Quantitative PET

Positron Emission Tomography (PET) allows imaging molecular targets down to picomolar concentrations. With suitable tracers, PET can even quantify tissue properties in absolute units. Therefore, PET has proven unique value for many in-vivo research domains. However, for real quantification the PET data has to be processed with sophisticated modeling techniques.

Modeling with PKIN

PMOD’s PKIN tool is the ideal solution for the model-based analysis of PET data. It offers a comprehensive toolbox which not only allows calculating quantitative information, but also features dedicated functionality to assess the meaningfulness of the results.

A palette of more than 40 kinetic model configurations is available.

Blood and tissue data can easily be imported into the user-friendly PKIN environment. A palette of more than 40 model configurations is available, including blood-based compartment models, reference tissue models, linearized models and many beyond. These models can be fitted to the data with various options ensuring reliability and reproducibility. As an extension to conventional modeling, multiple data sets may be fitted at once to incorporate physiological a-priori knowledge and thus improve the outcome.

A further contribution to a meaningful result is the support and modeling of all blood-related input data such as plasma and metabolite fractions.

In daily use by hundreds of PET researchers for more than 10 years, PKIN is arguably the best-validated modeling tool available today.

For an efficient results evaluation, the user is provided with convenient summaries and statistical decision criteria, which can easily be transferred to dedicated statistical programs.

PKIN Validation and Usage

Being in daily use by hundreds of PET researchers since more than 10 years, PKIN is arguably the best validated and most comprehensive modeling tool available today. The continuous feedback from our research users ensures that PKIN will also keep up with the future advances in the field.

PKIN user interface with the kinetic model configuration to the right, the tissue time-activity and the model curve in the upper left, and the residuals in the lower left.

Schematic of a 2-tissue compartment model which is often applied for dynamic PET quantification.
**Tissue Activity Models (> 40)**

The tissue models in PKIN predict the dynamic PET uptake, given a blood or reference tissue input curve. A fitting procedure varies the model parameters until the prediction most closely fits the measurement.

Model categories included:
- 1-, 2-, 3-Tissue compartment models
- Models with receptor saturation
- Models with additional metabolite input curve
- Models for acquisitions with multiple injections
- Patlak, Logan, Ito, RE-GP plots
- Reference tissue models
- Cardiac dual-spillover models

**Blood and Plasma Activity Models**

Often, blood activity measurements are scarce and noisy. The blood models in PKIN support fitting smooth functions to such data for interpolation and noise reduction purposes. Supported functions:
- Tri-exponential function
- Modified gamma functions
- Compartment functions

**Plasma Fraction**

PKIN supports the use of plasma fractions for the calculation of plasma activity from whole-blood activity curves. This function is particularly important when using online blood-sampling systems. Supported functions:
- Empirical function
- 3-exponential function

**Parent Fraction**

PKIN supports the use of parent fractions for the metabolite correction of plasma activity curves. Smooth parent fraction functions can be fitted to measured data, or used for population-based metabolite correction. Supported functions:
- Empirical function
- Hill function
- Watabe function
- Power-damped exponential function
- 1-, 2-, 3-exponential function

**Fitting Options**

PKIN implements various approaches for improving fitting reliability, including:
- Selective fixing/fitting of parameters
- Customizable sets of initial model parameters
- Initialization of compartment model parameters by a linear least squares fit
- Randomization of initial parameters to avoid local minima

**Options for Results Investigation**

PKIN not only provides fitting results, but also features several methods to assess their meaningfulness, such as:
- Standard error indication for resulting parameters derived from the covariance matrix
- Calculation of parameter correlation matrix and sensitivity functions
- Monte-Carlo simulations to address parameter variability
- Akaike, Schwarz criteria for comparison among models