MAGIA pipeline for automated PET-image processing and pharmacokinetic modelling

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Contents

- PET-processing & Magia toolbox overview
- How to use Magia
- Magia outputs and quality control results

Sources of variation in PET-data

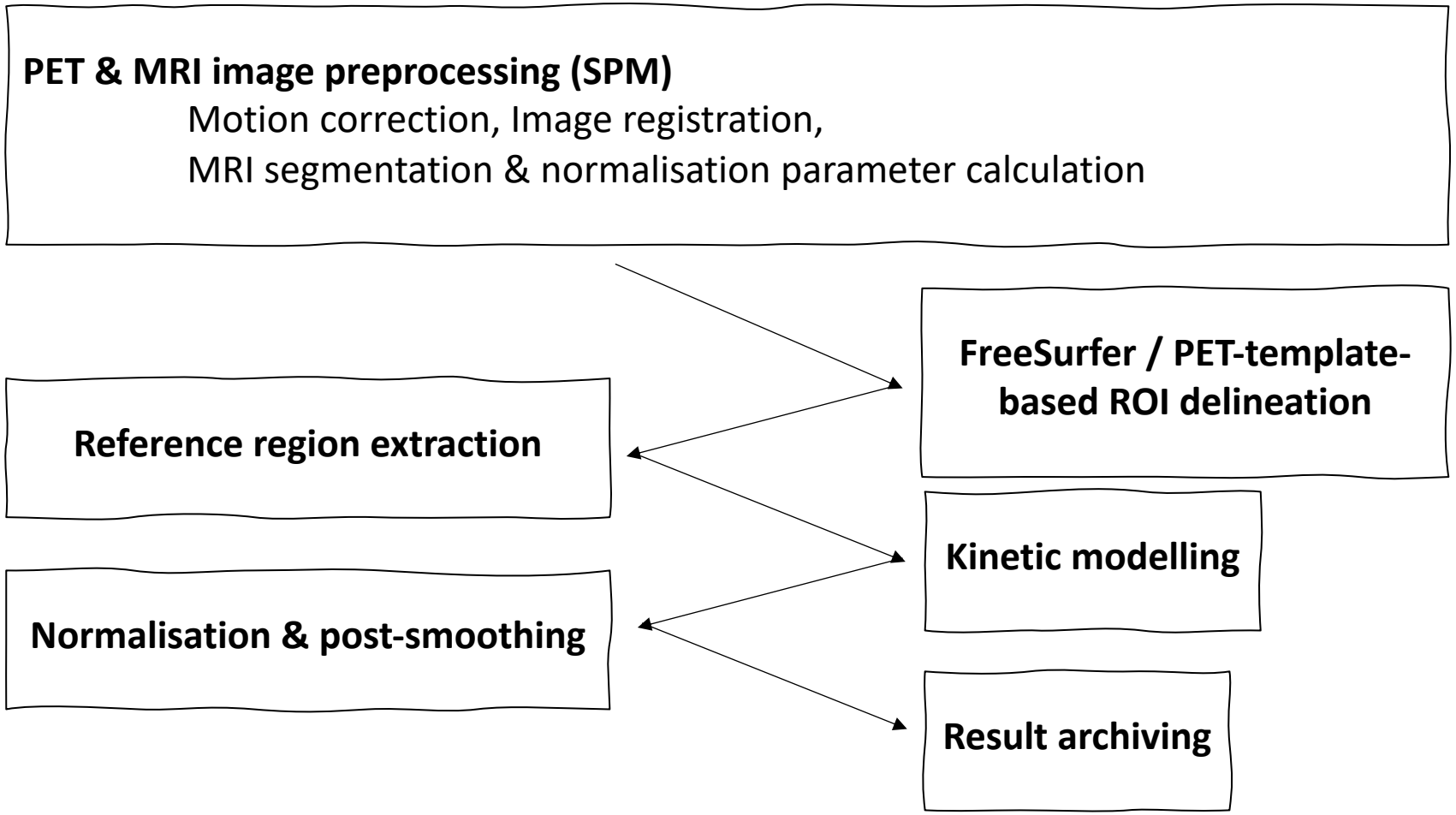
- Radioligand
- Dynamic or static study
- Frames
- Input (reference region / arterial)
- Kinetic model

⇾ Different PET data require different processing steps

Automated PET preprocessing and modelling

- Magia enables easy & automated PET data processing
  - Usable for wide range of different PET radioligands
  - Currently limited to human brain data
- Reduced manual work
- Increased reproducibility and reliability
  - scripts & automated image analysis
  - version control with GitHub
- Integration with Turku PET centre  AIVO database
  - Contains metadata from over 10 000 brain PET-images acquired in Turku

Magia processing flowchart



Magia ROI/voxel-level pharmacokinetic models

- SUV (Standardised Uptake Value) & SUV-ratio
- FUR (Fractional Uptake Ratio)

Reference tissue input :

- Simplified Reference Tissue Model (SRTM) (Lammertsma et al. 1996)
- Logan plot with reference tissue input (Logan et al. 1996)
- Patlak plot with reference tissue input (Patlak & Blasberg 1985)

