PMOD Software Release Notes

Version 3.6

PMOD Technologies

Printed on 10 October, 2016

PMOD Software Release Notes

Maintenance Builds of Release 3.6

Build 13 Oct. 10, 2016	⏩ PFUS: Fixed problem with probability maps normalization in fusion batch mode.
Build 12 March 4, 2016	⏩ VOI: A slight bug fixed for the "Move to Max/Min" function. ⏩ Report saving: On Windows systems it was not possible to save multiple times from the same dialog window.
Build 11 Jan. 7, 2016	⏩ Fusion initialization improved. Important for users working with the last Inveon version and using the PET/CT option.
Build 10 Oct. 21, 2015	⏩ Fix of report saving. After saving to a DICOM file the text input areas were inactive. ⏩ Java and WIBU drivers updated for compatibility with Windows 10 (Java SE 8 Update 60, WIBU Version 6.32). ⏩ Compatibility update of R console for El Capitan MacOSX. ⏩ DICOM: Fix for reading multiphase NM files. ⏩ DICOM: Fix for saving image data with slices filled with NaNs to Enhanced Objects. ⏩ DICOM: Added handling of slices direction for Siemens Mosaic files.
Build 9 Aug. 31, 2015	⏩ VOI: "Hypoxia index" introduced as an additional statistic (defined as the percentage of pixels in a VOI which are above a threshold specified by the operator). ⏩ PXMOD: Revision of iterative 2-tissue compartment model: Use of the parameter settings on the pre-processing tab in pixel-wise fitting. ⏩ R: Time mid used for TACs loaded form statistics files when sent to R-Console.
Build 8 July 24, 2015	⏩ PKIN: Bolus/Infusion model will always use Powell optimization, as Marquardt didn't work reliably. ⏩ PFUS: Fixed problem with application of manual transformations in fusion batch mode processing. ⏩ PXMOD: Fix to support the translation table in the C14-Autoradiography models. ⏩ Histogram external tool: Fix of number of bars calculated from width in VOI min / max range. ⏩ PSAMPLE: Resampling is restricted to return positive values. ⏩ DICOM: Incoming folder was sometimes deleted after importing data. ⏩ MicroPET: Improved handling of dynamic gated images. ⏩ Nifti: Support extended to allow selection of the source of the image orientation: qform or sform.
Build 7	⏩ PKIN: The activation time in the LSRTM model can now be fitted.

June 2, 2015	⏩ PFUS: Support for transformations paired with images in batch mode. ⏩ PFUS: Protocols of Fuse It now also include the data averaging range. ⏩ PNEURO: Problems with using small animal atlases in protocols fixed. ⏩ Batch pipeline: New result naming option for excluding tool names. ⏩ Batch pipeline: Bug fixed when only non-image results were configured for saving. ⏩ Segmentation: k-means clustering added (again) to the general segmentation tool. ⏩ VOI: Transformation improved for VOIs saved on images with smaller bounding box than current image. ⏩ Peak VOI: Fixed problem which occurred if the initial VOI was defined in X or Y direction. ⏩ Atlas creation: When creating an atlas from a VOI set, a PET and an MR template can now be specified. ⏩ DICOM: Some acquisition parameters (e.g. kVp) that are stored at the image slice level but have same value within the whole volume are now copied to the coregistered image. ⏩ P3D: Saving of last segmentation result as an image fixed. ⏩ PSAMPLE: After the correction TAC was closed, no other TAC could be loaded. ⏩ ITK: Unsuccessful filter loading had blocked the ATL and online versions.
Build 6 April 15, 2015	⏩ PNEURO: Possibility to use already normalized images for creating a Brain Norm added to the Norm Editor. ⏩ PNEURO: Improved handling of user-defined atlases without probability map definition. ⏩ PNEURO: Option in batch mode to create multiple protocols for the MR-only situation. ⏩ R Console: Restriction for aggregate size removed, and image size limit extended to 1500x1500 per slice. ⏩ R Console: "Linear Model" script renamed to "rm-Anova/Manova" for clarity; report plots performance improved. ⏩ R Console: configuration of printout font added. ⏩ PVIEW: TACs sent to PKIN now handle NaNs in the same way as Statistics. ⏩ VOI: Intersection when using a dynamic mask file corrected. The first mask frame was always used. ⏩ VOI: In pipeline operation statistics calculation relative to merged VOIs was fixed. ⏩ Database interface: Study date filter added. ⏩ PCARD: The actual units (eg. kBq/cc, SUV) of the image data are used to display curves, tables and polar plots. ⏩ Distance measurement: Fixed in zoomed fusion display. ⏩ Data aggregation: Series description column added to the component selection interface.
Build 5 Feb. 23, 2015	⏩ LSRTM model: Fixes in PKIN and PXMOD to accommodate series with gaps between acquisitions. ⏩ PKIN: Removed the filtering of very small stdvs in Monte Carlo simulations.

