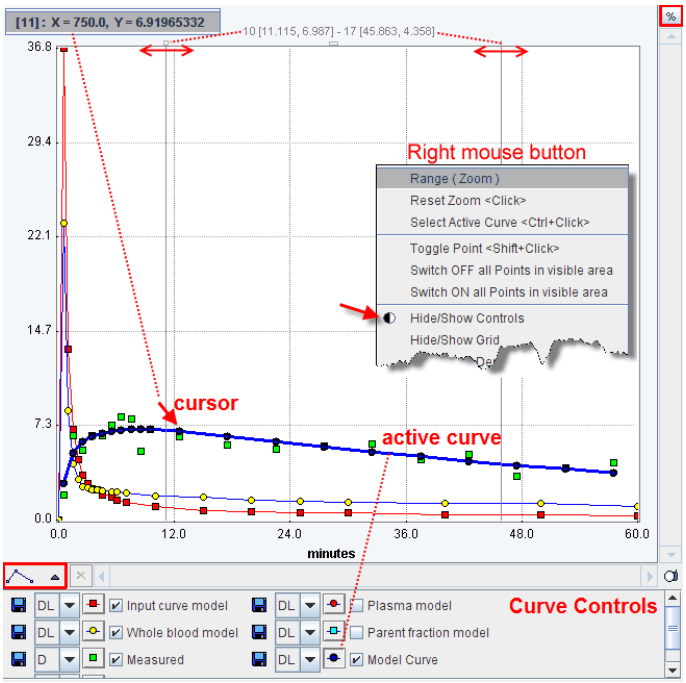


If the **Set** button is active the user may click into an image to define anatomical landmarks which are shown in the image. To avoid marker generation, hold `CTRL+SHIFT` when clicking. The slices can be scrolled by the mouse wheel or by `CTRL+DRAG`.

The spatial arrangement of landmarks can be saved for later use with . If the pushpin button is enabled , the clicks into the image will still produce markers even when the **Markers** pane is closed.

Curve Display

A common curve display object is used in all PMOD tools. It consists of a curve area and a controls area underneath.



In some contexts the control area may initially be hidden. The context menu can be used to show it

Curve Area

The curve area shows the curves which are enabled for display. There is always an *active curve*, which is shown in bold. A curve can be made active by holding down the `CTRL` key and clicking at one of its points, or by pushing its button in the controls area as illustrated with the **Model Curve** above.

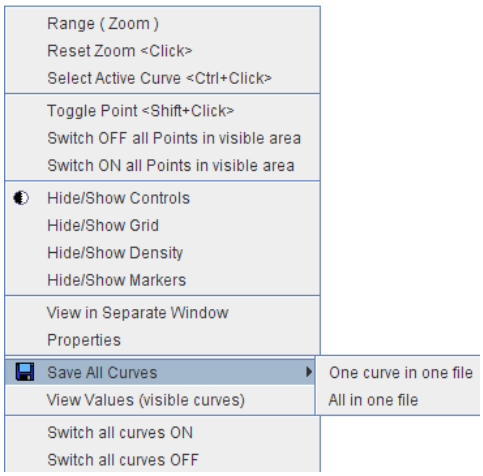
The definition of the active curve is relevant for the tools which interrogate the curve values:

- There are two small handles at the top of the curve area: a little rectangle to the left, and a line to the right. These are handles which can be moved left/right using the mouse, and the gray vertical lines move with them. The values at the top center of the curve area represent the interpolated (x/y) values of the active curve at the location of the handles. To get the measurements of a different curve just `CTRL+Click` at that curve to get the values updated.
- Only in some curve displays: When the cursor is brought close to a point of the active curve, its x/y value pair is shown at the upper left of the curve area.

To *zoom* into an area of the curve just click the left mouse button to the corner of the area of interest and drag a rectangle. After releasing the mouse button the display is zoomed into the defined rectangle. An alternative is to define the axes **Range** in the context menu. A single mouse click into the curve area is sufficient to reset the zoom.

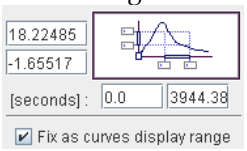
Context Menu

By clicking the right mouse button into the curve area a context menu with some additional options can be opened.



The functions are:

Range (Zoom) Set the range of the x- and y-axis by entering a numeric value.



If the box is checked, the range is maintained during all manipulations. Otherwise, a single click resets the range to the default.

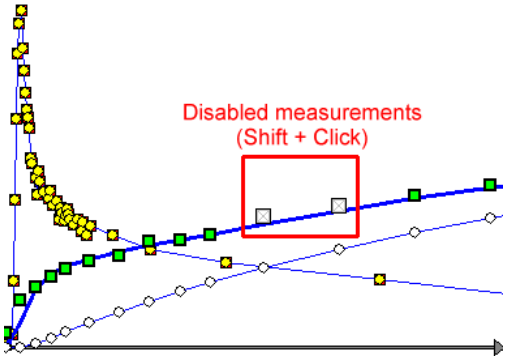
Reset Zoom To reset the curve range to the default full range. It is grayed if the display is not zoomed or the range is fixed.

Mouse operation: single `Click` into curve area.

Select Active Curve Selects the curve nearest to the point clicked with the right mouse button to open the context menu.

Mouse operation: `CTRL+Click` at a curve.

Toggle point Disable a measurement of the active curve. This is reflected by setting the symbol to gray.



In the context of model fitting measurements marked in gray are regarded as outliers and not considered when evaluating the cost function.

Mouse operation: select the relevant curve to active, then `SHIFT+Click` at measurement.

Switch ON/OFF all points in visible area — In combination with zooming this option allows to quickly disable/enable contiguous points of the active curve.

Hide/Show Controls — Allows hiding the controls if the curve display area is small, and to show them again.

Hide/Show Grid — Controls the display of the grid lines.

Hide/Show Density — Reflects the density (coded distance) of points in the graph as a colored map. More points close together produce a "higher" color.

Hide/Show Markers — Controls whether the measurement markers are shown.

View in Separate Window — With this option, the curve display can be opened in a separate, large window to closely examine the plot.

Properties — With this entry a configuration dialog is opened for setting the annotation **Font size**, and for enabling curve **Antialiasing** (smooth curve appearance).

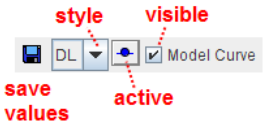
Save All Curves — Allows saving the numeric data of all curves in a single or separate text files.

View values (visible curves) — Opens a dialog window which shows the numeric values of all visible curves in a dialog window. The window contents can be copied to the **Clipboard** and pasted to a different application.

Save All Curves ON/OFF — To quickly change the visibility of all curves. When switching all off, the active curve is still shown.

Curve Control Area

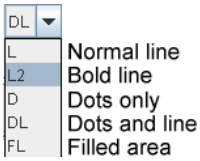
The control area lists the curves which are available for display. There are several elements to modify the curve appearance:



Show/Hide To show/hide a curve check/uncheck the *visible* box.

Active curve To set a curve to active click at the *active* button, or directly `CTRL+Click` on the curve itself. The line/symbols get bold.

Style The list selection can be used to change the style of a curve:



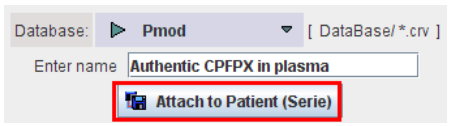
Further useful interface elements:

Connections Changes the shape of the lines defined by the measurements:

Note that calculations are not based on the display representation of a curve.

Saves the numeric data of a curve as a text file with two columns. These files obtain a **.crv** suffix and can easily be opened in Excel or a text editor.

When working with a database the curve can be attached to a particular image using the **Attach to Patient (Serie)** in the appearing dialog.



If this button is enabled, each curve is normalized to its own maximum and shown as percent values. This mode is helpful for comparing shapes when the dynamic range of the curves is very different.

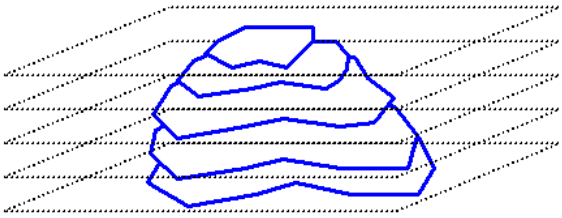
Creates a capture of the curve area. The captured image can be saved as a **JPEG**, **TIFF** or **DICOM** file. It can also be copied to the **Clipboard** to paste it into some office application.

Chapter 6
Volume-of-Interest (VOI) Analysis

The purpose of a VOI analysis is to calculate the distribution of pixel values within delineated tissue structures. There are several VOI definitions available in PMOD.

Contour VOIs

In PMOD a contour VOI is defined as a stack of planar, closed polygons which are named ROIs (region-of-interest). The contours are manually or semi-automatically outlined on the loaded images, and the pixels contained within the contour boundaries are considered for the VOI statistics.



There are a few principles to bear in mind when working with contour VOIs.

- The coordinates of the contour vertices are defined as the (x/y/z) triples. The x and y offsets are in [mm] from the image origin, whereas z represents the slice number. This makes the definition independent of the planar image resolution and the zoom factor. However, note that modification of the origin coordinate results in a shift of all VOIs defined for the image study.
- A contour VOI can be defined in each of the orthogonal directions. Naturally however, a single VOI can only consist of contours in the same direction.
- Contour VOIs consist of one ROI per slice.
- An ROI can have multiple independent contours per slice. For each contour the user can define, whether the included pixels should be included into the statistics or excluded from it. By defining contours with exclusion, VOIs with hollow parts can be created.
- Single pixels are a special case of contours. They can be easily added the VOI, or removed from the contour VOI.
- For dynamic data the VOI can be extended to the temporal dimension as well. This means that the VOI may have a varying shape or location at different acquisitions, allowing to track moving organs over time. As long as the VOI has only been defined at one time point, it is applied equally at all times (static VOI). When defining the VOI differently at different times, care must be taken that the VOI is defined at *all* times.
- Many studies can be loaded and processed in parallel. Hereby it is possible to have individual VOIs for the different studies, but the VOIs can also be shared among spatially matched images.

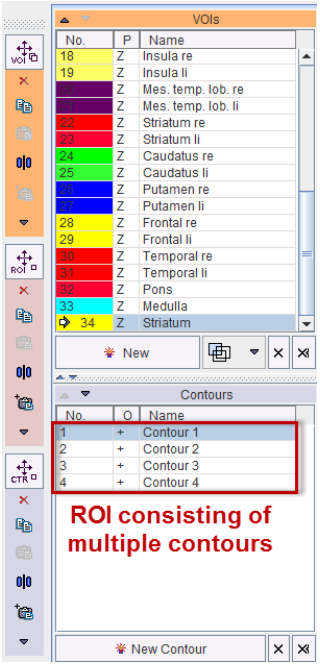
This hierarchy of three levels

1) VOI, consisting of ROIs in different slices

ROI, consisting of contours within a slice

Contour, a closed polygon

is reflected in the VOI user interface. Each level has a corresponding tool bar for object manipulations. For instance, when selecting the VOI button and shifting, the contours in all slices will be shift. When selecting the ROI button and shifting, only the contours in the current slice will be shifted.



Template VOIs

A template VOI is an image file which contains numeric label information for the different anatomic structures as the image information. This VOI information can be loaded into PMOD and used for statistics. The template VOI approach has the advantage that the structures can be arbitrarily complex, and that the results of external segmentation programs can easily be used within PMOD. The disadvantage is that the VOI definition cannot be modified. However, in PMOD it is simple to convert template VOIs into contour VOIs.

Often, template VOIs are used in combination with atlas images. Brain atlas images are representative images of the (human, rat, etc.) brain imaged with a certain modality (PET, SPECT, T1 MR, T2 MR, etc.) showing a normal brain. Usually, the images of many normal subjects are brought into alignment and are then averaged. This results in somewhat blurry template images which show the characteristic pattern of the brain in the particular modality. The template images are used as a basis for the standard analysis of individual images. First, the images are spatially normalized (elastic warping) to the template, and then a set of standard VOIs is applied to the normalized images to obtain regional statistics. Typically, the VOIs in the template space are template VOIs which are universally applicable, not contour VOIs which are program-specific.

The PMOD softrware includes a human brain template VOI (AAL), a rat brain template VOI (W. Schiffer) and a mouse template VOI (M. Mirrione) with corresponding normalization templates in the image fusion tool. For using the template VOIs a user should first spatially normalize the individual brain images using the corresponding normalization template.

Map VOIs

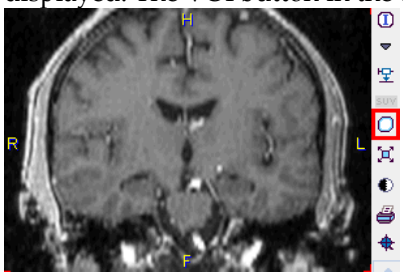
A map is a file, which contains label numbers in all pixels which identify different objects in the image. PMOD can load and analyze such a file and create a VOI template out of it. A special case are the object maps (*.obj) resulting from segmentations in AnalyzeAVW. These can directly be loaded as Map VOIs.

Mask VOIs

A mask is a binary file, which contains 1 in all pixels belonging to the tissue of interest, and 0 in all other pixels. It is most likely the result of some threshold or segmentation operation of the images to be analyzed. A mask-based VOI analysis provides two pixel distributions, from the tissue of interest and from the background. Any image can be loaded and used as a mask VOI. If it is not a binary image, the user can specify the threshold below which the pixels are converted to 0, while the other pixels are converted to 1.

Starting VOI Analysis

PMOD supports the access to VOI analysis in almost all situations when an image is displayed. The VOI button in the tools list next to the image

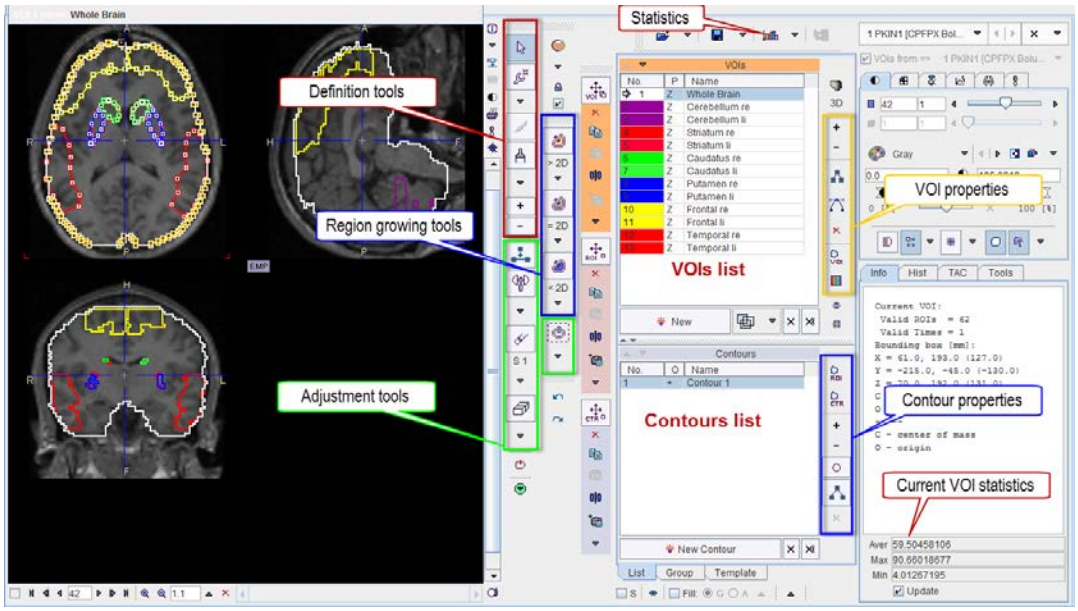


immediately starts the VOI tool with the current images. In the PVIEW tool, there is a separate tab **VOIs** for entering the VOI definition mode.

In This Chapter

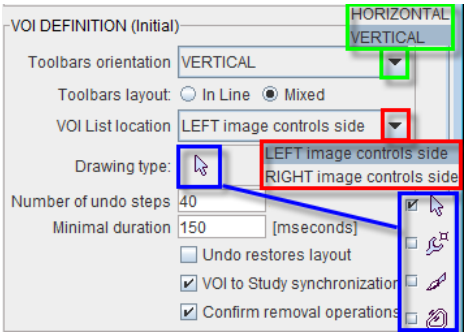
VOI Interface

When starting VOI definition a set of user interface items appears.



Layout Options

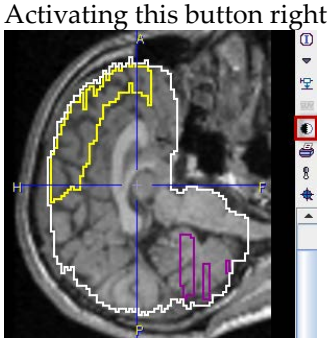
Note that a substantial part of the functionality is grouped on toolbars which can be detached and dragged to a suitable location by their handle ⋮⋮. The VOI toolbars can be organized vertically as illustrated above or horizontally, according to the **Toolbars Orientation** in the **Display/Report** pane of the ***tool configuration*** (on page 25).



Tool Hiding Options

If during image inspection the image space is too much reduced by the VOI tools, there are two ways to reduce the tool area:

Activating this button right to the image



will hide all the tools. Activating it again recovers the original layout.

This toggle button hides the list of VOIs and contours, while giving still access tot the VOI definition and editing tools. Another activation brings the list back.

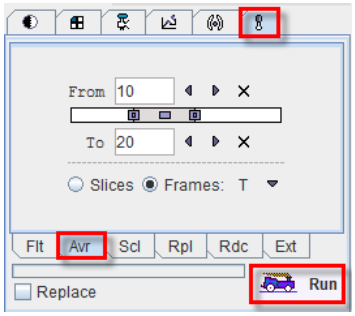
Using Contour VOIs

Preparations

Before starting contour definitions it is recommended to first take the time to locate the slice of interest, zoom and pan, so that the structures to be delineated are clearly seen. Also, it should be decided which of the orientations is best suited for the outlining.

VOIs for Dynamic Studies

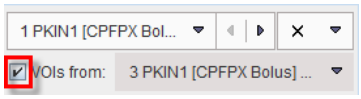
Often the anatomical information in dynamic studies is not sufficient to delineate VOIs. In some cases, averaging of a part of the acquisitions provides a clearer picture. A quick way for time-averaging is to select the tools tab and average some frames without replacing the study.



Another method is to define the VOIs in matched anatomical images of the same patient. Such a set of VOIs can then be applied to the dynamic study to derive time-activity curves.

Using Multiple Files Simultaneously

When multiple images have been loaded (or additional ones have been created by averaging frames as shown above), each of them has its own set of VOIs. The image series and the VOIs can be switched using the selection at the top

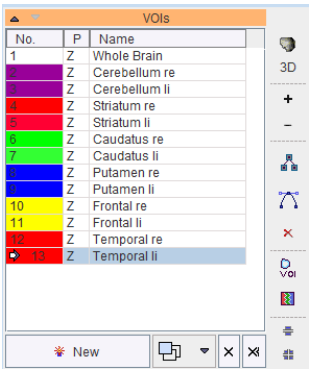


Please note the synchronization box **VOIs from**. If it is checked, the studies and the VOIs can be selected independent from each other. If it is not checked, each study uses its own VOIs, and the VOI selection is not active.

CAUTION: If VOIs are to be defined in one study and used in another, the two studies must be matched beforehand, meaning that both of them have the image origin at exactly the same anatomical location. This type of matching can be performed with the PMOD Image Fusion tool.

VOI Level Properties

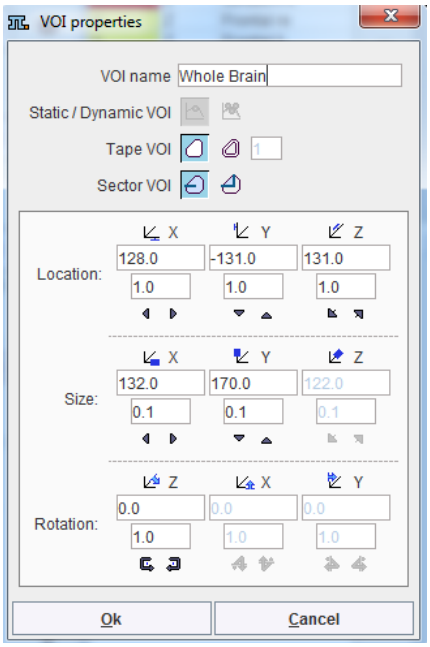
The **VOIs** section on the **List** tab contains the list of defined contour VOIs, and VOIs which are in the progress of outlining.



The **New** button creates an empty VOI in the list, with the plane direction **P** according to the currently selected plane in the image area. The buttons serve for deleting the selected VOI, or all VOIs, respectively. The arrow buttons on top of the list allow changing the VOI ordering by moving the selected VOI. represents the mode, how VOI overlapping is handled. The **+** and **-** buttons to the right set all contours of the selected VOI to **+** and **-** respectively as described ***below*** (on page 185). Similary, the and set the contour mode to straight line or B-spline connection.

VOI Properties

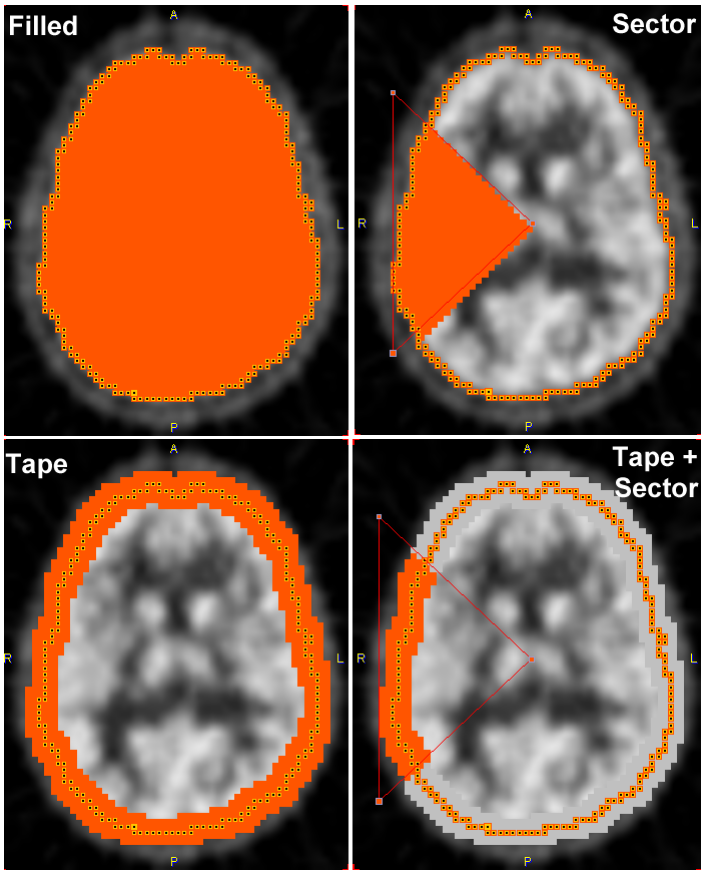
In addition to the plane orientation a VOI has several properties, which can be changed using the button. It shows the VOI properties dialog window illustrated below.



The window allows changing the properties, and immediately updates the display for providing a visual feedback. The property elements have the following meaning:

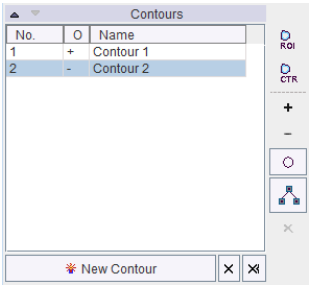
	**Static VOI**  : This property is only relevant for dynamic series. If a VOI is static, the same VOI definition is applied and shown at all times. **Dynamic VOI**  : This property is only relevant for dynamic series. For dynamic VOIs, a different VOI definition can be used at different times. Note that a dynamic VOI is only shown when viewing the images of the time frame it was defined on. As long as only one VOI is defined, statistics calculation will apply this VOI at all times as with a static VOI. However, as soon as VOIs have been defined at more than one time, it is required that VOIs are defined at *all* times. Here the VOI propagate functionality may be helpful.
	**Filled VOI**  : All pixels inside the contours belong to the VOI. **Tape VOI**  : The contour is interpreted as the center line of a VOI which includes pixels inside a band along the contour. The number of pixels inside and outside can be specified. This type of VOI was introduced for myocardium VOIs.
	**Full VOI**  : Uses pixels from all directions. **Sector VOI**  : Only the pixels in a defined angular sector will be considered. The sector angle can be defined in the **VOI Action** Mode using the handles at the angle corners. This type of VOI was introduced for myocardium VOIs.
Location	X, Y and Z position of the VOI relative to the origin in [mm]. The location can be changed by entering new coordinates or using the incrementing arrow buttons.
Size	Size of the VOI bounding box in mm. The sizes can be changed and result in a proportional scaling in the corresponding direction. The sizes can be edited or incremented by the arrow buttons. Note that for contour VOIs consisting of planar ROIs the scaling is only supported within the ROI planes, not orthogonal to it. Object VOIs can be scaled in all directions.
Rotation	The VOI can be rotated in space. Note that for contour VOIs consisting of planar ROIs rotation is only supported around the axis orthogonal to the ROI plane. Object VOIs can be rotated around all directions. The angles can be numerically specified in degrees, or incremented using the arrow buttons.
	**Color Palette**. Allows changing the contour color. All contours belonging to a VOI have the same color.

The illustration below illustrates the effect of the different properties on the pixels used for VOI statistics.



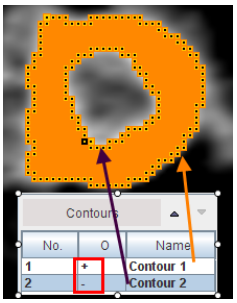
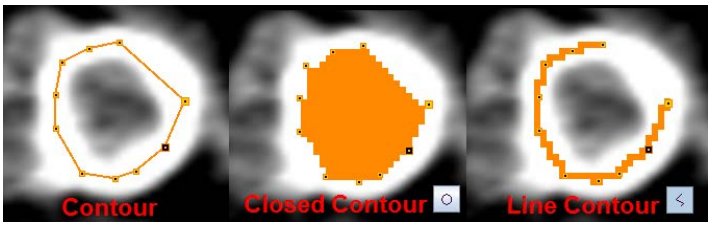
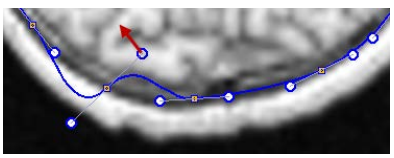
ROI and Contour Level Properties

The **Contours** section contains the list of the contours defined in the current slice of the image series for the VOI selected in the **VOIs** list. All contours belonging to a VOI in a single plane form together the planar ROI. When



The arrow buttons on top of the list allow changing the location of the selected contour in the list.

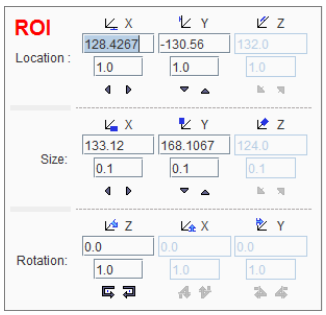
Each contour has properties, which can be changed with the buttons on the right of the list.

+	**Plus Contour**: This buttons sets all contours selected in the list to **+** in the operation column **O**. The meaning of a **+** contour is that the pixels enclosed by the contour are included in the statistics. This operation mode is equivalent to the OR set operation.
−	**Minus Contour**: This buttons sets all contours selected in the list to -. The meaning of a **-** contour is that all enclosed pixels are excluded from the statistics. This operation mode is equivalent to the AND NOT set operation. Cardiac example illustrating how a negative inner contour can be used to create a hollow VOI.  **CAUTION:** The first contour in the list needs to be a **+** contour.
Toggle	**Closed Contour**: The last vertex is connected to the first vertex, defining the VOI as the inner of the polygon. **Line Contour**: Only the pixels along the trajectory from the first to the last contour vertex are included into the VOI. 
Toggle	**Vertices Contour**: This is the default mode, whereby vertices are connected by straight lines. **B-Spline Contour**: After contours have been defined, they can be switched to B-Spline mode, whereby a spline function is calculated which passes through all vertices. Initially the lined will minimize the bending energy, but there are control handles at each vertex to change the boundary conditions. 

Similar to the VOI level, the size and angle can be changed on the contour level by two approaches.

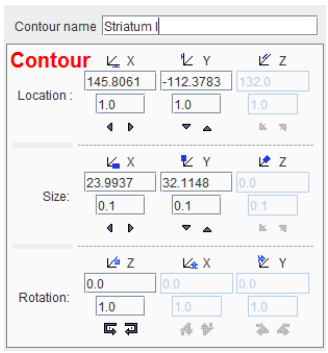
ROI Properties

All contours belonging to a VOI in a single plane form together the planar ROI. The properties of all ROI contours can be changed at once by the ROI button, which shows the dialog window below. It allows changing the **Location**, **Size** and **Rotation** angles of the ROIs. The translation and scaling operations are restricted within the contour plane plane, and the to rotation around the orthogonal.



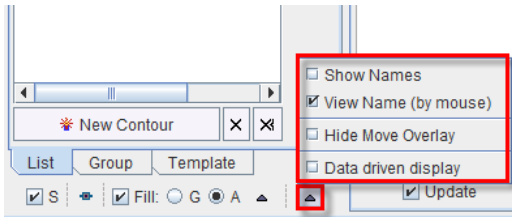
Contour Properties

The properties of individual contours can be changed by the CTR button, which works similar as the ROI button. It additionally offers changing the **Contour name**.



Contour Display Properties

In the lower right, there are some properties defining how the VOIs are displayed in the image overlay.



The following properties can be configured in the option menu:

Show Names	Shows the VOI names next to the contours in the image overlay. Note: The location of the names can not be changed.
View Name (by mouse)	Shows the names of the VOIs below the cursor in a separate section at the top of the image. Overlapping regions are shown as a list of names.
Hide Move Overlay	Hides the handle for moving the VOI to avoid obstructing the view with small VOIs. The VOI shifting/rotation operations have to be performed with the keyboard arrow cursors.
Data driven display	Determines the behavior of the image layout when switching between different series. If the box is checked, each image has its own properties such as layout, zoom, color etc. Otherwise, the images are shown with the same layout properties.

Usually contours are outlined on images displayed with interpolation, often combined with image zooming. In such a representation the images look smooth, even if the original pixels are big as with modalities suffering from low spatial resolution relative to the structure being outlined. To make sure that the right pixels are included in the VOI it is recommended - especially for small structures - to examine the VOI pixels as follows:

1) Check the **S** box. The display shows only the contours of the currently selected VOI to avoid confusion in the presence of multiple VOIs.

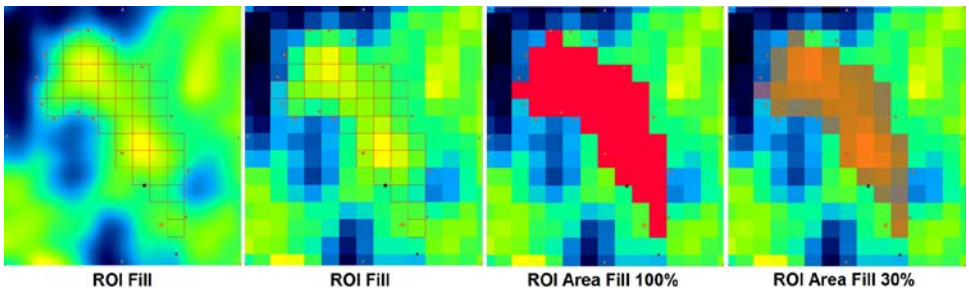
Check the icon. The VOIs vertexes are hidden.

Check the **Fill** box. The display now shows a grid with the VOI pixels (**G**). The grid can also be filled by setting the radio button to **A** (opaque filling). The degree of opacity can be change using the UP arrow right to the **A** button, whereby 100% indicates full opacity.

Disable image smoothing by disabling the

button in the image control section.

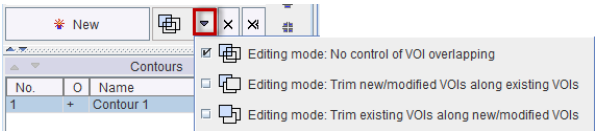
Modify the VOI contours with the **Fill** box checked, for instance by moving a vertex. The grid is updated as soon as the changes are completed.



Note: PMOD only considers the entire pixels for the statistics calculation which are visualized with the **Fill** functionality.

Overlapping Control

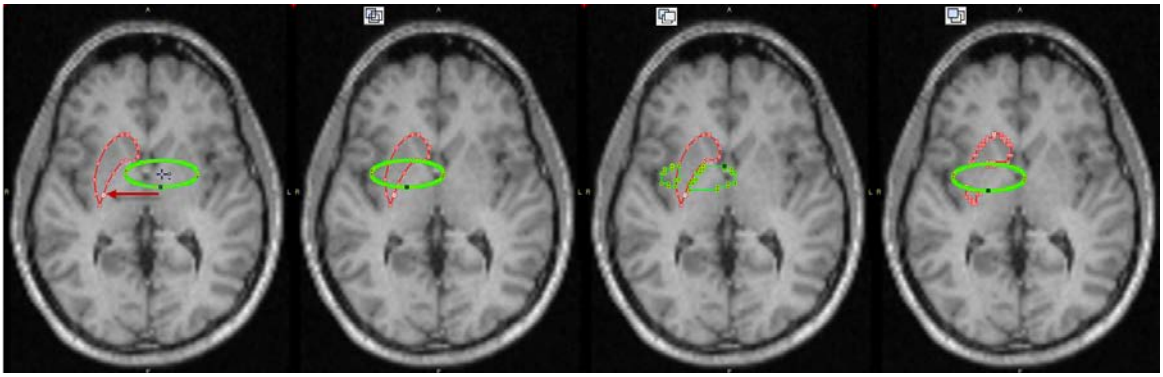
When defining several VOIs, the user may want to control whether they can overlap, or not. To this end, the editing can be set to one of three different modes as illustrated below.



Their effect is as follows.

	**No control of VOI overlapping**, contours can intersect arbitrarily.
	**Trim new/modified VOIs along existing VOIs**. The existing VOIs have priority. The new VOI is modified by removing any intersection area with the existing VOIs.
	**Trim existing VOI along new/modified VOIs**. The new VOI has priority. The existing VOIs are modified by removing any intersection area with the new VOI.

The example below illustrates the effect when shifting the green ellipse left in the different control modes.



Contour Definition Tools

VOI Contour Generation Modes

There are several methods for generating contours:

1) **Edit Mode:** Manually outlining a contour polygon by clicking with the left mouse button at vertex points. This will create a contour with relatively sparse vertices. It is easy to adjust, but tends to be coarse.

Draw Mode: Drawing a trajectory with closely spaced vertices by holding down the left mouse button and dragging along an anatomical structure. This will create a contour which is well-defined but relatively difficult to adjust because of the many vertices which have to be moved.

Iso-contour ROI Mode: There is a "pseudo-snake" function which follows pixels with similar values to enclose the largest object in the slice. It can look for cold or hot spots. This is an easy way to outline objects with a clear contrast to background in a single slice (**2D**), but can be extended in an easy way to consistently outline the same object in multiple slices (**3D**).

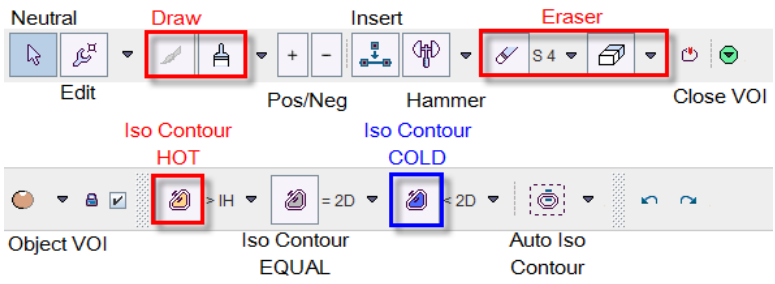
Iso-contour ROI Interactive Mode: Interactive 3D VOI outlining is based on region growing as long as the mouse button is hold. It can look for cold, hot or equal spots. Depending on the selected option, the algorithm is looking for the pixels above (for **HOT**), below (for **COLD**) or which equal (for **Maps**) the threshold, allowing or not the inner sparings.

Single Pixel Mode: The user can click at individual image pixels to add or remove them from a contour VOI. This way of defining VOIs is most flexible, and recommended when tight control is required, for example when working with small animal data.

Auto-Iso-contour Mode: This mode is similar to the **Iso-contour ROI Mode**, but is generating iso-contours at a well-defined threshold in a whole volume. The function can look for cold or hot objects, and can also generate multiple contours per slice to outline disconnected structures. Optionally, allows inner sparing, similar to the **Iso-contour ROI Interactive Mode**. In addition, the **Auto-Iso-contour Mode** algorithm can be restricted to a object VOI, within which the outlining is performed.

Regular VOIs: There is a list of regular objects (cube, sphere, etc) which can be generated centered at a defined point in the image. Some of the objects generate a stack of contours in a number of contiguous slices. After the creation they behave like normal contour VOIs. Other object VOIs remain analytically defined and can easily be scaled and moved in all directions. These VOIs are very helpful for cropping the image to a part of interest (for instance the brain in rat images), and also as restrictions to be applied in region-growing VOIs.

There is a toolbar in the VOI interface which collects the different VOI editing modes. Note that the arrangement can be horizontal as illustrated below, or vertical, depending on the tool configuration. The toolbar can also be detached for placing it at a convenient location on the screen.



Contour Outlining Process

After creation with **New**, a VOI is ready for the definition of a single contour per slice. Once a contour has been created in a slice, contour drawing is no more active. For adding another contour definition in the same slice, the user has to activate the **New Contour** button first.

During contour outlining or editing, it is important that the right VOI/contour is selected. A VOI can be selected by clicking at the entry in the **VOIs** list. If contours have already been outlined, the display will position on a slice with a contour of the selected VOI. Alternatively, a VOI can be selected by directly clicking at a contour vertex in the image.

It is recommended to complete the definitions of one VOI before the next is created. To this end, the user should work through the slices containing the object: In each slice outline the required contour(s) and then step to the next slice using the mouse wheel. Alternatively, if the contours are similar in neighboring slices, the contour(s) can be propagated to the next slice and then adjusted.

Undo/Redo/Neutral

VOI definition is a tedious task, and many situations may occur where the user would like to undo a change. To this end an **Undo** function for most manipulations of contour VOIs is available on a separate taskbar.

The arrow to the left undoes operations (goes back through history), while the button to the right redoes operations (goes forward through history).

Note: The Undo function is not applicable to changes to the image information itself.

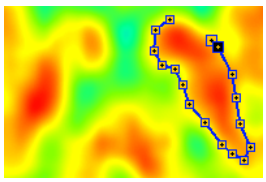
Neutral Mode

Browsing the image in the orthogonal layout involves clicking into the image. When VOI definition modes such as iso-contouring are active, clicks may introduce unwanted changes to the VOI definitions. This can be avoided by selecting the **Neutral Mode** with the  . Note that while working in a VOI editing mode, the VOI functionality can momentarily be disabled by holding down `CTRL+SHIFT` during clicking.

Vertex Edit Mode

In the **Edit Mode** the cursor changes to

By clicking the left mouse button into a slice without a contour of the selected VOI, the contour definition is immediately started and the first vertex appears. Additional clicks add more vertices to the ROI in the current plane.



There are two possibilities to close the contour,

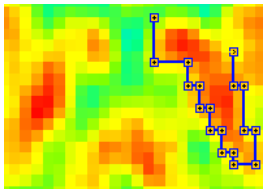
1) by double-clicking

by selecting the finish button  on the toolbar or the context menu.

Closing connects the last defined vertex with the first vertex. This operation can be undone by the unfinish button . Once a contour is closed, no vertices can be added any more, but the existing one can be moved by clicking at them and dragging them around.

Another option in **Edit Mode** is the cursor **Edit snap to grid:**

The snapping of the VOI polygon edges to the pixel grid during the drawing procedure clearly indicates the included pixels.

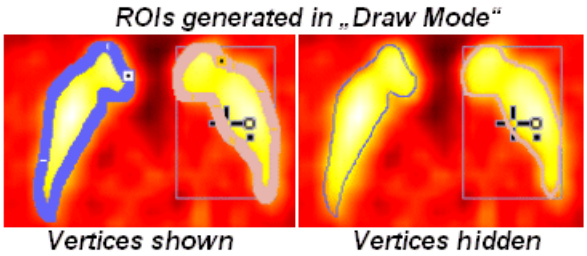


It is recommended to switch off the image **Interpolation** button when using this ROI definition mode.

Contour Drawing Mode

In the **Draw Mode** the cursor changes to

A contour can be generated by holding the left mouse button and dragging the cursor along the desired trajectory.

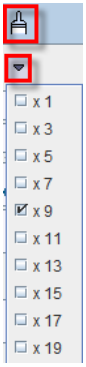


As soon as the mouse button is released, the contour is closed. This contouring mode generates many closely spaced vertices. To view the contour more clearly, the vertices can be hidden by checking the **Hide Vertices** box.

Paint ROI by Circle (2D)

In the **Paint ROI by circle (2D)** the cursor changes to

The 2D paint brush of the PMOD VOI tool is a circle and can have different sizes which may be selected from the option list close to the brush button.

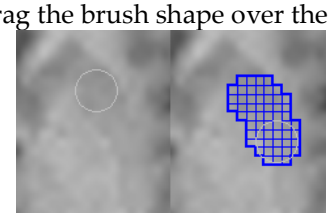


A contour can be generated by holding the left mouse button and dragging the brush along the desired area.

To create a contour VOI:

1) Activate the 2D paint brush button .

Drag the brush shape over the area which should be within the VOI.

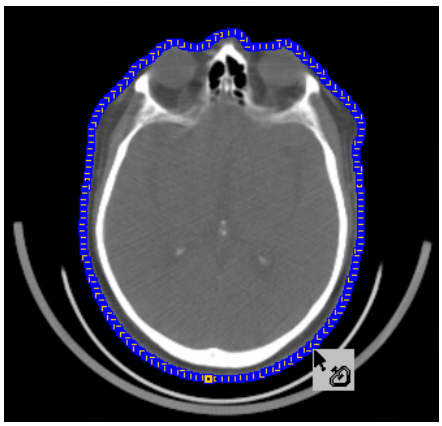


Iso-contour Mode (Pseudo-Snake)

In the **Iso-contour Mode** the cursor changes to

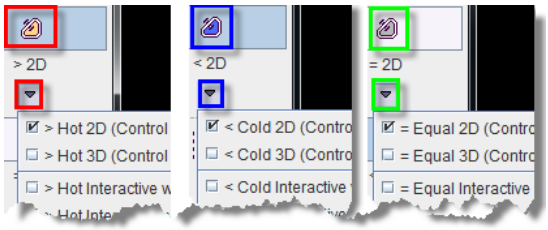
HOT or **COLD** or **EQUAL**

As soon as the left mouse button is clicked into an image, the pseudo-snake algorithm tries finding the largest closed iso-contour at the clicked image value and represents it as a closed polygon.



Note: Each time the button is clicked, the contour is replaced by a new iso-contour. This behavior is in contrast to the other drawing modes which require to first clear a contour, or opening it. To add a new iso-contour make sure you press the control button and the left mouse button simultaneously (CTRL+click)

The user can select the appropriate mode from the option list next to the iso-contour button as illustrated below. The automatic mode of iso-contouring can be 2D or 3D and dependent whether the user is aiming at a hot, cold or equal contour.



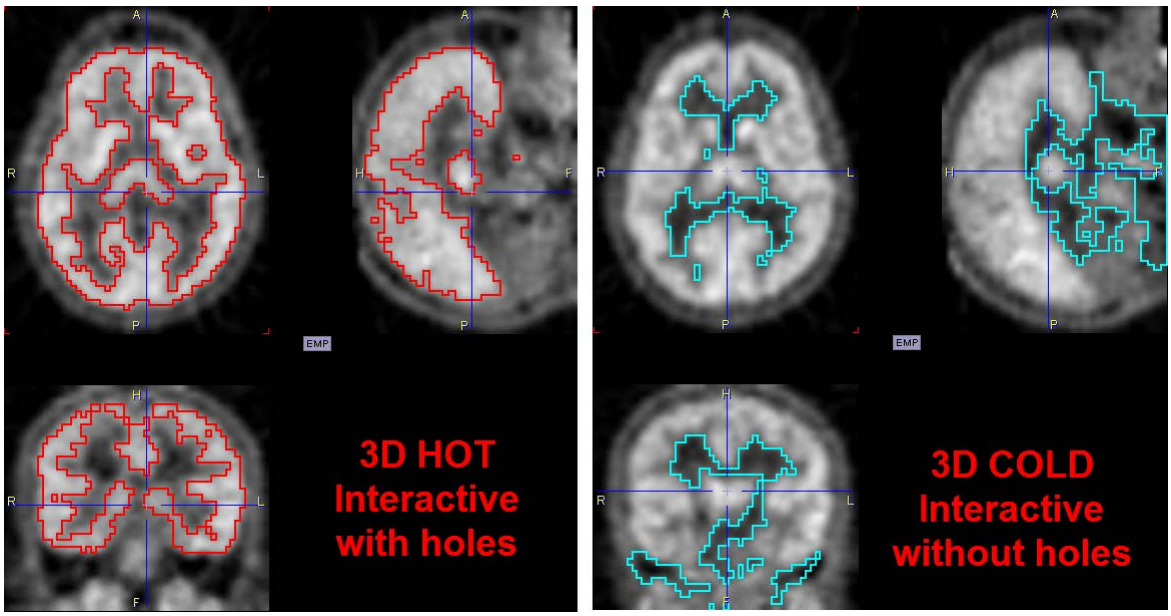
Iso-contour Interactive Mode

Similar to the **Iso-contour Mode (Pseudo-Snake)** the cursor changes to

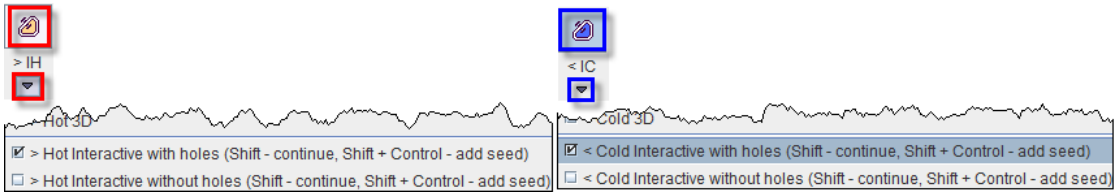
HOT  or **COLD**  or **EQUAL** 

Interactive 3D VOI outlining is based on region growing as long as the mouse button is hold. It can look for cold, hot or equal spots. Depending on the selected option, the algorithm is looking for the pixels above (for **HOT**), below (for **COLD**) or which equal (for **EQUAL**) the threshold, allowing or not the inner sparings.

Initially, the area to include within the VOI need to be located. Then the mouse button need to be clicked at the edge and held until the outlined VOI completely encompasses the area of interest. After completion of outlining, the VOI can still be extended. There are two options: the first (SHIFT+click+hold) allows continuing the region growing from the original seed, while the second (CTRL+click+hold) allows adding a new seed and continuing region growing from the new point.



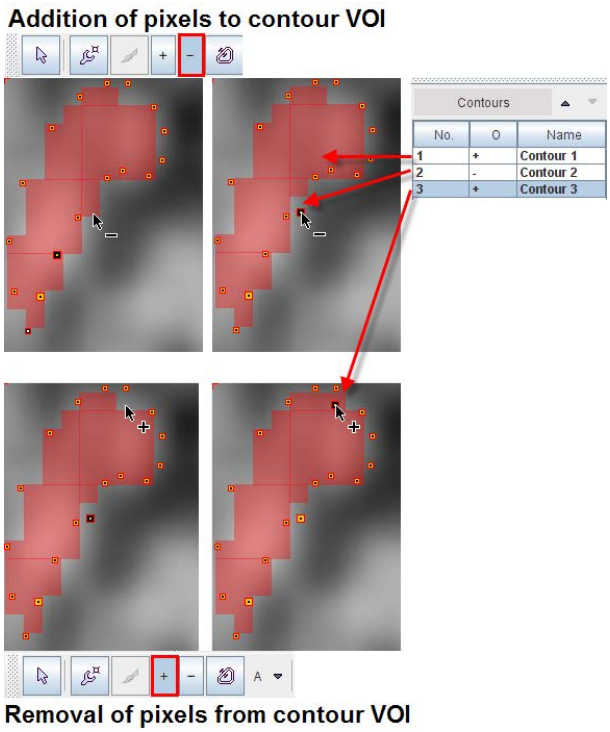
The user can select the appropriate mode from the option list next to the iso-contour button as illustrated below. The automatic mode of iso-contouring is 3D and dependent whether the user is aiming at a hot, cold or equal contour.



Adding/Removing individual Pixels

Whenever working with contour VOIs, the user can add or remove individual pixels as illustrated below. The initial **contour 1** is filled in transparent mode. First pixel removal is activated by selecting the **-** button in the toolbar. The cursor shape changes accordingly, and by clicking at a shaded pixel the negative **Contour 2** is created and the pixel removed (upper row). Whenever the user clicks into the image, the corresponding pixel will be removed from the VOI and a corresponding **-** contour is added to the list.

Pixel adding works in the same way. It is activated by selecting the **+** button in the toolbar, and the cursor shape changes accordingly. Whenever the user clicks into the image, the corresponding pixel will be added to the VOI and a corresponding **+** contour is added to the list (lower row).

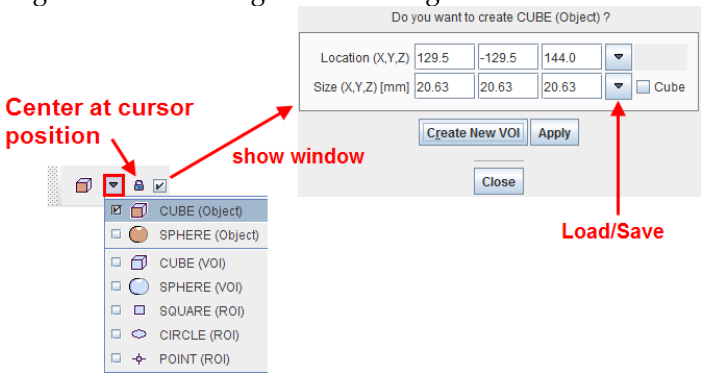


Note that it is possible to create VOIs which consist of individual pixels only. The **+** button is active as soon as a **New** VOI has been created.

Regular VOIs

The PMOD VOI functionality supports the easy generation of regular geometric objects. They are helpful for easily creating bounding boxes and for statistics based on regular objects like spheres of a certain size rather than free-form contours.

Regular VOIs can be generated using the multi-function button illustrated below.

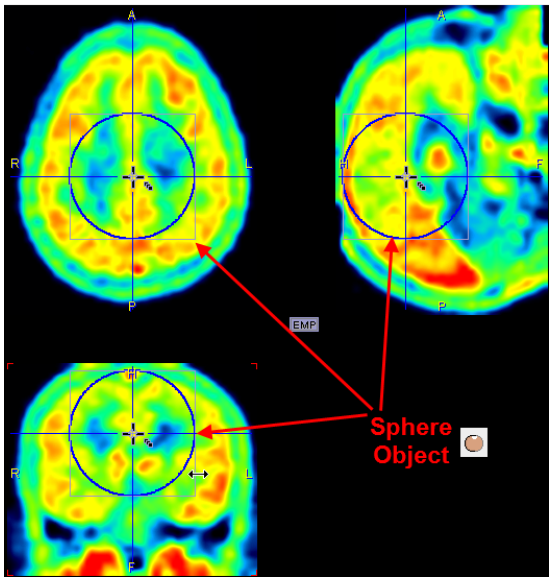


The list contains two sections. The **CUBE (Object)** and the **SPHERE (Object)** are based on an analytical definition of the shape and the center coordinate. The other VOIs are generated from an analytical description, but the result is a set of standard outline contours.

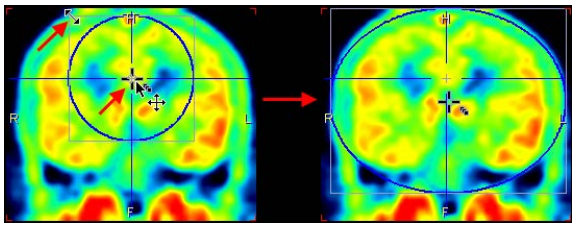
The regular objects are defined by the center location as well as some shape-dependent parameters. These definitions can be modified in a dialog window which is shown if the box indicated in the illustration above is checked. If it is not checked, the standard shape parameters will be applied. There are two modes for the center **Location** defined by the / toggle. In the position the location is defined by the last click into the image. In the position the location is not changed by mouse clicks. Activating **Yes** finally creates the object.

Object VOIs

The shapes can be scaled, so that ellipsoids of arbitrary sizes can be created from a **SPHERE (Object)**, and cuboids from a **CUBE (Object)**. The dialog window contains **Location** and **Size** fields for the exact object specification. If the box for proportional is checked (**Cube** in the illustration above), only one size field is shown. The **Create New VOI** button generates a new VOI in the list with the specified sizes, while the Apply button overwrites the currently selected VOI. The illustration below shows an example result with a sphere object.



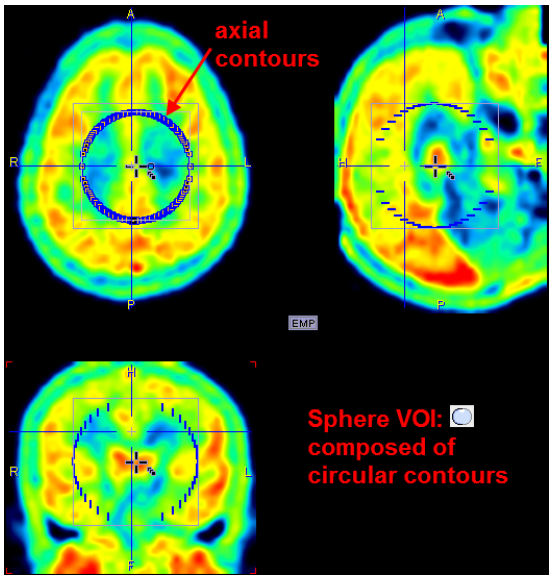
To change the location and size of the object please ensure that the **VOI Action** button is active , so that the handles for object manipulation are shown. The center of the object can then be dragged by the central handle with the left mouse button, and the shape can be scaled by dragging the sides or the corner of the bounding box in any direction. Note that holding the `SHIFT` key during dragging will maintain the aspect ratio in two dimensions. The result is an object with the shape of an ellipsoid.



Non-Object VOIs

The non-object regular VOIs are formed out of planar polygons. The example **SPHERE (VOI)** illustrated below has been created with the axial plane active. Therefore circular

contours were generate in the axial planes which together form a sphere. Such VOIs can be edited in the same way as normal contour VOIs. For instance they can be scaled within the definition (axial in the example) plane, but not in the other dimension.

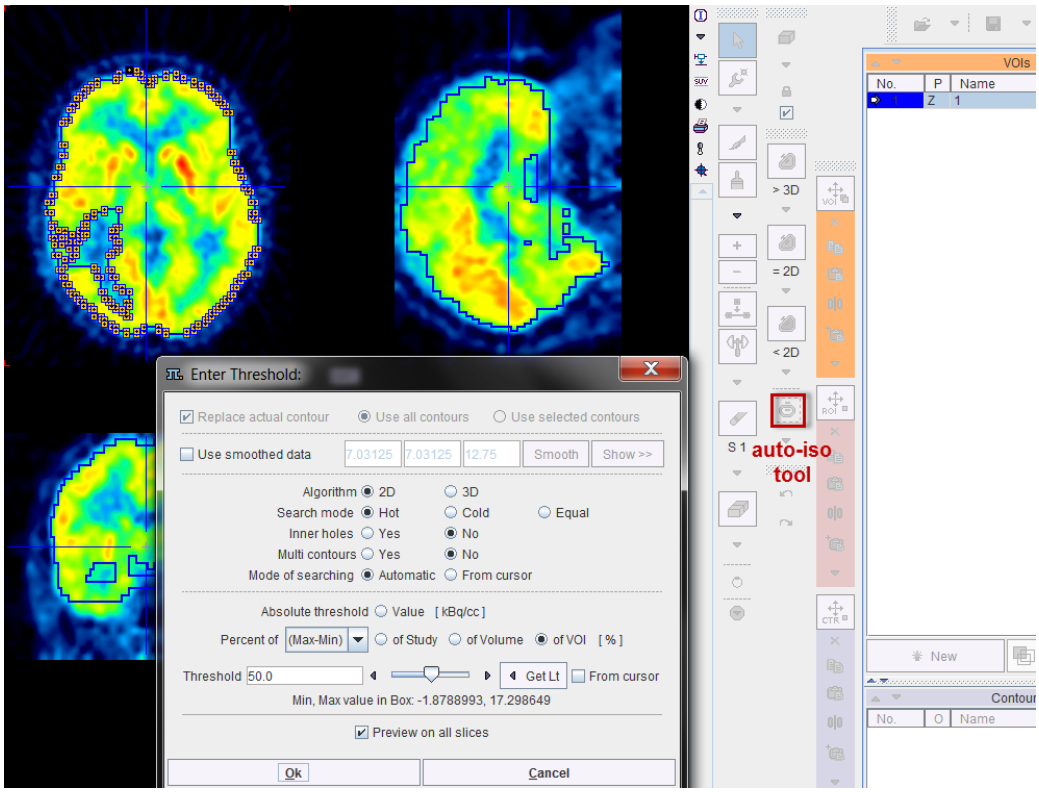


Auto Iso-contour VOIs

The auto iso-contour tool ("auto-iso") serves for the contouring of structures based on an intensity threshold by region growing. This process can be restricted within an existing VOI, otherwise it will work on the whole image volume.

Contouring without Restriction

The whole image volume will be processed, if the auto-iso tool is started without selecting a non-empty VOI in the **VOIs** list. This situation is given before VOI definitions have started yet, or by creating an empty **New VOI**. The situation below illustrates the initial situation when starting auto-iso on an FDG Brain image: One single **Hot** contour is shown at a threshold level of **50%**. without allowing **Inner holes.** The procedure operates in **2D** and defines the contours in the **Z** plane, because this plane was active at the time the tool was started.



