PMOD Release Notes

Version 3.2

π.pmod

PMOD Technologies

Release Notes of PMOD Software

Maintenance Builds of Release 3.2

Build 8 Dec 1, 2011	▸ VOIs: Speed improvement in cases where statistics and TAC updating is enabled. ▸ Units: %ID/cc added (percent injected dose per milliliter). This unit can be set, but the images cannot be converted from kBq/cc to %ID/cc within PMOD. ▸ Database: Images with size >5.5GB can now be saved. ▸ DICOM: Optimized loading of series containing multiple multi-frame objects. ▸ PFUS: In batch mode, some output format settings were ignored. ▸ User name in ATL version: The name could have changed when entering/exiting the Config facility.
Build 7 July 28, 2011	▸ DICOM RTSTRUCT (Radiotherapy structure set, RTSS): Improved handling of dicom objects with wrong fmi version specified in the header. Important for reading of Oncentra Master Plan RTSS objects. Improved UID handling when saving RTSS objects. ▸ DICOM: Fixed a problem with reading DICOM images with odd slice length in bytes (odd number of pixels and 8-Bit pixel representation). ▸ DICOM: Support for enhanced ultrasound images added. ▸ Interfile: Added support for loading 4-Byte unsigned integer image data. Capital characters in label strings are interpreted correctly. ▸ VOIs: Empty VOIs were used for labeling scatter plots and box plots. ▸ Screen capture: Representation of VOIs and the orthogonal crosshair improved.
Build 6 May 12, 2011	▸ PKIN: Initial values for blood models improved. ▸ PXMOD: If loaded protocol files contain a model not contained in the list of configured models, the needed model is automatically added to the list. ▸ VOIs: Improved synchronization of the orthogonal planes when clicking at a VOI. ▸ Fusion in PVIEW: There is now a choice whether reslicing for fusion should be relative to the origins or relative to the volume centers. ▸ PFUS: A bug fixed in the image algebra which resulted in the re-arrangement of the selected series after the results calculation and in an inappropriate naming. ▸ PFUS: Units of image algebra results adjusted according to the operation. ▸ DICOM: Improved reading of images from YAP-(S) PET systems. ▸ Study UID when saving derived image series: a new UID is created when patient or study info is modified or on user request. ▸ Loader for new native image file format: Varian FDF for micro MR systems (FDF - Flexible Data Format). ▸ Database: Integrity check improved. It is now also able to check the existence of the referenced files. ▸ Analyze Object Maps: Improved error handling in the case of inconsistent headers.

	▸ PALZ: Fixed a problem with calculating T-sum for image data missing part of the brain. The problem occured in version 3.1 and 3.2 prior to build 6.
	▸ Median Filter: The filter had no effect when called interactively from the tools.
Build 5 March 23, 2011	▸ Status check: The status check in the ToolBox now not only reports the availability of an update, but also the status of all transaction servers as well as the available memory.
	▸ PFUS: A new button for inverting the current transformation which may have been obtained by the combination of multiple transformations, including a normalization. For instance, if a PET has been matched to an MRI, and the MRI normalized to a template, the inverse of the combined transformation can be calculated. It will allow to transform VOIs from the template space to the PET space in a single operation.
	▸ PFUS: Fixed a problem with template loading which could result in a crash.
	▸ PFUS: Fixed a problem with using the inverse of a rigid transformations in a matrix combination.
	▸ PXMOD: Several changes to improve the overall operation.
	▸ PXMOD: The SRTM2 and BPnd (6 methods) models use SRTM from PKIN for the determination of k_2'. Due to the restriction of $R_1 <= 1$ the estimated k_2' was sometimes not optimal. This was corrected, and additionally k_2' is now determined with random fitting (N=20).
	▸ PKIN, Ito Plot: The Vt and Vtnd values were interchanged, and also the K_1 and K_1' values. The BPnd calculation had been missing.
	▸ PKIN: The standard deviations of slope and intercept were incorrectly calculated for the linear plots: Logan, Logan NonInvasive, Patlak, Patlak NonInvasive, RE-GP.
	▸ PKIN, Details panel: The panel contents was not always refreshed when switching regions.
	▸ MicroPET: "SPECT multiprojection acquisition" was added to the list of supported modes.
	▸ DICOM save: There was a problem when saving images without orientations that were processed by a mirror operation.
	▸ DICOM C-STORE: A problem occurred if the target DICOM server did not support the object to be sent.
	▸ DICOM: The saving of incomplete data (resulting from could interrupted loading) could cause a problem.
	▸ VOI: The size of object VOIs in the properties was a factor 2 too small.
	▸ VOI: The isocontouring is now applied to all selected contours of a VOI, not only the first in the list.
	▸ VOI: When pasting a VOI , its color is now changed to the color of the target VOI.
	▸ Atlas Template created from VOIs: If the name contained a space the loading failed.
	▸ PVIEW: In Compare layouts with only 1 or two rows the "Capture All" button has been added.
	▸ Component saving: Replacement of special characters in the exported component

	names is now optional, controlled by a checkbox.
	⏩ 3D: An error in texturing a static VR by a dynamic study was fixed.
	⏩ 3D: Newly saved protocols were unreadable.
Build 4 Jan 4, 2011	⏩ DICOM Server: Revision of message handling for clearer log output.
	⏩ DICOM: Support added for non-standard scaling factors in Bioscan data.
	⏩ File formats: Fix for a problem which occurred reading unsigned short values bigger than 32k.
	⏩ File formats: When multiple graphics files were loaded the first file was populated over all slices.
	⏩ VOI outlining: The outlining of a mask image now works on the selected frame instead of the first one.
	⏩ Bug fix of the origins which occurred in rotations and anatomical reformatting. The problem was only notable after saving and reloading.
Build 3 Dec. 8, 2010	⏩ PKIN: The axis labeling on the Blood tab was wrong for some models such as the Logan Plot.
	⏩ PKIN: The default setting for noise generation in Monte Carlo simulations was set to Model only.
	⏩ PBAS: The series date and time were added to the merging tool as an additional sorting criterion.
	⏩ PBAS: Fix for the origin location during some geometrical operations at loading such as rotations and in some conditions of anatomical reorientations.
	⏩ Database: Some data (Philips and some Enhanced objects) with additional units made PMOD freeze.
	⏩ Database: Scripts with a mySQL root password could not connect to the database.
	⏩ Database: There were two problems in the generation of transaction server scripts: A mySQL database could not be tested, and the script could contain a port number other than the defined one.
	⏩ Database: Image comment no more used to create Series comment when saved to database because of problems with line feeds.
	⏩ Fixed a bug which caused imageHistories being saved in the database.
	⏩ Database: Component name length increased to 15 characters.
	⏩ ATL: Selection of the audit trail database added, for instance to choose among annual databases.
	⏩ ATL: The report printing was restricted to a maximum of 100 pages.
	⏩ DICOM Server: shows the memory allocation and the file name of the log if the output is redierected (-o argument in command line).
	⏩ DICOM: Fixed a timing problem when there was a zone offset in the time string.
	⏩ MicroPET: Fixed a problem with the recognition of the nCi/cc unit.
	⏩ Study date added to the aggregation of voiStat files.
Build 2 Nov. 4, 2010	⏩ Database: Fix of a problem with the study time which occurred if there were fractional seconds in the DICOM file to be saved.
	⏩ DICOM: Fix of a problem when reading Enhanced DICOM objects containing a single slice only.

	‣ Alphabetical sorting of the Projects and Diagnosis lists.
	‣ Added configuration switch whether to include the patient name for the output filenames of batch operations.
Build 1 Oct. 27, 2010	‣ Initial upload of 3.2 version.

Product Release 3.2

The 3.2 release incorporates many improvements with the following focuses:

‣ Complete work-flow oriented revision of the PXMOD tool. Additionally, the image fusion tool is directly integrated into PXMOD to support the pixel-oriented comparison of parametric maps.

‣ Support for various automated partial-volume correction (PVC) methods. A VOI-based approach implements Rousset's GTM method. The VOIs can be manually outlined or automatically derived from standard VOI templates. A brain MRI based approach implements the method proposed by Muller-Gartner. It includes the required PET-MR matching as well as the MRI segmentation without the need for any user interaction.

