Preprocessing PET data with the Turku PET Center Pipeline

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Positron Emission Tomography allows in vivo quantification of the distribution of specific chemical compounds. It can thus be used for studying specific neurotransmitter systems.
Isotope production
$[^{11}\text{C}]^{18}\text{F}^{13}\text{N}^{15}\text{O}$

Cyclotron

$^{11}\text{CO}_2$

Radiochemistry

Precursor

Image of ligand distribution in brain

Positron camera

$^{11}\text{C}$-ligand
[11C] carfentanil
MOR tracer

[11C] MADAM
SERT tracer

[11C] raclopride
D2R tracer
What is meant by preprocessing of PET data?

- Dicom-to-Nifti conversion (SPM)
- Motion correction (SPM)
- Coregistration between MRI and PET (SPM)
- Generation of ROIs (FreeSurfer)
- ROI and voxel-level modeling (in-house scripts)
- Normalization to a standard space (SPM)
- Smoothing (SPM)

- Preprocessing creates inputs for population-level statistical analyses
Variation in PET data

• Tracer
• Dynamic or static
• Frames
• Input
• Model

→ Different PET data require different preprocessing steps
The Turku PET Center Pipeline: magia

• magia can preprocess wide range of different PET data in an easy-to-use way
  • Currently limited to human brain data
• Runs on Matlab
• Combines existing tools from SPM and FreeSurfer
• Available for all people doing neuroscience in PET centre
About raw PET data

• After image reconstruction, the data is available from PET Pacs Research
• The data is stored under PET Pacs Research in DICOM format
• 1 dicom = 1 slice of brain, consists of e.g. 256 x 256 pixels
• The data are converted into Nifti format, where 2D slices are combined into 3D images
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Dicom-to-Nifti conversion (SPM)

- magia starts by converting the dicoms into nifti format
- For dynamic scans, 4-dimensional images are generated
  - 4D means: a time-series of 3D images, all stored under the same file
Motion correction (SPM)
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Rigid-object transformation to match the brains inside the cubes
Motion correction (SPM)

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Coregistration between MRI and PET (SPM)
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Coregistration between MRI and PET is required when MRIs are used to aid normalization of PET images (recommended whenever MRI is available)
Generation of ROIs

• What do we need ROIs for?

1. Reference region
2. ROI-level analyses
Generation of ROIs (FreeSurfer)

• FreeSurfer automatically produces individual ROIs

Input: T1w MRI

Output: parcellation
Generation of ROIs (FreeSurfer)

• FreeSurfer-generated ROIs and manually drawn ROIs produce comparable time-activity curves for many tracers

[11C]raclopride cerebellum TAC from one representative subject

- - - Upper and lower bounds from manual delineation
- ------ Automatic parcellation
ROI and voxel-level modeling (in-house scripts)

• Produces parameter estimates reflecting how much the tracer accumulates in target tissue compared to plasma or reference tissue.
Normalization to a standard space (SPM)

• Large variation in brain size and shape across individuals
• However, the same anatomical structures are present in all brains
• Because we often want to do population-level inference across the whole brain, the brains need to be transformed into similar size and shape
Smoothing (SPM)

• The resulting parametric images are often very noisy
• One way to increase signal-to-noise ratio is to average the maps over neighboring voxels (smoothing)
• Cost: reduced spatial resolution
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The end product
How is the preprocessing done in TPC?

• **AIVO**: A centralized database
  - Contains metadata from over 10 000 neuro PET images acquired in Turku

• **magia**: Preprocessing pipeline
  - Runs on MATLAB
  - Fully automated
  - Standardized
  - Supports a wide range of different PET images
  - Provides quality control pictures and metrics
Select subjects
magia (Step 1/2)

Select subjects

Example: Select all studies of a project named Pleasure
Select subjects

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```
subjects = aivo_get_subjects('project','pleasure');
```
magia (Step 1/2)

Select subjects

Example: Select all studies of a project named Pleasure

```python
subjects = aivo_get_subjects('project','pleasure');
```
magia (Step 2/2)

Run preprocessing
magia (Step 2/2)

Run preprocessing

Example: Run preprocessing on previously selected subjects
Run preprocessing

Example: Run preprocessing on previously selected subjects

```plaintext
for i = 1:length(subjects)
    sub = subjects{i};
    run_magia(sub);
end
```
run_magia may take 10-20 hours to complete.
However, the FreeSurfer part only needs to be done once, after which re-runs take only less than 1 hour.
Advisable to run the FreeSurfer part in advance.
magia quality control: motion correction
magia quality control: coregistration
magia quality control: reference tissue
magia quality control: MRI

![Brain MRI histogram](image)

- $\mu_{GM} = 84.90$
- $\mu_{WM} = 104.69$
- $\Delta \mu = 19.80$ (23.32 %)
magia quality control: parametric images
magia quality control: ROI level fitting

Radioactivity concentration vs. time (min)

- $R1 = 1.13; \ k2 = 0.27; \ BPnd = 3.29$
AIVO + magia = WIN

• Together AIVO and magia allow efficient preprocessing of PET data:

1. The preprocessing only has to be run only once per study, after which the data is available for everyone to use in statistical analyses

2. Everyone can find the related metadata from one centralized database
   ○ This requires that someone inputs the data in AIVO in the first place (should be considered a routine step for new studies)

3. Allows analysis of massive (N >> 100) data sets easily

4. magia automatically saves quality control metrics into AIVO