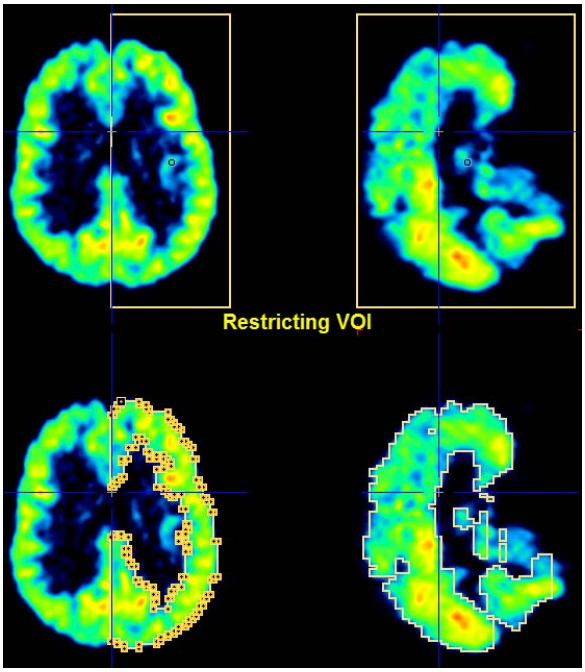
There are various parameters which change the behavior of the algorithm:

- **Threshold** options: The user can chose between various types of threshold definitions using the radio boxes. With **Absolute threshold** the iso-contouring value should be entered in image units into the **Threshold** number field. With **Percent of Study**, **Percent of Volume**, **Percent of VOI**, the value entered in the **Threshold** field is interpreted as a percentage of the dynamic range (**Max-Min**) of the whole study, the current frame of the study, or the enclosing VOI, respectively. Instead of the **Max-Min**, the percent threshold can be related to the **Max** only. There are two alternatives to entering the values manually: **Get Lt** copies the value of the lower threshold in the color table. With the **From cursor** check box enabled, the value is updated with the pixel value whenever one clicks into the image.
- **Algorithm**: **2D** processes each slice individually, whereas 3D performs the searching in all 3 dimensions.
- **Search mode**: **Hot** (**Cold**, **Equal**) is including pixels above (bllow, equal to) the threshold value, respectively.
- **Inner holes**: In the case of **Yes**, pixels not meeting the criterion which are fully enclosed by pixels meeting the criterion are removed from the resulting VOI. Otherwise, the VOI will be completely filled.
- **Multi contours**: With **Yes**, the generation of multiple VOIs is allowed. Otherwise, only the largest VOI will be returned.
- **Mode of searching**: Automatic is starting region-growing with the aim to detect structures of maximal volume, whereas **From cursor** allows to start the search from a manually defined location. In the latter case the **From cursor** checkbox next to **Get Lt** should also be enabled.

The updated contours are shown in the image, whenever a parameter is changed. For a complete visualization, **Preview on all slices** should be enabled. To accept the VOI definition, close the dialog window with the **Ok** button.

Contouring with Restriction

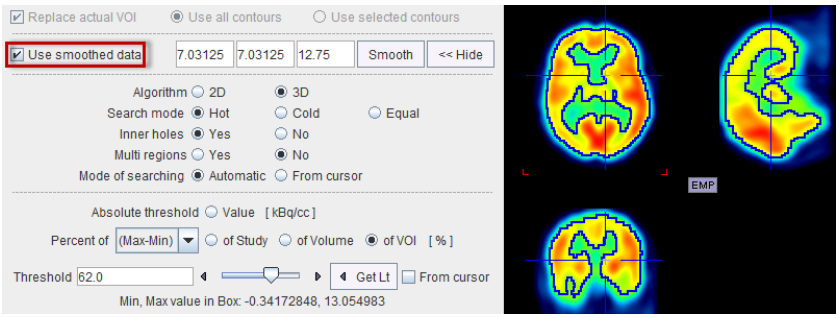
The process described above can be restricted to the volume of an existing VOI. To do so, select the restriction VOI in the VOIs list, and start the auto-iso tool. The example below illustrates contouring in a box VOI placed on the left brain hemisphere.



Depending on the setting of **Replace actual contour**, the bounding VOI will be overwritten, or a new VOI will be created with the contouring result.

Contouring with Smoothing

In order to get smoother contours than the original data supports, the procedure can work on a smoothed copy of the data. This functionality is activated with the **Use smoothed data** box. Each time the **Smooth** button is activated, the data copy is filtered with a Gaussian function using the three numbers as the FWHM in mm along x, y and z. By adjusting the filter sizes and repeated filtering, a gradually smoother copy and correspondingly smoother contours in the original image can be generated. The **Show>>** button can be activated to see the smoothed copy as illustrated below.

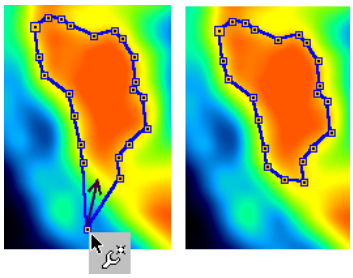


Editing Contour Shapes

The following tools are available for adjusting the shape of completed contours.

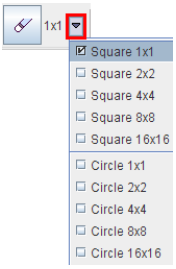
Moving Individual Vertices

When the **Edit Mode** is active, the user can click at individual contour vertices and then drag them to more appropriate positions. Clicking at contours from different VOIs will automatically select the corresponding VOI in the **VOIs** list.



Deleting Vertices

The eraser of the PMOD VOI tool can have different shapes and sizes which may be selected from the option list close to the eraser button.

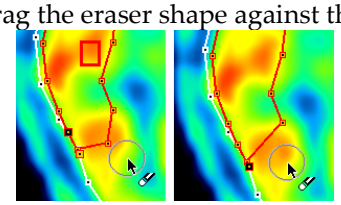


To delete pixels from a contour VOI:

1) Select the affected contour by selection in the **VOIs** and **Contours** list.

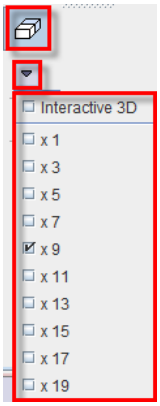
Activate the eraser button  .

Drag the eraser shape against the contour vertices which should be removed.



Erase 2D and erase 3D IH

The 2D eraser of the PMOD VOI tool is a circle which size can be selected from the option list:

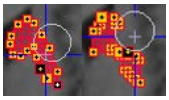


To delete parts from a contour VOI:

1) Select the affected VOI by selection in the **VOIs** list.

Activate the 2D eraser button .

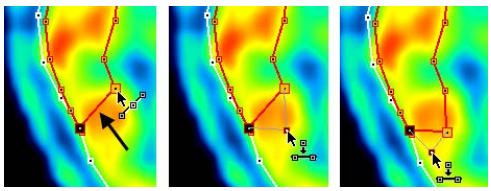
Click the eraser shape on the ROI area which should be removed.



The **Interactive 3D** removal is based on a sphere region growing algorithm. Initially, the area to be excluded from the VOI need to be located. Then the mouse button need to be clicked and held until the 'growing' sphere completely deletes the area of interest. After completion, the removal can still be extended simply by click+hold. The 3D removal based on region growing continues from the new point.

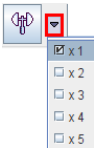
Inserting Vertices

It is also possible to insert vertices at any location into contours. As soon as the insertion tool is activated , the cursor shape changes accordingly. The contour to be edited can be selected by clicking at a vertex point, or by selection in the **VOIs** and **Contours** list. The segment into which a new vertex is inserted is determined by the vertex at which the user clicks, and is indicated by the emphasized vertices at both ends. When moving the cursor, the prospective two new segments are indicated by two faint lines. When the user clicks. the vertex is placed and the two new segments added. This procedure will continue for one of the created segments. To modify a different part of the contour please click at one of the vertices there. Note that the vertex locations cannot be changed in the insertion mode.



Shape Deformations

For the shape adjustment of densely populated contours a dedicated hammer tool is available. Similar to the eraser tool it can be configured for different sizes.

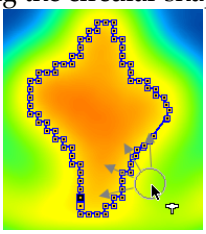


To change the contour shape with the hammer tool:

1) Select the affected contour by selection in the **VOIs** and **Contours** list.

Activate the hammer tool  .

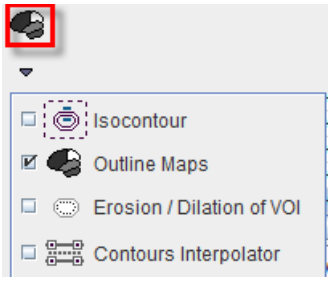
Drag the circular shape towards the contour vertices which are pushed radially away.



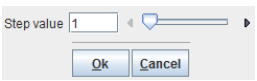
Outline Maps

A map is a file which contains integer pixel values called object labels. The labels typically identify different objects in the image volume. Such maps are often the product of segmentation procedures.

Map files in different image format can be loaded into PMOD. In the **VOI** page of the **View** tool map files can be converted in contour VOIs. The functionality is located in the **Auto Iso-contour** selection list.



When **Outline Maps** option is selected a dialog window appears which allows specifying the bin size for the label histogram.



A **Step value** of 1 should normally work fine. The file is scanned and for each label found a contour VOI is created. Now the names can be edited and the VOIs saved.

Contour Interpolation

Contour Interpolator is a fast way of outlining a VOI which contain two ROI outlined on different slices.

The procedure is simple:

1) To start, create a new VOI and outline two ROIs on different slices.

Select the **Contour Interpolator**. The algorithm finds contours which will be morphed from the first ROI to the second one.

Note: This tool makes interpolation between two contours and doesn't use data information. At least two ROIs contours need to be available before selecting the algorithm.

Operations on Objects

Contour VOIs are formed from a stack of planar ROIs, which themselves consist of a set of contours per slice. On each of these three levels a set of similar operations are supported.

- **Scaling**: The shape can be adjusted by dragging the edges of the object bounding box.
- **Clearing**: The contents of the object is cleared, but the object continues to exist and can be used again for a new definition.
- **Copy/Paste**: An object can be copied to the clipboard, and then pasted into an empty object on the same hierarchy level.
- **Mirroring**: An object can be mirrored with respect to the central axes of the image volume.
- **Propagation**: The aim of propagating an object is to easily get a copy of an existing object in a neighboring slice or frame. Propagation can work in both directions.

These operations are organized as function buttons on toolbars corresponding to the three levels. They can be configured to appear with a horizontal or vertical layout. The following sections illustrate the vertical layout.

Contour Operations

The contour toolbar

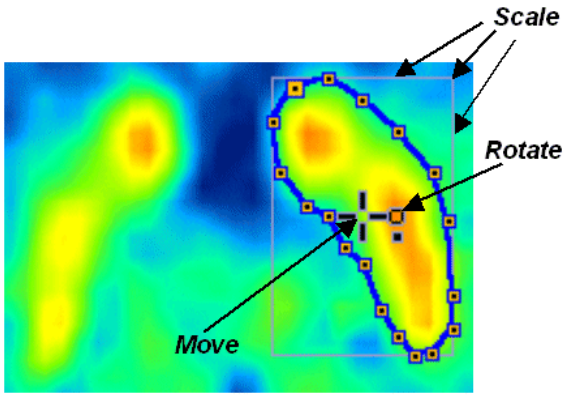
facilitates the operations related to contours. Note that only the selected contour is affected, whereas all others remain untouched.

	**CTR Action**. If this button is selected, a contour can be selected and then moved or scaled as described below.

	Clear. Clears the selected contour of the selected VOI in the current plane. The contour remains in the list, but has no defined polygon associated.
	**Copy**. Copies the selected contour to the clipboard.
	**Paste**. Pastes the contour from the clipboard into the current contour (which must be empty).
	**Mirror Vertical**. Mirrors the selected contour relative the vertical center line.
	**Mirror Horizontal**. Mirrors the selected contour relative the horizontal center line.
	**Propagate** option button. Propagation copies the selected contour of the current VOI and pastes it to a neighboring slice. Note that *all* existing contours in the target slice are *overwritten*. The different propagation variants are described below.

CTR Action

In the **CTR Action** mode an entire contour can be translated, rotated or scaled within the plane. If a VOI has multiple contours, select the target contour in the **Contours** list. As illustrated below, the operations can be performed using mouse dragging. The handle in the center of the contour allows translations and rotations. When dragging the edges of the bounding box, the contour is scaled.



Alternatively the keyboard cursor arrows can be employed:

`CURSOR UP, DOWN, LEFT, RIGHT`	Move contour accordingly
`CTRL + CURSOR UP, DOWN, LEFT, RIGHT`	Scale the contour
`SHIFT + CURSOR UP, DOWN, LEFT, RIGHT`	Rotate the contour
`ALT` + one of the above	Perform the operation 5 times faster

Individual vertices cannot be moved in CTR action mode. To edit individual vertices first switch back to the **Edit Mode** by selecting the corresponding button in the toolbar.

CTR Propagation

The following propagation options are available:

Contour Propagate -	Pastes to the next slice in one direction (depending on the plane sorting order).
Contour Propagate +	Pastes to the next slice in the other direction.
Contour ApplyToAll	Pastes to all slices of the series.
Contour SmartApply	Pastes to all neighbouring slices which have no defined contours.
Contour Follow Max -	Pastes to the next slice in one direction and centers the contour at the maximal value in the slice (eg to follow a vessel).
Contour Follow Max +	Pastes centered at the maximum in the other direction.

Contour propagation may have advantages in the following situations:

- if it is easier to adjust the propagated contour than to outline it from scratch, and
- to create a bounding VOI which roughly encloses a structure, and then using the iso-contour auto-VOI tool.

ROI Operations

The **ROI toolbar**

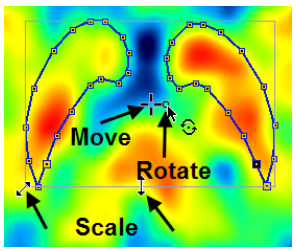
works in analogy to the **CTR** toolbar, except that all contours of the selected VOI in the current slice are changed at once.

	**ROI Action**. If this button is selected, al contours in the slice can be moved or scaled as described below.
	Clear. Removes the contours of the selected VOI in the current plane. The user can immediately begin defining a contour.
	**Copy**. Copies the contours to the clipboard.
	**Paste**. Pastes the contours from the clipboard into the current ROI (which must be empty).
	**Mirror Vertical**. Mirrors the contours relative the vertical center line.

	**Mirror Horizontal**. Mirrors the contours relative the horizontal center line.
	**Propagate** option button. Propagation means copying all contours of the current slice and pasting it to a neighboring slice. Note that existing contours in the target slice are *overwritten*. The different propagation variants are described below.

ROI Action

As illustrated below, a bounding box enclosing all contours of the selected VOI in the current slice appears together with the move/rotation handle in the center. When dragging the edges of the bounding box, all contours are scaled.



Alternatively the keyboard cursor arrows can be employed:

`CURSOR UP, DOWN, LEFT, RIGHT`	Move contours accordingly
`CTRL + CURSOR UP, DOWN, LEFT, RIGHT`	Scale the contours
`SHIFT + CURSOR UP, DOWN, LEFT, RIGHT`	Rotate the contours
`ALT` + one of the above	Perform the operation 5 times faster

Individual vertices cannot be moved in ROI action mode. To edit individual vertices first switch back to the **Edit Mode** by selecting the corresponding button in the toolbar.

ROI Propagation

The following propagation options are available:

ROI Propagate -	Pastes to the next slice in one direction (depending on the plane).
ROI Propagate +	Pastes to the next slice in the other direction.
ROI ApplyToAll	Pastes to all slices of the series.
ROI SmartApply	Pastes to all neighboring slices which have no defined contours.
ROI Follow Max -	Pastes to the next slice in one direction and centers at the maximal value in the slice (eg to follow a vessel).

ROI Follow Max +	Pastes centered at the maximum in the other direction.

VOI Operations

The **VOI toolbar**

supports operations related to the entire VOI definition. Note that all the contours are affected, not just the ones in the visible slice images.

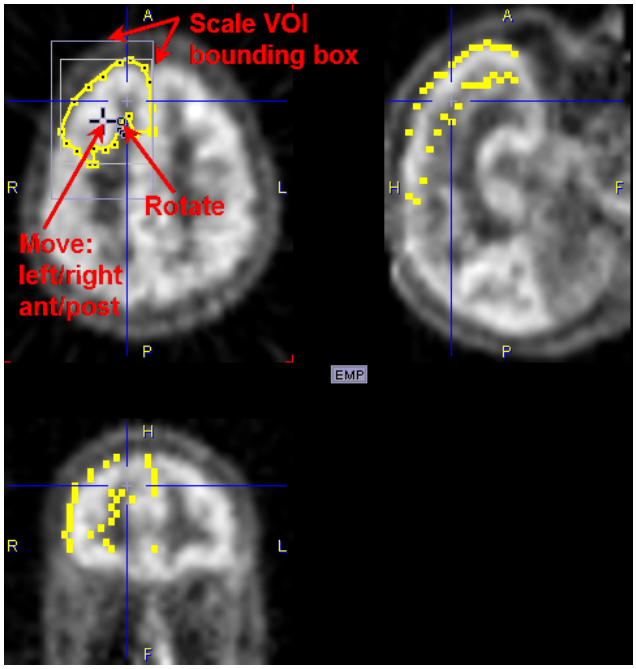
	VOI Action. If this button is selected, a VOI can be selected and then moved or scaled as described below.
	Clear. Clears all ROIs and contours of the selected VOI, leaving an empty definition.
	Copy. Copies the VOI to the buffer.
	Paste. Pastes the VOI from the buffer into the current VOI (which must be empty).
	Mirror Vertical. Mirrors the selected VOI relative the vertical center plane.
	Mirror Horizontal. Mirrors the selected VOI relative the horizontal center plane.
	Mirror Z. Mirrors the selected VOI relative the primary plane direction, ie across the slices.
	Center VOI to Min. Positions the center of the VOI bounding box at the pixel within the current VOI which has the minimal value. Note that multiple activations of the button may result in different positions.
	Center VOI to Max. Positions the center of the VOI bounding box at the pixel within the current VOI which has the maximal value. This function can be applied during a PERCIST evaluation to center the spheres at the lesion maxima.
	Propagate option button. Propagation for VOIs means copying a VOI from one time frame to another. This function is only available for dynamic series and VOIs which have the property set to dynamic. The different propagation variants are described below.

Usage of VOI Mirroring

This function can be used for creating a mirrored copy of a VOI as follows: Copy the VOI into the buffer, create a new VOI, and paste the VOI from the buffer. The two VOIs are now congruent, and one of them can be mirrored with a mirror button and moved to the destination place.

VOI Action

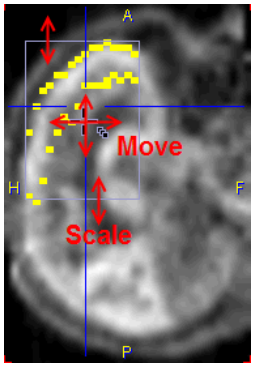
With the VOI Action mode all contours of a VOI can be modified at the same time. In most cases it will be advisable to use the orthogonal layout as illustrated below. After selecting the VOI by clicking at its contour or the entry in the **VOIs** list, several elements are shown in the overlay: the bounding box of the contours in the active slice, the bounding box of the VOI (maximum of the contour bounding boxes in all slices), and a handle for moving and rotating.



To move the VOI, drag the handle in the center with the left mouse button. Use the small rectangle for a rotation. To scale the VOI, drag the bounding box lines. After releasing the result will be updated in the other views. Note that not all operations are available in all directions:

- Scaling is only supported within the primary plane which was used for the contour definition. The reason for this behavior is the lack of contour interpolation across slices.
- Rotation is also only supported within the primary plane.
- Moving is supported in all directions. While it is arbitrary within the primary plane, shifts in the orthogonal direction (across the slices) are only possible in increments of the slice thickness.

Referring to the example above, the frontal VOI can only be scaled in the L/R and A/P directions, but not in the H/F direction. In the sagittal plane, there is no rotation handle, and the scaling is only active for the bounding box lines indicated in the illustration below (A/P).

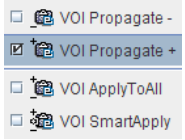


VOI Propagation

The **VOI Propagate** multi-function button serves for propagation over time and is therefore only active if

- the study is dynamic,
- and the properties of the VOI have been set to dynamic ( ).

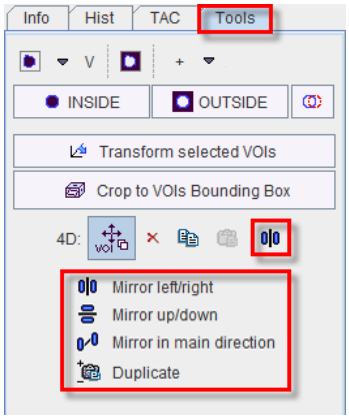
In this case, the VOI can consists of a differing definition at the different times. The button has the following options:



VOI Propagate -	Copies the current VOI, goes to the prior acquisition of the dynamic series, paste the VOI.
VOI Propagate +	Copies the current VOI, goes to the following acquisition of the dynamic series, and paste the VOI.
VOI ApplyToAll	Copies the current VOI and pastes it into all acquisitions.
VOI SmartApply	Copies the current VOI and pastes it into all subsequent acquisitions until an acquisition is encountered which already contains a VOI definition.

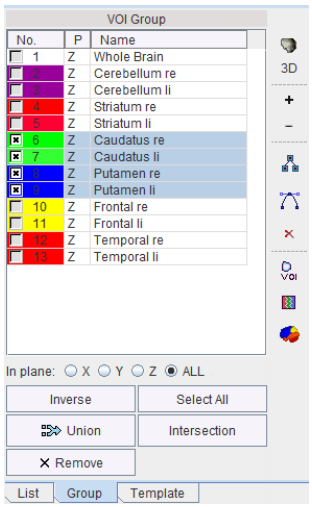
4D VOI Operations

When working with dynamic VOIs in dynamic series, an additional dimension needs to be considered, the time. Therefore, an area is available with similar tools as described above for the ROIs and VOIs. It is located on the **Tools** pane and allows a dynamic VOI to be cleared, copied, pasted, and mirrored in all frames at once.



VOI Grouping

The **Group** tab shows a list of all **List** VOIs with a selection box.



Initially, all VOIs are selected. The selection can be changed by dragging over the selection boxes and using `CTRL+Click` to selectively enable/disable VOIs. Additonally, `CTRL+A` or **Select All** selects all entries, and the **Inverse** button reverts the selection.

The buttons to the right act on the current selection. For instance, the **+** button sets the contours of all selected VOIs to positive.

VOI Union

The **Union** button serves for creating a new VOI from the selected ones. The resulting VOI includes the contours of all source VOIs, whereby the **+/-** ***property*** (on page 185) of these

contours is maintained. This function is useful for creating a VOI from sub-structures, but also to subtract a smaller VOI from a larger one.

VOI Intersection

The **Intersection** button outlines the intersection volume of two VOIs and adds it as a new VOI to the List. Two VOIs have to be selected in the **VOI** list in the **Group** tab.

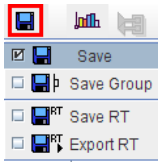
Operations on a Group of VOIs

While the **Group** tab is active rather than the **List** tab, the operations on the **VOI** toolbar will be applied to the entire group. For example, using **VOI Action**, all grouped VOIs can be moved, rotated, scaled at once. Furthermore, they can be cleared, mirrored, and masking applied.

The group operations can be refined using the radio buttons below the VOIs list. With **X pln** (**Y pln, Z pln**), only the selected VOIs with **X** (**Y**, **Z**) orientation will be included in the operation. With **ALL**, the operation will be applied to all selected VOIs.

Note: These group operations are only active as long as the **Group** tab is selected.

The grouped VOIs can also be saved together in a new VOI file, excluding the non-selected VOIs. To this end, use **Save Group** from the VOI saving menu.

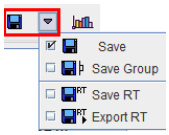


Furthermore, when calculating statistics, there is always a **Group** entry. It represents the statistics of the pixels in all the selected VOIs on the **Group** tab, even if the **Group** tab has never been actively selected.

VOI Save/Load

Saving

Once a set of contour VOIs has been defined for an image study the VOI definition can be saved using one of the **Save** option buttons



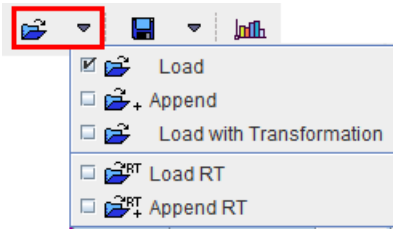
The buttons have the following function

Save	Saves all of the VOIs together with their names and color in a .voi file.
Save Group	Saves only those VOIs which are checked on the **Group** tab in a .voi file.

Save RT	Saves all VOIs as DICOM structure set objects in a file. Such DICOM structure set objects can be used in radiotherapy (RT) planning systems.
Export RT	This function also creates DICOM structure set objects, but allows to directly send them to an RT planning system using the DICOM network protocol. A dialog box pops up for selecting the target system among the configured DICOM nodes.

Loading

Conversely, contour VOI definitions can be retrieved from files using the **Load** option buttons



The buttons have the following function

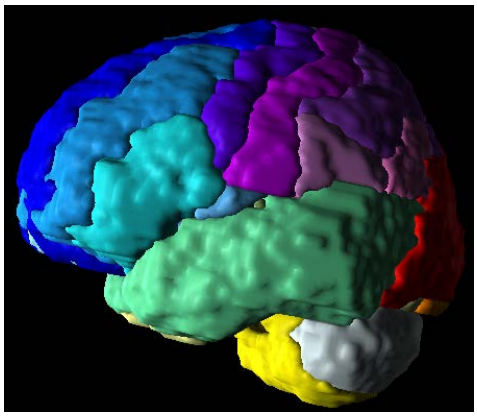
Load	First removes all current VOI definitions, then loads the ones from the selected VOI files.
Append	Loads the VOIs from the selected file and appends them to the current VOI definitions.
Load with transformation	First removes all current VOI definitions, loads the ones from the selected VOI files, and requests a spatial transformation which is applied to the VOIs. All transformations calculated in the PMOD Image Fusion tool are supported, rigid and elastic ones.
Load RT	First removes all current VOI definitions, then loads the VOIs from a file containing DICOM RT structure set objects.
Append RT	Loads the VOIs from a file containing DICOM RT structure set objects and appends them to the current VOI definitions.

3D VOI Visualization

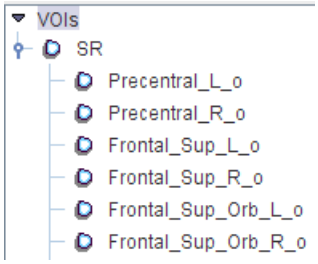
If the P3D option is installed on the system the button

is shown in the upper right corner of the VOI user interface. When it is activated, the contours can be rendered as ribbons with a width of the slice thickness, or as full surfaces.

The example shown below is a rendering of the VOIs derived from outlining the AAL template.



In the 3D tool, the VOIs are organized in a tree



so that each structure can individually be shown, hidden and colored. This might be helpful for interactive demonstration purposes to visualize the spatial relationship of the structures.

Using VOI Template Files

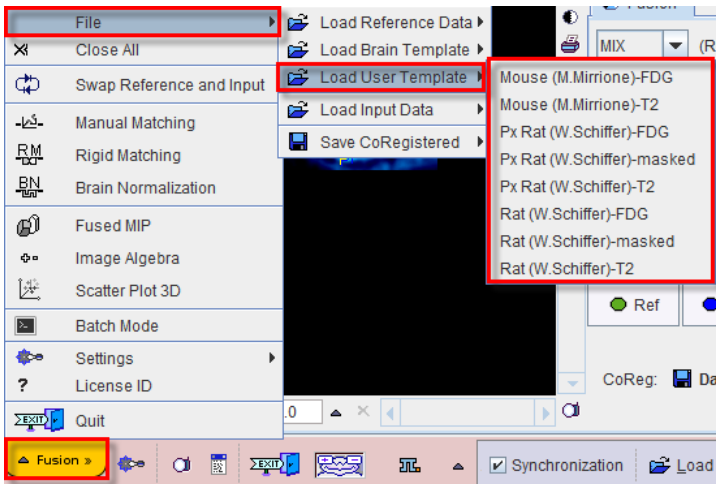
VOI templates are usually image files which represent a standard anatomy. The values in the image pixels are label numbers, and each label number corresponds to a certain anatomical region. The correspondence between label value and name is contained in a text file.

VOI Templates included in PMOD

PMOD includes several VOI templates ready to be used for data analysis. Because the experimental images first have to be brought into the standard anatomy, each template consists of a normalization template and a matched VOI template.

Spatial Normalization

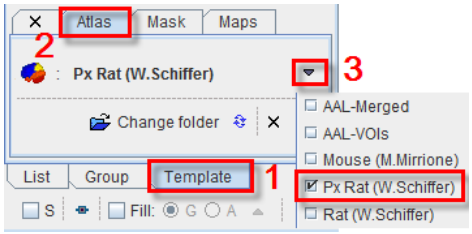
The spatial normalization can be done within the PMOD image fusion tool PFUS. There, a suitable reference image can selected from the menu as illustrated below.



Load Brain Template provides templates in the human MNI space for use with different modalities (PET, MRI), whereas the additional species templates can be loaded with **Load User Template**. After loading the reference, the user needs to load his own experimental images and perform a **Brain Normalization** processing.

VOI Template

On the resulting images, the corresponding VOI template can be applied for calculating regional statistics. It can be selected from the list of included templates as illustrated below.

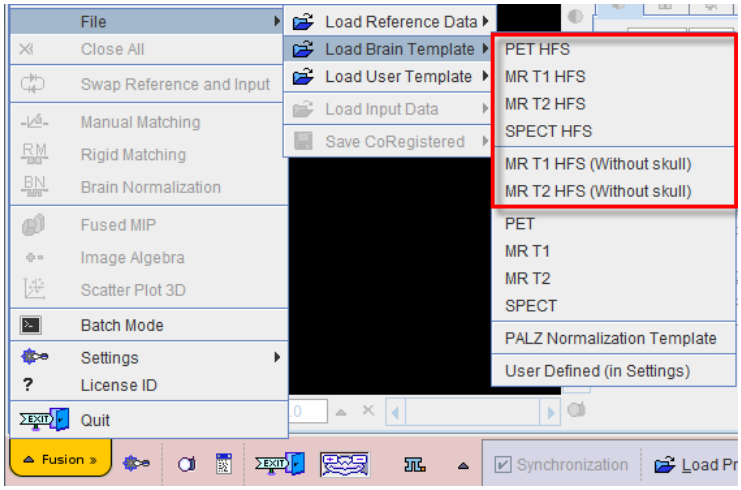


Single-Subject AAL Human Brain Template

For the analysis of human brain data the VOI template **AAL-VOIs** is available. It is the result of an automatic anatomical labeling [1] of the spatially normalized, single subject, high resolution T_1 MRI data set provided by the Montreal Neurological Institute (MNI)[2]. The template is provided in HFS orientation (radiological convention). All images which have been spatially normalized to one of the HFS templates in the PMOD image fusion tool can be analyzed with the AAL template.

Spatial Normalization

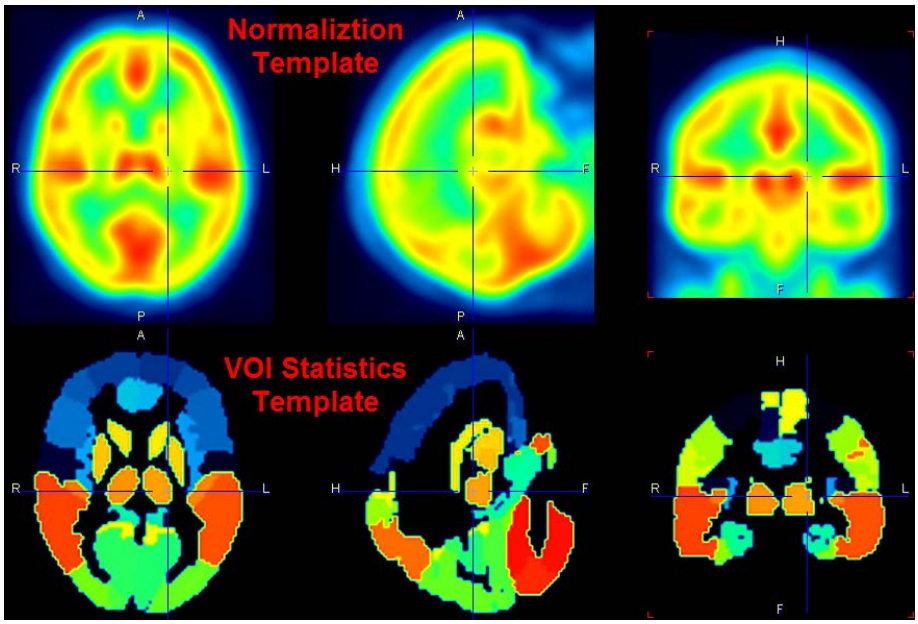
Several normalization templates are available in the fusion tool as menu entries **Fusion/File/Load Brain Template** as illustrated below.



The user should select the reference which is most similar to his experimental data. The images of these templates can be found in the *resources/templates* directory.

AAL VOI Template

For the statistical analysis, the VOI template **AAL-VOIs** can be selected in the list of included template VOIs. The corresponding files can be found in the *resources/templates/voitemplates/AAL-VOIs* directory.



There is also the VOI template **AAL-Merged** available wherein some of the small AAL regions have been combined.

Note: There is a slight asymmetry in the AAL template VOIs which corresponds to the natural asymmetry of normal brains and which is also part of the MNI template. The resolution of the AAL atlas is 2mm in all directions. Stereotactic data with other resolution must be interpolated to 2mm and brought into HFS orientation in order to apply the AAL template within PMOD.

---

[1] Tzourio-Mazoyer N, Landeau B, Papathanassiou D, Crivello F, Etard O, Delcroix N, et al. Automated anatomical labeling of activations in spm using a macroscopic anatomical parcellation of the MNI MRI single subject brain. Neuroimage 2002; 15: 273-289. ***DOI http://dx.doi.org/10.1006/nimg.2001.0978***

[2] Collins DL, Zijdenbos AP, Kollokian V, Sled JG, Kabani NJ, Holmes CJ, Evans AC. Design and construction of a realistic digital brain phantom. IEEE Trans Med Imaging. 1998 Jun;17(3):463-8.

Rat Brain Template

For the analysis of rat brain data the VOI template **Rat_W.Schiffer** [1] is available. We would like to thank Wynne Schiffer for providing the data and helping with the integrations. The coordinates of this template are the Paxinos coordinates.

Spatial Normalization

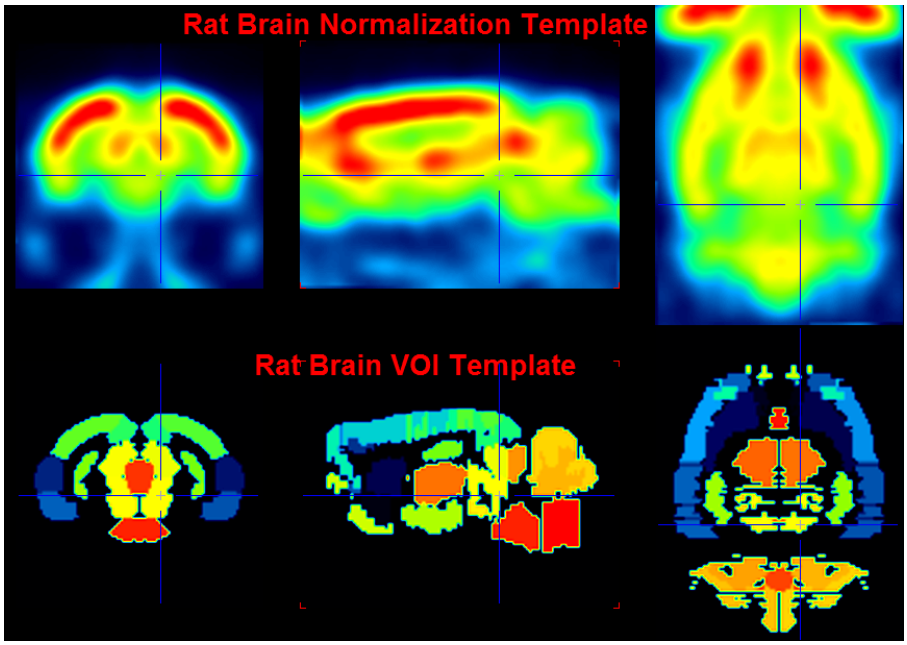
Three normalization templates are available in the fusion tool as menu entries in **Fusion/File/Load User Template**:

- **Rat_W.Schiffer-FDG**: This is an FDG PET template as illustrated below.
- **Rat_W.Schiffer-masked**: This is a masked version of the FDG PET which has been masked outside the brain. It may be helpful if the additional activity of the Haderian glands are not present in the rat images to be normalized.
- **Rat_W.Schiffer-T2**: This is a T_2-weighted MRI PET template which is in the same space as the PET templates.

The images of these templates can be found in the *resources/templates/usertemplates* directory.

VOI Template

The VOI template **Rat_W.Schiffer** can be selected in the list of included template VOIs. The corresponding files can be found in the *resources/templates/voitemplates/Rat_WSchiffer* directory.



Reference

[1] Schiffer WK, Mirrione MM, Biegon A, Alexoff DL, Patel V, Dewey SL. Serial microPET measures of the metabolic reaction to a microdialysis probe implant. J Neurosci Methods. 2006;155(2):272-84. ***DOI http://dx.doi.org/10.1016/j.jneumeth.2006.01.027***

Mouse Brain Template

For the analysis of mouse brain data the VOI template **Mouse_M.Mirrione** [1,2] is available. The species used were C57BL/6J mice. We would like to thank Martine Mirrione for providing the data and helping with the integrations.

Spatial Normalization

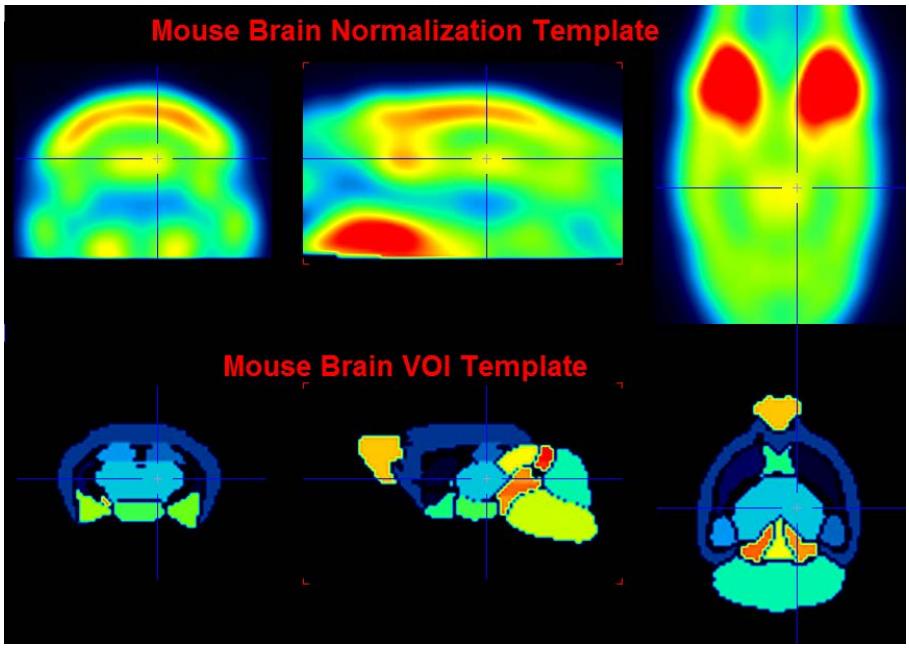
Two normalization templates are available in the fusion tool as menu entries from **Fusion/File/Load User Template**:

- **Mouse_M.Mirrione-FDG**: This is an FDG baseline PET template as illustrated below.
- **Mouse_M.Mirrione-T2**: This is a T_2-weighted MRI PET template which is in the same space as the PET templates.

The images of these templates can be found in the *resources/templates/usertemplates* directory.

VOI Template

The VOI template **Mouse_M.Mirrione** can be selected in the list of included template VOIs. The corresponding files can be found in the *resources/templates/voitemplates/Mouse_M.Mirrione* directory.



References

[1] Ma Y, Hof PR, Grant SC, Blackband SJ, Bennett R, Slatest L, McGuigan MD, Benveniste H. A three-dimensional digital atlas database of the adult C57BL/6J mouse brain by magnetic resonance microscopy. Neuroscience. 2005;135(4):1203-15. ***DOI http://dx.doi.org/10.1016/j.neuroscience.2005.07.014***

2. Mirrione MM, Schiffer WK, Fowler JS, Alexoff DL, Dewey SL, Tsirka SE. A novel approach for imaging brain-behavior relationships in mice reveals unexpected metabolic patterns during seizures in the absence of tissue plasminogen activator. Neuroimage. 2007;38(1):34-42. ***DOI http://dx.doi.org/10.1016/j.neuroimage.2007.06.032***

Cynomolgus Monkey Template

For the analysis of cynomolgus monkey (Macaca Fascialis) brain data the VOI template **Cynomolgus_CIMA-UN** [1] is available. We would like to thank Elena Prieto and Maria Collantes from the Centro for providing the data and helping with the integrations.

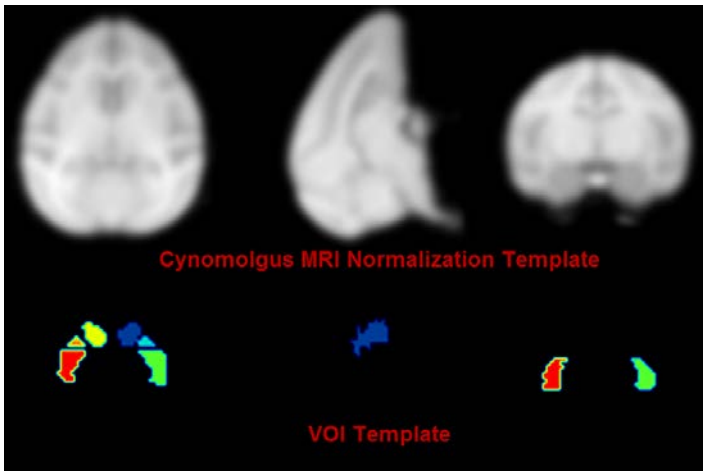
Spatial Normalization

A T_1-weighted MRI normalization template created from 15 healthy animals is directly available in the menu of the fusion tool as **Fusion/File/Load User Template**: **Cynomolgus_CIMA-UN-MRI**.

Two PET templates in the same space as are also available: **Cynomolgus_CIMA-UN-Dopa** and **Cynomolgus_CIMA-UN-DTBZ**. They can be loaded as a reference for normalization from **Fusion/File/Load Reference Data/Autodetect** from the *resources/templates/usertemplates/Cynomolgus_CIMA-UN* directory.

VOI Template

The VOI template **Cynomolgus_CIMA-UN** can be selected in the list of included template VOIs. The VOIs were hand drawn in the striatum (VOI size 400 mm^3) and occipital lobe (VOI size 310 mm^3) on axial MRI slices based on anatomical borders. The corresponding files can be found in the *resources/templates/voitemplates/Cynomolgus_CIMA-UN* directory.

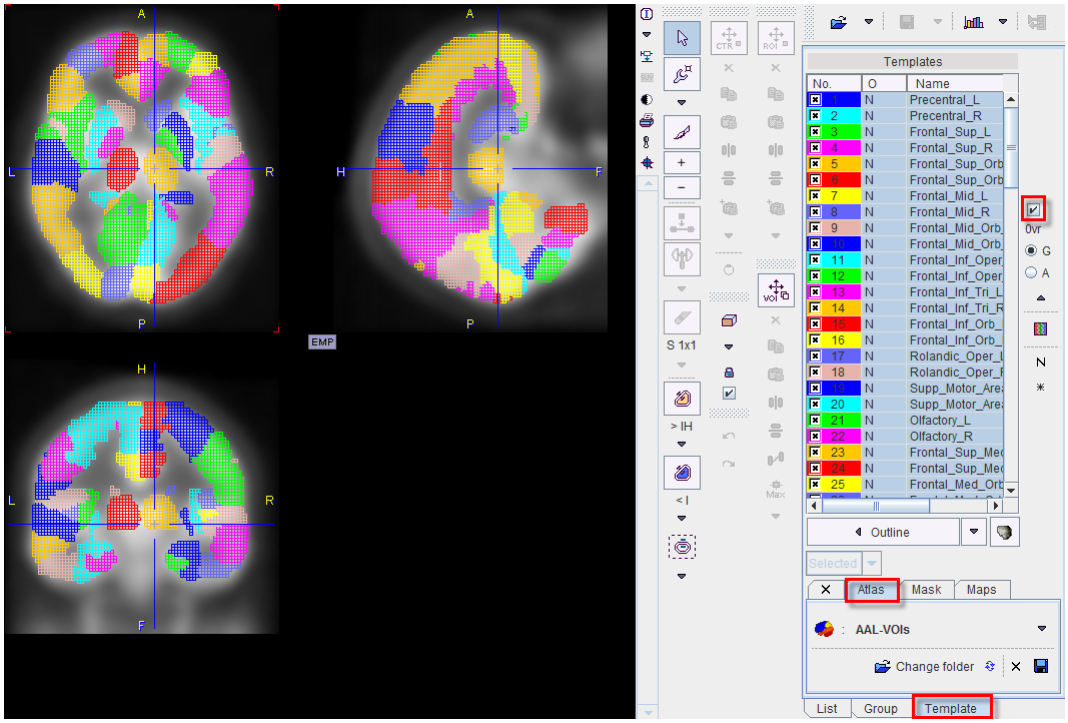


References

[1] Collantes M, Prieto E, Penuelas I, Blesa J, Juri C, Marti-Climent JM, Quincoces G, Arbizu J, Riverol M, Zubieta JL, Rodriguez-Oroz MC, Luquin MR, Richter JA, Obeso JA. New MRI, 18F-DOPA and 11C-(+)-alpha-dihydrotetrabenazine templates for Macaca fascicularis neuroimaging: advantages to improve PET quantification. Neuroimage. 2009;47(2):533-9.

Template-based VOI Statistics

When an image series has been loaded for which a suitable template exists, its use for VOI statistics is straightforward. First activate the VOI functionality, select the **Template** tab, and chose the template in the list on the **Atlas** pane.



The template description is read and the list of VOI labels populated. Initially, all regions are selected, and an overlay on the images marks their locations. The overlay can either show an open or a filled pixel raster, depending on the setting of the radio box above the **Ovr** check. To hide all template VOIs at once please un-check the **Ovr** box on the **Template** tab. To stop using the template VOIs select the **X** tab next to **Atlas**.

VOI Selection

Only the selected template regions are shown as VOIs and used for statistics calculations. The usual operations can be applied to select or de-select entries in the VOI list.

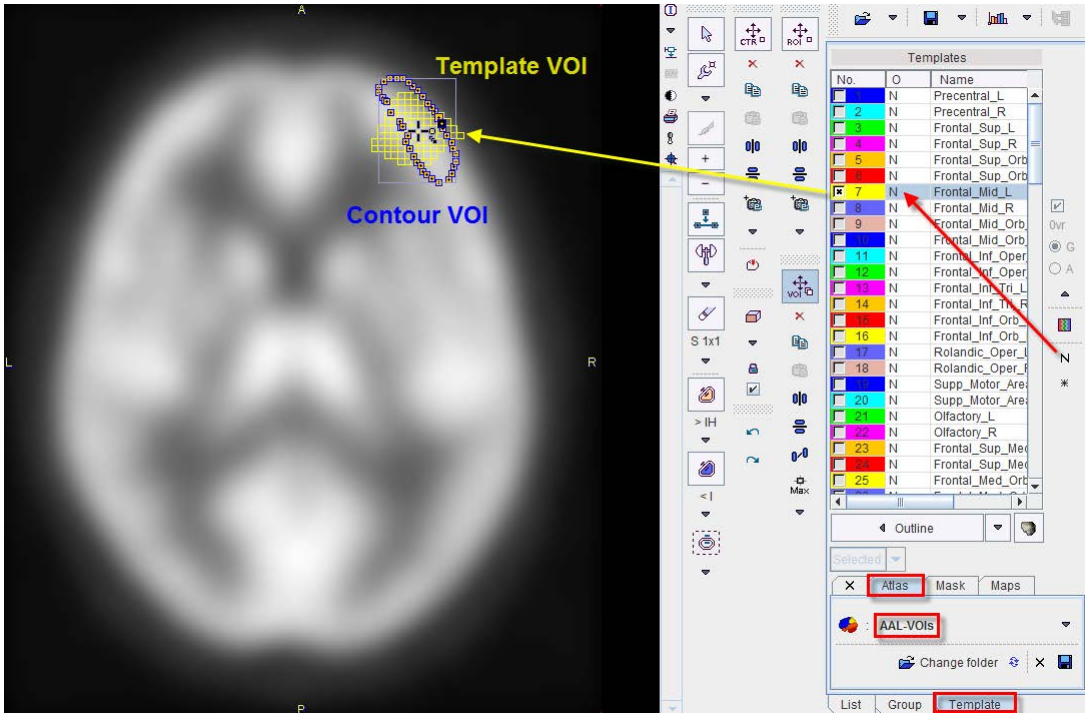
- `CTRL+A`: Select all entries.
- `CTRL+Click`: Check or un-check an entry without changing the others.
- `SHIFT+Click`: Select the range until the clicked entry.

VOI templates can co-exist with the standard VOI contours.

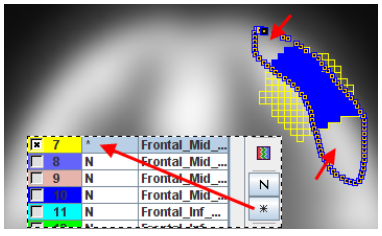
To modify the contour VOIs , select the **List** tab and use all of the functionality described for the contour VOIs sections above. **Statistics** calculates the statistics of the contour VOIs and the active template VOIs.

Using Template VOIs as Masks

In addition to using template VOIs for statistics, they can also be applied for masking contour VOIs. Illustrated below are a contour VOI from the **List** tab and a selected VOI from the **Template** tab which overlap. The indication in the **O** operation column is **N** for normal operation.

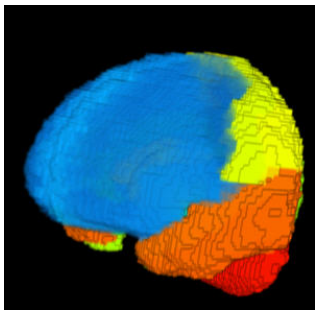


If the operation mode is changed to * for **Mask** operation by the indicated button, the template VOI acts as a mask for the contour VOI as shown below.



Template Visualization

If the 3D option has been purchased, the template can be rendered using the **View all in 3D** button located below the VOIs list.



Converting Template VOIs to Contour VOIs using Outline

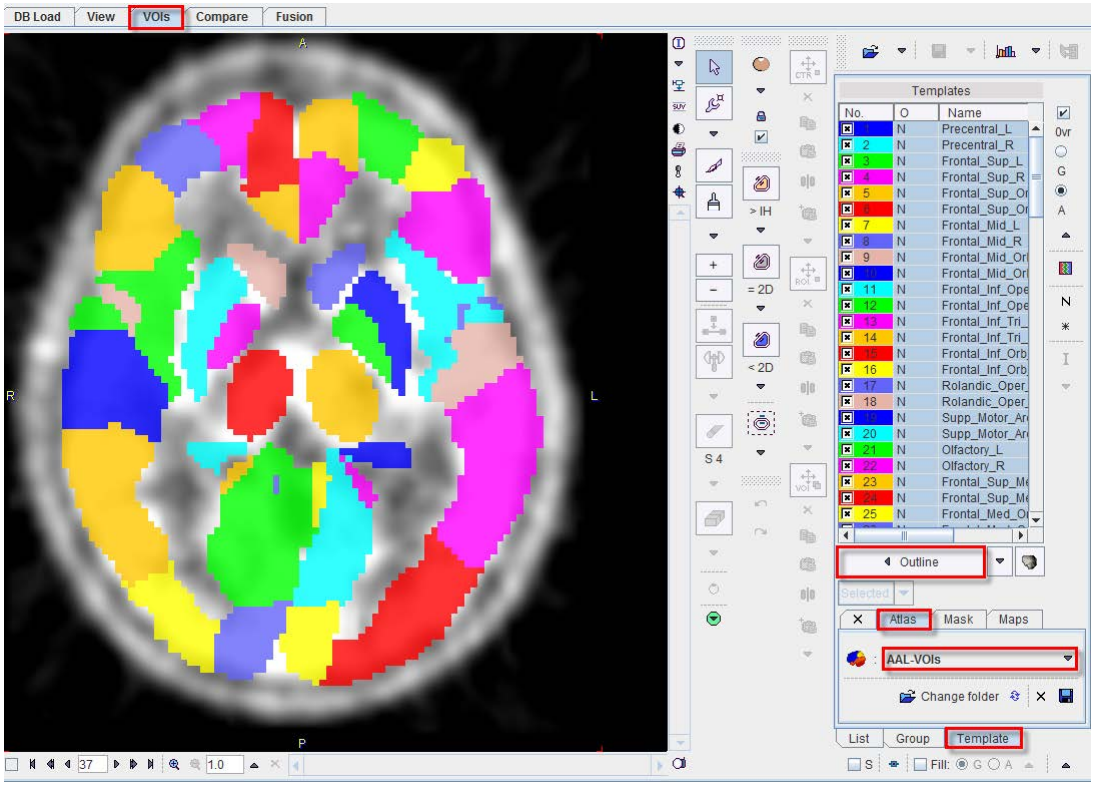
Unlike contour VOIs, template VOIs cannot be adjusted. Therefore, a mechanism has been implemented in the PMOD VOI tool to convert template VOIs into contour VOIs. The procedure is very simple:

1) Select the template VOIs for which contours should be generated (Template/Atlas/AAL-VOIs).

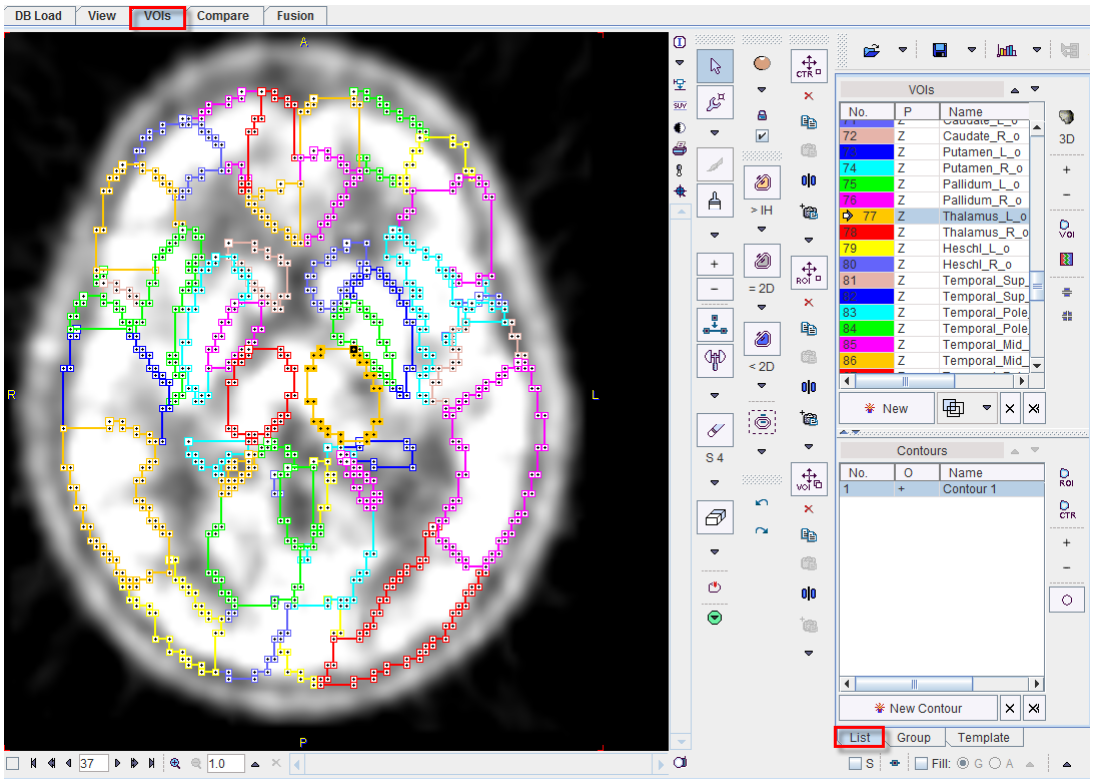
Activate the **Outline** button.

Save the contour VOIs.

The AAL template with filled overlay looks as follows.



Using **Outline** results in the following contour outlines shown on the **List** tab.



Converting Template VOIs to Contour VOIs using Normalize

A mechanism has been implemented in the PMOD VOI tool which allows transforming template VOIs into the study space.

NOTE: This approach will succeed ONLY if a well define strategy for data normalization is available in the Fusion.

The procedure is as follows:

1) Select the template VOIs for which contours should be generated (Template/Atlas/AAL-VOIs).

Activate the **Normalize** button.

A dialog window appears allowing to configure the normalization. Initally the normalization **Method** is selected. In this case **HUMAN**.

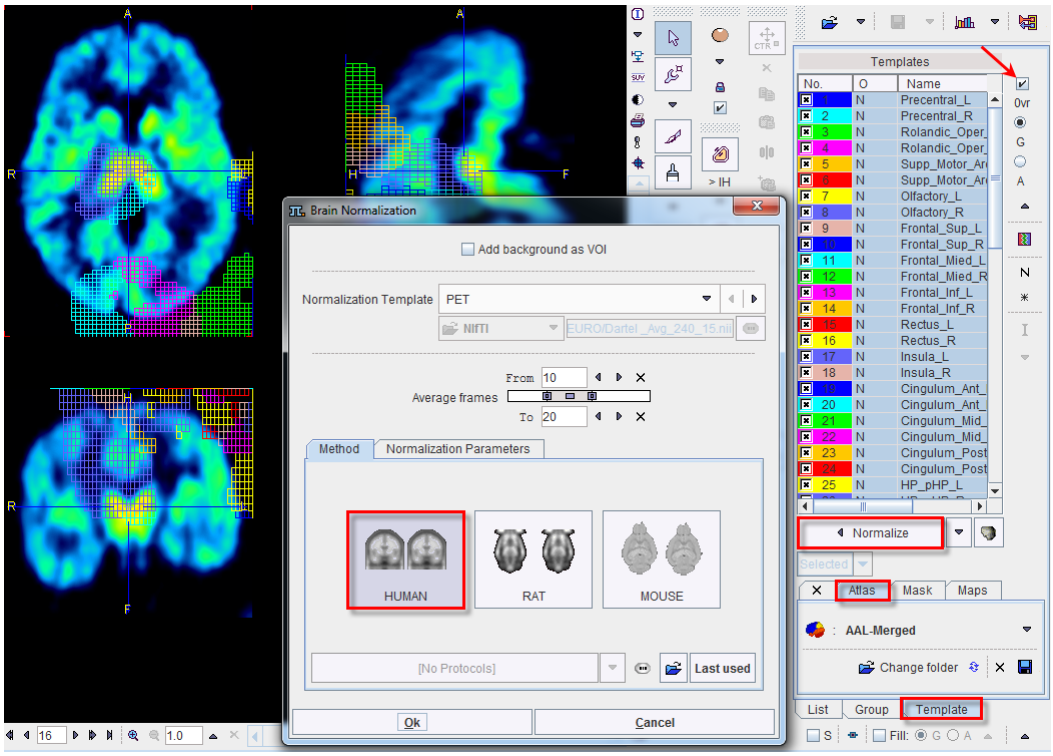
In the uppermost part of the window the normalization template can be set. In case dynamic data are analyzed, an **Average** over a range of frame can be defined.

