PBAS Image Processing and VOI Analysis

Biomedical Image Data Infrastructure

The PBAS tool represents the backbone of PMOD's software environment and is mandatory for any PMOD license. It provides an infrastructure for receiving and sending images via DICOM, importing images from all relevant proprietary formats, and organizing them in a database together with any derived information. If desired, databases can easily be shared in a network to provide a central repository among collaborating PMOD users.

PBAS supports the viewing and processing of images to an extent far beyond common reviewing software.

Image Viewing and Processing

PBAS supports the viewing and processing of images to an extent far beyond common reviewing software. In addition to standard image display options, PBAS offers many features for quantitative approaches, including the appropriate handling of calibration factors and value units, consideration of the acquisition timing as well as pertinent geometrical information. Additionally, a unique set of image processing solutions is included, ranging from gray/white matter segmentation of research MR images to the partial-volume correction of PET SUV values.

Volumes of Interest

Many types of quantitative analyses are based on the averaged signal within tissue structures. PBAS includes arguably the largest and most flexible set of tools for volumes of interest (VOI) definition. The definition types include contour outlines, regular geometric objects, object maps, linear VOIs and VOIs with holes. The VOIs can be created using many versatile tools, and they can be involved in advanced operations such as the calculation of their common pixels, intersections with probability maps, or transformations to the geometry of a different image from the same subject. A large number of statistics can be calculated within the VOIs, including 64 radiomics measures.

PBAS includes arguably the largest and most flexible set of tools for defining volumes of interest.

Statistics

PBAS includes an interface to the well-known R statistics environment. The interface allows for the transfer of the aggregated results from a group of subjects to R, and it supports research analysis using advanced scripts developed in collaboration with Prof. Karl Herholz.
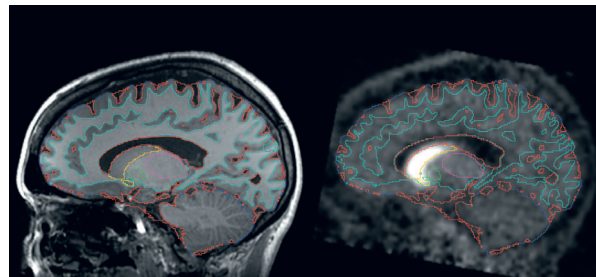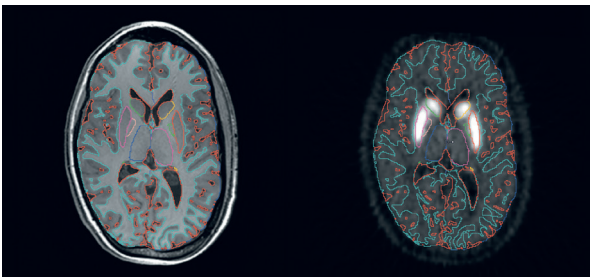
Brain region contour VOIs derived from MRI and applied to a registered raclopride PET.
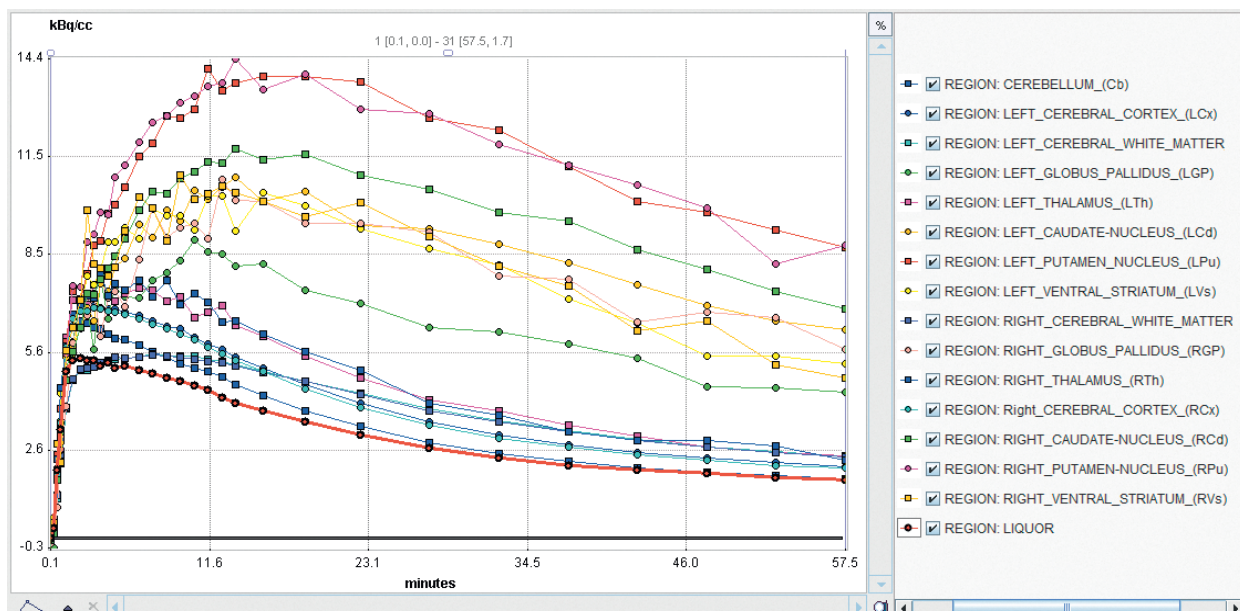
Regional statistics calculated from a dynamic raclopride PET and ready for transfer to kinetic modeling.