	⏩ PNEURO: Outlining fixed in the case of PET result space with transformation loaded from file. ⏩ PFUS/PFUSEIT: Batch mode save fix for the combination of Database input format and different output format. ⏩ PGEM: Graph synchronized with tree to select model elements. ⏩ R Console: generator for patient IDs added to simplify anonymization. ⏩ New option to reslice loaded series to common space and average at the same time. ⏩ DICOM: Fix for reading RTSS structures containing empty contours. ⏩ Normalization tool: Worked only when scaling (normalization) had been enabled. ⏩ Image history for motion correction fixed. The selected frame was always reported 0. ⏩ Scientific screen capture improved for switched series. ⏩ Saving of NaN values added for float DICOM and Database formats. ⏩ Cardiac MR module activated again.
Build 4 Jan. 13, 2015	⏩ Installation of upgrades improved to avoid database overwriting. ⏩ Additional status icon indicating the availability of a new version build. ⏩ PKIN: Sensitivity functions were calculated in "1/1" units rather than the indicated "%". ⏩ PKIN: The standard error of the slope was incorrectly scaled for the Logan Reference and RE-GP models. ⏩ PNEURO: A white-matter VOI is also generated for PET-only cases. ⏩ PNEURO/Mapping: VOIs used in parametric mapping can be created by VOI merging. ⏩ PNEURO/Mapping: A mask can be created from the brain matter segments or from a VOI selection. ⏩ Fuse It: Coupled cursor added to "Comparison" page. ⏩ Fuse It: Facility added for paring inputs and references which are loaded as separate lists. ⏩ Fusion: Problem fixed when loading motion correction transform without a reference. ⏩ PXMOD: Fix for PBnd_MRTM0 in 6 Calc Method. ⏩ Rat and mouse templates were converted to a right-handed coordinate system. ⏩ R: Repeated measures ANOVA added to LM analysis. ⏩ R: Fixed problem with plots for Mac and Linux. ⏩ R: Reconnection to R server more robust. ⏩ The “GM & WM & CSF Probability” external tool was renamed to “MRI Probability and Inhomogeneity". It allows saving of the denoised and inhomogeneity corrected MR images. ⏩ PGEM: 3D mesh generation possible without running an actual simulation. ⏩ PGEM: User interface for CFD case creation and the handling of cases improved. ⏩ PGEM: Update of the heartatlas structures.

	⏩ Dual-monitor option removed due to unpredictable results.
Build 3 Nov. 24, 2014	⏩ VOI: Fixed loading of RT Structure Sets without references to DICOM images. ⏩ VOI: Fixed average calculation for the last VOI in the list. ⏩ PNEURO: Saving of all results in batch mode fixed. ⏩ Fuse It: Markers matching improved when repeated markers adjustments are necessary. ⏩ PKIN: Sometimes not all regions were listed in the "View Par" window and NaNs were saved instead of the correct parameter values. ⏩ Gaussian filter in time domain added, with circular option (also for Median filter). ⏩ Configuration improvements for the ATL license.
Build 2 Nov. 4, 2014	⏩ R Console: Bartlett and Kruskal-Wallis results accumulated in tables; online helps added; improved descriptions and error handling; pm.base package version update; pixel dump script fix; variables shown after workspace loading; clean option for workspace loading. ⏩ "View aggregated" window unified to support combination with external data and transfer R Console in all places. ⏩ Peak VOI: Options to use a background threshold and require a minimal included fraction of the sphere volume inside the original VOI. ⏩ VOI atlas normalize function: uses the corresponding species presets directly. ⏩ PBAS segmentation: k-means clustering removed. ⏩ PSEG: New k-means clustering options whether to work on the dynamic data, each frame separately, or on the average. ⏩ PSEG: Option to outline all segments of the selected frame as VOIs. ⏩ Save to buffer option added to the "Save all" function of PFUS, PNEURO, PSEG. ⏩ Cropping box in PFUS, PNEURO, PSEG: edge sizes can numerically be defined. ⏩ PFUS: Unified options mm/pixel for sampling and smoothing in all matching methods. ⏩ P3D: Close all button added; online help introduced. ⏩ PMOD can be restarted directly after a configuration change. ⏩ License server: new "-lic[<pattern>]" commandline option for starting multiple license servers in a common installation, e.g. java -Xmx2G -jar pmtsvr.jar 5000 -ls -lic[1324] java -Xmx2G -jar pmtsvr.jar 5001 -ls -lic[427] These licenses can then be referred to in the client scripts with the -lsn[<PORT_NO>.<OPTIONAL_LICENSE_NO>@<IP_ADDRESS>] option.
Build 1 Oct. 17, 2014	Initial upload of 3.6 version.

Product Release 3.6

The 3.6 product release brings major functional improvements for pipeline processing which allows constructing comprehensive analysis procedures, a completely novel population statistics via the R console, and an additional tool (PFUSEIT) for image fusion with redesigned workflow and new features. Also added is a new tool (PGEM) for the development of geometric models. Additionally, many improvements were implemented for the various tools and the platform, whereby the list below only highlights the major points.

Features

General	Batch Pipeline Processing: Substantial extensions of functionality such as ⏩ Brain VOIs can be generated on anatomic images and applied to functional images for TAC generation. ⏩ Generated TACs can be submitted for kinetic modeling. ⏩ Quality-control options added: image viewing, VOI editing, JPEG image saving. ⏩ Results can directly be aggregated for population statistics. ⏩ Various external tools optimized for use with batch pipeline: CoRegistration and motion correction with interpolation choice; and VOI statistics with spatial transformation, morphological operations, and relative to reference region; VOI based PVC simplified; Interpolation tool can apply transformation; Background removal tool; Segmentation tool supports VOI outlining. VOIs: ⏩ New inclusion criteria for contour VOIs: 1) All pixels with a fractional part covered by the VOI are included, and the average is weighted according to the included pixel area. 2) Using pixels with 50% or 100% area included, with unweighted averaging. ⏩ SUV_{peak}: Generation of explicit sphere VOIs within an enclosing VOI. The positioning options are centering on the maximal pixel, or to maximize the average enclosed in the sphere. ⏩ Localization of a number of hottest pixels within a VOI. ⏩ Morphological operations (erosion, dilation etc.) of a whole group of VOIs, for instance to shrink automatically generated VOIs by 1 pixel. ⏩ Calculations of VOI pixel value histograms, which can be analyzed in R (skewness, kurtosis). ⏩ Use of predefined VOI name lists. ⏩ Tool for reducing the number of contour vertices. ⏩ Eraser working on all active VOIs when the Group tab is selected. Miscellaneous: ⏩ Java Version 8 is bundled with the distribution, now also for Mac. ⏩ Aggregation improved, particularly for group analysis. Group name and condition can be specified. ⏩ Animated GIF option for saving movies added.

