π.pmod Biomedical
        Image Quantification

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PMOD SOFTWARE RELEASE NOTES

MAINTENANCE BUILDS OF RELEASE 4.4

Build 5 June 26, 2024	‣ Licensing: Remote License Server availability, performance and stability improved. ‣ Licensing: Local license server started from Pmod 4.4 can now serve licenses for Pmod instances of versions older than 3.7. ‣ General: Compatibility of Pmod with Java version 17 and 21 provided. ‣ General: Manual data transformations (rotation, translation) are now tracked in image history and ATL log after data reslicing is applied. ‣ General: Fixed problem with data annotation for animal data in HFS position. ‣ General: Fixed problem with recalculating slice times after times edition – they are recalculated without the need of saving and reloading the data. ‣ PVIEW: All image processing operations executed from External Tools are logged in image history as well as ATL log. ‣ PVIEW: Possibility to crop all loaded studies restored. ‣ PFUS: Fixed problem with overwriting input data paths when loading from buffer option selected in fusing wizard. ‣ PNEURO: Fixed problem with loading 6TPM normalization transformation. ‣ PNEURO: Fixed problem with calculating statistics for SUV units at the end of Brain Parcellation workflow. ‣ PNROD: Fixed problem with PET only protocol retrieval. ‣ Rconsole: Communication with R 4.4 can be established with default settings. ‣ RConsole: Fixed problem with *pm.base* and *pm.ai* automatic packages installation during initial console configuration.
Build 4 September 14, 2023	‣ Dicom: Fixed problem with scaling CT data saved as Enhanced DICOM images saved by Paravision 360 scanners. Data were previously displayed as blank images. ‣ Fusion: Fixed problem with matching of the non-axial data. Matched data were either missing or visibly displaced. ‣ Fusion: Fixed problems with 2D deformation field masking for visualization. ‣ Fusion: Fixed problem with the segmentation results in PFUS. Resulting VOIs were dynamic even if the input data were static, which led to incorrect display. ‣ Statistics: Fixed problem with statistics calculation for group of VOIs for fraction mode. Group statistics were wrongly calculated for sum of VOIs in the group instead of the VOIs' union. ‣ Statistics: Fixed problem with Pmod hanging when calculating statistics either containing HotAveraged metric or group of VOIs. ‣ Statistics: Default statistics calculation speed improved.
Build 3 June 15, 2023	‣ General: Fixed problem with failed normalization in Normalization and Coregistration tool in pipe processing in installations with no PALZ license. ‣ General: Added Rconsole compatibility with R 4.3.

	▸ General: Fixed problem with wrong output from segmentation tool in Pipe Processing.
	▸ Database: Compatibility with drivers: MariaDB 3.1.4 and MySQL 8.0.33.
	▸ Database: Number of concurrent connections increased to 30.
	▸ VOI: Fixed problem with loaded VOI initially position outside image box (were inaccessible, predefined organ VOIs selection could fail due to this).
	▸ VOI: Fixed problem with disappearing VOI when switching from static to dynamic on frame different from VOI definition frame.
	▸ View: Fixed problem with drawing VOI with Paint 2D ROI with circular brush.
	▸ PAI: Fixed problem with failed segmentation with Humal LV RV model for dynamic data for selected frame mode.
	▸ PNEURO: Fixed problem with calculating volume when NaN. Was present in statistics for the first map.
	▸ PNROD: Fixed problem with masking segments in the functional input space (due to wrong mask segments were partially or completely removed).
	▸ PNROD: Fixed problem with application of inverse deformation field for reference different from the calculations (VOIs in functional space were rotated).
	▸ Dicom: Added support for reading images that use SQ type elements for dimension index (for example Bruker PV dwi images).
	▸ PATL: Transaction Server communication improvement for user plugins which save VOI statistics and VOI.
Build 2 Mar. 16, 2023	▸ General: Transactions Server management available in docked user interface.
	▸ General: External tools list can be scrolled for the lower resolution screens.
	▸ General: Project and Group lists are refreshed when changing DB during image saving operation.
	▸ VIEW: Hot key segmentation results are always the same independently of the loading method.
	▸ Database: Incoming folder working for standalone servers.
	▸ PAI: Classification is possible for all image reduction methods.
	▸ VOI: Overlay statistics removed from the display.
	▸ VOI: Problems with Tumor Volume Segmentation solved.
	▸ VOI: Statistics are calculated for object VOIs (e.g. spherical)
	▸ VOI: Interpolation of the contour interpolation is working correctly.
	▸ PKIN: Macro models parameters saving and retrieval fixed.
	▸ PKIN: Integration method retrieved for the cumulated activity model.
	▸ PKIN: Aggregation of kinPar files added.
	▸ PFUS/PNEURO/PNROD: Diffeomorphic normalization works for data acquired in all positions.
	▸ PNEURO/PNROD: Mapping execution is now possible after running LMA GTM correction first.
	▸ PNEURO: Protocol saving is possible on the Statistics tab.
	▸ PNEURO: Tool is working correctly without the need to have PAI tool licensed.
	▸ PSEG: VOIs sorting during PERCIST report segmentation problem solved.
	▸ PXMOD: Acceptance Test is performed correctly on macOS with ARM based processors (M1, M1X, M2 etc.).
	▸ PSEG: Pairing procedure of PERCIST regions improved.
	▸ PSEG: Problems with printing PERCIST report solved.
Build 1 Dec. 8, 2022	Initial upload of 4.4 version.

PRODUCT RELEASE 4.4

Highlights among the various improvements across all tools: (1) introduction of a **docked user interface** and further usability improvements, (2) **rigid matching** and basic **3D rendering** is now included in **PVIEW**, (3) optimized performance in **image** and **VOI display** as well as data loading, (4) a new, fast raster VOI functionality for images with huge resolution, (5) native support for the highly performing **Mac ARM** platform, (6) a new **image matching wizard** in **PFUS** to reduce complexity and improve speed for standard matching situations.

General	
	▸ NEW: Introduction of the docked user interface as default appearance. All main windows are now managed within a container for faster operation and compact handling. The legacy appearance can still be configured.
	▸ NEW: Combination of the loaders for DB, DICOM and Autodetect in a single unified page for streamlining the loading process.
	▸ NEW: Native support for the highly performing Mac ARM.
	▸ Image and VOI display performance optimized for big data.
	▸ Configuration option to block 3D functionality which is not supported for some systems or via remote desktop.
	▸ Ability to sort by name, date and size in file-based image loading.
	▸ Better sizing of the color bar in the Publication Capture functionality
	▸ Scaling tool extended (/TAC) so that for dynamic data the pixel values can be divided by the frame-wise VOI average.
	▸ Cropping for 2D data revised to avoid introducing a third dimension.
	▸ Interface of interpolation, cropping and filtering adjusted for 2D images.
	▸ ? mark to open documentation is now available on all toolbars.
	▸ Acceptance test unified across modules. The result when running globally for all tools is equivalent to running directly from a tool. Proper handling of tools which can´t be started due to system environment.
	▸ R console: R4.2 supported on all platforms; script RunPmod extended for Windows to allow starting R installed to non-system folder; package verification improved; appending of VOI statistics to workspace fixed.
	▸ Save all functionality previously reset the settings specified for image loading.
	▸ Memory leak fixed in pipeline segmentation.
PVIEW	▸ NEW: Manual rigid matching is now available on the Compare page when activating the Reslicing panel.
	▸ NEW: Basic 3D rendering of VOIs and the loaded images is now available.
	▸ Format cleanup in pipe processing and format conversion.
	▸ Saving interface improved for the situation of many files.
	▸ Improved time handling when merging PET images acquired with days in between the acquisitions.
	▸ Improved handling of the displayed VOIs when switching pages in the presence of multiple images and VOI sets.
	▸ Fix of acquisition time calculation for enhanced PET image with acquisition time prior to series time.
	▸ Fix of k-means segmentation.

Database	
	▸ Age field added on the series level.
	▸ Ability to save a list of selected files for restoring the selection later.
	▸ Performance of saving uncompressed data to a transaction server much improved.
	▸ Improved response time when changing the layouts of Database loading.
	▸ New button to inspect DICOM attributes of RTSTRUCT components.
	▸ Subject IDs cannot be changed to an already existing ID.
	▸ Mysql interface updated to support current version.
PAI	
	▸ NEW: Model added for the segmentation of trabecular bone from uCT images.
	▸ NEW: Framework extended to support classification neural networks. The prediction can be used in pipeline processing with the results being aggregated.
	▸ Serialization of environment for training sessions.
	▸ Configuration of GPU for prediction.
	▸ Automatic application of slice splitting when required by model.
	▸ Improved weights storage and handling.
	▸ Additional parameters for more effective control of training process.
	▸ Update to TensorFlow version 2.10.
	▸ Support of PyTorch Python library for AI training and prediction.
	▸ Image processing tool added which supports the comparison of image denoising with a NLM filter and AI based methods.
	▸ Multiple predictions are handled more efficiently.
	▸ Improvements of the diagnostics of the environment setup as well as data compatibility with the selected model.
	▸ Efficiency of transferring the prepared data to the training environment improved.
VOI	
	▸ NEW: Raster VOI functionality based on voxel masks which works much faster for huge images. They can be saved and exchanged as DICOM segmentation objects.
	▸ VOI statistics calculation performance improved by factors up to 6 fold.
	▸ Display degradation due to the presence of many VOIs fixed, improvement up to 5 times.
	▸ Fix of displaying VOIs created on cropped images on the original images when multiple images are displayed.
	▸ Fix of the visual feedback for interactive region growing.
	▸ Issue fixed for VOIs outside the image bounding box.
	▸ Object VOIs could disappear when the definition plane was changed.
	▸ Issue for spheres created from contours was corrected.
	▸ Iso-contouring of dynamic images could result in omitted frames.
	▸ The NumberOfPoints statistics was rounded when being exported.
PKIN	
	▸ NEW: Ability added to specify the initial parameters for the models in a macro.
	▸ Current blood delay is mirrored on the tissue parameters panel for better overview.
	▸ Parameter Explorer: Currently shown region is marked with *. When selecting a region the blood delay used in the regional fit is now also recovered.
	▸ Fix of visualization of Monte Carlo results via the fitting history.

