# PMOD Software Release Notes

**Version 3.5**

PMOD Technologies

Printed on 16 May, 2014

# PMOD Software Release Notes

## Maintenance Builds of Release 3.5

| | |
|---|---|
| **Build 7**<br>May 17, 2014 | ⏩ Java Runtime Environment updated to Java SE 7u55 for security and compatibility reasons (stability problems on Win8.1).<br>⏩ R: Problem fixed with installing additional packages.<br>⏩ R: Data extraction from aggregates improved.<br>⏩ VOI: Interactive 3D iso-contouring used wrong seed coordinate in the fusion display.<br>⏩ PNEURO: The statistics were not properly updated when using the "Relative to" mode, in case the image was changed.<br>⏩ PNEURO/Compare to Norm: When importing a Norm, the VOIs defined for results averaging were not properly handled.<br>⏩ PFUS: Saving the inverse of a manual transformation was fixed.<br>⏩ PFUS: The 3D scatter plot had only rendered the samples for one VOI.<br>⏩ Scaling tool: A facility was added to convert CT values to a value range useful for normalizing the image to the Clinical Toolbox template (http://www.mccauslandcenter.sc.edu/CRNL/clinical-toolbox).<br>⏩ DICOM: The image presentation information was not properly used when selecting a frame subset at loading.<br>⏩ Aggregation: When combining aggregates with external data, only the "Patient Name" key worked, not the "Patient ID".<br>⏩ MINC 1 format: Images stored in coronal and sagittal orientation are now also supported. |
| **Build 6**<br>March 11, 2014 | ⏩ PKIN: An inappropriate interpolation method had been shown when using the plasma fraction.<br>⏩ PKIN: It had not been possible to configure certain models.<br>⏩ PKIN: Models used in loaded data and not configured are automatically added.<br>⏩ PKIN: Improved refresh at the end of batch mode.<br>⏩ DICOM: Improvement of the extended association negotiation and the interoperability with the Mediso DICOM server.<br>⏩ PNEURO: A problem with parcellation in the absence of properties has been corrected.<br>⏩ PNEURO, PSEG: In the case of overlap (which is inappropriate) the affected VOIs are not added to the statistics and a warning message is shown.<br>⏩ R-Console: A problem with SUV units was fixed, and VOI names now may contain the "%" character.<br>⏩ Network license selection: If a customer has multiple license servers, the proper license server can be specified as a PMOD client command line option by: -lsn[<PORT_NO>.<OPTIONAL_LICENSE_NO>@<IP_ADDRESS>] |

| | |
|---|---|
| | ⏩ Transaction server configuration: The storage path is verified to ensure that data can be stored. |
| **Build 5**<br>Jan 27, 2014 | ⏩ PKIN: Fix of the model list shown for plasma activity loaded from file.<br>⏩ PKIN: Sum of 3 exponentials better initializes the begin time, namely to the signal maximum.<br>⏩ PNEURO: Option to selectively enable/disable sulci deformation for both the Maximum Probability and the Parcellation method (default = off). In parcellation it had previously always been applied.<br>⏩ PNEURO: Progress information improved.<br>⏩ PNEURO: 3D rendering problem fixed.<br>⏩ PFUS: Load protocol better supports data format changing.<br>⏩ Sizing of the curve control area improved. |
| **Build 4**<br>Jan 12, 2014 | ⏩ R console improvements and fixes: Plots did not work on Windows systems.<br>⏩ Pipe processing: Error handling improved so that errors terminate processing.<br>⏩ SUV external tool in pipe processing returns an error for zero injected activity in the data.<br>⏩ Data association functionality extended so that external segments can be used in the PVC external tool. In this case the MR segmentation step is omitted.<br>⏩ The external segmentation tool applies the same colortable as the processed data.<br>⏩ ATL database export: Speed (factor 2.5) and stability improvements.<br>⏩ PKIN: Curve zooming extended by a factor of 100.<br>⏩ PNEURO/Compare to Norm: Option added to limit z-score clusters by the minimal number of included pixels. |
| **Build 3**<br>Dec. 22, 2013 | ⏩ PNEURO, Norm Comparison: Cluster analysis with a specified maximal number of clusters.<br>⏩ PNEURO, Maximum Probability: Sulci bottom detection available as an additional segmentation option. It adjusts the VOIs such that they end in the sulci bottoms.<br>⏩ PNEURO, Maximum Probability: Support for user-defined atlases, which may also define animal brain VOIs (monkey, rat, mouse).<br>⏩ PKIN: Display layout showing the curves from all regions revised. All TACs, targets or model curves can now be shown.<br>⏩ R: Identity line option added to the scatter plot.<br>⏩ R: Support for box plots showing multiple variables.<br>⏩ R: Verification of packages at start time.<br>⏩ R: Data reduction procedure implemented for pixel-dump and image data, to increase loading speed.<br>⏩ PXMOD: If mask and VOIs are not manually saved when proceeding, a dialog window appears and simplifies saving.<br>⏩ PXMOD: VOIs used in preprocessing are initially switched off on the parametric maps.<br>⏩ Mapping of pixels defined in scatter plots back to the image space supported in the "Segmentation" procedures. |

| | |
|---|---|
| | ⏩ Arbitrary ROI definition in scatter plots via conversion into an image and usage of the standard VOI functionality.<br>⏩ Improved synchronization of the SUV units shown in the data inspector curve display.<br>⏩ DICOM Loading: Handling of Philips ADNI images with wrong high bit value.<br>⏩ DICOM Saving: Fix for using the proper output SOP selection.<br>⏩ Analyze: Improved handling of the origin for files stored in little endian.<br>⏩ Display: Inspector TAC updated also when triangulating via the MIP image. |
| **Build 2**<br>Nov. 11, 2013 | PNEURO: IMPORTANT - it is necessary to replace the parcellation resources for taking advantage of the improvements. This is most easily done by removing the directory Pmod3.5/resources/parcellation. When restarting and calling PNEURO, an appropriate download link will be shown.<br>⏩ PNEURO, Maximum-Probability method: Partial-volume correction improved. The VOI parts removed by gray-matter thresholding are considered as complementary VOIs and used for PVC.<br>⏩ PNEURO, Maximum-Probability method: Ventricles not affected by masking with the segments map.<br>⏩ PNEURO, Maximum-Probability method: White-matter VOIs are initially hidden.<br>⏩ VOI: Smoothing option introduced for the iso-contouring tool.<br>⏩ R: Improvements for sending pixel dump results to R. Preview, and support for multiple data files.<br>⏩ R: Revision of the scatter plot solution for better visualization.<br>⏩ Fusion: The separate color table used for fusion can be inverted separately.<br>⏩ External VOI-based PVC tool: The Hammers N30R83 atlas can also be selected, if PNEURO is licensed. |
| **Build 1**<br>Oct. 22, 2013 | Initial upload of 3.5 version. |

# Product Release 3.5

The 3.5 product release brings major improvements for the PNEURO and PKIN tools, as well as for the R statistics interface. Additionally, many improvements were implemented for the various tools and the platform, whereby the list below only highlights the major points.