	⏩ Yearly filter added to improve components listing speed. Important for large databases. ⏩ DB components loading speed optimization from large databases. Particularly relevant for PXMOD and PNEURO. ⏩ Automatic crop box calculation added based on subject end modality (PFUS, PALZ, PNEURO, PSEG). ⏩ Spline interpolation introduced for reslicing (PFUS, PALZ). Changed: ⏩ The Automatic Brain VOIs external tool is based on image matching technology and is therefore now bundled with the PFUS option.
PFUSEIT	The new "Fuse It" tool guides the user step-by-step from the input images to the registered and post-processed results. Common tasks can be achieved in only a few straightforward steps, whereas complications are handled separately by additional steps. The new tool is launched as a companion tool to the 3.6 version of the proven Fusion tool, for allowing users familiar with the old interface to continue their work as-is. This coexistence will be supported for some future versions, but new developments will mainly be included in the "Fuse It" tool. Novelties in "Fuse It": ⏩ generation of rotating MIP images fused from up to three sources, including animation over time; ⏩ explicit use of species information (HUMAN, RAT, MOUSE) for proper matching presets; ⏩ parallel viewing of up to 6 fused renderings; ⏩ whole-body layout for improved display of non-cubic data; ⏩ reference can be reoriented before the matching; ⏩ a "Run all" operation mode which applies the configured methods to data selected in the database; ⏩ support of overlapping criteria (Dice, Jaccard, volume difference, signed volume difference, specificity, Sensitivity) ⏩ transformation of markers after matching; ⏩ support for the normalization of CT brain images using a conversion of the HU values and template images from an elderly population (Clinical Toolbox, Chris Rorden).

R statistics Console	⏩ Population analysis implemented based methodology developed by Prof. K. Herholz ⏩ Statistical analysis of study data with numerous regional outcome values, which raises the problem of multiple comparisons. ⏩ Streamlined MANOVA and Linear Mixed Effects (LME) analysis workflows. ⏩ Scenarios covered include the comparison of groups, the interaction with regional effects, and the handling of covariates, such as age and gender. ⏩ Additional tests: Kruskal-Wallis, Variance analysis using the Bartlett test. ⏩ Import of data from SPSS, SAS, Systat, Stata, CSV and conversion to aggregates. ⏩ Improvements for pixel-dump analysis. ⏩ Own operating-system independent package pm.base.tar.gz added containing the scripts. ⏩ Multiple user interface improvements.
PKIN	New: ⏩ Fitting mode which sequentially shortens the data segment used. ⏩ The model history supports multiple new options. The change of a parameter across different fits (eg. shortening) can be visualized as a plot. ⏩ The configuration of all models (tissue, blood) can be saved in a single file. ⏩ The Sigmoid, Watabe and Hill functions can also be used as plasma fraction functions. ⏩ Sigmoid parent fraction function added which was described for [11C]-PBR28 by Owen et al. ⏩ Two-tissue compartment model developed by Rizzo et al. for the analysis of [11C]-PBR28 uptake in the human brain. ⏩ Alpert's Linearized Simplified Reference Tissue Model (LSRTM) for noninvasive detection of neuromodulatory changes in specific neurotransmitter systems added. Improved: ⏩ Handling of fitting failures: Regions are not shown in the parameter overview and not saved in the kmPar file. Failures in the reference region are not reported. ⏩ Monte Carlo simulations now use an independent seed for each data sample. Changed: ⏩ Runs test: The restriction of >8 runs and >16 samples was removed, and a correction for small sample sizes (N<50) was introduced. ⏩ Inclusion of the residual weighting scheme into the tissue model configuration file (.kmModel).

PNEURO	⏩ Animal brain atlases (mouse, rat, monkey) also supported. ⏩ Completely revised batch mode which allows defining a processing scheme for a whole list of input data. In this way processing variants can easily be applied to large data samples. ⏩ Automatic image cropping mode added so that the entire processing can run without user interaction. ⏩ Alternative normalization of MR images which uses the template images directly, rather than the tissue probability maps. ⏩ A Hammers atlas variant with 1mm resolution is available which provides more accurate VOIs in the MR space. ⏩ VOIs resulting from parcellation can also be obtained in the atlas space. ⏩ Parametric mapping can directly be performed in PNEURO, if the PXMOD tool is licensed. The VOIs can be applied to the maps, and the maps can also be used in norm comparisons.
PSEG	⏩ Automatic species recognition added based on the image volume. ⏩ The anatomic images (MR, CT) are directly resampled to the functional images. ⏩ K-means clustering added as an alternative method for generating cluster maps.
P3D	⏩ JOGL is used as 3D engine allowing 3D on Mac with Java 1.8. ⏩ New page for the generation of high-quality rotating MIPs. Up to 3 images may be fused. For dynamic scans, the temporal evolution of the images can be included in the rotations. ⏩ A scene consisting of surface objects can be saved to an STL file. The object tree is reconstructed after loading the STL ⏩ Support for the more compact binary STL format. ⏩ 3D properties can be set on the Segment page before rendering.
PXMOD	⏩ Alpert's Linearized Simplified Reference Tissue Model (LSRTM) for noninvasive detection of neuromodulatory changes in specific neurotransmitter systems ⏩ Image definition and loading are now done in a single step. ⏩ Several user interface optimizations.
PGEM	This new tool leverages the PMOD platform for supporting various types of simulations. A model builder allows for the construction of anatomic structures from VOIs, resulting in a geometric model. Such models can be enriched by multimedia annotations for creating educational 3D-scenes, and complemented by tissue properties. Based on the model construct, phantom images can easily be generated which represent a well-defined input for external simulators of image acquisition instruments or physiology, e.g., OpenFOAM® or Fluent®. An alternative output constitutes atlases which can be employed for automatic VOI generation.
Data Formats	⏩ Improved handling of floating point image data with NaN values (interpolation and smoothing). ⏩ Fixed problem with reading patient and acquisition information from de-identified files with no de-identification method element (0012,0063) included. ⏩ Information on image de-identification can be shown in the series info dialog, if present in the DICOM file.