The algorithm performs the data normalization using the **Basic** and **Advance** settings available in the **Normalization Parameters** tab. More informations about the settings are available in the PFUS documentation at Brain Norm. II Method section. It calculates the inverse transformation which is then applied to the VOI templates. Optionally, the

image background can be added to VOIs if **Add background as VOI** checkbox is enabled.

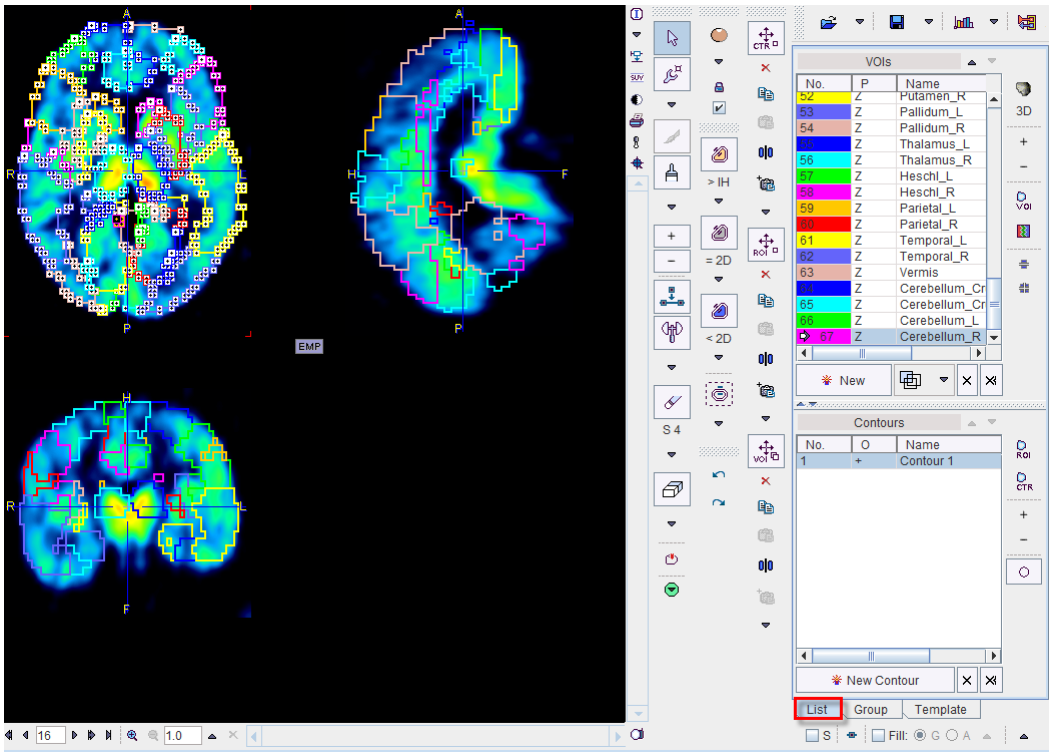
Finally, the transformed VOI template is outlined.

The AAL template with grid filled overlay looks as follows:



Note the misalignment of the template and the image before transformation.

The result of **Normalize** algorithm are shown below:



Preparation of VOI Template Files for PMOD

VOI label templates can be easily prepared for use in PMOD. Two sets of data are required, the

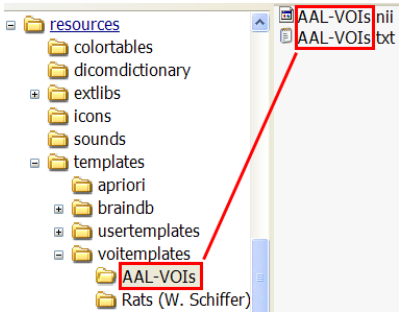
1) *Template images:* They must be prepared in the NifTI file format and contain an arbitrary number of labeled pixels as integer numbers. Non-integer values are rounded to the next integer value. We recommend using the HFS orientation (head first, supine = radiological convention).

Label list: A text file ending in .txt containing three columns. Each label is represented by a line of the form:

```
abbreviation1   label_name1   label_value1
abbreviation2   label_name2   label_value2
...
```

There must not be blank characters within the abbreviations or the names.

Included in the distribution are several templates. The naming and the arrangement of the files is illustrated below using the AAL template as an example.



Note that the name of the sub-directory in *resources/templates/voitemplates* must also be used for the template images and the label list. This name then shows up in the list of available templates in the VOI analysis tool. The labels in the AAL template are described in the file *AAL-VOIs.txt* by a list in the form

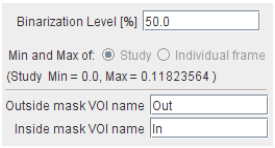
```
FAG   Precentral_L                    2001
FAD   Precentral_R                    2002
F1G   Frontal_Sup_L           2101
F1D   Frontal_Sup_R           2102
F1OG  Frontal_Sup_Orb_L       2111
F1OD  Frontal_Sup_Orb_R       2112
F2G   Frontal_Mid_L           2201
F2D   Frontal_Mid_R           2202
F2OG  Frontal_Mid_Orb_L       2211
F2OD  Frontal_Mid_Orb_R       2212
etc.
```

To add our own VOI template, just create a new sub-directory and add your files following the procedure described above.

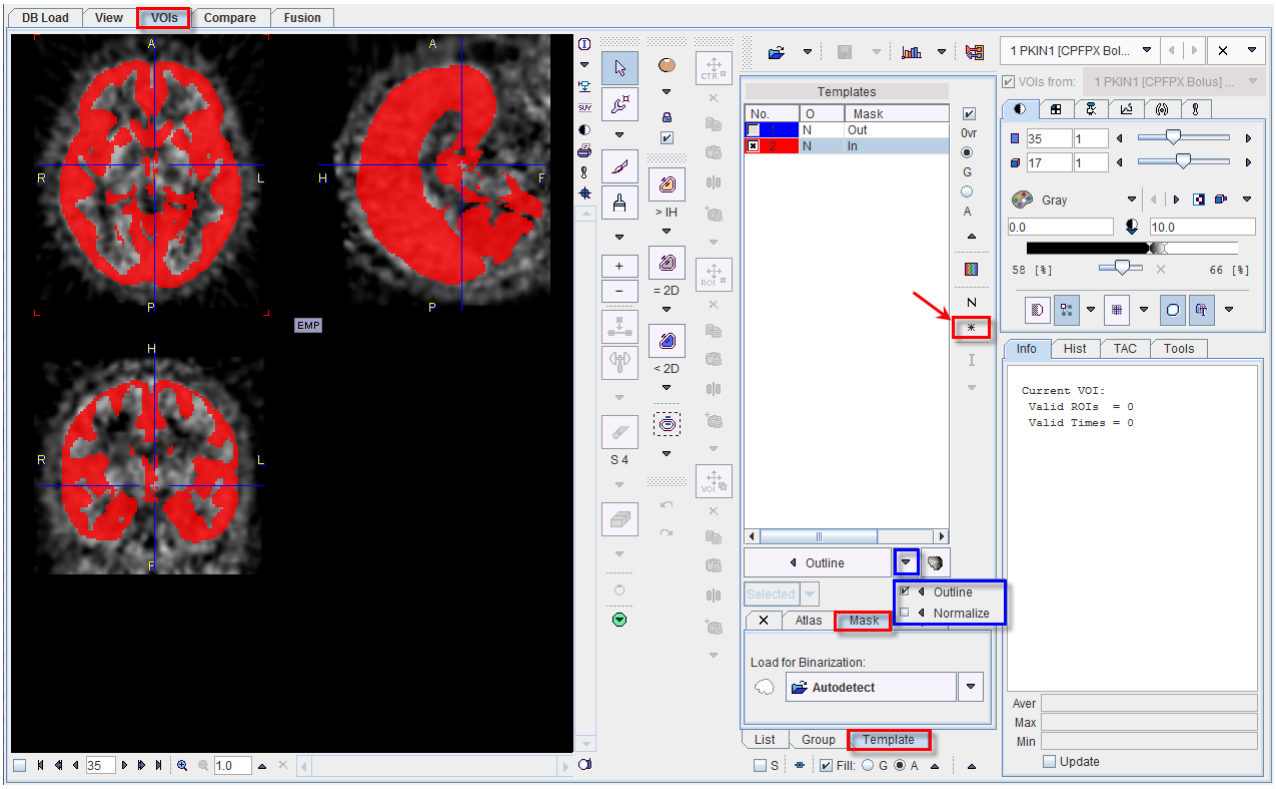
Using Mask Files

Standard templates can only be created and applied if it is possible to reliably map the organ of interest to a standard anatomy. Otherwise, masks created by some sort of thresholding or segmentation are often useful in individual analyses. Such binary masks can also be used for statistics calculations in PMOD.

To load a mask for VOI analysis first select the **Template** tab, and then **Mask**. A loading button becomes active and allows to loading a binary file. If the data in the file is not binary a dialog window appears



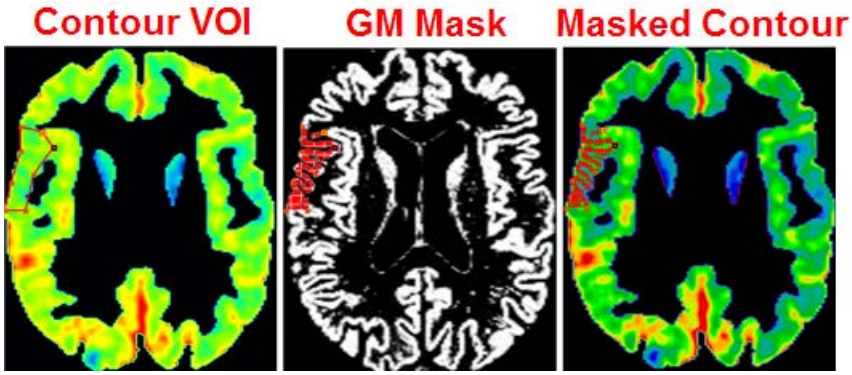
for defining the **Binarization Level [%]** and the names for the mask and the background.



A mask template only contains two VOIs, the **Mask** pixels **In**, and all background pixels **Out**. Most of the times only the **In** region will provide reasonable values, but the **Out** region can also be evaluated on demand.

The same operations are supported as for the ***template VOIs*** (on page 216): statistics can be calculated in the mask VOIs, contour VOIs can be defined in parallel and masked, and mask VOIs can be converted to contour VOIs by the **Outline** or **Normalize** option button. A notable application of masking is the restriction of contour VOIs to the gray matter pixels which can easily be achieved if a gray matter segment is available from a matched MRI data

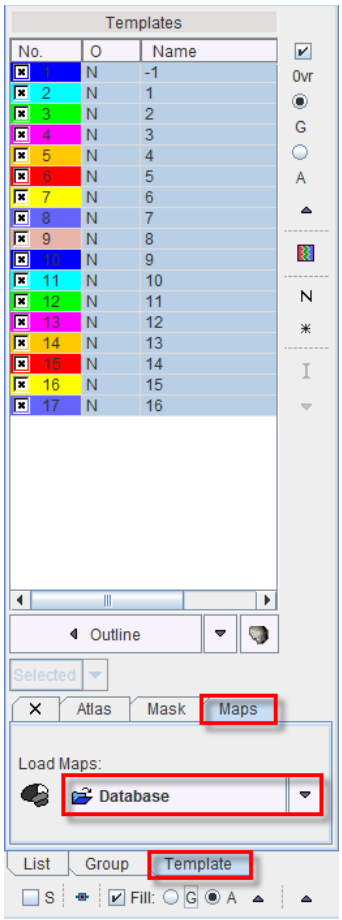
set. An example of restricting a contour VOI shown on a PET to gray matter is illustrated below.



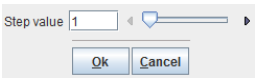
Using Maps Files

A map is a file which contains integer pixel values called object labels. The labels typically identify different objects in the image volume. Such maps are often the product of segmentation procedures.

PMOD is able to load and analyze map files and create a template VOI out of it. The functionality is located on the **Template** panel, in the **Maps** sub-panel as illustrated below.



To load a map file choose the file format in the **Load Maps** area and select the map file. A dialog window appears which allows specifying the bin size for the label histogram.



A **Step value** of 1 should normally work fine. The file is scanned and for each label found a list entry is created in the **Templates** list. Now the names can be edited, the VOIs outlined and further used as for the prepared ***template VOIs*** (on page 216).

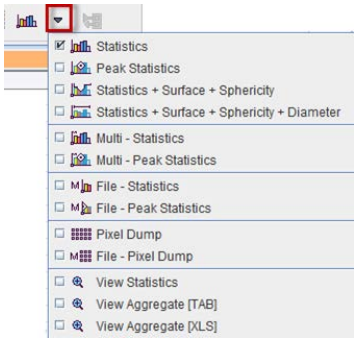
AnalyzeAVW Object Maps

Using the **Autodetect** format, PMOD can directly load AnalyzeAVW object maps (*.obj). It will not only create the VOIs, but also restore the VOI names and the VOI colors.

Operations with VOIs

Statistics

There is a multitude of ways how VOIs can be applied to images for calculating statistical measures which are available via the **Statistics** function button on the VOI panel.



Modes of Statistics Calculation

The following statistics modes are supported:

- **Statistics**: Apply the VOIs to the selected image and show the resulting statistics on a panel.
- **Multi-Statistics**: Apply the VOIs to all loaded images and show the resulting statistics on one panel per image. The outcome can then easily be merged into an aggregate.
- **File-Statistics**: Apply the VOIs to a set of image files and save the resulting statistics in a file. This procedure requires explicit image loading and is most useful when the images are in a normal (e.g. MNI) space, so that a standard set of VOIs can be applied.
- **Pixel Dump**: Extract the values in all VOI pixels of the selected image and save the values together with the pixel coordinates in a file. This procedure gives the user the full raw data and allows him implementing his own statistical analysis.
- **File-PixelDump**: Extract the values in all VOI pixels from a set of image files and save the values together with the pixel coordinates in a file.

VOIs used for Statistics

The following VOIs are considered in the interactive statistics calculation:

- All contour VOIs on the **List** tab.
- The VOI named **Group** which consists of all the contour VOIs which are selected on the **Group** tab.
- If on the **Template** tabs **Atlas** or **Mask** is active, the corresponding VOIs are also considered. Please enable the **Ovr** box to see these VOIs in the overlay.
- If a masking operation is configured on the **Atlas** or **Mask** sub-tab, it is applied to the contour VOIs during the statistics. Please enable the **Fill ROI** box to verify the actual coverage of the masked contour VOIs.

VOI Evaluation

The statistics are always calculated using the raw image pixel values, even when the images are shown with smoothing/interpolation enabled. Only full pixels are considered, no partial pixel areas are taken into account. Please enable the **Fill** checkbox to see which pixels will be included in the statistics calculation.

Statistics Measures

Except for the **Pixel Dump** different levels of statistics can be collected:

- **Statistics**: Standard descriptive statistics measures.
- **Peak Statistics**: The standard descriptive statistics evaluated in a sphere located at the maximum pixel in the VOI.
- **Statistics + Surface + Sphericity**: Standard descriptive statistics measures, a VOI surface estimate and an index of how sphere-shaped the VOI is.
- **Statistics + Surface + Sphericity + Diameter**: As above, plus the maximum VOI diameter.

The selected statistic type is calculated for each VOI.

Statistics Measures

The following basic descriptive statistics are calculated using the distribution of all pixel values in a VOI:

Averaged	Average of the pixel values.
Sd	Standard deviation of the pixel values.
Volume	Volume of the VOI pixels. It is based on the pixel size in x and y and the slice thickness in z.
Total(SUM)	Sum of the pixel values. The interpretation depends on the image contents. In the case of activity units the result will be total activity in the VOI.
Total(AVR*VOL)	Average of the pixel values multiplied by the VOI volume. The interpretation depends on the image contents. In the case of activity *concentration* units, the result represents total activity in the VOI. In the case of SUV units, the result is called *Total Lesion Glycolysis* (**TLG**).

	The TLG is usually calculated in combination with a lower range.
Min	Minimum pixel value.
Max	Maximum pixel value.
NumberOfPixels	Number of pixels included in the VOI.
HotAveraged	The highest pixel values averaged. The default **Number of Hottest Pixels** values to be averaged can be set in the User configuration, and can be changed in the upper part of the statistics window.
Median	Median value of the VOI pixel values.
AreaUnderCurve	Static data: **Averaged** times frame duration. Dynamic data: Integral of the **Averaged** curve.

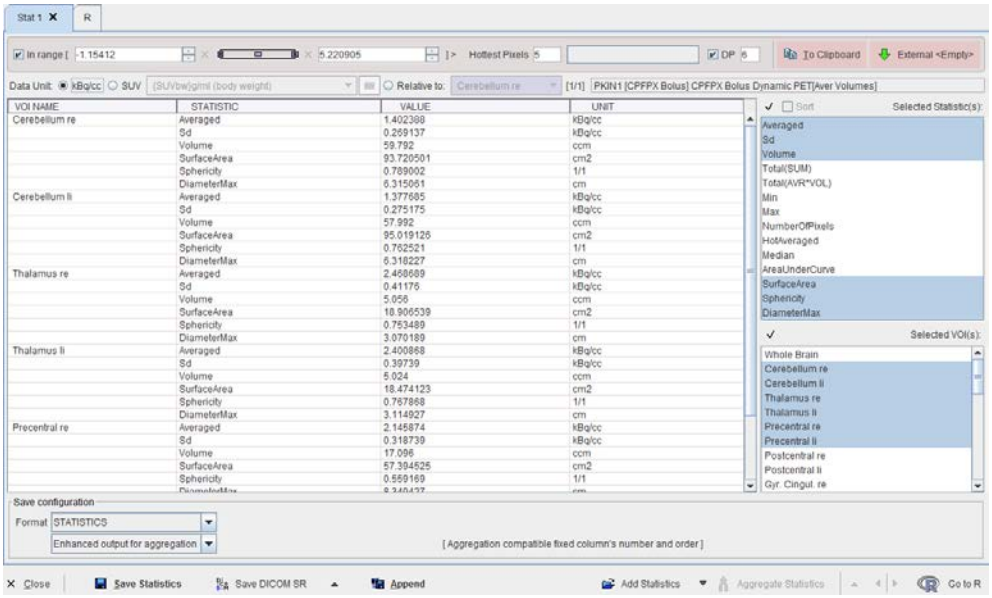
Additional Measures

The following additional VOI measures can be obtained with the corresponding statistics button:

SurfaceArea	Estimate of the VOI surface which is obtained by triangulating the contours and accumulating the triangle areas.
Spericity	Index of how spherical a VOI is. The values range between 0 and 1 (perfect sphere). ***Wikipedia http://en.wikipedia.org/wiki/Sphericity***
DiameterMax	Maximal distance between any two pixels in the VOI. The calculation can take substantial time and is restricted to VOIs enclosing less than 100'000 pixels.

Statistics Viewer

The dialog window for the statistics output is illustrated below. The R page only appears when ***R statistics*** (on page 251) is enabled.



The calculated information is comprehensive and can be tailored by several user interface elements.

Selected Statistics

The list to the right shows all available statistics figures. It serves for selecting the statistics of interest. Only the selected elements are be shown in the table and will be exported. The default selection includes the **Averaged** and the **Sd**.

Selected VOIs

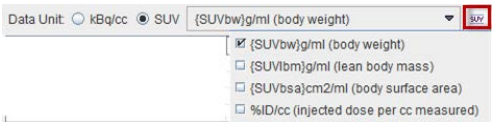
The second list in the lower right shows all available VOIs which were evaluated as well as a Group element. Only the selected elements are shown in the table and will be exported.

Range Restriction

Note the **In range** box which allows restricting the statistics to the subset of pixels with values in a specific range. For example, by setting the lower threshold to 40% of the maximum it is possible to calculate the average value and the volume of all pixels above 40%.

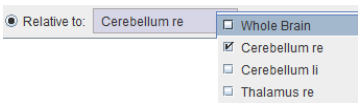
SUV Statistics

If the statistics are calculated for activity concentration images, the uptake results can be converted to different types of ***SUV*** (on page 127) images under the condition that the related activity information is available in the image header. If not, but the information is available, it can be entered after activating the SUV button



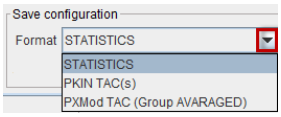
SUVR Statistics

The so-called SUVR statistics is the uptake divided by a reference uptake. It can easily be obtained by switching to the **Relative to** radio button and selecting the reference region from the VOI list.



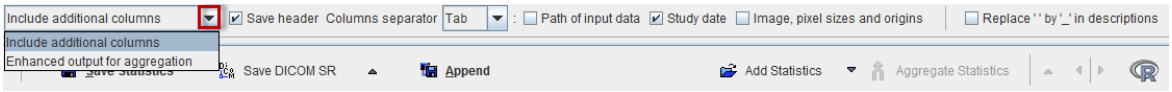
Saving Options

There are several options to chose from when saving the statistics. The **Format** selection has three choices.



STATISTICS is a tabular format aimed at statistics programs. **PKIN TAC(s)** is aimed at loading the save information as tissue curves into the kinetic PKIN tool. **PXMod TAC** will only export the time-activity curve of the **Group** VOI in a two-column format. This data is intended for use in the pixelwise modeling tool PXMOD.

The second option choice



is only available for the **STATISTICS** output.

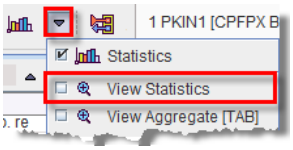
Please use **Save** for saving the data in a new tab-delimited text file, and **Append** for appending it to an existing statistics file.

Furthermore, the statistic results can be saved as a Dicom structured report with the **Save Dicom SR** option or exported as a structured report with the **Export Dicom SR**.

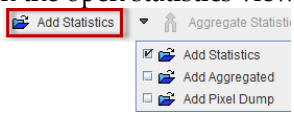
Load Statistics Files

Statistics files saved in the **STATISTIC/Enhanced output for aggregation** format can be loaded back into the statistics viewer. There are several ways to do so:

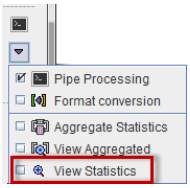
1) from the VOI interface using the **View Statistics** option in the **Statistic** selection list;



from the open statistics viewer using the **Add Statistics** option



from the lateral taskbar of the PVIEW tool



Once the statistic file is retrieved a dialog window opens and allows sending the data to R . Activating the **Go to R** button, the program automatically switches to the R interface while loading the available statistics data.

Multiple Statistics

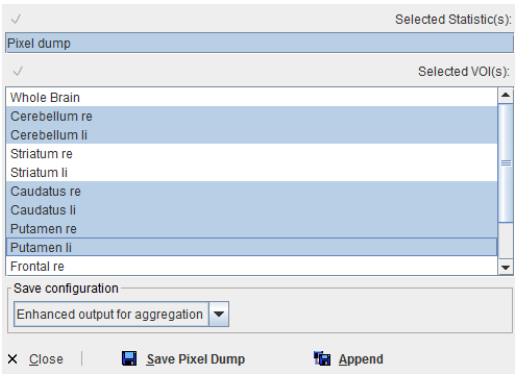
If the statistics is calculated for multiple files, the results are shown in the statistics viewer on separate pages. Similarly, when loading a statistics from a file, a new page is added to the statistics viewer. In this case, the **Aggregate Statistics** button becomes active and allows creating an aggregate from all open statistics pages.

Transfer to R

The statistics viewer includes an interface to the R statistics environment, if this feature is configured. The **Go to R** button will transfer all open data to the ***R console*** (on page 255).

Pixel Dump

The **Pixel Dump** serves for saving the raw values of all pixels included in the VOIs into a file. It shows a dialog window for defining the VOI selection.



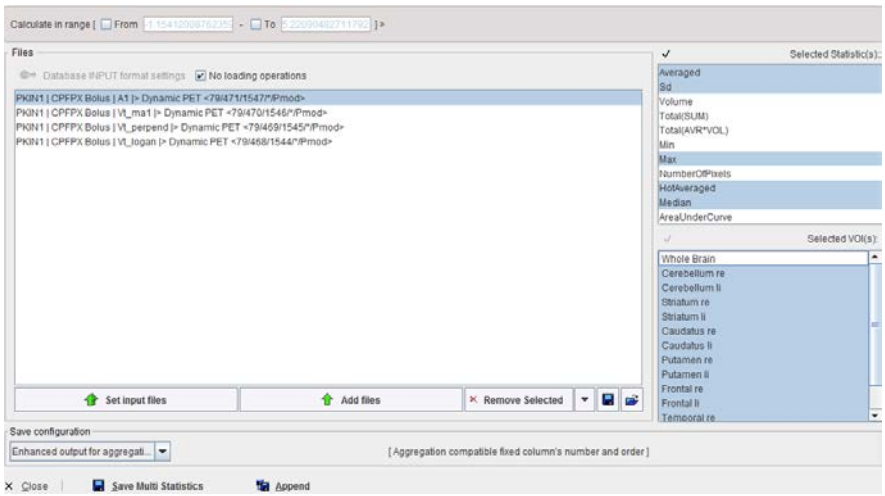
The results can be saved to a new file or appended to an existing one. The output has a tabular format, with the main part being the pixel coordinates and the value.

X [pixel]	Y [pixel]	Z [pixel]	Value [kBq/cc]
28	50	36	2.51422
28	51	36	2.506756
28	52	36	2.645055
28	53	36	2.725984
29	45	36	2.522795
29	46	36	2.58447
29	47	36	2.823405

It can easily be imported into statistics programs for a detailed analysis of the value distribution.

File-Based Statistics

The **File Statistics** allow applying the same statistics to a set of files in a batch mode operation. A dialog window appears for selecting the VOIs of interest and the files to be processed. Note that only files in a same format as the open image with the VOIs can be used.

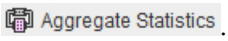


No loading operations	If the box is checked the image are loaded without any data transformation. Otherwise a pre-processing can be specified using the **INPUT format settings** button.
Set Input files	For selecting the images to be analyzed.
Add files	For adding additional files to the list.
Remove selected	For removing the selected files from the list.
Remove all	Clears the file list.
	For saving the file list as a configuration.
	For loading a list configuration.

After activating **Save**, PMOD will prompt for an output file name, and the calculations will be started.

Statistics Aggregation

The numeric output of several PMOD tools can be compiled into a single aggregate file for further statistic analysis. Typically, the results of a population (controls, patients) or a condition (test, retest) should be compiled into a single aggregate, and comparisons or tests performed between aggregates.

The following results can be aggregated: VOI statistics (.voistat), parameters from the PKIN tool (.kinPar), the PCARDP (.pcardRes) tool, the PCARDM (.mcardRes) tool, and the PALZ (.palzRes) tool. Each of the tools has an appropriate aggregation button 

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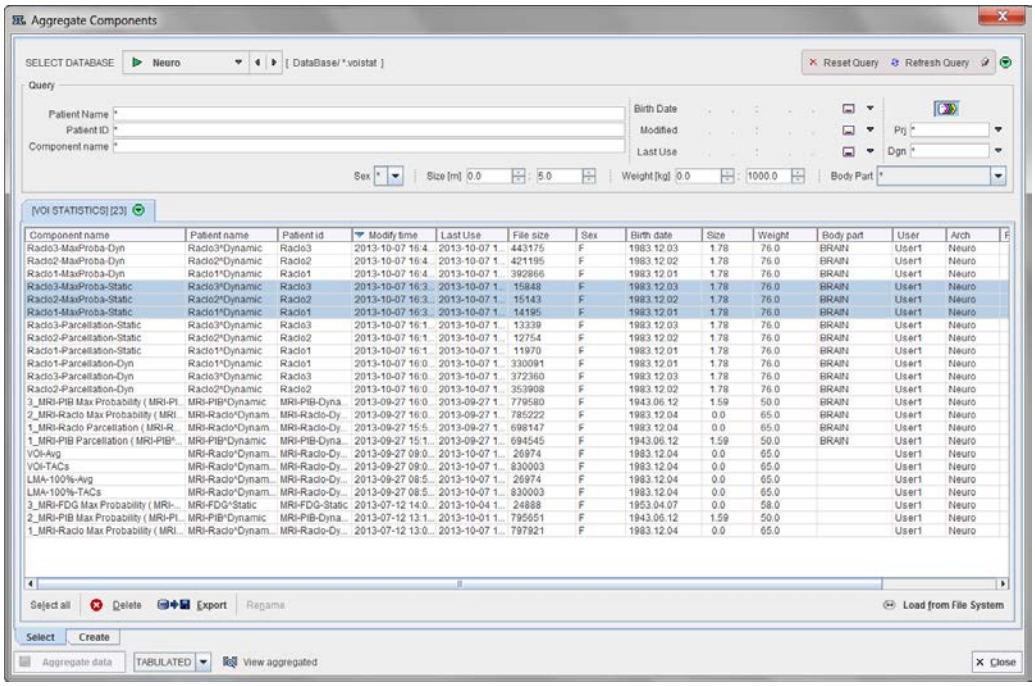
As an example, the aggregation of VOI statistics saved in **.voistat** files is described below. The aggregation window can be opened with **Aggregate VOI Statistics** from the **View** menu.

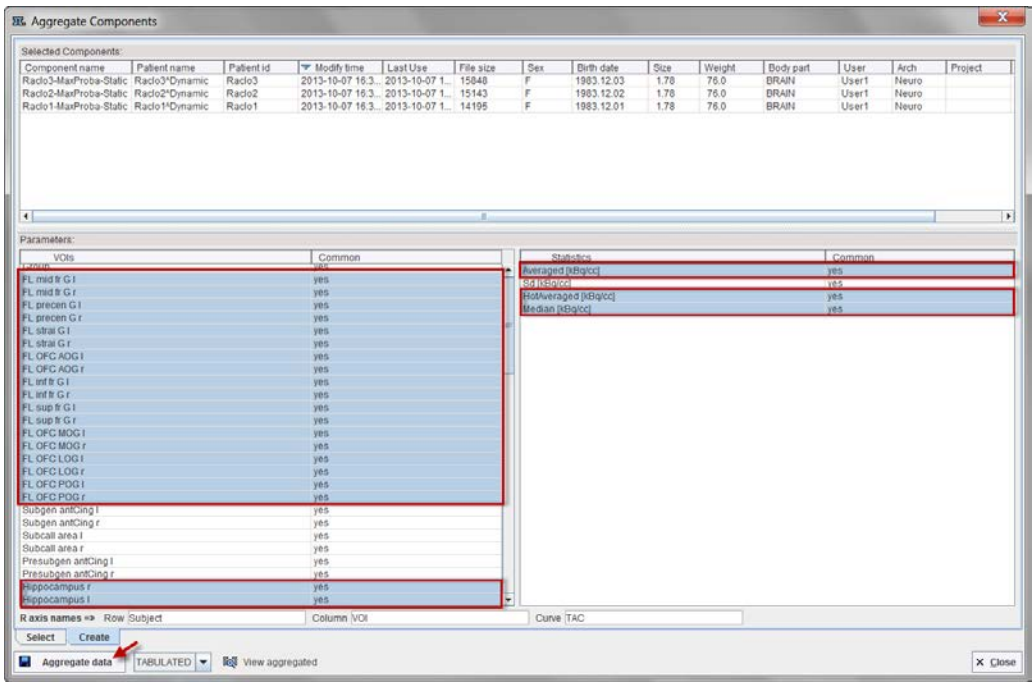


Selection of .voistat Files

The first step of aggregation is defining the files to aggregate from on the **Select** page. In the example above the data is selected from a database. The filters have been cleared by the **Reset Query** button so that all **.voistat** files are listed. The first aggregate will be created out of 3 data sets which are selected in the list and appear highlighted. If no database has been used for saving the .voistat files, the **Load from File System** has to be used instead.

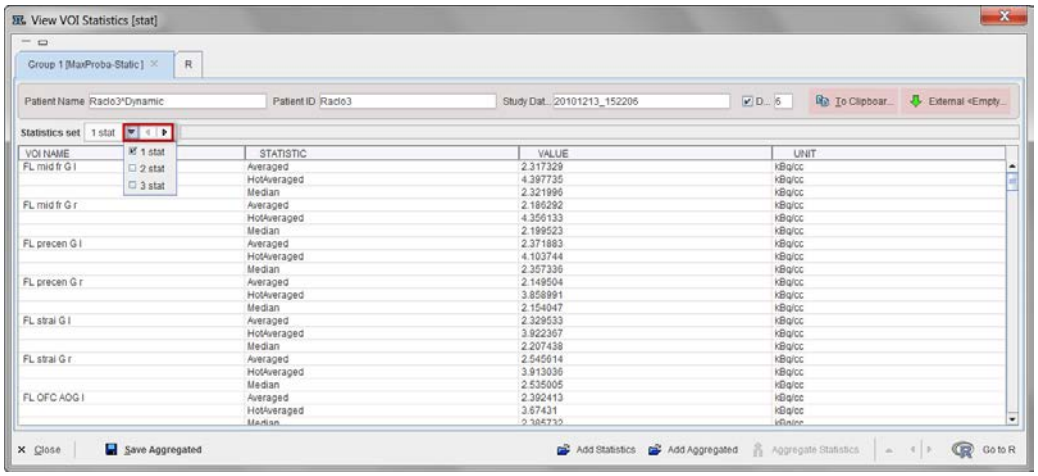
Aggregation of Information

Select the **Create** pane to prepare the aggregation.



The **Selected Components** area is for information only. The left part of the **Parameters** section lists all **VOIs** in the selected components, labeling the VOIs occurring in all of them as **Common=yes**. The **Statistics** area lists the VOI statistics types occurring in any of the files. Again, **Common=yes** labels the ones which are always available.

Use the **Aggregate data** button to create and aggregate file (.dbTab) and save it to a database or to the file system. The result can be inspected with the **View aggregated** button as illustrated below.



The information of a single .voistat file is shown in the list area. Using the arrows of the **Statistics set** to step through the different data sets.

Time-Activity Curve Generation and Link to PKIN

An important usage of the VOI analysis is the generation of time-activity curves (TAC) for subsequent kinetic modeling. This can easily be achieved in PVIEW by the following steps

1. Definition of the VOIs

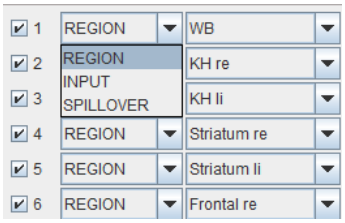
The image data is loaded as a dynamic series with the *correct acquisition times* and the *correct input units*. This is important, because otherwise the acquisition start/end times in kinetic modeling will be wrong, and the TACs may be different in magnitude with respect to the blood data. Such problems result in erroneous model parameters.

In dynamic image series there is generally not enough anatomical information to delineate VOIs. Often, averaging of a subset of the acquisition frames resolves the problem. The VOIs are then delineated in the summed images, transferred to the dynamic images, and optionally saved to a file.

2. TAC generation

Switch the tool to the dynamic study, and activate the button

A dialog window appears which allows defining the proper type of the calculated TACs (REGION = tissue TAC, INPUT = plasma curve, SPILLOVER= total blood curve)



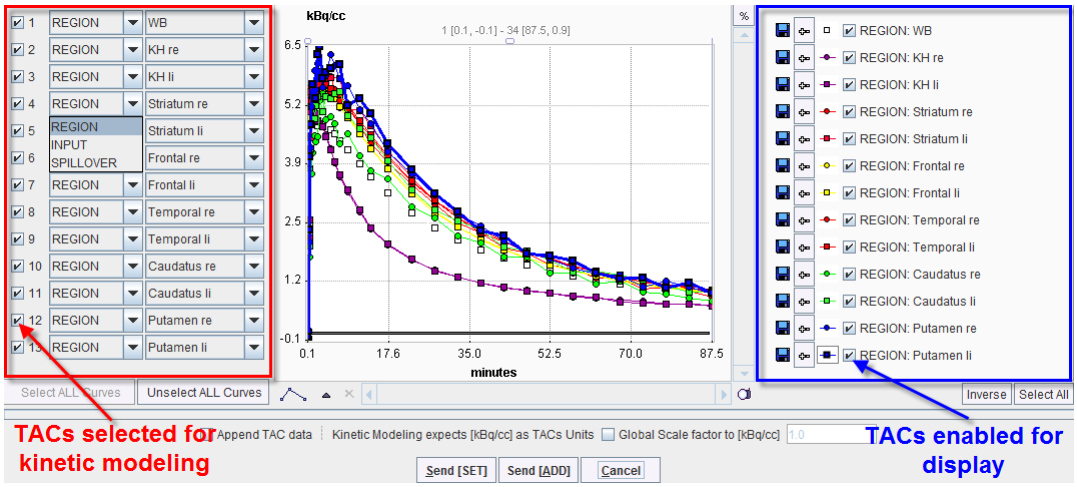
The window is organized in three panels:

1) The left panel (red) allows defining the proper type of the calculated TACs. All the TACs selected in this panel are going to be send to the **Kinetic modeling** tool.

The central panel is a plot which displays the calculated TACs.

The right panel (blue) allows the selection of the the TACs to be displayed in the graphic area.

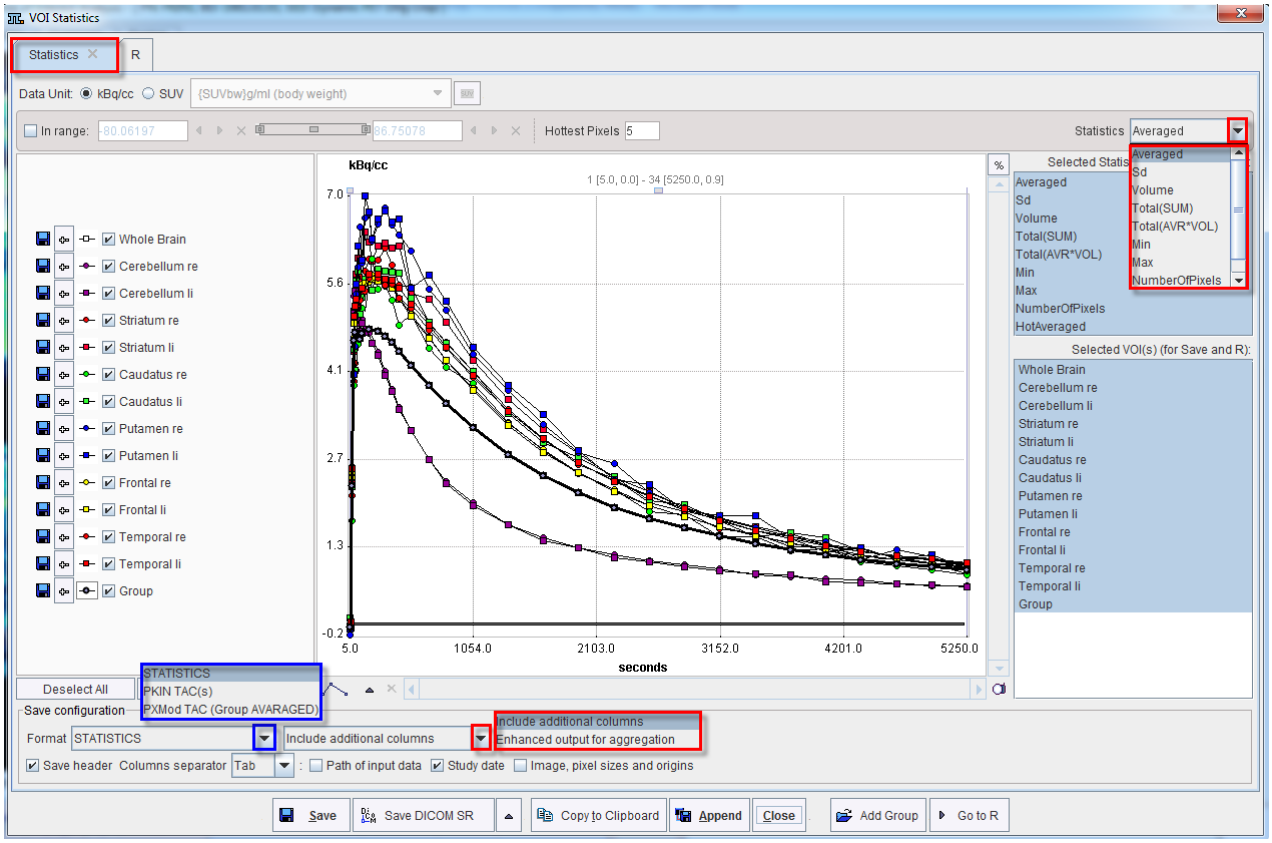
NOTE: The selection in the right panel (blue) does not affect the selection on the left panel (red) while the selection on left panel is immediately reflected in both display area and right panel.



The **Send** buttons initiate the transfer of the activity curve data to the PKIN tool. Selecting the **Send[SET]** button transfers the TAC data to the currently selected tab in the PKIN tool. If the **Append TAC Data** box is checked, the curves are appended as new curves to the data existing on the PKIN tab, otherwise the data is over-written. **Send[ADD]** first creates a new tab in PKIN, to which the data is added. If PKIN is not running, the tool is first started and the data added.

The **+-** button in the curve controls allow for simple operations such as curve scaling before sending the data to PKIN. Both the average value and the standard deviation within the VOIs are transferred, as well as patient and study information. The standard deviation may be used for weighted fits in PKIN.

If the PKIN option is not available, the TACs of a dynamic series can also by obtained with the statistics button as illustrated below.



The **In range** box allows restricting the TACs statistics to the subset of pixels with values in a specific range.

Note the radio box in the upper section which allows switching between **kBq/cc** and the **SUV**, if all required information is available. The **Statistic** type selection list allows choosing the type of statistics to be displayed in the graphic area.

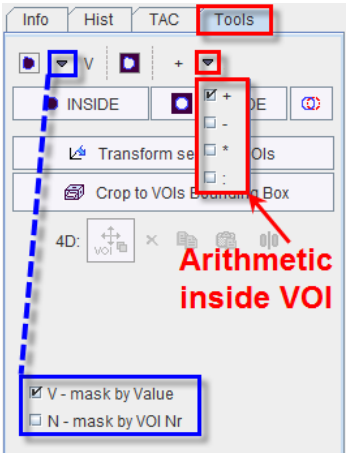
The statistics numbers selected in the **Selected Statistic(s) [For Save]** area of the VOIs selected in **Selected VOI(s) [For Save]** can be saved into a text file with **Save,** appended to an existing one using **Append**, copied to the **Clipboard** or sent directly to PMOD R interface with the **Go to R** button. The statistic results can be saved as a Dicom structured report with the **Save Dicom SR** option or exported as a structured report with the **Export Dicom SR**.

There are different statistic formats available for saving procedure:

- **STATISTICS** saves all selected information. The **Include additional columns** or the **Enhanced output for aggregation** selections are available for the **Statistic** format. We recommend using the **Enhanced output for aggregation** option for aggregation and further statistical analysis in R interface.
- **PKIN TAC(s)** saves the acquisition times and regional averages in a text file which can directly be loaded with the **Load Time Activity Curve** entry of the PKIN **Menu**.
- **PXMod TAC (Group AVERAGED)** saves the average of all grouped VOIs in a two-column text file suitable for usage with PXMOD.

Masking Inside and Outside of VOIs

The VOI **Tools** tab offers some **Masking & Algebra** functions. They will be applied to the selected VOIs when the **List** or **Group** tab is active, and also to the selected VOIs when using a **Template** or a **Mask**.



The buttons have the following function:

	Mask voxels inside. This button replaces the values of all pixels within a VOI by a constant value. There are two variants: If the configuration is set to **Va**, the selected VOI will be filled with the value entered in the number field below. If the configuration is set to **N**, then the selected VOIs will be filled with sequential number VOI numbers starting from 1.
	Mask voxels outside. All pixels outside the selected VOIs will be set to the value defined in the number field.
+	**Algebra**. The operation can be configured to addition, subtraction, multiplication or division. All pixels inside the selected VOIs will undergo the same operation. With * and a number of **2**, for example, the VOI pixel values will be doubled.

Interactive Masking

The interactive masking algorithm is based on the interactive outlining of a sphere. It allows the fast removal of disturbing parts in the image.

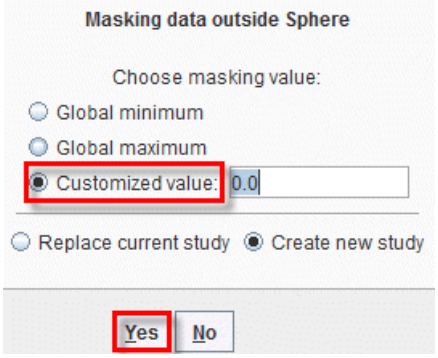
The algorithm consists in the following steps:

1) Select either inside or outside **Removal**.

Locate the center of the anatomic structure to be masked.

Click and hold the left mouse button until the image area of interest is located within the interactive sphere.

Upon the completion of the previous steps a dialog window appears. It allows specifying the masking value, creating a new study or replacing the current one.

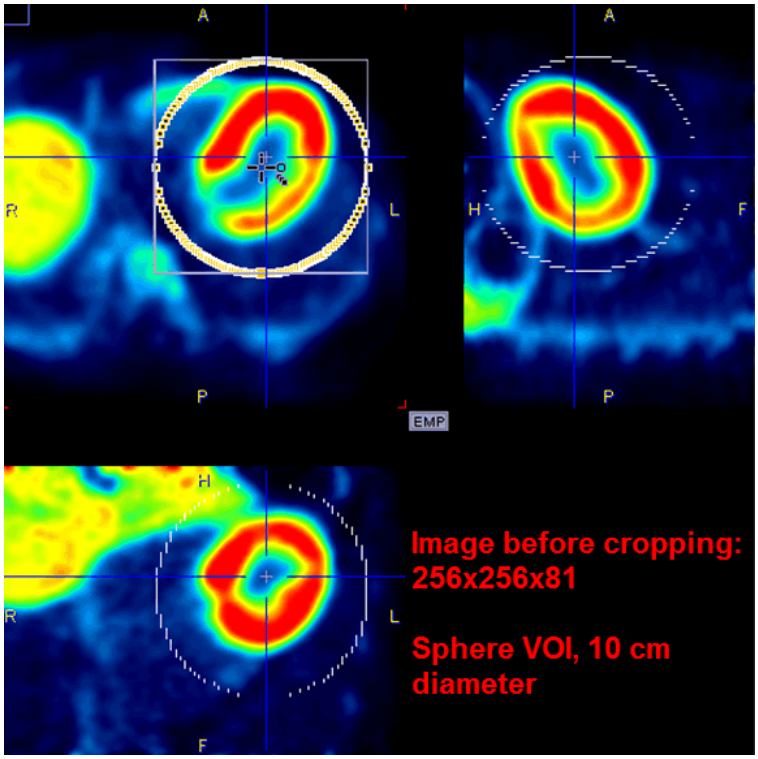


Finally, activate **Yes** to perform the interactive removal.

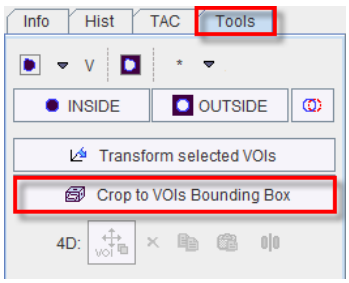
Note: The dialog window confirmation (Step 4) can be disabled. To do so, activate the **VIEW** configuration button and select the **Display** tab. In **VOI DEFINITION** area turn **OFF** the **Confirm removal operation** checkbox.

VOI-based Image Cropping

Contour VOIs can be used for cropping image series to a sub-volume of interest. The image below shows the images reconstructed from a cardiac study with a large field-of-view and a 256x256 matrix size. The orthogonal planes are displayed with a zoom factor of 3. A sphere VOI of 10 cm diameter has been positioned around the left ventricle with the purpose of defining the volume of interest.



The data was then cropped using the **Crop to VOI Bounding Box button** on the **Tools** tab.



The resulting series is shown below with a zoom factor of 1. It still contains the full information regarding the left ventricle, but requires a factor of about 40 less space.

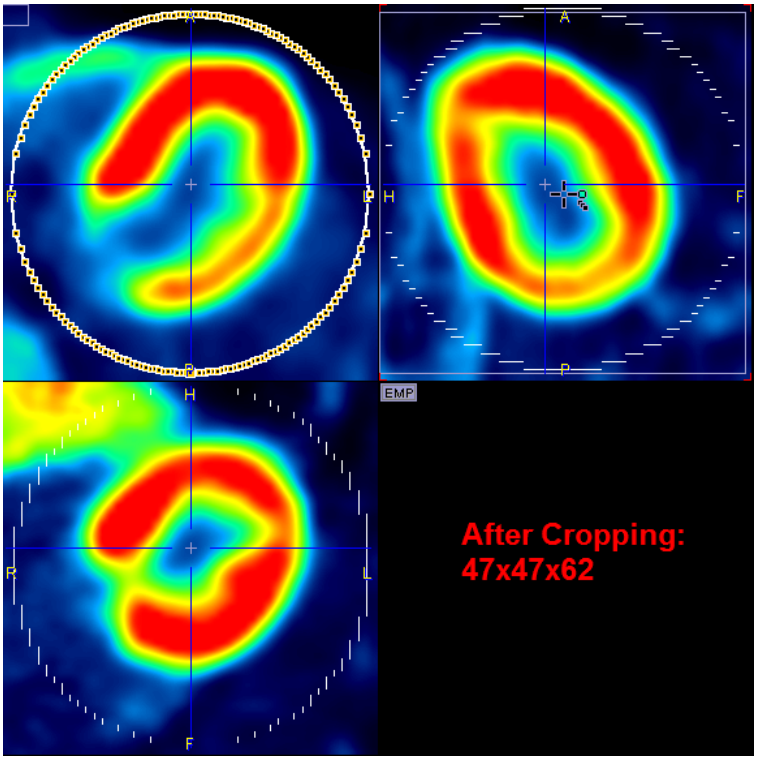


Image cropping is particularly useful as a pre-processing step to image registration. When matching a dynamic series to high-resolved MRI or CT images as a reference, it is highly recommended to crop the reference to the organ of interest before the registration. Hereby, the RAM requirements are reduced by factors without losing information, and processing speed is improved accordingly.

Creation of Template VOIs

An image series for which a set of contour VOIs has been defined can easily be converted into a VOI template as follows:

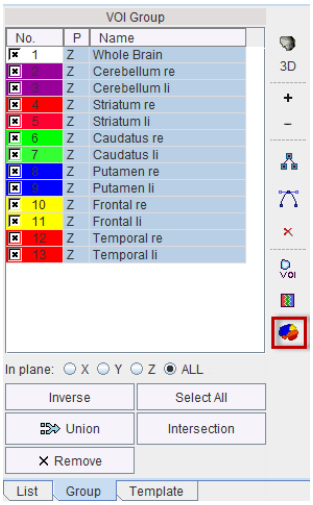
1) Load the image series in the PVIEW tool.

Outline a set of contour VOIs in the **VOIs** page.

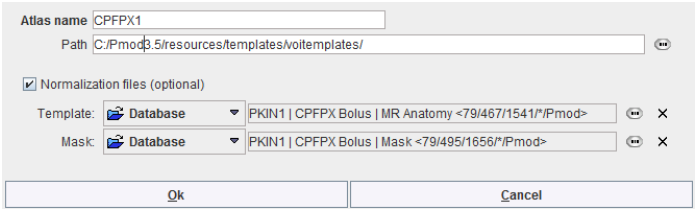
On the **Group** tab, select the VOIs to be included in the template.

Important: do NOT include VOIs (such as a whole-brain VOI) which cover other VOIs.

Activate the **Create Template Atlas** icon available on the right side of the **VOI Group**. The same icon is available in the lateral taskbar.



A dialog window appears which requests a name for template. Using this name a subdirectory is created in *resources/templates/voitemplates*, where the image series is saved in NifTI format, and a text file with the VOI names is created. After activating the refresh button in the **Atlas** panel of **Template**, the new template appears and can be used for statistics.



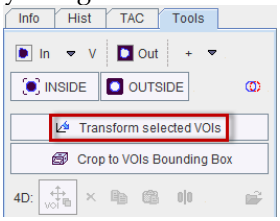
Optionally, files for the spatial normalization can be defined for the template. To this end enable the **Normalization files (optional)** box. Using the above configuration, the CPFPX subdirectory is created in *resources/templates/voitemplates*. The VOI label image is saved in NifTI format, with a text file to assign VOI names to lable values. Additionally, a **normalization** folder is created with the normalization image in NifTI format (norm_template.nii) and a **mask** folder where the mask image is saved in NifTI format (mask.nii).

Spatial VOI Transformation

If the user has a set a VOIs defined on a different image and a spatial transformation which maps the other image to the current, this transformation can be applied to the VOIs in two ways:

1) By applying the transformation during the ***loading operation*** (on page 213),

or by using the **Transform selected VOIs** button in the **VOI Tools** panel.



Note that the **Transform selected VOIs** button also works on template VOIs.

Chapter 7

R Statistics in PMOD

R is an open-source statistical environment and programming language for data analysis and graphical display (***R-project http://www.r-project.org/***). Recently it has gained increased attention in the analysis of biomedical data, see for example the overview article of Tabelow et al: *Image analysis and statistical inference in neuroimaging with R*. Neuroimage 2011, 55(4):1686-1693. ***DOI http://dx.doi.org/10.1016/j.neuroimage.2011.01.013.***.

The PMOD **R** console provides an interface to the R package and leverages the entire R functionality including the statistical analysis of PMOD results from populations. The methods can be applied to the outcome of VOI statistics, regional kinetic modeling, cardiac perfusion quantification and the PALZ analysis.

Standard analysis types are directly supported via the graphical user interface. They can be as simple as a performing scatter plots, but range to more complicated techniques such as ANOVA, test-retest analysis or Bland-Altman comparison.

Beyond using the graphical interface for invoking R functionality, users can also develop their own analysis scripts in a command window interface. In this situation, the PMOD **R** console serves as a prototyping interface which allows to enter R code, execute it, inspect the result, and improve the code.

In This Chapter

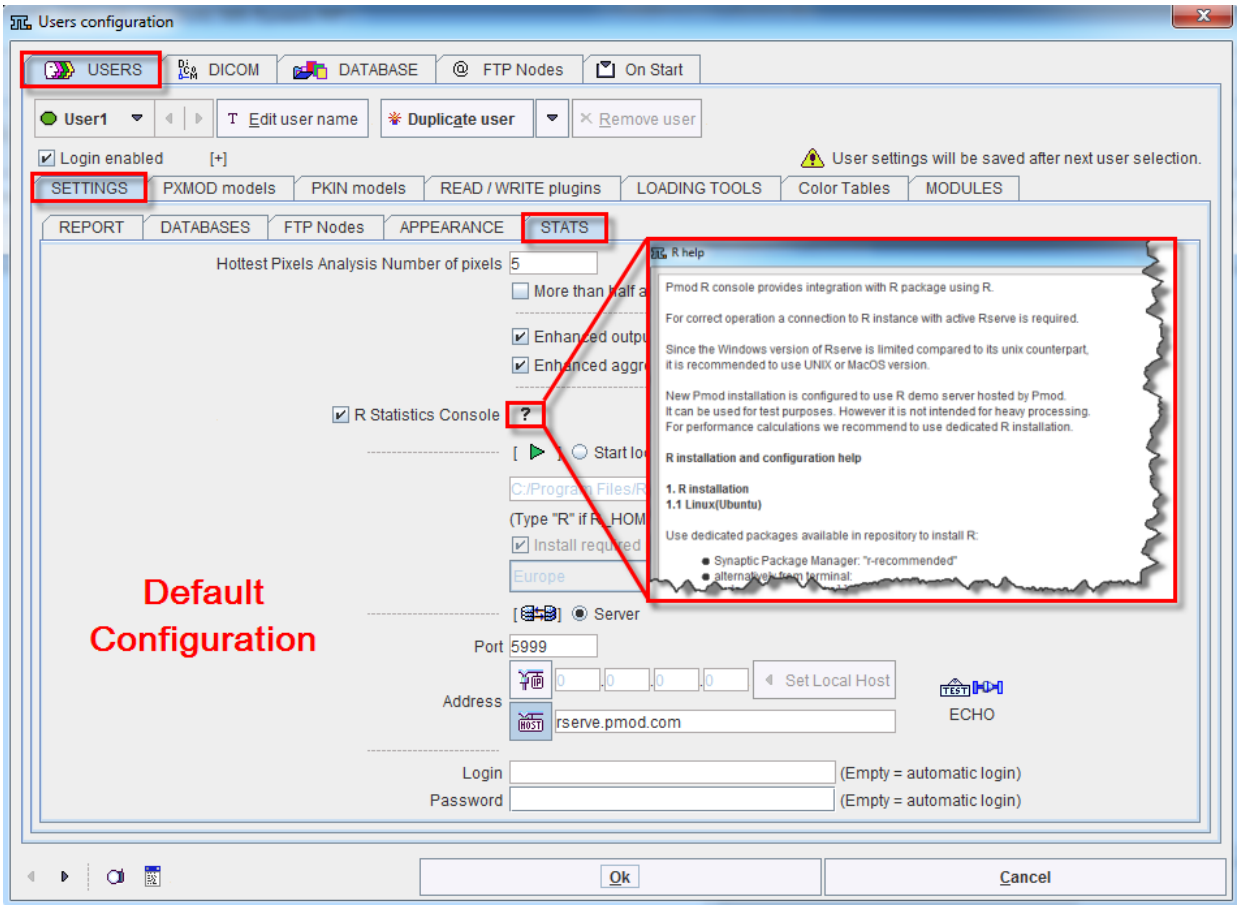
R Installation and Configuration

R Server

R can be set up as a processing server which is listening on a certain IP port. The server can receive data from a client and save it to an internal workspace. It can also receive processing commands, apply them to the data, and return the results to the client on the same channel. PMOD uses this R server mechanism for implementing R-based statistics and therefore relies on a responding R server.

PMOD Configuration for Using R Statistics

The R server to be used for statistics is configured in the **Users configuration** window, **SETTINGS/STAT** tab as illustrated below.



Per default, PMOD comes with enabled R statistics using an R server hosted on a PMOD machine (**rserve.pmod.com:5999**). However, this R server should only be used for tests, and not for productive data processing. We recommend users to set up their own R server, which is easy to do and free of charge. There are two alternative setups:

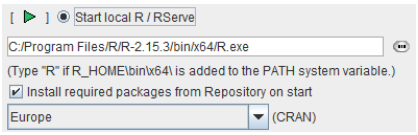
1) In a multi-user environment it is possible to set up a single R server interacting with several PMOD clients. However, due to limitations of the R server on Windows, the R server should be installed on a Mac or Linux system in this case.