‣ Ability to calculate and apply the inverse of all transforms (rigid and elastic) calculated in the fusion tool. Furthermore, VOIs can now also be transformed, not only images. Together, these new features allow easily transferring template VOIs to the patient images for performing the template-based statistics on the original PET images.

‣ A new version (ATL) was developed which supports all the features required for CFR part 11 compliant data analyses. It is mainly intended for CROs and includes full audit trails, data protection and advanced reporting.

Features

General	New:
	‣ External tool for VOI-based partial volume (GTM method proposed by Rousset).
	‣ External tool for the partial volume correction of brain PET images based on the gray/white matter segmentation of a matched MRI series (method proposed by Muller-Gartner).
	‣ External tool with two variants for the skull-stripping of MRI brain images.
	‣ Support request facility: the user can capture screens illustrating the problem, combine them with the console output and a problem description, and send the material with a single mouse-click to the PMOD support.
	‣ Mouse-operated zooming: Holding down the "Ctrl" and scrolling the mouse wheel activates zooming.
	‣ Focus during zooming: The hot spot of the image (selected VOI or planes triangulation point) now always remains visible during zooming.
	‣ Lower threshold default: The user can now configure that the lower threshold of the color table defaults to zero, not the minimal value (excluding HU).
	‣ Color of the orthogonal crosshair lines can be defined.
	‣ Split to slices tool added.

	� Use of the selected patient info selected in the database for filling the DICOM Q/R information.
	⋙ The keyboard shortcuts have been extended and can be listed from the context menu.
	⋙ Report paper size configuration: A4, letter.
	Changed:
	⋙ Interactive zooming can now be performed in all planes, not only the active one.
	⋙ Improvements of the compare mode in the viewing tool.
	⋙ General information such as Origins, Pixel Size etc moved from the Data Inspector window to the Info window.
	⋙ The external tools can now also be called from a new button in the image side bar, and interrupted during execution.
PXMOD	The PXMOD user interface was completely revised to clarify the work-flow and improve the ease of use. Furthermore, several functional improvements were introduced. Existing users are kindly referred to the update documentation and to the examples in the PMOD Workbook.
	New:
	⋙ Parallel processing: The PXMOD models requiring significant processing time have been parallelized so that the calculation time is decreased by a factor approximately proportional to the number of processing cores (1 core is always spared).
	⋙ New model: Basis function method for 2-tissue compartment model according to Hong and Fryer, Neuroimage. 2010;51(1):164-72. This model is particularly suitable to estimate the individual rate constants of irreversible tracers in addition to the flux.
	⋙ New model: Graphical model (RE-GP Plot) developed by Zhou Y et al, Neuroimage. 2010;49(4):2947-57. This model is an alternative to the Logan plot which is not prone to bias due to high noise levels. While the results of VOI analyses are equivalent, the performance of the Zhou plot should be better with pixel-wise data.
	⋙ Model combination: The six different reference models for calculating BPnd have been incorporated into a convenience model which calculates BPnd using all methodologies of interest.
	⋙ An optional segmentation step was introduced which allows interactively creating a mask for the restriction of the pixel-wise calculation.
	⋙ A VOI outlining step was integrated into the workflow for avoiding the necessity to create VOI data in a different processing session.
	Changed:
	⋙ The partial volume correction models PVE and PVE2 were retired. A much improved PVC functionality is now generally available in the external tools.
PKIN	Note: The graphical plots which have non-standard time on the x-axis have been re-implemented, so that t* can be specified in plain acquisition time. This makes it simpler to use the same value segment for all regional TACs. The old implementations

	are still available, now with "Legacy" in the name.
	New:
	⇥ Coupled studies fitting: Data from different acquisitions can now be processed in a common fit which allows the coupling of parameters across data sets. A parameter coupling can be REGIONAL (a common value is estimated in all coupled regions with the same name, e.g. for k_3) or GLOBAL (a common value is estimated in all coupled regions, e.g. for k_4).
	⇥ Residual weighting: Additional flexibility was added to the weighting for taking the effects of radioactive decay and frame duration into account.
	⇥ The weighted and/or the raw residuals can be shown. Randomized fitting can now also be applied in couple fitting.
	⇥ The Patlak Reference model was added.
	⇥ A new graphical method was added. It allows calculating Vt, Vnd, and therefore also BPnd. Furthermore, the shape of the plot gives an indication whether there is specific binding or not not. Ito H et al, A new graphic plot analysis for determination of neuroreceptor binding in positron emission tomography studies. Neuroimage. 2010;49(1):578-86.
	⇥ Loader for the Gamma Medica blood sampler format.
	⇥ The curve control elements can be configured to be shown beside the curves rather than below. This improves the layout for 16:9 screens.
	Changed:
	⇥ The fitting history now also includes the weighting and valid point definition (not yet the configuration of the different blood items).
	⇥ Copy to clipboard: the precision was extended to 16 digits.
	⇥ The %SE of the macroparameters is now also retrieved from a KM file.
	⇥ If a file is loaded for which the model is not configured, it is automatically added to the model list.
PFUS	New:
	⇥ All matching procedures can optionally calculate the inverse transform.
	⇥ Rigid Matching: dedicated presets for the matching of human or animal images are available.
	⇥ The matching tools can now also be used in the external tools and therefore in pipe processing.
	⇥ The template image used in the PALZ tool is now included in the list of brain templates. Normalizations can therefore be prepared for PALZ in a batch matching mode.
	Changed:
	⇥ Rigid transforms (manual, automatic) have been unified and can be used interchangeably.
VOIs	New:
	⇥ Transformation of contour and template VOIs using the transformation matrices

	obtained in image matching. This allows for instance to transform the standard AAL VOIs to the patient space and apply them to the original PET images.
	⏴ A VOI template for mouse images was added (courtesy of Martine Mirrione, BNL).
	⏴ Button for centering the VOI at the enclosed Max or Min pixel.
	⏴ Object VOI properties: The different properties of a VOI can now be edited in a dialog window. For example, object VOIs can have well-defined sizes in all dimensions (e.g. as an ellipsoid) and rotated around all directions.
	⏴ VOI bounding boxes are visualized in the MIP images.
	⏴ Object maps (*.obj) of the Analyze software can be loaded in PMOD, used for statistics, converted into vertex VOIs, etc.
	⏴ Load multiple VOI files at the same time.
	⏴ Option to show the VOI name if mouse is moved over VOI in the image. Works for both contour and template VOIs.
	⏴ Outlining function which turns an image object map (objects are represented by distinct integers) into a set of contour VOIs.
	⏴ The statistics results can be copied to the clipboard.
	⏴ Cropping is now also supported for template VOIs.
	Changed:
	⏴ Synchronization of VOIs and data sets: the initial setting of the synchronization box can now be configured per PMOD module.
	⏴ Additional information is saved to the pixel dump file.
	⏴ Cropping now allows creating a new study instead of overwriting.
	⏴ The iso-contouring can now also be restricted by a template VOI.
Database	New:
	⏴ Saving in "real" number format: Some data require the representation as real numbers to be saved accurately enough. In this case databases can now be configured to allow saving in dedicated PMOD DICOM objects which support real numbers.
	⏴ The information of the selected patient can be used in the DICOM Query/Retrieve window.
	⏴ Filter extensions: the availability of components such as Captures or VOIs can be used for filtering.
	⏴ Ability to "pair" two image series for applying PVC in a batch.
	⏴ The project definition is now inherited from the loaded images to the result images.
	⏴ Images are now written to the database in the new "Enhanced" object definition.
	⏴ When images are exported the fields edited in the database are replaced in the corresponding DICOM elements. Furthermore, the output IOD can be selected.
	⏴ A private definition for saving float values to the database was introduced, ensuring highest numeric precision. These objects are converted into standard DICOM objects when exported from the database.

	Changed: ⯈ If more than one database is configured, PMOD remembers the least recently used one after restarting.
PVIEW	New: ⯈ Support for the fused viewing of images from hybrid acquisitions. ⯈ Split to slices tool added. ⯈ Tool to transfer images from PMOD to ImageJ. ⯈ Scaling of curves (for calibration purposes) when sending them to the PKIN tool.
P3D	Changed: ⯈ The "Texture" tab was removed. All loaded data sets can now used for texturing.
PCARD	Changed: ⯈ The automatic procedures for short-axis reorientation and myocardium detection were improved for ^{82}Rb data. ⯈ The PMOD-specific segmentation of the myocardium was removed from the configuration.
Data Formats	⯈ DICOM Special Cases: can now be exported and imported and therefore easily shared. ⯈ Workaround to support the loading of Bioscan CT DICOM data. ⯈ Interpretation of private information for loading dynamic GE SPECT DICOM images with proper values scaling. ⯈ When a DICOMDIR file is dragged into PMOD all series listed by the DICOMDIR are loaded.