PFUS	⯈ NEW: Wizard to reduce complexity and improve speed for standard matching situations.
	⯈ Display performance improved when using cubic interpolation.
	⯈ Display performance significantly improved on the fused MIP page.
	⯈ ANTS: Percentage of used voxels introduced for the affine step. Support for application in 2D.
	⯈ Reslicing extended to handle data beyond 2^{31}-1 voxels per volume.
	⯈ The option to conserve total amount rather than concentration when applying an SPM transformation was retired.
	⯈ Fix of effective motion correction range when applied in batch mode.
	⯈ Motion correction relative to previous frame was not working properly.
PNEURO/PNROD	⯈ NEW: ANTS affine and deformable registration added as normalization methodology.
	⯈ NEW: ICBM templates made available for non-T1 based workflows (termed "Other").
	⯈ Revision of the image labeling on the Save All configuration panel.
	⯈ Optimized transformation handling for workflows with already matched functional/anatomical images.
	⯈ Template selection for normalization verification when using Hammers 1mm atlas improved (PNEURO).
	⯈ Inappropriate loading of segments removed from PNROD.
	⯈ Confirmation dialog before applying a cropping box is removed.
	⯈ Default of enforcing 0 as lower display threshold removed for better experience with CT data.
	⯈ Duplication of Split White Matter check box in batch configuration corrected (PNEURO).
	⯈ Acceptance test revision to avoid failure for specific Windows environments.
	⯈ Revised enabling/disabling of the action buttons depending on the current status, eg. after protocol running.
	⯈ Better handling of cropping information from protocols.
	⯈ Loading of tissue probability maps in PNEURO resulted in a blocked state.
	⯈ Some fixes of workflow specific default parameters.
	⯈ Fix of a small shift when applying the deformation transformation resulting from the 6 tissue probability normalization (PNEURO).
P3D	⯈ Display synchronization of input frame and segmentation result for dynamic images added.
PXMOD	⯈ Deconvolution of dispersion improved for blood data not starting at time zero and having relatively distant samples.
PCARDM	⯈ Ability to reorient the input images, as this may improve segmentation performance.
	⯈ Iso-contouring is now also supported for LV segmentation.
	⯈ Model-based volume extrapolation procedure added for 2D data.
	⯈ Wall-thickening analysis also supported for 2D data.

PCARDP/PCAR DM	▸ Optional filter for the volume curve implemented to cope with segmentation failing in some gates.
Image File Formats	▸ DICOM: Improvements for loading images with empty reference time element (non conformant with the standard). ▸ Paravision 360: Support for reading B_0 values. ▸ ITK Metalmage (mhd): Raw file format to read AI challenge data added.
PATL	▸ Mandatory comment introduced for deleting and lock/unlock operations. ▸ Project tracker uses database configured for current user.
PGEM	▸ GUI fixes and improvements.
PSEG	▸ Definition of the liver Reference VOI in the PERCIST workflow resulted in an exception.

Zurich, December 8, 2022

MAINTENANCE BUILDS OF RELEASE 4.3

Build 5 February 16, 2023	▸ PAI: Usage of R package Reticulate 1.24 enforced, since the latest Reticulate version could cause PAI prediction to hang. ▸ VOI statistics: Peak VOI calculated on static 3D data can now be retrieved correctly in dynamic 4D data. ▸ VOI properties edition corrected. ▸ PKIN: Integration method in Cumulative Activity (OLINDA, IDAC) can be edited and applied to the model. ▸ PFUS: Motion Correction values are saved correctly, not shifted by 1, when saved. ▸ PFUS: Motion Correction range is applied correctly instead of correcting the whole data. ▸ PFUS: Transformation with reslicing to Talairach bounding box is applied correctly. ▸ PNROD: List of available Partial Volume Effect correction methods limited to only VOI based ones. ▸ Micropet data with not defined manufacturer and storing data offsets as 2 32-bits integers are loaded correctly. ▸ PVIEW: Defacing external tool is available under PVIEW license. ▸ Frame times for Enhanced DICOM object are retrieved correctly after series time update. ▸ Series dates earlier than 01.01.1970 are correctly saved to DICOM objects.
Build 4 July 15, 2022	▸ Poor display performance in the presence of many VOIs: scrolling or triangulation is now much faster. ▸ VOI statistics: The in-range function didn't work properly when SUV units were selected. ▸ SUV panel: Propagation of date/time values was corrected.

	▸ PFUS: The functionality of user-defined reference image was not available in batch operation. ▸ PFUS: Support for changing the matching parameters in the batch dialog window was improved. ▸ PFUS: Content of the ANTS configuration in image history was corrected. ▸ PFUS: Functionality related to visualization of deformation fields was revised. ▸ PKIN: Adding/removing of models in the main configuration was not working properly. ▸ PKIN: Issue occurring in the Parameter Explorer after deleting TACs was fixed. ▸ PKIN: Running a fitting macro failed when it contained a model which was not configured. ▸ DB: Split of the series of one subject into new subjects was revised. ▸ PNROD: Acceptance test could fail due to modified properties. ▸ Enhanced PET images from PMOD version <3.7: Timing issue when loading in current version was fixed. ▸ Fix for loading of old GE Advance data. ▸ MicroPET images from old Bruker PET insert with header version 6.3: Dedicated fix introduced. ▸ DB export of updated PET objects: Fix for instances missing the element (54,0101).
Build 3 March 31, 2022	▸ PFUS: Color tables are now included in reports generated from the Comparison page. ▸ PFUS, PNEURO: Initialization of ANTS matching was not proper for some images with oblique orientation. ▸ PFUS: Fix for the use of mask in combination with ANTS in batch processing. ▸ PKIN: Plot area was not updated when changing the current region from the parameter explorer by double-clicking. ▸ PKIN: "Fit model, all regions" could result in small differences when repeated due to an issue in multi-threading. Fixed and performance increased by up to 60%. ▸ PKIN: When using macros in batch fitting only the result of the last model in the macro was saved. ▸ VOI: When a group of non-intersecting VOIs were rotated, intersections could be observed sometimes in the result. Behavior improved. ▸ VOI: Iso-contouring within VOI was improved for dynamic data. ▸ VOI in PCARDP, PCARDM: suffix "_iso" is suppressed when iso-contouring a VOI. ▸ VOI: Name was not updated when changed in properties. ▸ VOI: Intersection of VOI with a mask was not working correctly. ▸ PCARDP: Bounding box was wrong by 1 pixel when a VOI was retrieved from file. ▸ PCARDP: Minimal differences between step-wise procedure and protocol execution were fixed. ▸ PCARDM: Segmentation issue was corrected. ▸ PNEURO: Issue when calculation relative TACs was fixed. ▸ PNEURO, PNROD: Workflow for already matched data had a problem in certain conditions. ▸ PNEURO, PNROD: Use of the template mask was changed to optional and set to off by default. ▸ PNROD: Issue with user-defined templates was fixed.

	⇒ PNROD: For PET/MR data matching was always performed, even if "Already matched" was selected. ⇒ PSEG: Organ segmentation was not working for data with initial empty frames. ⇒ DICOM loading dialog: Sorting according to dates was improved. ⇒ DB export information: Sex, age, organ, project, group are now included. ⇒ DB export with anonymization: file name creation was improved according to DICOMDIR convention.
Build 2 Dec. 21, 2021	⇒ Iso-contouring VOI: Option to create separate VOIs for disconnected parts fixed; changing of planes in preview prevented when getting threshold from cursor; proportional tolerance (10^{-6}) added to the threshold; preview synchronized with selected frame in dynamic series. ⇒ Segmentation processing tool: could not be selected in batch configuration. ⇒ PFUS: Improvements of ANTS in batch processing. ⇒ PFUS: Initial alignment improved for images without orientation definition. ⇒ PFUS: In repeated matching, the rigid part of the previous matching operation is used as starting configuration (also extracted from deformable registrations). ⇒ PAI: Better portability of exported learning sets and models. ⇒ P3D: Two of the example protocols (MR-AAL, AAL-VOIs 3D) were not working. ⇒ PVIEW: Issue with the images generated in the VOI-based PVC tool. ⇒ PKIN: Behavior of model propagation (without parameters) corrected: establishes current default of "Conversion" switch is off, otherwise applies conversion procedure. ⇒ PKIN: AIC and R2 added for Logan Ref, Patlak Ref and RE_GP models. ⇒ PNEURO: Atlas smoothing check box added for SPM-based normalization. ⇒ R console: Saving of tables failed sometimes. ⇒ Saving of single slice TIFF images fixed. ⇒ Fix for saving histogram data.
Build 1 Oct.28, 2021	Initial upload of 4.3 version.

PRODUCT RELEASE 4.3

Besides improvements across all tools as listed below the following achievements are particularly noteworthy: (1) major improvements of the **PAI** solution and use thereof in the **PCARDM** tool, (2) revision of the **PCARDM** workflow for cardiac cine MR images and launch as an independent module, (3) drastic display speed boost in **PFUS** in situations with multiple fused images, (4) ANTS deformable registration in **PFUS**, (5) revision of the **PKIN** user interface in combination with improving access and performance of fitting macros, (6) faster **VOI** functionality for very large images.

General	⇒ Execution of protocols from the system command level, including replacement of the files to process (PVIEW, PNEURO, PNROD, PFUS, PXMOD, PCARDP, PCARDM, PSEG). ⇒ Printable Acceptance Test Report for all tools. ⇒ Revised reporting after check for upgrade availability.

	‣ Update of Java engine in distribution (OpenJDK Runtime Environment 11.0.12+7) for better performance and security.
	‣ Ability to collect multiple pixel-wise TACs in the data inspector.
	‣ Cropping box improvements: issue with slice scrolling solved, scaling by edge drawing.
	‣ Display now supports MIPs over time for dynamic series.
	‣ Display of timing information improved in multiple places.
	‣ SUV panel: clearer problem messages.
	‣ Slice direction cosines added to slice information viewer.
	‣ R: The use of rserve has been abandoned. Local R installation is now required and direct communication used for performance reasons.
	‣ R: Cleanup of temporary data revised to make it more fail safe.
	‣ Database: Performance optimization for name filtering. Subject age field introduced on series level.
	‣ Revised procedure for listing the available file system volumes to avoid delays due to not accessible volumes.
	‣ Garbage collection improved to reduce RAM leakage.
	‣ New optional commandline switch "-brkr": Adds the default Paravision DICOM server, configures the small animal settings and the Nimbus Look & Feel.
	‣ On Windows the commandline switch "-Dfile.encoding=UTF-8" is included in RunPmod to ensure portable data generation.
	‣ R installation allows interactive selection of CRAN repository.
PVIEW	‣ Convenience tool for automatic splitting image series with 3 or 4 mice into separate data sets.
	‣ AI functionality added (if PAI licensed): Supports model development and prediction (segmentation and classification).
	‣ AI-based segmentation supported in the segmentation plugin to be used in batch processing.
	‣ Defacing tool for MR and CT head images for anatomical anonymization introduced.
	‣ Merging of slices was only working if PFUS had been licensed too.
	‣ Merging of static series into dynamic: better timing checks, error messages and defaults for decay correction; preview of the resulting dynamic series.
	‣ Otsu segmentation migrated from ITK library to native Java.
	‣ Segmentation tool: In presence of a VOI the histogram within the VOI is shown.
	‣ "Fusion" page renamed to "Hybrid" to make clear that only matched images can be fused.
	‣ Protocols now also include the VOIs, not only the images.
	‣ Vertical value profile was not properly updated in the data inspector.
	‣ ITK filters removed.
	‣ The atlas VOI names were missing when using the automatic brain VOI tool.
	‣ The "Replace Image" functionality was not always working in batch pipeline.
PAI	‣ User interface, robustness and functionality improved in many respects, please refer to the *PAI User Guide*.
	‣ Support for classification applications by SVM (Support Vector Machine).
	‣ Facility for evaluating a trained model with a set of test samples.
	‣ Loss function value is plotted during the training process to monitor the learning progress.