The typical case, however, is installation of an R server on every machine running PMOD.

Information about the installation of R on Window systems is given below. Please refer to the explanations available via with the **?** button to install an R server on Mac and Linux systems.

Local R Server on Windows

To set up a local R server on a windows machine please proceed as follows. Download and perform a local installation of the R package as described on the ***R download http://cran.r-project.org/mirrors.html*** website. Then configure the R section as follows:



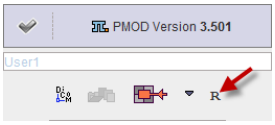
Enable the **Start local R/RServe** radio button and point to the executable *R.exe* of your installation (e.g. *C:/Program Files/R/R-2.15.3/bin/x64/R.exe*). Check **Install required packages ...** and set the **CRAN** package repository according to your country. This repository will be used for the loading of particular processing packages. This is only needed for the first time the R server is started, or when new packages should be added. Confirm the settings with **OK** and close PMOD.

IMPORTANT: In order to complete the R installation PMOD needs to be started once with administrator privileges. To do so, please right-click the PMOD starting script RunPmod.bat and select the option **Run as administrator** from the context dialog. During startup, R activities such as package loading will be reported. After they complete, PMOD can be restarted in the normal user mode and the **Install required packages ...** check removed.

Starting the R Console

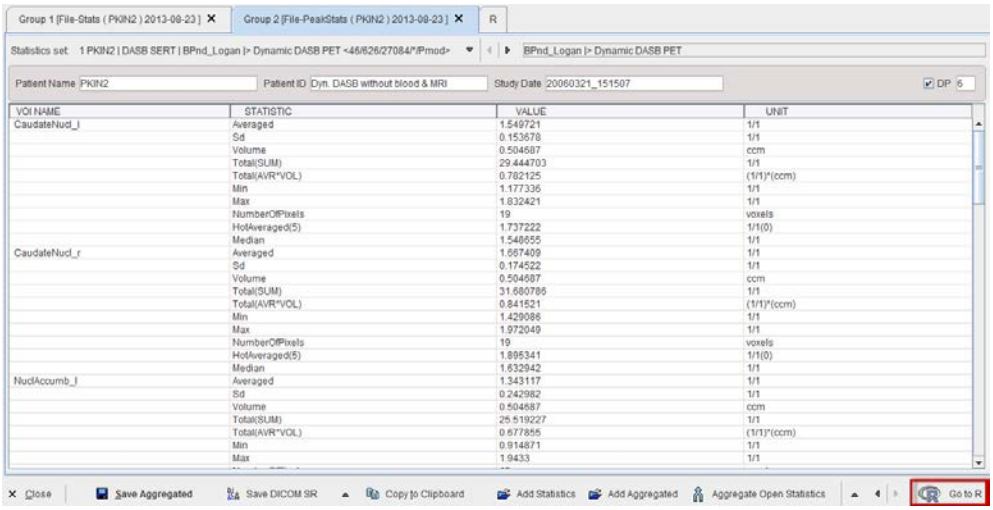
The PMOD R console can be started in different ways:

1) From the PMOD ToolBox



using the keyboard keys `SHIFT+CTRL+R`,

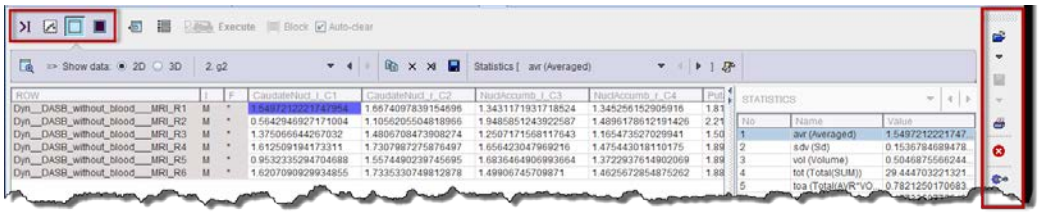
by transferring data using the **Go to R** button from the PMOD statistics or aggregate viewers illustrated below.



The console opens as a dialog window. If **Go to R** has been invoked, the workspace will contain data which is already shown in the user interface. When starting with an empty console, data needs to be loaded using the loading button from the lateral taskbar.

R Console Organization

The user interface of the R console has a main part and a taskbar to the right.



Main Window

The main part may have 4 different layouts depending on which of the indicated buttons in the upper left is selected:

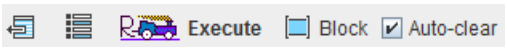
Command layout: Allows invoking existing analysis scripts as well as editing and executing native R commands on the loaded data.

Plotting layout: Allows producing different plots of the data, and inspecting the plots produced by analysis scripts.

Table layout: Allows inspecting the data variables of the R workspace. Initially, the loaded data appear as variables g1, g2, etc. Scripts add variables to the workspace. Data can be copied to the clipboard for external usage.

Image layout: Allows visualizing images.

Next to the layout buttons is an area containing several buttons



which are related to programming in R and effective in different contexts:

Generates R code for extracting parts of the workspace variables.

Lists the variables in the workspace and inserts the selected variable into the command line.

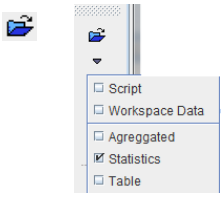
Executes the whole code in the command window.

Executes the selected code in the command window.

Clears the contents of the command window after execution.

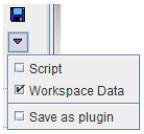
Lateral Taskbar

The elements in the taskbar have the following functionality:



Loading of

- R-specific data: R scripts (**Script**, .r file), a saved R workspace (**Workspace Data**, .RData file), saved R tables (**Table,** .RTable file);
- PMOD statistics data: **Aggregated** (.dbTab file)**, Statistics** (.voistat file).



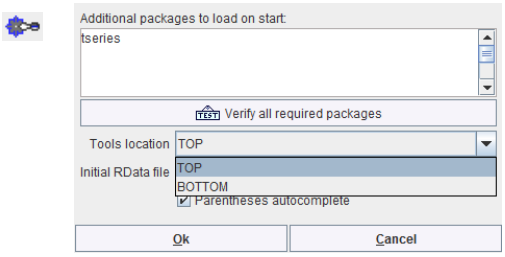
Saving of

- the contents of the command window in two ways: as a new **Script** , which can be loaded, or as a **plugin**, which can directly be selected from a list;
- all data variables as an R workspace (**Workspace Data**, .RData file) which can be loaded back into the PMOD R console, but also directly to R or other graphical front-ends of R (e.g. R Studio).

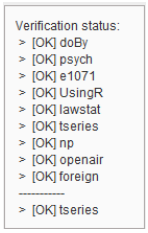
Printing a report which may include plots, tables and/or images, depending on the analysis performed.

Clears all the variables in the R workspace.

Opens the configuration settings window:



If user scripts require additional R packages, they can be typed into the **Additional packages ...** window and checked with the **Verify ...** button.



Tools location is layout option. The tools section may be arranged at the **Top** (as in this documentation), or at the **Bottom**.

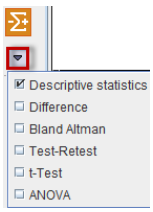
Initial RData file directs the R console to load an R workspace file whenever it is started. This file might include R functions developed by the user.

? Help information concerning R installation and configuration, R interface and references.

Captures the entire screen (not only the PMOD window) and adds it to a console buffer.

Opens the **Console** dialog window for checking the log output and *reporting problems* (on page 29) to support@pmod.com.

Shortcut for opening the scripts selection. System scripts are listed first, followed by scripts which were saved as plugins.



Data Loading

Input Data

The following data generated by PMOD can be loaded into the R console:

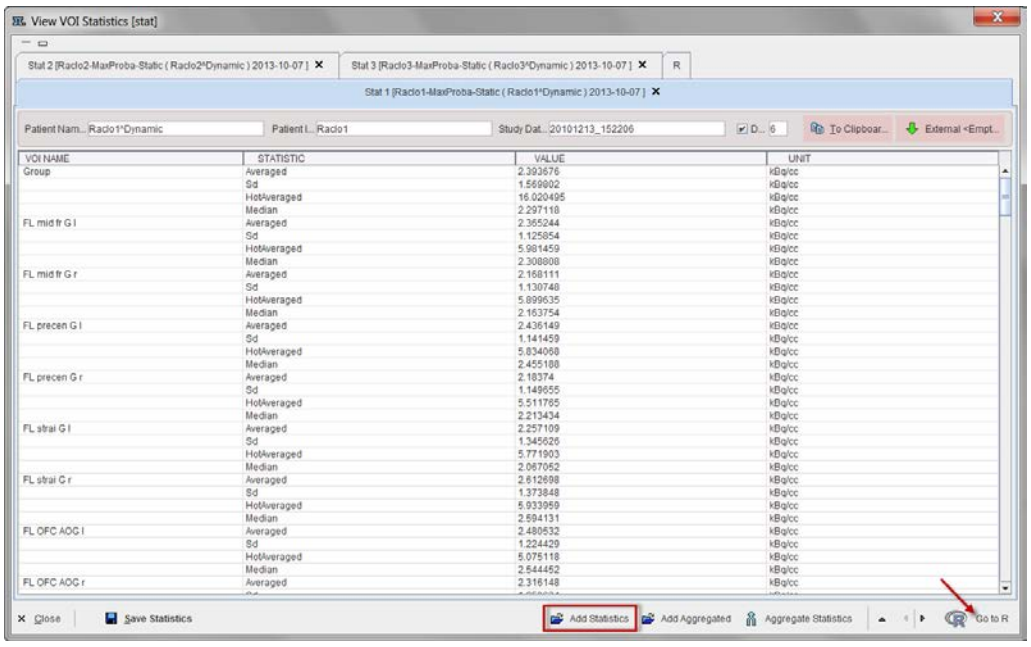
- Saved VOI statistics results, applied to a single image or multiple images (.voistat files). The **Enhanced output format** and **Enhanced aggregation format** should be enabled in the ***configuration*** (on page 16). Note that the statistics may included a time dimension if the image file was dynamic.
- ***Aggregated PMOD results*** (on page 239) from multiple result files. Typically, the results of a population (controls, patients) or a condition (test, retest) should be compiled into a single aggregate.
- Images, which can be transferred to R via the ***R console*** (on page 140) entry in the **External Tools**. At this time, however, no dedicated statistics on images are yet provided through the PMOD R console.

Transfer of Statistics to R

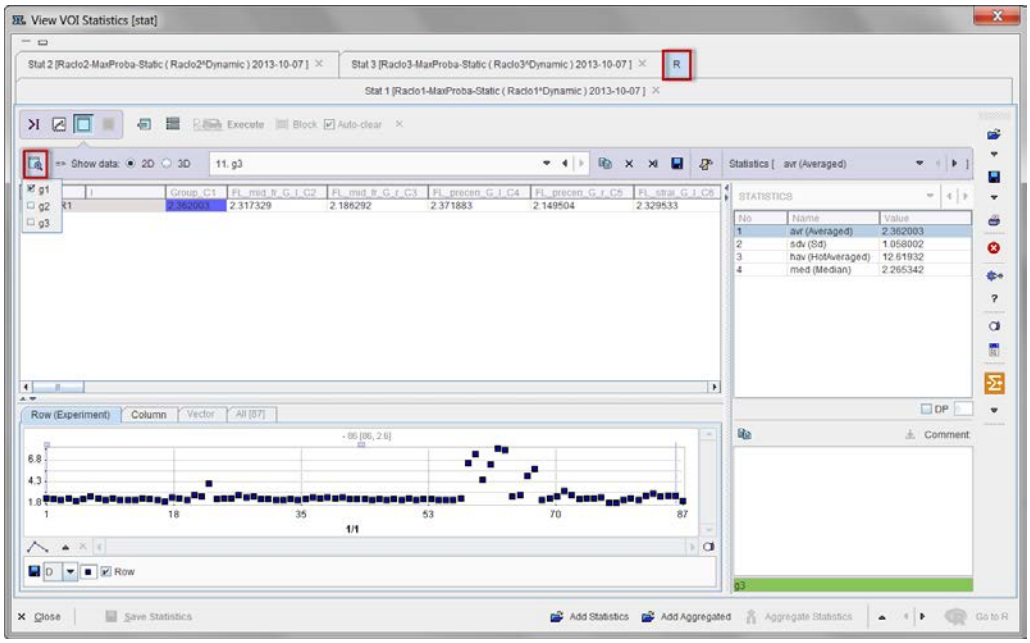
The **Go to R** button transfers the data of all open statistics to the R server, generating one R variable per tab in the R workspace. The variables are labeled sequentially in the order of the tabs as **g1**, **g2**, .. etc.

Load Statistics Files

Use **View statistics** in the lateral taskbar or the menu for loading one or multiple statistics (.voistat) files. A dialog window opens with a **Stat** page per statistics file, and an **R** page. Further statistics files can be added by the **Add Statistics** button.

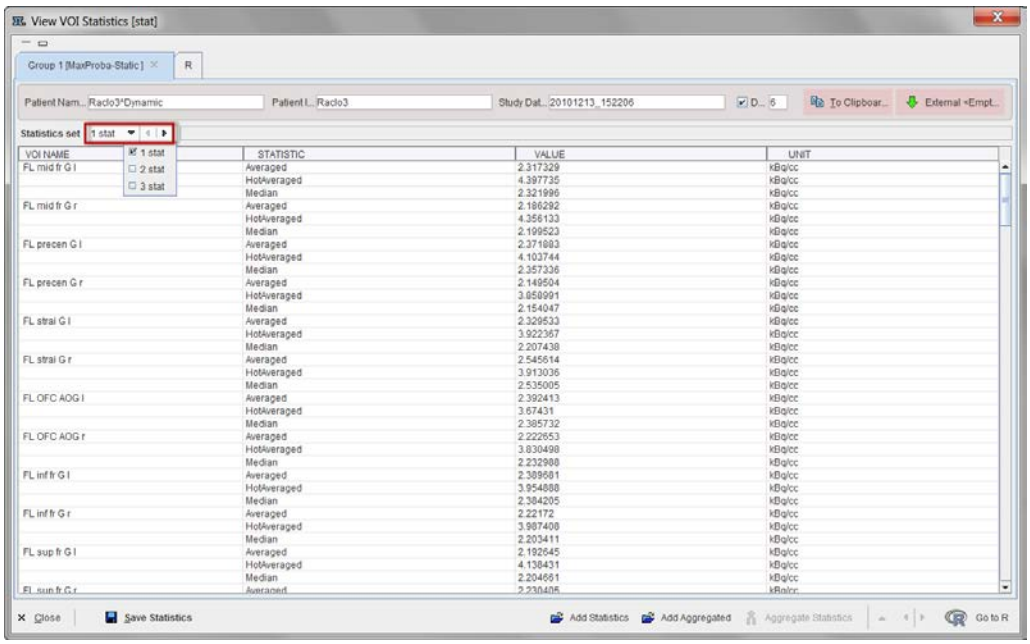


The **Go to R** button transfers the data of all open statistics to the R server, generating one R variable per tab in the R workspace. Note that the variables are labeled sequentially in the order of the tabs as **g1**, **g2**, .. etc. The result of the example is illustrated below.

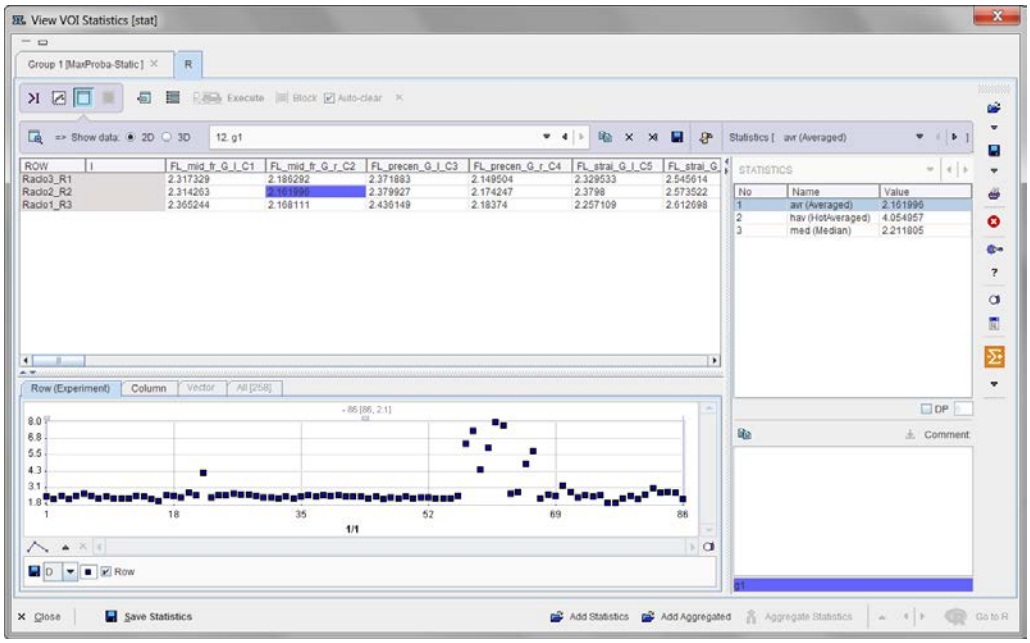


Load Aggregate Files

View aggregated works similarly as **View statistics**, except that aggregates typically contain data from multiple data sets. Correspondingly, there is a **Statistic set** selection for switching the data set. Aggregates can be incrementally added using the **Add Aggregated** button.



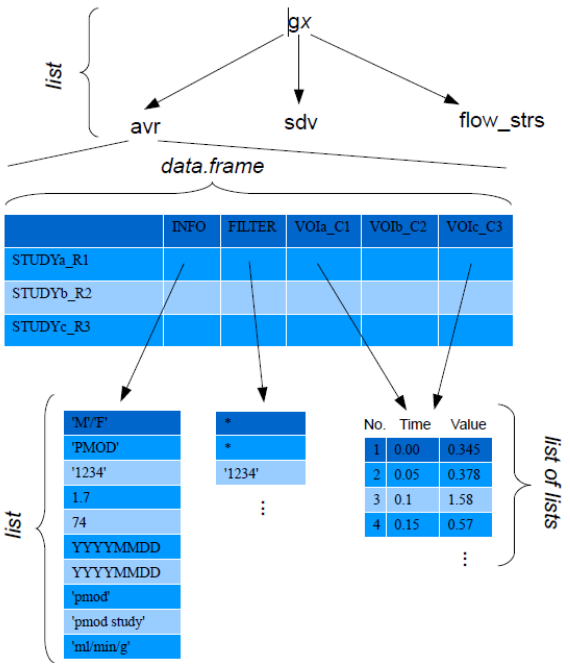
After transferring the data to r with **Go to R** there is only one variable **g1** with one row per data set.



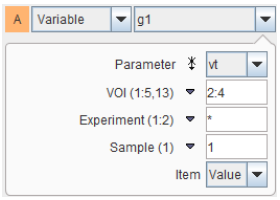
R Variable Structure

The variables **g1, g2** etc. created by the transfer of statistics and aggregates to R have the following structure:

- The highest level consists of a list corresponding to the different statistic types such as average and standard deviation for VOI statistics, Vt for aggregated modeling results, etc.
- The next level is a data frame with a header line and data rows. The data rows correspond to the rows in an aggregate and are thus dependent on the aggregated data. Typically, the rows correspond to the different subjects in a population.
- Each cell in the data frame table is in itself a list. The list structure depends on the aggregated table and on the column. An INFO list contains demographic data, while a VOI list contains 3 lists for the elements "number", "time" and "value".



Most PMOD scripts require the specification of which part of a variable should be processed. Therefore, they show dialog windows such as the one illustrated below.



After choosing a **Variable**, the elements in the lower part are updated according to the variable contents. **Parameter** represents the statistics to be analyzed. The **VOI** selection corresponds to the columns, the **Experiment** to the rows, and the **Sample** to the location in the **value** or **time** list. **Item** finally allows switching from **Value** to **Time**, if the acquisition timing rather than the sample value is needed.

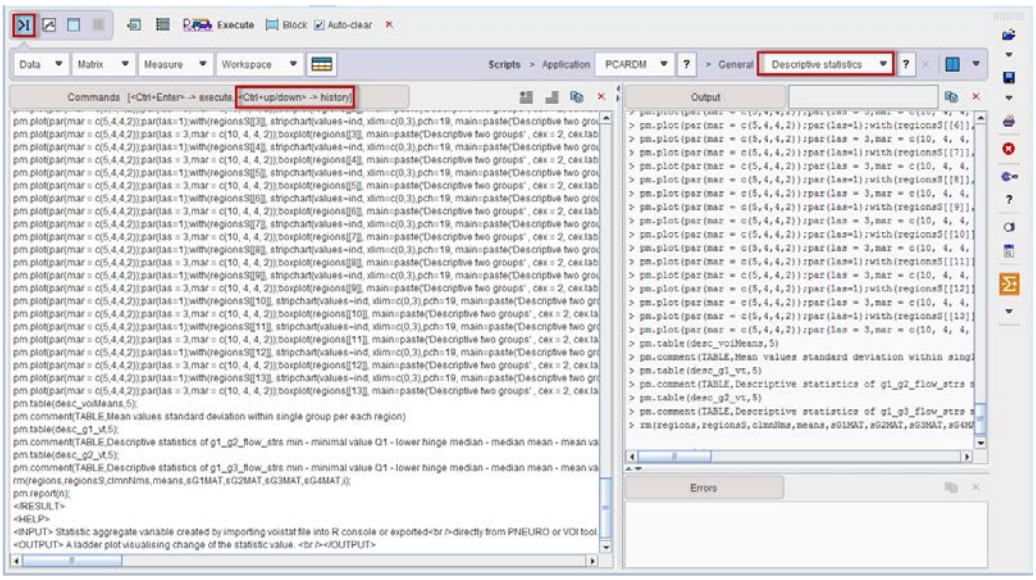
The selections in text fields represent standard R expressions, for example:

- Use all available elements, eg all VOIs: "*****"
- Use a range, eg. elements 2 to 4: "**2:4**"
- Use one specific element, eg the first: "**1**". It can be combined with a range in the form of e.g. "**1, 3:5**".

As a convenience, the shortcut button  propagates the "*" definition to all components.

Command Window

The command window provides a graphic user interface for developing and executing R commands and scripts. The illustration below shows the organization using the horizontal layout.



Commands Area

The **Commands** area serves the following purposes:

1) Interactive R command execution: R commands can be manually typed into the are and executed with the Execute button. If multiple code lines were entered, execution can be restricted to a highlighted part by the Block button.

Code generated by Scripts: Whenever a scripts is called, its R code is copied to the **Commands** area and then executed.

Execution history: Whenever the **Commands** contents is executed, it is copied to a history butter. If the **Auto-clear** box is checked, the **Command** area is cleared after command execution. However, using the keyboard keys `Ctrl+up-arrow` and `Ctrl+down-arrow`, prior execution code can be retrieved from the history for inspection/modification. For users interested in R it may be of interest to recall and review the code of in-built scripts.

Output Area

The

```
Connecting to the server localhost ... Connected.
Loading default settings ... Loaded.
R version 2.15.3 (2013-03-01)
Loading input data 1/2... Loaded.
Loading input data 2/2... Loaded.
```

```
> summary(g1);
   Length Class      Mode
vt 16     data.frame list

> ls();
[1] "g1"          "g2"          "pm.getc"     "pm.gete"
"pm.getf"
[6] "pm.geti"     "pm.getm"     "pm.getp"     "pm.getr"
"pm.getslc"
[11] "pm.getv"     "pm.getx"     "pm.mutualc"  "pm.mutualr"
"pm.mutualrc"
[16] "pm.setc"     "pm.setm"     "pm.setp"     "pm.setr"
"pm.setslc"
[21] "pm.size"     "pm.sortc"    "pm.sortr"    "pm.sortrc"
"pm.trim"
[26] "zz"
```

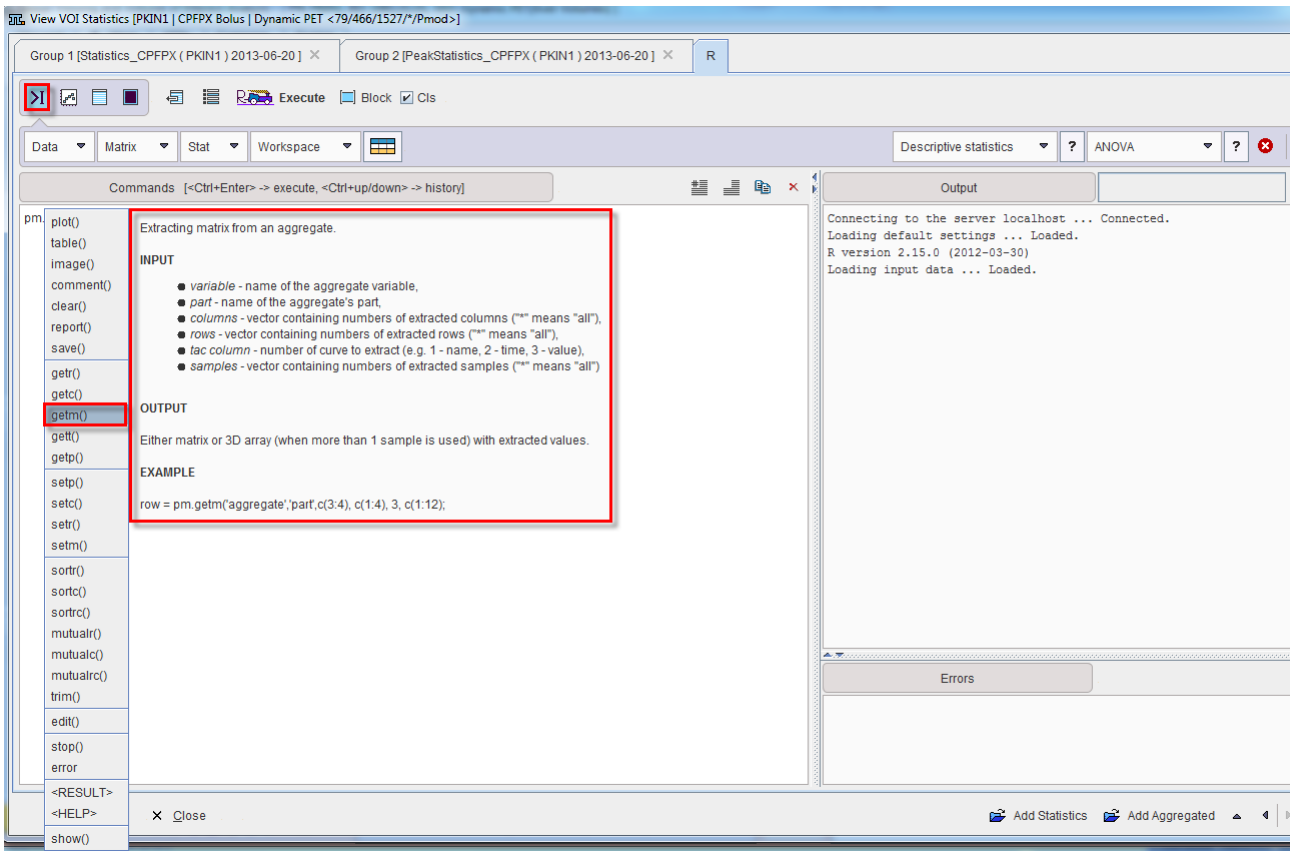
Errors Area

The l

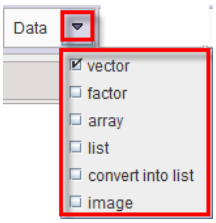
PMOD R Commands and Code Generator

PMOD has implemented a set of commands for the manipulation of the R variables created .

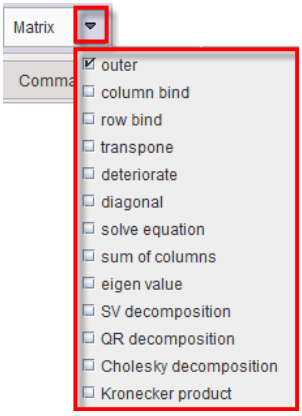
commands dedicated to the PMOD **Command** console. This commands list is accessible typing the **pm.** in the **Command** console. Their description is available upon selection from the pop-up menu as shown below:



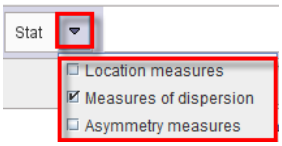
Data — Creation of new data structures such as vector, array or list



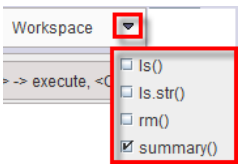
Matrix — Basic operations on matrices.



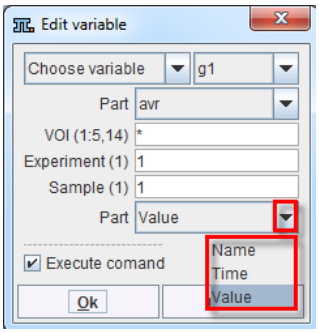
Stat — Allows applying predefined statistic operations to the variables available in the workspace.



Workspace — Allows performing various quick operation like listing (ls()), removing(rm()) and accessing the summary (summary()) of the variables available in the workspace. The results are displayed in the **Output** console.

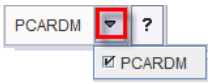


Allows editing a variable available in the workspace. Upon activation the list of variables available in the workspace is displayed. The data type is detected automatically. Two options are available: either **Choose variable** or **Define expression**.

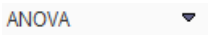


The user can decide which **Part** of the selected variable has to be edited: Name, Time or Value. The confirmation of the settings opens a dialog window which allows perfroming the editing.

Allows selecting and running PMOD tool specific predefined R scripts available in the PMOD-R interface. The predefined scripts are available for selection with the small arrow closed to the button.

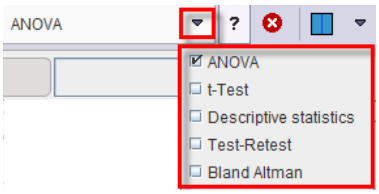


If any help section is available for the selected script, this can be visualized activating the **?** icon close to the scripts selection list.



Allows selecting and running general predefined R scripts. Detailed information of the scripts is available in the dedicated section in this documentation.

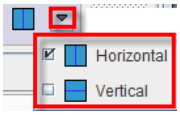
The predefined scripts are available for selection with the small arrow closed to the button. To add a R script to the predefined list, please copy the ***.r** file in the Pmod installation folder *in C:\Pmod3.5resources\extlibs\r*



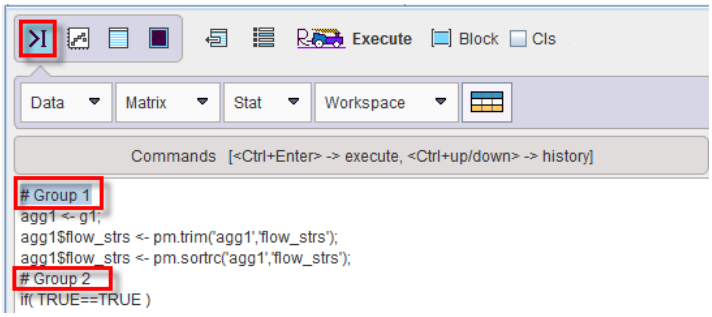
If any help section was included in the script this can be visualized activating the **?** icon close to the scripts selection list.

Allows deleting a script from the scripts predefined list.

Allows switching between the two layout options: horizontal and vertical.



Allows commenting the command lines. First, the lines have to be selected and the icon activated.



Allows uncommenting the selected command lines in the command console. First, the lines have to be selected and the icon activated.

In the **Commands** console: allows copying commands console to the clipboard.

In the **Output** console: allows copying output content to clipboard.

In the **Errors** console: allows copying the errors messages to the clipboard.

In the **Commands** console: allows deleting the content of the command console.

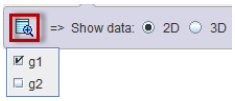
In the **Output** console: allows clearing the output content .

In the **Errors** console: allows deleting the errors messages.

Data Inspection and Visualization

Variable Selection

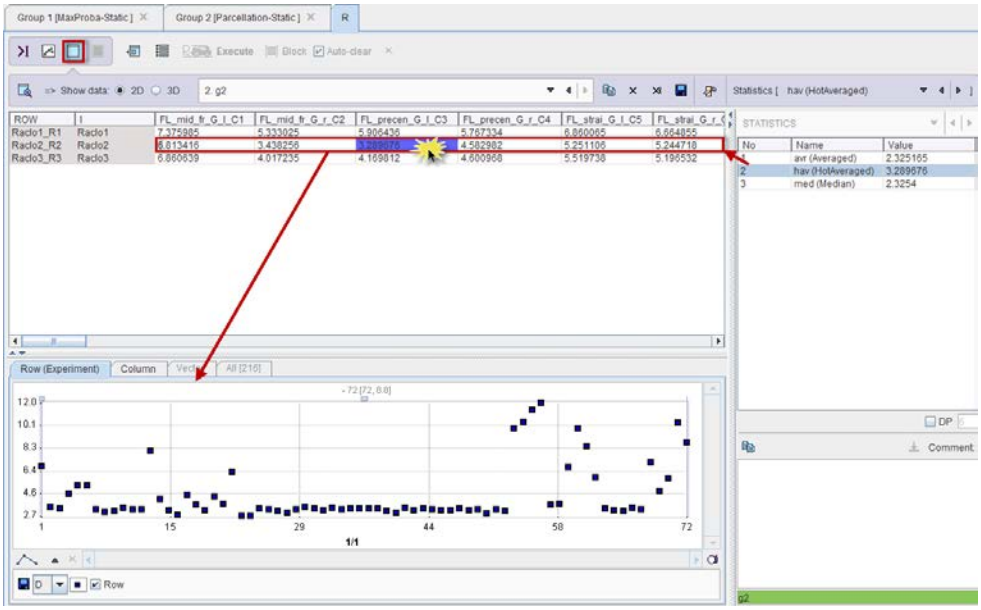
The  button activates the **Table layout** for inspecting the data in the R workspace. The R variables can be selected from the **Preview** list indicated below.



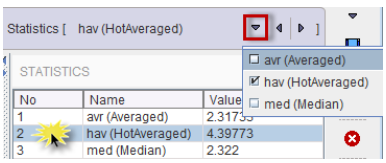
The list will show the original variables as well as variables created by the scripts and R commands.

Table View Layout

After selecting a variable, its content can be inspected. The default **2D** view illustrated below shows the table of the data frame.



The lower plot area shows scatter plots of a data **Row** or **Column**. One variable may have different data frames for different aggregated outcome statistics such as **avr**, **hav**, and **med**. The **Statistics** selection can be used to change between statistics, as well as direct double-clicking into the **STATISTICS** list.



In order to keep track of the variable meaning, comments can be added in the lower right. Please select the variable of interest, enter the comment, and then activate the copy button illustrated below. When saving the R workspace, this comment will be included, so that it will be available when resuming work.

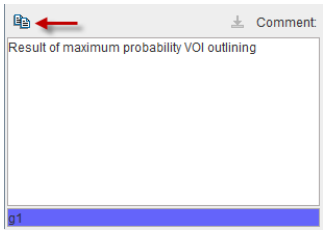
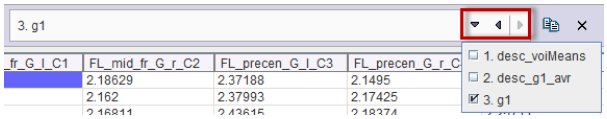


Table Buffer

Note that each visualization of a table is stored in a buffer list so that it can be quickly recalled. While a variable exists only once, there might be multiple entries in the buffer which may represent the visualization of different variable parts.



The buffer list can be edited with the buttons to its right:

 Remove current table from the list.

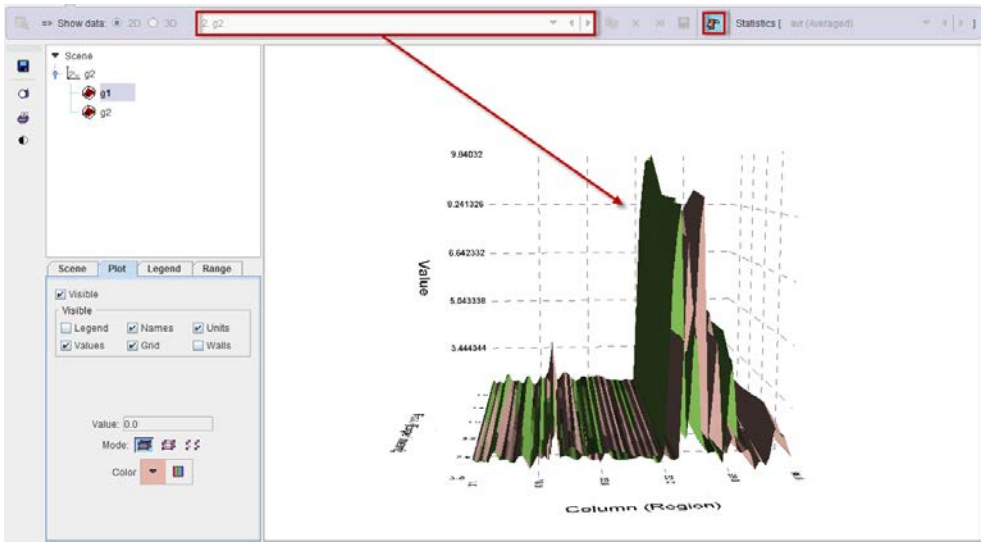
 Save all list tables into a file.

 Copies the current table to the clipboard.

 Clear the buffer list.

Surface Plot Visualization (Option)

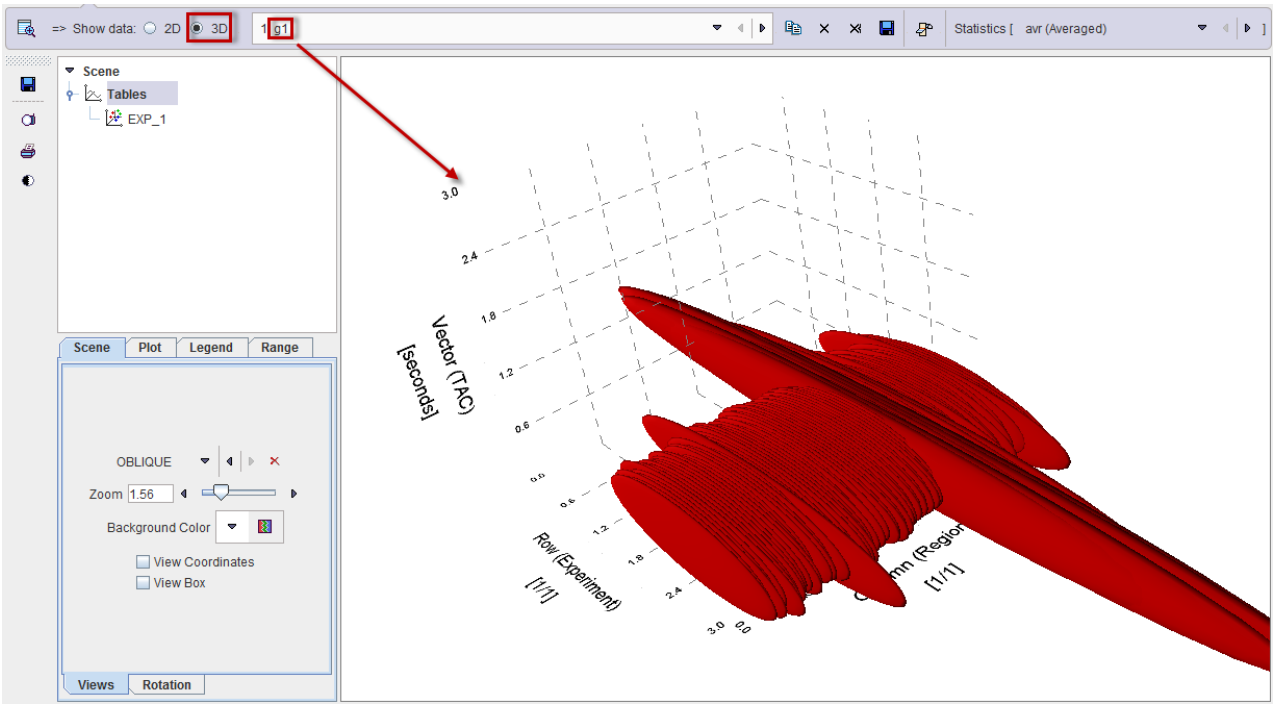
The tables from the buffer can also be visualized as 3D surfaces as illustrated below.



It is essential, that before enabling this display the buffer is prepared so that only meaningful tables remain. Please remove the other tables with the **x** button. For information about the 3D rendering please refer to the *PMOD 3D Rendering User's Guide*.

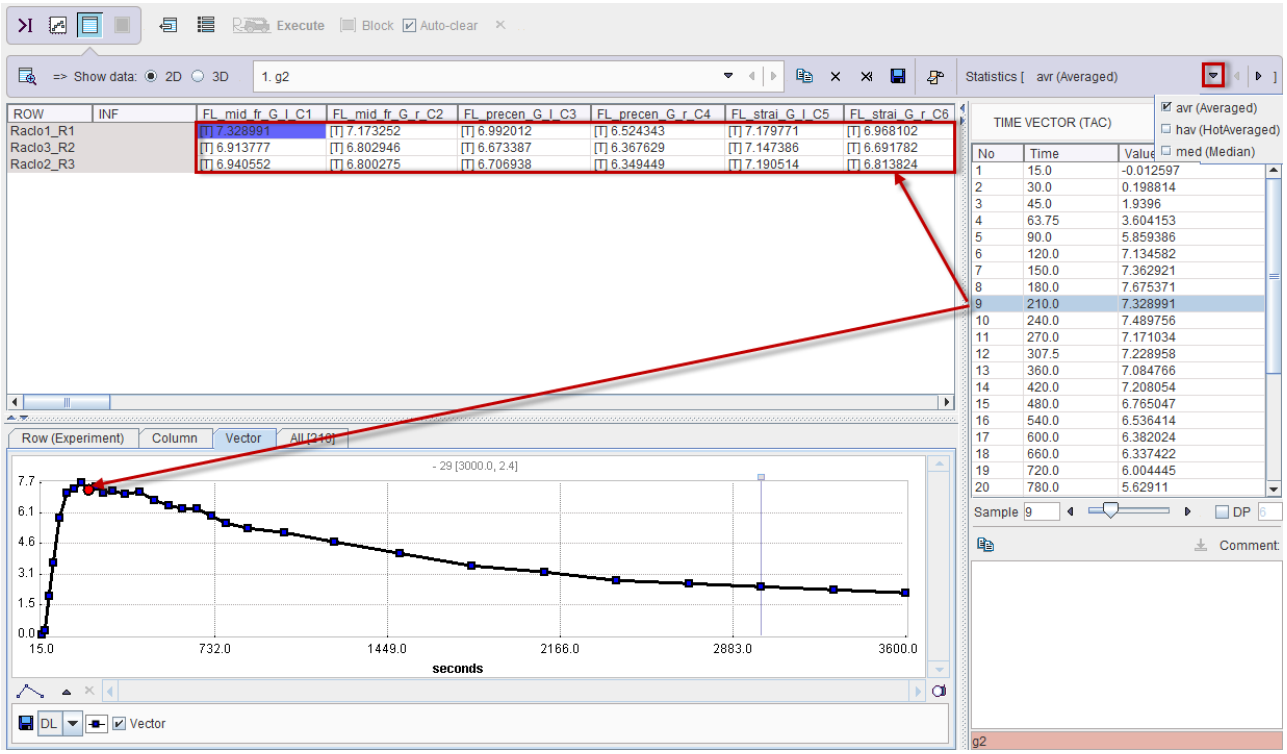
3D Visualization (Option)

When the **3D** radio button is enabled, the selected buffer table is displayed as shown below.



Dynamic Data

If the loaded statistic has a time dimension, the table represents the values at a certain time which can be selected in the **TIME VECTOR** list or by moving the **Sample** slider.

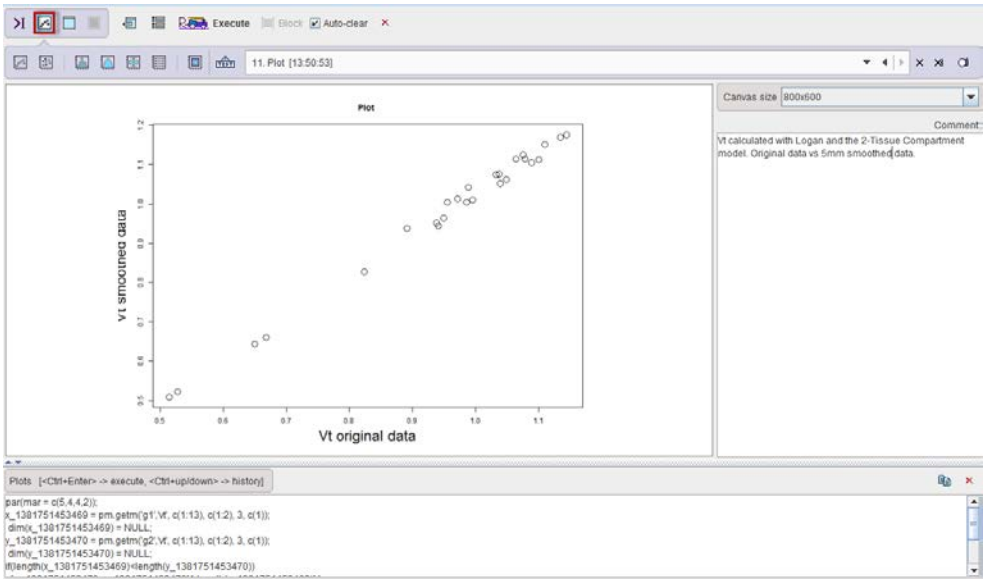


The TAC corresponding to the selected cell (subject/VOI) and the selected **Statistics** is plotted in the **Vector** tab, and all TACs in the **All** tab.

Data Plotting

The contents of variables in the R workspace can be plotted in various ways. Note, however, that the structure of the aggregates used for comparative plotting (eg. scatter plots) needs to be identical, meaning that the number of rows and columns as well as the sorting order must be the same. *No attempt is made to pair corresponding data.*

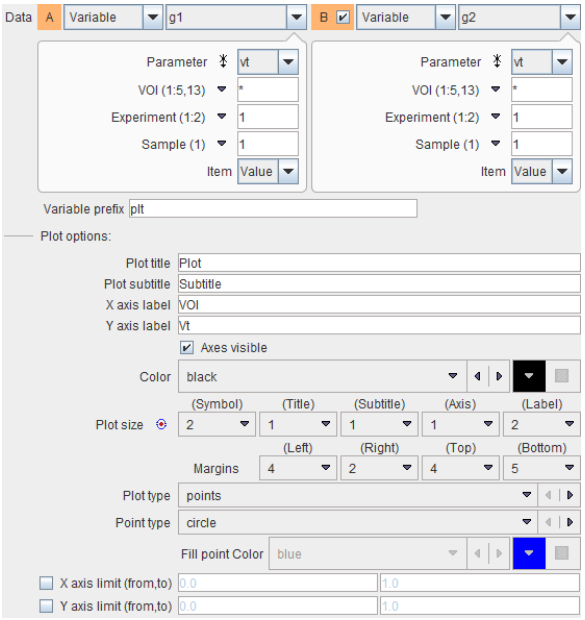
The  button switches the R console to the **Plotting Layout** as illustrated below.



The different available types of plots are represented by the icons in the upper left. When one of the plot icons is activated, it shows a dialog window for the specification of the input data and the plotting parameters.

Plotting User Interface

The interface for the different plots shares common features. The example below shows the **Plot** interface.



The upper part represents the specification of the data to be plotted, as described ***above*** (on page 261). Depending on the situation, one or more data sets labeled **A**, **B**, **C** can be plotted. Some plots may generate variables which are of general interest. They are labeled with **Variable prefix** so that they can easily be identified in the workspace.

Most **Plot options** are straightforward, except for the **Plot size**. It relates to the default size of the R plotting function, which is variable. The plot sizes may need adjustment, when the canvas size is changed.

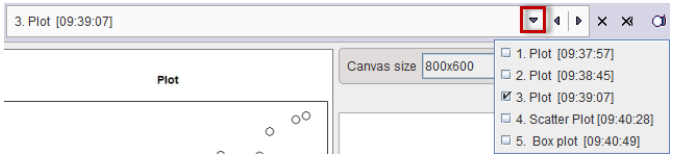
Plotting Code

From the specification in the dialog window R code is generated. If the **Execute** flag is enabled, the code is immediately executed and the graphics is shown in the main window. Otherwise the code is added to the history of the **Plots** command window and may be edited before execution, for instance to change a plotting option.

All executed code is added to the history of the **Plots** command window. On demand prior code can be recovered using the keyboard keys `Ctrl+Up-arrow` and `Ctrl+Down-arrow` similar to the ***command window*** `(on page 263).`

Plot Buffer

The plots created by any plotting actions (including scripts) end up in a plot buffer, so that they can be inspected at any time during a processing session by simply switching the list.



The buffer list can be edited with the buttons to its right:

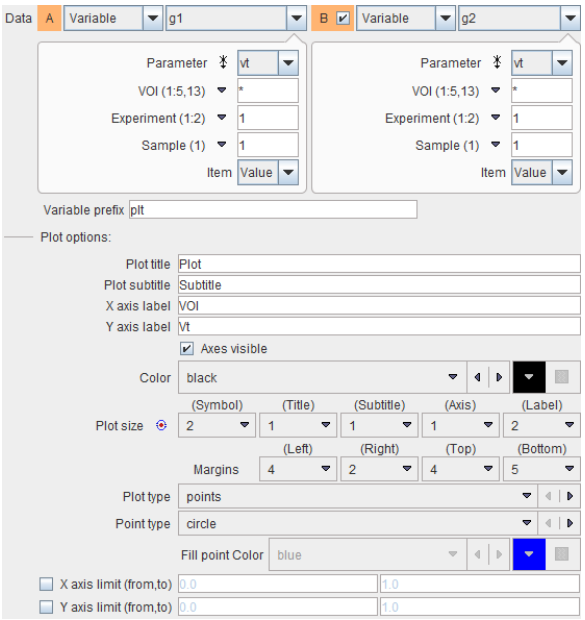
Remove current table from the list.

Clear the buffer list.

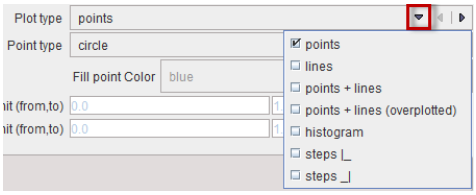
Save the graphics to a file.

Data Plots

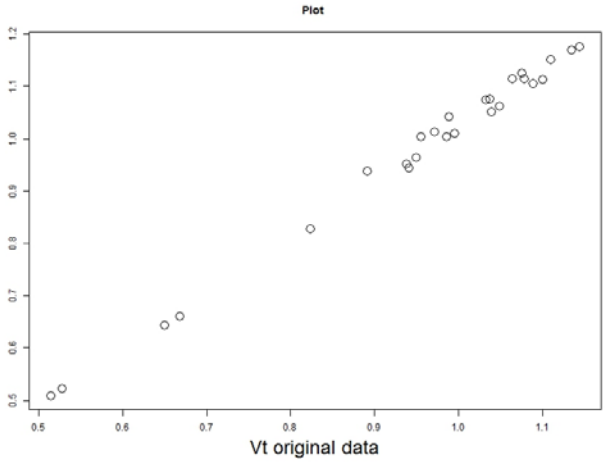
There is a general plotting procedure which can be called with the icon. The user interface allows tailoring it to the plotting task.



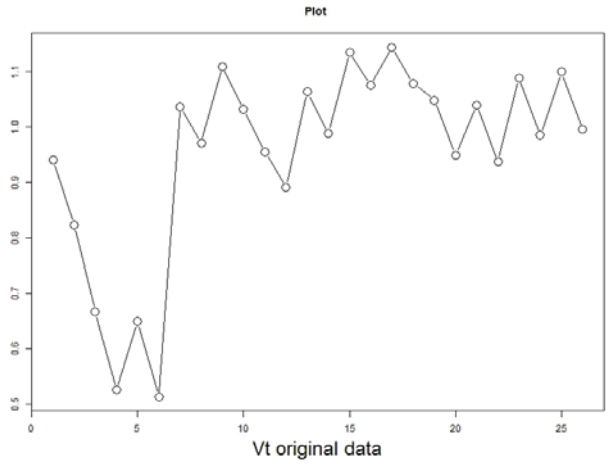
This function is more suited for plotting a single data vector, but x-y plots of two data vectors with equal length are also possible. The **Plot types** list offers the following choices for the plot presentation:



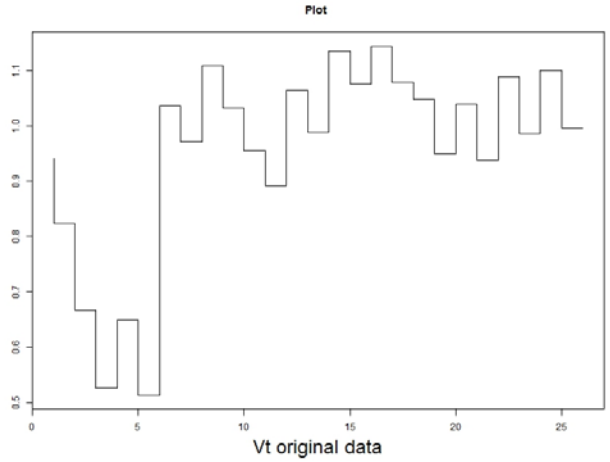
Some example plots: **points** plot with two variables **A** and **B**. Note that regression fits are not supported in this function.



Points + lines plot with a single data vector

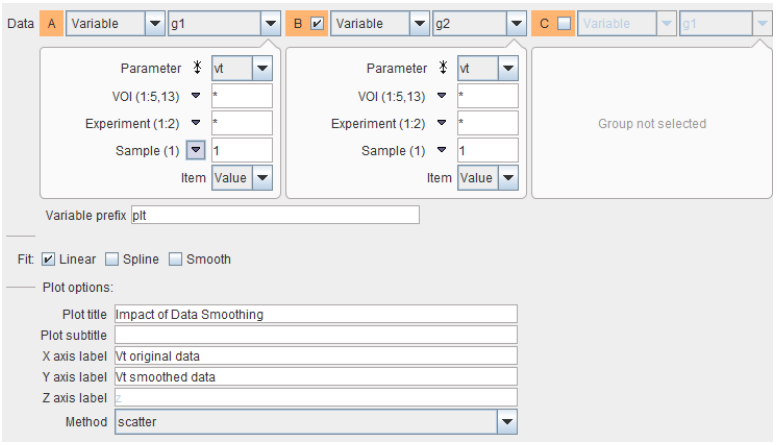


Steps plot with a single data vector



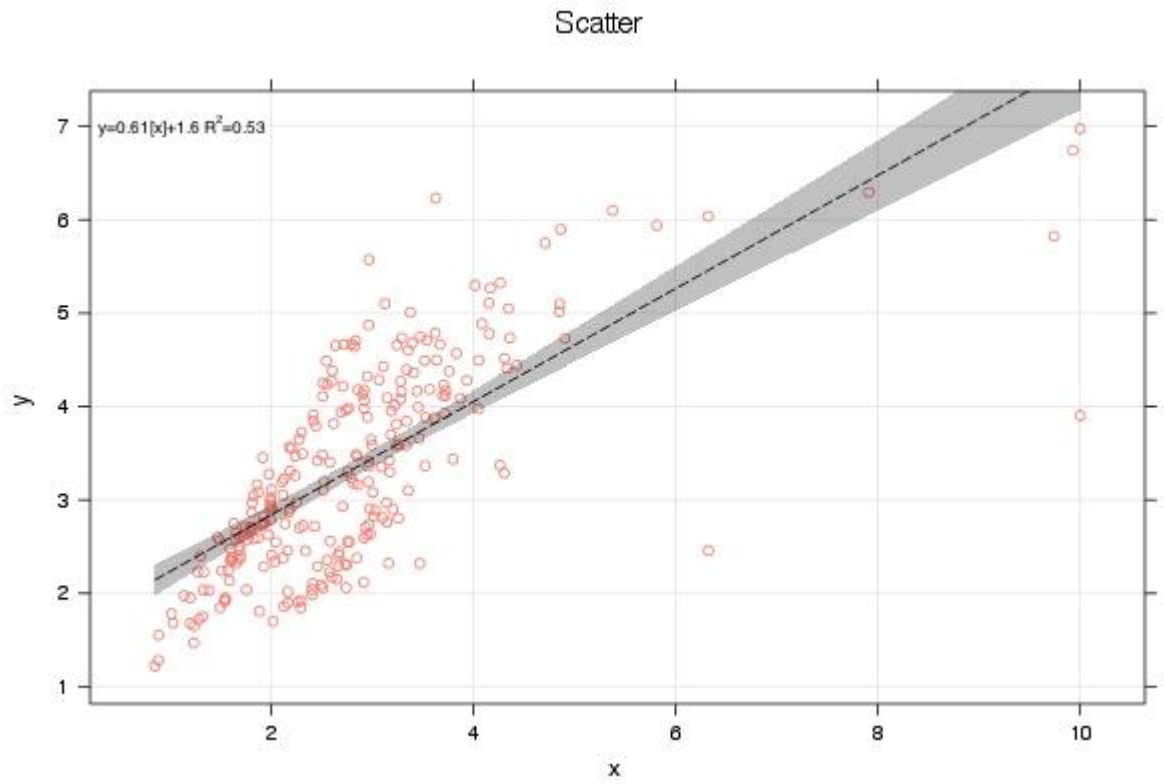
Scatter Plots

The scatter plotting function is called with the button and opens the following dialog window.



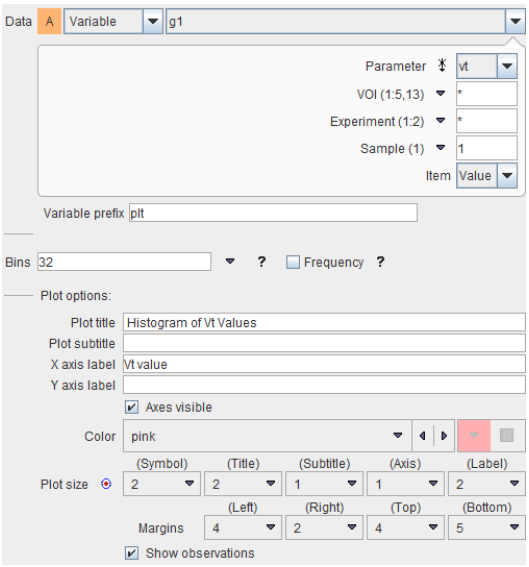
Typically, the values of variable **A** will be plotted against variable **B**. If a third variable **C** is enabled (option), the plot is shown as a 3D scene in the PMOD 3D rendering tool.