	⏩ Corrected encoding of HU for DICOM enhanced images. ⏩ DICOM Incoming folder support for MicroPET and Interfile. Device specific folders with an initial transformation.

Zürich, October 17, 2014

Maintenance Builds of Release 3.5

Build 10 Oct. 16, 2014	⏩ Local R installation improvements: No administration privileges required for package installation. ⏩ PKIN: Displayed weighed residuals were wrong: division by stdv instead of stdv^2. ⏩ PKIN: In Monte Carlo stdvs<1e-4 had been masked, which is inconvenient for rate constants with small values.
Build 9 Aug. 7, 2014	⏩ PNEURO: Fixes for reducing RAM consumption during batch operation. ⏩ PNEURO, Maximum Probability Method: Fix for a situation when splitting of the hemispheres fails. In this case white matter is not separated into left and right parts. ⏩ PNEURO: Crop box is saved in protocols without explicit cropping during protocol preparation. ⏩ PKIN: For the blood-related interpolation models calculated weights did not include the decay effect. ⏩ R Console: Statistics calculated using atlas VOIs could not directly be transferred to the R console.
Build 8 June 4, 2014	⏩ Java compilation error fixed which manifested itself when loading a transformation. ⏩ PFUS: Fix of a synchronization problem in triple fusion. ⏩ PXMOD: The k2 map of the SRTM2 model had been incorrect. ⏩ PKIN: The correction of the AIC for small sample sizes had been inactive. ⏩ PKIN: Default of third exponential half-time slightly adjusted for plasma fractions.
Build 7 May 17, 2014	⏩ Java Runtime Environment updated to Java SE 7u55 for security and compatibility reasons (stability problems on Win8.1). ⏩ R: Problem fixed with installing additional packages. ⏩ R: Data extraction from aggregates improved. ⏩ VOI: Interactive 3D iso-contouring used wrong seed coordinate in the fusion display. ⏩ PNEURO: The statistics were not properly updated when using the "Relative to" mode, in case the image was changed. ⏩ PNEURO/Compare to Norm: When importing a Norm, the VOIs defined for results averaging were not properly handled. ⏩ PFUS: Saving the inverse of a manual transformation was fixed. ⏩ PFUS: The 3D scatter plot had only rendered the samples for one VOI. ⏩ 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). ⏩ DICOM: The image presentation information was not properly used when selecting a frame subset at loading. ⏩ Aggregation: When combining aggregates with external data, only the "Patient Name" key worked, not the "Patient ID".

	⏩ MINC 1 format: Images stored in coronal and sagittal orientation are now also supported.
Build 6 March 11, 2014	⏩ PKIN: An inappropriate interpolation method had been shown when using the plasma fraction. ⏩ PKIN: It had not been possible to configure certain models. ⏩ PKIN: Models used in loaded data and not configured are automatically added. ⏩ PKIN: Improved refresh at the end of batch mode. ⏩ DICOM: Improvement of the extended association negotiation and the interoperability with the Mediso DICOM server. ⏩ PNEURO: A problem with parcellation in the absence of properties has been corrected. ⏩ 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. ⏩ R-Console: A problem with SUV units was fixed, and VOI names now may contain the "%" character. ⏩ 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 Jan 27, 2014	⏩ PKIN: Fix of the model list shown for plasma activity loaded from file. ⏩ PKIN: Sum of 3 exponentials better initializes the begin time, namely to the signal maximum. ⏩ 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. ⏩ PNEURO: Progress information improved. ⏩ PNEURO: 3D rendering problem fixed. ⏩ PFUS: Load protocol better supports data format changing. ⏩ Sizing of the curve control area improved.
Build 4 Jan 12, 2014	⏩ R console improvements and fixes: Plots did not work on Windows systems. ⏩ Pipe processing: Error handling improved so that errors terminate processing. ⏩ SUV external tool in pipe processing returns an error for zero injected activity in the data. ⏩ 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. ⏩ The external segmentation tool applies the same colortable as the processed data. ⏩ ATL database export: Speed (factor 2.5) and stability improvements. ⏩ PKIN: Curve zooming extended by a factor of 100.

	⏩ PNEURO/Compare to Norm: Option added to limit z-score clusters by the minimal number of included pixels.
Build 3 Dec. 22, 2013	⏩ PNEURO, Norm Comparison: Cluster analysis with a specified maximal number of clusters. ⏩ PNEURO, Maximum Probability: Sulci bottom detection available as an additional segmentation option. It adjusts the VOIs such that they end in the sulci bottoms. ⏩ PNEURO, Maximum Probability: Support for user-defined atlases, which may also define animal brain VOIs (monkey, rat, mouse). ⏩ PKIN: Display layout showing the curves from all regions revised. All TACs, targets or model curves can now be shown. ⏩ R: Identity line option added to the scatter plot. ⏩ R: Support for box plots showing multiple variables. ⏩ R: Verification of packages at start time. ⏩ R: Data reduction procedure implemented for pixel-dump and image data, to increase loading speed. ⏩ PXMOD: If mask and VOIs are not manually saved when proceeding, a dialog window appears and simplifies saving. ⏩ PXMOD: VOIs used in preprocessing are initially switched off on the parametric maps. ⏩ 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. ⏩ Improved synchronization of the SUV units shown in the data inspector curve display. ⏩ DICOM Loading: Handling of Philips ADNI images with wrong high bit value. ⏩ DICOM Saving: Fix for using the proper output SOP selection. ⏩ Analyze: Improved handling of the origin for files stored in little endian. ⏩ Display: Inspector TAC updated also when triangulating via the MIP image.
Build 2 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. ⏩ 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. ⏩ PNEURO, Maximum-Probability method: Ventricles not affected by masking with the segments map. ⏩ PNEURO, Maximum-Probability method: White-matter VOIs are initially hidden. ⏩ VOI: Smoothing option introduced for the iso-contouring tool. ⏩ R: Improvements for sending pixel dump results to R. Preview, and support for multiple data files.