	▸ Training can be interrupted interactively. ▸ Export and import of learning sets implemented. ▸ 2D multichannel NN architecture added. ▸ Models developed for the LV segmentation of cardiac cine MR images (human, mouse) ▸ Model developed for the segmentation of trabecular bone in CT images. ▸ Model developed for the segmentation of the deep nuclei in human MR brain images. ▸ Model developed for the classification of Amyloid PET images as positive or negative.
VOI	▸ VOIs of two rodent cradles included for rapid bed masking in the image. ▸ Algorithm redesign to make iso-contouring workable for big data with >1300^3 voxels. ▸ Multi-threading of time-consuming processes. ▸ Support for iso-contouring in a VOI group. ▸ Name generation of iso-contoured VOIs improved. ▸ Region-growing: The orthogonal neighborhood was not strictly observed, under some conditions oblique neighbors were also considered. ▸ Interactive eraser didn't work properly in Group mode. Is now blocked. ▸ An additional VOI was shown sometimes in addition to the ones selected on the Group panel. ▸ VOIs can now directly be 3D rendered from the lateral taskbar of the PVIEW tool.
PKIN	▸ Macro functionality fundamentally revised and a new format .kmMacro introduced to save macro definitions. ▸ Three basic macros included in distribution for calculation of Vt, BPnd or FDG Flux. ▸ Batch mode revised to offer simplified processing based on macros. ▸ Revision of Look & Feel to be more similar to the other modules. ▸ QC captures can be generated from model fitting in batch pipeline. ▸ Blood delay fitting is automatically disabled for models without blood information. ▸ After data loading, text was not correctly updated on the Comment tab.
PFUS	▸ Drastic display speed improvements, particularly with multiple fused images on the Comparison page. ▸ Inclusion of the ANTS methodology for elastic registration. ▸ Completion of the list of standard brain normalization templates. ▸ Improved fusion slide behavior when only one data set is loaded. ▸ Protocol improvements: loading of parameters without execution supported; better handling of data units.
PSEG	▸ New batch mode introduced which features the cloning approach and supports VOI statistics. ▸ Default for masking set to None. ▸ Standard morphological segmentations were added. ▸ Segmentation of a dynamic series now generates dynamic VOIs.

P3D	‣ P3D engine updated to support Java 11 using the libraries Java 3D 1.7 and JogAmp 2.4. ‣ New headlight scene lighting option. ‣ Unused elements removed from cutting panel, and interface behavior improved. ‣ VRML support discontinued.
PXMOD	‣ Improved handling of image units in protocols. ‣ Better robustness of batch operation. ‣ Transfer of resting state fMRI correlation matrix to PVIEW for inspection was added.
PCARDM	‣ Relaunched as separate module independent of the cardiac PET (PCARDP) module. ‣ Completely revised workflow for the analysis of gated cardiac cine MR images. ‣ Implementation of AI-based segmentation for the left ventricle (requires PAI option); applicable to human and mouse data. ‣ Parameter settings are derived from species selection. ‣ Serialization and protocol support now covers all settings.
PCARDP	‣ Creation of normal databases supported for gated studies. ‣ Polar plots can be saved as DICOM Secondary Capture objects.
PNROD and PNEURO	‣ Multiple improvements in batch mode: Better robustness of batch operation. QC captures now also available for MR only workflow. QC captures of parametric maps added. QC captures of TACs added. More descriptive series descriptions for parametric maps. VOI statistics are evaluated on all parametric maps. Results are saved in the database corresponding to the input images. ‣ VOI statistics of parametric maps could not be saved to file system, only to database. ‣ Issue occurred if an atlas only had a CT template, but no MR template. ‣ Improvement of partial-volume correction performance. ‣ Issue solved with NaN in parametric maps if TACs were also calculated in the same workflow. ‣ Protocol correctly restores the frame averaging settings. ‣ Relative statistics were not saved in batch operation. ‣ In batch operation, QC captures were not saved in the selected folder.
PGEM	‣ Acceptance test uses DTI workflow instead of CFD.
PSAMPLE	‣ The first twilite generation with serial interface is not supported anymore.

Zurich, October 28, 2021

MAINTENANCE BUILDS OF RELEASE 4.2

Build 6 Nov. 23, 2021	‣ PVC: The procedure failed in the presence of empty VOIs. ‣ Segmentation tool: Saving the result as atlas was fixed.

	▸ PFUS batch: The saving/retrieving of a job list was not working properly. ▸ DICOM: Loading of images with missing isotope half-life was improved. ▸ DICOMDIR: Support for the use of other character sets than UTF-8 introduced. ▸ PKIN: Export format OLINDA 2 enabled for Cumulated Activity model results. ▸ VOI: After trimming a VOI it was not correctly displayed in the orthogonal planes.
Build 5 July 21, 2021	▸ The behavior of the fusion display was slowed down by Internet look-ups. The implementation as been changed, resulting in much better display performance of PFUS. ▸ PVIEW/Compare page: A third row could appear when creating an image capture. ▸ PVIEW/Batch/Segmentation: Maximal number of clusters and minimal cluster size options added. ▸ PVIEW/Reslicing to common slice thickness: An empty slice could appear at the edge. ▸ PNROD: The results could not be obtained in the subject space for the affine normalization. ▸ PNEURO: Slight differences could occur when executing protocols with a certain crop box definition. ▸ PKIN: Saving of the standard deviation from the curve plot are was not working properly. ▸ DICOM: The energy windows are now also saved in derived NM objects. ▸ DICOM: Fixes for loading and handling of Segmentation objects. ▸ Two fixes correcting wrong image orientation information after manual transformation of biped data. ▸ Adding of the image frames during loading was fixed.
Build 4 May 26, 2021	▸ PSEG/PERCIST: Issue solved with Reference VOI if mask was not defined. ▸ Image scaling tool: Allows also value normalization by image average or z-score. ▸ PNROD in ATL version: Issue with atlas selection fixed. ▸ Image series merging: New option to decay correct to injection time. ▸ DICOM element (0020,0013) included in single frame images for compatibility with AW station. ▸ PKIN/Coupled fitting: Delay could not be fitted. ▸ PKIN/Display type "Blood": Was not working. ▸ TAC calculation fixed for images with per slice scaling and non-zero start time. ▸ Information from original images is better propagated to screen captures saved as DICOM objects. ▸ Fix for handling PET images with a single uniform value. ▸ PNEURO/PVC: Percent difference was not calculated for dynamic TACs. ▸ PVC (VOI based) tool was not working. ▸ PVC in PNEURO/PNROD/PSEG: VOI adjustments by user were not taken into account.
Build 3 March 16, 2021	▸ VOI: Problems fixed when using eraser. Overlap control improved for adding a small VOI inside a large one. Undo operation improved to fix VOI disappearance in specific situations. Orthogonal display issue fixed for complex VOIs. VOI filling did only work in one direction when the Group panel was active. ▸ ATL version: Unnecessary network traffic due to project tracker eliminated. Atlas template was not properly loaded. License monitoring improved. Default configuration of VOI statistics changed to basic measures.

	‣ PNEURO, PNROD batch: Aggregation failed when saving to One Folder.
	‣ PNROD: Generated segments are trimmed within the normalization mask for removing artefacts.
	‣ PSEG: Segmentation based on artificial intelligence was not working from protocol.
	‣ PAI: Problem with blocking by rserve in case of a failure situation fixed.
	‣ PKIN Batch: An unnecessary file was created.
	‣ Cardiac MR: Was not working for single-slice data.
	‣ PGEM: User interface improvements.
	‣ Cloud license: Support for two security certificates, for licensing and data exchange.
	‣ Batch Pipeline: In the case of a list of pipelines, non-image results were always saved to default database.
	‣ Transfer of statistics to R: Variable name can be defined.
	‣ Global Acceptance Test: P3D and PGEM excluded to avoid system overload due to high resource consumption.
	‣ Paravison MR data: Fix for loading images with repeated value tags.
	‣ DICOM: Fix for loading NM images missing correct image type definitions. Support for reading files missing 132 bytes of the file header. Fix in merging of series which could result in a failure during image saving.
	‣ Incoming folder: Performance improved by skipping known non-image files.
	‣ ATL: Access to help system improved in case Internet is not available.
Build 2 Jan. 22, 2021	‣ Tape VOI: Issues with generating the VOI pixels along the contour and NaN statistics solved.
	‣ PKIN: The residuals of the model fit to the plasma activity were incorrectly plotted.
	‣ PKIN: Problem fixed when closing the tool configuration window.
	‣ PAI: Test introduced to check whether R is working correctly and Python/TensorFlow is installed; improved error handling in case of data loading problems or data inconsistency; installation help links introduced for Python/TensorFlow; installation of reduced set of R packages is possible for PAI-only use; option to anonymize the training data; manifest file added to record model configuration and training history.
	‣ R Package installation fixed for MacOSX Big Sur and Linux.
	‣ PFUS: Saving of manual transformation improved so that it can be combined with other transformations.
	‣ Reslice to standard orientation did not work properly for data with left-handed coordinate system.
	‣ Cropping box was not correct in sagittal plane of whole-body layout.
	‣ DICOM Capture of sagittal plane in whole-body layout: improved capture size.
	‣ DICOM: Fix for reading enhanced images that do not include measurement units code sequence (0040,08ea).
	‣ DICOM Query: Improved handling of faulty requests.
	‣ DICOM Save: Performance improvements for saving to NAS storage systems; bug fixed when saving concatenated data >1GB.
	‣ Improved handling of units stored with protocols (PXMOD, PFUS, PCARD, PNEURO, PNROD, PGEM): the stored units did override the units in the loaded data.
	‣ Fix for saving histogram data.

Build 1 Oct.28, 2020	Initial upload of 4.2 version.

PRODUCT RELEASE 4.2

Two exciting new tools are introduced with version 4.2:
1. **PNROD** has been developed for the analysis of rodent brain images. **PNROD** takes the nature of typical rat and mouse data into account for a solution which is simplified in terms of operation, yet extended regarding the methodology. Particularly, CT images are supported for matching to the atlas templates.
2. **PAI** is a framework which allows users to leverage artificial intelligence (AI) methodology for the segmentation of images. It covers the learning as well as the prediction part. **PAI** is an add-on to the **PSEG** module.

Please refer to the various documentation materials for **PNROD** and **PAI** details.

The previously existing modules were further improved and extended, including the points described below.