Zürich, Oct. 26, 2010

Maintenance Builds of Release 3.1

Build 7 Aug. 15, 2010	⯈ PKIN: Fixes for inconsistencies in the fitted start time of the MA1 and MA2 models. ⯈ MySQL: Fix for compatibility with the latest MySQL 5.1.41. ⯈ Merging of files into a dynamic study: At the end of the merging process the Edit Times dialog window is shown so that the user can verify the timing and correct of necessary. ⯈ Interfile: Added the times for static tomographic images, not only dynamic ones. ⯈ PXMOD: With some DICOM objects only one parametric map was saved due to a naming problem. ⯈ DICOM: Fixed reading of DICOMDIR with references to non image objects. The problem caused repeated entries for the same image on the selection list. ⯈ DICOM: Improvements for Philips enhanced MR DICOM objects to support DTI images. ⯈ DICOM: Fixed special case "Image start time not at zero". It resulted in a wrong

	timing and a message about missing time in the file.
	⧔ DICOM loading window: Fixed a problem with de-selecting files by double-clicking.
Buil.d 6 May 30, 2010	⧔ PKIN: Fix of a bug in the B/I optimization model which occurred with coupled fitting, and when optimizing a tissue TAC together with the plasma curve.
	⧔ PKIN: Bug fixed in MP4A RLS Model which caused an exception during fitting.
	⧔ PKIN: Dual Ligand, Cold model did not consider the cold tracer from the second injection at times after the third injection.
	⧔ PXMOD: Batch mode loading error messages were not added to the final message.
	⧔ PFUS: For some combinations of pixel size and bounding box a wrong bounding box was obtained after normalization.
	⧔ Anatomical orientation: Fix of a problem with missing orientations after the initial loading operations AVERAGE_VOLUMES, VOLUMES_SUM and INTEGRATE_VOLUMES.
	⧔ Anatomical orientation: The reorientation tool in combination with certain data types could result in obviously wrong value scaling.
	⧔ DICOM: Fix of a problem with with UN elements (unknown value representation).
	⧔ DICOM: Loading procedure modified to correctly sort retired NM objects with wrong image orientation (old GE data).
	⧔ PALZ: New normalization setting "Compensate Origins displacement (Difference between origins of Template and Normalized)" added to improve normalization robustness.
	⧔ A setup was tested for Solaris on SPARC systems and has been found running, with the exception of license key support and the native ITK libraries. In such a configuration a network license must be employed which is served by one of the officially supported system.
Build 5 March 29, 2010	⧔ SUV values: There was a SUV calculation problem for GE and PMOD data if a non-zero value for the post-injection activity had been entered. This problem was in Builds 1-4 of version 3.1, but not in version 3.0.
	⧔ Image loading: When only a subset of the frames of a dynamic data set was loaded the timing could be incorrect.
	⧔ Philips ImageIO: The image data were loaded with a scale factor 1/1 and the units set to kBq/cc, even if the specified units were not kBq/cc. This could introduce a scaling error of the data.
	⧔ DICOM: Images are now loaded even if the FMI header length in the file is incorrect (GE Signa Excite).
	⧔ IRW DICOM: Fix of a slice scaling bug which occasionally occurred and was obvious in the loaded images. Version 3.0 did not suffer from this problem.
	⧔ DICOM Sever: Starting of the server with the provided script failed.
	⧔ PKIN: Retrieving of default settings for the metabolite correction did not work properly.
	⧔ PKIN: The Print Report function generated a plot that did not correctly display the metabolite data.
	⧔ VOI: When sending curves to PKIN the specified curve operations such as adding

		an offset were not applied.
	▸	VOI: VOIs with different definitions for different frames were not correctly saved.
	▸	If the distance was measured on two synchronized data sets, minor distance differences could occur.
	▸	Pipe processing: The definition files were changed to be smaller and faster interpreted. Saved Pipe processing definitions may require recreation.
	▸	Report printing of RGB images: The proportional scaling of the image was change to better exploit the image area.
	▸	The zoom factor in the zoom list was not adjusted after zoom manipulations.
Build 4 Feb. 2, 2010	▸	**Dramatic speed improvement of database operations** by a factor of 100 and more. Taking advantage of the improvement requires *updating the database structure* as follows: After installation of Build 4 select the **Config** button on the ToolBox. In the **Users configuration** window select the **DATABASE** tab, and then the local data source. First perform a backup of the database tables with the **Save SQL Backup** button. Then start database upgrading with the **Update** button. Note that remote Transaction Server databases need to be upgraded on the machine hosting the database.
	▸	**PMOD Workbook** added to the distribution: It is provides step-by-step tutorials for the major tools using the example data available after PMOD installation. The workbook can also be downloaded after the login into the Support area of the PMOD website.
	▸	PKIN: Loading multi-column text files with more column headers than data columns caused a program failure.
	▸	PFUS: Motion correction with the "previous" or "following" frame as reference did not work properly.
	▸	VOI: The contour names had not been saved with the VOI definition.
	▸	Pipe processing: Adding the specified prefix to the file name did not always work.
	▸	"Interpolation" external tool: support for manual transformations had been missing.
	▸	Ecat saving: Activity dose changed from MBq to Bq. Patient height changed from m to cm.
	▸	Analyze, NiFTi, Interfile, microPET, Afni image loading: importing the acquisition times from a file reset the scaling factor, so that wrong values were loaded.
	▸	Analyze, Afni, Neurostat, Graphic image loading: the times from the preceding loading operation was not remembered.
	▸	WIBU USB key: Drivers for Debian/Ubuntu Linux systems added to the distribution.
Build 3 Dec. 1, 2009	▸	VOI: Propagation on the ROI level caused contours to change from "-" to "+".
	▸	VOI: The time of VOIs created with the iso-contour tool and "Apply to all frames" in dynamic series were all set to zero.
	▸	Edit times: The change of acquisition times acquisition start not from zero were not correctly saved.
	▸	Saving DICOM: the saving as NM DICOM objects caused a program error in certain conditions.

	‣ Rat template (W.Schiffer): the template included some distorted regions.
	‣ AAL-VOIs template: The image origin was adjusted to that of the other templates in the MNI space.
	‣ NifTI: Fix for the 2 files mode to store frame times.
Build 2 Nov. 11, 2009	‣ VOI: Compatibility fix required to compensate changes in the treatment of origins and pixel sizes.
	‣ SUV dialog window: Synchronization of the list and the entered half-life.
	‣ Edit frame time: Improvement of time generation by step and duration.
Build 1 Oct. 26, 2009	‣ Initial upload of 3.1 version.

Product Release 3.1

The 3.1 release incorporates more than 130 improvements with main highlights in VOI and kinetic modeling functionalities.

CAUTION: There are important improvements in kinetic modeling which may change the fitting results, please see below.

General	New: ‣ During the installation of the new version the configuration of the previous version can be imported. ‣ A new button on the ToolBox allows for checking whether the installation is up to date. ‣ New color tables added. ‣ The list menu of the color tables now includes icons representing the coloring of the different tables. ‣ New interface to the ITK (Insight Toolkit). It is exploited by a new external tool which allows to apply 28 image processing filters, and in the segmentation tool which offers ITK-based segmentations. ‣ A pipe tool was introduced for multistudy processing. For example: Loading [scaling | smoothing | replacing] saving. ‣ A new external tool was added for starting scripts of the operating system. ‣ Dual-screen support: Menus are correctly shown, and dialog windows are shown on the secondary screen. ‣ Printing of the help pages is supported. Changed: ‣ When merging loaded series into a dynamic study the user can define which series are used and in which order. ‣ When merging loaded series which cover parts of an object (table positions) into a single study the user can define which series are used and in which order.