	⏩ R: Revision of the scatter plot solution for better visualization. ⏩ Fusion: The separate color table used for fusion can be inverted separately. ⏩ External VOI-based PVC tool: The Hammers N30R83 atlas can also be selected, if PNEURO is licensed.
Build 1 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: ⏩ New VOI statistics: surface estimation, maximum diameter, sphericity and area under curve. ⏩ Use of B-Splines between vertices to create smooth contours. ⏩ SUVR calculation easily possible in statistics panel. ⏩ Multiple user interface improvements of statistics panel: VOI merging, sorting, show only selected information. ⏩ Improvements of VOI tree handling. ⏩ VOI/ROI/Contour toolbars reorganized. Miscellaneous: ⏩ 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. ⏩ Aggregation: highlighting of common parameters, adding of covariates to the data, control over the aggregation order. ⏩ 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. ⏩ Pipe processing and external tools improvements in: SUV conversion; histogram calculation; median filter in time domain; pipe organization and results saving. ⏩ Interference of automatic reorientation and macros solved in several tools. ⏩ 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. Standard analysis types are directly supported via the graphical user interface. They can be as simple as a performing scatter plots, but range to more complicated techniques such as ANOVA, test-retest analysis or Bland-Altman comparison. Beyond using the graphical interface for invoking R functionality, users can also develop their own analysis scripts in a command window interface. In this situation, the PMOD R console serves as a prototyping interface which allows to enter R code, execute it, inspect the result, and improve the code. Compared to version 3.4 the whole functionality, including data preparation, was revised and extended.
PKIN	New: ⏩ Multi-model fitting: Support for fitting data with multiple models at once. ⏩ Filtering options for tailoring the model list to the actual data (e.g. models with/without blood data, reversible/irreversible configurations, etc). ⏩ Saving of the model fitting history in the km file such that prior configurations can easily be recalled. ⏩ New tissue model: 2-tissue compartment model with k_5 efflux. ⏩ New tissue model: 3 sequential tissues described for FDG in skeletal muscle. ⏩ New tissue model: Multi-linear approach for estimating the influx of irreversible tracers (MLAIR). ⏩ New tissue model: Utility for calculating OLINDA-ready residence times in dosimetry studies. ⏩ New blood model: Gamma function peak plus two exponentials. ⏩ New plasma fraction: linear plasma/whole-blood ratio. ⏩ New composite data format for importing all data parts at once. ⏩ New curve tools: Decay correction, decay un-correction, volume edition, acquisition times trimming. Improved: ⏩ Batch mode: Support for composite data format and multi-model fitting. ⏩ The organization of the blood data has been unified for all input curves of models with more than only a single input curve. Changed: ⏩ Modified gamma functions 1 and 2 deprecated. ⏩ Model for cardiac water PET with geometrical correction removed.
PNEURO	New: ⏩ 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. ⏩ Parcellation now also estimates Hippocampus and Amygdala from the knowledge base. ⏩ Parcellation performs a sulci optimization with the cortical VOIs. ⏩ Support for the AAL-Merged atlas as well as user-defined atlases in the MNI space. ⏩ Introduction of the tree structure for the AAL atlases. ⏩ Addition of regions to the AAL atlas for making it more comparable to the N30R83 atlas. Improved: ⏩ Harmonization of the workflow and the resulting VOIs across the two brain VOI approaches. ⏩ Brain norm editor better streamlined and the probability map normalization added. ⏩ Additional parameters made available for segmentation and matching. Changed: ⏩ 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. ⏩ List of cropping sizes adjusted to species selection. ⏩ Instead of overwriting existing VOIs with the same name, structures can now also be appended. ⏩ If an anatomical image is loaded, it is pre-selected for fusion with the segments. ⏩ Hot region growing added to the default VOI tools.
PCARDP	New: ⏩ Facility to replace the LV curve by an externally created curve (e.g. obtained with an online blood sampler). ⏩ New crop box sizes suitable for rodents. ⏩ Simplified data loading by associating rest and stress scans in database. Improved: ⏩ Behavior of data loading for creating factor images for water bolus studies. Changed: ⏩ 2-tissue compartment model for Rb: Vd removed corresponding to differential equation system.

P3D	New: ⏩ Smoothing added to VOI rendering protocols. ⏩ Markers defined in images are rendered when transferring the images to P3D. Improved: ⏩ Functionality of Segmentation page. ⏩ Tree allows multiple nodes with the same name.
PXMOD	⏩ Transfer of pixel-TACs to PKIN optimized. ⏩ Improvements of workflow.
PALZ	⏩ Crop box added.
PFUS	⏩ Additional brain normalization procedure using tissue probability map information. ⏩ Facility to map points localized in a 2D scatter plot ROI back to the image space. ⏩ Scatter plot analysis tool. ⏩ Support for a prefix to the original file name when saving multiple matched series.
Data Formats	⏩ Bruker Paravision MR loader added. ⏩ MINC 1 loader added. ⏩ 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 May 17, 2014	⏩ Java Runtime Environment updated to Java SE 7u55 for security and compatibility reasons (stability problems on Win8.1). ⏩ PNEURO: Parcellation could be started even when both deep nuclei and cortex parcellation were switched off. ⏩ PNEURO: Fixed problem of loading gray matter template in parcellation in case of previous loading of dynamic series by Autodetect. ⏩ PKIN: Incorrect times had been used when switching from Logan to the B/I model. ⏩ ATL version: Incoming folder processing could close DICOM Server.
Build 8 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. ⏩ PKIN/PXMOD, Patlak Reference Plot: Independent of the t* setting, the whole data segment had been used for the linear regression. ⏩ 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. ⏩ VOI: Loading with transformation could result in truncated VOIs when they were outside the field-of-view. ⏩ VOI: Statistics within a range did not work properly when invokeded repeatedly. ⏩ VOI: Intersection of dynamic VOIs was not correct for frames beyond the first one. ⏩ VOI: Compatibility option for statistics saved with the 3.3 version replacing the space character by "_" in descriptions. ⏩ DICOM: Support for fixed color scale in the generation of SC DICOM output.
Build 7 July 12, 2013	⏩ P3D: Improvement of protocols including VOI renderings. ⏩ PNEURO: Initial 3D rendering limited to VOIs, but the skull-stripped MR is also made available for rendering. ⏩ Fix for a VOI undo problem in PNEURO and PSEG. ⏩ Pipe processing: path definitions were not working for data other than DICOM or database files. ⏩ PCARDP: Protocols for ammonia didn't store the flag for calculation of the MBF maps. ⏩ PCARDP: Stress/rest is now detected in the series description when performing the factor analysis for water PET studies. ⏩ ECAT: Improved support of the origin coordinates. ⏩ Save all: better handling of the settings across the saved files.

