Biomedical
Image Quantification

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Preview of PMOD Version 4.0

(available in October 2018)

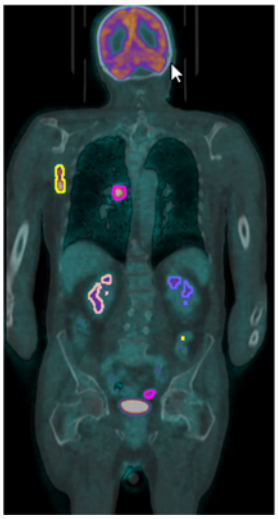
Extended Support for Oncology Research

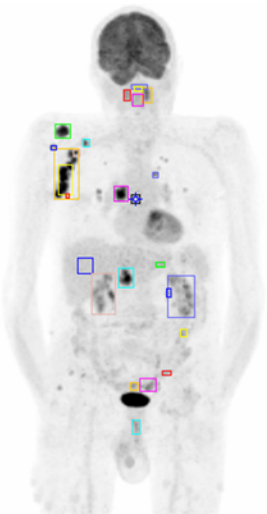
The effort to improve functionality and usability for oncology research already started with version 3.9 and resulted in a number of highly valuable features such as:

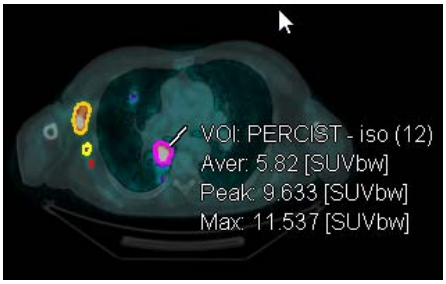
- Convenient selection of various SUV variants for display and statistics.
- Quick, keyboard-driven definition of SUV_{peak} and isocontouring VOIs on adaptive or absolute SUV thresholds.
- In line with a PERCIST evaluation, simple placement of a 3cm reference sphere and segmentation of VOIs on a SUV threshold derived from reference uptake and variance.
- Lesion VOI sorting according to SUV_{peak}, SUV_{max}, SUV_{mean}, MTV or longest diameter.
- Improved lesion documentation by overlaying VOI statistics in the image and keyboard-driven image capturing.

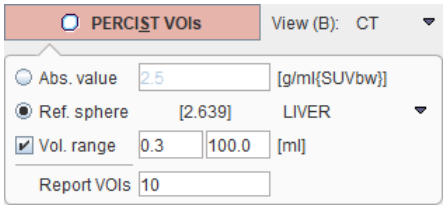
The upcoming annual version 4.0 leverages this functionality to introduce a dedicated and flexible workflow for oncologic lesion segmentation and assessment. The workflow is being provided in the **PSEG** tool. It progresses as follows:

- Load hybrid PET/CT images with optional cropping or interpolation to arbitrary resolution.
- Create a mask to restrict lesion segmentation, e.g. within the bones.
- Place a reference sphere into tissue or blood to calculate a minimal tumor uptake threshold as described in PERCIST. Alternatively, define an absolute SUV threshold.
- Generate iso-contour lesion VOIs with volume in a specified range. If needed, interactively define additional VOIs on either the PET or the CT image using the various tools.
- Sort the lesion VOIs according to relevant criteria including SUV_{peak} and diameter.
- Generate a report listing uptake and size measures along with the lesion position.
- 3D render the lesions together with the images to illustrate lesion shape and location.









De-identification Facility for GDPR-compliant Data Export

Since May 2018, the General Data Protection Regulation (GDPR) of the European Union is in force. Its introduction strengthened the awareness of privacy concerns. Therefore, de-identification functionality was improved to conveniently remove personal information from images and derived data including VOI definitions, VOI statistics, kinetic modeling files and results, etc. An algorithm converts patient name and ID into a code, optionally producing a reference list for bulk anonymizations.

Improvements and Extensions in the PMOD Tools

All PMOD tools are continually subject to a rigorous revision and improvement process. Some highlights, to be extended towards the date of release:

VOI Functionality

– While the VOI functionality has been growing in features, its organization in the user interface has become somewhat spread out. PMOD 4.0 introduces a new, compact layout easing access and adding clarity.
– VOI statistics speed was greatly improved, particularly for dynamic series.

Dynamic whole-body FDG PET

– Support has been added to accurately interpret and handle the slice-dependent timing of such studies. This timing is considered when transferring pixel-wise or averaged TACs from PBAS to the PKIN tool, and in the subsequent modeling.
– Two PXMOD models were tailored for the data of dynamic whole-body FDG PET protocols. They facilitate mapping of glucose consumption by Patlak or basis function analysis.

PKIN

– A dual-input model developed for FDG studies of liver inflammation by Wang et al, (2018) was added. The portal vein input is derived from the aorta activity by convolution.
– A sigmoid-like parent fraction function for the analysis of dynamic ammonia perfusion scans of the heart with a 2-compartment model was added.
– For data transferred directly from PBAS (dynamic data + VOIs required), synthetic images can be generated using the result parameters, the fitted model curves, or the original TACs.
– Fitting macros created from the model filter interface provide shortcuts for frequently applied model testing sequences.
– A “Comments” tab was added to the main interface for ease of documenting analysis progress.

PFUS

– Alignment initialization by use of origin information was improved.
– Cross-correlation as a measure to compare normalizations using template alternatives was added.

PGEM

– 4D Flow data analysis improvements: Additional data formats supported; pathlines added; tracking revised; parametric mapping in PXMOD resulting in velocity flow field, vorticity and helicity.