General	- Acceptance tests are now available for all modules. They test that the functionality works properly after installation. All tests can be initiated at once from the "On Start" panel in the configuration. - The whole-body orthogonal layout is now available for all displays including fusion. It features better usage of the display area for non-cubic data such as human or rodent whole-body acquisitions. - A new "M" button at the image border serves for quickly enabling/disabling the MIP display in the orthogonal layouts. - Improved appearance of curve plots: Axis ticks are rounded, curve names can be shown in the plot area, and the maximal value of the active curve can be overlaid. - Triangulation in zoomed image fixed: The triangulation point has not always been visible in all planes. - Improved description and encoding of the ~100 normalization templates in the system. Manifest files were introduced for the templates to specify species and anatomical space. - Support for more association types to define data roles (whole-blood data, input curve, mask, etc) particularly for PXMOD and Machine Learning. - Mechanism (association) to automatically organize relations between images such as T1, T2, Flair. This information can be used when batch processing a big number of data sets, e.g. in Machine Learning. - New command-line option "-version" to extract PMOD version information. - R workspace saving: Optimization for size reduction. - Implementation of a cloud license server which allows dongle-less PMOD operation. - R Console: Improved testing and management of the required R packages. Start-up test and report in the case of configuration problems.
VOI	Organ Shape VOIs: To simplify organ delineation, VOIs with typical organ shapes can easily placed at the triangulation point and adjusted to the actual anatomy in the image. Organ VOI sets are available for humans, rats and mice. Users can create their own set of standard VOIs.

	⇥ VOI rotation is not limited any more to one axis. VOIs can be rotated (and scaled) in any direction. ⇥ Interpolation of contours across slices is working much faster now. An new choice allows restricting the interpolation to a sub-range. ⇥ Faster VOI outlining and masking for big data. ⇥ MNI Atlas creation: Additional option to create an entry "SPACE=MNI" in the manifest, so that the standard set of normalization templates will be available. ⇥ Objects defined in STL files can be converted to VOIs. ⇥ Larger brush sizes supported for painting and erasing. ⇥ Tape VOIs: For some VOI types the functionality didn't work properly. ⇥ Loading VOIs with transformation: Only the first VOI had been transformed. ⇥ Former "Enhanced statistics" format is now exclusively used.
PKIN	⇥ New model for renal kinetics added with two parallel tissue compartments (Gulaldi et al. Biomed Res Int. 2013). ⇥ Average VOI TACs transferred from PVIEW can be used in a similar was as the pixel-wise TACs to create parametric maps and dynamic phantom images. In contrast to the pixel-wise case, the information in the VOIs will be homogeneous. ⇥ Simplification of menu entries for loading blood-related files: sub-menus are now only shown (parent, metabolite), if a model with metabolite input curve has been selected ⇥ Introduction of acceptance test verifying 26 model configurations. ⇥ Correction of t* estimation for Logan plot: negative prediction values had not been taken into account. ⇥ t* estimation for MA1 and MA2 divided the deviation by the measurement, not the predicted value as the other models. This was harmonized. ⇥ "Fit all" does not complain any more about the failed reference tissue, and lists all regions where fitting failed. ⇥ Noise addition to several selected curves was not working properly. ⇥ Models including a metabolite input function: harmonization so that the "Authentic fraction" can also be used for calculating the metabolite input function from total plasma activity.
PFUS	⇥ The legacy fusion tool has now been retired. Its matching part has been migrated to the new tool as an alternative option. ⇥ Normalization presets for rodent species were adjusted. ⇥ Initialization has been improved for non-axial images resulting from SPM anlyses. ⇥ Some harmonizations and simplifications of the user interface were implemented
PSEG	⇥ Integration of PAI covering the learning as well as the prediction part. Users can prepare sets of images with their corresponding segmentation. Such learning sets can then be submitted to TensorFlow for training a neural network of suitable structure. The resulting network can finally be applied to segment input images with characteristics similar to the ones in the learning set. ⇥ Two masking methods added: bone mask for CT images, brain mask for MR and PET. ⇥ Whole-body layout can be configured as default for oncology users.
PVIEW	⇥ New page added where the statistics results are permanently available. ⇥ Protocol support added which is used for the new acceptance test and which is generally useful for repeated data loading.

	‣ The publication capture is now also supporting SUV units. ‣ Fix for pipeline use of the brain extraction tool.
PXMOD	‣ Improvement for batch processing: protocols can be generated by cloning an existing protocol (similar as in PNEURO). Depending on the model used, the functionality requires association of VOIs and blood data to the image.
PCARD	‣ Improvements in the segmentation of rat PET images by refining the model and adjusting the segmentation presets. ‣ Overlay information for the transmural perfusion analysis changed for consistency reasons.
PNEURO	‣ Rodent atlases removed. The processing of rodent brain images requires tailored workflows now available in PNROD. ‣ Split brain box (to divide the white matter segment) moved to the page where the result space is defined. ‣ Issue fixed when executing a protocol and adjusting manually the registration with the anatomical image. ‣ Revision of PVC method naming.
PGEM	‣ Pixel-wise boundary conditions (velocity or pressure) for CFD simulation can now be specified by loading image data. ‣ Improvements in saving and loading CFD simulation protocols.
PSAMPLE	‣ Acceptance test introduced which verifies connectivity with device.
Data Formats	‣ Nifty extension to include Biped/Quadruped attribute, which is used to provide correct anatomical labels for the normalization templates. ‣ DICOM: Support for attribute (0012,0050) clinical trial time point ID. ‣ CT DICOM images: Exposure time is now used as frame duration instead of the default 1sec. ‣ Fix for reading CT images with unknown SOP class. ‣ Anonymization: Option to keep patient name and ID (for data with code information in the name field). ‣ Improved handling of data with missing slices. ‣ Support for 32 bit integer raw data. ‣ Generation of synthetic patient/study name for data without patient information: use of sub-directory structure in the incoming folder for generating the patient and study level information. ‣ Strategy to avoid file name lengths beyond operating system support when exporting component information from the database.

Zürich, October 28, 2020

MAINTENANCE BUILDS OF RELEASE 4.1

Build 6 Dec. 7, 2021	‣ Reading of gated Bruker Paravision images fixed.

	⇥ DB: fix of an issue which occurred when querying the DB during an update process. ⇥ P3D protocol: Spurious object appeared when loading a protocol.
Build 5 Sept 15, 2020	⇥ PXMOD/protocols: The saved mask file was not considered in the processing. ⇥ PXMOD: For some DICOM data with missing frame durations a wrong timing could result so that modeling failed. ⇥ PFUS: Configuration of the legacy PFUS was not possible if only the fusion tool was licensed. ⇥ PFUS: Calculation of the rotation matrix from affine an transformation was improved. ⇥ PNEURO: Manual adjustment of rigid matching resulted in a segmentation failure. ⇥ PVIEW: Image saving from sidebar used DICOM SOP from previous operation. ⇥ P3D: MIP configured as initial landing page caused an exception. ⇥ Import of information from database to image series: Only limited information was used. ⇥ DICOM: The Study Instance UID is kept for the generation of derived objects (Secondary Capture, processing results) as long as the patient-related information is not changed. ⇥ DICOM: Support for faulty NM data encoding each slice in a file. ⇥ DICOM: Fix to read certain legacy Paravision data. ⇥ DICOM: Special handling to read data from the Total Explorer (missing frame duration, wrong decay correction). ⇥ DICOM: Graceful handling of missing slices when loading data. ⇥ DICOM: Problems occurred if the folder containing DICOM data was itself named DICOMDIR. ⇥ DICOM: If only a sub-range of slices was loaded, the SUV information was missing. ⇥ Transaction server: Automatic generation of the port number improved.
Build 4 June 4, 2020	⇥ PXMOD: Parametric mapping using non-DICOM images was affected by a timing problem (only models which support slice-wise timing). ⇥ PKIN: Enabling of the options in the lateral taskbar (e.g. randomized fitting, LLS initialization) had the side effect of changing the model in all regions to the model applied in the current region. ⇥ PNEURO/Batch: "Brain split" was not applied in batch processing when the dedicated checkbox was enabled. The "split brain" setting in the step-by-step Neuro interface overrode the batch setting. ⇥ PNEURO/Comparison to normal database: VOIs belonging to a database disappeared when loading NORMALIZED images twice in a row. ⇥ PNEURO: The normalized PET images saved from the lateral taskbar are now prefixed with NORMALIZED in the description. This allows skipping the normalization procedure in the comparison to a normal database. ⇥ PNEURO acceptance test was not working properly if not executed at program start. ⇥ VOI: Scaling is now supported also in the direction orthogonal to the contour definition plane. ⇥ VOI: Undo/redo functionality improved. ⇥ Image processing tools: When applied to multiple images in replace mode the first image was overwritten.

	‣ Image loading with operations: Now the operation can be defined individually for all selected series. Previously, the operation defined for the first series was applied to all selected series. ‣ R console: Supports the latest R4.0 version on all operating systems. ‣ Spaces were omitted in text output after recent Linux updates. The default Look & Feel was changed to "System" to avoid the problem. ‣ Image algebra results in a long series description which is used as file name in certain formats. This created saving problems due to file names longer than supported by the operating system. ‣ DICOM/Segment saving: Binary maps are now supported in addition to probability maps. ‣ P3D: FreeSurfer surfaces can be directly loaded and displayed. ‣ PGEM: Acceptance test improvements. ‣ Update check and help access were changed to support the https protocol. ‣ Client-side functionality added to connect to a cloud license server.
Build 3 March 3, 2020	‣ VOI iso-contouring: The selection "Inner Holes" Yes/No was not working properly. ‣ VOI: Save of pixel dump failed for dynamic image data and if the VOI was defined on a single frame. ‣ P3D: Fix for protocols including database VOIs. ‣ P3D: Added loading and rendering of FreeSurfer surfaces. ‣ PKIN: Naming of the menu entries for loading blood components improved when using the model filter. Subtle revision of behavior when switching model filter between transferring TACs and loading blood data. ‣ PNEURO: The MR normalization templates for mouse and rat were not properly prepared. ‣ PNEURO: The PET only workflow did not work, if Hammers 1mm was selected and FDG or AV45 controls etc. were used as templates. ‣ PNEURO, PSEG: PVC calculations for images larger than 256x256x256 voxels failed. ‣ PCARD: Improvements of the apex segmentation for PET MBF data by using irregular sampling. ‣ PCARD for MR: Wall thickening calculation improved; volume units changed to [ml] for small animal data. ‣ PGEM: Toolbar functionality extended by polymesh loading and STL saving. ‣ PGEM: VOIs were not displayed after adding new elements to a model. ‣ PGEM: Report of track statistics revised. ‣ R: Automatic R package installation supported on Linux; conversion of VOI pixel dump into an image fixed; image saving supported from R console. ‣ The configuration "Communication with www.pmod.com" was not serialized. ‣ DICOM: When loading images saved from PMOD other than PET or Enhanced the shifting of frame times to zero resulted in wrong times. ‣ DICOM: Improvements of the output SOP handling when saving multiple files at once. ‣ MicroPET format: Improvements to load Digimouse images. ‣ FreeSurfer format added for loading. The surface description is converted into a volumetric representation suitable for data processing.
Build 2 Dec. 12, 2019	‣ PNEURO: "Save all" didn't correctly handle the change of the output modality in subsequent calls. Protocol fix: The settings for VOI intersection with the tissue segments were not restored.