### Features

| | |
|---|---|
| **General** | VOIs:<br>⏩ New VOI statistics: surface estimation, maximum diameter, sphericity and area under curve.<br>⏩ Use of B-Splines between vertices to create smooth contours.<br>⏩ SUVR calculation easily possible in statistics panel.<br>⏩ Multiple user interface improvements of statistics panel: VOI merging, sorting, show only selected information.<br>⏩ Improvements of VOI tree handling.<br>⏩ VOI/ROI/Contour toolbars reorganized.<br>Miscellaneous:<br>⏩ Flexible marker use: set markers by coordinates specification; distance map for a set of markers; sum of distances between two sets of markers; intensity profile along a set of markers; spatial transformation of markers.<br>⏩ Aggregation: highlighting of common parameters, adding of covariates to the data, control over the aggregation order.<br>⏩ Database: Replication facility for migrating the database information to a new database without actually moving the data; response accelerated; facility for adding project/diagnosis/comment when saving to database; C_STORE option for data export; "last month" and "last year" filter added.<br>⏩ Pipe processing and external tools improvements in: SUV conversion; histogram calculation; median filter in time domain; pipe organization and results saving.<br>⏩ Interference of automatic reorientation and macros solved in several tools.<br>⏩ Linear regression added to 2D scatter plots. |

| | |
|---|---|
| R statistics Console | 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.<br><br>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.<br><br>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.<br><br>Compared to version 3.4 the whole functionality, including data preparation, was revised and extended. |
| **PKIN** | New:<br>⏩ Multi-model fitting: Support for fitting data with multiple models at once.<br>⏩ Filtering options for tailoring the model list to the actual data (e.g. models with/without blood data, reversible/irreversible configurations, etc).<br>⏩ Saving of the model fitting history in the km file such that prior configurations can easily be recalled.<br>⏩ New tissue model: 2-tissue compartment model with $k_5$ efflux.<br>⏩ New tissue model: 3 sequential tissues described for FDG in skeletal muscle.<br>⏩ New tissue model: Multi-linear approach for estimating the influx of irreversible tracers (MLAIR).<br>⏩ New tissue model: Utility for calculating OLINDA-ready residence times in dosimetry studies.<br>⏩ New blood model: Gamma function peak plus two exponentials.<br>⏩ New plasma fraction: linear plasma/whole-blood ratio.<br>⏩ New composite data format for importing all data parts at once.<br>⏩ New curve tools: Decay correction, decay un-correction, volume edition, acquisition times trimming.<br><br>Improved:<br>⏩ Batch mode: Support for composite data format and multi-model fitting.<br>⏩ The organization of the blood data has been unified for all input curves of models with more than only a single input curve.<br><br>Changed:<br>⏩ Modified gamma functions 1 and 2 deprecated.<br>⏩ Model for cardiac water PET with geometrical correction removed. |
| **PNEURO** | New:<br>⏩ Batch mode support for brain VOI generation. |

| | |
|---|---|
| | ⏩ The landmarks required for the brain parcellation are now automatically generated, making this method batch-able and easier to use.<br>⏩ Parcellation now also estimates Hippocampus and Amygdala from the knowledge base.<br>⏩ Parcellation performs a sulci optimization with the cortical VOIs.<br>⏩ Support for the AAL-Merged atlas as well as user-defined atlases in the MNI space.<br>⏩ Introduction of the tree structure for the AAL atlases.<br>⏩ Addition of regions to the AAL atlas for making it more comparable to the N30R83 atlas.<br>Improved:<br>⏩ Harmonization of the workflow and the resulting VOIs across the two brain VOI approaches.<br>⏩ Brain norm editor better streamlined and the probability map normalization added.<br>⏩ Additional parameters made available for segmentation and matching.<br>Changed:<br>⏩ New knowledge base for the parcellation, now including 26 rather than 14 normal subjects (all non-smokers; female: 3, left-handed:1, age: 34±12, min 19, max 29). |
| **PSEG** | ⏩ Species selection: HUMAN WB and HUMAN BRAIN added.<br>⏩ List of cropping sizes adjusted to species selection.<br>⏩ Instead of overwriting existing VOIs with the same name, structures can now also be appended.<br>⏩ If an anatomical image is loaded, it is pre-selected for fusion with the segments.<br>⏩ Hot region growing added to the default VOI tools. |
| **PCARDP** | New:<br>⏩ Facility to replace the LV curve by an externally created curve (e.g. obtained with an online blood sampler).<br>⏩ New crop box sizes suitable for rodents.<br>⏩ Simplified data loading by associating rest and stress scans in database.<br>Improved:<br>⏩ Behavior of data loading for creating factor images for water bolus studies.<br>Changed:<br>⏩ 2-tissue compartment model for Rb: Vd removed corresponding to differential equation system. |

| | |
|---|---|
| **P3D** | New:<br>⏩ Smoothing added to VOI rendering protocols.<br>⏩ Markers defined in images are rendered when transferring the images to P3D.<br>Improved:<br>⏩ Functionality of Segmentation page.<br>⏩ Tree allows multiple nodes with the same name. |
| **PXMOD** | ⏩ Transfer of pixel-TACs to PKIN optimized.<br>⏩ Improvements of workflow. |
| **PALZ** | ⏩ Crop box added. |
| **PFUS** | ⏩ Additional brain normalization procedure using tissue probability map information.<br>⏩ Facility to map points localized in a 2D scatter plot ROI back to the image space.<br>⏩ Scatter plot analysis tool.<br>⏩ Support for a prefix to the original file name when saving multiple matched series. |
| **Data Formats** | ⏩ Bruker Paravision MR loader added.<br>⏩ MINC 1 loader added.<br>⏩ DICOM: Preview facility for the DICOM Special Cases; export/import of nodes list; various improvements for different devices. |

Zürich, Oct. 18, 2013

# Maintenance Builds of Release 3.4

| | |
|---|---|
| **Build 9**<br>May 17, 2014 | ⏩ Java Runtime Environment updated to Java SE 7u55 for security and compatibility reasons (stability problems on Win8.1).<br>⏩ PNEURO: Parcellation could be started even when both deep nuclei and cortex parcellation were switched off.<br>⏩ PNEURO: Fixed problem of loading gray matter template in parcellation in case of previous loading of dynamic series by Autodetect.<br>⏩ PKIN: Incorrect times had been used when switching from Logan to the B/I model.<br>⏩ ATL version: Incoming folder processing could close DICOM Server. |
| **Build 8**<br>Sept. 23, 2013 | ⏩ PKIN/PXMOD, Patlak plot: The plasma activity had only been integrated from the time of the first sample. Corrected to add area of linearly integrated blood activity assumed zero at time 0.<br>⏩ PKIN/PXMOD, Patlak Reference Plot: Independent of the t* setting, the whole data segment had been used for the linear regression.<br>⏩ PNEURO: Partial-volume correction had not considered the parts of the activity outside the gray-matter intersected VOIs. Complementary VOIs are now included in the correction.<br>⏩ VOI: Loading with transformation could result in truncated VOIs when they were outside the field-of-view.<br>⏩ VOI: Statistics within a range did not work properly when invokeded repeatedly.<br>⏩ VOI: Intersection of dynamic VOIs was not correct for frames beyond the first one.<br>⏩ VOI: Compatibility option for statistics saved with the 3.3 version replacing the space character by "_" in descriptions.<br>⏩ DICOM: Support for fixed color scale in the generation of SC DICOM output. |
| **Build 7**<br>July 12, 2013 | ⏩ P3D: Improvement of protocols including VOI renderings.<br>⏩ PNEURO: Initial 3D rendering limited to VOIs, but the skull-stripped MR is also made available for rendering.<br>⏩ Fix for a VOI undo problem in PNEURO and PSEG.<br>⏩ Pipe processing: path definitions were not working for data other than DICOM or database files.<br>⏩ PCARDP: Protocols for ammonia didn't store the flag for calculation of the MBF maps.<br>⏩ PCARDP: Stress/rest is now detected in the series description when performing the factor analysis for water PET studies.<br>⏩ ECAT: Improved support of the origin coordinates.<br>⏩ Save all: better handling of the settings across the saved files. |