The example below shows a scatter plot with a fitted regression line.

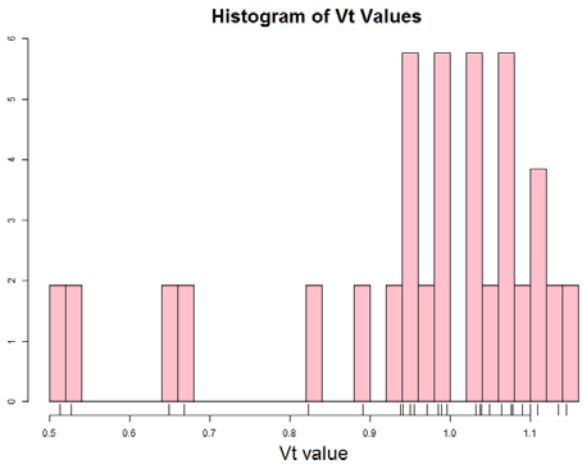


Histogram Plots

The third button  serves for plotting a histogram of a data vector.



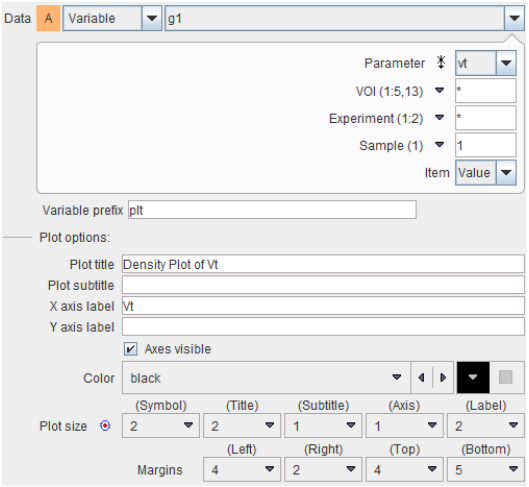
The number of **Bins** can be entered numerically or automatically calculated by 3 methods (**Sturges**, **Freedman-Diaconis**, **Scott**). The example results in the histogram below.



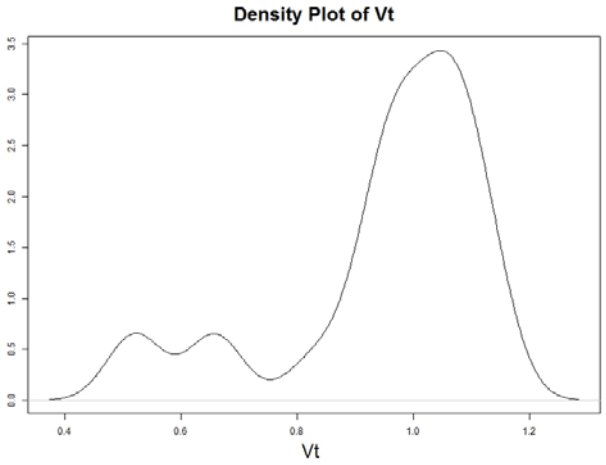
Note the indication of the values and the value ranges because **Show observations** and **Axes visible** are enabled.

Density Plots

The fourth button  provides access to density plotting. This is an extension of the histogram approach and has the advantage that it doesn't depend on a bin size. The setting

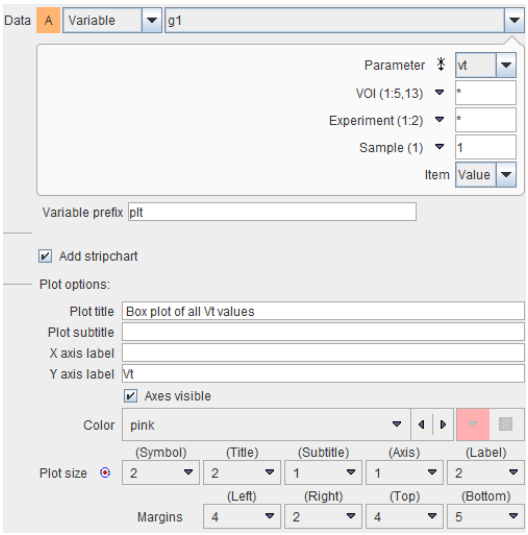


uses the Vt from all VOIs and Experiments (= analysis methods in the example data) and results in the plot below.

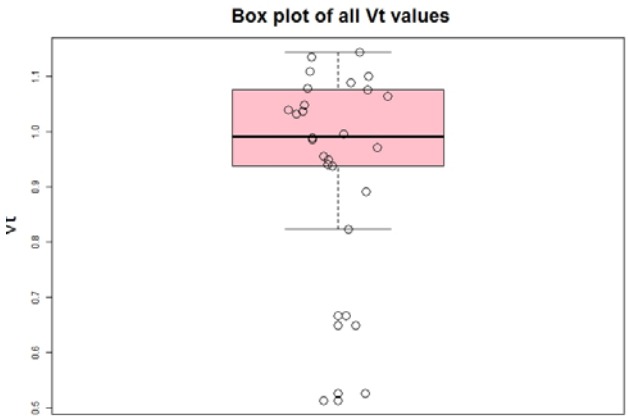


Box Plots

Box plots are widely used in descriptive statistics. They are particularly useful for comparing populations. The button opens the box plot interface.



It produces from the data vector a plot with the following structure.

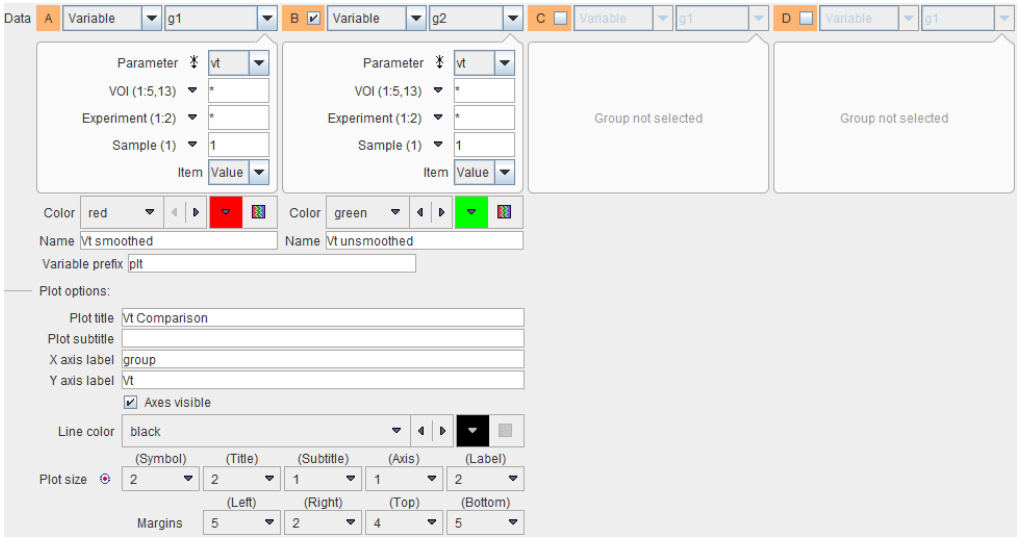


The lines of the box represent the first and third quartiles (Q1, Q3). The bold line in the box represents the median. The whiskers are calculated from the data according to Tukey's method from the interquartile distance (Q3-Q1) and the data. Data points outside the whisker range are outliers.

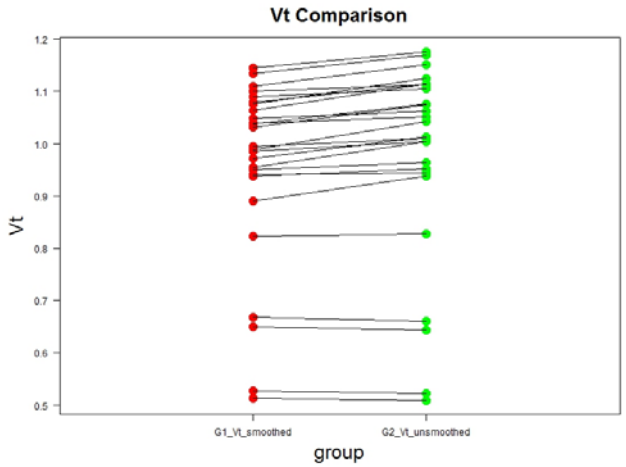
Note that the box plot is applied in the **Descriptive Statistics** script.

Ladder Plots

Ladder plots visualize the relation of a test variable in two or more conditions, for instance pre-and post-treatment. It is called with the button.



Up to 4 conditions can be connected. However, note that the implementation requires identical ordering of the subjects in the data vectors. The example below illustrates a comparison between two conditions.



Analysis Scripts for Aggregates

PMOD has developed several scripts to support users with the statistical analysis of results arising in the comparison of populations or analysis methods. To use them efficiently, the outcome measures should be organized in groups by ***aggregation*** (on page 239).

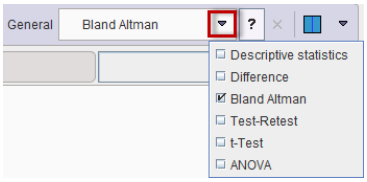
For example, if healthy controls are studied twice to determine the repeatability of an acquisition/data processing methodology, the results of the first study should be aggregated in a test group g1, and the results of the second study in a retest group g2. These groups can then be loaded into the R-console of PMOD, and analyzed with the **Test-Retest** script.

Another typical example is the comparison of analysis methods. The same set of population data will be processed twice with different methods, for instance to calculate the regional binding potential BP_{nd}. All BP_{nd} estimates resulting from method 1 are aggregated into a group g1, and all BP_{nd} estimates resulting from method 2 in group g2. The method comparison is then done by applying the script **Bland Altman Plot** to g1 and g2.

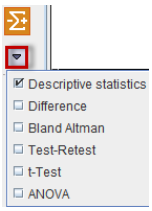
The scripts generate and execute native R code which can be inspected in the command console and serve as a basis for users to develop their own, modified scripts.

Invoking Scripts

After loading the data to be analyzed, scripts can be called either from the **General** list of the command layout



or via the lateral taskbar by the indicated arrow button



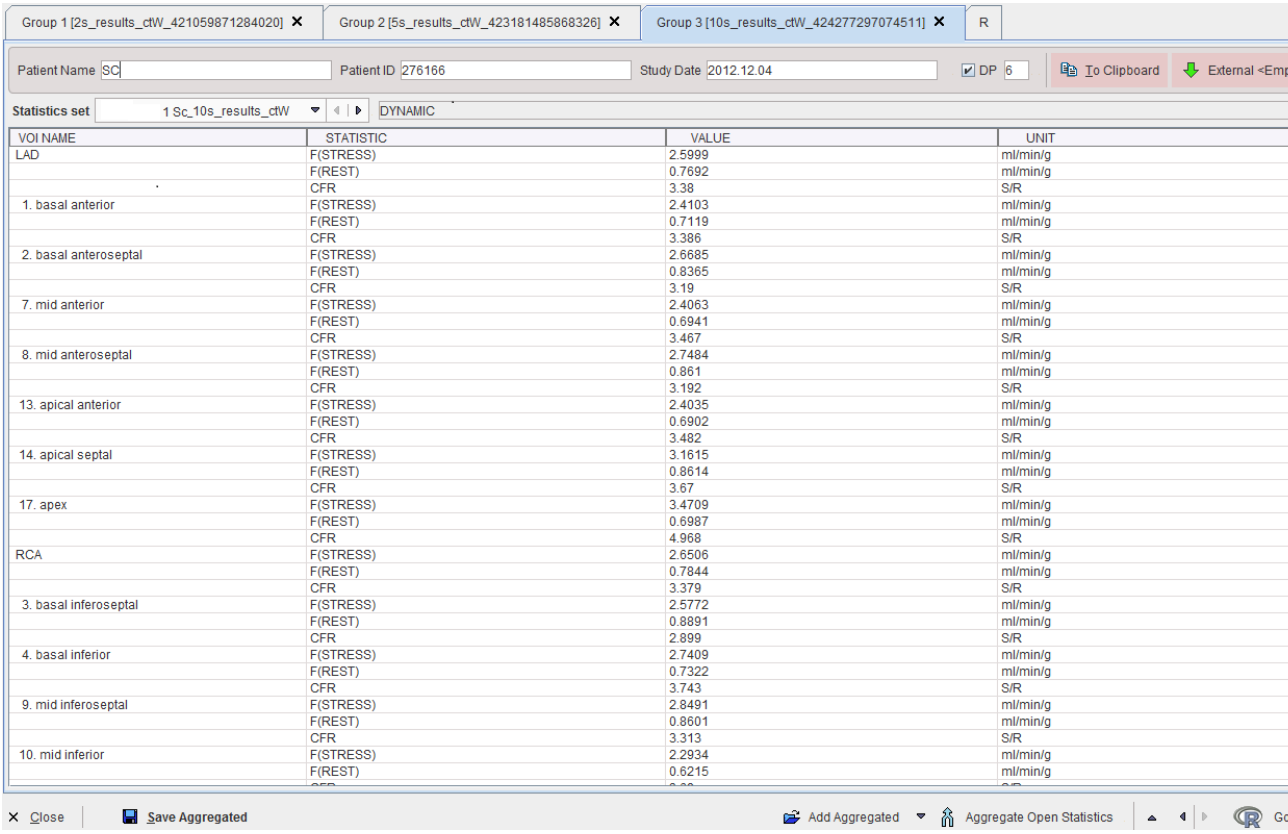
The following sections describe each of the scripts. Most practical details are included in the **Descriptive Statistics** section, so ülease make sure to read this section first.

Descriptive Statistics

The **Descriptive statistics** script serves for summarizing the statistical properties of outcomes assembled in one or several PMOD aggregates.

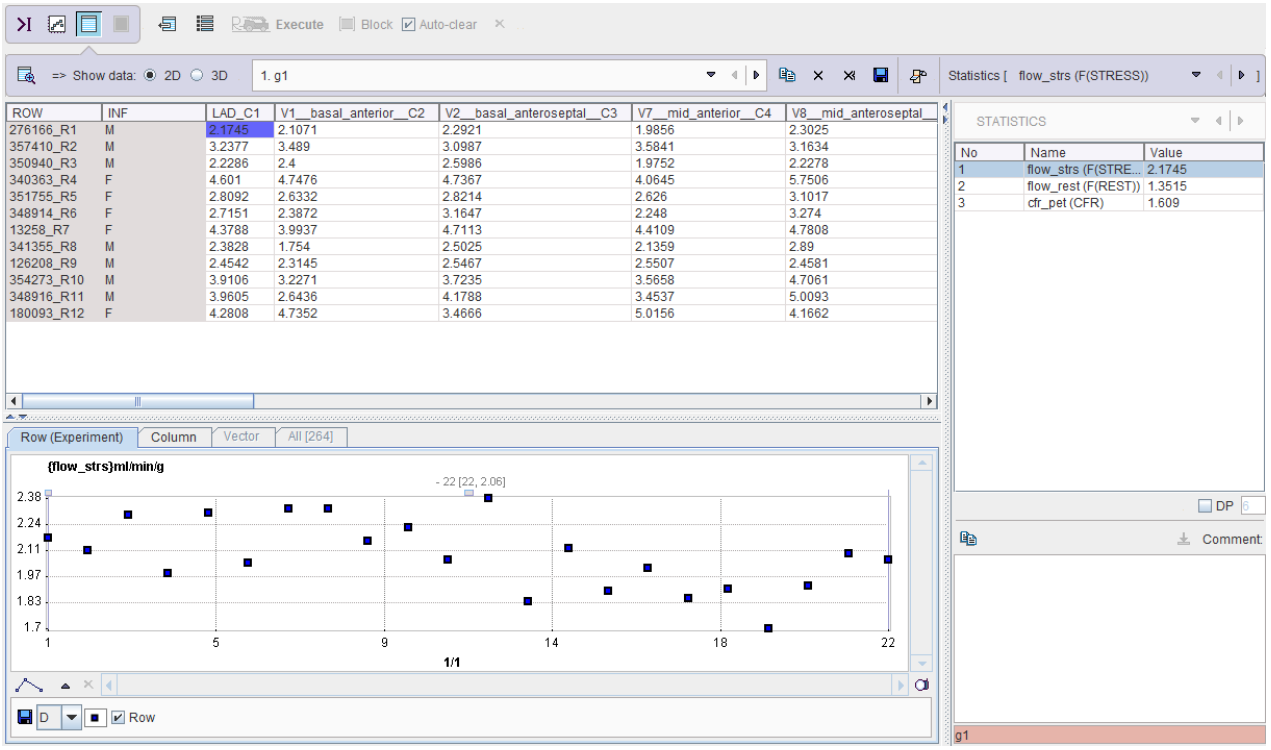
Preparation

The example below uses three aggregates from the quantification of myocardial perfusion by PCARDP. The purpose of the study was to evaluate the impact of the initial frame rate on the perfusion estimate. Correspondingly, the aggregates represent 2 sec, 5 sec and 10 sec sampling. Each of the aggregates has 12 datasets (**Statistics set**) with 3 **STATISTIC** results, the stress flow **F(STRESS)**, the rest flow **F(REST)**, and the coronary flow reserve **CFR** in 17 VOIs (=cardiac sebments, **LAD**, ...). Illustrated below is the R console with the three aggregates loaded.

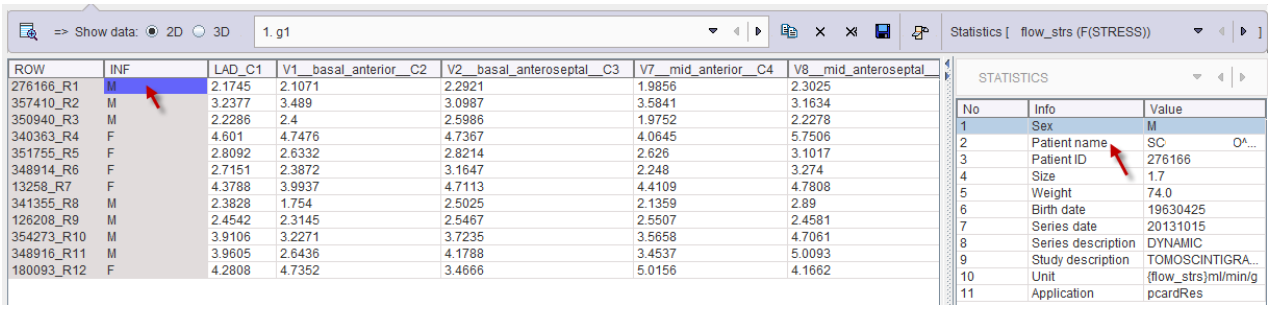


VOI NAME	STATISTIC	VALUE	UNIT
LAD	F(STRESS)	2.5999	ml/min/g
	F(REST)	0.7692	ml/min/g
	CFR	3.38	S/R
1. basal anterior	F(STRESS)	2.4103	ml/min/g
	F(REST)	0.7119	ml/min/g
	CFR	3.386	S/R
2. basal anteroseptal	F(STRESS)	2.6685	ml/min/g
	F(REST)	0.8365	ml/min/g
	CFR	3.19	S/R
7. mid anterior	F(STRESS)	2.4063	ml/min/g
	F(REST)	0.6941	ml/min/g
	CFR	3.467	S/R
8. mid anteroseptal	F(STRESS)	2.7484	ml/min/g
	F(REST)	0.861	ml/min/g
	CFR	3.192	S/R
13. apical anterior	F(STRESS)	2.4035	ml/min/g
	F(REST)	0.6902	ml/min/g
	CFR	3.482	S/R
14. apical septal	F(STRESS)	3.1615	ml/min/g
	F(REST)	0.8614	ml/min/g
	CFR	3.67	S/R
17. apex	F(STRESS)	3.4709	ml/min/g
	F(REST)	0.6987	ml/min/g
	CFR	4.968	S/R
RCA	F(STRESS)	2.6506	ml/min/g
	F(REST)	0.7844	ml/min/g
	CFR	3.379	S/R
3. basal inferoseptal	F(STRESS)	2.5772	ml/min/g
	F(REST)	0.8891	ml/min/g
	CFR	2.899	S/R
4. basal inferior	F(STRESS)	2.7409	ml/min/g
	F(REST)	0.7322	ml/min/g
	CFR	3.743	S/R
9. mid inferoseptal	F(STRESS)	2.8491	ml/min/g
	F(REST)	0.8601	ml/min/g
	CFR	3.313	S/R
10. mid inferior	F(STRESS)	2.2934	ml/min/g
	F(REST)	0.6215	ml/min/g

Transferring the data to R with **Go to R** creates the 3 workspace variables **g1**, **g2** and **g3**. The table layout illustrated below shows the structure of **g1** with the subjects in the rows, the VOIs in the columns, and the statistics as a selection.

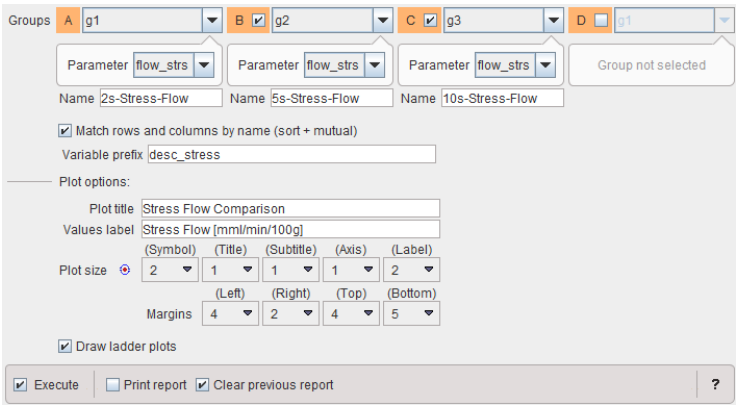


Note the **INF** column which can be used to show selected demographic data, the gender in the example above. To change to a different information item please double-click an element in the **INF** column. The **STATISTICS** list is switched to the demographic information, and the element of interest can be selected.



Descriptive Statistics Configuration

The **Descriptive Statistics** script shows the following dialog window.

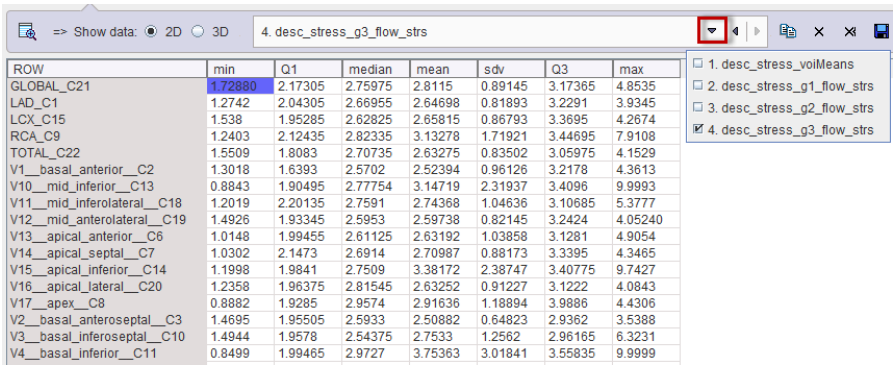


Note that up to 4 data sets can be compared. In the example case 3 **Groups** are selected and the variables **g1**, **g2** and **g3** assigned such that the sampling time is increasing. Only one statistic can be compared at a time, to be selected from the **Parameter** list. If the parameter names don't match, the program will complain, but still perform the calculation.

The results will include tables as well as graphic plots. To group the table results a **Variable prefix** can be specified. **Plot title** and **Values label** should be edited such that the plots are meaningfully annotated. The **Draw ladder** plot option allows visualizing each data point across the three data sets.

Descriptive Statistics Results

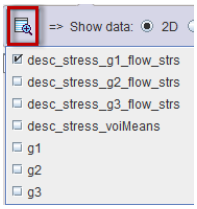
After running the script the workspace is populated with new variables, and plots have been generated and added to the plot history. The R console is in the table layout and shows a statistic summary table of the third group **g3**. For each VOI the **desc_stess_g3_flow_strs** table shows minimum, first quartile (Q1), median, mean, standard deviation. third Quartile (Q3) and maximum across the 12 subjects.



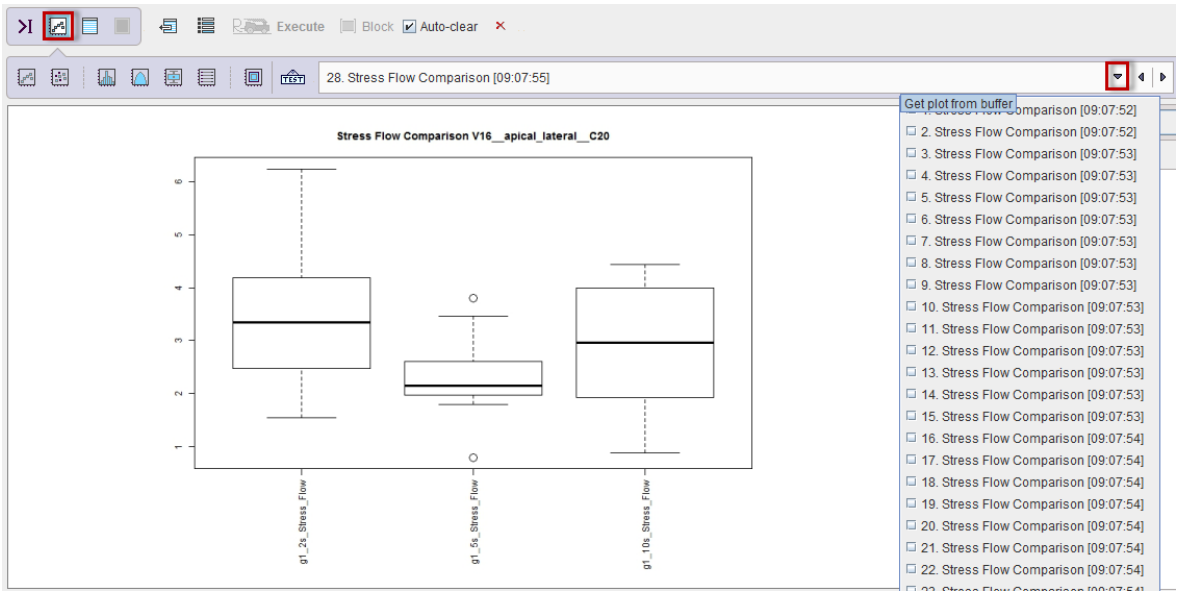
ROW	min	Q1	median	mean	sdv	Q3	max
GLOBAL_C21	1.72880	2.17305	2.75975	2.8115	0.89145	3.17365	4.8535
LAD_C1	1.2742	2.04305	2.66955	2.64698	0.81893	3.2291	3.9345
LCX_C15	1.538	1.95285	2.62825	2.65815	0.86793	3.3695	4.2674
RCA_C9	1.2403	2.12435	2.82335	3.13278	1.71921	3.44695	7.9108
TOTAL_C22	1.5509	1.8083	2.70735	2.63275	0.83502	3.05975	4.1529
V1__basal_anterior__C2	1.3018	1.6393	2.5702	2.52394	0.96126	3.2178	4.3613
V10__mid_inferior__C13	0.8843	1.90495	2.77754	3.14719	2.31937	3.4096	9.9993
V11__mid_inferolateral__C18	1.2019	2.20135	2.7591	2.74368	1.04636	3.10685	5.3777
V12__mid_anterolateral__C19	1.4926	1.93345	2.5953	2.59738	0.82145	3.2424	4.05240
V13__apical_anterior__C6	1.0148	1.99455	2.61125	2.63192	1.03858	3.1281	4.9054
V14__apical_septal__C7	1.0302	2.1473	2.6914	2.70987	0.88173	3.3395	4.3465
V15__apical_inferior__C14	1.1998	1.9841	2.7509	3.38172	2.38747	3.40775	9.7427
V16__apical_lateral__C20	1.2358	1.96375	2.81545	2.63252	0.91227	3.1222	4.0843
V17__apex__C8	0.8882	1.9285	2.9574	2.91636	1.18894	3.9886	4.4306
V2__basal_anteroseptal__C3	1.4695	1.95505	2.5933	2.50882	0.64823	2.9362	3.5388
V3__basal_inferoseptal__C10	1.4944	1.9578	2.54375	2.7533	1.2562	2.96165	6.3231
V4__basal_inferior__C11	0.8499	1.99465	2.9727	3.75363	3.01841	3.55835	9.9999

Using the history, the table can easily switched to the other groups, as well as the **voiMeans** table which just shows the VOI means and standard deviations. Note the copy and save buttons in the buffer controls for exporting the table data.

Note that the workspace now has 4 additional variables, with the defined prefix.



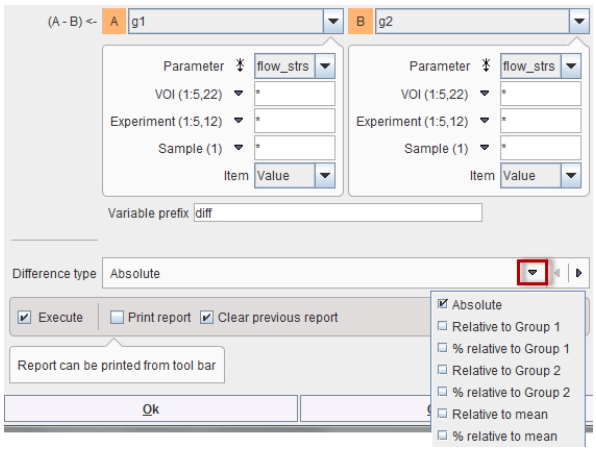
The same information as in the tables is visualized by one ***box plot*** (on page 279) per VOI, providing a convenient side by side comparison of the groups. Please activated the plot layout and use the buffer arrows to browse through the different VOIs.



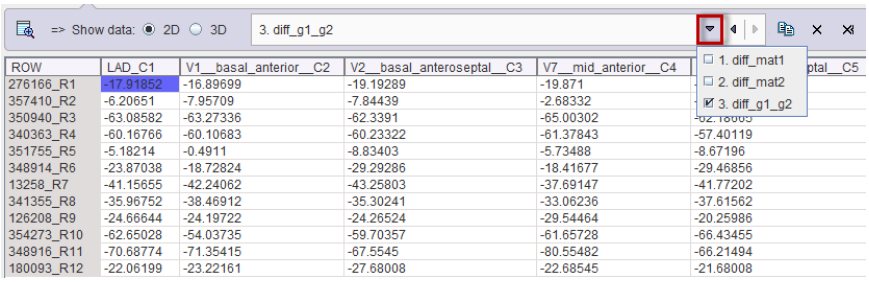
If the **Ladder** plot option was enabled, box plots are alternated with ***ladder plots*** (on page 280).

Difference

The **Difference** script is a simple facility for calculating the difference between two groups. Besides the **Absolute** difference there are various relative differences available, which can be configured with the **Difference type** option list.



The result of the script are three tables, available through the buffer



ROW	LAD_C1	V1__basal_anterior__C2	V2__basal_anteroseptal__C3	V7__mid_anterior__C4
276166_R1	-17.91852	-16.89699	-19.19289	-19.871
357410_R2	-6.20651	-7.95709	-7.84439	-2.68332
350940_R3	-63.08582	-63.27336	-62.3391	-65.00302
340363_R4	-60.16766	-60.10683	-60.23322	-61.37843
351755_R5	-5.18214	-0.4911	-8.83403	-5.73488
348914_R6	-23.87038	-18.72824	-29.29286	-18.41677
13258_R7	-41.15655	-42.24062	-43.25803	-37.69147
341355_R8	-35.96752	-38.46912	-35.30241	-33.06236
126208_R9	-24.66644	-24.19722	-24.26524	-29.54464
354273_R10	-62.65028	-54.03735	-59.70357	-61.65728
348916_R11	-70.68774	-71.35415	-67.5545	-80.55482
180093_R12	-22.06199	-23.22161	-27.68008	-22.68545

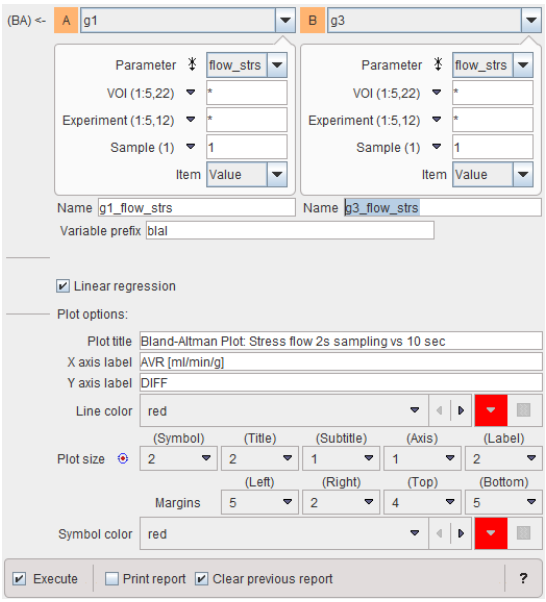
diff_g1_g2 represents the calculated difference, whereas **diff_mat1** and **diff_mat2** contain the extracted input data for the calculation.

Bland Altman Plot

The Bland-Altman plot is aimed at comparing two measurement methods [1]. It simply plots the difference between the measurements against their average. The mean difference is the estimated bias, and from the standard deviation of the differences the 95% limits of agreement can be calculated (mean±1.96std).

Bland Altman Plot Configuration

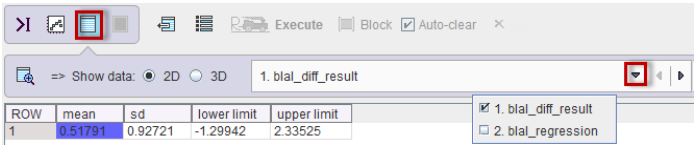
The **Bland Altman Plot** script shows the following dialog window.



Two variables have to be defined, which will be sorted so that the correspondence between samples is ensured. The **Linear regression** convenience option allows getting a scatter plot with a regression line at the same time as the Bland Altman plot.

Bland Altman Plot Results

There are two numeric result tables: the information related to the Bland Altman plot in the **diff_result** table

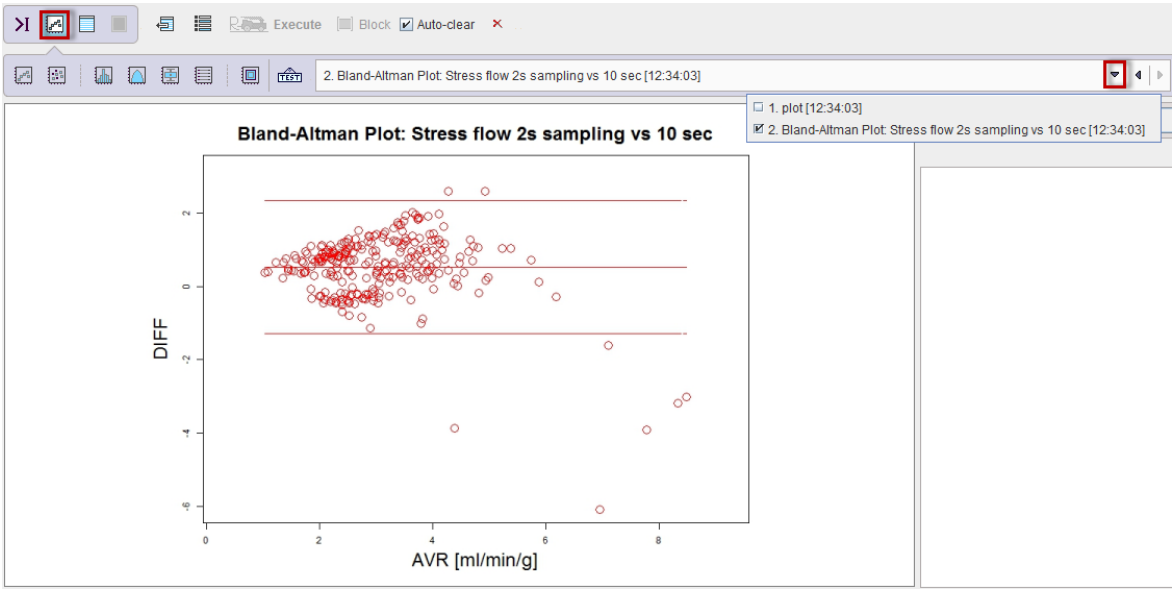


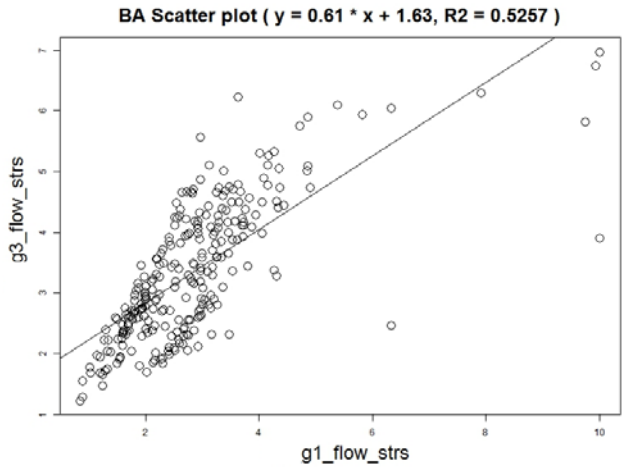
ROW	mean	sd	lower limit	upper limit
1	0.51791	0.92721	-1.29942	2.33525

with the mean and standard deviation of the difference, and the limits of agreement, and the equation of the linear regression in the **regression** table.

ROW	Slope	Intercept	R squared
1	0.61	1.63	0.5257

The corresponding plots can be inspected in the plot layout.





Reference:

1. Bland JM, Altman DG: Statistical methods for assessing agreement between two methods of clinical measurement. Lancet 1986, 1(8476):307-310.

Test-Retest

Once a quantitative methodology has been established, the variability of the outcome parameters needs to be assessed in order to find out, what effect sizes can be detected.

Test-Retest Variability and ICC

A test-retest study should be performed with about 10 subjects to evaluate the variability of the relevant outcome parameters. Each subject is studied twice, whereby the physiological and experimental conditions should be as similar as possible. Due to biologic variability, both acquisitions are preferably done on the same day.

The data quantification method in question is applied for all regions of interest and the results from all subjects pooled. The test-retest variability (VAR, also called within subject variability) is then calculated for each region as follows:

$$VAR = \frac{1}{N}\sum_{i=1}^{N}\frac{\left|test_i - retest_i\right|}{(test_i + retest_i)/2}\cdot 100\%$$

where N represents the number of subjects and $test_i$ and $retest_i$ the result values of the quantification method. Hence, the test-retest variability represents the average percent difference of the regional results across the subjects. As an example, the variability of the macro-parameters (Vt, BP_{ND}) in PET is typically in the range of about 5–10%. Brain perfusion is known to be subject to significant physiological variability, and therefore has 20% test-retest variability.

The same data can be used to calculate the variability across the study population. This between-subject variability for a specific region is defined as the coefficient of variation BS(%COV) of the outcome across the population, hence

$$COV = \frac{SD}{Mean}\cdot 100\%$$

where SD represents the standard deviation of the results across subjects.

Another important measure which can be calculated from test-retest data is the intraclass correlation coefficient (ICC). It estimates the reliability of the measurement per region by comparing the within-subject (WS) variability to the between-subject (BS) variability. For the test-retest situation it can be calculated as follows:

$$ICC = \frac{BSMSS - WSMSS}{BSMSS + WSMSS}$$

whereby the MSS represents mean sum of squares and is calculated for the WS and the BS situation by

$$WSMSS = \frac{\sum_{i=1}^{N}\sum_{k=1}^{2}(m_{ik} - \overline{m_i})^2}{N}$$

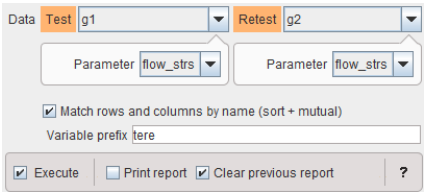
$$BSMSS = \frac{\sum_{i=1}^{N}2(\overline{m_i} - \overline{m})^2}{N-1}$$

m_{ik} represents a result of subject i (k=1 test, k=2 retest), $\overline{m_i}$ the test-retest mean of subject i, and $\overline{m}$ the overall mean across all studies and subjects.

The ICC ranges between -1 (no reliability) and 1 (maximum reliability, achieved in the case of identity between test and retest), and is negative in case more differences are observed within than between subjects. See [1] for an application in PET modeling.

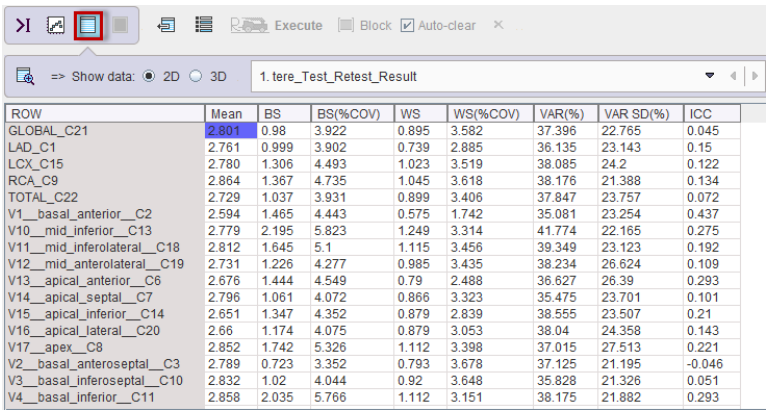
Test-Retest Configuration

The Test-Retest script performs the calculations described above between two variables in the workspace for all VOIs. The only choices in the user interface are the variables, and the statistics within the variables (**Parameter**)



Test-Retest Results

This script only provides a result table **Test_Retest_Result**



ROW	Mean	BS	BS(%COV)	WS	WS(%COV)	VAR(%)	VAR SD(%)	ICC
GLOBAL_C21	2.801	0.98	3.922	0.895	3.582	37.396	22.765	0.045
LAD_C1	2.761	0.999	3.902	0.739	2.885	36.135	23.143	0.15
LCX_C15	2.780	1.306	4.493	1.023	3.519	38.085	24.2	0.122
RCA_C9	2.864	1.367	4.735	1.045	3.618	38.176	21.388	0.134
TOTAL_C22	2.729	1.037	3.931	0.899	3.406	37.847	23.757	0.072
V1__basal_anterior__C2	2.594	1.465	4.443	0.575	1.742	35.081	23.254	0.437
V10__mid_inferior__C13	2.779	2.195	5.823	1.249	3.314	41.774	22.165	0.275
V11__mid_inferolateral__C18	2.812	1.645	5.1	1.115	3.456	39.349	23.123	0.192
V12__mid_anterolateral__C19	2.731	1.226	4.277	0.985	3.435	38.234	26.624	0.109
V13__apical_anterior__C6	2.676	1.444	4.549	0.79	2.488	36.627	26.39	0.293
V14__apical_septal__C7	2.796	1.061	4.072	0.866	3.323	35.475	23.701	0.101
V15__apical_inferior__C14	2.651	1.347	4.352	0.879	2.839	38.555	23.507	0.21
V16__apical_lateral__C20	2.66	1.174	4.075	0.879	3.053	38.04	24.358	0.143
V17__apex__C8	2.852	1.742	5.326	1.112	3.398	37.015	27.513	0.221
V2__basal_anteroseptal__C3	2.789	0.723	3.352	0.793	3.678	37.125	21.195	-0.046
V3__basal_inferoseptal__C10	2.832	1.02	4.044	0.92	3.648	35.828	21.326	0.051
V4__basal_inferior__C11	2.858	2.035	5.766	1.112	3.151	38.175	21.882	0.293

with the following results per VOI:

Mean The mean value of the test and retest data.

BS The between subject variability.

BS (%COV) The between subject coefficient of variation.

WS The within subject variability.

WS (%COV) The within subject coefficient of variation.

VAR (%) Test-retest variability.

VAR SD (%) Test-retest variability standard deviation.

ICC The intraclass correlation coefficient.

1. Parsey RV, Slifstein M, Hwang DR, Abi-Dargham A, Simpson N, Mawlawi O, Guo NN, Van Heertum R, Mann JJ, Laruelle M: Validation and reproducibility of measurement of 5-HT1A receptor parameters with [carbonyl-11C]WAY-100635 in humans: comparison of arterial and reference tissue input functions. J Cereb Blood Flow Metab 2000, 20(7):1111-1133. ***DOI http://dx.doi.org/10.1097/00004647-200007000-00011***

t-Test

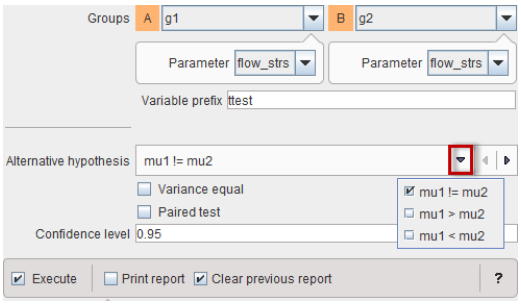
An instructive summary of the background and the application of the t-test can be found on ***Wikipedia https://en.wikipedia.org/wiki/Student's_t-test*** [1]. Briefly, it is a family of statistical hypothesis tests which can be used to determine if two sets of data are significantly different from each other.

Depending on the application case (null hypothesis, data) different test statistics formula need to be applied to the data. They all result in a t-value, which can be converted into a p-value using a table of values from Student's t-distribution.

The p-value is the probability of the obtaining at least the observed t-value, assuming that the null hypothesis is true. Therefore, if the calculated p-value is below the threshold chosen for statistical significance (usually the 0.10, the 0.05, or 0.01 level) and therefore highly unlikely, the null hypothesis is rejected in favor of the alternative hypothesis.

t-Test Configuration

The **t-Test** script in the R console implements a t-test between two samples. Its configuration window has the following form.

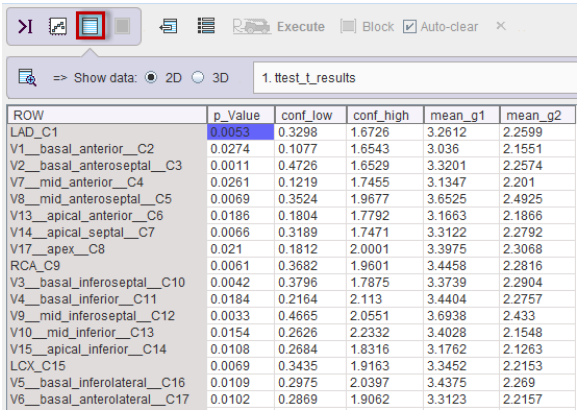


Note the **Alternative hypothesis** selection which allows configuring a two-sided test (**mu1!=mu2**) or one-sided tests (**mu1>mu2**, **mu1<mu2**). If the variance in the two samples is equal, the **Variance equal** box should be checked for using the pooled variance rather than

an approximation. The **Paired test** should only be enabled in if this condition is met by the two samples. In this case, the data will be sorted for appropriate sample pairing.

t-Test Results

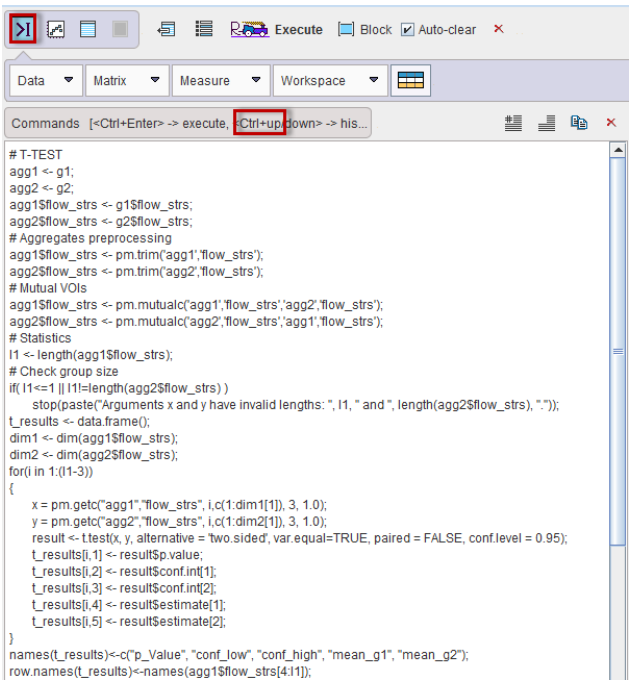
The script only returns numeric results in the form of the **ttest_t_results** table. The example below illustrates the outcome with an unpaired two-sided test.



ROW	p_Value	conf_low	conf_high	mean_g1	mean_g2
LAD_C1	0.0053	0.3298	1.6726	3.2612	2.2599
V1__basal_anterior__C2	0.0274	0.1077	1.6543	3.036	2.1551
V2__basal_anteroseptal__C3	0.0011	0.4726	1.6529	3.3201	2.2574
V7__mid_anterior__C4	0.0261	0.1219	1.7455	3.1347	2.201
V8__mid_anteroseptal__C5	0.0069	0.3524	1.9677	3.6525	2.4925
V13__apical_anterior__C6	0.0186	0.1804	1.7792	3.1663	2.1866
V14__apical_septal__C7	0.0066	0.3189	1.7471	3.3122	2.2792
V17__apex__C8	0.021	0.1812	2.0001	3.3975	2.3068
RCA_C9	0.0061	0.3682	1.9601	3.4458	2.2816
V3__basal_inferoseptal__C10	0.0042	0.3796	1.7875	3.3739	2.2904
V4__basal_inferior__C11	0.0184	0.2164	2.113	3.4404	2.2757
V9__mid_inferoseptal__C12	0.0033	0.4665	2.0551	3.6938	2.433
V10__mid_inferior__C13	0.0154	0.2626	2.2332	3.4028	2.1548
V15__apical_inferior__C14	0.0108	0.2684	1.8316	3.1762	2.1263
LCX_C15	0.0069	0.3435	1.9163	3.3452	2.2153
V5__basal_inferolateral__C16	0.0109	0.2975	2.0397	3.4375	2.269
V6__basal_anterolateral__C17	0.0102	0.2869	1.9062	3.3123	2.2157

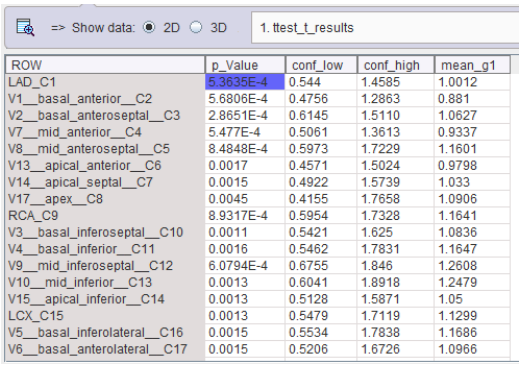
For each region the **p_value**, the lower and upper confidence intervals (**conf_low**, **conf_high**) as well as the means of the two groups (**mean_g1**, **mean_g2**) are listed. In the example above, all regional means are significantly different, since the p-values are below 5%.

As an example, the R code for this analysis can easily be inspected in the command layout, entering `Ctrl+Up-arrow` with the keyboard.




```
# T-TEST
agg1 <- g1;
agg2 <- g2;
agg1$flow_strs <- g1$flow_strs;
agg2$flow_strs <- g2$flow_strs;
# Aggregates preprocessing
agg1$flow_strs <- pm.trim('agg1','flow_strs');
agg2$flow_strs <- pm.trim('agg2','flow_strs');
# Mutual VOIs
agg1$flow_strs <- pm.mutualc('agg1','flow_strs','agg2','flow_strs');
agg2$flow_strs <- pm.mutualc('agg2','flow_strs','agg1','flow_strs');
# Statistics
l1 <- length(agg1$flow_strs);
# Check group size
if( l1<=1 || l1!=length(agg2$flow_strs) )
    stop(paste("Arguments x and y have invalid lengths: ", l1, " and ", length(agg2$flow_strs), "."));
t_results <- data.frame();
dim1 <- dim(agg1$flow_strs);
dim2 <- dim(agg2$flow_strs);
for(i in 1:(l1-3))
{
    x = pm.getc("agg1","flow_strs", i,c(1:dim1[1]), 3, 1.0);
    y = pm.getc("agg2","flow_strs", i,c(1:dim2[1]), 3, 1.0);
    result <- t.test(x, y, alternative = 'two.sided', var.equal=TRUE, paired = FALSE, conf.level = 0.95);
    t_results[i,1] <- result$p.value;
    t_results[i,2] <- result$conf.int[1];
    t_results[i,3] <- result$conf.int[2];
    t_results[i,4] <- result$estimate[1];
    t_results[i,5] <- result$estimate[2];
}
names(t_results)<-c("p_Value", "conf_low", "conf_high", "mean_g1", "mean_g2");
row.names(t_results)<-names(agg1$flow_strs[4:l1]);
```

Analyzing the same data with at paired t-test (which is actually justified), the significance of a different mean is even higher. Note that the conf_low and conf_high as well as mean_g1 are now related to the difference values.



ROW	p_Value	conf_low	conf_high	mean_g1
LAD_C1	5.3635E-4	0.544	1.4585	1.0012
V1__basal_anterior__C2	5.6806E-4	0.4756	1.2863	0.881
V2__basal_anteroseptal__C3	2.8651E-4	0.6145	1.5110	1.0627
V7__mid_anterior__C4	5.477E-4	0.5061	1.3613	0.9337
V8__mid_anteroseptal__C5	8.4848E-4	0.5973	1.7229	1.1601
V13__apical_anterior__C6	0.0017	0.4571	1.5024	0.9798
V14__apical_septal__C7	0.0015	0.4922	1.5739	1.033
V17__apex__C8	0.0045	0.4155	1.7658	1.0906
RCA_C9	8.9317E-4	0.5954	1.7328	1.1641
V3__basal_inferoseptal__C10	0.0011	0.5421	1.625	1.0836
V4__basal_inferior__C11	0.0016	0.5462	1.7831	1.1647
V9__mid_inferoseptal__C12	6.0794E-4	0.6755	1.846	1.2608
V10__mid_inferior__C13	0.0013	0.6041	1.8918	1.2479
V15__apical_inferior__C14	0.0013	0.5128	1.5871	1.05
LCX_C15	0.0013	0.5479	1.7119	1.1299
V5__basal_inferolateral__C16	0.0015	0.5534	1.7838	1.1686
V6__basal_anterolateral__C17	0.0015	0.5206	1.6726	1.0966

One-way ANOVA for 3 or 4 Groups

The one-way ANOVA compares the means between the groups and determines whether any of those means are significantly different from each other.

The NULL hypothesis (H_0) assumes that all group population means are equal. The alternative hypothesis (H_a) is that there are at least two group means that are significantly different from each other. If the result is statistically significant, the alternative hypothesis is accepted.

The one-way ANOVA is a statistic test can only detect that least two groups are different, but not which ones. To this end a *post-hoc* comparison test needs to be applied. The **ANOVA** script applies the Tukey's HSD (Honest Significant Difference) test.

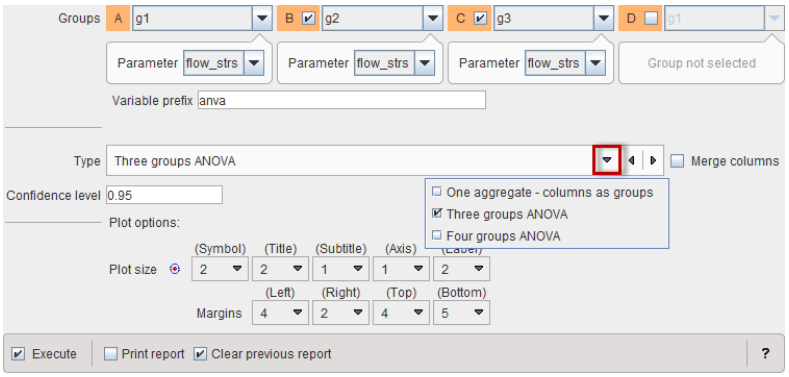
Assumptions

The results of a one-way ANOVA can be considered reliable as long as the following assumptions are met:

- the response variable (the dependent variable) is normally distributed;
- the samples are independent;
- the variances of populations are equal.

ANOVA Configuration

The configuration window is illustrated below.



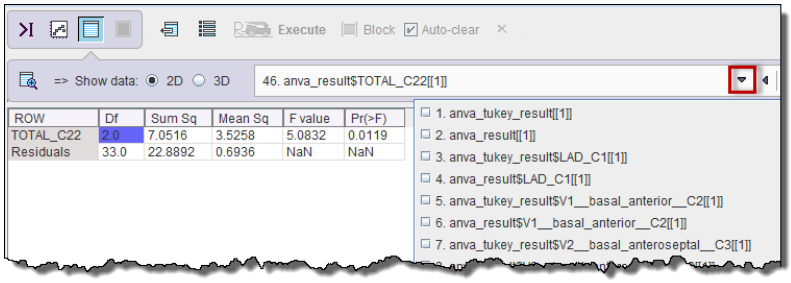
Basically, there are two usage types:

1) The groups to be compared are arranged as the columns in a single aggregate. This situation is reflected by the **One aggregate - columns as groups** selection as the analysis **Type**.

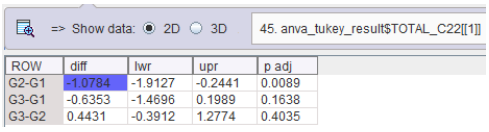
The groups to be compared are organized in separate aggregates. The script can handle 3 or four groups. If **Merge columns** is enabled, the data of all columns will be pooled, otherwise the ANOVA analysis is performed per column.

ANOVA Results

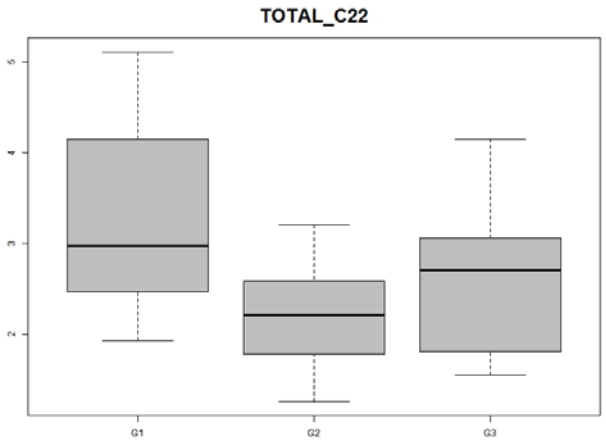
The script produces result tables related to the ANOVA (**anva_result**) and Tukey (**anva_tukey**) as well as plots for the results visualization.