	‣ PSEG: Texture analysis enabled for all segmentations; texture results are cleared when closing the underlying data. ‣ PKIN: Export to Olinda 2 cas files extended by female model. ‣ VOI: Better handling of duplicate names when appending from a VOI file. ‣ Big data (with >2^{31}-1 voxels per frame): Fixes of reduction procedure and of filters. ‣ DICOM: Fixed problem with reading multi-frame images saved from PMOD as single slice MR; fixed issue with missing orientations in dynamic RECON TOMO NM objects. ‣ Viewing tool: Cropping can be applied to more than one of the loaded images. ‣ Batch processing: Reduction and reslicing loading operations didn't work properly; incompatibility with some 4.0 batch definitions including registration fixed. ‣ Segmentation tool: Fix of 2D active model segmentation. ‣ Fusion display: Triangulation in zoom mode fixed. ‣ MR inhomogeneity tool: Method based on 6 probability maps added. ‣ PGEM: Several issues fixed in the report; vessels in the heart model extended and improved; protocol execution fixed; spatial offset between streamlines and VOIs fixed.
Build 1 Oct. 30, 2019	Initial upload of 4.1 version.

PRODUCT RELEASE 4.1

As with every PMOD release, functionality and stability have been improved in all modules. Major enhancements can be found in PXMOD, PFUS, PCARD and PSEG as detailed below.

General	‣ Image reduction options for coping with large data sets: Slice selection in increments supported in loading operations dialog window; cropping and interpolation facility added on the View page of the viewing tool. Single slice cropping is now possible. ‣ Handling of variable slice times improved to handle different variants of storing the times in DICOM. ‣ New facility on the image information window for inspecting the slice locations. ‣ Python script added as example for using the External Script tool. ‣ Revision of the units list, grouping the more relevant ones at the top. ‣ R: Undo option for R-Console command editor added; conversion of aggregate structure into flat table, which can be easily exported; keyboard Ctrl+B executes the highlighted command block; 'Max lines in printout' configuration added. ‣ Copying of dates in the information dialog window: can now be restricted to empty elements only. ‣ Color tables: new list organization; defaults updated; perceptually uniform sequential color maps added. ‣ Segmentation tool: Histogram can be restricted to a VOI; information about segment number was always using the result from the first frame; ‣ ATL password hashing without external library. ‣ Configuration: Main configuration (species, oncology) are now on user level; box to enable update checking moved from toolbox to configuration; ‣ The 'Last used dialog size' now only relates to the application window.

	‣ All images in the console buffer can be saved at once. ‣ Reorganization of the templates in the resources folder. ‣ Client for support emailing updated to javax.mail.jar 1.6.2. ‣ Scientific image capture: now uses display unit; numeric precision of color bar annotation configurable; serialized behavior. ‣ Image value inspector: now also active on MIP; value probe at cursor location in the image can be enabled from the context menu. ‣ Database: Whole database export/import removed; data export directory added to configurable paths.
VOI	‣ Texture analysis now includes 64 indexes: 23 are based on the pixel histogram within a VOI, 25 based on the gray level co-occurrence matrix (GLCM) and 16 based on the gray level run length matrix (RLM). The calculations have been implemented and tested according to the report of the Image Biomarker Standardisation Initiative ([IBSI Documentation](#)). ‣ Performance improvements: atlas outlining; maximum diameter calculation (by factors); undo/redo; iso-contouring. ‣ Statistics: Multi-statistics result can be aggregated also if R is not configured. In fraction classification mode, the median statistics is now using the unchanged voxel values. ‣ Naming of VOIs using predefined lists directly by right-clicking. ‣ Possibility to reduce VOIs created on high-resolution images for use at lower resolution. ‣ Statistics viewer: Copy to Clipboard using system locale number format option added to improve compatibility with Excel number formats. ‣ Compatibility classification deprecated. ‣ Arithmetic operation in VOI with masking outside fixed.
PXMOD	‣ Harmonization of the methods for determination of k_2' for reference tissue modes requiring fixed k_2': (1) Entered k_2' (2) k_2' fitted using target TAC (3) k_2' obtained as median value of k_2' map calculated by SRTM, with outlier removal. Available for Logan, SRTM2, MRTM2 and 6 BPnd Methods. ‣ Correct handling of variable times across slices in multiple blood-based models (Patlak, Logan, DV methods, 2-Compartment models, 3-Compartment sequential model, MLAIR, Spectral SAIF). ‣ Specification of the target tissue is now optional in the models, except when it is required to establish reasonable parameters for iterative fitting (2-Compartment models). ‣ The masking parameter now allows to specify a percentage of excluded pixels (least energy). ‣ Various user interface improvements: Graphical elements to clarify the meaning of different sections in the panels; adjustment of the preprocessing plots to layouts similar as in PKIN (e.g. unused samples set to grey); revision of the entries in the VOI list related to the blood data; TAC preparation step is skipped if no VOIs are outlined; model-switching retains more of the common configuration settings; better control of the panels which are shown in the different models; explanatory tooltips added for preprocessing options. ‣ Distinction between Load Protocol (data and model definition) and Load Settings (only model definitions) clarified. ‣ Watabe model: derived high- and low-flow curves are not shown any more. ‣ MBF parametric mapping for NH3 data: vRV fitting set tp optional (reduces some noise); usage of data only up to 240sec for fitting.

	⇒ TKE (turbulent kinetic energy) model for 4D flow velocity image data.
PCARD	⇒ Perfusion model for dynamic 99m-Tc Tetrofosmin SPECT images added (Shrestha et al.) ⇒ Presets added for the pig species and segmentation optimized. ⇒ Heart model size specification: interactive adjustment improved; can be shifted away from the center; different specifications for rest and stress possible; moved from status line to the control area ⇒ 3D rendering of the epi/endo meshes for gated images. Allows to generate movies of the beating heart optionally with slice images and surface texture. ⇒ Segmentation: performance for high resolution data improved. ⇒ Results are harmonized between the PET and the MR cardiac tools. ⇒ The polar plots resulting from a transmural analysis integrate the epi- and endocardial results. ⇒ Gated analysis: supported if contours are only defined at two timepoints (systole/diastole); volume curve added to results panel and to report (MR). ⇒ 3D: Sampling point visualization improved; texture on LV mesh fixed; ⇒ Rest/stress perfusion polar plots can be scaled to a common maximum. ⇒ Deprecated: centerline segmentation deprecated; setting model size using markers.
PFUS	⇒ User interface improvements: tooltips added; label revisions; status line info improved; option selection for workflow type instead of a series of buttons; ⇒ Workflow for hybrid data added which directly ends on the 'Comparison' page. ⇒ Hot spot alignment initialization: New dialog window to define a common location in the input and reference images. ⇒ MIP page: the color table thresholds of the MIP images can be defined in absolute values. ⇒ Comparison page: MIP can be enabled/disabled; various options to propagate the color tables among the displayed series. ⇒ Image operations on 'Image Algebra' do not switch back to the 'Reference' step. ⇒ Scientific output of fusion display uses interpolation defined in the main display. ⇒ Matching using only the information in a box improved. ⇒ Scatter plot: Now offeres Bland-Altman plot, box plot and Passing Bablok regression analysis. ⇒ Fixed problem with 3D deformation field visualization when arrows were visible and color was changed to solid. ⇒ Deprecated: Triple fusion page.
PSEG	⇒ Improvements of PERCIST Report page: Summary line of the listed lesions; comparison of the current analysis with a previous one listing new lesions, vanished lesions and the change of the various parameters for the persisting lesions. VOI pairing based on names and progression analysis is directly done after loading the comparison report. ⇒ Synchronization of texture analysis configuration across direct analysis and PERCIST analysis.
PNEURO	⇒ T2 and PET anatomical reference added as fusion image on the VOIs page. ⇒ Filling of the atlas VOIs on X and Y planes improved (stable and faster).

	▸ Fixed problem of relative (SUVR) statistics when using protocol execution. ▸ The generated VOIs are directly available on the parametric maps (VOI and Fusion tab). ▸ White matter parcellation enabling box is now on the 'Brain Segments' page.
PKIN	▸ In batch mode it is now possible to first fit the blood function(s) to the blood data before the tissue model is fitted. ▸ Support for Olinda 2: The residence times calculated for dosimetry data can be saved Olinda 2 case; a new name list containing the organ names used in Olinda 2 is available for proper VOI naming during the organ outlining.
PGEM	▸ Heart Model: added new VOI definitions for both frames for Left Atrium and the Pulmonary Veins. ▸ Added support of Siemens 4D flow DICOM image data, with separate series for each velocity direction. ▸ Behavior of 3D button dependent on the context. ▸ User interface streamlined. ▸ Facility to edit the timing of models.
P3D	▸ 3D: Improved speed of cutting multiple large surfaces. ▸ Faster display of big scatter data.
Data Formats	▸ Images with kBq/ml units are converted to kBq/cc. ▸ Special handling for faulty Philips Achivea DICOM anonymized by Synarc with wrong dimension pointers 00209165, 00209167 in the Dimension Index Sequence 00209222. ▸ Saving images with short representation in memory as DICOM had no padding in the first volume. ▸ Set PMOD as derived data producer in the enhanced DICOM objects.

Zürich, October 30, 2019

MAINTENANCE BUILDS OF RELEASE 4.0

Build 6 Oct. 23, 2019	▸ **CAUTION with PSEG/PERCIST report**: TLG and SUV mean were not correct. Indication of the segmentation threshold in the report was incorrect. ▸ PSEG: Texture analysis statistics can now be saved correctly. ▸ PNEURO: Fixed save problem of a combined field transformation. Fixed segment alignment for already matched PET and MR using the 6 probability maps normalization for the segmentation. ▸ VOI: Repeated outlining of atlas VOIs failed after the second time. ▸ DICOM: Fixed issue related to DICOM saving of images without orientation information after mirroring. Improved loading of series consisting of multiple NM objects (Xeleris). Fixed timing issue when converting gated PET images as enhanced DICOM objects. ▸ PCARD/Gated: Improved polar plot generation for septal basal area. ▸ PKIN: Fixed problem with improper revision numbering when using Fit All. ▸ Fixed problem with input format selection for batch anonymization. ▸ Pipeline processing: All formats used the saving path configured for DICOM.

