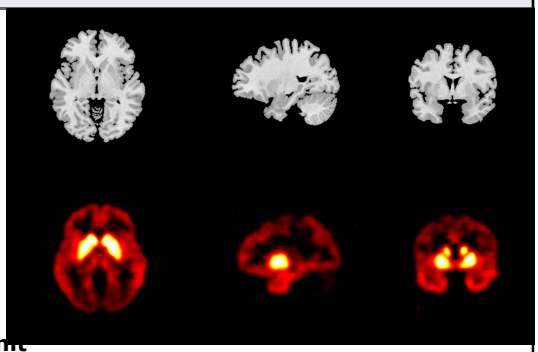
Analysis and kinetic modeling of real PET dataset

Claus Svarer MSc PhD



Neurobiology Research Unit
Copenhagen University Hospital, Rigshospitalet
Denmark

Overview

- PET dataset
- PVElab – extraction of time activity curves
- Import into PMOD
- PMOD modeling:
  - Reference tissue modeling
  - 2TC modeling

AZ dataset – reference method

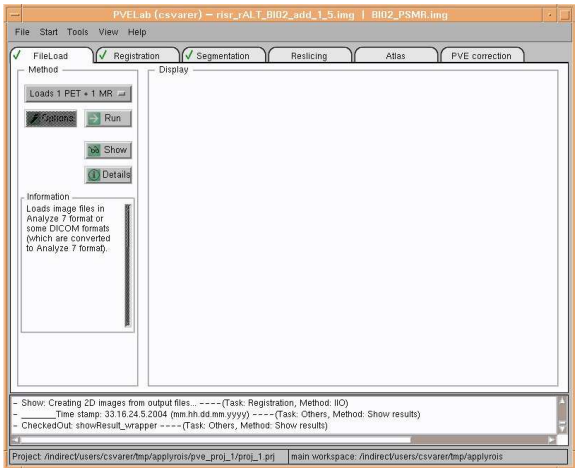
- Radioligand [11C]AZ10419369 used for imaging the serotonin 5-HT1B receptor binding in the brain
- Functional dynamic dataset (90 minutes, 36 frames)
  - HRRT scanner (256x256x207 voxels, 1.2x1.2x1.2 mm, resolution <3mm)
- Structural dataset
  - Siemens 3T MR Prisma scanner (256x256x256 voxels, 1x1x1 mm)

CUMI dataset – 2 TC modeling

- Radioligand [11C]CUMI-101 used for imaging the serotonin 5-HT1A receptor binding in the brain
- Functional dynamic dataset (120 minutes, 38 frames)
  - HRRT scanner (256x256x207 voxels, 1.2x1.2x1.2 mm, resolution <3mm)
- Structural dataset
  - Siemens 3T MR Prisma scanner (256x256x256 voxels, 1x1x1 mm)
- Blood sampling (automatic blood sampler for the first 10 minutes, and manual blood samples drawn during the total scan)

PVElab for estimation of TAC's

- Matlab based GUI:



pvelab: Implemented methods

pvelab:
- software for control and logging of the image processing pipeline (NRU)

Fileload:
- Software for loading and converting analyze and dicom image files

Registration (MR and PET):
- Interactive Image Overlay (IIO, NRU)
- Interactive Point Selection (IPS, NRU)
- Interface to SPM co-registration (Statistical Parametric Mapping)
- Interface to AIR registration (Automatic Image Registration)
- Load AIR file (registration done otherwise)

Segmentation (MR):
- QMCI segmentation (Naples, uses 3 MR images T1, T2, and PD)
- Interface to SPM segmentation (Statistical Parametric Mapping)
- Interface to BrainSeg segmentation (Canterbury)
- Load segmentation volume (segmentation done otherwise)

pvelab: Implemented methods

Reslice (MR to PET):
- Interface to ResliceWarp (using Brain Warp, Kjems, DTU)
- Interface to AIR reslicing (Automatic Image Registration)
- Reslice (pure matlab)

Atlas (defines VOI's (volumes of interest)):
- Talairach based (Naples, 16 VOI's)
- MNI based (Naples, requires T1, T2 and PD images)
- applyrois (NRU, 37 VOI's)

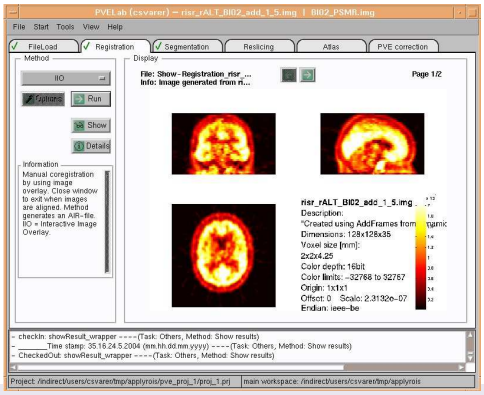
PVE correction:
- PVE correction (Naples), including Rousset, Meltzer, and Müeller-Gartner methods

