

General Kinetic and Pixelwise Modeling

PMOD's PKIN tool facilitates interactive testing of the full range of models for tissue-activity curves (TAC) from extended tissue volumes, and yields numerical tables for statistical processing. The PXMOD tool is complementary. It applies similar modeling techniques directly to the signals arising in the individual image pixels. Therefore, the results are again images, known as parametric maps, showing the value of a model parameter in each image pixel. Hereby, tissue functions or properties are visualized and can easily be compared against information from other sources, such as autoradiography. As the maps are quantitative, they can also be analyzed statistically, for example to compare population groups.

PXMOD is the leading parametric mapping solution for quantitative PET and SPECT.

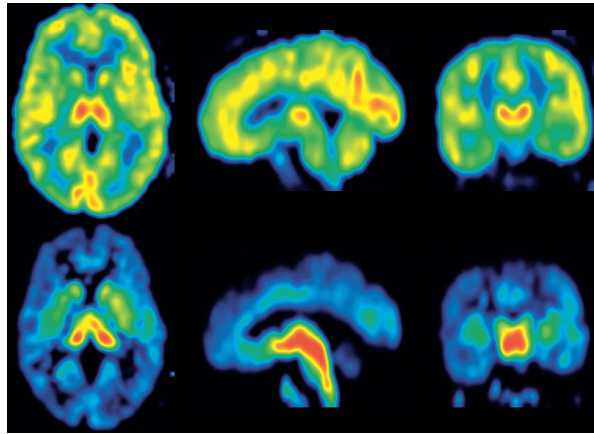
Modeling with PXMOD

PMOD's PXMOD tool is the leading workflow-oriented solution for quantitative parametric mapping of PET, SPECT and fMRI data. The user is guided through all tasks involved in a step-by-step fashion, namely data loading, mask generation, blood data import and correction, tissue VOI definition, parameter configuration and target map specification.

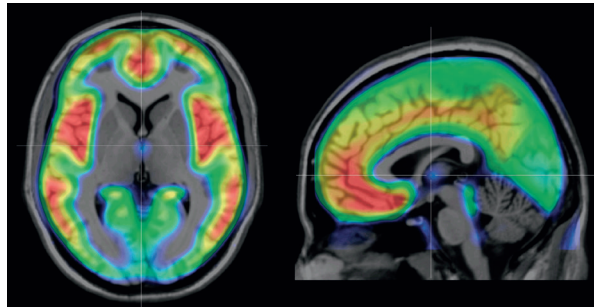
Once the parametric maps are calculated, PXMOD offers versatile tools for inspection of the results. There is a direct interface to the PKIN tool, which facilitates the transfer of pixelwise TACs and analysis in the powerful, interactive PKIN environment. In this way, the PXMOD outcome can be verified and the cause of problematic results in certain pixels studied. An alternative is the comparative analysis of the maps in the embedded fusion component, for instance to study the outcome obtained with alternative modeling approaches.

A seamless interface facilitates the transfer of pixelwise TACs and analysis in the powerful, interactive PKIN tool.

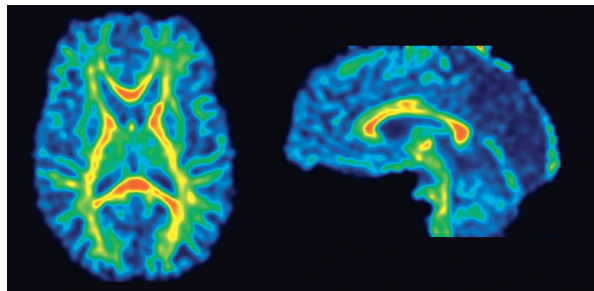
More than 30 models are available in PXMOD, both for situations with and without blood input. They range from simplified, robust, methods to full compartment models requiring iterative fitting. To make the latter more reliable, variants are available which implement priors and/or constraints. As some of the model calculations require considerable computing power, processing has been parallelized to take advantage of the multi-core computing systems now commonly available.



Parametric maps calculated using a reference model: Relative perfusion (top), SERT BP_{nd} (bottom).



Population average of serotonin 5-HT1A BP_{nd} maps fused with representative MRI. Courtesy of A. Hahn, M. Savli, R. Lanzenberger, Med. University Vienna. <http://www.meduniwien.ac.at/neuroimaging/>.



Parametric map of fractional anisotropy (FA) calculated from diffusion-weighted MR imaging.

Input and Result Data

A dynamic image series is expected in any of the supported formats. Care has to be taken that the acquisition timing in the image header is accurate. If it is missing or wrong, the times can be corrected in PXMOD. The blood-based PET models require the preparation of the plasma tracer activity in a simple tab-delimited text file. Alternatively, if whole-blood activity is applicable for modeling, the input file can be replaced by a VOI-derived input curve. The resulting parametric maps can be saved in multiple formats, including direct transfer to a DICOM server. For reproduction and adjustment of the data processing at a later time, the complete configuration of a processing session can be saved in a protocol file.

Parametric Mapping for Radiotracers

The radiotracer models (> 30) in PXMOD predict the dynamic PET or SPECT uptake, given a blood or reference tissue input curve. A fitting procedure determines the model parameters yielding the prediction closest to the measurement. Model categories include:

- Standard 1-, 2-tissue compartment models
- 1-tissue compartment model with time-weighted integral solution
- 1- and 2-tissue tissue compartment models with ridge regression
- 2-tissue compartment model fitted by a basis function approach
- Logan and Patlak plots
- Autoradiographic methods for MRGlu, CBF and CBV
- Spectral analysis for tracers with irreversible binding
- Simplified reference tissue model with fixed and fitted k_2'
- Three multi-linear reference tissue methods
- Reference variants of Logan and Patlak plots
- Parametric mapping for dynamic whole-body FDG data with slice-wise timing, as acquired with a PET scanner that moves the imaging field-of-view dynamically during the acquisition

Parametric Mapping of fMRI Data

The structure of PXMOD lends itself to other types of parametric mapping based on dynamic data, such as fMRI images:

- Calculation of fractional anisotropy (FA), various diffusivity maps and the diffusion tensors from DTI MR images
- Perfusion calculation from pCASL MRI
- Seed-based analysis of resting state fMRI
- Quantification of blood flow from 4D Flow MR images

Utilities

Additionally, some general analysis methods for data with a time dimension are available (correlation, regression, Fourier analysis, fractal analysis).

Options for Investigation of Results

PXMOD not only provides parametric maps, but also features several methods for their investigation, such as:

- Inspector for parameter values in pixels
- Image fusion of input data and parametric maps
- Image algebra calculations among maps
- Transfer of pixelwise TACs to PKIN for interactive modeling