	‣ Saving during data splitting generates unique file names to avoid overwriting. ‣ PVC VOI based plugin: Now accepts NaNs in the images; viewing tool could not be closed after VOI adjustments.
Build 5 July 12, 2019	‣ PXMOD: Fix of the Logan method. The provided target TAC had an influence on the selection of the time points included in the fit. No impact in case of target TAC with normal SNR. ‣ PSEG: Button added to generate the reference sphere as alternative to using Ctrl+Shift+U. ‣ PSEG: Report saving via transaction server had a problem. ‣ VOI: Split of VOI into slice ROIs was added, and is also working for grouped VOIs. ‣ VOI: NaN supported as background value in VOI masking. ‣ VOI: Minor problem solved relating to Number of Pixels statistics for dynamic series. ‣ Texture: Sub-millimeter GLCM distances are now supported. Run Length Matrices and the RLM based metrics are applicable to dynamic input data. ‣ PVIEW: Region growing segmentation supports multiple seeds defined as markers. ‣ PVIEW: New loading tool added for handling series with varying slice thickness. ‣ PVIEW: Merge slices procedure improved to handle series with varying slice thickness. ‣ PVIEW/Batch: Improved GUI for anonymization during pipe processing. Parameters of Reduction and Volume Reslicing tools during loading are serialized. ‣ PCARD: Segmentation step triggered by auto-check works correctly now. ‣ DICOM: Server support added for storing DICOM information objects not used in PMOD. ‣ DICOM: Reading DICOM images improved to handle enhanced objects with incomplete information of dimension organization. ‣ DICOM commitment: Configurable response delay implemented. ‣ R console: Support added for R versions 3.5 and 3.6. ‣ NifTI data: Support for meter and micrometer spatial dimension units. Issue with reading some compressed images fixed. ‣ General: UI adaptations to make clear that PMOD is for research use only (RUO).
Build 4 April 3, 2019	‣ SUV information: Panel also available for SPECT, not only PET. ‣ VOI: Calculation of fractal dimension fixed for specific situation (single slice VOI in coronal plane). ‣ VOI: NaN supported as value for outside VOI masking (was replaced by 0 before). ‣ PNEURO: Problem of merging PVC results fixed. ‣ PNEURO: Merged VOI was previously not added to "Relative to" VOI list. ‣ PSEG: Fix for PERCIST report. It failed in "Oncology" mode when contouring was performed on fixed threshold. ‣ PKIN: All TACs display: Proper display of X axis and units for graphical models. ‣ PKIN: Layout improvement reducing space of the control area. ‣ PKIN Parameter Explorer: Only content visible in the table is copied to clipboard. ‣ PKIN: Units of MLAIR regression coefficients corrected. ‣ Fuse It: External tools are restricted to the page with image loading. ‣ fMRI DICOM: Improved image sorting in the case of undetermined volume times. ‣ PET DICOM: Fixed problem with frame reference time when converting Enhanced to regular PET objects.

	▸ DICOM: Fixed problem with dynamic high resolution images (over 2 gigabytes per volume, 16bit integer representation). ▸ DICOM: Fix for reading images with unparsable/missing acquisition time. ▸ DICOM: Improved support for storage commitment. ▸ Database: Export/import of whole database is discontinued.
Build 3 Feb. 25, 2019	▸ ATL: Audit Log DB optimization for large databases. ▸ PNEURO: VOI merge problem fixed. ▸ PNEURO: Batch mode saving the results to the input data location uses the same image format as loading. ▸ PKIN: Blood delay was not updated properly from the fitting history. ▸ PXMOD: R1 threshold added to MRTM2 for masking low-perfusion voxels. ▸ PSEG: Mask generation using Otsu method fixed. ▸ Texture analysis: Verified according to Image Biomarker Standardisation Initiative. Only fix of run lenght matrix calculation required. (Reference: Zwanenburg A, Leger S, Valli6eres M, Lock S. Image biomarker standardisation initiative. arXiv preprint arXiv:1612.07003). ▸ VOI: Volume statistics was not saved under certain condition (VolumeWithout-NaN deselected). ▸ PCARD MR: Protocol extended; results saving improved; manual VOI definition fixed. ▸ PSAMPLE: Support for the new twilite 3. ▸ Database import of non-DICOM data: Name generation improved to avoid name duplication. ▸ Database: Fixed problem of deleting images from DBs connected via transaction server. ▸ DICOM: 12bit jpeg decoder added. ▸ R Console: Communication problem with R 3.5.2 fixed. ▸ Batch pipeline: Problem of selecting QC plug-in in the interface fixed. ▸ Support for CT Liver segmentation via "CT VOI Generation" tool discontinued. ▸ Atlas "Rhesus (RIKEN)" removed. "Rhesus Macaque (INIA19)" provides more details.
Build 2 Dec. 21, 2018	
	▸ **CAUTION:** A vulnerability has been detected in the drivers of the WibuKey used for PMOD license protection. The provider has fixed the issue and the new drivers should be installed. So after downloading Build 2, please start the installer in the Pmod4.0/install/hksetup directory and install the new driver version 6.50. Alternatively, the WibuKey driver can directly be downloaded using the link https://www.wibu.com/support/user/downloads-user-software.html
	▸ Linux systems: Default installation directory changed to user folder. This avoids permission problems in case the same person who installed PMOD is also its user. For a multi-user installation the /opt directory and a permission change with chmod is still recommended. ▸ Config/USERS/MODULES: Showed FuseIt even when Fusion was not licensed. ▸ VOI: Morphological operations improved (settings serialization, speed, interruption).

	⇥ VOI: New "Accelerated" classification mode with substantial performance improvement for display and statistics. Recommended for all VOIs generated by automatic methods.
	⇥ File loading path history: The loading and saving paths are not treated separately any more (for non DICOM images and non image components).
	⇥ DB: Facility added to dump patient, acquisition and tracer application information of multiple studies from the database via the DB Export function.
	⇥ DB: New filter (single vs. multiple file series) to distinguish ENHANCED PET from PET encoding.
	⇥ INIA19 rhesus atlas: Brain only MR template added.
	⇥ Pipe processing: Setting of "Replace Patient Information" is serialized.
	⇥ PKIN: Behavior of saving fit results from parameter explorer changed. If "Use last region fits for table" is enabled in the configuration, the most recent model fit from the history is used. Otherwise, the current parameters are used, even if a fit was not successful.
	⇥ PKIN: If target and reference region are the same, no fitting is performed.
	⇥ PXMOD: Better handling of batch failure. Subtle problem fixed with incorrectly setting the first parameter by a protocol or the default button.
	⇥ PNEURO: Sulci deformation option removed, but still working if enabled in old protocols. Default probability thresholds for masking with GM and CSF changed to 0.5 (previously 0.3).
	⇥ PCARD: Interpolation on/off | 48 | 64 option added. Polar plots on the "Compare" page are also interpolated. %Max shown as overlay. Z-score values are shown in overlay. %lt/ut of the report images are based on the value range in the myocardial VOI. Comparative image report can be also printed from "Compare" page. "Baseline correction" switch available on dialog starting kinetic modeling. Configuration possibility for "Mixed"/"Compact" VOI layout.
	⇥ PSEG: Display unit selection supported by protocols.
	⇥ PGEM Heart model: Pulmonary veins added, aortic arch branches updated, left atrium improved.
	⇥ ATL: Configuration improved. Internal columns removed from the export of the audit log viewing dialog. Details which are too too long to fit into a DB record are now split into multiple records instead of truncation.
Build 1 Oct. 28, 2018	Initial upload of 4.0 version.

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In addition to the individual improvements detailed two major areas are further developed in the new version.

1. While highly flexible and with unique functionality, the VOI user interface had reached a overwhelming complexity. Therefore, in version 4.0, the interface has been reorganized in a new "Compact" layout. It covers less space and provides better functional grouping. As we are confident that it will make VOI analysis easier and more efficient, it is the new default layout. However, the previous layout is still available for users who prefer continuing their proven workflows.
2. The PSEG tool has been extended by a new workflow intended for users with a need to assess hot lesions in static PET images. It includes the PERCIST methodology for objectively outlining and documenting the uptake in oncologic whole-body scans, but offers additional features: The lesion outlining result can be combined with texture analysis, and can directly be converted into training data sets for machine learning.

General	
	‣ Global Oncology setting supports specification of default SUV variant.
	‣ SUV display units: Warning symbol next to colorbar if required information is not complete.
	‣ Fusion balance can be shifted by mouse wheel while holding down the "F" key.
	‣ Image information dialog window: Slice times and species editor added.
	‣ DICOM anonymization added to file format conversion.
	‣ Direct starting of DICOM loader after creation of DICOMDIR file supported.
	‣ Restart possible after global configuration change; starting possible at the end of installation wizard.
	‣ DB extended query revised: image filter added; only patients/series are listed which contain elements corresponding to the applied filter.
	‣ Rebinning of dynamic series. Down-sampling: The area under the curve in each pixel is maintained. Up-sampling: Uses spline interpolation between frame mid-times.
	‣ Time domain filter: Despiking with 9 samples median absolute deviation method (MAD9) added.
	‣ Partial Volume Correction external tool: GTM speed improvement by multithread calculation; PVC (Brain MR based) extended by white matter correction.
	‣ Pipeline: Improved names of aggregates generated pipeline lists; tool added to calculate similarity measures relative to a mask; Option to scan a directory tree to build the list of input files.
	‣ Active model segmentation: Extended by median filter size and myocardial width restriction; parameter optimization by specification of target mask.
	‣ Segmentation: restriction by template VOIs supported.
	‣ Incoming folder functionality can use script alternative to pipeline.
	‣ Noise addition external tool extended: Poisson and uniform distributions added; definition of noise amplitude; amplitude and stdv based on reference VOI; conditional based on pixel value ($<$, $>$, ==).
	‣ Texture analysis of dynamic data results in dynamic texture measures.
	‣ Scaling external tool: *IMG option added to scale pixelwise by an image.
	‣ Handling of NaN values in image interpolation improved.
VOI	
	‣ New layout of the VOI user interface layout, called "Compact".
	‣ Statistics calculation: Results are displayed in display units (e.g. SUV); configuration list for defining the statistics of interest; time-consuming statistics moved from statistics menu to configuration list; indication of time-consuming elements in the list; default statistics menu entry; calculation speed improvements.
	‣ Iso-Contouring tool: Fundamentally revised; Average percentage threshold option added.
	‣ VOI naming using lists now also works on group level. A <number> at the end of the VOI name is used for generating label maps in PSEG.
	‣ New "Neutral" mode for selecting VOIs directly by clicking at them in the image or in the MIP. Single clicking into the VOIs list does not switch to contour definition plane, only double-clicking does.
	‣ <Ctrl+B> adds a prefix "{UNCLEAR}" to the name of the selected VOI.
	‣ "Peak" sphere volume can be defined for human, rat, mouse.
	‣ Speed improvement of VOI overlay display.
	‣ Properties dialog window reorganized; new property for locking contours.
	‣ Column in the VOI list indicating its role in tracking (seed etc) restricted to PGEM.

PSEG	⇥ Completely new (PERCIST) workflow for static oncologic PET scans introduced, see documentation.
	⇥ Texture analysis: measures based on run-length added.