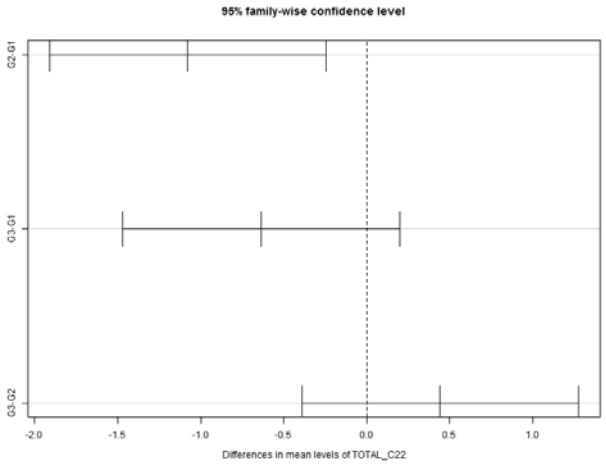
Note the p-value which is below 0.95, indicating that there is a significant difference which can be localized for **G2-G1** in the Tukey table below. For r **G2-G1** $p<0.05$ where it is >0.05 for the other comparisons.



The plot layout contains a ***box plot*** (on page 279) per VOI, showing the characteristics of the groups next to each other. In the example below the difference between G1 and G2 is supported.



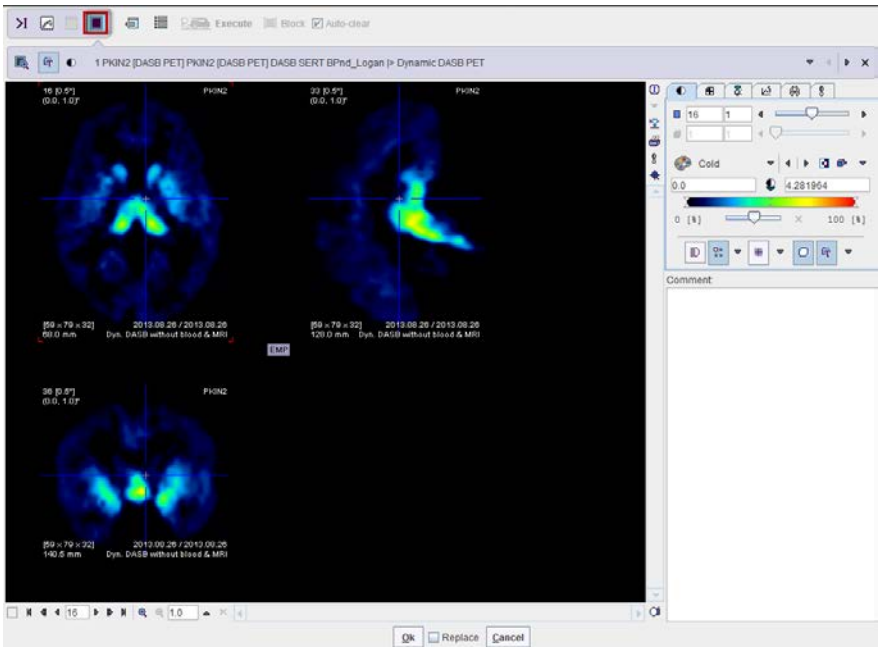
The second plot which is available per VOI visualizes the 95% confidence interval of the group differences.



If zero is not included in the confidence interval, the difference is significant.

Image Data

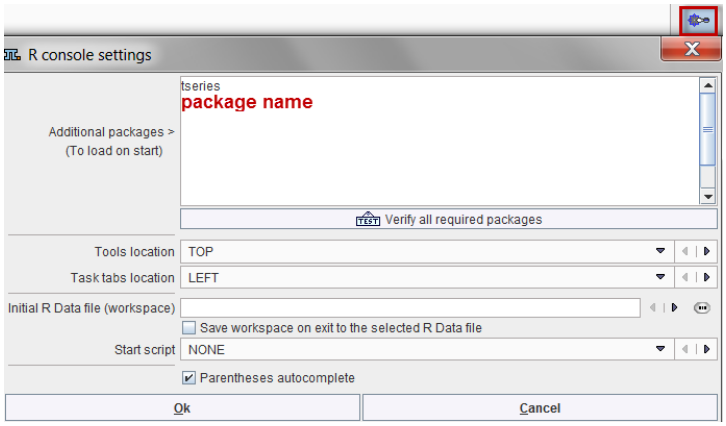
The image window serves for the visualization of the image data transferred to the R interface using the **R console** ***external tool*** (on page 131).



User Programming and Scripts

Package Use

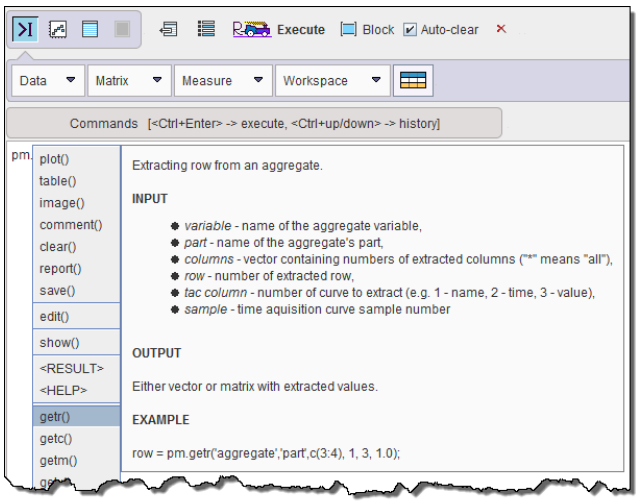
There is a huge number of public packages available covering a large spectrum of functionality. Users may want to use functions contained in such packages for their own developments. To do so, the package name needs to be added to the **Additional packages** list



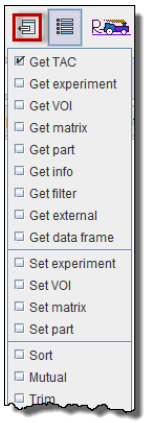
and then enable **Install required packages from Repository on Start** in the configuration. After restarting PMOD, the package should be loaded and become available.

Accessing PMOD R Variables

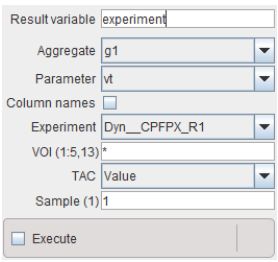
The structure of PMOD R variables is described ***above*** (on page 261). A user may want to program scripts which address and process such variables. A list of functions can be obtained by simply typing `"pm."` into the command window. Moving the cursor over the list entries pops up a window with a syntax description and an example.



Another approach which is particularly helpful when beginning with scripts is using the extraction button



After selecting an entry, a dialog window is shown, in the case of **Get experiment**



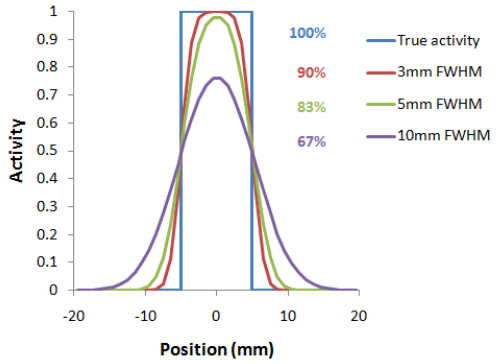
When confirming the window, corresponding R code is generated

```
experiment = pm.getr("g1", "vt",c(1:13), 1, 3, 1.0);
```

Partial-Volume Correction (PVC)

which can be seen if the **Execute** box is not enabled.

PET and SPECT images are inherently affected by the *partial-volume effect*. This term means that the measured tracer activity concentrations are not accurate due to the relatively low image resolution and the limited tissue sampling. Basically, the low resolution causes a blurring of the image, so that high activities (from a hot lesion) are spread to the surrounding as illustrated below. This effect is called *spill-out*. The same effect also causes a *spill-in* of background activity into the volume of interest.



As a consequence, hot lesions tend to appear less aggressive (reduced maximum) but bigger (spreading) than they are in reality.

Spill-in and spill-out depend on the geometry of the objects, the activity distribution of the tracer, and on the resolution of the scanner which may vary across the imaging field-of-view. Therefore, practical correction approaches have to assume certain conditions and can only be approximate. For a nice overview of the topic please refer to the publication of Soret et al. [1].

Solutions Implemented in PMOD

PMOD provides two PVC solutions:

1) **PVC VOI-based:** This correction is based on the assumption, that the imaging volume can be separated into tissue volumes (VOIs) with homogeneous uptake. If the resolution of the PET scanner is known, the mutual signal contaminations across the VOIs can be calculated and corrected for. This method is known as the GTM (Geometric Transfer Matrix) method and was introduced by Rousset et al. [2,3].
   The implementation in PMOD allows the user applying the GTM correction with any set of manually outlined VOIs. Additionally, for the analysis of human brain uptake, the user may take advantage of standard VOIs which are automatically adjusted to the patient's anatomy.

PVC Brain MR based : This correction is based on the assumption that white matter uptake is homogeneous. All brain pixels are classified as white matter (WM) or grey matter (GM) and sorted into respective segments. Based on these segments and the assumed PET resolution the spill-out from WM to GM can be estimated and subtracted. Similarly, the spill-out from GM to the surroundings can be estimated and compensated for. The result is a grey matter image with corrected activity values in all pixels. This method was introduced by Muller-Gartner et al. [4].
Given a brain PET and an anatomical MRI of a patient, the implementation in PMOD allows the user performing the segmentation and apply the Muller-Gartner PVC in a fully automated way.

The two PVC methods are implemented as ***external tools*** (on page 143), although they have a much broader scope and require more user interaction than typical external tools. Therefore, their implementations are described in the respective sub-sections below.

Step-wise and Background Calculation Modes

The different PVC methods typically involve several processing steps, some of them using input parameters. There are two ways how a user can apply the PVC calculation:

1) **Background calculation:** The user enters all required information and adjusts the different parameters, and then starts the processing. The tool window closes, the computations run in a separate thread in the background, and finally returns the corrected images for statistical analysis.

Step-wise processing: The user performs the processing steps one by one interactively with a button, and inspects the intermediate results in the tool. If required, he can change a parameter and initiates the calculation again. After the last step, the final results are returned and the tool closed.

The step-wise processing mode has the advantage that all intermediate data remains available, and processing can be repeated from any intermediate step. When data is returned, it is already quality checked, whereas in the background mode the user can not always be sure that all processing steps were successful without inspecting some of the supplementary images returned by the tool.

The **All Steps** button performs all processing steps sequentially, but does not close the dialog window so that after a first run the different steps can be interactively explored.

Note that the parameters can always be reset to the recommended default values by the button to establish a well defined situation after some experiments.

Common Requirements for Partial-volume Correction in PMOD

The PVC methods implemented in PMOD assume a homogeneous, Gaussian-shaped point-spread function (PSF) of the scanner which is specified by its full-width at half maximum (FWHM) in all directions. The user needs to determine reasonable FWHM values for his reconstructed images and specify them to the algorithm. If possible, a PET reconstruction method with homogeneous resolution should be used, so that the assumption of a stationary PSF is justified. Furthermore, the brain PET images should be reconstructed with a small pixel size not larger than 2.5 mm.

Important Note: The PVC tools expect that the image data is loaded in the HFS orientation. It is a precondition for segmentation and matching procedures.

PVC based on Manual and Brain Template VOIs

Methodology Description

The GTM method according to Rousset [2] restricts the partial volume correction to the signal of the true objects which are constituted by VOIs. The relation of measured PET values (affected by the partial-volume effect) to the true PET values is given by the matrix equation below

$$\vec{C}_{measured} = [GTM] \times \vec{C}_{true}$$

with the following notations:

C_{true} Vector of the true average activity concentration in the different VOIs of interest. The vector length n equals the number of object VOIs.

$C_{measured}$ Actually measured average activity concentration in the different VOIs.

GTM Geometric Transfer Matrix which describes the spill-over among all the VOIs. The matrix is square with nxn weighting elements $w_{i,j}$ which express the fraction of true activity spilled over from VOI_i into VOI_j.

In practice, $w_{i,j}$ is calculated as follows: A binary map is created with 1 in all pixels of VOI_i and 0 elsewhere. The map is convolved with the imaging Point-Spread Function (PSF), and in the resulting spillover map the average of all VOI_j pixels calculated.

The GTM equation above represents a system of linear equations. Once the weights have been calculated, the system can be solved for the true values C_{true} by matrix inversion. Rousset [2] has shown that this algorithm is robust to noise propagation during the correction process.

Implemented VOI-based PVC Variants

The **PVC (VOI based)** method provides three variants which are based on the same GTM methodology. The difference is, how the VOIs are obtained.

1) Manual VOIs: The user outlines all VOIs manually.

Template VOIs based on standard masks: VOI templates defined in the MNI space are used and adjusted to the PET image. This method can only be applied for human brain images.

Template VOIs based on individual masks: The same VOI templates as above are used. The difference is, that the user has to provide an anatomical MRI image which is employed for a better individual adjustment for the VOIs.

Template VOIs based on Plain VOIs: the same VOI templates as above are used. No Anatomical MRI image is needed.

Methods 2,3 and 4 can only be applied for human brain images, whereas method 1 is generic. Note that the user may also derive himself contour VOIs from standard VOI templates, adjust them to the subject anatomy, and apply method 1. This allows him to take advantage of the rat and mouse templates for which an automated work-flow is not yet available.

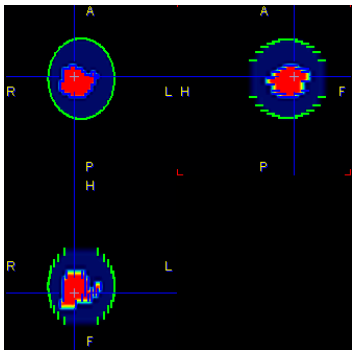
The details of the methods are explained in the corresponding sections below.

Common Requirements

The VOI-based PVC methods can be applied to PET or SPECT images, both static and dynamic. A set of VOIs is required which define objects of common functional properties.

Important Note: The VOIs used for PVC may not be overlapping each other! If they do, a warning message will be shown. All activities in the neighborhood of the target should be taken into consideration and included into appropriate VOIs.

When closing the dialog window, the results of VOI-based partial-volume correction are returned in the form of an additional image series, indicated in the description by a **VOI based PVE corrected** string. In these images, all pixels belonging to a VOI are set to the value obtained as the partial-volume corrected average value of that VOI. Pixels not included in a VOI are set to 0. The example below illustrates a case with only two manually outlined VOIs, a tumor VOI and an enclosing background VOI.

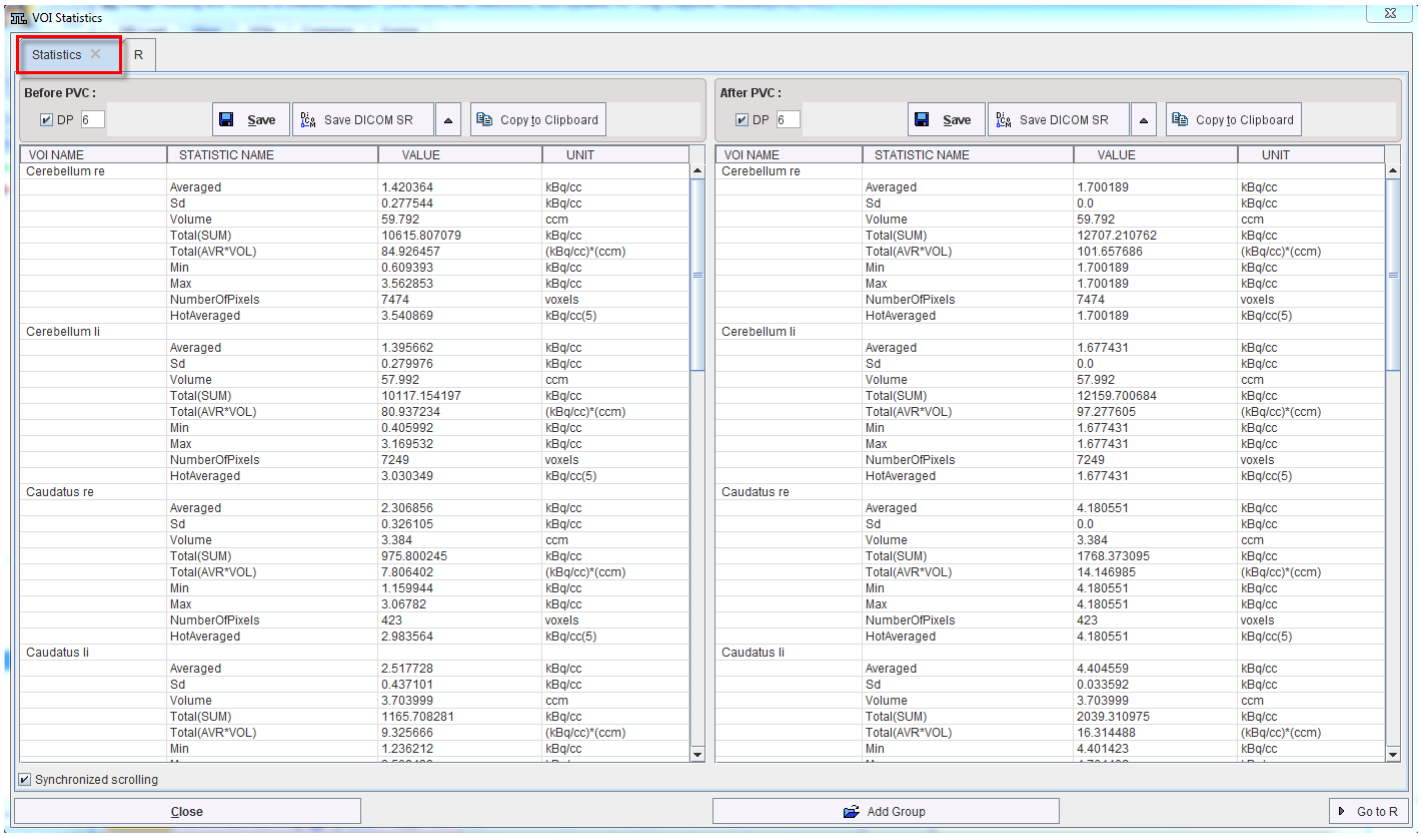


To obtain the partial-volume corrected VOI averages please open the result images in the VOI tool, load the VOIs employed for the PVC, and calculate the statistics.

Note that if the **Replace** box is checked the original images are replaced by the partial-volume corrected images.

Statistics in Step-wise Mode

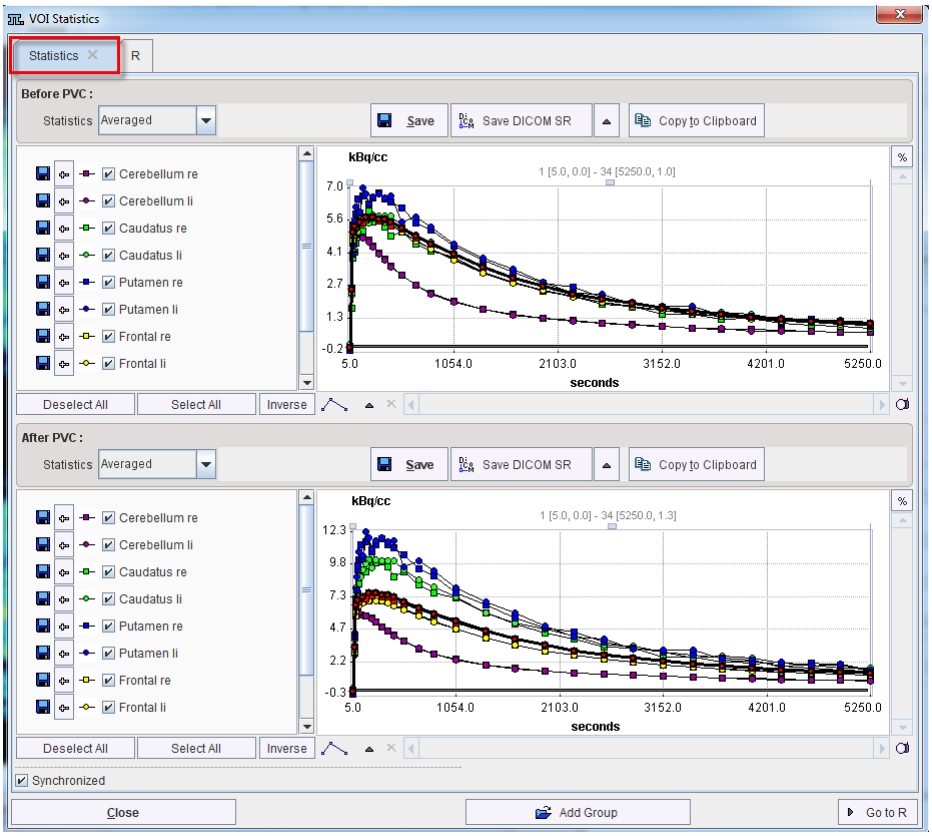
The step-wise mode has the advantage, that the statistics can directly be calculated with the **View Statistics** button. For static series, simple VOI statistics will be generated which are shown in a side-by-side manner as illustrated below.



VOI NAME	STATISTIC NAME	VALUE	UNIT
Cerebellum re			
	Averaged	1.420364	kBq/cc
	Sd	0.277544	kBq/cc
	Volume	59.792	ccm
	Total(SUM)	10615.807079	kBq/cc
	Total(AVR*VOL)	84.926457	(kBq/cc)*(ccm)
	Min	0.609393	kBq/cc
	Max	3.562853	kBq/cc
	NumberOfPixels	7474	voxels
	HotAveraged	3.540869	kBq/cc(5)
Cerebellum li			
	Averaged	1.395662	kBq/cc
	Sd	0.279976	kBq/cc
	Volume	57.992	ccm
	Total(SUM)	10117.154197	kBq/cc
	Total(AVR*VOL)	80.937234	(kBq/cc)*(ccm)
	Min	0.405992	kBq/cc
	Max	3.169532	kBq/cc
	NumberOfPixels	7249	voxels
	HotAveraged	3.030349	kBq/cc(5)
Caudatus re			
	Averaged	2.306856	kBq/cc
	Sd	0.326105	kBq/cc
	Volume	3.384	ccm
	Total(SUM)	975.800245	kBq/cc
	Total(AVR*VOL)	7.806402	(kBq/cc)*(ccm)
	Min	1.159944	kBq/cc
	Max	3.06782	kBq/cc
	NumberOfPixels	423	voxels
	HotAveraged	2.983564	kBq/cc(5)
Caudatus li			
	Averaged	2.517728	kBq/cc
	Sd	0.437101	kBq/cc
	Volume	3.703999	ccm
	Total(SUM)	1165.708281	kBq/cc
	Total(AVR*VOL)	9.325666	(kBq/cc)*(ccm)
	Min	1.236212	kBq/cc

VOI NAME	STATISTIC NAME	VALUE	UNIT
Cerebellum re			
	Averaged	1.700189	kBq/cc
	Sd	0.0	kBq/cc
	Volume	59.792	ccm
	Total(SUM)	12707.210762	kBq/cc
	Total(AVR*VOL)	101.657686	(kBq/cc)*(ccm)
	Min	1.700189	kBq/cc
	Max	1.700189	kBq/cc
	NumberOfPixels	7474	voxels
	HotAveraged	1.700189	kBq/cc(5)
Cerebellum li			
	Averaged	1.677431	kBq/cc
	Sd	0.0	kBq/cc
	Volume	57.992	ccm
	Total(SUM)	12159.700684	kBq/cc
	Total(AVR*VOL)	97.277605	(kBq/cc)*(ccm)
	Min	1.677431	kBq/cc
	Max	1.677431	kBq/cc
	NumberOfPixels	7249	voxels
	HotAveraged	1.677431	kBq/cc(5)
Caudatus re			
	Averaged	4.180551	kBq/cc
	Sd	0.0	kBq/cc
	Volume	3.384	ccm
	Total(SUM)	1768.373095	kBq/cc
	Total(AVR*VOL)	14.146985	(kBq/cc)*(ccm)
	Min	4.180551	kBq/cc
	Max	4.180551	kBq/cc
	NumberOfPixels	423	voxels
	HotAveraged	4.180551	kBq/cc(5)
Caudatus li			
	Averaged	4.404559	kBq/cc
	Sd	0.033592	kBq/cc
	Volume	3.703999	ccm
	Total(SUM)	2039.310975	kBq/cc
	Total(AVR*VOL)	16.314488	(kBq/cc)*(ccm)
	Min	4.401423	kBq/cc

In the case of dynamic series the results are TACs as illustrated below.



The statistic results can be saved as a Dicom structured report with the **Save Dicom SR** option or exported as a structured report with the **Export Dicom SR**. In alternative, the content of the statistic page can be **Copy to Clipboard** and paste in Excel.

Using the **Go to R** button located on lower right corner, the statistic results can be send directly to the PMOD R interface for further statistic analysis.

PVC using Manual VOIs

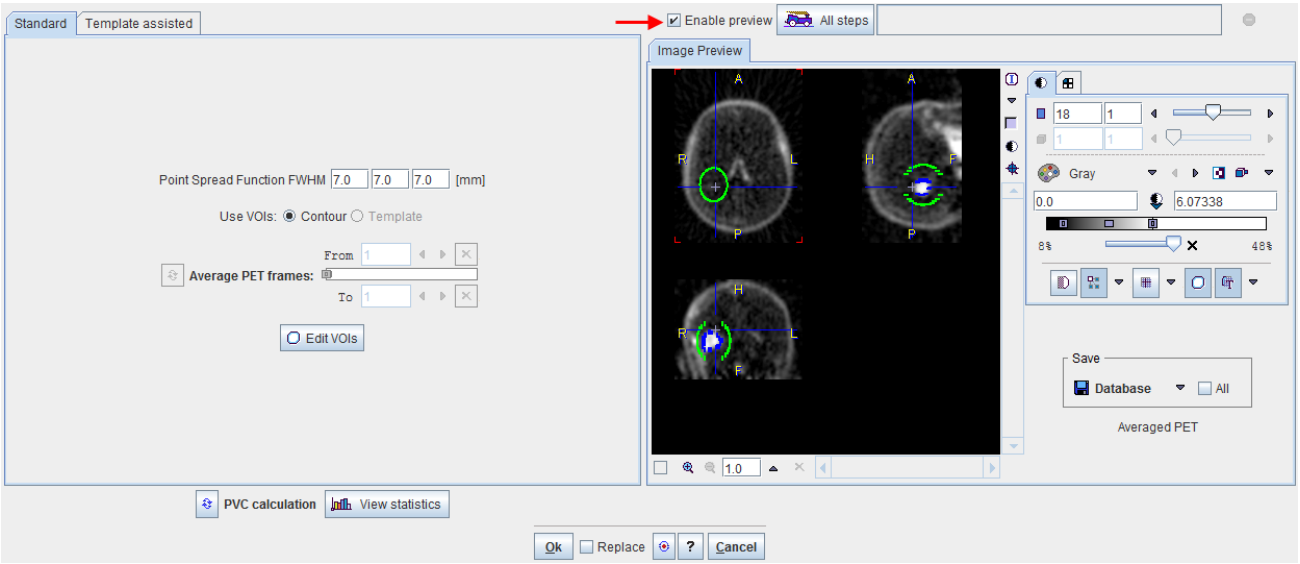
Overview

The most general case of VOI based PVC is, that the user himself generates a set of suitable VOIs to which he applies the GTM correction as described below.

Starting the PVC

As a first step, load the PET images into the PVIEW tool. Define or load a set of VOIs. Then activate the button to the right of the image and select the **PVC (VOI based)** method from the list of external tools. A dialog window is shown which allows performing the processing in a step-by-step mode or as a background process.

Select the **Standard** tab for performing a correction based on your manually defined VOIs.



Step-by-Step PVC Processing Mode

The step-wise mode is activated by checking the box next to the **Enable preview** label. It activates buttons for the individual processing steps, as well as the **Edit VOIs** and once the PVC was calculated also the **View statistics** buttons.

Point Spread Function FWHM:

The PSF is assumed to be a three-dimensional Gaussian function. The FWHM values in the three directions have to be specified according to the resolution of the reconstructed image. Default is 7 mm isotropic FWHM.

Use VOIs:

Both contour VOIs and template VOIs can exist in parallel. If two definitions exist, the user has to decide whether to use the **Contour** or the **Template** VOIs.

Average PET frames:

If the study is dynamic, this option gets active in the step-wise mode. The purpose is to provide an averaged PET image for the purpose of VOI outlining. This averaging step is optional, and PVC will always be performed on the original images. The **Averaged PET** will also be shown in the **Image Preview** window

Edit VOIs:

This button opens a VOI tool dialog window showing the averaged PET images. If VOIs were defined beforehand, they can be edited, and VOIs can be loaded from a file. To return modified VOIs, close the window with the **Ok** button, otherwise **Cancel**.

PVC Calculation:

This button performs the actual PVC calculation. The result is returned in the form of an image series and shown in the **Image Preview** window.

View Statistics:

This button calculates the VOI statistics in the original and the PVC corrected images. Depending on the input images the results are simple statistics, or tissue time-activity curves.

Returning the Results:

To return the results close the window with the **Ok** button.

Background PVC Processing Mode

If no interactive processing is desired, the user interaction is minimal.

1) If desired, edit the FWHM parameters, or reset them by the button.

Start the PVC calculation with the **Ok** button.

The window will be closed and processing will run in the background. The processing time depends on the number of VOIs and the FWHM. Once the result was calculated and returned to PVIEW, a confirmation message will be shown.

PVC using Template VOIs based on Standard Masks

Overview

PMOD provides templates of human brain VOIs in the standard MNI space, as well as masks of the grey and white matter pixels. The PVC method described below employs this prior information for constructing a set of individual brain VOIs matching a PET scan as follows:

1) The template VOIs are intersected with the GM mask to obtain standard GM VOIs.

The WM mask is converted into a WM VOI.

The PET image is normalized to the MNI PET template using the **Brain Norm. II** method.

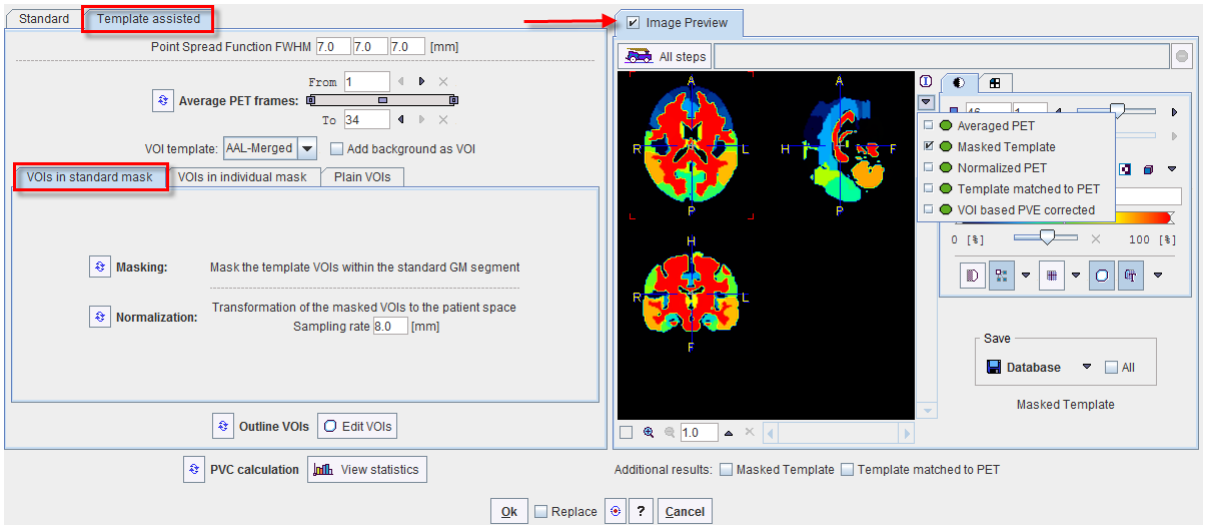
The standard GM and WM VOIs are transformed to the space of the PET image using the inverse normalization transform.

A contouring procedure is applied to get contour definitions of all VOIs, which the user can view together with the PET image and edit.

The GTM PVC method is applied to the original PET series using this set of template-based VOIs.

Starting the PVC

As a first step, load the PET images into the PVIEW tool. Then activate the button to the right of the image and select the **PVC (VOI based)** method from the list of external tools. A dialog window is shown which allows performing partial-volume correction in a step-by-step mode or as a background process.



Step-by-Step PVC Processing Mode

The step-wise mode is activated by checking the box next to the **Image Preview** label. Note the buttons which are used to start the individual processing steps. Initially, several of them are inactive because the prior steps are missing.

The result images of the different steps are collected in the **Image Preview** area. In the image selection list, available results appear with a green mark, while yet unavailable ones are marked in red. The example above shows the **Masked Template** calculated by step 2. The selected image series can be exported for later use by the **Save** button.

The advantage of step-wise processing is that steps can be repeated with different parameters until the outcome is satisfactory.

Point Spread Function FWHM:

The PSF is assumed to be a three-dimensional Gaussian function. The FWHM values in the three directions have to be specified according to the resolution of the reconstructed image. Default is 7 mm isotropic FWHM.

Average PET frames:

Dynamic images can be processed and will result in a corrected dynamic series. However, for the **Normalization** step, a static PET image showing anatomical information is required. Therefore, the user should define a suitable range for averaging time frames, and then activate . In the case of a static scan this step is not required and the button therefore not active. The **Averaged PET** is shown in the **Image Preview** window.

Masking:

The masking requires no parameters. It shows the **Masked Template** in the **Image Preview** window.

Normalization:

The normalization of the averaged PET image to the MNI PET template has one parameter, **Sampling rate**. After calculating the normalization, the normalization inverse is applied to transform the masked template to the PET space. The results **Normalized PET** and **Template matched to PET** are shown in the the **Image Preview** window.

Outline VOIs:

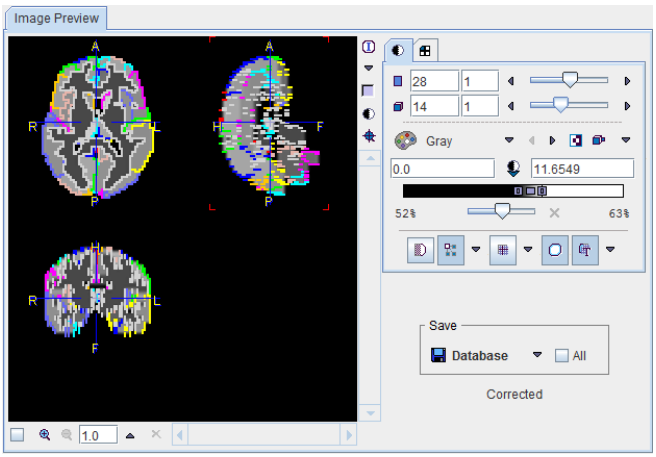
This step calculates contour VOIs from **Template matched to PET** and shows them together with the **Averaged PET** in the **Image Preview** window. This is the VOI set which will be used in the PVC.

Edit VOIs:

This button opens a VOI dialog window showing the VOIs on top of the **Averaged PET**. Note the extended **White Matter** VOI which has been derived from the WM mask. The VOIs can be inspected and edited, or saved for later use. To return modified VOIs, close the window with the **Ok** button, otherwise **Cancel**.

PVC Calculation:

This step performs the actual PVC calculation. Because of the large number of VOIs contained in the standard templates the processing takes a while. The result is returned in the form of an image series and shown in the **Image Preview** window. If the input series was dynamic, the result is also dynamic as in the example below.



View Statistics:

This button calculates the VOI statistics in the original and the PVC corrected images. Depending on the input images the results are simple statistics, or tissue time-activity curves.

Returning the Results:

Make sure that the **Additional results** of interest are checked. Then close the window with the **Ok** button to return the results.

Background PVC Processing Mode

If no interactive processing is desired, the user interaction is minimal.

1) If desired, edit the FWHM parameters, or reset them by the button.

If the PET series is dynamic, define an appropriate frame range for averaging.

Make sure that the **Additional results** of interest are checked.

Start the PVC calculation with the **Ok** button.

The dialog window will be closed and processing will run in the background. Once the result were calculated and returned, a confirmation message will be shown.

PVC using Template VOIs based on Individual Masks

Overview

PMOD provides templates of human brain VOIs in the standard MNI space. The PVC method described below combines this information with the grey and white matter masks derived from an individual patient MR image as follows:

1) The anatomical MRI of the patient is segmented and the GM and WM masks calculated.

The MR image is normalized to the MNI MR template using the **Brain Normalization** method.

The VOI template is transformed to the MR space using the inverse of the normalization transform.

The transformed VOI template is intersected with the GM mask to obtain the GM VOIs in the MR space.

The WM mask is converted into a WM VOI.

The PET images are rigidly matched to the MR images.

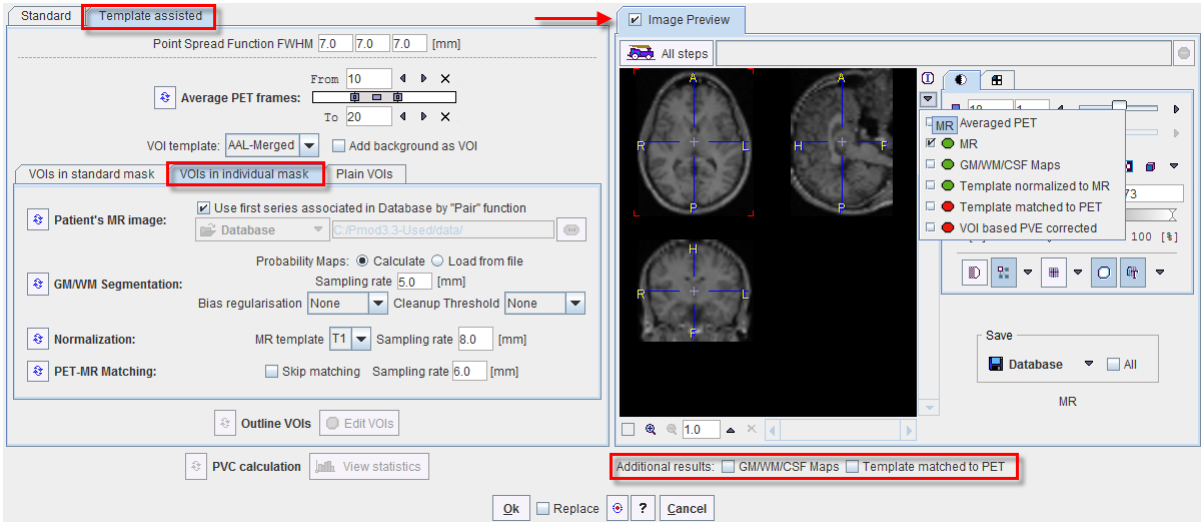
The GM and WM VOIs are transformed to the PET space using the inverse rigid transform.

A contouring procedure is applied to get contour definitions of all VOIs, which the user can view and edit.

The GTM PVC method is applied to the original PET series using this set of template-based VOIs.

Starting the PVC

As a first step, load the PET images into the PVIEW tool. Then activate the button to the right of the image and select the **PVC (VOI based)** method from the list of external tools. A dialog window is shown which allows performing partial-volume correction in a step-by-step mode or as a background process.



Step-by-Step PVC Processing Mode

The step-wise mode is activated by checking the box next to the **Image Preview** label. Note the buttons which are used to start the individual processing steps. Initially, several of them are inactive because the prior steps are missing.

The result images of the different steps are collected in the **Image Preview** area. In the image selection list, available results appear with a green mark, while yet unavailable ones are marked in red. The example above shows the **MR** loaded by step **Patient's MR image**. The images selected in the **Image Preview** can be exported for later use by the **Save** button.

The advantage of step-wise processing is that steps can be repeated with different parameters until the outcome is satisfactory.

Point Spread Function FWHM:

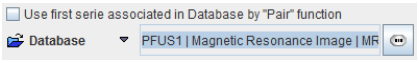
The PSF is assumed to be a three-dimensional Gaussian function. The FWHM values in the three directions have to be specified according to the resolution of the reconstructed image. Default is 7 mm isotropic FWHM.

Average PET frames:

Dynamic images can be processed and will result in a corrected dynamic series. However, for the **PET-MR Matching** step, a static PET image showing anatomical information is required. Therefore, the user should define a suitable range for averaging time frames and then activate . In the case of a static scan this step is not required and the button therefore not active. The **Averaged PET** is shown in the **Image Preview** window.

Patient's MR image:

The user must specify an anatomical MR image of the same patient which will be segmented. He can choose the format, select the image and then activate for loading the MRI.

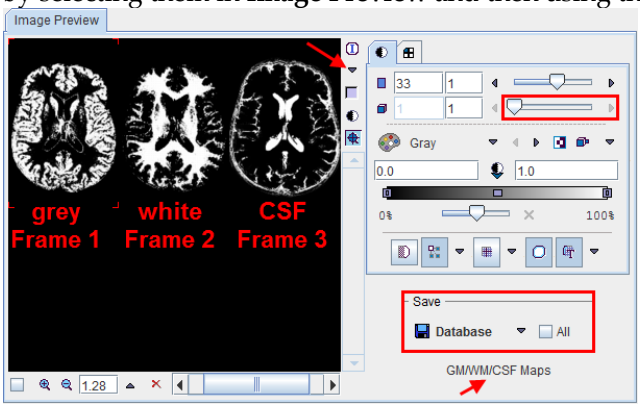


The **Use first series associated in Database by "Pair" function** box allows taking advantage of the feature that two series can be associated as a pair in PMOD databases.

GM/WM Segmentation:

This step needs to provide the different tissue segments. If **Probability Maps** is configured as **Calculate**, the button calls a segmentation procedure which may take several minutes to complete. The procedure has three parameters: **Sampling rate** determines the density of pixels considered in the calculation. **Bias Regularisation** serves for compensating modulations of the image intensity across the field-of-view. Depending on the degree of the artifact, a corresponding setting can be selected from the list. **Cleanup** is a procedure for rectifying the segmentation along the boundaries. It is recommended to use the default settings and only experiment with other parameter values if the segmentation fails.

The results are three segments, WM, GM and CSF. They are arranged as frames in a "dynamic" series. In the illustration below, the three frames are arranged in three columns. Because the calculation takes long, it may be helpful to save the segment images for later use by selecting them in **Image Preview** and then using the **Save** button.



If segment images are already available, **Probability Maps** can be configured as **Load from file**, and the corresponding segment file selected. Note that the segment images must be matched to the MR image and different segments should appear as dynamic frames in the indicated order. In this case the button just loads the segments.

Normalization:

The normalization of the MR image to the MNI template has two parameters, the **MR template** which should be set to T_1 or T_2 as appropriate, and the **Sampling rate**. After calculating the normalization its inverse is applied for transforming the VOI template to the MR space. It is then intersected with the individual GM mask, and the WM mask is used to create the WM VOI. The resulting VOI template is shown in the **Image Preview** window as **Template normalized to MR** .

PET-MR Matching:

Upon activating the button, the PET image is rigidly matched to the selected MR image. The inverse transformation is applied for transforming the VOI template from the MR to the PET space. The result **Template matched to PET** is shown in the **Image Preview** window.

If the PET and MR images are already matched, the **Skip Matching** box can be checked to skip this processing step. However, please note that in this case the MRI and the PET images must have identical pixel size and image matrix. If the automatic matching in the PVC tool is not feasible, matching can be performed manually in the fusion tool and the results saved for use in the PVC tool.

Outline VOIs:

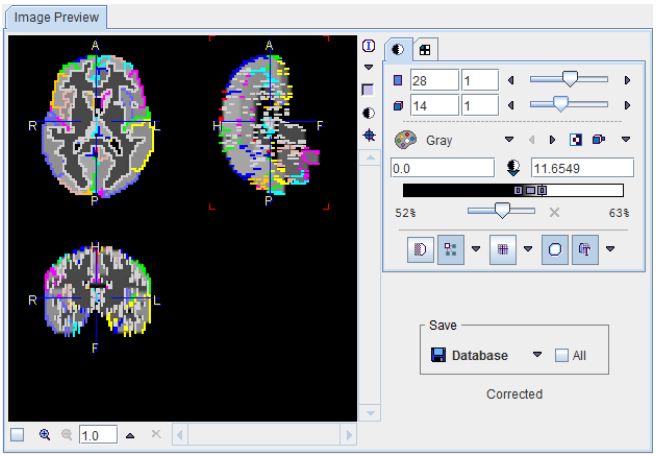
This step calculates contour VOIs from **Template matched to PET** and shows them together with the **Averaged PET** in the **Image Preview** window. This is the VOI set which will be used for PVC.

Edit VOIs:

This button opens a VOI dialog window showing the VOIs on top of the **Averaged PET**. Note the extended **White Matter** VOI which has been derived from the WM mask. The VOIs can be inspected and edited, or saved for later use. To return modified VOIs, close the window with the **Ok** button, otherwise **Cancel**.

PVC Calculation:

This step performs the actual PVC calculation. Because of the large number of VOIs in the standard templates the processing takes a while. The result is returned in the form of an image series and shown in the **Image Preview** window. If the input series was dynamic, the result is also dynamic as in the example shown below.



View Statistics:

This button calculates the VOI statistics in the original and the PVC corrected images. Depending on the input images the results are simple statistics, or tissue time-activity curves.

Returning the Results:

Make sure that the **Additional results** of interest are checked. Then close the window with the **Ok** button to return the results.

Background PVC Processing Mode

If no interactive processing is desired, the user interaction is minimal.

1) If desired, edit any of the parameters, or reset them by the button.

If the PET series is dynamic, define an appropriate frame range for averaging.

Select the anatomical MRI of the same patient.

Make sure that the **Additional results** of interest are checked.

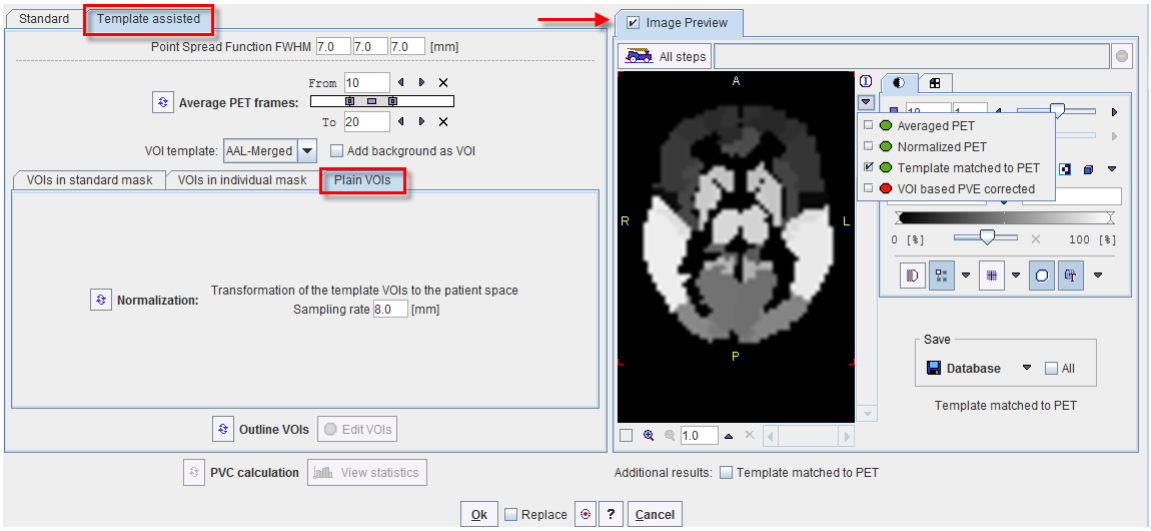
Start the PVC calculation with the **Ok** button.

The dialog window will be closed and processing will run in the background. Once the result were calculated and returned to PVIEW, a confirmation message will be shown.

PVC using Template VOIs based on Plain VOIs

Starting the PVC

As a first step, load the PET images into the PVIEW tool. Then activate the button to the right of the image and select the **PVC (VOI based)** method from the list of external tools. A dialog window is shown which allows performing partial-volume correction in a step-by-step mode or as a background process.



Step-by-Step PVC Processing Mode

The step-wise mode is activated by checking the box next to the **Image Preview** label. Note the buttons which are used to start the individual processing steps. Initially, several of them are inactive because the prior steps are missing.

The result images of the different steps are collected in the **Image Preview** area. In the image selection list, available results appear with a green mark, while yet unavailable ones are

marked in red. The example above shows the **Template matched to PET**. The images selected in the **Image Preview** can be exported for later use by the **Save** button.

The advantage of step-wise processing is that steps can be repeated with different parameters until the outcome is satisfactory.

Point Spread Function FWHM:

The PSF is assumed to be a three-dimensional Gaussian function. The FWHM values in the three directions have to be specified according to the resolution of the reconstructed image. Default is 7 mm isotropic FWHM.

Average PET frames:

Dynamic images can be processed and will result in a corrected dynamic series. However, for the **Normalization** step, a static PET image showing anatomical information is required. Therefore, the user should define a suitable range for averaging time frames, and then activate  . In the case of a static scan this step is not required and the button therefore not active. The **Averaged PET** is shown in the **Image Preview** window.

Normalization:

The normalization of the averaged PET image to the MNI PET template has one parameter, **Sampling rate**. After calculating the normalization, the normalization inverse is applied to transform the masked template to the PET space. The results **Normalized PET** and **Template matched to PET** are shown in the the **Image Preview** window.

Outline VOIs:

This step calculates contour VOIs from **Template matched to PET** and shows them together with the **Averaged PET** in the **Image Preview** window. This is the VOI set which will be used in the PVC.

Edit VOIs:

This button opens a VOI dialog window showing the VOIs on top of the **Averaged PET**. The VOIs can be inspected and edited, or saved for later use. To return modified VOIs, close the window with the **Ok** button, otherwise **Cancel**.

PVC Calculation:

This step performs the actual PVC calculation. Because of the large number of VOIs contained in the standard templates the processing takes a while. The result is returned in the form of an image series and shown in the **Image Preview** window. If the input series was dynamic, the result is also dynamic as in the example below.

View Statistics:

This button calculates the VOI statistics in the original and the PVC corrected images. Depending on the input images the results are simple statistics, or tissue time-activity curves.

Returning the Results:

Make sure that the **Additional results** of interest are checked. Then close the window with the **Ok** button to return the results.

Background PVC Processing Mode

If no interactive processing is desired, the user interaction is minimal.

1) If desired, edit the FWHM parameters, or reset them by the button.

If the PET series is dynamic, define an appropriate frame range for averaging.

Make sure that the **Additional results** of interest are checked.

Start the PVC calculation with the **Ok** button.

The dialog window will be closed and processing will run in the background. Once the result were calculated and returned, a confirmation message will be shown.

Note: This PVC procedure do not used grey matter mask to intersect with the VOI template. This is the difference respect to PVC using Template VOIs based on Standard Masks.

Recommendations

Findings by Rousset et al. [2]

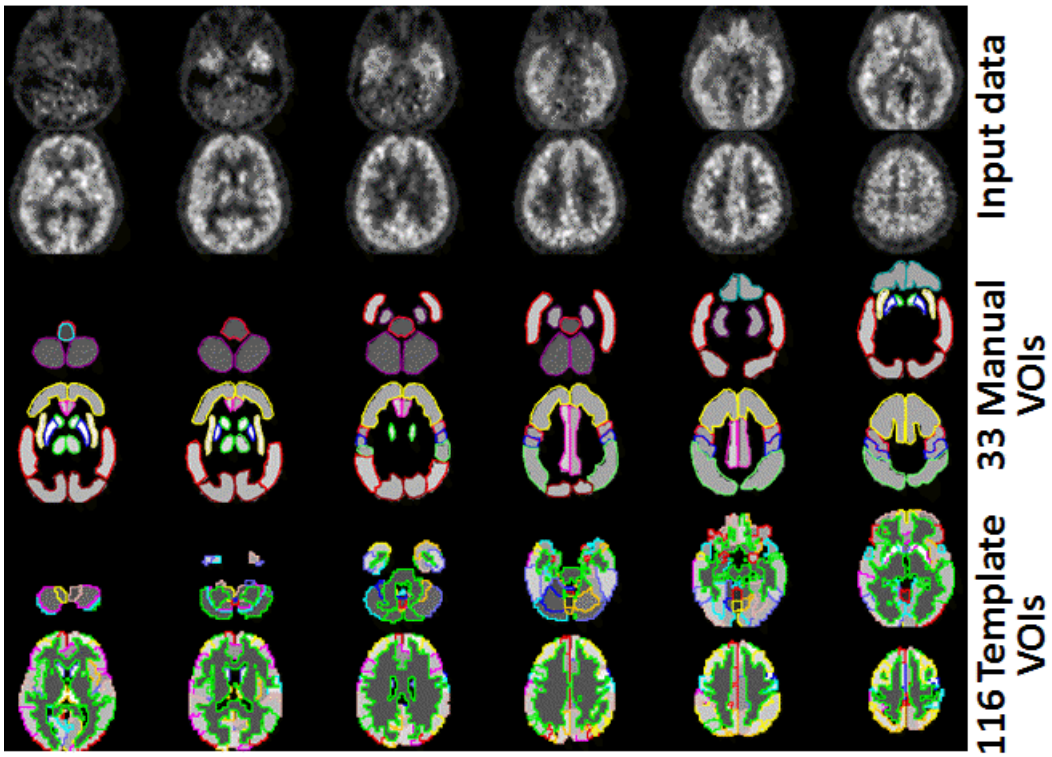
According to Rousset et al. [2], the accuracy of the GTM method depends primarily on the proper identification of the tissues which have different functional properties. If this is the case, the GTM algorithm is capable of accurately correcting the regional concentration within small structures such as the human basal ganglia. Furthermore, the propagation of statistical noise during partial-volume correction was found to be easily predictable and suitable for the application in dynamic PET.

Findings with the PMOD Implementation

The application of the GTM method to simulated PET images with realistic, spatially variant PSF resulted in the following observations (unpublished work Olivier Barret, PhD, Institute for Neurodegenerative Disorders, New Haven, CT, USA):

- GM VOIs are always corrected into the right direction, up- and downwards.
- A FWHM of 7mm is a reasonable default setting for the Gaussian PSF.
- If a patient MRI is available, the individual segments result in a better partial-volume correction than the standard GM, WM and CSF segments.

Shown below is an example of a patient data set corrected with 33 manually outlined VOIs, and with 116 VOIs derived from the AAL template combined with individual segments. Note the homogeneous values within the VOIs which are equal the partial-volume corrected average value of each VOI.



PVC of Brain Images based on MRI Segmentation

Methodology Description

The **PVC (Brain MR based)** method implemented in PMOD consists of the following steps:

1. Segmentation of the Anatomical MRI

To perform the segmentation, a normalization transform of the patient MRI anatomy to the MNI anatomy (or *space*) is calculated. In the MNI space, there are probability maps available for grey matter (GM), white matted (WM) and cerebrospinal fluid (CSF).

These priors are inversely transformed to the MRI space and employed in the image segmentation. The results are three probability images in the MRI space, called the GM, WM and CSF segments. They form the basis for the PVC.

2. Matching of the PET and MR Images

In order to perform the PVC, the information of the MRI and the PET must be aligned. Because the GM segments are relatively fine, they cannot be resampled to a typical PET resolution without severe information loss. Therefore, the PET image is rigidly matched to the MRI, and the PVC performed in the MRI space on the up-sampled PET images.

3. Partial-volume Effect Correction

First, the uptake in WM is obtained either by analyzing the PET uptake in pixels with very high WM probability, or by using a value provided by the user. Then, the following correction formula of Muller-Gartner is applied:

$$C_{PVC-GM} = \frac{C_{measured} - C_{WM} \times (WM \otimes PSF)}{GM \otimes PSF}$$

Corrects WM spill-in

Corrects GM spill-out

with the following notations:

C_{PVC-GM} Corrected activity concentration. This is the result of the PVC correction in each GM pixel.

$C_{measured}$ Actually measured activity concentration in a GM pixel which may be distorted due to spill-out and spill-in.

C_{WM} Activity concentration in WM which is assumed to be homogeneous and just blurred by the PSF.

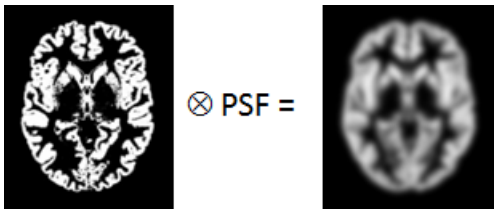
WM, GM — WM (GM) segment image which represents the WM (GM) probability of each pixel in the image as a value between 0 and 1. These images are assumed to represent the true anatomy with ideal resolution.

PSF — Point-spread function of the imaging system which is assumed to be constant across the image and represented by a three-dimensional Gaussian function.

WM⊗PSF — Mathematical convolution of the WM segment image with the PSF. The result represents the image of the ideal WM segment when detected with a real imaging system characterized by the PSF function.

The expected WM image is obtained by scaling WM⊗PSF by the WM concentration C_{WM}. It is subtracted from the measured image to compensate for spill-in from WM to GM.

GM⊗PSF — Mathematical convolution of the GM segment image with the PSF.



A division of the WM-corrected image by GM⊗PSF represents a deconvolution operation and corrects for the spill-out effect from GM. The operation of division may introduce over-corrections at the GM boundary. Therefore, the result image is masked at a certain threshold of the convolved GM image

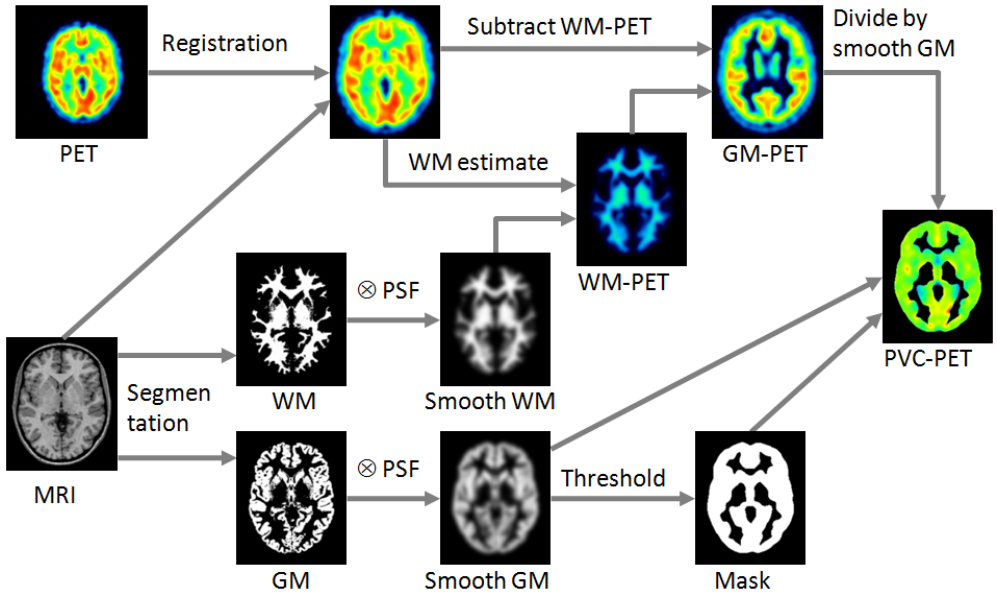
Spill-out Correction Only

If, however, the segmentation of white and grey matter fails, the correction can be reduced to a spill-out only correction. In this case a *Brain* segment is formed from all pixels which are not CSF. This segment is convolved with the PSF, and the PET image divided by the result as described by the equation below.

$$C_{PVC-Brain} = \frac{C_{measured}}{Brain \otimes PSF}$$

Schematic of the Correction Workflow

The following illustration provides a graphical overview of the different processing steps as well as the resulting intermediate images.