	‣ The logging was improved.
Database	New: ‣ Free text search in the study and series descriptions.Viewer for loading JPEG and TIFF images which are saved in the database. ‣ Free text comments which are related to certain image series can be saved in the DB. ‣ New "Flat" selection mode with all series in a single list. ‣ Ability to switch off list updating after every change of a filter element. ‣ Transaction Server: A facility was added which generates an operating-system specific starting script for the transaction server. ‣ Arrow buttons added for stepping through the patients list. ‣ It is now possible to filter for more than one modality by an OR combination. Fixed: ‣ Sometimes entries remained in the Projects list although all related data had been removed. ‣ Sometimes could disappear from a patient, although the user had chosen not to delete the attached components when deleting images.
VOIs	New: ‣ **Regular geometric VOIs** were added which are not consisting of ROIs, so that they can be scaled in all directions. With this function an enclosing VOI can much quicker be defined. ‣ **Single pixels** can be added or removed from a VOI. ‣ Extended operations on the contour level. **Contours** can be **additive** (adding the included pixels) **or subtractive** (removing the including pixels) for the VOI. ‣ Facility for applying operations at the contour level. ‣ Extended operations on the VOI level. VOIs can be merged to form new VOIs. During the merge, **VOIs** can be **additive** or **subtractive**, as the contours. This allows to easily create VOIs with hollow inclusions. ‣ **AND** operation **with a mask** (eg gray matter). Only VOI pixels are considered in the statistics which are also in the mask. ‣ Definition of a new VOI which consists of the pixels along a line. ‣ New solution for the case when the data origin has changed which causes the VOIs to be shifted. The VOI origin can be adjusted to the new data origin. ‣ Splitting of a VOI into a set of VOIs on the ROI or contour level. ‣ The VOI ordering in the list can be changed. ‣ Insertion of vertices into a closed contour at any position is now possible. ‣ An eraser of configurable size and shape was added for quickly removing ranges of vertices.

	⇥ The hammer tool now has a configurable size.Default sizes for the regular objects can be saved.
	⇥ Drawing contours and Iso-Contours are now also possible in NxM layouts.
PKIN	**CAUTION:**
	Significant Change related to Compartment Models: In prior versions the whole-blood contribution in the operational equation was calculated by interpolation of the whole-blood activity at frame midpoint and multiplication with the frame duration. The calculation has now been changed to the integration of whole-blood activity during the frame duration using the interpolation model of the whole-blood curve. This calculation represents a better approximation of the imaging physics and tends to result in a better modeling of the initial part of the TACs.
	As a result of this change, the model curves calculated with version 3.1 differ from that of prior versions, and correspondingly fitting results will also differ. Particularly, the default value of vB may have to be revised.
	Change of the Lumped constant for the FDG models. The old default value of 0.437 was replaced by a new value of 0.89. This value had been determined by Graham et al (J Nucl Med 2002; 43:1157–1166) using [11]C Glucose and FDG in 2002. Their results: Normal brain: 0.89+/-0.08; cerebellum: 0.78+/-0.11.
	New:
	⇥ Support for **Randomized fitting**. Random sets of initial parameters are generated and the data fitted. The parameter set among the results with has minimal chi squared is returned as the fitting estimate. Hereby the potential of getting stuck in a local minimum is reduced.
	⇥ Option for **Automatic parameter initialization** of compartment models using linear least squares estimates before starting the fit.
	⇥ Facility for establishing **User-defined initial parameters** per model.
	⇥ Improvement of the **History functionality**. It is now a list to which the user can add manually, and from which he can delete entries. The list shows the model configuration with the estimated parameters and fit criteria. Therefore it can also be used for quickly comparing the results with different model configurations.
	⇥ Support for **Data cloning** into an additional window which can be used for a side-by-side comparison of models.
	⇥ Comments can be added to a data set, and later edited.
	⇥ Noise can be added to TACs in the Edit Data dialog.
	⇥ Whole-blood and plasma data can be loaded from a single file.
	⇥ New model: linear least squares method for 1- and 2-tissue compartment models with blood spillover.
	⇥ The definition of the valid samples can now be copied to all regions.

PXMOD	New:
	⏵ New model: Iterative fitting of a 2-tissue compartment model with ridge regression. This model allows controlling the degree how much the individual parameters may be adjusted from their initial values.
	⏵ Option for separating the blood curves and the tissue TACs into two separate curve displays to improve visibility on small displays.
	Changed:
	⏵ 2-tissue compartment model: was extended by additional output parameters (Vt, Vs, k3/k4, flux, ssq).
	⏵ Partial volume correction method 2: the gray matter threshold is now applied to the smoothed segment, not the original. This reduces the overcorrection problem along the mask boundaries.
	CAUTION: The lumped constant for the FDG models was corrected from the old default value of 0.437 to a new value of 0.89.
PFUS	New:
	⏵ Brain Normalization II: Default configurations which sets appropriate parameters for human or small animal applications. (Note: Brain Normalization I should NOT be used for small animal applications).
	⏵ Templates of the rat brain added for normalization, matching and VOI statistics (courtesy of Wynne Schiffer).
	⏵ Added the functionality to save all registered images at once.
	⏵ Optional identity line added to the 2D scatter plots of VOI pixel values.
	Changed:
	⏵ VOIs can now also be enabled in the Scientific Output of PFUS.
P3D	New:
	⏵ Selection of objects directly in the scene by double-clicking.
	⏵ When rendering VOIs, their color is used for surface shading.
	⏵ Support for more than one set of orthogonal planes.
	⏵ By using thresholds, the pixels below a certain value can be set to transparent in the planes.
	⏵ Plane definitions are also saved in protocols.
	⏵ Support for more than one marker.
	⏵ Choice to enable automatic refreshing after changing the VR properties.
	⏵ Various ITK segmentations available.
	Changed:
	⏵ Revision of the user interface of the control section.
	⏵ Planes are now also objects in the tree.
	⏵ Organization of the color profiles for volume rendering improved.

	▸ Navigator window is no more hidden in certain situations.
PCARD	New:
	▸ Save protocol function for easily saving all information related to a data processing (data, transformations, VOIs). Allows to exactly reproduce a data analysis.
	▸ New default for setting the start time of the first frame to zero.
	▸ New default for rotating the loaded images to anatomical orientation. This makes the automatic reorientation procedure more robust.
	▸ Different default reorientation for Humans and Animals.
	Changed:
	▸ Scaling in the reorientation function was disabled.
	▸ More significant numbers are shown in the data investigator of the polar plot.
	▸ RV and LV VOIs are no more required for the processing of static scans.
Data Formats	New:
	▸ Native support for JPEG compressed DICOM loader which avoids the use of the JAI ImageIO library which was not available on Mac.
	▸ DICOM Advanced settings: Default button added.
	▸ DICOM Server: A facility was added which generates an operating-system specific starting script for the DICOM server.
	Fixed:
	▸ DICOMDIR: Under certain conditions (records including sequences) the system hanged after deleting a file based on the DICOMDIR listing.
	▸ DICOM: When scanning a read protected folder an error occurred (mainly MAC, Linux)
Java Runtime Environment (JRE)	▸ On Windows and Linux systems a dedicated JRE is installed together with PMOD and used for the execution of the program. Therefore, automatic upgrading of Java by the operating system should not affect the PMOD installation.
	▸ On Mac OS X systems the internal JRE is used and therefore the PMOD installation might be more vulnerable to system updates. PMOD 3.1 has been tested on Snow Leopard (10.6) and Java(TM) SE Runtime Environment (build 1.6.0_15-b03-219) Java HotSpot(TM) 64-Bit Server VM (build 14.1-b02-90, mixed mode)

Zürich, Oct. 26, 2009

Maintenance Builds of Release 3.0

Build 11 Nov, 2009	▸ PXMOD: Problem fixed when updating curves from "VOIs on Sum" functionality.
	▸ PFUS: Improvement in the randomized grid usage, so that the matching results are now exactly reproducible.