| | |
|---|---|
| **Build 6**<br>April 22, 2013 | **PSEG Tool Released**: New tool for the semi-automatic segmentation of dynamic rodent PET series is available. Please refer to the product description on www.pmod.com for details.<br>⏩ PNEURO: Support added for using the MR segments calculated in a prior PNEURO session. They can be loaded together with their transformation to the atlas space.<br>⏩ PNEURO: Improvement of the parcellation result by removing spurious isolated pixels.<br>⏩ PCARD: The factor images generated for water studies can be cropped before short-axis reorientation.<br>⏩ PCARD: Protocols include recalculation and cropping of factor images.<br>⏩ PFUS: Fix for an initial slice offset due to differing slice thicknesses of the reference and the input series.<br>⏩ PVIEW: Fix of a problem in the Split slices and Split frames procedures.<br>⏩ Save All function: Revised interface fixing a bug in propagation of changes.<br>⏩ Series description added to Data Inspector title bar.<br>⏩ Option to switch off automatic checking of available updates.<br>⏩ Fixed problem when saving reports with multiple pages as DICOM SC objects. |
| **Build 5**<br>March 7, 2013 | ⏩ PNEURO: The VOIs are saved with the protocol definition to preserve manual edits.<br>⏩ PNEURO: Facility for saving all intermediate results of interest at once with a save all button in the lateral taskbar.<br>⏩ PKIN: Handling of time-overlaps occurring due to erroneous DICOM time encodings.<br>⏩ R statistics: Multiple functional improvements.<br>⏩ Scaling tool: new options (divide by VOI average, scale to 1 or 255 max).<br>⏩ VOI: Masking inside VOI using its own VOI average.<br>⏩ DICOM: Improved handling of PET frame reference time values. Automatic calculation of frame start and end times for PET images referring the time of average activity.<br>⏩ External Histogram tool: extended with "In VOI" option.<br>⏩ PCARDP: Zero time setting had not been applied when using factor analysis.<br>⏩ Transaction server: improvements in starting and status reporting.<br>⏩ Default configuration: Raw and Query data loaders added.<br>⏩ Distribution: Java updated to JRE 1.7.0_17. WIBU Key driver files updated to 6.11.1057.500. |
| **Build 4**<br>Jan. 14, 2013 | ⏩ PNEURO: Cortical VOIs are created using the approach of the Maximum Probability tool.<br>⏩ PNEURO: FDG or other PET images with anatomical information can be used for determining the normalization transform, replacing the role of the MRI.<br>⏩ PNEURO: Organization of the Hammers VOIs in a hierarchical tree. This also allows simplified merging functions. |

| | |
|---|---|
| | ⏩ PNEURO: Facility to save the different transformations between the spaces.<br>⏩ PNEURO: The VOI volume is calculated instead of the value average in the case of MR-only analyses.<br>⏩ PNEURO: Partial-volume correction now also considered the complementary white-matter parts of masked VOIs. Improved interface for adding scanners.<br>⏩ PNEURO: Protocols can be used for loading configurations without starting processing.<br>⏩ PNEURO: Fix of unit support in protocols.<br>⏩ PNEURO: Volume-weighted averaging of curves added on Statistics page.<br>⏩ PCARDP: Improvements of the factor image reorientation for water data.<br>⏩ PCARDP: Simplified loading from the side bar of dynamic and transmission images for factor analysis.<br>⏩ PFUS: The data of scatter plots can be saved as statistics from the context menu.<br>⏩ PFUS: RGB images can be fused with monochrome images.<br>⏩ PKIN: Regions containing "cerebellum" or "reference" in the name are now pre-selected for the reference region after data import.<br>⏩ PKIN: Fix of the Ito plot results. The result parameters were interchanged (Vt <-> Vnd, K1<->K1') and BPnd not calculated.<br>⏩ PKIN: Dedicated filters for loading data didn't work.<br>⏩ VOI: Multiple VOI sets of an image can be converted into mask files.<br>⏩ VOI: Masking by average value in VOI added. |
| **Build 3**<br>Nov. 24, 2012 | ⏩ PXMOD: The program could freeze for some model configurations when running all processing steps.<br>⏩ Acceptance tests fixed for the ATL version.<br>⏩ PNEURO: Fix in the calculation of the lateral frontal horn thickness.<br>⏩ PNEURO: Improvements when switching between workflows.<br>⏩ PNEURO: Denoising option added to Maximum Probability solution.<br>⏩ PCARDM: Improved compatibility with prior protocols. |
| **Build 2**<br>Nov. 8, 2012 | **CAUTION:** Due to Java-related errors users are strongly recommended migrating from Build 1 to Build 2.<br>⏩ Java: A severe bug was detected in the Oracle JRE 1.7.0_07 distributed with Build 1 which caused unpredictable numerical errors. The PMOD installation packages were updated with JRE 1.7.0_09.<br>⏩ PNEURO: New normalization procedure for T1-MR images which dramatically improves the quality of the VOIs in the Maximum Probability module.<br>⏩ PNEURO: Time-weighted average statistics added for dynamic PET scans.<br>⏩ PKIN: Tissue model curves and compartment model curves shown in HD.<br>⏩ VOI statistics aggregation: Improvements and fix in handling of old format statistics.<br>⏩ Cardiac PET: List of recognized ammonia strings extended.<br>⏩ Cardiac PET: Fix for handling a problem with manually shifted EPI/ENDO |

| | |
|---|---|
| | contours.<br>⏩ Cardiac PET: The excess ENDO TAC was removed.<br>⏩ Cardiac PET: Static input creates polar plot with average values in AHA sectors instead of the individual samples.<br>⏩ R statistics console: More plots added (histogram,scatter plot, box plot, density plot).<br>⏩ DICOM: Fixed problem with saving private slices orientation and position elements for NM objects with more than 1365 frames when explicit transfer syntax is used. |
| **Build 1**<br>Oct. 16, 2012 | Initial upload of 3.4 version. |

# Product Release 3.4

The 3.4 product release includes a completely revised and functionally extended tool for the analysis of human brain images, as well as a new module for the quantification of cardiac MRI images. Further, in order support the users with their statistics analysis, an interface was developed to the "R" statistics server.