Infrastructure

Organization of images and other information objects:
– DICOM server and client, see conformance statement
– Data management by embedded Java database
– Proprietary middleware for sharing data among PMOD installations

Image Formats

Images can be read in more than 20 formats and saved in a subset thereof, including:
– DICOM (read/write)
– ECAT (read/write)
– Interfile (read/write)
– NIfTI (read/write)
– Analyze (read/write)
– MicroPET (read)
– Bruker Paravision (read)
– Philips par/rec files (read)
Units, calibration factors and acquisition timing in the image headers are meticulously interpreted.

Image Viewing

Visualization of volumetric images, tailored for dynamic series:
– Tiling and orthogonal layouts
– Maximum/minimum intensity projections
– Cines across slices and time (dynamic)
– System and user-defined color tables
– SUV inspection; various types supported
– Pixel-wise time-activity curves
– Raw pixels, various interpolation methods

Image Processing

Basic and advanced image processing procedures, including:
– Merging static into dynamic series
– Averaging in time or across slices
– Spatial filtering (Gaussian, median, Deriche)
– Morphological operations
– Interpolation to different pixel or field-of-view sizes
– Gray/white matter segmentation of brain MR images
– Skull-stripping of brain MR images
– Brain MR-based and VOI-based partial volume effect correction of PET SUV values
– Interface to ITK filtering and ImageJ

Volumes of Interest (VOIs)

Unique VOI definition functionality, including:
– Import/export of DICOM RTSTRUCT VOI definitions
– Interactive contour delineation using boundary clicking, pencil drawing, iso-contouring
– Contour interpolation across slices
– Regular VOIs in 2D (circle, rectangle, point) and 3D (ellipsoid, cuboid)
– Region growing methods for hot and cold structures in 2D and 3D
– Automatic brain VOI generation based on atlas templates
– Interpretation of pixel-defined object maps
– Predefined VOIs for the human, rat and mouse brain (stereotactic spaces), and organs
– Support for user-defined VOI atlases
VOI-based operations:
– Statistics of VOI pixels; time-activity curves for dynamic series
– Dumping of all pixel values in the VOIs into a text file
– Shrinking or expansion of VOIs (morphological operations)
– Common pixels of VOIs, intersection with probability map
– Merging and subtraction of VOIs
– Masking inside or outside of VOIs
– Cropping image series to a VOI bounding box
– VOI-based partial-volume effect correction (Rousset method)
– Spatial transformation of VOIs between images
– Texture analysis (64 measures)

Pipeline Processing

The functionality of PBAS and that of other PMOD tools can be arranged into processing pipelines, which may be applied to the data of a whole study population. Example pipeline: motion correction of a dynamic PET series → registration to a brain MRI → automatic MR-based brain VOI outlining → regional TAC calculation → kinetic model fitting → result parameter aggregation.

Statistics

Powerful statistics based on the R environment:
– Aggregation of regional results
– Transfer to R statistics environment
– Interactive data exploration
– Descriptive statistics and standard tests
– Sophisticated tests including handling of multiple comparisons (rm-ANOVA, Linear Mixed Effects Model)

Computer System Requirements

For productive work with real research data:
– Operating system: Windows, Mac OS X, Linux
– RAM: $\geq$ 32 GB
– Cores: $\geq$ 4 ($\geq$ 8 for PNEURO tool)
– Graphics: dedicated mid- to high-range board
– USB connector