	‣ DICOM: Improved support for the DICOM dialects of NanoSpect and Radworks.
Build 10 Oct, 2009	‣ Fix for an incompatibility found with Snow Leopard (10.6) on Mac OS X systems. ‣ PFUS: Motion correction with match to previous did not work. ‣ PFUS: A problem was corrected which occurred with Brain Normalization II with certain origins. ‣ PKIN: A Problem when loading some files without metabolite corrections was fixed. ‣ DICOM: When SUV-related information was changed and then the file saved multiple times, only the first information was used. ‣ DICOM: For some specific data sets the study date was incorrectly interpreted. ‣ DICOM: For "Check incoming folder" the relative path definition "./DCMIN" was not supported. ‣ Database: " ‣ Set Acquisition Times to zero" was not working when loading data from the database. ‣ Philips ImageIO data: A problem related to the timing information was fixed. ‣ Raw data: If the saving name contained dots, they were removed from the name.
Build 9 Sept, 2009	‣ PKIN: The metabolite correction was turned off as soon as the interpolation model of the plasma curve was changed. ‣ PALZ: Normalization problem fixed (affected: Build 7 and 8). ‣ PFUS: There had been a relatively small limit for manually shifting the images in interactive registration. Increased by a factor of 20. ‣ PCARD: The number of polar plot circles was calculated from the VOI axial bounding box of all VOIs (not only Myocardium). As result if the RV or LV was defined higher than last basal Myocardium ROI the number of circles was too small. Changed to use the Myocardium VOI only. ‣ HRRT Data: Interpretation of (mm/dd/yyyy), (mm:dd:yyyy) dates added. For better handling of dob and study date with HRRT files created in the US.
Build 8 July, 2009	‣ Mac OSX: Apple has fixed a bug in Java 1.5 which had required a work-around in PMOD. This fix caused buttons to change in size. The workaround in PMOD was removed to recover the user interface. ‣ PFUS: Fix of z-axis shift equal to half the pixel size difference of the input and reference image (transformations for motion correction). ‣ PFUS: Update of contours list in the fusion display was not active.
Build 7 June, 2009	‣ PFUS: Since Build 4 there was a shift in the z-axis equal to half the pixel size difference of the input and reference image (manual transformation). ‣ PFUS: Division by 0 was not handled in the %Dif arithmetic operation. ‣ PXMOD: Problem fixed which occurred when updating TACs from VOIs after switching between models. ‣ PXMOD: The behavior when using VOI templates for updating the TACs was not correct. ‣ PXMOD: When sending data to PKIN form the data inspector only the input curve

	was transferred, not both the input curve and the whole-blood curve.
	‣ PXMOD: An error was not handled when all model parameters were disabled from fittting.
	‣ DICOM data: When saving dynamic data as NM DICOM objects the timing was not correctly saved if there were gaps between successive acquisitions.
	‣ AFNI data: The origin was interpreted differently when loading the images directly than when showing the loading dialog. This caused VOI problems.
	‣ NEUROSTAT data: The non-standard encoding as floating-point is now supported.
	‣ NIFTI data: Images created by PMOD were confusing to SPM5. The sform matrix was corrected.
	‣ Fixed a slight problem with the context menu of the color bar for setting the window to the upper third of the value range.
Build 6 May, 2009	‣ PXMOD: Selection of the mask file caused replacement of the original input data by the mask data.
	‣ PXMOD: When "Interactive loading" was initially selected, changing of the input data was not possible thereafter.
	‣ VOI: In fusion mode the iso-contour VOI was always calculated on the "A" image.
	‣ VOI: In zoom mode, edition of the vertices with the "Hammer" tool resulted in unpredictable shifts.
	‣ VOI: In the case of zoom and image shift "Unfinish" resulted in a wrong starting point.
	‣ DICOM: On Windows platform a problem with reading JPEG lossless compressed DICOM data was fixed.
	‣ DICOM: The limitation of file names to eight capital characters was dropped. This behavior caused the "Save all" feature in PXMOD to sometimes generate only a single file.
	‣ DICOM: The regular scanning of an input directory by the DICOM server was not working.
	‣ TIFF: Fix for saving results in tiff format.
	‣ Matlab data loading: There was a misleading scaling factor from previous loading which is now set to 1.
	‣ Set Pixel Size: After changing the pixel size the display was not been updated properly.
Build 5 April, 2009	IMPORTANT: JRE 1.6 update 12 introduced an incompatibility which causes all prior PMOD versions to stop working. This incompatibility has been fixed in the current Build 5. For prior PMOD version please use a JRE below 1.6 update 12.
	‣ PXMOD: Fix for the BP calculation in the MRTM2 model. A wrong k2' had been applied for the BP calculation in the earlier builds of version 3.0.
	‣ PKIN: Bug fixed in the AIC calculation. Chi squared had been used in the calculation instead of the reduced Chi squared ("n" had been missing in Math.log(rss/n)).
	‣ PCARD: Change of the Herrero 2-compartment model for Rb data. The spillover

	contribution from the RV VOI had been used instead of the LV VOI.
	⇉ Transaction server: added command line argument -noLS which can be used for running multiple database transaction servers in parallel without affecting the interactive session.
	⇉ VOIs: In orthogonal layouts, the VOI was only zoomed in the axial image, but not in the coronal and sagittal image.
	⇉ VOIs: In planar layouts with multiple images, VOIs were only displayed in the upper left image.
	⇉ VOIs: When outlining VOIs in the fusion mode and an active zoom factor, there was an offset between the cursor and the appearing vertices.
	⇉ Query/Retrieve: Bug fixed which occurred when the source and the target of the retrieval were identical.
	⇉ MicroPET: Loading a sub-set of slices from dynamic MicroPET data resulted in incorrect sorting.
	⇉ Nifti data format: Fix introduced for saving correct origins.
	⇉ "Settings" button removed in the loading dialog window to avoid confusion.
Build 4 Feb. 2, 2009	⇉ License server: Fixing a problem which caused the license server to lose connection with the USB key after about 5 days of operation.
	⇉ Configuration of the Transaction Server: behavior when switching between Derby and MySQL improved.
	⇉ PKIN: Fix for an interpolation problem before the first measured sample of the parent fraction. A value of 0 instead of 1 was assumed at time 0. The error only occurred for the "Measured" parent model.
	⇉ PKIN: A fitting problem was fixed for 4 rarely used models (Ichise MRTM0, Ichise MA1, Ichise MA2, MP4A RLS).
	⇉ PKIN: When TAC data with two time columns (start end) were loaded as plasma curve, the time of the first column was used as the blood sampling time. Was changed to use the mid-time of both columns.
	⇉ P3D: Improvement for calculation of transparency/opacity profiles and color for volume rendering in case of images with few values.
	⇉ PFUS: Brain normalization II extended so that it also works for images with very small pixel sizes (mice).
	⇉ External Tools, Interpolation: Fix for a shifting problem by half a pixel size. The problem was only in version 3, Build 3, and affected the "Number of pixels" and "Pixel size" modes.
	⇉ VOI: Crop to VOI bounding box was changed to exact cropping (previously, one pixel was added).
	⇉ VOI: Contours were only shown in the first image of a NxM layout.
	⇉ Security certificate *properties/system/security/pmod_store* updated. Important for secure DICOM transfer and encrypted access to the License Server.
	Several changes related to image formats for improving format conversions:
	⇉ Conversion Explore Vista Interfile -> DICOM: more data fields are interpreted.
	⇉ DICOM special cases are not applied for images created by PMOD itself.

	‣ DICOM special case "Time start not at zero (move to zero) "added: To make sure the acquisition times start from time 0.
	‣ PMOD now reads and writes energy windows (DICOM NM, DICOM PET, Ecat).
	‣ PMOD reads/writes decay factor and relative to what time it must be applied (DICOM).
	‣ PMOD reads/writes decay correction factor (ECAT).
	‣ PMOD preserves the original series date/time if the image data is not modified. Note: series date/time is stored only in DICOM PET objects.
Build 3 Dec. 9, 2008	‣ Installer for the Linux 64-Bit USB-key drivers replaced by WIBU pre-release (WkRt-Lin64-5.21.500-1.x86_64.rpm).
	‣ Correction of handling the image origins while rotating and mirroring images during loading.
	‣ Improved origin support for NIfTI image files.
	‣ AAL VOI template image (ROI_MNI_V4.nii) replaced by a new file with origins compatible with SPM templates.
	‣ P3D: Fix for the 3D rendering of VOIs. It was only functional for VOIs defined in the z-plane.
	‣ PKIN: Fix of a bug which could result in endless looping when fits encounter a certain error condition.
	‣ PKIN: Default metabolite correction set to Fixed, not Measured.
	‣ PKIN Fix: The model on the Metabolites tab was not reset when loading new data.
	‣ VOIs: Fix for ROI propagation with "ROI Follow Max". It was only functional for VOIs defined in the z-plane.
	‣ "New Contour" added to the context menu of VOI definition.
	‣ PFUS: Fix fixed problem of the rotation center when combining a normalization transformation with other transformations.
	‣ PFUS: Support for the combination of rigid transformations with rotation centers not in image center (calculated with initial parameters from principal axis or center of mass methods).
	‣ PFUS: Fix for using VOIs defined as part of VOI templates in scatter plots.
	‣ PFUS: Menu entry for user-defined templates which must be prepared in the *resources/templates/usertemplates* subdirectory as NIfTI files.
	‣ PCARD: Correction of the calculation of the segmental TACS from the polar plot samples. The resulting TACs are smaller in magnitude (the division was by the number of samples minus one before) and composed of slightly different polar samples (boundary samples were considered in more than one segment). Note: This change produces different results as compared to the prior versions by up to 10% in individual segments, particularly in apical segments. The effect is smaller for territories and global values.
	‣ PCARD: Fix for a problem of VOI positioning after manual VOI adjustments.
	‣ PCARD: Fix for static series. They were smoothed even if the box for the automatic application was not checked.
	‣ PCARD: Fix for the time averaging if the frames are not contiguous.
	‣ PXMOD: The parallel processing of some models (Ichise variants, SRTM, SRTM2,