PNEURO	⇥ Rhesus macaque brain atlas added (INIA19, https://www.nitrc.org/projects/inia19/).
	⇥ Handling of orientations (human/small animal) is based on selected atlas (manifest); error message in the case of species mismatch between subject and atlas.
	⇥ Atlas viewer also shows the tissue probability maps.
	⇥ Percent difference between partial-volume corrected and uncorrected result is saved with statistics.

PKIN	⇥ Single pixel TACs from data inspector: coordinate added to name; dialog window not closed.
	⇥ TAC from viewing tool: filter choice for target models extended.
	⇥ Sigmoid-like parent fraction model added.
	⇥ Residuals on Plasma panel were incorrect if plasma/whole-blood fraction was used.
	⇥ Comments facility moved to a main interface tab.
	⇥ Configuration in the model filter dialog window can be saved as a macro, which can be called in batch or from the taskbar.
	⇥ Interruption possible for all types of multiple fittings, except for macros.

PXMOD	⇥ Parametric mapping of energy loss from 4D Flow velocity field.
	⇥ Improvements in models with multi-file selection for Interfile, Paravision and Varian formats.

PCARD	⇥ Cardiac MR: Motion correction transformation saved in protocol; wall thickening calculation added; acceptance test fix.
	⇥ Cardiac PET: use of "MBF" and "MFR" according to Consensus paper "Clinical Quantification of Myocardial Blood Flow Using PET".
	⇥ Cardiac PET: LV object VOI for interactive definition of model size added.
	⇥ Gated PET: Reversibility values fixed; wall thickening values added.

PFUS	⇥ Automatic reslicing when switching using the VOI button instead of going through matching.
	⇥ "Origin alignment" improved to include rotations for initial transformation of matched data with different orientations.
	⇥ Cross-correlation quality measure of matching added. Has been used in literature to select the more adequate template (controls vs Alzheimer's).
	⇥ Color table and species persistence improved.

PGEM	⇥ 3D: In-scene colorbar with units; streamlines have arrows showing directions; possibility to add additional images when inspecting results; data profile from cutting with oblique plane.
	⇥ 4D Flow: user interface revision; adjusted units for helicity and vorticity maps; recalculation without starting from data loading; muli-frame mask; pathlines as alternative to streamlines; NaN handling in streamline tracking; tracking defaults for aorta and brain vessels.

	▸▸ CFD: boundary condition setting improved; velocity boundary from 4D flow image data supported; serialization of case creation parameters.
R Statistics Console	▸▸ LASSO method implemented as discrimination alternative. ▸▸ Cumulative sum curve added to histogram and density plot. ▸▸ Function converting vectors and matrices into aggregates for using predefined scripts. ▸▸ Rows and columns selection extended by select all. ▸▸ Improved reporting of text and tables exceeding printout page size. ▸▸ Script development: pm.copyColumns function added; multiple result sections supported, not only one at the end of script. ▸▸ Predefined scripts support aggregates with time dimension.
Data Formats	▸▸ Database import: Improved filling of series description and patient id for non DICOM data. Better handling of formats using two files. ▸▸ Database: Split series of a patient into new patients with one series each. ▸▸ DICOM Server: Storage Commitment SOP added. ▸▸ DICOM: Usage of PET units (activity concentration) when loading image data with multiple units. ▸▸ DICOM: Dual gated data timing improved. ▸▸ DICOM: Improvements in reading trigger times with Special Case: "Multivolume MR (sort by trigger times)". ▸▸ Merging of GE DICOM data produced by dynamic whole body scanning: improved handling of decay correction. ▸▸ Philips: PAR/REC format updated to handle modified column names (version 4.2). DICOM 4D Flow files can be loaded with Special Case: "Multiframe (Sort by slice position)". ▸▸ Micropet: support for reconstruction method added.

Zürich, October 28, 2018

MAINTENANCE BUILDS OF RELEASE 3.9

Build 10 July 10, 2019	▸▸ VOI: Sphericity statistics calculation problem fixed. ▸▸ VOI: Statistics of the VOI group were not saved in file.
Build 9 Dec. 21, 2018	▸▸ **CAUTION:** A vulnerability has been detected in the drivers of the WibuKey used for PMOD license protection. The provider has fixed the issue and the new drivers should be installed. So after downloading Build 9, please start the installer in the Pmod3.9/install/hksetup directory and install the new driver version 6.50. Alternatively, the WibuKey driver can directly be downloaded using the link https://www.wibu.com/support/user/downloads-user-software.html ▸▸ VOI: Massive speed improvement for the "Hottest Connected Voxels" VOI calculation. ▸▸ Pipeline processing without user interface: fix for reading all command switches in script, particularly -lsn[...] for specifying the license server.

	‣ PCARD: Fixed problem of reading gated protocols saved in version 3.908.
Build 8 Oct 11, 2018	‣ VOI: polygon vertexes were shown as circles instead of the customary squares. ‣ PCARD: Radial maximum sampling added a zero ring to the polar plot for certain settings of the crop box. ‣ Database: Potential database creation problem on MacOS X Mojave fixed which related to missing control of locale information (language, regional settings).
Build 7 Sept 18, 2018	‣ **PALZ CAVEAT**: Since version 3.9 the PALZ results were different from previous versions. This is corrected, restoring the pre-3.9 behavior. *PALZ users are strongly advised to install Version 3.9 Build 7!* ‣ Global "Oncology" flag: Impact including the statistics image overlay is restricted to PVIEW, PFUS, PSEG. ‣ PNEURO: Fixed loading of gm/wm/csf map and normalization transformation in Brain Parcellation processing. ‣ DICOMDIR creation: more graceful handling in case required elements are missing in the data. ‣ SUV_{lbm}: BMI calculation according to Janmahasatian method fixed. ‣ Overwriting of non-image files fixed (Linux system bug only). ‣ Correction of bug when splitting of dynamic series to individual slices. ‣ NaN values handling added for trilinear, cubic spline and sinc interpolation.
Build 6 July 5, 2018	‣ Anonymization when exporting data from a database improved: Complete removal of name etc from images and all components (statistics, VOIs, etc). Option to use synthetic name generated from the DB name by encryption algorithm. Option to indicate the name is already anonymized. ‣ Privacy disclaimer added to start-up dialog (GDPR). ‣ VOI: Statistics selection did not work properly. Statistics measures different from the selected ones could be saved. ‣ VOI: Group surface area is also calculated for VOIs with fraction classification. ‣ Dynamic VOI: Isocontouring % threshold is calculated individually for each frame. ‣ Mouse (Ma-Benveniste-Mirrione) atlas: inferior colliculi corrected. the separation of the inferior colliculi into a left and a right part was faulty. ‣ Merging of files: Decay correction corrected to properly handle multiframe DICOM data. ‣ LMA GTM partial volume correction: Problem corrected which occurred for small % included pixels (PNEURO, PSEG for segmentations other than Organ separation). ‣ PNEURO: When loading old protocols, the new option CSF masking is now enabled. Adjustable border for brain autocropping implemented for improving the reliability of MR/PET matching in batch runs. ‣ PCARD: Sector overlays with values added to input data polar maps. Cosmetic change. Compare tab cosmetics related to polar maps. ‣ PGEM: Save data profile for oblique cutting planes.
Build 5 April 19, 2018	‣ VOI statistics selection, new default: Only Averaged and SD are initially selected and the configuration dialog is displayed before first run. ‣ VOI statistics of dynamic data: Bug fixed (introduced in Build 4). ‣ Peak VOI for dynamic data: Peak calculation is now correctly done for each frame, and save/retrive of dynamic peak VOIs was fixed. ‣ Iso-contouring VOI for dynamic data: Restricting VOI was not handled correctly.

	‣ Fuselt: Protocol behavior fixed; correctly retrieves data and transformation. ‣ PNEURO: Batch mode could be blocked by a dialog window appearing due to a mapping problem.
Build 4 March 22, 2018	Main innovation: added features for assessing and documenting oncologic lesions. Please refer to the dedicated flyer in the News section on the PMOD website. ‣ Global oncology configuration establishes the following defaults: SUV display units, show MIP image in inverted gray, show patient name and ID, use terms "MTV" and "TLG" in statistics. ‣ Hot-key (Ctrl+Q) driven placement of a peak VOI in lesion. ‣ Hot-key (Ctrl+L) generation of an iso-contour VOI of lesion based on %SUVmax, %SUVpeak, or absolute SUV. ‣ Hot-key based assessment of lesions relative to liver: (Ctrl+Shift+U) places 3cm sphere as reference, (Ctrl+U) performs iso-contouring at minimal level of tumor uptake and calculates SUVpeak. ‣ Generation of an iso-contour VOI of lesion based on %SUVmax, %SUVpeak, or absolute SUV. ‣ Configuration of the hot-key VOIs and the overlay statistics in a new panel of the data inspector. ‣ Overlay of relevant VOI statistics (average, peak, max, MTV) in image. ‣ Sorting of VOI list by descending SUVpeak, SUVmax, SUVmean, MTV, diameter. ‣ Statistics units synchronized with display units (SUV type). ‣ Lesion documentation via screen capture (Ctrl+E). Other improvements and changes: ‣ Slowness on computer without internet connection due to update and documentation checking: improved, but it is recommended to install the documentation locally and switch off the update checking. ‣ PNEURO: Saving both parametric maps and TACs in batch mode. ‣ PXMOD: ssq map added to the SRTM2 model. ‣ PKIN/Parametric mapping: Lack of synchronization between curve and parameter update fixed. ‣ Texture analysis: NaN support, applicable for dynamic series. ‣ PGEM: Export of OpenFOAM's volume mesh to Fluent format. ‣ VOI statistics: Fixed problem in sphericity (was always zero). ‣ Build installation: existing start scripts are not overwritten. ‣ Database: Compatibility with current mySQL established. ‣ R Statistics: Bland-Altman works with NaN. ‣ File saving: Prevent file system write error for file names longer than 255 chars.
Build 3 Jan. 15, 2018	‣ Database of demo data extended by PCARDM and PGEM (CFD) examples. ‣ PXMOD: Two models (Patlak, irreversibe 2-compartment model with basis function fitting) added for the parametric mapping of dynamic FDG whole-body data. They account for the slice-wise timing definitions in the image header. ‣ Slice-wise timing for TAC transfer to PKIN: average TAC uses timing of the slice in the VOI center; pixel-wise TAC uses timing of individual slice. ‣ PKIN: Reference curve was not shown when reference region was the first in the list. ‣ Amyloid Cortical Composite atlas added. It contains the definition of the most commonly used composite region for analyzing amyloid data, as well as several reference regions.