### Features

| | |
|---|---|
| **PNEURO**<br>**- EXTENDED** | The former PBRAINDB tool has been completely revised and extended. In addition to the normal brain database functionality two modules were added for the automatic generation of human brain VOIs, one using the Hammers N30R83 maximum probability atlas, the other parcellating $T_1$-MR images. See product brochure for more details. |
| **PCARDM**<br>**- NEW** | A new tool for cardiac MR was jointly developed with the CMR research group of ETH Zurich, Switzerland. Using PCARDM, researchers in the field of CMR may apply the state-of-the art perfusion quantification approaches to their data and compare them with the standard qualitative outcome or an external gold standard. For version 3.4, the cardiac MR tool is bundled with the cardiac PET tool. See product brochure for more details. |
| **General** | A lot of effort was devoted for assembling numerical PMOD results and connecting PMOD with the "R" open-source statistics environment (www.r-project.org). The idea is that the user can easily aggregate results for comparing methods or populations and analyze them in "R". A variety of numerical results can be analyzed in this manner like VOI statistics and modeling parameters.<br><br>New:<br>⏩ The PMOD distribution includes the latest Java 7 version.<br>⏩ R-console: facility for connecting to "R" servers, transfer data, send commands for analyzing the data, retrieve the results and visualize them.<br>⏩ Direct saving of aggregates as an Excel file.<br>⏩ The "PMOD Version" area in the ToolBox acts as a drop-box for files: When a file is dropped (image file, protocol file, pipe, etc) the linked module starts.<br>⏩ PSAMPLE and the R console can start automatically after user login.<br>⏩ New association in the DB interface to support grouping of PET and MR segments for partial-volume correction.<br><br>VOIs:<br>⏩ New statistical measures added: median, area-under-curve (AUC), peak statistics in sphere centered at the VOI maximum.<br>⏩ Statistics can be calculated on all loaded images at once and the results shown on tabbed pages.<br>⏩ Interactive region growing and shrinking holding down the "Ctrl" key.<br>⏩ Brush mode for creating VOIs and deleting from VOIs.<br>⏩ Contour generation with the criterion of equality. |

| | |
|---|---|
| | ⏩ New contour editing modes which disallow overlapping VOIs.<br>⏩ VOI template for cynomolgus monkeys added.<br>⏩ Intersection of VOI template with list contours.<br>⏩ Statistics output window is not blocking any more.<br>⏩ Saving of VOI statistics as DICOM Structured Report.<br>Improved:<br>⏩ Pipe processing: Functionality extended for running multiple pipe definitions subsequently. Macros and VOI statistics are now also supported in pipes. Partial-volume corrections revised so that they can also be used in pipes.<br>⏩ Time editing facility improved. Simplified shifting of time vectors and calculation of start/end times from mid-times.<br>⏩ New options in replace tool using the magnitude.<br>⏩ Network license server supports multiple license files.<br>⏩ License client can view state of licenses on the server. |
| **PKIN** | New:<br>⏩ Simplified fitting of the blood delay together with the tissue compartment model, both for a single TAC as well as coupled TACs.<br>⏩ Spectral analysis model added.<br>⏩ Power-function damped three-exponential metabolite correction added (requested for use with $^{11}$C-DASB). It handles the situation where the parent fraction starts at a low value and then increases, before dropping.<br>⏩ Blood delay parameter included in the model history.<br>⏩ Visualization of min/max parameters in summary lists: min = green, max = red. Columns with constant values are marked in blue.<br>Improved:<br>⏩ Bug fix in the handling of a delayed input curve: There was an impact in cases in which the inherent assumptions of the kinetic data are not met. Particularly, if the input curve had significant contributions before time zero, and when the PET frames were not started at time zero (=injection time).<br>⏩ Simplified user interface for curve loading.<br>⏩ Monte Carlo functionality for coupled fitting integrated into the Monte Carlo tab.<br>⏩ Simplified selection of the regions to be coupled with long region lists.<br>⏩ Units of curve plots revised. |
| **PCARDP** | New:<br>⏩ Definition of the endo- and epicardial boundaries as an alternative to the centerline heart model definition.<br>⏩ Cardiology-style report page showing the average uptake images of stress and rest in the different orientations.<br>⏩ Calculation of parametric MBF maps for ammonia using a basis function method.<br>⏩ UCLA model for MBF quantification with ammonia. |

| | |
|---|---|
| | ⏩ Facility for cropping the images around the heart which is particularly useful when the reconstructed images are not zoomed onto the heart.<br>⏩ Visual support for optimizing time-averaging of the early and late uptake phases.<br>⏩ Facility for saving the VOIs in the space of the MBF maps for comparison purposes.<br>⏩ Support for the aggregation of the result statistics.<br>⏩ Vertical taskbar for data loading and results processing.<br>⏩ Configuration option to reduce the number of visible VOI tools to the most relevant ones.<br>Improved:<br>⏩ Unified numerical results organization for dynamic and static studies.<br>⏩ Protocols for water studies with factor analysis fixed. |
| **P3D** | New:<br>⏩ Completely new page for the object segmentation. The image space is larger, and segment generation is easier and more flexible.<br>⏩ When VOIs are directly submitted for 3D rendering from the viewing tool the user is offered the choice between the rendering modes (surface, stripes).<br>⏩ Texture color interpolation can be switched off, for instance for the visualization of parcellated brain segments.<br>⏩ Example protocol showing elements of the heart anatomy.<br>Improved:<br>⏩ Better support for the STL (STereoLithography) format. Surface renderings can be saved in STL and used for flow simulations (ANSYS Fluent) and for printing 3D prototypes (Materialize MiniMagic). Loaded STL objects can be surface textured.<br>⏩ Faster and smoother surface rendering of VOIs.<br>⏩ Better control for the rendering of dynamic VOIs.<br>⏩ More accurate visualization of the pixels to be included before the actual segmentation. |
| **PALZ** | New:<br>⏩ Lateral taskbar for loading and closing of the image data.<br>⏩ Facility for aggregating the statistics results of the PALZ analysis (only in non-simplified mode). |
| **PFUS** | New:<br>⏩ Masking facilities for restricting the information used in matching and normalization.<br>⏩ Motion correction can be used in batch mode and in pipe processing.<br>⏩ In batch mode and the interpolation tool the user can choose to use the resolution of the input study, for instance in the case of a low-resolution reference. |

| | |
|---|---|
| **PVIEW** | New:<br>⏩ Stitching tool which automatically determines the overlap of two acquisitions and creates a combined data volume. |
| **PXMOD** | New<br>⏩ Model for the calculation of MBF maps from dynamic cardiac NH3 PET series. The model applies a basis function approach and includes right and left ventricular spillover. |
| **PSAMPLE** | Improved:<br>⏩ Calculation of the calibration factor from a single calibration acquisition. Two areas can be interactively positioned on the calibration curve: one for calculating the average dark count rate (no activity in catheter), and the other for calculating the average signal plus dark counts (filled catheter). |
| **Data Formats** | Improved:<br>⏩ Interfile: Extension for saving SUV-related information, patient information, and the image orientation.<br>⏩ Nifti: Support for multi-layer images added.<br>⏩ MicroPET: Support for reading pre- and postinjection activities.<br>⏩ MicroPET: Fixed a problem with reading large Inveon data (>2GB).<br>⏩ Revision of series date default when the information is not contained in file.<br>⏩ DICOM Element viewer: supports copy to clipboard. |
| **ATL** | New:<br>⏩ Flat view shows seriesDBID and patiendDBID in ATL.<br>⏩ SOP class of exported data is included in the log.<br>⏩ ATL ip, version and build date are added to details on application level.<br>⏩ View of license state extended by the possibility to clean up licenses. |