	2-tissue compartment model) could potentially result in inconsistent results and was switched off.
	▸ License server: Change to make it more robust against short-term communication problems with the USB key.
Build 2 Nov. 20, 2008	▸ VOI: VOIs from prior versions were not loaded properly.
	▸ VOI: Fill VOI was not correct in the fused display of PFUS.
	▸ VOI: Fixes for operations with grouped VOIs.
	▸ VOI: Context menu changed (4D removed; instead added "New Contour").
	▸ DB: Preferred DB selection per user corrected.
	▸ DB: Problem fixed when replication data from a mySQL database to a JavaDB database.
	▸ DB: The transaction server had a potential problem with saving component data (not images). The effect only occurred with slow databases and fast disks.
	▸ DB: During a delete operation blocking of the Delete button could be undone by a new selection.
	▸ PKIN: When loading data from DB the patient information in the file is overwritten by the DB contents (as with image data).
	▸ PKIN: Fix of the standard deviation calculation in Edit Data when averaging curves.
	▸ PKIN: Added "Curve by Curve operations" to "Edit Data" to for supporting curve divisions, multiplications etc.
	▸ PKIN: Fitting algorithm adjusted to improve behavior close to restrictions.
	▸ PXMOD: Load blood data without units in the file. The configured units not properly interpreted.
	▸ PXMOD: Batch with a single input file failed with exception.
	▸ PFUS: Saving of AUTO transformations was not possible.
	▸ PFUS: The SPECT Template provided for brain normalization was flipped L/R.
	▸ PFUS: "Crop to VOI" blocked (caused problems when used after reslicing).
	▸ PFUS: There was a problem with brain normalization in case of (0,0,0) origins in the template.
	▸ PCARD: Calculation of the segment average values from the polar plot was corrected (sum of samples was divided by n-1, instead of n; n= number of samples in segment). The effect is a general, slight decrease of the calculated flow values in the range 1-6%.
	▸ DICOM server: Configuration user interface was not complete for users with 2.9 licenses.
Build 1 Oct. 30, 2008	▸ Initial upload of 3.0 version.

Zürich, Oct. 10, 2009

Product Release 3.0

General	New:
	▸ Inclusion of the database and DICOM server functionality (which were a separate option) into the base license.
	▸ During installation, a java runtime environment is extracted together with the PMOD program. This runtime will be used for running PMOD. The advantage is that it will not be changed by automatic updates, and that all libraries are properly included.
	▸ Export functionality for the values of all curves in the curve area.
	▸ High-quality capture of image are including color bar (Scientific Output).
	▸ Additional color lookup tables.
	▸ Selectable width for grid overlay to appropriately cover animal studies.
	▸ Different shapes for the plane intersection point in the orthogonal display.
	▸ Value inspection window when pointing at points in curve area.
	▸ Selection of different PET nuclides in the SUV dialog.
	▸ External plug-in for averaging of slices and/or time frames.
	▸ External plug-in for Segmentation and mask generation.
	▸ External plug-in for basic numeric transformations (log, exp,..).
	▸ Division function in the scaling tool.
	▸ Calculation of the average/stdv image as a new tool in PVIEW.
	▸ Loading: Interpolation to an arbitrary pixel size.
	▸ Some tools moved to detachable taskbars.
	Changed:
	▸ The Gene-PET (GENEPET) tool is no longer in PMOD's offering.
	▸ No license checkout for servers (DICOM, Database)
	▸ The configuration of internal precision was removed. The need for float precision is now automatically determined.
	▸ More flexible annotations in reports.
Database	New:
	▸ Support for an **embedded database** (JavaDB, also called "derby"). MySQL is still supported, but not provided any more with the distribution.
	▸ Functionality for the replication of data between databases is now available in the database image loader.
	▸ Testing of database response in the configuration, similar to DICOM C_ECHO.
	▸ Support for encrypted/compressed communication with remote databases.
	Fixed:
	▸ There was a potential problem when saving component data (VOIs etc.) to a transaction server, depending on the disk performance of the server. To avoid this

	problem both the transaction server and the clients should use version 3.0
VOIs	New:
	‣ Mask by VOI number for generating template images.
	‣ Contours can now also be outlined in the **coronal or sagittal orientations**.
	‣ **Undo** function for contour VOIs.
	‣ Cropping the image volume to VOI bounding boxes.
	‣ Single-button creation of an atlas from an image and the outlined contours.
	Changed
	‣ Revised user interface to enlarge the available image space.
	‣ Calculation of TACs: up to 5 times faster.
	‣ Creation of VOI masks from a number of hottest pixels (external tool).
	‣ Creation of VOI masks using segmentation techniques (external tool)
PKIN	New:
	‣ Functionality for **metabolite correction** which includes fitting of parent fractions with different models and the usage of population correction curves.
	‣ Ability to directly copy of the parameters from the overview panel to the clipboard. Can be pasted into Excel.
	‣ "Details" tab with new fit quality parameters (coefficient of determination, residuals root mean square) and criteria for model comparison (Schwartz criterion, Runs test).
	Changed:
	‣ Menu reorganized and moved to the lower left corner.
	‣ When loading .km files from a database, patient/study information is overwritten by the contents in the database.
	Fixes:
	‣ Bolus/Infusion Optimization had a problem when measured weights were used during fitting and simultaneous fitting of the plasma parameters was enabled.
	‣ The calculation of the sensitivity function used parameter changes which were too big (100% instead of 1%).
	‣ Blood delay fitting sometimes failed due to a problem in resampling with negative times.
	‣ Fix for calculation of standard deviations in curves created in the Edit Data tool.

PXMOD	New:
	⤷ SRTM2 model for BPnd calculation with fixed k2'.
	⤷ 1-tissue compartment model with ridge regression (Zhou GRRSC).
	⤷ Threshold parameter in the model pre-processing section to allow for background masking.
	⤷ Possibility to outline VOIs and save them as TAC definitions for the PXMOD models.
	⤷ Mask files can now be selected for masking the processing.
	Changed:
	⤷ The MA1 model was removed as a standalone model; it is included in the model which calculates the distribution volume by 3 different methods.
	⤷ It is no longer possible to directly return a corrected input curve from PKIN to PXMOD.
	⤷ The whole blood activity must be defined in the blood dialog, not any more in the pre-processing dialog (2-tissue compartments model, 1-tissue compartment models).
	⤷ When a model processing is interrupted, the calculated pixels are displayed.
	Fixed:
	⤷ Some problems with batch mode were solved.
	⤷ BPnd values calculated with SRTM method were not correct in early builds of version 2.95.
	⤷ The configuration of value units was not properly applied when loading certain blood files.
	⤷ Batches with only a single batch operation failed.
PFUS	New:
	⤷ Automatic matching and normalization can be started for all loaded series, not only one-by-one.
	⤷ Support for independent manual transformations of the frames of a dynamic study.
	⤷ Toolbar with shortcut buttons for the most important tasks.
	Changed:
	⤷ Brain normalization II now includes a resampling grid randomization to avoid local minima. Consequently, the result may vary slightly between runs.
	⤷ Adjusted order of the rotation buttons for a more intuitive behavior.
	⤷ Transformations are always applied when data is loaded ("Auto" check box removed).
	Fixed:
	⤷ Due to an interpolation problem there had been a slight shift of the resliced images by 1/2 of the original pixel size.