Further:
- Programs for visualization of images (NRU)
- Programs for correction of analyze files (headers)
- Other tools for correcting images

pvelab: Registration

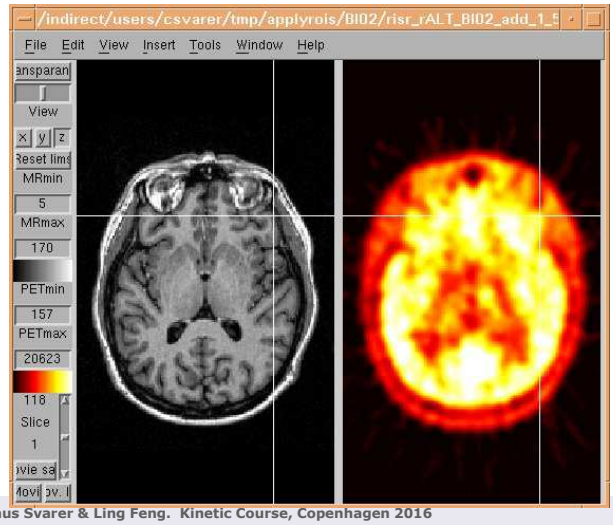
Possible methods:
- Interactive Image Overlay (IIO)
- Interactive Point Selection (IPS)
- SPM (co-registration)
- AIR (alignlinear)

Inspecting Results:



pvelab: Registration

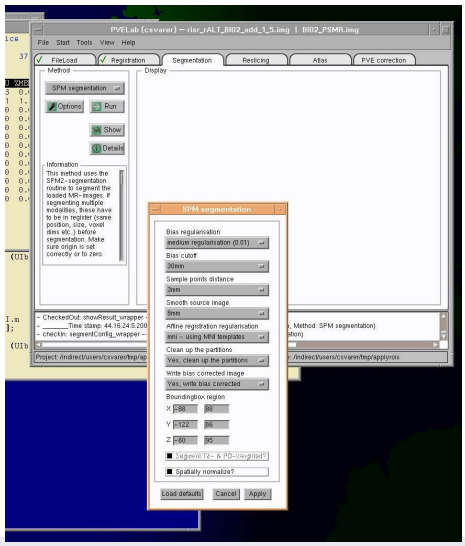
Controlling registration more carefully using pvelab -> View -> Inspect



pvelab: Segmentation

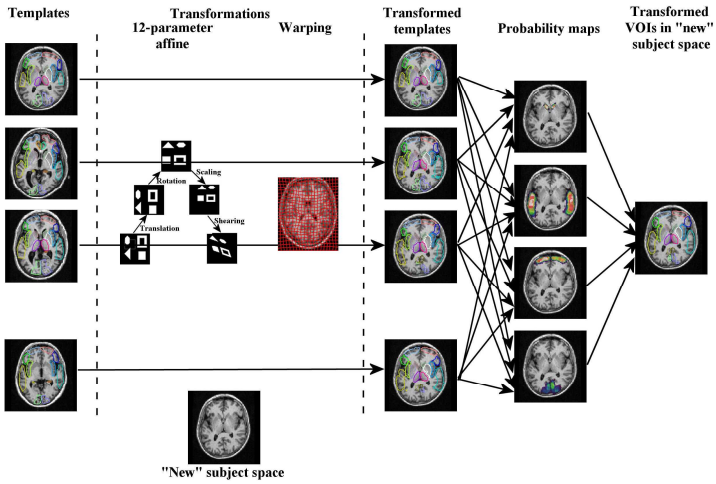
Parameters for each of the implemented methods can be changed by selecting options.

E.g. SPM2/5/8 segmentation:



pvelab: Atlas – VOI definition - applyrois

Svarer et al, MR-based automatic delineation of volumes of interest in huma
brain PET images using probability maps, Neuroimage, Feb. 2005



PVElab

- **Module for doing correction for PVE** (partial volume correction) using Meltzer (correcting for none-brain), Mueller-Gartner (correcting for none-brain and GM/WM difference), and Rousset (GTM) method – region based
- **Module for extracting TAC data for regions**
- **And it is GUI based and fast** (takes less than 20 minutes at data from a clinical scanner, takes 1.5 hour for a HRRT dataset)

Blood data – sampling and corrections

- Data acquisition (whole blood):
  - Data from manual samples (0-120 min)
  - Data from autosampler (0-10 min) is adjusted and corrected using the manual samples (0-10 min)
  - Whole blood/plasma ratio (from manual samples) is applied to get plasma samples
  - Metabolite (HPLC) data is used for correcting plasma samples for metabolites (that doesn't pass the BBB)
- Autosampler and manual data combined to generate a input curve for the experiment (120 min)

Import into PMOD

- PMOD requires a strict format of input files
  - Timing information
  - Values
- Scripts have been created that fully-automatically create these files from the output from PVElab)
- PMOD can also do voxels based modeling – this we will not do!

- And then to the examples:
  - SRTM/MRTM modeling
  - 2TC kinetic modeling with a plasma input curve