Zürich, Oct. 16, 2012

# Maintenance Builds of Release 3.3

| | |
|---|---|
| **Build 10**<br>Dec. 7, 2012 | ⏩ PKIN: Fix of the Ito plot results. The result parameters were interchanged (Vt <-> Vnd, K1<->K1') and BPnd not calculated.<br>⏩ PCARD: Improved loading of water protocols using the factor analysis.<br>⏩ PCARD: "Oxygen-water O^15^ / ^15^Oxygen" added to accepted tracers list.<br>⏩ DICOM: Files are now accepted using defined length sequences with wrong length values.<br>⏩ MicroPET: Fixed problem with loading Inveon dynamic gated images. |
| **Build 9**<br>Sept 4, 2012 | ⏩ VOI: In version 3.303 multiple VOI definitions were saved in the files. The statistics were still correct, but performance suffered. A function was added to the VOI Tools panel for correcting this problem.<br>⏩ DICOM: Default transfer syntax for creating DICOM files on local disk is changed from implicit little endian to explicit little endian in favor of compatibility with other programs.<br>⏩ DICOM: Problem fixed in conversion of NM objects to PET objects during export from PMOD DB.<br>⏩ DICOM: Problem fixed in conversion of Compressed DICOM objects during export from PMOD DB. The image closing item was missing missing and made the images unreadable in PMOD as well as other programs.<br>⏩ Pipe Processing: SUV tool fixed to work with pipe processing. The relevant information has to be available in the input files. |
| **Build 8**<br>July 9, 2012 | ⏩ PXMOD: Bug fixed with handling the units of blood files.<br>⏩ PSAMPLE: Fix of a problem with integration times longer than 1 sec. They could result in timeouts.<br>⏩ PFUS batch processing: Fixed a problem with missing origins when image data was resliced with a rigid transformation (DICOM or NiFTI affected, not Analyze).<br>⏩ DICOM: Improved handling of dicom multiframe images with wrong number of slices specified in element 0054,0081.<br>⏩ External tools: A tool was added which allows correcting images in case of DICOM objects with wrong endian endcoding.<br>⏩ Database: When exporting files from a database the patient size and weight is not replaced in the file, if it already exists.<br>⏩ Database: Connection timeout increased from 2 to 5 seconds to accommodate slow WAN connections and heavy loaded systems. |
| **Build 7**<br>May 14, 2012 | ⏩ PFUS: Improved support for combining of rigid and manual transformations.<br>⏩ PXMOD: STRM2 model had not been visible.<br>⏩ VOI: VOI histogram had not been correctly displayed.<br>⏩ Pipe processing: problem of scale tool fixed.<br>⏩ Initial reformatting of images: A blank screen could be shown when reading floating point image data with initial reformatting. |
| **Build 6**<br>April 2, 2012 | ⏩ PFUS: Fixed a reslicing problem in brain normalization if the reference had a pixel size of exactly 1mm. In this case warping was incomplete. |

| | |
|---|---|
| | ⏩ PKIN: Correction of the formula used for calculating the Watabe parent fraction: 1 / [ 1 + A*t$^{B}$]$^{C}$ had been used instead of 1 / [ 1 + (A*t)$^{B}$]$^{C}$.<br>⏩ PALZ: New option added for calculating the patient age based on the birthdate and the PET study date. Previously, only calendar years were used.<br>⏩ SUV calculation: In some situations incorrect units were shown for SUV or %ID, and when saving calculated SUV images a wrong unit might have been saved to the file.<br>⏩ PCARD: The markers are not cleared any more by the generation of new VOIs, and they are available in the overlay of all image types.<br>⏩ PCARD: Improved synchronization between the polar plots and the images on the "Modeling" page. Clicking into a polar plot causes the corresponding pixel being triangulated in the images if synchronization is enabled.<br>⏩ DICOM: Fixed handling of the private Philips scaling factor. It is now only applied if the image units are counts. |
| **Build 5**<br>Feb. 28, 2012 | ⏩ PKIN: The plasma fraction model had not been saved if there was no loaded plasma fraction data.<br>⏩ PKIN: The prescribed weighting had not been functional for the blood model fitting.<br>⏩ PCARD: Myocardium sampling range is now limited within the defined wall thickness (instead of 3 times the pixel size) centered at the contour line.<br>⏩ PCARD: There are now two different orthogonal layouts, the default 1x3 layout and a 1x4 layout also showing the MIP.<br>⏩ DICOM Server: Stability improved, now handling more than 10'000 objects in a single transfer.<br>⏩ Scientific Output: A grid of adjustable size can optionally be added to the overlay. |
| **Build 4**<br>Jan. 26, 2012 | ⏩ VOI: Fixed a problem with growing disk size when VOI files were loaded and saved again. The problem was not affecting the VOI definition and resulting statistics.<br>⏩ VOI: There was a problem to read 3.3 multi-contour VOIs with parts outside the target bounding box in prior PMOD versions. To be readable in those versions, VOIs have to be loaded/saved again with 3.3 Build 4.<br>⏩ PFUS: Change of the color synchronization. The reference and input displays are permanently data driven to support the modality dependent color tables.<br>⏩ Basic operation external tool: the optical density transformation [-log10(v)] was added.<br>⏩ Frame averaging based on the number of included frames always used the total number of frames independent of the selected frame range. Time-weighted averaging was correct.<br>⏩ PCARD: The flow areas (LAD, LCX, RCA) were added as color-coded overlays to the polar plots of the kinetic results. |
| **Build 3**<br>Dec. 10, 2011 | ⏩ PKIN: List of default models extended.<br>⏩ PKIN: New model added which calculates the AUC of the tissue TAC and the input curve as a function of time, as well as their ratio.<br>⏩ PKIN: The region names are now shown in the curve control area. |