	‣ The combination of set landmark and manual matching are now correctly saved/replayed in protocols. ‣ SPECT template replaced (left and right were mirrored before).
P3D	New: ‣ Synchronization of two movies with the real time scale. ‣ Ghost objects to configure rendering options beforehand. ‣ Interpolation to isotropic pixel size during loading to reduce the flipping effects of VR objects. ‣ Control over smoothing during segmentation. ‣ Segmentation of a definable number of hottest pixels. ‣ Annotation in the 3D scene by adding a Note Changed: ‣ VR controls are now also in the properties area, not in a separate dialog window. ‣ More control over opacity function ‣ Some detachable taskbars.
Data Formats	‣ Memory usage optimized for large DICOM objects ‣ Added: Loader for NeuroStat files ‣ Philips format: support for SUV-related information. ‣ Philips format: Support for Syntegra CT data.

Zürich, Oct. 30, 2008

Maintenance Release 2.95

General	‣ **Most Important - Compatibility with the "Leopard" OS on Mac:** The Leopard (10.5) release of the Mac OSX turned out to be incompatible with all PMOD versions. The reason was the missing support for some of the user interface widgets used by PMOD. The whole PMOD user interface was revised to avoid the affected elements. As a result, PMOD has now a platform-specific look on Mac systems. On Linux and Vista systems, both the cross-platform look (used traditionally by PMOD) and the system look are now available. The selection is available as a configuration switch in the "Config" functionality. ‣ New plug-in "Basic Operations" in the external tools with some basic pixel-wise operations (ln, exp, 1/x, etc). ‣ Bug fixed which occurred when loading the acquisition timing from a file, if the number of frames did not match the number of file entries. ‣ The database "Save Query" now also remembers the last used database.
PKIN	‣ Fix of "Batch Mode" which was trapped in a never ending loop. ‣ Fix of a problem occurring during Drag & Drop of a data file. ‣ Fix of a saving problem with "Create Synthetic KM File" if a new, dense sampling was defined. ‣ Fix of a problem with "Edit Data" which occurred when deleting TACs in studies without blood data.
PXMOD	‣ Pre-processing stage: Derived parameters (which have no effect on the way how the calculations are performed) are indicated more clearly. ‣ Fixed problem with "VOIs on Sum": After creating VOIs, the "Update PMOD Curves" did not produce valid time-activity curves. ‣ Saving of the parametric maps using the file "File" menu did not work correctly. The input data were saved rather than the results.
PFUS	‣ Separate color table for the fusion overlay. ‣ Support for dynamic studies in "Image algebra". ‣ New menu entries as shortcuts for Fusion MIPs, Image Algebra, and Scatter Plots.
PVIEW VOIs	‣ Fixes for different problems occurring with iso-contour VOIs. The functionality was reduced and corrected to work more robustly. ‣ Fix for a problem with splitting a dynamic sequence into static frames. ‣ Fix of a protocol saving with transformations calculated by automatic methods.

P3D	▸ Surface cutting of SR objects is now also supported in addition to the existing cutting of VR objects.
	▸ Unrelated elements in the objects can be selected (with CTRL+Click) and their properties modified at once.
	▸ Cutting parameters are now also saved in protocol files.
	▸ New facility for enlarging the image area during the segmentation definition.
	▸ Selective rendering of VOIs (as stripes or surfaces) is supported without loading images.
	▸ Fix in loading protocols: the data format was not always correctly detected.
	▸ Fix in the texturing of small objects.
	▸ Optimization of memory usage for VR rendering.
	▸ Support for textures sizes which are not a power of two.
Data Formats	▸ MicroPET: extended so that the CT images from Inveon systems can also be loaded.

Adliswil, February 26, 2008

Product Release 2.9

PCARD	▸ The perfusion difference can be calculated as an alternative to the perfusion reserve to avoid artifacts by the division of very low perfusion values.
	▸ Visualization of the myocardium sampling points is now available for quality control. They are represented as circles in the short axis images. If the P3D option is available, they can more accurately be rendered as spheres in a 3D scene together with the left ventricle shape.
	▸ A polar plot of the Chi squared criterion of the kinetic model fit was added as an option.
	▸ A new sampling mode "Radial Max, Averaged" was added. This mode adds immediate neighbor pixels of the samples at the radial maximum to reduce noise effects.
	▸ Water model: The TAC results of a first analysis can be used for a subsequent new Factor Analysis.
	▸ DeGrado cardiac NH3 model only considers the first 4 minutes for fitting and disables later measurements which are not supported by the model. Problems are avoided by this behavior if a user loads longer-lasting acquisitions.
	▸ Rb 1-compartment model: The default parameters used for the flow-dependent extraction function according to the paper Lortie et al. Quantification of myocardial blood flow with 82Rb dynamic PET imaging. Eur J Nucl Med Mol Imaging. 2007 (in press).
	▸ A bug was corrected in the calculation of the apical TACs. Some pixels from the apex had also included in their calculation.
	▸ The division into basal, mid-ventricular and apical slices in the short-axis images was revised to more closely approach three equal thirds.

PKIN	‣ A history of fitted models is maintained for each region, through which one can browse quickly.
	‣ Data Editor to rename, rearrange, average, scale, and delete regional TACs from the data set.
	‣ Points of the input curve which are switched off will not be used for the linear interpolation of the blood data.
	‣ The applicability of sensitivity functions was extended to more non-compartment models.
	‣ Fix for a conversion problem when loading vector data in µCi/cc.
	‣ Fix for a problem when generating synthetic PXMOD data (occurring only with ny=1).
PXMOD	‣ Parametric maps are differently organized, not any more as the frames of a dynamic series. Dynamic series resulting from PVE and PVE2 processing are also available in the parametric maps area.
	‣ Optimization of batch operation.
PFUS	‣ The user interface was slightly adjusted to make the image algebra clearer.
	‣ A new non-linear matching method was added which is SPM5 compatible.
PVIEW VOIs	‣ New function to split a VOI into single-slice VOIs.
	‣ Iso-contour Auto-VOI: real-time outline on all slices and other improvements
	‣ Direct 3D visualization of VOIs (requires P3D option).
	‣ VOI Templates: Automatic contouring of the different labels was added to create an outline version of the template.
P3D	‣ Selection of colors for surface rendered objects from a palette is now possible.
	‣ The properties of an entire branch in the object tree can be manipulated, for instance be set to invisible.
	‣ Significant improvements in RAM consumption.
Data Formats	‣ A new loader format called "Autodetect" was added: It allows selecting data in different image formats and recognizes the format type automatically from the file contents.
	‣ Nifti: Support for writing was added.
	‣ MicroPET: A flag was added in the loading dialog to take into account the branching factor to the data values (division by the fraction). This is only a compatibility flag and not needed with new data, which has the branching ratio already applied.
	‣ Philips Mosaic SUV data: The unit section of a loading dialog was extended with a choice for units defined within the file. That choice is only available when PMOD recognizes more than one unit defined in the file.
DICOM	‣ Native support for Lossless Compression was added. The JAI installation is only needed for data with lossy compression.
	‣ Support for compressed connections.
General	‣ Rounding of x-axis tick numbers improved to avoid identical ticks.
	‣ External tool for image interpolation: The user can now also specify the pixel size of the image volume which is calculated from the original data by image

	interpolation.
	▶▶ Users button in toolbar renamed to Config.
	▶▶ Data Inspector bug fix: when interrogating in the z-planes, values from the neighboring plane (slice number decremented by 1) were reported.