Requirements

The MRI-based PVC is only applicable to PET or SPECT images of the human brain. It can be applied to static or dynamic series. A well resolved anatomical T_1- or T_2-weighted brain MR image of the same patient is required, but there is no need for matching the two image series beforehand.

Performing MRI-based PVC

Starting the PVC

As a first step, load the brain PET images into the PVIEW tool. Loading of the MR series is not required at this stage. Then activate the button to the right of the image and select the **PVC (Brain MR based)** method on the list of external tools. A dialog window is shown which allows performing the processing in a step-by-step mode or as a background process.

Note the following:

1) Minimally, the user has to provide an anatomical MRI image.

It is recommended to inspect and analyze the outcome of the PVC procedure, for instance the outcome of the segmentation and the PET-MR matching. To this end, **Additional results** can be returned. The user should make sure that with in the background mode the corresponding boxes **PET matched to MR**, **Brain Segments** and **Grey mask** are enabled before closing the window with the **Ok** button.

If the **Replace** box is checked the original images are replaced by the partial-volume corrected images.

Step-by-Step PVC Processing Mode

The step-wise mode is activated by checking the box next to the **Enable preview** label. Note the buttons along the left border which are used to activate the individual processing steps. Initially, most of them are inactive because the prior steps are missing. In the example above, steps 1 - 3 have been performed. Therefore, step 4 can also be started, but step 5 not yet as it requires that the images have already been matched.

Note that the result images of the different steps are collected in the **Image Preview** area. In the image selection list, available results appear with a green mark, while yet unavailable ones are marked in red. The example above shows the WM map calculated by step 3. The images selected in the **Image Preview** can be exported for later use by the **Save** button.

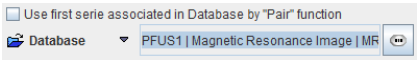
The advantage of step-wise processing is that the steps can be repeated with different parameters until the outcome is satisfactory.

1. Average PET frames:

Dynamic PET images can be processed and will result in a corrected dynamic series. However, for the matching in step 4, a static PET image showing anatomical information is required. Therefore, the user should define a suitable range for averaging time frames and then activate . In the case of a static scan, as in the example above, this step is not required and therefore not active.

2. Patient's MR image:

The user must specify an anatomical MR image which will be segmented. He can choose the format, select the image and then activate for loading the MRI.



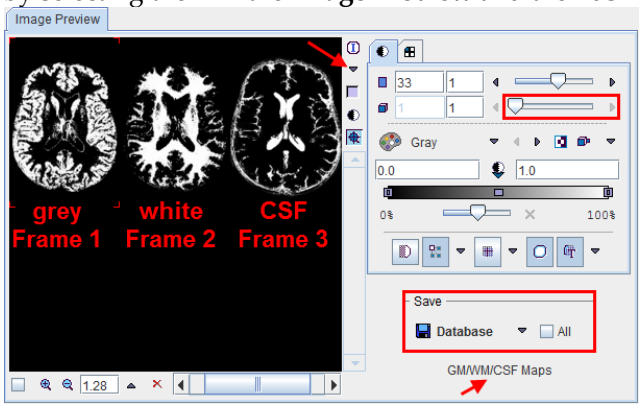
The **Use first series associated in Database by "Pair" function** box allows taking advantage of the feature that two series can be associated as a pair in PMOD databases.

3. GM/WM Segmentation:

This step needs to provide the different tissue segments. If **Probability Maps** is configured as **Calculate**, the button calls a segmentation procedure which may take several minutes to complete. The procedure has three parameters: **Sampling rate** determines the density of pixels considered in the calculation. **Bias Regularisation** serves for compensating

modulations of the image intensity across the field-of-view. Depending on the degree of the artifact, a corresponding setting can be selected from the list. **Cleanup** is a procedure for rectifying the segmentation along the boundaries. It is recommended to use the default settings and only experiment with other parameter values if the segmentation fails.

The results are three segments, WM, GM and CSF. They are arranged as frames in a "dynamic" series. In the illustration below, the three frames are arranged in three columns. Because the calculation takes long it may be helpful to save the segment images for later use by selecting them in the **Image Preview** and then using the **Save** button.



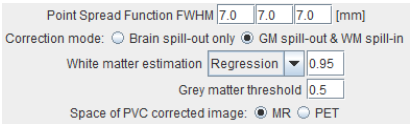
If segment images are already available, **Probability Maps** can be configured as **Load from file**, and the corresponding segment file selected. Note that the segment images must be matched to the MR image and different segments should appear as dynamic frames in the indicated order. In this case the button just loads the segments.

4. PET-MR Matching:

Upon activating the button, the PET image is rigidly matched to the selected MR image. If the matching fails, the **Sampling rate** can be reduced and matching tried again. In case the images are known to be already matched, the **Skip Matching** box can be checked in order to skip the matching step. However, please note that in this case the MRI and the PET images must have identical pixel size and image matrix. If automatic matching in the PVC tool is not feasible, matching can be performed manually in the fusion tool and the results saved for use in the PVC tool.

5. PVC Calculation:

The last step is the actual partial-volume correction procedure which has several parameters.



The **Point Spread Function FWHM** represents the assumed point-spread function. Default is 7 mm isotropic FWHM.

The **Correction mode** is normally set do **GM spill-out and WM spill-in**. If, however, the segmentation of white and grey matter does not give an accurate result, the correction can be reduced to **Brain spill-out** only.

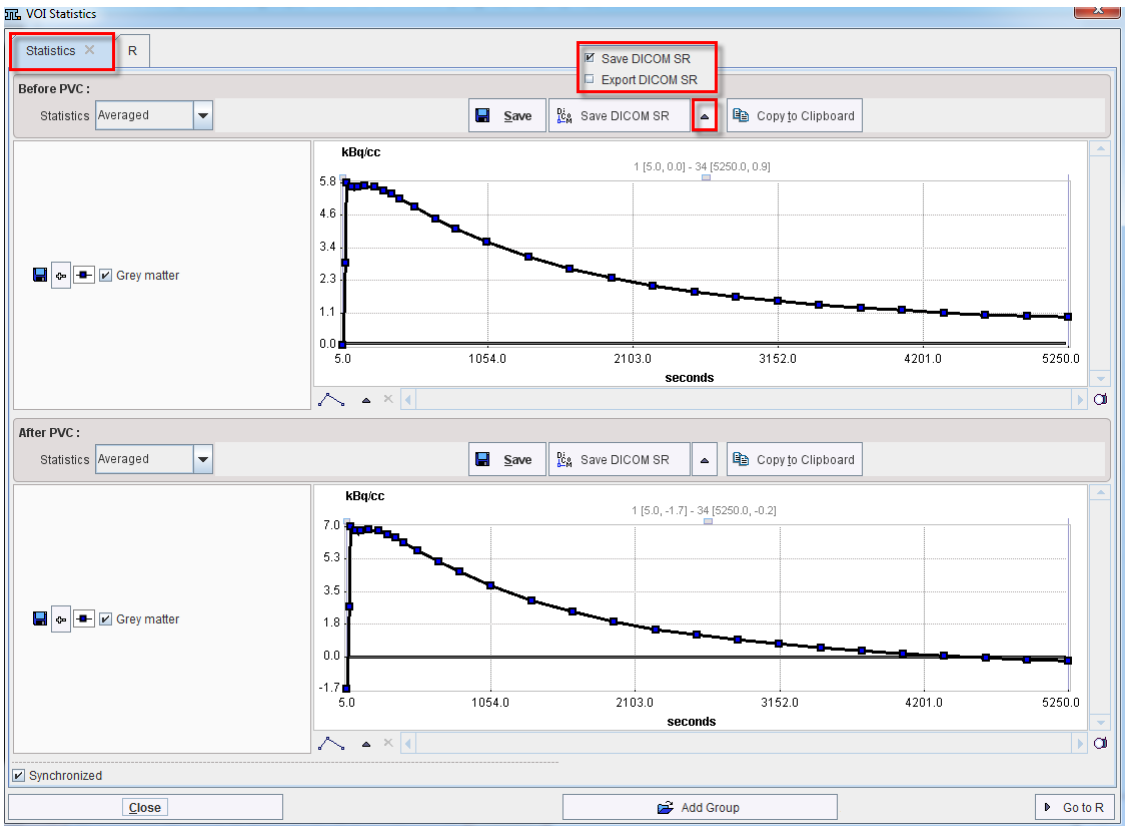
The **White matter estimation** provides three choices: Default is the **Regression** approach. It collects the PET uptake of all pixels with a WM probability higher than the specified value (e.g. **0.95**), and performs a linear regression to estimate the WM value at the probability of 1. [5] With **Average**, the average is calculated instead of using the regression. Finally, the user can specify a known WM uptake value with the **Fixed value** setting.

The PVC is only appropriate for GM pixels. All other pixels in the corrected image may therefore not be evaluated and are masked. To this end, a **Grey matter threshold** can be specified. It is applied to the convolved GM segment for getting a smooth appearance. Note that if the threshold is small, outlier values might appear along the mask boundaries as over-correction artifacts.

The PVC correction is always performed in the space of the MR image using the matched, interpolated PET image. If **Space of PVC corrected image** is set to **MR**, this corrected PET series is returned as-is. With the **PET** setting, however, the corrected series is transformed to the PET space using the inverse of the PET to MR transform.

6. View Statistics:

This button calculates the VOI statistics in the original and the PVC corrected images. Depending on the input images the results are simple statistics, or tissue time-activity curves for the gray matter.



The statistic results can be saved as a Dicom structured report with the **Save Dicom SR** option or exported as a structured report with the **Export Dicom SR**. In alternative, the content of the statistic page can be **Copy to Clipboard** and paste in Excel.

The **Go to R** button allows sending directly the statistic results to the PMOD R interface for further analysis.

Returning the Results:

Before closing the window make sure that the appropriate **Additional results** boxes are checked, then select the **Ok** button.

Background PVC Processing Mode

If no interactive processing is required, the PVC procedure is very easy. Only the following actions are required:

1) If the PET data is dynamic, the averaging range has to be defined.

The anatomical MRI has to be selected.

If desired, some of the parameters can be edited in the different processing steps, or they can be reset by the button.

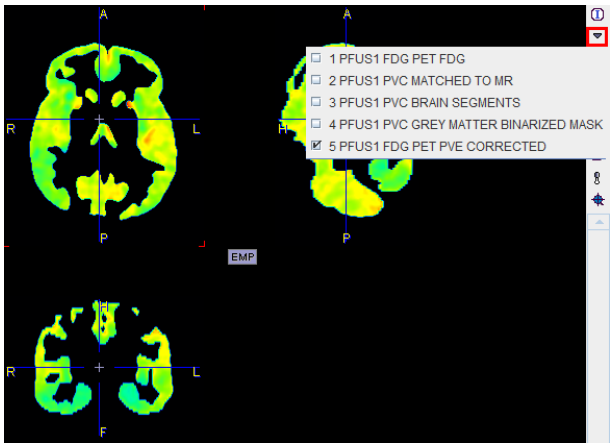
The appropriate **Additional results** boxes should be checked.

The PVC can be started with the **Ok** button.

The window will be closed and processing will run in the background for several minutes. Once the results were calculated and returned to PVIEW, a confirmation message will be shown.

Result Images

The results are returned as additional image series, as illustrated below. The original data is the first on the list, then come three auxiliary image series, and the last series marked by **PVE CORRECTED** is final outcome of PVC. Note the masking which may cause the disappearance of GM pixels if the cortex is thin and the PET resolution low.



Validation and Recommendations

Validation

The performance of the **PVC (Brain MR based)** method has been studied by Olivier Barret, PhD, Institute for Neurodegenerative Disorders, New Haven, CT, USA, and the results presented at the Symposium on Functional Neuroreceptor Mapping of the Living Brain 2010 in Glasgow. The abstract is reproduced below.

Performance Evaluation of PMOD integrated Partial Volume Correction Method for Brain PET data

Partial volume effects in emission tomography (PET) come from the limited resolution of the cameras and are due to two factors: the underlying heterogeneity of the tissues (grey and white matter in brain tissue) and the cross contamination of adjacent regions by the point spread function (PSF) of the tomographs. The result of these effects is an erroneous estimation of the true local tissue radioactivity concentration and in studies where quantitative estimates are required, it is often essential to perform partial volume corrections (PVC), in particular to take into account pathological or structural changes for instance as these can have a significant impact. Several correction methods, often requiring an additional structural imaging, have been proposed to attempt recovery of the true signal, and among these, one of the correction the most commonly used is an MR-based solution.

We report here of a fully integrated implementation of such an MR-based correction in the PMOD software, where the MR is automatically segmented into grey matter and white matter maps and subsequently registered with the PET image. Activity concentration in white matter is automatically determined by linear regression and the functional image is corrected by the maps smoothed by the PSF of the system, approximated by a 3-dimensional Gaussian distribution with a full-width half-maximum (FWHM) adjustable by the user. At the end of the process, the user is presented with a grey matter partial volume corrected functional image. The correction has been validated using simulated subjects from a Monte Carlo database built using the PET-SORTEO simulator which implements a realistic model of the ECAT EXACT HR+ tomograph. Ten subjects simulated with a FDG functional model were used to estimate the recovery coefficient as a function of the set FWHM and to evaluate the robustness of the correction with regard to the white matter activity concentration estimate.

Results for the simulated subjects show a very good recovery of the cortical regions with corrected values within 3% of the simulated activity concentration for an optimal FWHM around 6-7mm, in agreement with an effective resolution of the space-variant published resolution of the simulated scanner. The recovery coefficient also showed good stability against the user defined FWHM, with variation of 4-5% for a FWHM set between 5mm and 9mm. The method was shown to be robust against the white matter activity concentration estimates, with variation of only 2-3% of the final grey matter corrected values for large errors of 10% in the WM estimates.

An MR-based PVC method fully automated and integrated with all the steps necessary to perform the correction has been implemented in the PMOD software and validated against a simulated data set. The pertinence of the correction is being evaluated for different tracers (FDOPA from the PET-SORTEO database) and also for patient data from the ADNI database, in particular for the beta amyloid PIB tracer where this correction might prove to be critical because of the high white matter uptake.

Recommendations

The **PVC (Brain MR based)** method is a fully automatic procedure which has been tested in detail. However, the user should be aware that in practical situations there are several sources of potential errors which may affect the PVC outcome, particularly

- distortions of the grey and white matter segments, and
- inaccurate matching of the PET to the MRI.

Therefore the user is advised to inspect the additional PVC results. He should fuse the segment images with the anatomical MRI, and the matched PET image with the MRI to ensure that the anatomical information, which is used for the PVC, is correct and aligned.

Furthermore, VOI statistics should be calculated both with the original as well as with the PVC corrected images in order to detect consistencies in the data.

PVC References

1) Soret M, Bacharach SL, Buvat I. Partial-volume effect in PET tumor imaging. J Nucl Med. 2007;48(6):932-45

Rousset OG, Ma Y, Evans AC. Correction for partial volume effects in PET: principle and validation. J Nucl Med. 1998;39(5):904-11.

Rousset OG, Collins DL, Rahmim A, Wong DF. Design and implementation of an automated partial volume correction in PET: application to dopamine receptor quantification in the normal human striatum. J Nucl Med. 2008;49(7):1097-106.

Muller-Gartner HW, Links JM, Prince JL, Bryan RN, McVeigh E, Leal JP, Davatzikos C, Frost JJ. Measurement of radiotracer concentration in brain gray matter using positron emission tomography: MRI-based correction for partial volume effects. J Cereb Blood Flow Metab. 1992;12(4):571-83.

Giovacchini G, Lerner A, Toczek MT, Fraser C, Ma K, DeMar JC, Herscovitch P, Eckelman WC, Rapoport SI, Carson RE. Brain incorporation of 11C-arachidonic acid, blood volume, and blood flow in healthy aging: a study with partial-volume correction. J Nucl Med. 2004;45(9):1471-9.

Chapter 8

PMOD Image Viewing and VOI Tool (PVIEW)

PVIEW is a versatile image and Volume-of-Interest (VOI) analysis tool which belongs to the base installation of PMOD. It supports many operations for image reviewing and scientific data analysis including:

- Loading medical images in different formats, including DICOM.
- Viewing the images with different color tables and in different layouts.
- Calculating new slice images in arbitrary new orientations.
- Performing many image processing and manipulation operations.
- Displaying fusion images of matched data sets (image registration is a separate option).
- Performing volume-of-interest analyses and the calculation of time-activity curves from dynamic studies.
- Saving images in different formats, including DICOM, and directly C-STORE them to a DICOM server.

The PVIEW tool is started from the PMOD ToolBox with the

Like many other PMOD tools it organizes the functionality on different pages which can be selected by the upper tabs.

In This Chapter

Database Loading - Page 1 (Option)

The first page **DB Load** shows the database interface. It is only available if the database functionality is enabled and a local or remote database has been configured to access images in DICOM format. Note that it is highly recommended to use the database for accessing DICOM images, because the image access is much slower otherwise. The database load page offers an efficient interface for loading images stored in one of the configured databases. A detailed description can be found in the ***Image Data Load section*** (on page 84).

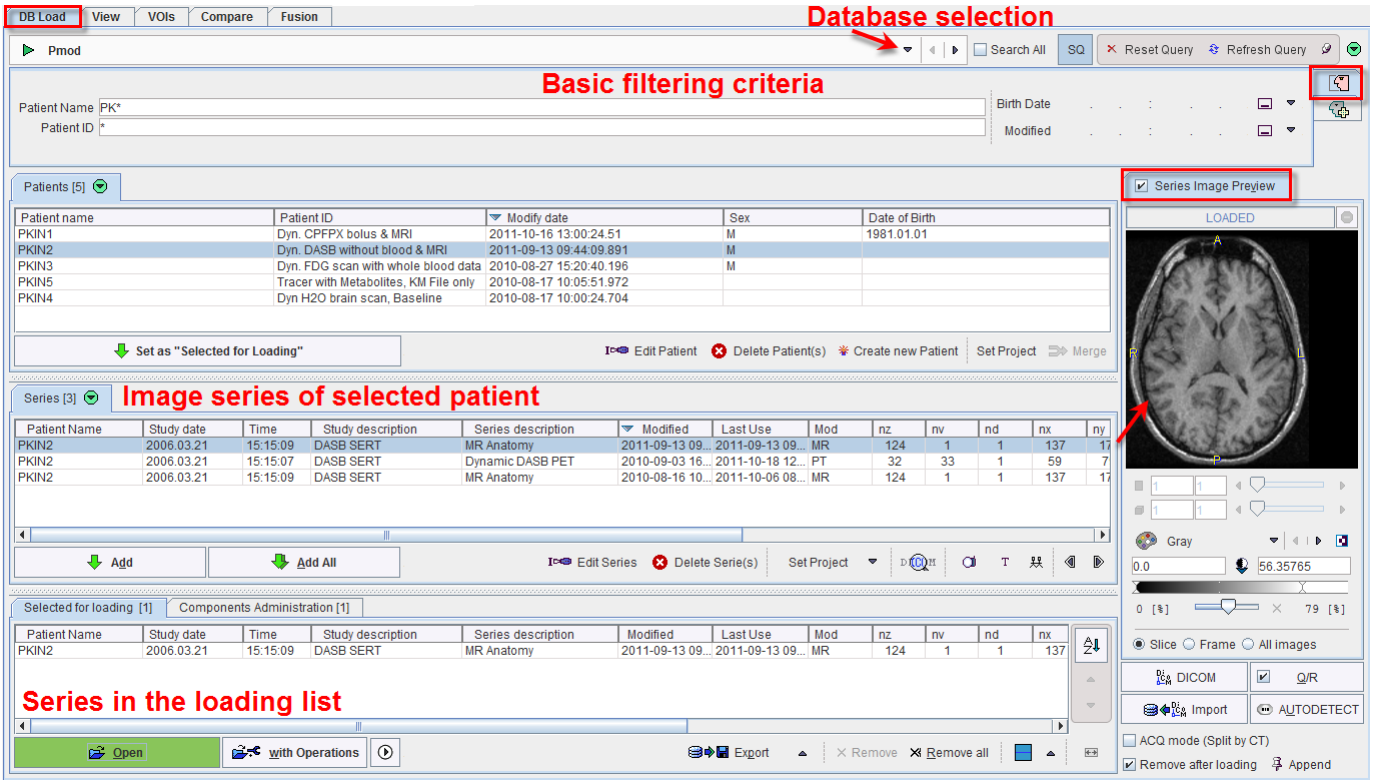
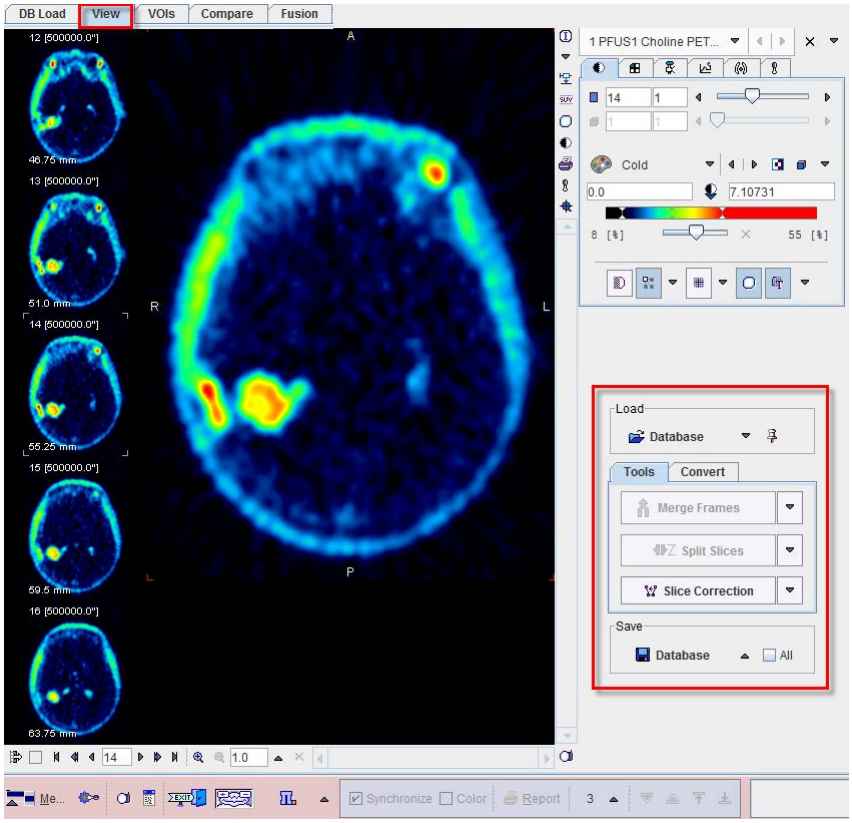


Image Viewing - Page 2

The purpose of the **View** page is

- loading images in all kinds of image formats,
- viewing the loaded images and performing processing operations, and
- saving (modified) images in one of the supported output formats.

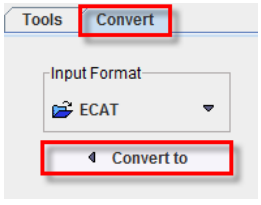


Several images can be loaded, but only one at the time can be viewed on this page. The **View** page essentially implements the basic PMOD capabilities which are described in the ***Image Loading*** (on page 58) and the ***Image Display*** (on page 106) sections. Additionally, there are some extra functions available which are accessible by the tabs in the lower right.

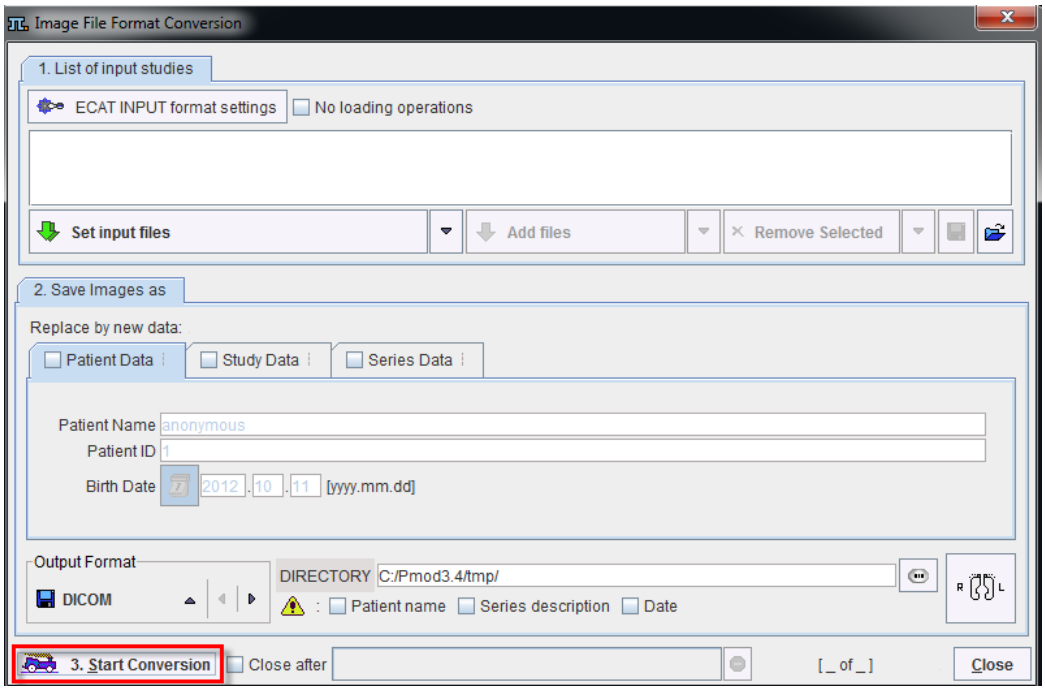
The **Load/Save** sections contains the **Load** and the **Save** buttons, configurable to different image formats. Note the **All** box which can be checked to save all loaded images at once.

Batch Format Conversion

The **Convert** tab is used for batch format conversion.



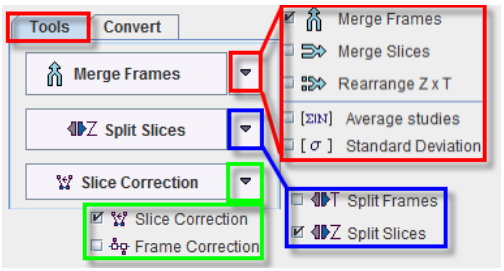
Begin by setting the **Input Format** then activate the **Convert to** button. A dialog appears, which allows selecting the files to be converted, and to define processing and output properties as well as the **Output format**.



The contents of the dialog window may differ depending on the selected formats. The first step is to select the files to be converted using the **Set input files** button. Activating the **INPUT format settings** button brings up the loading dialog, where data pre-processing operations (eg. rotations, filtering) can be specified. Another dialog is shown when selecting the **Output Format** settings button. In the DICOM example shown above the output modality and the patient position can be specified. Finally, an output path must be defined in the **DIRECTORY** section. After activating **Start Conversion**, PVIEW reads, converts and saves the selected series in the prescribed manner.

Tools

In addition to standard image viewing the PVIEW tool allows performing the following distinct operations available on the **Tools** tab:



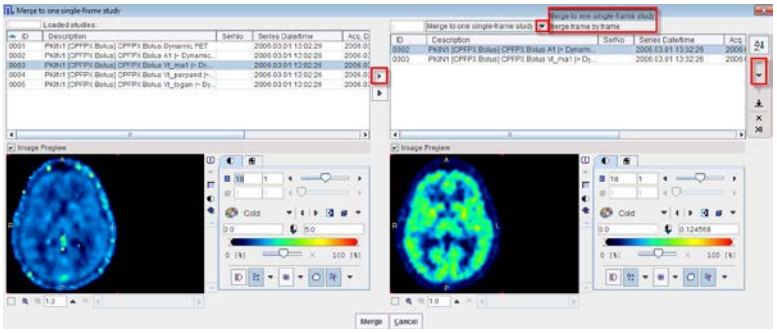
Most functions only get active when more than one image series have been loaded into PVIEW.

Functionality:

Merge Slices

Merging of a number of static image series in axial direction.

Activating **Merge Slices** opens a dialog window for choosing among the loaded series and changing their order. The studies selected for merging are then combined in the axial direction to form a static series with extended coverage.



There re two option available for merging: **Merge one single frame study** and **Merge frame by frame**.

This function is only reasonable for image series covering aadjacent axial fields-of-view such as in whole-body scanning.

Note that at least two studies have to be selected for mearging

Merge Frames

Merging a number of static image series into one dynamic study.

Activating **Merge Frames** opens a dialog window for choosing among the loaded series and changing their order. The result of the merge operation is a dynamic study which most likely has inappropriate timing information. Please use the ***study information button*** (on page 109) to change the acquisition times. After that, save the study using an image format which supports acquisition times (DICOM, Interfile, Ecat).

This function is only reasonable for image series having identical geometry.

Rearrange Z&T

The result is a one multiframe study with a new number of slices and frames.

Average studies

Calculating the average value of each pixel across the loaded image series.

Result is the average image series, while the individual image series are removed from PVIEW.

Standard Deviation

Calculating the standard deviation of the values in each pixel across the loaded image series.

Result is the standard deviation image series, while the individual

image series are removed from PVIEW.

Split Frames *Splitting a dynamic image series into a set of static series.*

Activating the button causes PVIEW to split the current dynamic series into a set of static series (one per time frame) which can be separately displayed.

If the **To disk** box is checked, the **Output Format** selection becomes active. In this configuration, a saving dialog appears when the **Split Volumes** button is activated, and the new static series can be saved to disk.

Split Slices *Splitting a 3D static image into a set of 2D static series.*

If the **To disk** box is checked, a dialog window appears allowing to select the **Output Format**.

Slice corr. *Calculates a rigid 2D transformation between marker pairs defined on slices.*

The first slice with valid markers serves as the reference. This function could be useful when merging slices which have been acquired separately (eg. by autoradiography of small animals) into a volume.

Note that at least three markers on two slices need to be defined.

Frame corr. *Motion correction for a dynamic series with external markers (translations only).*

Calculates the transformation between frames and corrects them based on the assumption that the maximal value contained in a VOI should remain stable.

Note that at least one VOI must be defined (in case of multiple VOIs the first one on the list is going to be used during the correction). It is important that VOIs are in dynamic mode.

Volume-of-Interest Analysis - Page 3

The purpose of the **VOIs** page is to support Volume-of-Interest analyses on the currently loaded image series. This functionality is described in detail in a ***previous chapter*** (on page 177).

Image Comparison - Page 4

After images have been loaded, the user can switch to the parallel image viewing page by selecting the **Compare** tab. PVIEW now shows three horizontal image display layouts. There are two display modes available, regular image display, and image fusion.

Regular Image Display Mode

The example below illustrates the regular image display mode, whereby each of the studies may have an independent layout. Note the **Synchronize** (for *Synchronize compare display 1,2,3*) and **Color** boxes highlighted in red. If they are checked, PVIEW switches all three rows to the same layout and synchronizes the images shown. This will only be successful for studies which have the origin at the same location and which cover the same image volume (the pixel size, however, might differ as in the case of a PET/CT study with the same reconstructed field-of-view).

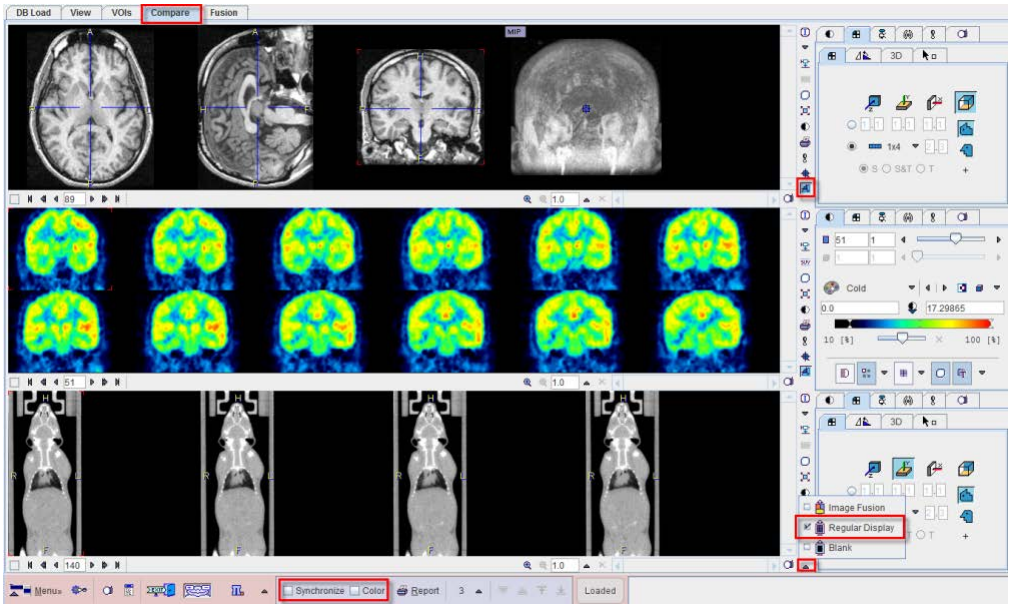
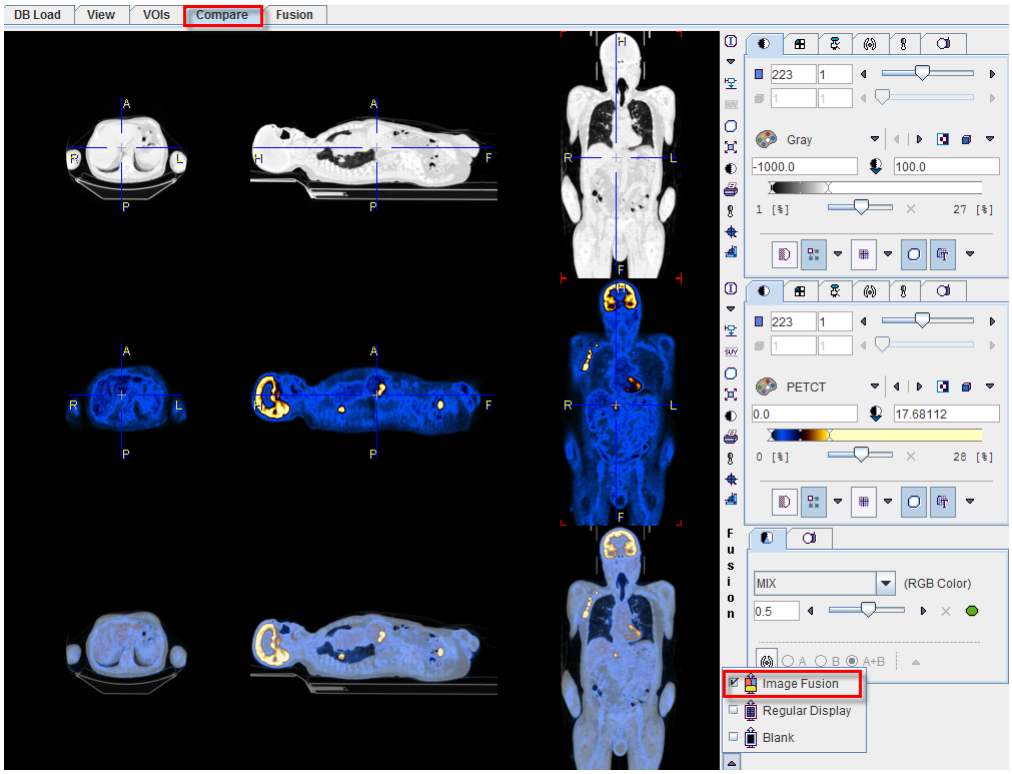


Image Fusion Display Mode

In the fusion display mode the studies in the upper two rows are synchronized, while the third row shows the fusion image. As for synchronized image comparison, the studies must have the origin at the same location and cover the same image volume. A PET/CT example is shown below.



In the fusion mode all ***fusion renderings*** (on page 163) are available to prepare a meaningful fusion image. Additionally, by activating the **Fusion** tab it is possible to bring up a larger display of the active fusion image.

Switching the Display Mode

The display modes can be switched using the button close to the right lower corner, which changes according to the situation.

 Selects the image fusion mode.

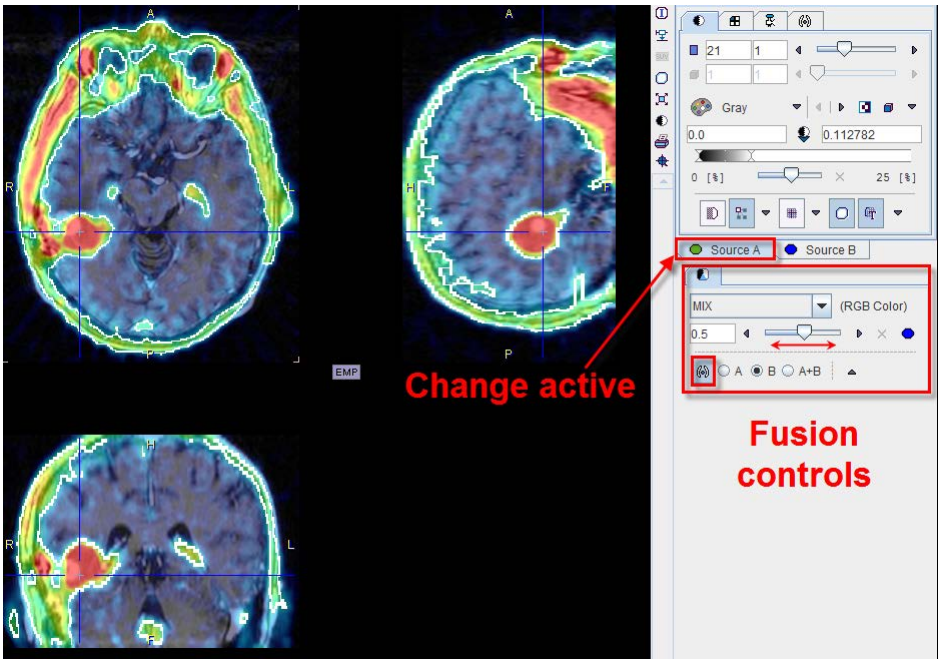
 Selects the regular image display mode with independent series.

 Sets the third row to blank.

Image Fusion - Page 5 (Optional)

The fusion images in the third row of the **Compare** page are relatively small. To investigate them closer please select the **Fusion** tab which shows a page with just the fusion image and the image controls.

Note: the **Fusion** page is only available if the image fusion tool (PFUS) has been purchased.



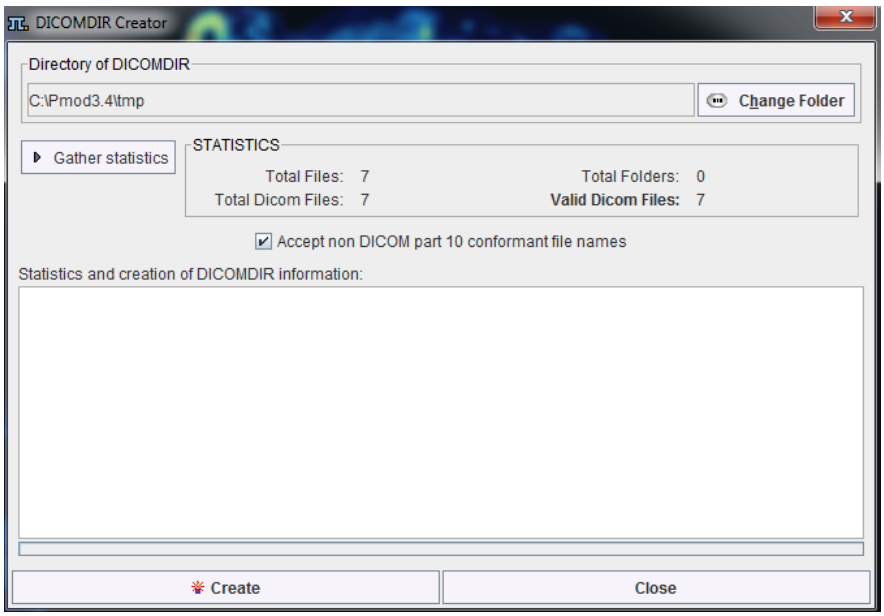
To adjust the color of the studies, either of the tabs **Source A** or **Source B** must first be selected. To show different studies on this page, please go back to the **Compare** page and display them in the upper two rows, then switch again to **Fusion**. All fusion capabilities are available, and the fused representation can be saved in JPEG or in DICOM format.

Note: In contrast to the image fusion tool it is not possible to outline VOIs directly in the fusion images. Selecting the VOI button just switches the display back to the **VOIs** page.

Creation of a DICOMDIR File

The DICOMDIR file format has been defined to organize the access to off-line DICOM part 10 files. For instance, DICOM-compliant data CDs contain a DICOMDIR at the root level which contains a description and access information for all the studies on the CD. In PMOD, the DICOMDIR similarly describes the DICOM files residing under a root directory, eg. *Pmod3.5/data/dicom*. This file can be maintained by PMOD's DICOM server which updates the information after receiving and storing new images (see also the ***PMOD DICOM Functionality*** (on page 31)).

The PVIEW tool has a handy function to create a DICOMDIR file which registers all DICOM files contained in a directory tree (see also the section ***DICOM Part 10 Data Loading*** (on page 86)). This function is called by the **Create Dicomdir** entry in the menu **View** and opens the following dialog.

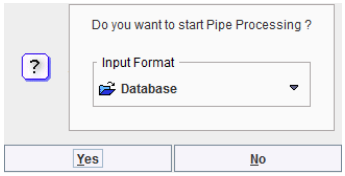


The **Change Folder** opens a file browser to select the root directory of the tree containing the DICOM files to be registered. When **Gather statistics** is activated, all files in the directory tree are analyzed, and the information in the **STATISTICS** section updated. However, to really create the DICOMDIR file, the **Create** button must be activated.

Batch Mode Pipe Processing

The PVIEW tool has a mechanism for concatenating ***external tools*** (on page 143) into a processing pipeline. The output of each step in the pipeline serves as the input to the next step, producing the end result after the last step.

The configuration of such a pipeline can be started with the **Batch Mode Pipe Processing** item in the **View** menu. Since pipe processing is restricted to a single image format, a dialog window appears first for defining the **Input Format**.



Next, the configuration window appears for setting the pipe up. The left area serves for defining the input images and the output format, whereas the sequentially applied external tools are defined to the right. The example below illustrates the situation, where FDG brain images are converted to SUV units, spatially normalized, and then the SUV statistics in a set of standard brain regions is calculated.

Please proceed as follows for setting up a pipe processing job:

1) Use **Set input files** for selecting the images to be processed.

On the first tab in the PIPE PROCESSING DEFINITION select the first external tool to be applied from the **Processing Tool** list.

Adjust the parameters of the selected tool.

Use the **+** button to add another processing tab, select the **Processing Tool** and adjust its parameters. Intermediate results may be helpful for quality control purposes and trouble-shooting. Their saving can be enabled by the **Save** box, and an optional **Prefix** defined for clarification of the results.

Continue adding processing tabs as required.

Use **Save Processing** to save the pipe definition. Note that such pipe definitions can be chained on the **List of Pipes** panel.

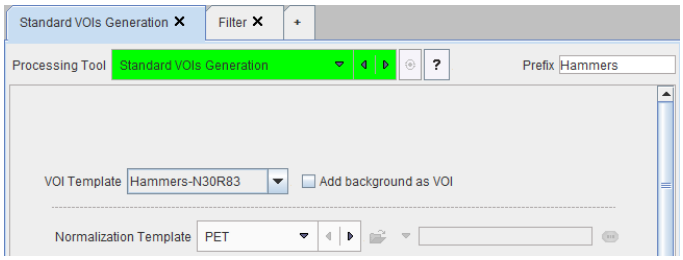
Select a representative series in the **List of input studies** and enable **Preview** for testing the pipe. The result is shown in the image window. If the result is not convincing, adjust some tools parameter and **Refresh**, to test the new configuration.

Define the output options in the lower left: If needed, **Patient**, **Study** or **Series** information can be replaced. Depending on the processing, the results may include VOI definitions and statistics. Using the radio button choices, select which parts of the result are to be saved. The **Output Format** is used for defining the image output format, but might behave differently, depending on the radio button setting. For instance, if **Only VOIs and Statistics** are needed, there is no image format choice available.

Start Processing.

VOI Statistics

The **Standard VOIs Generation** ***tool*** (on page 155) is specific in that it in the pipe it will not only produce the VOI definition, but also calculates and saves the VOI statistics in the current image, if **Statistics** is included in the save options.



Chapter 9

PMOD Installation

Please read the following information carefully and perform the installation of PMOD and the required supplementary components as described in the sections for the different operating systems.

In This Chapter

Supported Platforms

Operating Systems

Currently, the full functionality of the PMOD modules is offered on three platforms:

- Windows Operating Systems starting from Windows 7
- Linux
- MacOSX

Java Compatibility

PMOD is based on the Java Runtime Environment (JRE) which evolves over time. In order to avoid compatibility problems PMOD is deployed since version 3.1 with a tailored JRE on Windows and Linux systems. On MacOSX systems, however, the JRE is a part of the operating system and can therefore not be tailored. If a MacOSX upgrade happens to cause an incompatibility, PMOD Technologies will react and provide a new build of the current release to be freely downloaded using the customer's support login on the PMOD website. Note, however, that versions prior to the current PMOD release will not be fixed. In these cases, JRE upgrading should be avoided.

Performance

The performance of PMOD is crucially dependent on the the following system characteristics:

- CPU clock: Java performance increases approximately linearly with the CPU clock; a better internal organization of a CPU usually does not compensate a higher clock rate.
- Processing Cores: The PKIN, PXMOD and PNEURO tools supports parallel calculations, if a system has more than two cores or CPUs and will be significantly faster. For using the parcellation methodology in PNEURO eight cores or more are recommended.
- Operating system: To process real-life data sets it is *mandatory to use 64-Bit operating systems*. With 32-Bit systems, the RAM available to PMOD is limited to about 1.2-1.5GB which is not sufficient for real image processing!
- RAM: The equipment of the system with at least 8GB RAM (on 64-Bit systems) is required to avoid swapping and running out of memory. For PNEURO 16GB or more is highly recommended.

Windows Installation

The installation for all types of PMOD systems starts with the software extraction from the installation DVD. No other installation is required for PMOD network clients. For PMOD standalone systems and PMOD license server systems, the USB protection key drivers must then be installed and the dedicated license file copied to the *properties/system/lcs* folder.

Note that the USB key driver installation requires administrator privileges.

Installation Overview

PMOD supports two licensing schemes: stand-alone and network licenses.

Licensing, Stand-alone License

The PMOD software stand-alone licensing mechanism consists of two components:

1) a **USB protection key** (WIBU-Box/RU, WIBU-SYSTEMS AG, *http://www.wibu.com*), and

a license file **pstarter.lcs** (in sub-directory *properties/system/lcs* of the PMOD installation).

During PMOD startup the license information encoded in the USB key is read and compared to that in the license file. Only if the two informations match, startup proceeds. Next is a check whether the PMOD version purchased allows running the currently installed version. If all checks are successful, the PMOD ToolBox appears showing the purchased modules, and processing can start. Note that the USB key must remain in place while running PMOD.

Licensing, Network License

The PMOD network licensing scheme consists of a PMOD license server which manages a pool of purchased licenses, and an arbitrary number of PMOD clients which can check out unused licenses from the server. As soon as the PMOD program on a client is closed, the license is returned to the managed server pool. If the PMOD client crashes for some reason, the license is re-collected to the pool after about 15 minutes. On the other hand, if the license server is stopped, the clients show a warning message to the user and allow to continue work for a few minutes. Then, the clients will be stopped, unless the server has been started again.

On the license server PMOD is installed in the same way as for a stand-alone license with the USB key, but the license file turns it into a license server.

On the clients PMOD is also installed in the standard way, *except* that

- installation of the drivers for the USB protection key is not required;
- no license file is required.

Note the following:

- The license server PMOD installation is only intended for server purposes and not for data processing.
- The license server must be running and the USB key must be connected at all times.
- The license server and the clients must run the same PMOD version.
- It is not required that the license server and the clients have the same operating system.

Java Runtime Environment (JRE)

The entire PMOD software has been programmed in Java and therefore requires an appropriate Java Runtime Environment (JRE) to be executed. During PMOD installation on Linux and Windows systems, an appropriately configured JRE is extracted into the *java* sub-directory of the PMOD installation. This dedicated JRE will then be used for running PMOD. By this controlled environment, PMOD will remain unaffected from changes due to

automatic upgrade procedures on Windows and Linux. Only on MacOSX systems, the built-in JRE will be used.

Installation Steps

The installation of the PMOD software consists of the following steps which should be performed in the proposed sequence. They are explained in detail in the system-specific installation sections.

1) Extraction of the PMOD program files, the JRE, and the example data to the *Pmod3.5* directory in a user-defined directory.
This installation step is required for: **Stand-alone Installation, License Server, Network Clients.**

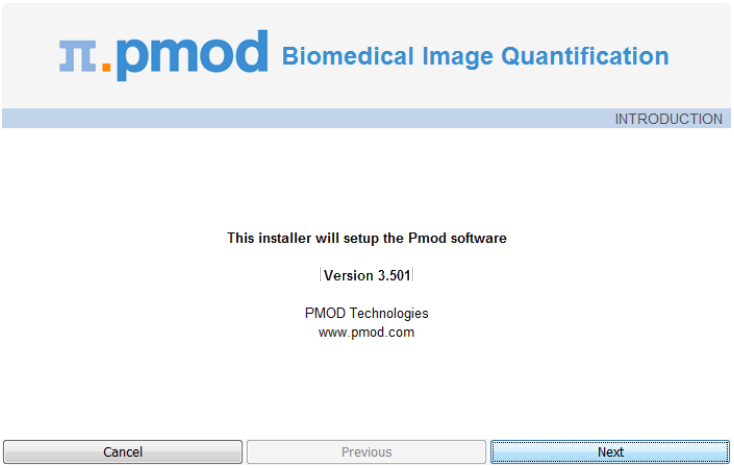
Installation of the USB protection key drivers for reading the information from the WIBU-Box/RU plugged into the USB port. *Please do not connect the PMOD USB protection key before this installation has been completed.*
This installation step is required for: **Stand-alone Installation, License Server.**

Installation of the PMOD license file *pstarter.lcs*. The license file can be downloaded from the **Support** area of the PMOD ***website http://www.pmod.com/technologies/support/enter-support.php*** after the personalized login (please refer to the delivery note of your PMOD package for login information).
This installation step is required for: **Stand-alone Installation**, **License Server**.

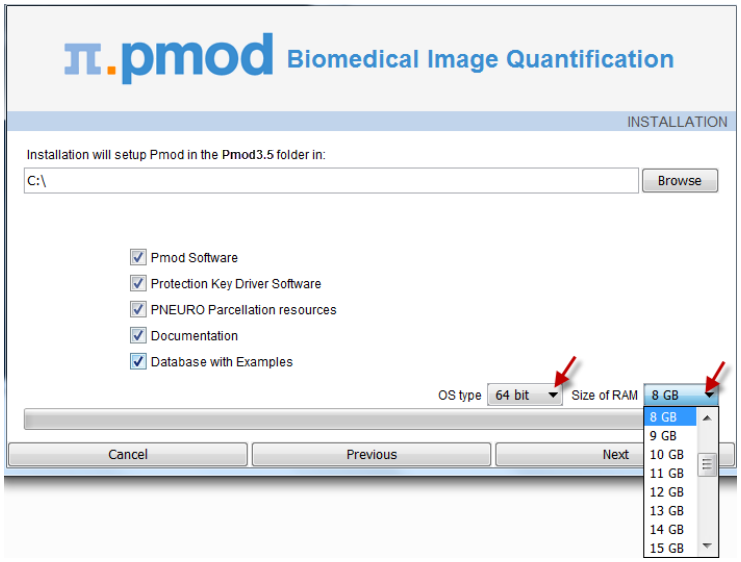
PMOD Software Extraction

The following software extraction procedure must be performed for standalone PMOD installations, for PMOD servers, and also for all PMOD network clients.

Please begin by inserting the PMOD installation DVD. Then start the installer by starting the **RunSetup.bat** in the *Setup/Windows* directory on the DVD by double-clicking. The following installation screen appears



Please use **Next** to proceed and accept the license agreement in the appearing dialog window. After activating **Next** the window for configuring the installation appears.



Please perform the following configurations:

Installation Path

Use the **Browse** button to select the parent directory for the installation. There, the installer will create a new directory **Pmod3.5** for the program files and the data. Please make sure that 450MB of free space is available.

Packages

It is highly recommended to install all four packages, the **Software**, the **Protection Key Driver Software**, the **Documentation**, and the **Example Database**. The **Example Database** requires about 120MB and will show up as database called **Pmod**. This database will be a great help for getting acquainted with the programs because it contains examples for the different types of data analysis. Furthermore, you will already have a database for storing your data.

Properties of Operating System and RAM

Current operating systems (**OS**) support the 64-Bit capability of new hardware. The main advantage of using a 64-Bit OS is the extended address space for the applications, in this case PMOD. Consequently, the data size is virtually unlimited for a 64-Bit OS (only limited by hardware RAM), while it is limited to <<2GB for a 32-Bit system. As there is a clear trend towards rapidly increasing image data sizes, we strongly advise against using 32-Bit systems for PMOD.

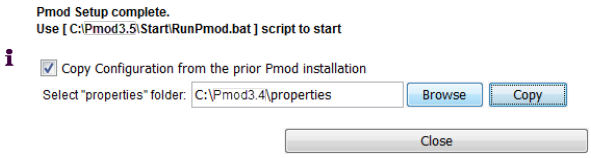
If the operating system of your target computer is 32-Bit, then please set the **OS type** selection to **32-Bit**. Correspondingly, only **Size of RAM** of **1GB** or **1.2GB** can be selected, preferably **1.2GB**.

Normally the operating system of your target computer should be 64-Bit. In this case please set the **OS type** selection to **64-Bit,** and **Size of RAM** can be set to any size. However, if the

specified size exceeds the physical RAM, the system will start swapping after RAM space is exhausted and will become very slow. Therefore it is recommended setting **Size of RAM** < physical RAM.

Installation of the PMOD Environment

The installation is started by the **Install** button. The Pmod3.5 directory is created wherein all PMOD-related files are extracted. At the end of the installation a dialog window is shown. It indicates the command script for starting Pmod3.5, and allows importing the configurations from a prior version. To this end, select the **properties** folder of your prior PMOD installation with the **Browse** button as illustrated below, and activate **Copy Configurations**. This import will also copy the license file, so that Pmod3.5 should immediately run with the familiar environment if your license is valid with the Pmod3.5 version.



PMOD Stand-alone License Installation

Install USB Key Drivers

All the files required for the driver installation have been extracted during the installation of the PMOD software and stored in the PMOD directory tree. The following two steps must be performed to install the USB protection key hardware drivers.

1) **Driver installation:** The purpose of this step is to install programs for reading the information from the WIBU-Box/RU plugged into the USB port. The driver installer is located in the directory *Pmod3.5/hksetup/Windows.*
   Please start the program **WkRuntime.exe** which includes the drivers for both 32-Bit and 64-Bit systems, and perform a standard installation procedure. Then *reboot the system*.

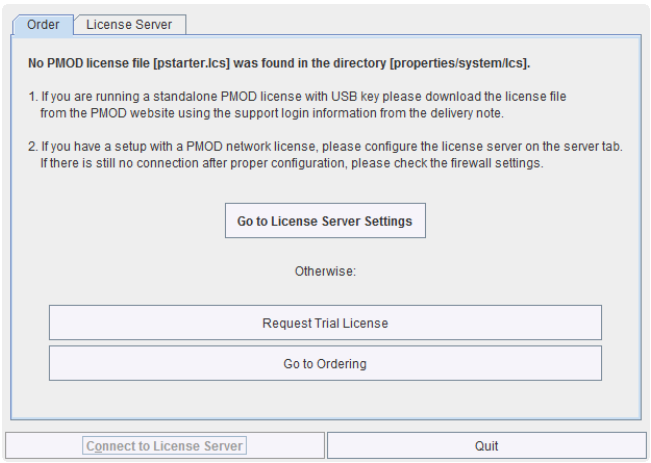
Now the USB key can be connected to any of the free ports.

Note: If you experience problems during driver installation, you are recommended to download the most recent drivers for the WIBU-KEY (Runtime Kit) from ***http://wibu.com/download_user.php*** (***http://wibu.com/download_user.php***) and try the installation again.

Copy License File

The delivery note that you have received with the PMOD DVD contains account information for logging into the support area of ***www.pmod.com*** (***http://www.pmod.com/technologies/support/enter-support.php***). There you will find a license report, and a button for downloading the license file (pstarter.lcs) for your purchased configuration. Please download pstarter.lcs and copy it to the directory *Pmod3.5/properties/system/lcs.*

If the license file is missing when PMOD is started, the following dialog window is shown.



The button **Request Trial License** opens a web browser and points to the location, where the user can fill out a form for requesting a trial license file. The button **Go to ordering** opens a web browser and points to the PMOD ordering form.

The **Go to License Server** panel is only applicable for network licenses. In this case please refer to the next ***section*** (on page 348).

Important Note: Please do not change pstarter.lcs in any way - a modified license file will not be accepted. Do not open pstarter.lcs in any program, do not rename it, and if you transfer it per FTP, use binary transfer.

Starting PMOD

PMOD can now be started with the command script **RunPmod.bat** in *Pmod3.5/Start*. Example:

```
C:
cd "C:\Pmod3.5"
.\java\jre\bin\java -version
.\java\jre\bin\java -Xmx8000M -jar pmod.jar
pause
```

Notes:

The starting script has been tailored to the installation directory. Therefore, if the Pmod3.5 directory is moved to a different location, the path needs to be adjusted.

The **-Xmx8000M** option specifies the maximum heap memory (8000 MB) that PMOD can allocate. To process large data sets this number should be increased. However, please note that there is an operating-system dependent *limitation on 32-Bit operating systems*: only a maximum of 1500M can be allocated, even if the physical RAM size is larger. Increasing -Xmx beyond 1500M will result in an error *Could not reserve enough space for object heap*. Caution: The P3D tool may crash, when the reserved space approaches the physical RAM size.

Create a PMOD Starter Shortcut on your Windows desktop:

1) Start a Windows explorer and drag the file *Pmod3.5/Start/RunPmod.bat* to the Desktop while pressing `CTRL+SHIFT` simultaneously.

Then rename the shortcut to *PMOD*.

Change its icon by pressing the right mouse button on the shortcut, select **Properties**, and then in **Change Icon** point to *Pmod3.5/resources/icons/Pmod.ico***.**

PMOD Network License Installation

PMOD License Server Installation

PMOD Software Installation

The computer for the PMOD license server doesn't require a high performance, but needs to be running continually. Therefore, a robust, vintage machine is well suited as a PMOD license server. Preferably, it is also dedicated to serving the PMOD license, because the license server is a standard process rather than a Windows service.