| | |
|---|---|
| | ⏩ PKIN: The default weighting function for the different blood models was changed from relative to constant weighting.<br>⏩ PKIN: Loading of blood data without having loaded tissue TACs previously could cause an error or lock the system.<br>⏩ VOI: The HOT 2D/3D and COLD 2D/3D methods have now also the Ctrl+Shift option for adding structures to the same VOI.<br>⏩ VOI: The original VOIs can optionally be removed after merging.<br>⏩ VOI: Problem to read dynamic (multiframe) VOIs with ROIs fully out of image bounding box fixed.<br>⏩ PFUS: Manual motion correction has not been possible because the "Copy to all" button and the "Fixed" transformation check were incidentally hidden.<br>⏩ PXMOD: The loading of mask files was changed to avoid unwanted initial transformations.<br>⏩ PCARD: Protocol functionality extended to allow changing the image series.<br>⏩ Database: Redesign of the dialog window for setting the Project/Diagnosis/Locked properties to make it more flexible.<br>⏩ Database: Button added to hide/show the image preview area. |
| **Build 2**<br>Nov. 12, 2011 | ⏩ PFUS: Initialization simplified by moving the transformation parameters from the main interface to the image reslicing interface.<br>⏩ PFUS: The transformation parameters can now be copied to the clipboard in the transformation inspection panel.<br>⏩ VOI: The VOI list part of the user interface can be hidden in case the horizontal screen space is limited.<br>⏩ VOI: When saving a VOI atlas, the destination folder can be selected instead of always saving to the system location.<br>⏩ PXMOD: Default unit values can now be configured for image file formats lacking the units.<br>⏩ PKIN: Two models were missing from the configuration, Ichise's MA1 method and the 4 compartment model with metabolites.<br>⏩ PKIN: The initial model parameters of loaded KM files are added to the history.<br>⏩ PKIN: Model configurations which are loaded now also switch the model appropriately instead of reporting a problem in case a different model was active. |
| **Build 1**<br>Oct. 30, 2011 | ⏩ Initial upload of 3.3 version. |

# Product Release 3.3

The 3.3 product release was focused on stability and user interface improvements. In addition, the functionality was further extended as described below.

### Features

| | |
|---|---|
| **PSAMPLE** | The gold standard of PET quantification is kinetic modeling using information about the tracer concentration in arterial blood. To promote wider use of PET quantification Swisstrace (www.swisstrace.ch) has introduced a new online blood sampling device for humans and animals. It is highly sensitive and accurate due to coincidence counting with LYSO crystals, and the unique design makes it fully MR compatible. PMOD is proud to provide the PSAMPLE data acquisition software for this sophisticated instrument. |
| **General** | New:<br>⏩ Introduction of a buffer which allows using data created in one tool in another tool without saving them first to disk.<br>⏩ New option to collapse user interface elements which are rarely used. This is particularly useful with smaller computer screens.<br>⏩ Definition of the default color tables for the major modalities (PET, SPECT, MR, CT<br>⏩ Support for modality-specific color table presets.<br>⏩ New display option which allows including the color bar directly into the image area.<br>⏩ Saving of color table presets with absolute thresholds. This is particularly useful for CT images.<br>⏩ New split color table optimized for assessing difference images.<br>⏩ Improved visual support for the reorientation of images in the loading window.<br>⏩ Generalized facility for the short-axis reorientation of cardiac PET data.<br>⏩ Direct import of DICOM images into a PMOD database without requiring a DICOM server.<br>⏩ Better SUV inspector, which also allows displaying % injected dose per ml.<br>⏩ Configuration which remembers all window sizes and applies when the window is opened again.<br>⏩ Replacement of a value range by a single value.<br>⏩ Visual assistant for loading images which are not in standard orientation.<br>⏩ Monitors for the status of the DICOM and transaction servers can be started from the ToolBox.<br>⏩ PVC (MR based) extended by gray matter statistics calculation and comparison (corrected vs. non corrected PET).<br>⏩ Temporal MIP which works in the time domain: For each pixel it uses the maximal value of all time frames to create a volumetric data set. |

| | |
|---|---|
| **PALZ** | New:<br>⏩ Acceptance test to verify the tool operation.<br>⏩ Option to use a streamlined and simplified user interface.<br>⏩ The new criterion "PET Score" was implemented according to Herholz et al., "Evaluation of a calibrated FDG PET score as a biomarker for progression in Alzheimer's disease and mild cognitive impairment", J Nucl Med, 2011 52:1218-1226.<br>⏩ When loading data different from FDG PET a notification message appears.<br>Changed:<br>⏩ Redesign of the report pages.<br>⏩ The page for the normalization inspection has been reduced to showing a single, big fusion image with the template. |
| **PKIN** | New:<br>⏩ Support for the conversion of whole blood activity into plasma activity by the use of a plasma fraction function. Plasma fractions can be loaded and models fitted to the plasma. Furthermore, population functions can also be applied if no data is available.<br>⏩ Representation of the model curves in a high-density fashion to more accurately see the shape which is used in the calculations.<br>⏩ Support for saving particular sets of model parameters either under a specific name, or as the global default parameters for a model.<br>⏩ Inclusion of the area-under-the-curve (AUC) calculations.<br>⏩ Buttons to step through the loaded data sets.<br>Changed:<br>⏩ The curves available for display are controlled by the selected panel. Preferences of the user are maintained during a session.<br>⏩ The compartment models with a spillover contribution (vB>0) may result in slightly different model curves. This is due to a correction in the averaging procedure of whole-blood. |
| **PFUS** | Substantial user interface improvements were done to make data processing more intuitive. In particular, the first page was significantly revised to make it easy for the user to start with a reasonable initial match. The automatic matching methods now always take into account manual adjustments of the user.<br>New:<br>⏩ Calculation of the inverse of the current transformation is always possible. By this approach, the inverse of any series of combined transformation can be obtained.<br>⏩ Ability to shift the input series in the large fusion mode.<br>⏩ Defaults added for mouse brain normalization.<br>⏩ Rigid matching: Two new options are available allowing to enable/disable the fitting of rotation angles and scaling factors. |

| | |
|---|---|
| | Changed:<br>⏩ The automatic methods now always take into account the initial positioning which can be done by aligning the centers of the data volumes, their origins, two manually placed landmarks, or the result of manual adjustments.<br>⏩ Transform saving has been revised to always encompass all of the applied transformations.<br>⏩ Reslicing is refreshed when the pixel size is changed. |
| **VOIs** | The VOI functionality was again significantly extended with an emphasis on region growing methods.<br>New:<br>⏩ 3D region growing method for hot and cold lesions.<br>⏩ Interactive 3D region growing, which also allows extending VOIs.<br>⏩ Drawing mode in which the vertexes snap to the pixel edges, and where the contours have staircase shape enclosing exactly the including pixels.<br>⏩ Interpolation of contour VOIs across slices.<br>⏩ Morphological operations on existing VOIs (Erosion, Dilation, Opening, Closing).<br>⏩ Calculation of the intersection VOI of a group of VOIs.<br>⏩ Interactive removal of data from an image by growing a sphere.<br>⏩ Direct outlining of segmented structures into contour VOIs in the external segmentation tool.<br>⏩ Automatic generation of standard brain VOIs in the patient space based on the available atlas templates.<br>Changed:<br>⏩ Representation of VOIs by closed contour lines in all three plane orientations.<br>⏩ VOI filling is applied in all three plane orientations, with variable degree of transparency.<br>⏩ Improvements of reading and writing VOIs as DICOM RT Structure Sets. |
| **Database** | New:<br>⏩ Direct loading of DICOM data into a database without the need for a running a DICOM server.<br>⏩ Direct conversion of native images to database format without an intermediate data set to minimize changes.<br>⏩ Better control of sorting in the list of selected series.<br>⏩ The user-defined ordering and sizing of the columns in the DB loading panel is remembered.<br>Changed:<br>⏩ Improvements of database configuration, transaction server script generation, data replication, automatic backups and integrity testing. |