Adliswil, October 2007

Maintenance Release 2.85

NEW: Network Licensing	Implementation of a network licensing scheme: A license server manages a number of purchased licenses. When starting PMOD on client machines within a network, the license server is contacted to request a free license. If one is available, it is checked out from the license pool, and PMOD starts. Otherwise, the user is informed that currently there is no license available. Since only the server requires the USB key, sharing of PMOD licenses is much easier.
Installation Running	▶▶ The RAM usage has been improved, so that the memory needs during continuous processing are markedly reduced. ▶▶ The blocking disclaimer dialog window at start-up has been removed. ▶▶ If only one user is configured, an explicit log in after start-up is no longer required. ▶▶ Improvements for starting individual tools from the command line. ▶▶ In some installation the generation of Quicktime movies fails because of library problems. It is therefore recommended to install the **Java** Media Framework (JMF) which can be downloaded from: *http://java.sun.com/products/java-media/jmf/2.1.1/download.html* ▶▶ In some installation the reading of compressed DICOM data fails because of library problems. It is therefore recommended to install the **Java Advanced Image I/O Tools** (jre) which can be downloaded from: *https://jai-imageio.dev.java.net/binary-builds.html*
General	▶▶ Better support for NaN (Not a Number) values in Ecat, Matlab and Analyze files. ▶▶ More filtering options instead of only Gaussian smoothing are now available in the tools section.
PCARD	▶▶ The MBF values are now reported in [ml/min/g], assuming a cardiac tissue density of 1.04 g/ml. ▶▶ Streamlining of the Coronary Flow Reserve report which now also includes a bar representation of the segmental flow reserves. ▶▶ Changes in the layout so that the images of the horizontal long axis view have now the apex on top, and the annotations are in cardiology style. ▶▶ If the automatic short-axis reorientation procedure fails, the user can define a marker in the left ventricle cavity. With this information, reorientation works more robustly. ▶▶ A new shortcut has been introduced to quickly apply average rotation parameters, bringing the images roughly to short-axis reorientation. This can serve as a starting point for manual reorientation.
PKIN	▶▶ A new reference model suitable for the non-invasive quantification of the acetylcholinesterase activity with the MP4A tracer was added.

	▶▶ A new variant of the dual-input curve model (with metabolites entering tissue) was added which includes a transfer coefficient linking the exchangeable compartments in tissue.
	▶▶ A reference model has been implemented in which the target tissue is modeled by a 1-tissue model, whereas the *reference tissue is described by a 2-tissue model* (Watabe et al,).
	▶▶ The Logan plot model now additionally calculates the slope using the perpendicular distances from the regression line. The resulting distribution volume should be less biased in the presence of a high noise level.
	▶▶ Unit change of kinetic parameters: "ml tissue" was replaced by ccm (cm^3). ml is now only used for fluid volumes.
	▶▶ Name changes of composed parameters. The new notations are: Vt = total distribution volume Vs = distribution volume of specific binding Vnd = distribution volume of non-displaceable uptake (K1/k2) Vns = Distribution volume of non-specific binding (k5/k6)
	▶▶ Coupled Fit: a bug in the %COV of the derived parameters was fixed (they represented values from the single fits).
PXMOD	▶▶ A new reference model suitable for the non-invasive quantification of the acetylcholinesterase activity with the MP4A tracer was added.
	▶▶ An new model was implemented which calculates the distribution volume with three methods at once: the standard Logan plot, the Logan plot using the perpendicular distances, and Ichise's MA1 method. In this order, the methods have less bias, but increasing variance. The advantage is that three Vt-maps are available in a single run.
PFUS	▶▶ Improved batch mode to allow arbitrary Reference/Reslice pairs instead of a global reference only.
	▶▶ Simplified user interface for creating rotating MIPs of fused images.
PVIEW VOIs	▶▶ The isocontour auto-VOI can now work on all frames of a dynamic series, for instance to measure the volume changes of a vessel in dynamic microscopy images.
	▶▶ The isocontour auto-VOI now supports multiple contours per slice for outlining disconnected structure components.
Database	▶▶ A new backup procedure was developed which saves the database tables together with the actual data files into a zip archive. The data from such archives can be restored into an existing database at later times.
Data Formats	▶▶ Reading and writing of Ecat data was further improved.
	▶▶ A reader was added to load blood data directly from the ABSS blood sampler file (*http://www.allogg.se*; corrected singles).
DICOM	▶▶ Query/Retrieve improvements: With some systems (eg. GE Advantage Windows) Q/R from PMOD failed because some unsupported elements were requested. By reducing the number of requested elements Q/R from PMOD now works more widely.

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Product Release 2.8

Licensing	The use of the *single-user* PMOD license is more strictly controlled. PMOD may now only be used by a single person at a time who may run up to two concurrent sessions (for side-by-side comparisons). **Caution:** *When PMOD is started a third time, the first session is stopped.*
Installation Running	‣ The 2.8 version *requires the current Java version JRE 1.5.* ‣ The individual PMOD tools can also be started directly from the command line (and therefore from other programs). Files to be loaded are specified as command line arguments. For instance, the fusion tool could be started from a different application with a reference and a reslice study loaded.
General	‣ Configuration of plug-ins such as models or loaders is easier because model name and explanation is available. ‣ The zoom factor can be entered numerically.
PCARD	The cardiac modeling tool is undergoing a *complete revision*. The improvements in the current version include ‣ Improved documentation ‣ Stress/Rest side-by-side processing. ‣ General pre-processing for anatomical blood volume and myocardium images. ‣ Automatic procedure to transform the data into standard short axis orientation. ‣ Automatic outlining of the left ventricle and right ventricle VOIs, as well as the myocardium centerline. ‣ New polar resampling for more flexibility in the segment model definition. ‣ AHA 17-segment model. ‣ Calculation of the Coronary Flow Reserve from the rest and stress results. The revision will continue and is scheduled for completion in the 2.85 version.
PXMOD	The pixel-wise modeling tool has also be revised and significantly improved: ‣ Tabs added to allow for the parallel processing of multiple data sets. ‣ Improved documentation. ‣ Button to pop up a short model explanation. ‣ The TACs from single pixels can directly be transferred to the PKIN tool together with the blood data. ‣ Parametric maps can directly be sent to the PFUS tool for a comparison. ‣ Menu newly structured. ‣ New Patlak Reference Model for calculating K_{occ} for FDOPA studies. ‣ The file names can not be edited any more. To redefine a file the **...** button must be used. ‣ After activating the **x** button processing will start from scratch including all data loading.

PKIN	‣ New button to pop up a short model explanation.
	‣ Undo/redo button to switch back and forth between models which have already been fitted.
	‣ New model for cardiac perfusion with NH_3 model: 2 compartments (Hutchins) with exponential metabolite correction (van den Hoff).
	‣ New model for cardiac perfusion with ^{11}C acetate model (van den Hoff) with corrections for metabolite buildup and flow-dependent extraction fraction.
	‣ The interpolation of blood values before the first sample was changed. In earlier versions, all blood values before the first sample were considered as 0. Now, the blood values are linearly interpolated assuming a blood value of 0 at time 0. To avoid unexpected results the user should define a blood value of 0 at a suitable time.
	‣ "Fit blood param" check box has been moved to the first tab for more ease of use.
P3D	‣ Improved documentation.
	‣ Loading of VRML data sets improved to integrate Amira results in PMOD scenes.
PFUS	‣ Batch application of an existing transformation matrix to a set of studies.
	‣ Normalization templates switched from the Analyze to the Nifti format.
	‣ Direct transfer of matched studies to the 3D tool.
	‣ Support for user-defined templates with corresponding masks.
PVIEW VOIs	‣ Split to disk exception fixed.
	‣ Improved implementation of saving VOIs as DICOM RT Structure sets.
Database	‣ *mySQL 5 is now required* (supporting local character sets). If a mySQL 4.x server is running, please first un-install, then install the new 5.x version. Finally copy the *data* directory containing the database tables from the old to the new mysql version.
	‣ Migration between databases is much faster.
	‣ Backup of database tables to file system (automatic schedule or manual).
Data Formats	‣ New loader added for images in the Nifti format (http://nifti.nimh.nih.gov/nifti-1).
	‣ TIFF loader improved; data from AIDA systems can now be loaded.
DICOM	‣ Support for national character sets (Umlaute) added.
	‣ Fix for situations where character set is not encoded in the object (Xeleris). The new Advanced DICOM configuration "Use selected character set if not present in object". It is recommended to define "ISO-8859-1" as the default (Latin-1 character set for Western Europe).
	‣ New **Query** loader allows to display images from a remote DICOM server without first saving the data to disk.
	‣ Database import server: Specification of a directory which is scanned continuously by the DICOM server. Found DICOM image series are imported into a database or can be converted to another format.
	‣ Flag to suppress the saving of SUV-related information which is encoded in private GE attributes (can cause problems on some older systems).
	‣ Studies with multiple acquisitions in one series can now be loaded. The different acquisitions are shown as separate series.

	⇥ Bug fixed with with NM Recon Tomo objects. Acquisition time was 1000 times to big.

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