Build 6 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. ⏩ 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. ⏩ PNEURO: Improvement of the parcellation result by removing spurious isolated pixels. ⏩ PCARD: The factor images generated for water studies can be cropped before short-axis reorientation. ⏩ PCARD: Protocols include recalculation and cropping of factor images. ⏩ PFUS: Fix for an initial slice offset due to differing slice thicknesses of the reference and the input series. ⏩ PVIEW: Fix of a problem in the Split slices and Split frames procedures. ⏩ Save All function: Revised interface fixing a bug in propagation of changes. ⏩ Series description added to Data Inspector title bar. ⏩ Option to switch off automatic checking of available updates. ⏩ Fixed problem when saving reports with multiple pages as DICOM SC objects.
Build 5 March 7, 2013	⏩ PNEURO: The VOIs are saved with the protocol definition to preserve manual edits. ⏩ PNEURO: Facility for saving all intermediate results of interest at once with a save all button in the lateral taskbar. ⏩ PKIN: Handling of time-overlaps occurring due to erroneous DICOM time encodings. ⏩ R statistics: Multiple functional improvements. ⏩ Scaling tool: new options (divide by VOI average, scale to 1 or 255 max). ⏩ VOI: Masking inside VOI using its own VOI average. ⏩ 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. ⏩ External Histogram tool: extended with "In VOI" option. ⏩ PCARDP: Zero time setting had not been applied when using factor analysis. ⏩ Transaction server: improvements in starting and status reporting. ⏩ Default configuration: Raw and Query data loaders added. ⏩ Distribution: Java updated to JRE 1.7.0_17. WIBU Key driver files updated to 6.11.1057.500.
Build 4 Jan. 14, 2013	⏩ PNEURO: Cortical VOIs are created using the approach of the Maximum Probability tool. ⏩ PNEURO: FDG or other PET images with anatomical information can be used for determining the normalization transform, replacing the role of the MRI. ⏩ 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. ⏩ PNEURO: The VOI volume is calculated instead of the value average in the case of MR-only analyses. ⏩ PNEURO: Partial-volume correction now also considered the complementary white-matter parts of masked VOIs. Improved interface for adding scanners. ⏩ PNEURO: Protocols can be used for loading configurations without starting processing. ⏩ PNEURO: Fix of unit support in protocols. ⏩ PNEURO: Volume-weighted averaging of curves added on Statistics page. ⏩ PCARDP: Improvements of the factor image reorientation for water data. ⏩ PCARDP: Simplified loading from the side bar of dynamic and transmission images for factor analysis. ⏩ PFUS: The data of scatter plots can be saved as statistics from the context menu. ⏩ PFUS: RGB images can be fused with monochrome images. ⏩ PKIN: Regions containing "cerebellum" or "reference" in the name are now pre-selected for the reference region after data import. ⏩ PKIN: Fix of the Ito plot results. The result parameters were interchanged (Vt <-> Vnd, K1<->K1') and BPnd not calculated. ⏩ PKIN: Dedicated filters for loading data didn't work. ⏩ VOI: Multiple VOI sets of an image can be converted into mask files. ⏩ VOI: Masking by average value in VOI added.
Build 3 Nov. 24, 2012	⏩ PXMOD: The program could freeze for some model configurations when running all processing steps. ⏩ Acceptance tests fixed for the ATL version. ⏩ PNEURO: Fix in the calculation of the lateral frontal horn thickness. ⏩ PNEURO: Improvements when switching between workflows. ⏩ PNEURO: Denoising option added to Maximum Probability solution. ⏩ PCARDM: Improved compatibility with prior protocols.
Build 2 Nov. 8, 2012	**CAUTION:** Due to Java-related errors users are strongly recommended migrating from Build 1 to Build 2. ⏩ 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. ⏩ PNEURO: New normalization procedure for T1-MR images which dramatically improves the quality of the VOIs in the Maximum Probability module. ⏩ PNEURO: Time-weighted average statistics added for dynamic PET scans. ⏩ PKIN: Tissue model curves and compartment model curves shown in HD. ⏩ VOI statistics aggregation: Improvements and fix in handling of old format statistics. ⏩ Cardiac PET: List of recognized ammonia strings extended. ⏩ Cardiac PET: Fix for handling a problem with manually shifted EPI/ENDO

	contours. ⏩ Cardiac PET: The excess ENDO TAC was removed. ⏩ Cardiac PET: Static input creates polar plot with average values in AHA sectors instead of the individual samples. ⏩ R statistics console: More plots added (histogram,scatter plot, box plot, density plot). ⏩ 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 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 **- 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 **- 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. New: ⏩ The PMOD distribution includes the latest Java 7 version. ⏩ R-console: facility for connecting to "R" servers, transfer data, send commands for analyzing the data, retrieve the results and visualize them. ⏩ Direct saving of aggregates as an Excel file. ⏩ 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. ⏩ PSAMPLE and the R console can start automatically after user login. ⏩ New association in the DB interface to support grouping of PET and MR segments for partial-volume correction. VOIs: ⏩ New statistical measures added: median, area-under-curve (AUC), peak statistics in sphere centered at the VOI maximum. ⏩ Statistics can be calculated on all loaded images at once and the results shown on tabbed pages. ⏩ Interactive region growing and shrinking holding down the "Ctrl" key. ⏩ Brush mode for creating VOIs and deleting from VOIs. ⏩ Contour generation with the criterion of equality.