| | |
|---|---|
| **PVIEW** | New:<br>⏩ The MRI-based partial-volume correction optionally produces a new map indicating the pixels which were used for the white-matter activity calculation.<br>⏩ After image series merging the loaded series does not automatically disappear. |
| **PXMOD** | New<br>⏩ A new loading tool which automatically performs a short-axis reorientation of the input data, allowing to easily specify a left ventricle VOI as the input curve.<br>⏩ If processing tools are applied to calculated maps, the result is also available on the fusion page. |
| **P3D** | New:<br>⏩ Improved speed of volume rendering on multi core systems by calculating textures in parallel.<br>⏩ Introduction of an acceptance test which characterizes the properties of the graphics system and its suitability for P3D.<br>⏩ New HD option for the improved rendering of non-isotropic data.<br>⏩ Optional surface lighting to improve the realistic impression<br>⏩ Additional predefined protocols.<br>⏩ Predefined protocols can be applied to loaded images.<br>⏩ New variants of predefined protocols.<br>⏩ Collapsing of user interface elements for cleaner interface. |
| **PCARD** | New:<br>⏩ Acceptance test to verify the tool operation.<br>⏩ Overlay on the polar plots.<br>⏩ Results viewer supports the loading of two data sets for side-by-side comparison.<br>⏩ Collapsing of user interface elements for cleaner interface. |
| **Data Formats** | ⏩ Multiple DICOM Servers can be easily configured and starting scripts generated.<br>⏩ Support for Enhanced US DICOM objects.<br>⏩ New loaders for Brainvisa and Bruker small animal MR images. |

Zürich, Oct. 31, 2011

# Maintenance Builds of Release 3.2

| | |
|---|---|
| **Build 8**<br>Dec. 1, 2011 | ⏩ VOIs: Speed improvement in cases where statistics and TAC updating is enabled.<br>⏩ 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.<br>⏩ Database: Images with size >5.5GB can now be saved.<br>⏩ DICOM: Optimized loading of series containing multiple multi-frame objects.<br>⏩ PFUS: In batch mode, some output format settings were ignored.<br>⏩ User name in ATL version: The name could have changed when entering/exiting the Config facility. |
| **Build 7**<br>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.<br>⏩ DICOM: Fixed a problem with reading DICOM images with odd slice length in bytes (odd number of pixels and 8-Bit pixel representation).<br>⏩ DICOM: Support for enhanced ultrasound images added.<br>⏩ Interfile: Added support for loading 4-Byte unsigned integer image data. Capital characters in label strings are interpreted correctly.<br>⏩ VOIs: Empty VOIs were used for labeling scatter plots and box plots.<br>⏩ Screen capture: Representation of VOIs and the orthogonal crosshair improved. |
| **Build 6**<br>May 12, 2011 | ⏩ PKIN: Initial values for blood models improved.<br>⏩ 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.<br>⏩ VOIs: Improved synchronization of the orthogonal planes when clicking at a VOI.<br>⏩ Fusion in PVIEW: There is now a choice whether reslicing for fusion should be relative to the origins or relative to the volume centers.<br>⏩ 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.<br>⏩ PFUS: Units of image algebra results adjusted according to the operation.<br>⏩ DICOM: Improved reading of images from YAP-(S) PET systems.<br>⏩ Study UID when saving derived image series: a new UID is created when patient or study info is modified or on user request.<br>⏩ Loader for new native image file format: Varian FDF for micro MR systems (FDF - Flexible Data Format).<br>⏩ Database: Integrity check improved. It is now also able to check the existence of the referenced files.<br>⏩ Analyze Object Maps: Improved error handling in the case of inconsistent headers.<br>⏩ 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.<br>⏩ Median Filter: The filter had no effect when called interactively from the tools. |
| **Build 5** | ⏩ Status check: The status check in the ToolBox now not only reports the availability |

| | |
|---|---|
| March 23, 2011 | of an update, but also the status of all transaction servers as well as the available memory.<br>⏩ 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.<br>⏩ PFUS: Fixed a problem with template loading which could result in a crash.<br>⏩ PFUS: Fixed a problem with using the inverse of a rigid transformations in a matrix combination.<br>⏩ PXMOD: Several changes to improve the overall operation.<br>⏩ 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).<br>⏩ 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.<br>⏩ PKIN: The standard deviations of slope and intercept were incorrectly calculated for the linear plots: Logan, Logan NonInvasive, Patlak, Patlak NonInvasive, RE-GP.<br>⏩ PKIN, Details panel: The panel contents was not always refreshed when switching regions.<br>⏩ MicroPET: "SPECT multiprojection acquisition" was added to the list of supported modes.<br>⏩ DICOM save: There was a problem when saving images without orientations that were processed by a mirror operation.<br>⏩ DICOM C-STORE: A problem occurred if the target DICOM server did not support the object to be sent.<br>⏩ DICOM: The saving of incomplete data (resulting from could interrupted loading) could cause a problem.<br>⏩ VOI: The size of object VOIs in the properties was a factor 2 too small.<br>⏩ VOI: The isocontouring is now applied to all selected contours of a VOI, not only the first in the list.<br>⏩ VOI: When pasting a VOI , its color is now changed to the color of the target VOI.<br>⏩ Atlas Template created from VOIs: If the name contained a space the loading failed.<br>⏩ PVIEW: In Compare layouts with only 1 or two rows the "Capture All" button has been added.<br>⏩ Component saving: Replacement of special characters in the exported component names is now optional, controlled by a checkbox.<br>⏩ 3D: An error in texturing a static VR by a dynamic study was fixed.<br>⏩ 3D: Newly saved protocols were unreadable. |
| **Build 4** | ⏩ DICOM Server: Revision of message handling for clearer log output. |