To install the PMOD license server first perform the steps described in the ***Stand-Alone PMOD installation*** (on page 346) including copying of the license file and plugging the USB key in.

Multiple Licenses Management

A license server can manage multiple licenses simultaneously. In order to use this feature please rename the different license files (pstarter.lcs) by appending the license numbers (pstarter860.lcs, pstarter912.lcs, ...) and copy them into the *Pmod3.5/properties/system/lcs* folder.

Starting the License Server

The PMOD license server can then be started by executing the *Pmod3.5/Start/RunLcsSvr.bat* script containing the following lines

```
C:
cd "C:\Pmod3.5"
.\java\jre\bin\java -Xmx2G-jar pmtsvr.jar 5000 -ls -d
Pause
```

The meaning of the command arguments is:
`5000`: IP port over which the license server communicates
`-ls`: license server only, no data sharing
`-d`: verbose output

Note: The script has been tailored to the installation directory. Therefore, if the Pmod3.5 directory is moved to a different location, the path needs to be adjusted. The USB key needs to remain connected at all times during license server operation.

Log Output

The command window will show startup information and log the checking out/in events as illustrated below. In this example, two clients are started, and then the one of them is stopped again.

```
C:\Pmod3.5\Start>C:
C:\Pmod3.5\Start>cd "C:\Pmod3.5"
C:\Pmod3.5>.\java\jre\bin\java -Xmx1200M -jar pmtsvr.jar 5000 -ls -d
***
 Started on license [912]
***
License Server [Version 3.501 A  (c) 1996 - 2012 by PMOD
Technologies]
Verbose: true, Secure: false, Compressed: false
***
 Port: 5000
 Started on: PMOD-ASUS/192.168.55.109
 License Server: [ ON ] STANDALONE, Number of Server Licenses: 3
 Memory Assigned: 1160 MB
--> License Server started [Tue Oct 25 15:38:19 CEST 2011] : on port
5000
 [20111025 15:39:27.890] LCS: ADDED CLIENT [192.168.55.102-
192.168.55.102].
 Active LCS clients:
 1) 192.168.55.102-192.168.55.102
 Number of free licenses: 2

 2011.10.25 - 15:39:28 [5000] -> 192.168.55.102 -> GET TS Version ->
3.501

[20111025 15:39:41.156] LCS: ADDED CLIENT [192.168.55.102-
192.168.55.102].
Active LCS clients:
 1) 192.168.55.102-192.168.55.102
 2) 192.168.55.102-192.168.55.102
 Number of free licenses: 1

2011.10.25 - 15:39:41 [5000] -> 192.168.55.102 -> GET TS Version ->
3.501
[20111025 15:39:54.234] LCS Command: REMOVED CLIENT [192.168.55.102-
192.168.55.102]. Active clients:
 1) 192.168.55.102-192.168.55.102
 Number of free licenses: 2
```

Emergency Restart

In the case of connection or license management problems the following procedure is recommended for restoring clean license handling:

1) Stop the license server.

Delete the contents of the *Pmod3.5/properties/system/lcs/lct/* directory.

Start the license server again.

If this procedure is completed within 5 minutes, no shutdown of running PMOD clients is required.

Client Processing on License Server Machine

Although it is not recommended, client processing can be done on the same machine. To do so, a second PMOD installation has to be prepared as follows:

1) Copy Pmod3.5 to Pmod3.5LS. Pmod3.5 will be used for client processing, Pmod3.5LS for license serving.

Ensure that the license file (pstarter.lcs) is copied to Pmod3.5LS/properties/system/lcs.

Remove the license file from Pmod3.5/properties/system/lcs.

Modify Pmod3.5LS/Start/RunLcsSvr.bat to use the new path (Pmod3.5LS). Remove the other .bat files from this Start directory.

Remove RunLcsSvr.bat from Pmod3.5/Start.

Use Windows Switch User to login as different user (dedicated to run the License Server) e.g.: admin.pmod.

Start Pmod3.5LS/Start/RunLcsSvr.bat as admin.pmod user.

Switch back to the standard user and run Pmod3.5/Start/RunPmod.bat. Provide the computer name or the local IP to access the license server.

Please note that you need to provide proper RW privileges:

- admin.pmod - RW access to Pmod3.5LS
- other Pmod users - RW access to Pmod3.5
- all other non-Pmod users - no access to Pmod3.5 nor Pmod3.5LS

In this way the License Server will be running for all users, as long as the computer is not shut down.

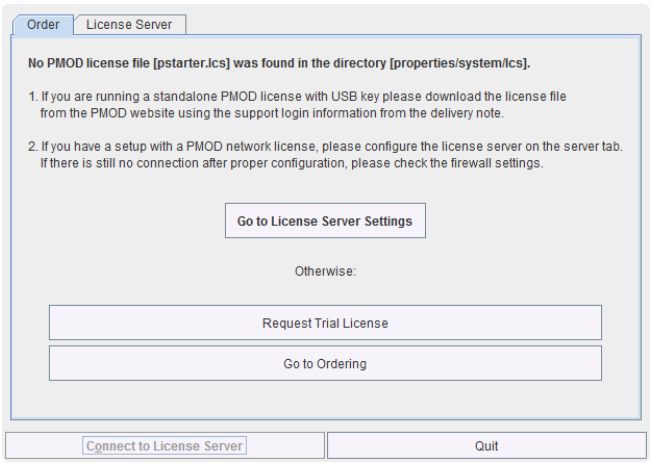
PMOD Network Clients Installation and Configuration

PMOD Software Installation

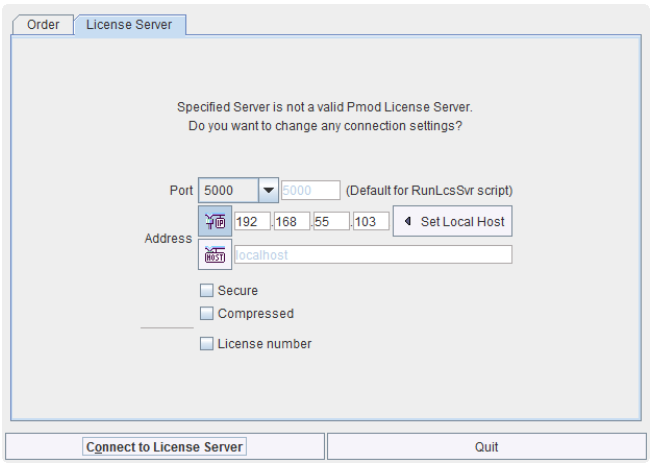
For a PMOD client only the software extraction of the ***Stand-Alone PMOD installation*** (on page 346) is required. *The license file should not be copied.*

Configuration of the License Server

The PMOD client can then be started by the command script **RunPmod.bat** in the *Pmod3.5/Start* directory. Because no license file is found, the following dialog window is shown.

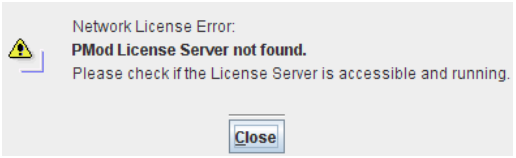


Please select the **Go to License Server Settings** button to open the **License server** panel illustrated below.



Please configure the same **Port** that you have configured for the license server (or transaction server), and specify the server **Address** either by entering its IP address, or by entering its host name. If the process employed for license serving uses compression or encryption, please check the appropriate boxes. If the license server manages several licenses at the same time, enable the **License number** box and enter the number of the license to which you want to connect. Then activate **Yes**.

If the connection succeeds, the dialog window disappears and PMOD starts up. Otherwise the dialog window



is shown. In this case, please check the configuration of the license server and try again.

If a customer has multiple license servers, the proper license server can also be specified in **RunPmod.bat** as a client command line option by:

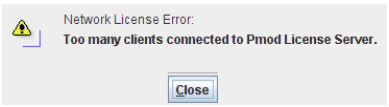
-lsn[<PORT_NO>.<OPTIONAL_LICENSE_NO>@<IP_ADDRESS>]

Starting and Stopping a PMOD Client

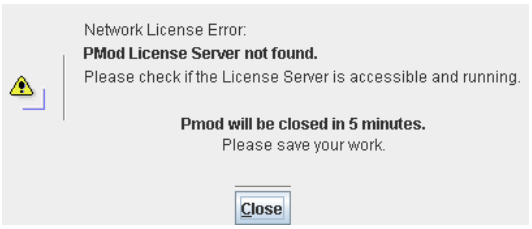
After the license server has been properly configured, PMOD can be started in exactly the same way as with a stand-alone installation. However, for stopping PMOD the main **Quit** button of the ToolBox should always be used. This will initiate a proper shutdown procedure which returns the license to the license server. Otherwise, when simply killing the client, it will take about 15 minutes until the license server diagnoses loss of connection and reclaims the lost license.

Connection Problems

If at client startup no more licenses are available from the license server because all are in use, the **License Server** connection dialog window is shown again to give the user a chance for connecting to a different license server. In case the connection is repeated with the same server following message is shown.



If a connection problem with the license server occurs while working, the **License Server** connection dialog window is shown. If it is not possible to re-establish the connection (for instance by restarting the license server) the following warning is displayed



and after five more minutes the PMOD client is finally stopped.

Combination of License and Database Server

Please note that the license server process is based on the transaction server mechanism used for publishing a database. Therefore, if the user is already running a transaction server process on the server system (RunDbSvr.bat, see *Setting up a Transaction Server* (on page 53)), it is *not* necessary to start a dedicated process (RunLcsSvr.bat) just for the license management. The clients can use the same port for requesting a license as for requesting data from the transaction server.

In this context the transaction server option
`-noLS`: database server only

is relevant. This option should be used when running multiple transaction servers. In this case, only one of the transaction servers should started without `-noLS`, namely the one used for license serving.

Troubleshooting

Error reporting

Internal errors typically leave messages of the form

```
java.lang.NullPointerException
at
pmclass.applications.pmgateway.PMgatewayDefaults.getConvertionSettin
gs(PMgatewayDefaults.java:143)
at
pmclass.applications.pmgateway.PMgatewayFrame.convert(PMgatewayFrame
.java:854)
at
pmclass.applications.pmgateway.PMgatewayFrame.run(PMgatewayFrame.jav
a:911)
at java.lang.Thread.run(Thread.java:484)
```

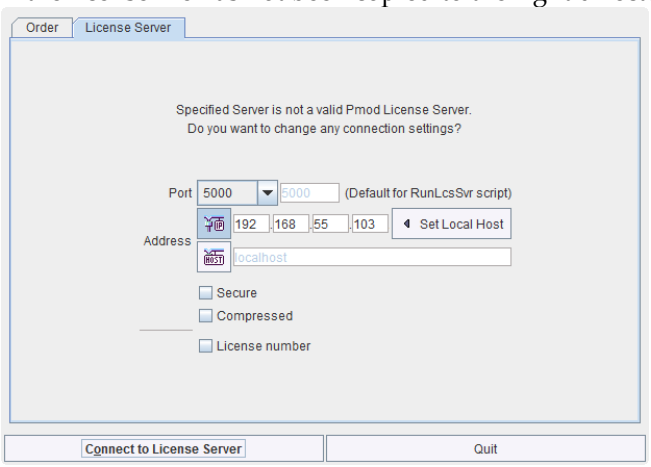
in the command window or the log file.

To allow PMOD Technologies tracking the problem please report the error using the in-built reporting mechanism as described in the problem reporting section. If this is not possible due to a firewall problem please log into the support section on the www.pmod.com website and fill the error message together with a description into the problem report form.

License Errors

Some of the most likely license errors are:

- If the license file has not been copied to the right directory, you will see a message dialog



  Please make sure you copy *pstarter.lcs* to *Pmod3.5/properties/system/lcs.*

- If the license file has been modified somehow, you will see a message *License Error. Invalid license file (2)*
  Please try extracting *pstarter.lcs* again from your e-mail without any modifications.

- If the USB key cannot be interrogated, because it is not connected or because the driver installation is not up to date, you will see an error message *Hardware license key not accessible*, with additional details.

Please make sure that the USB key is connected and the installation was done as described. The driver installation may have to be repeated after an operating system upgrade.

Linux Installation

The installation for all types of PMOD systems starts with the software extraction from the installation DVD. No other installation is required for PMOD network clients. For PMOD standalone systems and PMOD license server systems, the USB protection key drivers must then be installed and the dedicated license file copied to the *properties/system/lcs* folder.

Some parts of the PMOD installation may require root privileges. If your account does not have these rights, please ask your IT support to perform the following installation steps.

Installation Overview

PMOD supports two licensing schemes: stand-alone and network licenses.

Licensing, Stand-alone License

The PMOD software stand-alone licensing mechanism consists of two components:

1) a **USB protection key** (WIBU-Box/RU, WIBU-SYSTEMS AG, *http://www.wibu.com*), and

a license file **pstarter.lcs** (in sub-directory *properties/system/lcs* of the PMOD installation).

During PMOD startup the license information encoded in the USB key is read and compared to that in the license file. Only if the two informations match, startup proceeds. Next is a check whether the PMOD version purchased allows running the currently installed version. If all checks are successful, the PMOD ToolBox appears showing the purchased modules, and processing can start. Note that the USB key must remain in place while running PMOD.

Licensing, Network License

The PMOD network licensing scheme consists of a PMOD license server which manages a pool of purchased licenses, and an arbitrary number of PMOD clients which can check out unused licenses from the server. As soon as the PMOD program on a client is closed, the license is returned to the managed server pool. If the PMOD client crashes for some reason, the license is re-collected to the pool after about 15 minutes. On the other hand, if the license server is stopped, the clients show a warning message to the user and allow to continue work for a few minutes. Then, the clients will be stopped, unless the server has been started again.

On the license server PMOD is installed in the same way as for a stand-alone license with the USB key, but the license file turns it into a license server.

On the clients PMOD is also installed in the standard way, *except* that

- installation of the drivers for the USB protection key is not required;
- no license file is required.

Note the following:

- The license server PMOD installation is only intended for server purposes and not for data processing.
- The license server must be running and the USB key must be connected at all times.
- The license server and the clients must run the same PMOD version.
- It is not required that the license server and the clients have the same operating system.

Java Runtime Environment (JRE)

The entire PMOD software has been programmed in Java and therefore requires an appropriate Java Runtime Environment (JRE) to be executed. During PMOD installation on Linux and Windows systems, an appropriately configured JRE is extracted into the *java* sub-directory of the PMOD installation. This dedicated JRE will then be used for running PMOD. By this controlled environment, PMOD will remain unaffected from changes due to

automatic upgrade procedures on Windows and Linux. Only on MacOSX systems, the built-in JRE will be used.

Installation Steps

The installation of the PMOD software consists of the following steps which should be performed in the proposed sequence. They are explained in detail in the system-specific installation sections.

1) Extraction of the PMOD program files, the JRE, and the example data to the *Pmod3.5* directory in a user-defined directory.
This installation step is required for: **Stand-alone Installation, License Server, Network Clients.**

Installation of the USB protection key drivers for reading the information from the WIBU-Box/RU plugged into the USB port. *Please do not connect the PMOD USB protection key before this installation has been completed.*
This installation step is required for: **Stand-alone Installation, License Server.**

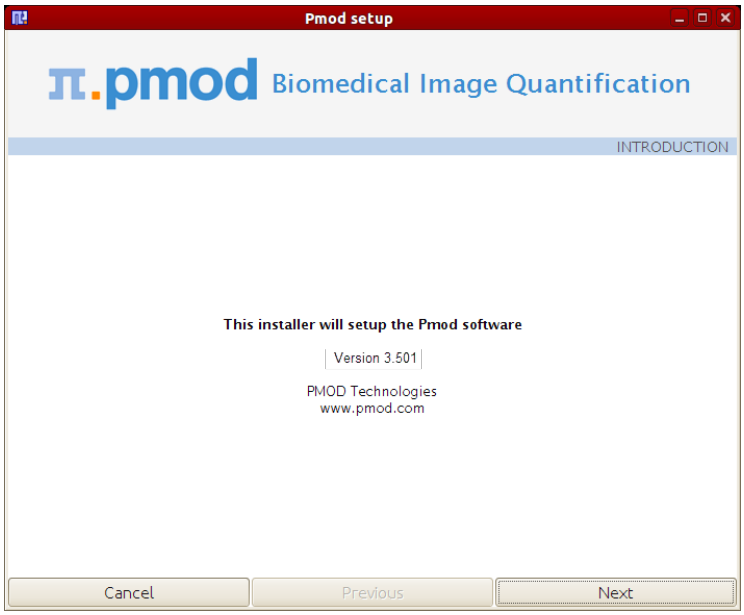
Installation of the PMOD license file *pstarter.lcs*. The license file can be downloaded from the **Support** area of the PMOD ***website http://www.pmod.com/technologies/support/enter-support.php*** after the personalized login (please refer to the delivery note of your PMOD package for login information).
This installation step is required for: **Stand-alone Installation**, **License Server**.

PMOD Software Extraction

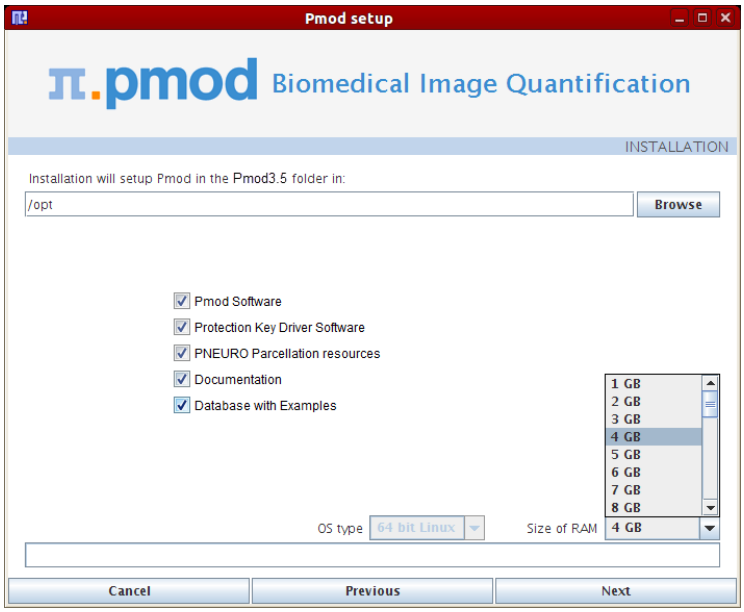
The following software extraction procedure must be performed for standalone PMOD installations, for PMOD servers, and also for all PMOD network clients.

Please begin by inserting the PMOD installation DVD. Then start the installer by executing **RunSetup_32** or **RunSetup_64** in the *Setup/Linux* directory on the DVD by double-clicking, depending on your operating system. New systems are typically 64 Bit, so it is recommended to try **RunSetup_64** first.

The following installation screen appears



Please use **Next** to proceed and accept the license agreement in the appearing dialog window. After activating **Next** the window for configuring the installation appears.



Please perform the following configurations:

Installation Path

Use the **Browse** button to select the parent directory for the installation for which the installing user has writing permissions. There, the installer will create a new directory **Pmod3.5** for the program files and the data. Please make sure that 450MB of free space is available.

Packages

It is recommended to install all four packages, the **Software**, the **Protection Key Driver Software**, the **Documentation**, and the **Example Database**. The **Example Database** requires about 120MB, but will be a great help for getting acquainted with the programs because they provide examples for the the different types of analysis. Furthermore, you will already have a database for storing your data.

Properties of Operating System and RAM

Current operating systems (**OS**) support the 64-Bit capability of new hardware. The main advantage of using a 64-Bit OS is the extended address space for the applications, in this case PMOD. Consequently, the data size is virtually unlimited for a 64-Bit OS (only limited by hardware RAM), while it is limited to <2GB for a 32-Bit system. As there is a clear trend towards rapidly increasing image data sizes, we strongly advise against using 32-Bit systems for PMOD.

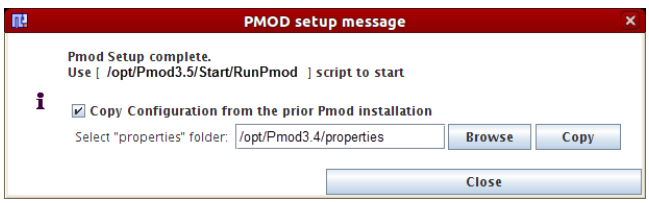
If the operating system of your target computer is 32-Bit, then please set the **OS type** selection to **32-Bit**. Correspondingly, only **Size of RAM** of **1GB** or **2GB** can be selected, preferably **2GB**.

If the operating system of your target computer is 64-Bit, then please set the **OS type** selection to **64-Bit**. In this case, **Size of RAM** can be set to any size. However, if the specified size exceeds the physical RAM, the system will start swapping after RAM space is exhausted and will become very slow. Therefore it is recommended setting **Size of RAM** < physical RAM.

Installation of the PMOD Environment

The installation is started by the **Install** button. The Pmod3.5 directory is created wherein all PMOD-related files are extracted. If the installing user has no write permission in the parent directory, a dialog window appears which reports an installation problem. In this case please change the writing permissions of the installation as root user, or try the installation again using a different installation directory.

At the end of the installation a dialog window is shown. It indicates the command script for starting Pmod3.5, and allows importing the configurations from a prior version. To this end, select the **properties** folder of your prior installation with the **Browse** button as illustrated below, and activate **Copy Configurations**. This import will also copy the license file, so that Pmod3.5 should immediately run with the familiar environment if your license is valid with the Pmod3.5 version.



PMOD Stand-alone License Installation

Install USB Key Drivers

All the files required for the driver installation have been extracted during the installation of the PMOD software and stored in the PMOD *hksetup* sub-directory. For Linux, it includes four installation files, the 32-Bit and 64-Bit installers for RedHat/Fedora as well as Ubuntu/Debian systems. The driver installation should be performed as *root* user.

On Ubuntu/Debian Linux systems double-click **WkRt-Lin32_6.0.501_i386.deb** (32-Bit) or **WkRt-Lin64_6.0.501_amd64.deb** (64-Bit) depending on the architecture of your host system, and then install the package.

Similarly, on RedHat/Fedora Linux systems use **WkRt-Lin32-6.0.501_i386.rpm** (32-Bit) or **WkRt-Lin64-6.0.501_amd64.rpm** (64-Bit). If the installation per double-clicking does not work open a terminal and enter the command

```
cd /opt/Pmod3.5/hksetup/Linux
rpm -i WkRt-Lin64-6.0.501_amd64.rpm
```

(or `rpm -i WkRt-Lin32-6.0.501_i386.rpm`)

If a message *usbutils conflicts with WkRt-Lin-5.20.500-1* occurs on the console, please cancel the installation of WkRt-Lin-5.20.500-1.i386.rpm and enter the command:

```
rpm -e --nodeps usbutils
```

to uninstall conflicting USB support.

If messages occur in the console window indicating a conflict with an older version of the driver please uninstall that prior version (eg. WkRt-Lin-5.10.501-1.i386) by entering the command:

```
rpm -e WkRt-Lin-5.10.501-1.i386
```

After these cleaning procedures try the installation again.

Note: If you experience problems during driver installation, you are recommended downloading the most recent drivers for the WIBU-KEY (Runtime Kit) from ***http://wibu.com/download_user.php*** (***http://wibu.com/download_user.php***) and try the installation again. Also, in some cases, a reboot may be required after driver installation.

License File

The delivery note you have received with the PMOD CD contains account information for logging into the support area of ***www.pmod.com*** (***http://www.pmod.com/technologies/support/enter-support.php***). There you will find a license report, and a button for downloading the license file for your purchased configuration. Please download pstarter.lcs and copy it to the directory *Pmod3.5/properties/system/lcs.*

Important Note: Please do not change pstarter.lcs in any way - a modified license file will not be accepted. Do not open pstarter.lcs in any program, do not rename it, and if you transfer it per FTP, use binary transfer.

Start PMOD

PMOD can now be started with command script **RunPmod** in *Pmod3.5/Start.* Example:

```
!/bin/sh
cd /opt/Pmod3.5
.\java\jre\bin\java -version
.\java\jre\bin\java -Xmx8000M -jar pmod.jar
```

Notes:

The script has been tailored to the installation directory. Therefore, if the Pmod3.5 directory is moved to a different location, the path needs to be adjusted.

The **-Xmx8000M** option specifies the maximum heap memory (8000 MB) that PMOD can allocate. To process large data sets this number should be increased. However, please note that currently there is an operating-system dependent *limitation on 32-Bit operating systems*: only a maximum of 1800M can be allocated, even if the physical RAM size is larger. Increasing -Xmx beyond 1800M might result in an error *Could not reserve enough space for object heap*. Caution: The P3D tool may crash, when the reserved space approaches the physical RAM size.

Change Permission Settings of Directories for writing

To allow other users than root the full usage of PMOD it is important to open some PMOD directories for writing:

```
chmod -R ugo+w /opt/Pmod3.5/properties
chmod -R ugo+w /opt/Pmod3.5/data/
```

There may be other directories you have to open for writing later on, if several users are working with the same PMOD installation.

PMOD Network License Installation

PMOD License Server Installation

PMOD Software Installation

The computer for the PMOD license server doesn't require a high performance, but needs to be running continually. Therefore, a robust, vintage machine is well suited as a PMOD license server. Preferably, it is also dedicated to serving the PMOD license.

To install the PMOD license server first perform the steps described in the ***Stand-alone PMOD Installation*** (on page 360) including copying of the license file and plugging the USB key in.

Multiple Licenses Management

A license server can manage multiple licenses simultaneously. In order to use this feature please rename the different license files (pstarter.lcs) by appending the license numbers

(pstarter860.lcs, pstarter912.lcs, ...) and copy them into the *Pmod3.5/properties/system/lcs* folder.

Starting the License Server

The PMOD license server can then be started by executing the **RunLcsSvr** script in *Pmod3.5*/*Start* containing the following lines

```
!/bin/sh
cd /opt/Pmod3.5
.\java\jre\bin\java -version
.\java\jre\bin\java -Xmx2G -jar pmtsvr.jar 5000 -ls -d
```

The meaning of the command arguments is:
`5000`: IP port over which the license server communicates
`-ls`: license server only, no data sharing
`-d`: verbose output

Note: The script has been tailored to the installation directory. Therefore, if the Pmod3.5 directory is moved to a different location, the path needs to be adjusted.

Log Output

The command window will show startup information and log the checking out/in events as illustrated below. In this example, two clients are started, and then the one of them is stopped again.

```
MD03845:/opt # Pmod3.5/Start/RunLcsSvr
***
***
 Started on license [912]
***
License Server [Version 3.501 A  (c) 1996 - 2011 by PMOD
Technologies]
Verbose: true, Secure: false, Compressed: false
***
 Port: 5000
 Started on: PMOD-ASUS/192.168.55.109
 License Server: [ ON ] STANDALONE, Number of Server Licenses: 3
 Memory Assigned: 1160 MB
--> License Server started [Tue Oct 25 15:38:19 CEST 2011] : on port
5000
 [20111025 15:39:27.890] LCS: ADDED CLIENT [192.168.55.102-
192.168.55.102].
 Active LCS clients:
 1) 192.168.55.102-192.168.55.102
 Number of free licenses: 2

 2011.10.25 - 15:39:28 [5000] -> 192.168.55.102 -> GET TS Version ->
3.501

[20111025 15:39:41.156] LCS: ADDED CLIENT [192.168.55.102-
192.168.55.102].
Active LCS clients:
 1) 192.168.55.102-192.168.55.102
 2) 192.168.55.102-192.168.55.102
```

```
 Number of free licenses: 1

2011.10.25 - 15:39:41 [5000] -> 192.168.55.102 -> GET TS Version ->
3.501
[20111025 15:39:54.234] LCS Command: REMOVED CLIENT [192.168.55.102-
192.168.55.102]. Active clients:
 1) 192.168.55.102-192.168.55.102
 Number of free licenses: 2
```

Emergency Restart

In the case of connection or license management problems the following procedure is recommended for restoring clean license handling:

1) Stop the license server.

Delete the contents of the *Pmod3.5/properties/system/lcs/lct/* directory.

Start the license server again.

If this procedure is completed within 5 minutes, no shutdown of running PMOD clients is required.

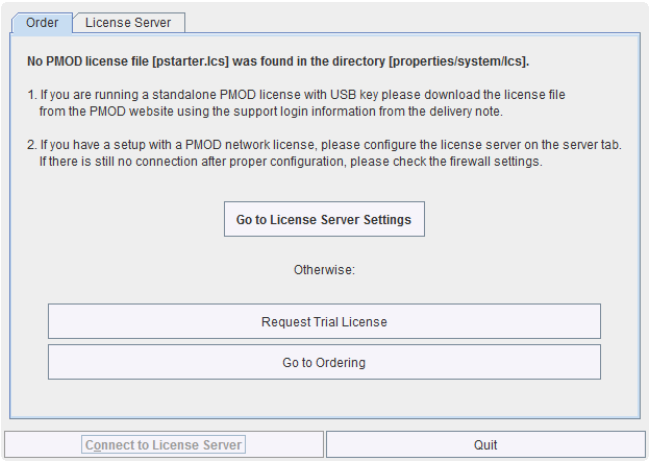
PMOD Network Clients Installation and Configuration

PMOD Software Installation

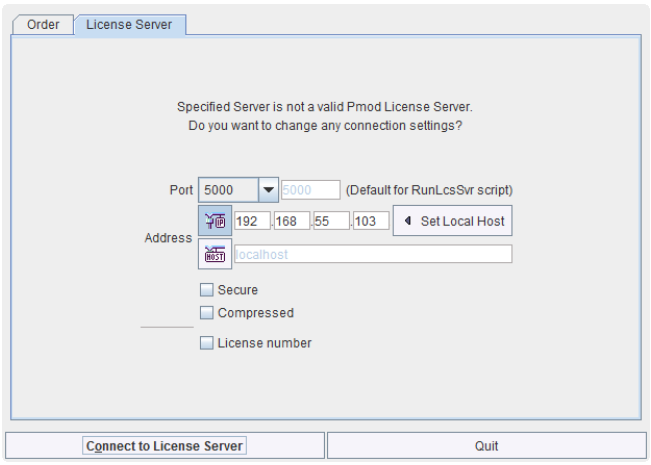
For a PMOD client only the software extraction of the ***Stand-Alone PMOD installation*** (on page 346) is required. *The license file should not be copied.*

Configuration of the License Server

The PMOD client can the be started by the command script **RunPmod** in the *Pmod3.5/Start* directory. As no license file is found, the following dialog window is shown.

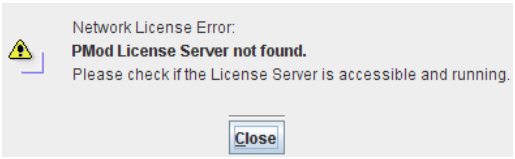


Please select the **Go to License Server Settings** button to open the License server panel illustrated below.



Please configure the same **Port** that you have configured for the license server (or transaction server), and specify the server **Address** either by entering its IP address, or by entering its host name. If the process employed for license serving uses compression or encryption, please check the appropriate boxes. If the license server manages several licenses at the same time, enable the **License number** box and enter the number of the license to which you want to connect. Then activate **Yes**.

If the connection succeeds, the dialog window disappears and PMOD starts up. Otherwise the dialog



is shown. In this case, please check the configuration of the license server and try again.

If a customer has multiple license servers, the proper license server can also be specified in **RunPmod** as a client command line option by:
-lsn[<PORT_NO>.<OPTIONAL_LICENSE_NO>@<IP_ADDRESS>]

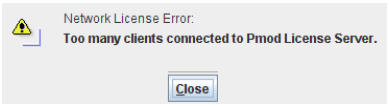
Starting and Stopping a PMOD Client

After the license server has been properly configured, PMOD can be started in exactly the same way as with a stand-alone installation. However, for stopping PMOD the main **Quit** button of the ToolBox should always be used. This will initiate a proper shutdown procedure which returns the license to the license server. Otherwise, when simply killing the client, it will take about 15 minutes until the license server diagnoses loss of connection and reclaims the lost license.

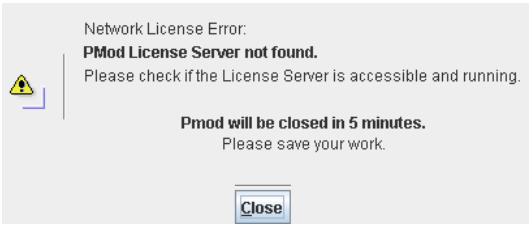
Connection Problems

If at client startup no more licenses are available from the license server because all are in use, the **License Server** connection dialog window is shown again to give the user a chance

for connecting to a different license server. In case the connection is repeated with the same server following message is shown.



If a connection problem with the license server occurs while working, the **License Server** connection dialog window is shown. If it is not possible to re-establish the connection (for instance by restarting the license server) the following warning is displayed.



and after five more minutes the PMOD client is finally stopped.

Combination of License and Database Server

Please note that the license server process is based on the transaction server mechanism used for publishing a database. Therefore, if the user is already running a transaction server process on the server system (RunDbSvr, see ***Setting up a Transaction Server*** (on page 53)), it is *not* necessary to start a dedicated process (RunLcsSvr) just for the license management. The clients can use the same port for requesting a license as for requesting data from the transaction server.

In this context the transaction server option
`-noLS`: database server only
is relevant. This option should be used when running multiple transaction servers. In this case, only one of the transaction servers should started without `-noLS`, namely the one used for license serving.

Troubleshooting

Error reporting

Internal errors typically leave messages of the form

```
java.lang.NullPointerException
at
pmclass.applications.pmgateway.PMgatewayDefaults.getConvertionSettin
gs(PMgatewayDefaults.java:143)
at
pmclass.applications.pmgateway.PMgatewayFrame.convert(PMgatewayFrame
.java:854)
at
pmclass.applications.pmgateway.PMgatewayFrame.run(PMgatewayFrame.jav
a:911)
at java.lang.Thread.run(Thread.java:484)
```

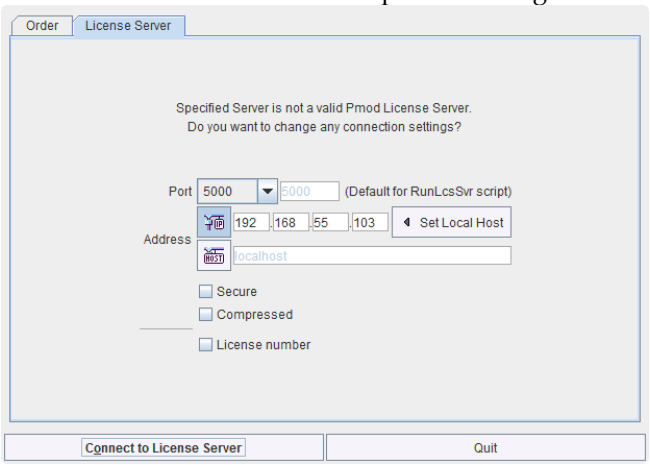
in the command window or the log file.

To allow PMOD Technologies tracking the problem please report the error using the in-built reporting mechanism as described in the problem reporting section. If this is not possible due to a firewall problem please log into the support section on the www.pmod.com website and fill the error message together with a description into the problem report form.

License Errors

Some of the most likely license errors are:

- If the license file has not been copied to the right directory, you will see a message



  Please copy *pstarter.lcs* to *Pmod3.5/properties/system/lcs*

- If the license file has been modified somehow, you will see a message *License Error. Invalid license file (2)*
  Please try to extract *pstarter.lcs* again from your e-mail without any modifications.

- If the USB key cannot be read because it is not connected or because the driver installation is not up to date, you will see an error message *Hardware license key not accessible* with additional details.
  Please make sure that the USB key is connected and the installation was done as described. The installation may have to be repeated after an operating system upgrade.

- In order to be able to run PMOD with the USB key, the JNI must be found during startup. To this end the environment variable LD_LIBRARY_PATH must contain the path */usr/lib*. The most appropriate location to define it would be in a global definition file, eg */etc/csh.cshrc*. If not already defined so, add

```
setenv LD_LIBRARY_PATH /usr/lib
```

Mac OS X Installation

The installation for all types of PMOD systems starts with the software extraction from the installation DVD. No other installation is required for PMOD network clients. For PMOD standalone systems and PMOD license server systems, the USB protection key drivers must then be installed and the dedicated license file copied to the *properties/system/lcs* folder.

Some parts of the PMOD installation may require administrator privileges. If your account does not have these rights, please ask your IT support to perform the following installation steps.

Installation Overview

PMOD supports two licensing schemes: stand-alone and network licenses.

Licensing, Stand-alone License

The PMOD software stand-alone licensing mechanism consists of two components:

1) a **USB protection key** (WIBU-Box/RU, WIBU-SYSTEMS AG, *http://www.wibu.com*), and

a license file **pstarter.lcs** (in sub-directory *properties/system/lcs* of the PMOD installation).

During PMOD startup the license information encoded in the USB key is read and compared to that in the license file. Only if the two informations match, startup proceeds. Next is a check whether the PMOD version purchased allows running the currently installed version. If all checks are successful, the PMOD ToolBox appears showing the purchased modules, and processing can start. Note that the USB key must remain in place while running PMOD.

Licensing, Network License

The PMOD network licensing scheme consists of a PMOD license server which manages a pool of purchased licenses, and an arbitrary number of PMOD clients which can check out unused licenses from the server. As soon as the PMOD program on a client is closed, the license is returned to the managed server pool. If the PMOD client crashes for some reason, the license is re-collected to the pool after about 15 minutes. On the other hand, if the license server is stopped, the clients show a warning message to the user and allow to continue work for a few minutes. Then, the clients will be stopped, unless the server has been started again.

On the license server PMOD is installed in the same way as for a stand-alone license with the USB key, but the license file turns it into a license server.

On the clients PMOD is also installed in the standard way, *except* that

- installation of the drivers for the USB protection key is not required;
- no license file is required.

Note the following:

- The license server PMOD installation is only intended for server purposes and not for data processing.
- The license server must be running and the USB key must be connected at all times.
- The license server and the clients must run the same PMOD version.
- It is not required that the license server and the clients have the same operating system.

Java Runtime Environment (JRE)

The entire PMOD software has been programmed in Java and therefore requires an appropriate Java Runtime Environment (JRE) to be executed. During PMOD installation on Linux and Windows systems, an appropriately configured JRE is extracted into the *java* sub-directory of the PMOD installation. This dedicated JRE will then be used for running PMOD. By this controlled environment, PMOD will remain unaffected from changes due to

automatic upgrade procedures on Windows and Linux. Only on MacOSX systems, the built-in JRE will be used.

Installation Steps

The installation of the PMOD software consists of the following steps which should be performed in the proposed sequence. They are explained in detail in the system-specific installation sections.

1) Extraction of the PMOD program files, the JRE, and the example data to the *Pmod3.5* directory in a user-defined directory.
This installation step is required for: **Stand-alone Installation, License Server, Network Clients.**

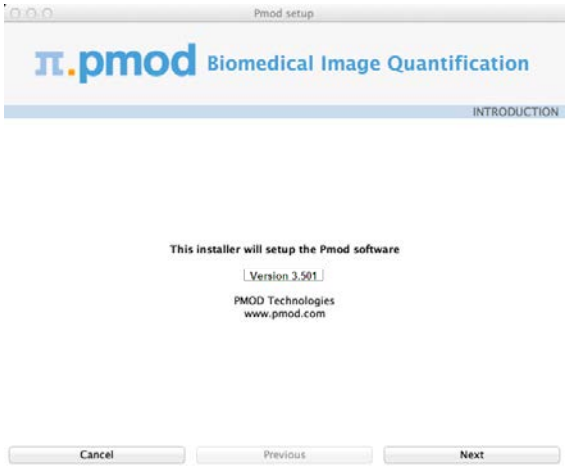
Installation of the USB protection key drivers for reading the information from the WIBU-Box/RU plugged into the USB port. *Please do not connect the PMOD USB protection key before this installation has been completed.*
This installation step is required for: **Stand-alone Installation, License Server.**

Installation of the PMOD license file *pstarter.lcs*. The license file can be downloaded from the **Support** area of the PMOD ***website http://www.pmod.com/technologies/support/enter-support.php*** after the personalized login (please refer to the delivery note of your PMOD package for login information).
This installation step is required for: **Stand-alone Installation**, **License Server**.

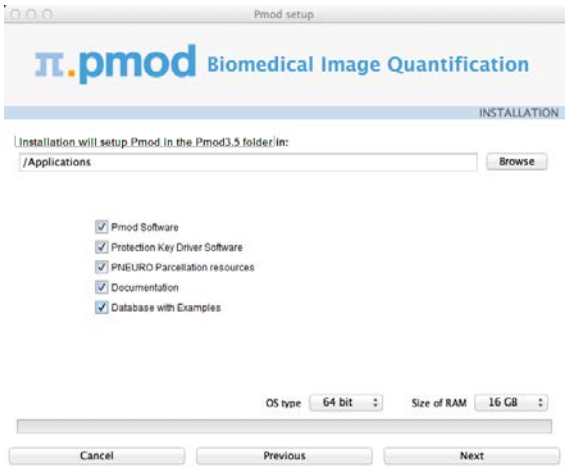
PMOD Software Extraction

The following software extraction procedure must be performed for standalone PMOD installations, for PMOD servers, and also for all PMOD network clients.

Please begin by inserting the PMOD installation DVD. Then start the installer by double-clicking **seup.jar** in the *pmod* directory on the DVD. The following installation screen appears.



Please use **Next** to proceed and accept the license agreement in the appearing dialog window. After activating **Next** the window for configuring the installation appears.



Please perform the following configurations:

Installation Path

Use the **Browse** button to select the parent directory for the installation. There, the installer will create a new directory **Pmod3.5** for the program files and the data. Please make sure that 450MB of free space is available.

Packages

It is recommended to install all three packages, the **Software**, the **Documentation**, and the **Example Database**. The **Example Database** requires about 120MB, but will be a great help for getting acquainted with the programs because they provide examples for the the different types of analysis. Furthermore, you will already have a database for storing your data.

Properties of Operating System and RAM

Current operating systems (**OS**) support the 64-Bit capability of new hardware. The main advantage of using a 64-Bit OS is the extended address space for the applications, in this case PMOD. Consequently, the data size is virtually unlimited for a 64-Bit OS (only limited by hardware RAM), while it is limited to <2GB for a 32-Bit system. As there is a clear trend towards rapidly increasing image data sizes, we strongly advise against using 32-Bit systems for PMOD.

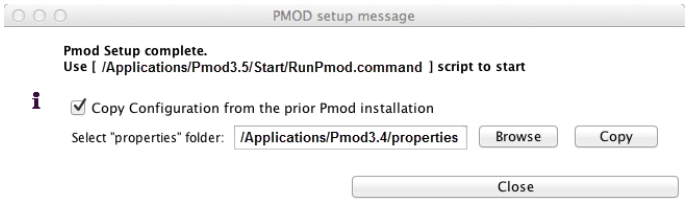
If the operating system of your target computer is 64-Bit, then please set the **OS type** selection to **64-Bit**. In this case, **Size of RAM** can be set to any size. However, if the specified size exceeds the physical RAM, the system will start swapping after RAM space is exhausted and will become very slow. Therefore it is recommended setting **Size of RAM** < physical RAM.

Note: As opposed to other platforms, the Java environment of the Mac OS X operating system is used. Mac OS X 10.6 and later are a 64-Bit operating systems, so please select **64-Bit** for those versions.

Installation of the PMOD Environment

The installation is started by the **Install** button. The Pmod3.5 directory is created wherein all PMOD-related files are extracted. If the installing user has no write permission in the parent directory, a dialog window appears which reports an installation problem. In this case please change the writing permissions of the installation as root user, or try the installation again using a different installation directory.

At the end of the installation a dialog window is shown. It indicates the command script for starting Pmod3.5, and allows importing the configurations from a prior version. To this end, select the **properties** folder of your prior installation with the **Browse** button as illustrated below, and activate **Copy Configurations**. This import will also copy the license file, so that Pmod3.5 should immediately run with the familiar environment if your license is valid with the Pmod3.5 version

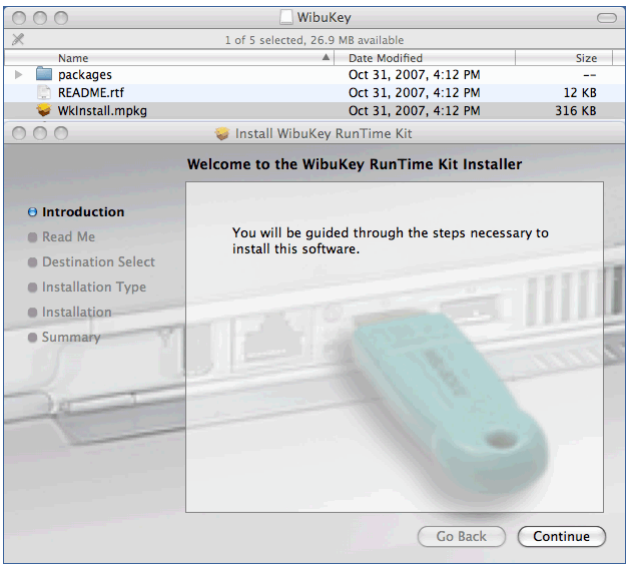


PMOD Stand-alone License Installation

Install USB Key Drivers

All the files required for the driver installation have been extracted during the installation of the PMOD software and stored in the PMOD directory tree. Browse to the directory */Applications/Pmod3.5/hksetup/MacOSX*

First double-click **WkRuntimeUser_6.0.501.dmg**, then **WkInstall.pkg,** and perform a standard installation



Note: If you experience problems during driver installation, you are recommended downloading the most recent drivers for the WIBU-KEY (Runtime Kit) from ***http://wibu.com/download_user.php*** (***http://wibu.com/download_user.php***) and try the installation again. Also, in some cases, a reboot may be required after driver installation.

License File

The delivery note you have received with the PMOD CD contains account information for logging into the support area of ***www.pmod.com*** (***http://www.pmod.com/technologies/support/enter-support.php***). There you will find a license report, and a button for downloading the license file for your purchased configuration. Please download pstarter.lcs and copy it to the directory */Applications/Pmod3.5/properties/system/lcs.*

Important Note: Please do not change pstarter.lcs in any way - a modified license file will not be accepted. Do not open pstarter.lcs in any program, do not rename it, and if you transfer it per FTP, use binary transfer.

Start PMOD

PMOD can now be started by double-clicking the **RunPmod.command** script in */Applications/Pmod3.5/Start/*. Depending on the selected configuration it contains the following commands:

32-Bit (= JRE 1.5):

```
cd /Applications/Pmod3.5
java=/System/Library/Frameworks/JavaVM.framework/Versions/1.5/Home/b
in/java
$java -version
$java -Xmx1800M -jar pmod.jar
```

64-Bit (= JRE 1.6):

```
cd /Applications/Pmod3.5
java=/System/Library/Frameworks/JavaVM.framework/Versions/1.6/Home/b
in/java
$java -version
$java -Xmx8000M -jar pmod.jar
```

Alternatively, the script can be dragged once from the finder to the Mac OS X taskbar to create a shortcut. From then on, PMOD can be started using this shortcut.

Notes:

The script has been tailored to the installation directory. Therefore, if the Pmod3.5 directory is moved to a different location, the path needs to be adjusted.

The **-Xmx8000M** option specifies the maximum heap memory (8000 MB) that PMOD can allocate. To process large data sets this number should be increased. However, please note that currently there is an operating-system dependent *limitation on 32-Bit operating systems*: only a maximum of 1800M can be allocated, even if the physical RAM size is larger.

Increasing -Xmx beyond 1800M might result in an error *Could not reserve enough space for object heap*. Caution: The P3D tool may crash, when the reserved space approaches the physical RAM size.

Change Permission Settings of Directories for writing

To allow other users than root the full usage of PMOD it is important to open some key PMOD directories for writing:

```
chmod -R ugo+w /Applications/Pmod3.5/properties
chmod -R ugo+w /Applications/Pmod3.5/data
```

There may be other directories you have to open for writing later on, if several users are working with the same PMOD installation.

PMOD Network License Installation

PMOD License Server Installation

PMOD Software Installation

The computer for the PMOD license server doesn't require a high performance, but needs to be running continually. Therefore, a robust, vintage machine is well suited as a PMOD license server. Preferably, it is also dedicated to serving the PMOD license, because the license server is a standard process rather than a Windows service.

To install the PMOD license server first perform the steps described in the ***Stand-alone PMOD Installation*** (on page 371) including copying of the license file and plugging the USB key in.

Multiple Licenses Management

A license server can manage multiple licenses simultaneously. In order to use this feature please rename the different license files (pstarter.lcs) by appending the license numbers (pstarter860.lcs, pstarter912.lcs, ...) and copy them into the *Pmod3.5/properties/system/lcs* folder.

Starting the License Server

The PMOD license server can then be started by executing the **RunLcsSvr.command** script in */Applications/Pmod3.5/Start* containing the following lines (64-Bit version)

```
cd /Applications/Pmod3.5
java=/System/Library/Frameworks/JavaVM.framework/Versions/1.6/Home/b
in/java
$java -Xmx2G -jar pmtsvr.jar 5000 -ls -d
```

The meaning of the command arguments is:

`5000`: IP port over which the license server communicates
`-ls`: license server only, no data sharing
`-d`: verbose output

Note: The script has been tailored to the installation directory. Therefore, if the Pmod3.5 directory is moved to a different location, the path needs to be adjusted.

Log Output

The command window will show startup information and log the checking out/in events as illustrated below. In this example, two clients are started, and then the one of them is stopped again.

```
MD03845:/Applications/Pmod3.5/Start/RunLcsSvr.command
***
 Started on license [912]
***
License Server [Version 3.501 A  (c) 1996 - 2011 by PMOD
Technologies]
Verbose: true, Secure: false, Compressed: false
***
 Port: 5000
 Started on: PMOD-ASUS/192.168.55.109
 License Server: [ ON ] STANDALONE, Number of Server Licenses: 3
 Memory Assigned: 1160 MB
--> License Server started [Tue Oct 25 15:38:19 CEST 2011] : on port
5000
 [20111025 15:39:27.890] LCS: ADDED CLIENT [192.168.55.102-
192.168.55.102].
 Active LCS clients:
 1) 192.168.55.102-192.168.55.102
 Number of free licenses: 2

 2011.10.25 - 15:39:28 [5000] -> 192.168.55.102 -> GET TS Version ->
3.501

[20111025 15:39:41.156] LCS: ADDED CLIENT [192.168.55.102-
192.168.55.102].
Active LCS clients:
 1) 192.168.55.102-192.168.55.102
 2) 192.168.55.102-192.168.55.102
 Number of free licenses: 1

2011.10.25 - 15:39:41 [5000] -> 192.168.55.102 -> GET TS Version ->
3.501
[20111025 15:39:54.234] LCS Command: REMOVED CLIENT [192.168.55.102-
192.168.55.102]. Active clients:
 1) 192.168.55.102-192.168.55.102
 Number of free licenses: 2
```

Emergency Restart

In the case of connection or license management problems the following procedure is recommended for restoring clean license handling:

1) Stop the license server.

Delete the contents of the *Pmod3.5/properties/system/lcs/lct/* directory.

Start the license server again.

If this procedure is completed within 5 minutes, no shutdown of running PMOD clients is required.

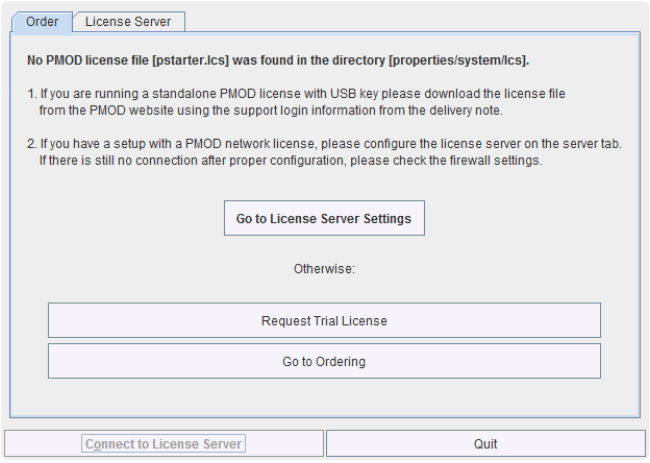
PMOD Network Clients Installation and Configuration

PMOD Software Installation

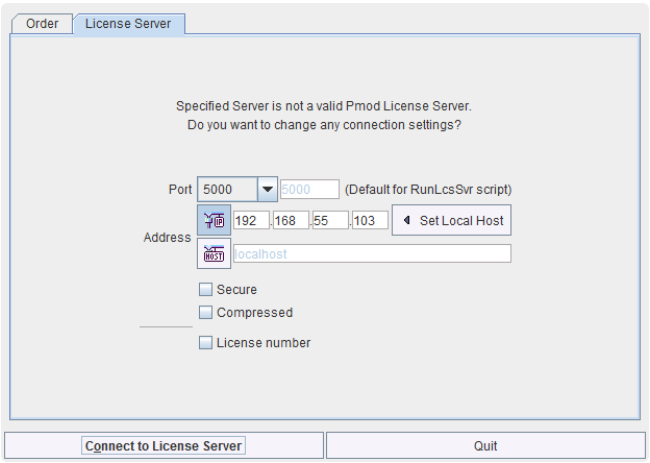
For a PMOD client only the software extraction of the ***Stand-Alone PMOD installation*** (on page 346) is required. *The license file should not be copied.*

Configuration of the License Server

The PMOD client can then be started by the command script **RunPmod.command** in the *Pmod3.5/Start* directory. As no license file is found, the following dialog window is shown.



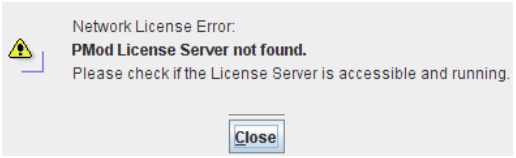
Please select the **Go to License Server Settings** button to open the License server panel illustrated below.



Please configure the same **Port** that you have configured for the license server (or transaction server), and specify the server **Address** either by entering its IP address, or by entering its host name. If the process employed for license serving uses compression or encryption, please check the appropriate boxes. If the license server manages several licenses at the same

time, enable the **License number** box and enter the number of the license to which you want to connect. Then activate **Yes**.

If the connection succeeds, the dialog window disappears and PMOD starts up. Otherwise the dialog



is shown. In this case, please check the configuration of the license server and try again.

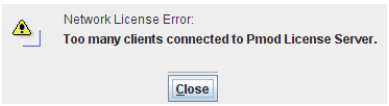
If a customer has multiple license servers, the proper license server can also be specified in **RunPmod.command** as a client command line option by:
-lsn[<PORT_NO>.<OPTIONAL_LICENSE_NO>@<IP_ADDRESS>]

Starting and Stopping a PMOD Client

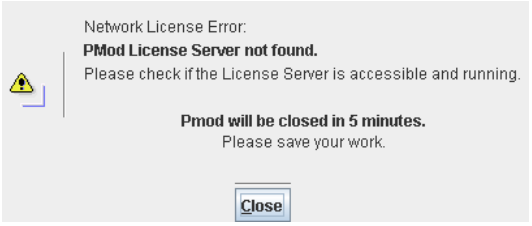
After the license server has been properly configured, PMOD can be started in exactly the same way as with a stand-alone installation. However, for stopping PMOD the main **Quit** button of the ToolBox should always be used. This will initiate a proper shutdown procedure which returns the license to the license server. Otherwise, when simply killing the client, it will take about 15 minutes until the license server diagnoses loss of connection and reclaims the lost license.

Connection Problems

If at client startup no more licenses are available from the license server because all are in use, the **License Server** connection dialog window is shown again to give the user a chance for connecting to a different license server. In case the connection is repeated with the same server following message is shown.



If a connection problem with the license server occurs while working, the **License Server** connection dialog window is shown. If it is not possible to re-establish the connection (for instance by restarting the license server) the following warning is displayed



and after five more minutes the PMOD client is finally stopped.

Combination of License and Database Server

Please note that the license server process is based on the transaction server mechanism used for publishing a database. Therefore, if the user is already running a transaction server process on the server system (RunDbSvr.command, see ***Setting up a Transaction Server*** (on page 53)), it is *not* necessary to start a dedicated process (RunLcsSvr.command) just for the license management. The clients can use the same port for requesting a license as for requesting data from the transaction server.

In this context the transaction server option
`-noLS`: database server only
is relevant. This option should be used when running multiple transaction servers. In this case, only one of the transaction servers should started without `-noLS`, namely the one used for license serving.

Troubleshooting

Error reporting

Internal errors typically leave messages of the form

```
java.lang.NullPointerException
at
pmclass.applications.pmgateway.PMgatewayDefaults.getConvertionSettin
gs(PMgatewayDefaults.java:143)
at
pmclass.applications.pmgateway.PMgatewayFrame.convert(PMgatewayFrame
.java:854)
at
pmclass.applications.pmgateway.PMgatewayFrame.run(PMgatewayFrame.jav
a:911)
at java.lang.Thread.run(Thread.java:484)
```

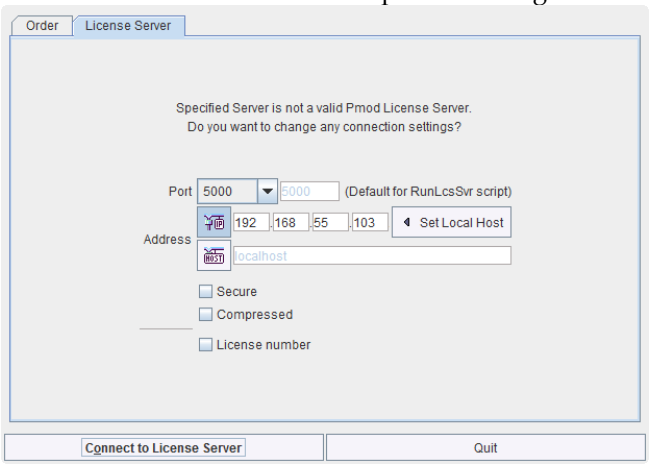
in the command window or the log file.

To allow PMOD Technologies tracking the problem please report the error using the in-built reporting mechanism as described in the problem reporting section. If this is not possible due to a firewall problem please log into the support section on the www.pmod.com website and fill the error message together with a description into the problem report form.

License Errors

Some of the most likely license errors are:

- If the license file has not been copied to the right directory, you will see a message



  Please copy *pstarter.lcs* to */Applications/Pmod3.5/*properties/system/lcs

- If the license file has been modified somehow, you will see a message *License Error. Invalid license file (2)*
  Please try to extract *pstarter.lcs* again from your e-mail without any modifications.

- If the USB key cannot be read because it is not connected or because the driver installation is not up to date, you will see an error message *Hardware license key not accessible* with additional details.
  Please make sure that the USB key is connected and the installation was done as described. The installation may have to be repeated after an operating system upgrade.

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