	⏩ New contour editing modes which disallow overlapping VOIs. ⏩ VOI template for cynomolgus monkeys added. ⏩ Intersection of VOI template with list contours. ⏩ Statistics output window is not blocking any more. ⏩ Saving of VOI statistics as DICOM Structured Report. Improved: ⏩ 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. ⏩ Time editing facility improved. Simplified shifting of time vectors and calculation of start/end times from mid-times. ⏩ New options in replace tool using the magnitude. ⏩ Network license server supports multiple license files. ⏩ License client can view state of licenses on the server.
PKIN	New: ⏩ Simplified fitting of the blood delay together with the tissue compartment model, both for a single TAC as well as coupled TACs. ⏩ Spectral analysis model added. ⏩ 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. ⏩ Blood delay parameter included in the model history. ⏩ Visualization of min/max parameters in summary lists: min = green, max = red. Columns with constant values are marked in blue. Improved: ⏩ 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). ⏩ Simplified user interface for curve loading. ⏩ Monte Carlo functionality for coupled fitting integrated into the Monte Carlo tab. ⏩ Simplified selection of the regions to be coupled with long region lists. ⏩ Units of curve plots revised.
PCARDP	New: ⏩ Definition of the endo- and epicardial boundaries as an alternative to the centerline heart model definition. ⏩ Cardiology-style report page showing the average uptake images of stress and rest in the different orientations. ⏩ Calculation of parametric MBF maps for ammonia using a basis function method. ⏩ 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. ⏩ Visual support for optimizing time-averaging of the early and late uptake phases. ⏩ Facility for saving the VOIs in the space of the MBF maps for comparison purposes. ⏩ Support for the aggregation of the result statistics. ⏩ Vertical taskbar for data loading and results processing. ⏩ Configuration option to reduce the number of visible VOI tools to the most relevant ones. Improved: ⏩ Unified numerical results organization for dynamic and static studies. ⏩ Protocols for water studies with factor analysis fixed.
P3D	New: ⏩ Completely new page for the object segmentation. The image space is larger, and segment generation is easier and more flexible. ⏩ When VOIs are directly submitted for 3D rendering from the viewing tool the user is offered the choice between the rendering modes (surface, stripes). ⏩ Texture color interpolation can be switched off, for instance for the visualization of parcellated brain segments. ⏩ Example protocol showing elements of the heart anatomy. Improved: ⏩ 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. ⏩ Faster and smoother surface rendering of VOIs. ⏩ Better control for the rendering of dynamic VOIs. ⏩ More accurate visualization of the pixels to be included before the actual segmentation.
PALZ	New: ⏩ Lateral taskbar for loading and closing of the image data. ⏩ Facility for aggregating the statistics results of the PALZ analysis (only in non-simplified mode).
PFUS	New: ⏩ Masking facilities for restricting the information used in matching and normalization. ⏩ Motion correction can be used in batch mode and in pipe processing. ⏩ 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: ⏩ Stitching tool which automatically determines the overlap of two acquisitions and creates a combined data volume.
PXMOD	New ⏩ 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: ⏩ 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: ⏩ Interfile: Extension for saving SUV-related information, patient information, and the image orientation. ⏩ Nifti: Support for multi-layer images added. ⏩ MicroPET: Support for reading pre- and postinjection activities. ⏩ MicroPET: Fixed a problem with reading large Inveon data (>2GB). ⏩ Revision of series date default when the information is not contained in file. ⏩ DICOM Element viewer: supports copy to clipboard.
ATL	New: ⏩ Flat view shows seriesDBID and patiendDBID in ATL. ⏩ SOP class of exported data is included in the log. ⏩ ATL ip, version and build date are added to details on application level. ⏩ View of license state extended by the possibility to clean up licenses.