| | |
|---|---|
| Jan 4, 2011 | ⏩ DICOM: Support added for non-standard scaling factors in Bioscan data.<br>⏩ File formats: Fix for a problem which occurred reading unsigned short values bigger than 32k.<br>⏩ File formats: When multiple graphics files were loaded the first file was populated over all slices.<br>⏩ VOI outlining: The outlining of a mask image now works on the selected frame instead of the first one.<br>⏩ Bug fix of the origins which occurred in rotations and anatomical reformatting. The problem was only notable after saving and reloading. |
| **Build 3**<br>Dec. 8, 2010 | ⏩ PKIN: The axis labeling on the Blood tab was wrong for some models such as the Logan Plot.<br>⏩ PKIN: The default setting for noise generation in Monte Carlo simulations was set to Model only.<br>⏩ PBAS: The series date and time were added to the merging tool as an additional sorting criterion.<br>⏩ PBAS: Fix for the origin location during some geometrical operations at loading such as rotations and in some conditions of anatomical reorientations.<br>⏩ Database: Some data (Philips and some Enhanced objects) with additional units made PMOD freeze.<br>⏩ Database: Scripts with a mySQL root password could not connect to the database.<br>⏩ 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.<br>⏩ Database: Image comment no more used to create Series comment when saved to database because of problems with line feeds.<br>⏩ Fixed a bug which caused imageHistories being saved in the database.<br>⏩ Database: Component name length increased to 15 characters.<br>⏩ ATL: Selection of the audit trail database added, for instance to choose among annual databases.<br>⏩ ATL: The report printing was restricted to a maximum of 100 pages.<br>⏩ DICOM Server: shows the memory allocation and the file name of the log if the output is redierected (-o argument in command line).<br>⏩ DICOM: Fixed a timing problem when there was a zone offset in the time string.<br>⏩ MicroPET: Fixed a problem with the recognition of the nCi/cc unit.<br>⏩ Study date added to the aggregation of voiStat files. |
| **Build 2**<br>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.<br>⏩ DICOM: Fix of a problem when reading Enhanced DICOM objects containing a single slice only.<br>⏩ Alphabetical sorting of the Projects and Diagnosis lists.<br>⏩ Added configuration switch whether to include the patient name for the output filenames of batch operations. |

| | |
|---|---|
| **Build 1**<br>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:<br>- External tool for VOI-based partial volume (GTM method proposed by Rousset).<br>- 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).<br>- External tool with two variants for the skull-stripping of MRI brain images.<br>- 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.<br>- Mouse-operated zooming: Holding down the "Ctrl" and scrolling the mouse wheel activates zooming.<br>- Focus during zooming: The hot spot of the image (selected VOI or planes triangulation point) now always remains visible during zooming.<br>- 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).<br>- Color of the orthogonal crosshair lines can be defined.<br>- Split to slices tool added.<br>- Use of the selected patient info selected in the database for filling the DICOM Q/R information.<br>- The keyboard shortcuts have been extended and can be listed from the context menu.<br>- Report paper size configuration: A4, letter.<br>Changed: |

| | |
|---|---|
| | ⏩ Interactive zooming can now be performed in all planes, not only the active one.<br>⏩ Improvements of the compare mode in the viewing tool.<br>⏩ General information such as Origins, Pixel Size etc moved from the Data Inspector window to the Info window.<br>⏩ 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.<br><br>New:<br>⏩ 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).<br>⏩ 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.<br>⏩ 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.<br>⏩ 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.<br>⏩ An optional segmentation step was introduced which allows interactively creating a mask for the restriction of the pixel-wise calculation.<br>⏩ A VOI outlining step was integrated into the workflow for avoiding the necessity to create VOI data in a different processing session.<br><br>Changed:<br>⏩ 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.<br><br>New:<br>⏩ 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 $k_4$).<br>⏩ Residual weighting: Additional flexibility was added to the weighting for taking the effects of radioactive decay and frame duration into account.<br>⏩ The weighted and/or the raw residuals can be shown.Randomized fitting can now also be applied in couple fitting.<br>⏩ The Patlak Reference model was added.<br>⏩ A new graphical method was added. It allows calculatingVt, 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.<br>⏩ Loader for the Gamma Medica blood sampler format.<br>⏩ The curve control elements can be configured to be shown beside the curves rather than below. This improves the layout for 16:9 screens.<br>Changed:<br>⏩ The fitting history now also includes the weighting and valid point definition (not yet the configuration of the different blood items).<br>⏩ Copy to clipboard: the precision was extended to 16 digits.<br>⏩ The %SE of the macroparameters is now also retrieved from a KM file.<br>⏩ If a file is loaded for which the model is not configured, it is automatically added to the model list. |
| **PFUS** | New:<br>⏩ All matching procedures can optionally calculate the inverse transform.<br>⏩ Rigid Matching: dedicated presets for the matching of human or animal images are available.<br>⏩ The matching tools can now also be used in the external tools and therefore in pipe processing.<br>⏩ 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.<br>Changed:<br>⏩ Rigid transforms (manual, automatic) have been unified and can be used interchangeably. |
| **VOIs** | New:<br>⏩ 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.<br>⏩ A VOI template for mouse images was added (courtesy of Martine Mirrione, BNL).<br>⏩ Button for centering the VOI at the enclosed Max or Min pixel.<br>⏩ 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.<br>⏩ VOI bounding boxes are visualized in the MIP images.<br>⏩ Object maps (*.obj) of the Analyze software can be loaded in PMOD, used for statistics, converted into vertex VOIs, etc.<br>⏩ Load multiple VOI files at the same time.<br>⏩ Option to show the VOI name if mouse is moved over VOI in the image. Works for both contour and template VOIs.<br>⏩ Outlining function which turns an image object map (objects are represented by distinct integers) into a set of contour VOIs.<br>⏩ The statistics results can be copied to the clipboard.<br>⏩ Cropping is now also supported for template VOIs.<br>Changed:<br>⏩ Synchronization of VOIs and data sets: the initial setting of the synchronization box can now be configured per PMOD module.<br>⏩ Additional information is saved to the pixel dump file.<br>⏩ Cropping now allows creating a new study instead of overwriting.<br>⏩ The iso-contouring can now also be restricted by a template VOI. |
| **Database** | New:<br>⏩ 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.<br>⏩ The information of the selected patient can be used in the DICOM Query/Retrieve window.<br>⏩ Filter extensions: the availability of components such as Captures or VOIs can be used for filtering.<br>⏩ Ability to "pair" two image series for applying PVC in a batch.<br>⏩ The project definition is now inherited from the loaded images to the result images.<br>⏩ Images are now written to the database in the new "Enhanced" object definition.<br>⏩ When images are exported the fields edited in the database are replaced in the corresponding DICOM elements. Furthermore, the output IOD can be selected.<br>⏩ 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.<br>Changed:<br>⏩ If more than one database is configured, PMOD remembers the least recently used one after restarting. |

| | |
|---|---|
| **PVIEW** | New:<br>⏩ Support for the fused viewing of images from hybrid acquisitions.<br>⏩ Split to slices tool added.<br>⏩ Tool to transfer images from PMOD to ImageJ.<br>⏩ Scaling of curves (for calibration purposes) when sending them to the PKIN tool. |
| **P3D** | Changed:<br>⏩ The "Texture" tab was removed. All loaded data sets can now used for texturing. |
| **PCARD** | Changed:<br>⏩ The automatic procedures for short-axis reorientation and myocardium detection were improved for $^{82}$Rb data.<br>⏩ 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.<br>⏩ Workaround to support the loading of Bioscan CT DICOM data.<br>⏩ Interpretation of private information for loading dynamic GE SPECT DICOM images with proper values scaling.<br>⏩ When a DICOMDIR file is dragged into PMOD all series listed by the DICOMDIR are loaded. |

Zürich, Oct. 26, 2010

# PMOD Copyright Notice



**PMOD Technologies Ltd**
Sumatrastrasse 25
8006 Zürich
Switzerland
+41 (44) 350 46 00
support@pmod.com
http://www.pmod.com