	⇶ Mouse atlas renamed to "Mouse (Ma-Benveniste-Mirrione)" to credit the work of Ma and Benveniste who did the extensive atlas groundwork.
	⇶ PFUS/PNEURO: Normalization templates derived from ADNI data (FDG, AV45 for AD and controls) added to the list of predefined templates. Brain masking for AV45 templates improved.
	⇶ Pig Brain Atlas (CH. Malbert) labels fixed: Left/right corrections, Superior_cerebellar_peduncle moved to the non-lateralized Posterior_fossa.
	⇶ PNEURO: User defined MNI atlases automatically offer the standard normalization templates if MNI is mentioned in the atlas manifest.
	⇶ PNEURO: Option for enabling/disabling CSF masking and CSF threshold slider added.
	⇶ PNEURO: Transformation results of a PET/MR workflow are cleared before PET-only protocol execution.
	⇶ PNEURO: Anatomical reference control added to batch mode panel.
	⇶ PNEURO/Compare to Norm: Variance pooling estimation corrected. Missing statistics VOIs fixed when repeating analysis with modified parameters.
	⇶ VOI/RTSS: Fixed problem with conversion to RTSS when contours were defined in different plane orientations. Fixed issue with loading of RTSS data. Fixed problem with wrong series instance UID in RTSS objects created by PMOD.
	⇶ VOI: Problem of calculating fractal dimension for VOIs defined in X and Y directions fixed.
	⇶ VOI: Texture analysis can be started from Calculate Statistics menu of VOI Tool.
	⇶ PCARD: Segmentation parameters for mouse data has been adjusted (active models + valve plane fitting).
	⇶ PCARD: Manually edited VOIs are now saved correctly to protocols. Protocols for data with changed frame times are now retrieved correctly.
	⇶ PCARD: Specific protocol retrieval panels for cardiac MR applications.
	⇶ Pipeline processing: Can be started from command line script and run with or without user interface. Fixed problem with updating the QC tool state.
	⇶ Interpolation tool: Fixed reading of transformation when deformation field was previously loaded. Fixed saving of resliced image using deformation field transformation.
	⇶ PGEM: Improved conversion of CFD results to images for comparison with tomographic data.
	⇶ PGEM: Image data can be loaded while visualizing CFD results.
	⇶ R Console: Aggregate filtering in the presence of NA values fixed; scatter plot fixes.
	⇶ R Console: Linear Mixed Effect Models is now working with data containing NA values (which are excluded from the analysis).
	⇶ Network license: More detailed information in license server dialog. If all licenses are occupied there is an information that no license is available and connection can terminate other Pmod instance.
	⇶ Philips PAR/REC images: Now assumes miliseconds as trigger times units. Improved slice sorting and timing.
Build 2 Nov. 9, 2017	⇶ Dynamic Data with slice-dependent timing: Use of the VOI center location timing when transferring VOI TACs to PKIN. Automatic reformatting improved for handling of per-slice information.
	⇶ VOI: Configuration of the statistics measures of interest introduced for minimizing calculation time.
	⇶ VOI: Tumor volume segmentation method fixed and improved. Is now working for group of selected VOIs, and a VOI called "Bck" is automatically selected as background VOI.

	▸ PXMOD/Resting state model: Fix to avoid masking of correlation matrix. ▸ PXMOD/VOIs tab: fraction mode is new default for interactively outlined VOIs. ▸ PCARDP/Gated: Segmentation method limited to EPI/ENDO Active Model. ▸ PCARDP/Perfusion: Problem in sector TAC calculation fixed. ▸ PCARDM: Segmentation parameters units unified to mm. ▸ PCARD protocols: VOI saving in protocols fixed. ▸ Texture analysis: Information in the tab titles improved. ▸ PGEM: DTI report problem fixed when patient information was missing. ▸ Fusion: Parameters of motion correction transformation can be presented as a graph.
Build 1 Oct. 30, 2017	Initial upload of 3.9 version.

PRODUCT RELEASE 3.9

New Features and Revisions

General	▸ Improved handling of the data path history when selecting from the file system rather than the database. ▸ SUV dialog window and inspector revised. Support for SUV_{lbm} by Janmahastian method. Use of UCUM units (e.g. g/ml{SUVlbm(Janma)} when saving SUV images to enhanced DICOM objects, otherwise the DICOM SUV Type definition (0054,1006). ▸ Texture analysis within VOIs. ▸ Command line execution of pipeline definitions which include an input file list (e.g. ./java/jre/bin/java -Xmx1200M -jar pmod.jar PIPELINE[noGUI] pipe_definition_file.pipeProc). ▸ Pipeline processing: Restriction that a file can only appear once on the input list was removed. ▸ DICOM server starting a pipeline processing with the received data: all non-image data are also saved. ▸ External tool for calculation z-score values relative to the average and the standard deviation within a specified VOI (frame-wise operation for dynamic data). Useful for transforming the data as input to the supervised clustering method). ▸ New option to keep triangulation at the same 3D coordinate when switching between images in a viewport. ▸ Layout panel: "Go to coordinate origin" and "Go to x/y/z coordinate" buttons to support well-defined triangulation. ▸ Extended list of isotopes and radiopharmaceuticals. ▸ Proper units are set for images generated in situations beyond parametric mapping. ▸ Skeletonization added to "Segmentation" external tool. ▸ New automatic VOI generation approach resulting in the hottest connected voxels within a VOI. ▸ External tool for calculation of texture features within VOIs.

PNEURO	▸ Template, Atlas and Parcellation resources converted to compressed images for saving space
	▸ White matter parcellation added, resulting in a white matter VOI for each atlas VOI.
	▸ Masking of grey matter regions by CSF improved for the maximum probability method.
	▸ Revision of the tree organization for better organizing the additional VOIs.
	▸ Batch mode improved in several ways: support for mapping added; option to create and save a quality control image showing the generated VOIs on top of the images; new interface item element for specifying the averaging range of dynamic series; saving of TACs, parametric maps, transformations and protocols.
	▸ Option to select the dynamic PET instead of the average PET after the VOIs have been outlined.
	▸ Support for user-defined atlases in parcellation improved. Supported also in batch mode.
	▸ Warning added when a loaded transformation doesn't match the space of input data.
PKIN	▸ Grid fitting: Start iterative fitting with initial parameter combinations which cover the whole physiologic parameter space.
	▸ Monte Carlo: Randomized fitting supported.
	▸ Monte Carlo: Noise can be added to tissue TAC instead of model curve. This allows studying situations where the model underlying the data differs from the fitted model.
	▸ Monte Carlo: The generated data and the fits can be added to the fitting history for inspection and export.
	▸ Monte Carlo: Noise generation using bootstrap method.
	▸ Parameter explorer: The listed results correspond either to the current model parameters, or to the latest successful fit. Previously non-fitted regions were omitted.
	▸ Fitting history included in parameter explorer to browse histories across regions more easily.
	▸ Parameter sensitivity to acquisition duration is now also supported for coupled fits. Creates history entries with the same revision number.
	▸ Number of fits required for convergence is also added to the fit details list.
	▸ Batch fitting with specified model configuration: Only the tissue model is replaced, the blood configuration now remains unchanged.
	▸ Fitting can be stopped after calling "Fit all".
	▸ Negative values allowed in blood data.
	▸ Blood curve resampling improved. Didn't work properly in all configurations.
	▸ "non-blood" model filter introduced which is default until blood data is loaded.
	▸ Averaging window introduced in "Plasma Ratio" model for use with bolus/infusion data, where the ratio equals Vt.
	▸ Standard error supported in the aggregation of kinetic modeling results.
	▸ Support for TACs with different timing across regions. This is particularly relevant for dynamic whole-body and dosimetry studies.
	▸ Dosimetry model: Output of cumulated activities for the IDAC2.1 dosimetry program (www.idac-dose.org).
	▸ Massive speed improvements for the transfer of pixel-wise TACs.

PXMOD	
	⇥ Revised SRTM2 model, allowing to calculate k2' as the median for the SRTM results in a region and restricted to a physiological range.
	⇥ Model for DWI MR images. Supports different calculations of the ADC maps including fit of mono exponential.
	⇥ Model for PCASL MR images which are organized in two dynamic series (control, label), and a proton density image. Supports calculation of average perfusion.
	⇥ Model for the seed-based correlation analysis of resting state fMRI data. A matrix showing the correlation between the signals of multiple VOIs is shown as image and can be explored with the data inspector probe.
	⇥ Individual timing is supported for each pixel. This feature is particularly relevant for dynamic data acquired with continuous bed motion.
PCARD	
	⇥ Gated PET: Improved volume and wall-thickening accuracy based on a new interpolated data set (called VOLUME).
	⇥ Gated PET: More precise valve plane fitting.
	⇥ Cardiac PET: Acceptance test revised.
	⇥ Perfusion PET: Transmural gradient for flow areas calculated from the ratio of the endo and epi averages of the relevant segments.
	⇥ Contours are smoothed.
	⇥ Optional correction of myocardium TACs for activity remaining from previous scan.
	⇥ Cardiac MR: Active model segmentation added; can be initialized by markers.
PSEG	
	⇥ Clustering method when using external TACs replaced: the supervised clustering algorithm developed by Turkheimer et al. (2007) for PK11195 is now used instead of k-means.
	⇥ Brain extraction added to the masking step.
PFUS	
	⇥ Color table lt/ut propagation in absolute values supported.
P3D	
	⇥ Functionality useful for vessel rendering and analysis: Skeletonization of a segment and creation of a vectorized path; creation of planes which can be moved along the path and always are orthogonal to; cutting of object by this plane.
	⇥ Cutting of SR objects by use of a circle.
	⇥ Texture display on oblique planes.
PGEM	
	⇥ CFD: Integration with new CFD calculation engine OpenFoam 5.0.
	⇥ CFD: Use of 4D-Flow derived flow boundary conditions.
	⇥ CFD: Improvements in case creation GUI, case status detection, case downloading, log display and error detection.
	⇥ CFD: Cutting interface shows loaded image data.
	⇥ Added possibility of loading 4D flow data to a scene presenting CFD simulations results.
	⇥ Added possibility of generating and using skeletons of geometric structures, and cutting those structures by planes perpendicular to the skeletons.
	⇥ Loaded image data available on 3D page for all processing types.
	⇥ Heart model updated.
	⇥ Model with brain regions added.

R Statistics Console	▸ NaN are not removed when statistics are transferred to R Console. ▸ Master table only includes mutual VOIs included in all aggregates ▸ New function "pm.copyColumns()" for copying columns between aggregates. ▸ GUI of Linear Models is not freezing any more during execution. ▸ Improved NA handling when filtering variable is equal NA. ▸ Version control introduced for required packages.
Data Formats	▸ Handling of wrongly formatted injection date in some versions of Albira microPET files. ▸ Matlab image loader extended to read 4D matrices as dynamic images. ▸ Improved handling of reversed image indices in the PET DICOM object. ▸ Fix for handling of DICOMDIR files with icon images. ▸ Initial reading support for the evolving quantitative PET extension of the BIDS data standard (bids.neuroimaging.io), including encoding of ancillary information in the JSON format.

Zürich, October 30, 2017

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