Zürich, Oct. 16, 2012

Maintenance Builds of Release 3.3

Build 10 Dec. 7, 2012	⏩ PKIN: Fix of the Ito plot results. The result parameters were interchanged (Vt <-> Vnd, K1<->K1') and BPnd not calculated. ⏩ PCARD: Improved loading of water protocols using the factor analysis. ⏩ PCARD: "Oxygen-water O^15^ / ^15^Oxygen" added to accepted tracers list. ⏩ DICOM: Files are now accepted using defined length sequences with wrong length values. ⏩ MicroPET: Fixed problem with loading Inveon dynamic gated images.
Build 9 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. ⏩ 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. ⏩ DICOM: Problem fixed in conversion of NM objects to PET objects during export from PMOD DB. ⏩ 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. ⏩ Pipe Processing: SUV tool fixed to work with pipe processing. The relevant information has to be available in the input files.
Build 8 July 9, 2012	⏩ PXMOD: Bug fixed with handling the units of blood files. ⏩ PSAMPLE: Fix of a problem with integration times longer than 1 sec. They could result in timeouts. ⏩ PFUS batch processing: Fixed a problem with missing origins when image data was resliced with a rigid transformation (DICOM or NiFTI affected, not Analyze). ⏩ DICOM: Improved handling of dicom multiframe images with wrong number of slices specified in element 0054,0081. ⏩ External tools: A tool was added which allows correcting images in case of DICOM objects with wrong endian endcoding. ⏩ Database: When exporting files from a database the patient size and weight is not replaced in the file, if it already exists. ⏩ Database: Connection timeout increased from 2 to 5 seconds to accommodate slow WAN connections and heavy loaded systems.
Build 7 May 14, 2012	⏩ PFUS: Improved support for combining of rigid and manual transformations. ⏩ PXMOD: STRM2 model had not been visible. ⏩ VOI: VOI histogram had not been correctly displayed. ⏩ Pipe processing: problem of scale tool fixed. ⏩ Initial reformatting of images: A blank screen could be shown when reading floating point image data with initial reformatting.
Build 6 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}. ⏩ PALZ: New option added for calculating the patient age based on the birthdate and the PET study date. Previously, only calendar years were used. ⏩ 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. ⏩ 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. ⏩ 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. ⏩ DICOM: Fixed handling of the private Philips scaling factor. It is now only applied if the image units are counts.
Build 5 Feb. 28, 2012	⏩ PKIN: The plasma fraction model had not been saved if there was no loaded plasma fraction data. ⏩ PKIN: The prescribed weighting had not been functional for the blood model fitting. ⏩ PCARD: Myocardium sampling range is now limited within the defined wall thickness (instead of 3 times the pixel size) centered at the contour line. ⏩ PCARD: There are now two different orthogonal layouts, the default 1x3 layout and a 1x4 layout also showing the MIP. ⏩ DICOM Server: Stability improved, now handling more than 10'000 objects in a single transfer. ⏩ Scientific Output: A grid of adjustable size can optionally be added to the overlay.
Build 4 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. ⏩ 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. ⏩ PFUS: Change of the color synchronization. The reference and input displays are permanently data driven to support the modality dependent color tables. ⏩ Basic operation external tool: the optical density transformation [-log10(v)] was added. ⏩ 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. ⏩ PCARD: The flow areas (LAD, LCX, RCA) were added as color-coded overlays to the polar plots of the kinetic results.
Build 3 Dec. 10, 2011	⏩ PKIN: List of default models extended. ⏩ 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. ⏩ 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. ⏩ PKIN: Loading of blood data without having loaded tissue TACs previously could cause an error or lock the system. ⏩ VOI: The HOT 2D/3D and COLD 2D/3D methods have now also the Ctrl+Shift option for adding structures to the same VOI. ⏩ VOI: The original VOIs can optionally be removed after merging. ⏩ VOI: Problem to read dynamic (multiframe) VOIs with ROIs fully out of image bounding box fixed. ⏩ PFUS: Manual motion correction has not been possible because the "Copy to all" button and the "Fixed" transformation check were incidentally hidden. ⏩ PXMOD: The loading of mask files was changed to avoid unwanted initial transformations. ⏩ PCARD: Protocol functionality extended to allow changing the image series. ⏩ Database: Redesign of the dialog window for setting the Project/Diagnosis/Locked properties to make it more flexible. ⏩ Database: Button added to hide/show the image preview area.
Build 2 Nov. 12, 2011	⏩ PFUS: Initialization simplified by moving the transformation parameters from the main interface to the image reslicing interface. ⏩ PFUS: The transformation parameters can now be copied to the clipboard in the transformation inspection panel. ⏩ VOI: The VOI list part of the user interface can be hidden in case the horizontal screen space is limited. ⏩ VOI: When saving a VOI atlas, the destination folder can be selected instead of always saving to the system location. ⏩ PXMOD: Default unit values can now be configured for image file formats lacking the units. ⏩ PKIN: Two models were missing from the configuration, Ichise's MA1 method and the 4 compartment model with metabolites. ⏩ PKIN: The initial model parameters of loaded KM files are added to the history. ⏩ 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 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: ⏩ Introduction of a buffer which allows using data created in one tool in another tool without saving them first to disk. ⏩ New option to collapse user interface elements which are rarely used. This is particularly useful with smaller computer screens. ⏩ Definition of the default color tables for the major modalities (PET, SPECT, MR, CT ⏩ Support for modality-specific color table presets. ⏩ New display option which allows including the color bar directly into the image area. ⏩ Saving of color table presets with absolute thresholds. This is particularly useful for CT images. ⏩ New split color table optimized for assessing difference images. ⏩ Improved visual support for the reorientation of images in the loading window. ⏩ Generalized facility for the short-axis reorientation of cardiac PET data. ⏩ Direct import of DICOM images into a PMOD database without requiring a DICOM server. ⏩ Better SUV inspector, which also allows displaying % injected dose per ml. ⏩ Configuration which remembers all window sizes and applies when the window is opened again. ⏩ Replacement of a value range by a single value. ⏩ Visual assistant for loading images which are not in standard orientation. ⏩ Monitors for the status of the DICOM and transaction servers can be started from the ToolBox. ⏩ PVC (MR based) extended by gray matter statistics calculation and comparison (corrected vs. non corrected PET). ⏩ 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: ⏩ Acceptance test to verify the tool operation. ⏩ Option to use a streamlined and simplified user interface. ⏩ 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. ⏩ When loading data different from FDG PET a notification message appears. Changed: ⏩ Redesign of the report pages. ⏩ The page for the normalization inspection has been reduced to showing a single, big fusion image with the template.
PKIN	New: ⏩ 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. ⏩ Representation of the model curves in a high-density fashion to more accurately see the shape which is used in the calculations. ⏩ Support for saving particular sets of model parameters either under a specific name, or as the global default parameters for a model. ⏩ Inclusion of the area-under-the-curve (AUC) calculations. ⏩ Buttons to step through the loaded data sets. Changed: ⏩ The curves available for display are controlled by the selected panel. Preferences of the user are maintained during a session. ⏩ 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. New: ⏩ 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. ⏩ Ability to shift the input series in the large fusion mode. ⏩ Defaults added for mouse brain normalization. ⏩ Rigid matching: Two new options are available allowing to enable/disable the fitting of rotation angles and scaling factors.

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

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

Zürich, Oct. 31, 2011

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