Arterial input (requires manual processing):

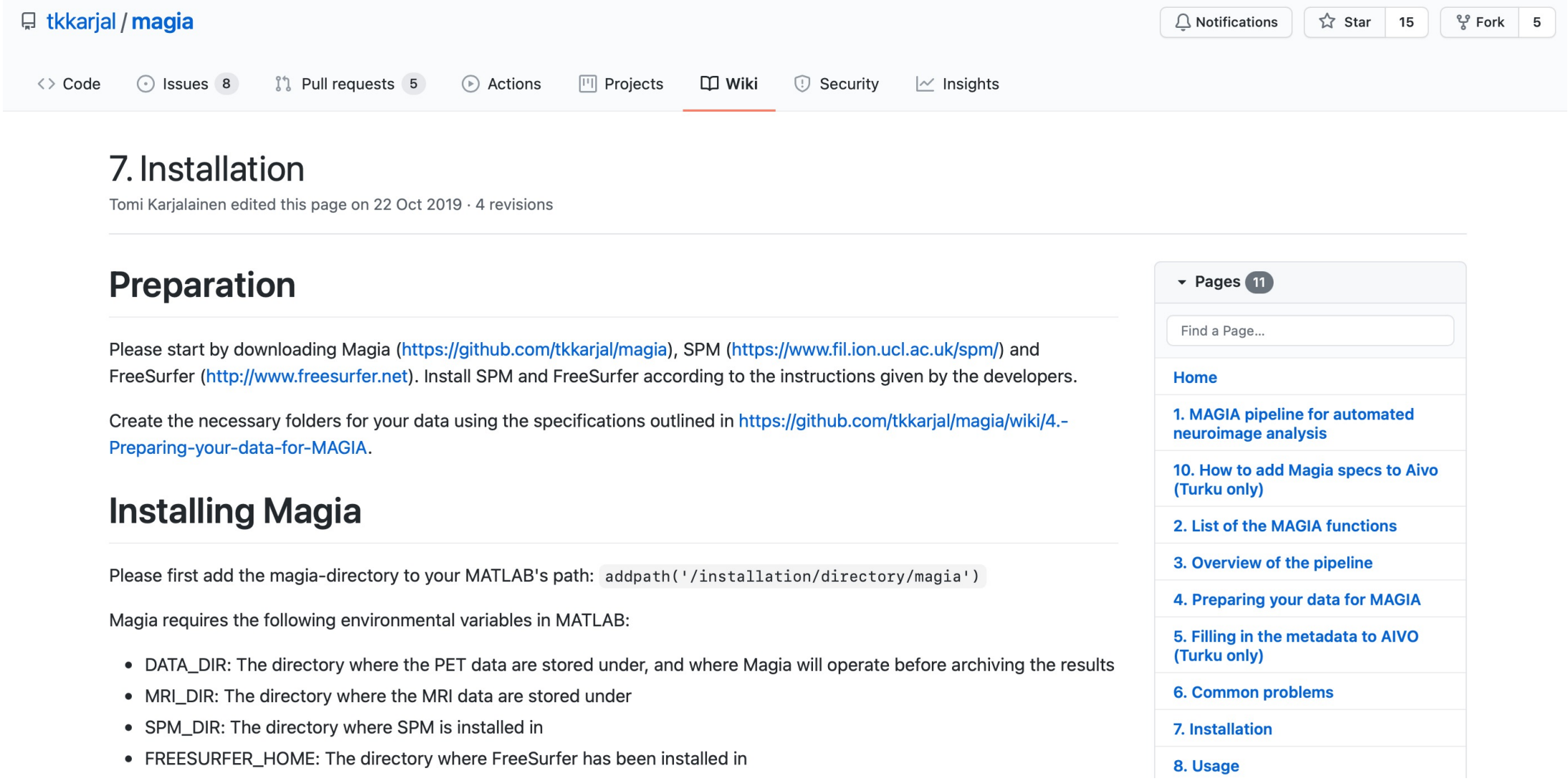
- Logan plot (Logan et al. 1990)
- Patlak plot (Patlak et al. 1983)
- Ichise's multillinear analysis 1 (Ichise et al. 2003)
- Two-tissue compartment model (2TCM)

Tested to compare with TPClib models; More models added eventually…

Magia requirements

- MATLAB
- SPM (Statistical Parametric Mapping)
- FreeSurfer
  - Supported operating systems: Linux & Mac

Installation: (https://github.com/tkkarjal/magia)



tkkarjal / magia

Notifications | Star 15 | Fork 5

Code | Issues 8 | Pull requests 5 | Actions | Projects | Wiki | Security | Insights

7. Installation

Tomi Karjalainen edited this page on 22 Oct 2019 · 4 revisions

Preparation

Please start by downloading Magia (https://github.com/tkkarjal/magia), SPM (https://www.fil.ion.ucl.ac.uk/spm/) and FreeSurfer (http://www.freesurfer.net). Install SPM and FreeSurfer according to the instructions given by the developers.

Create the necessary folders for your data using the specifications outlined in https://github.com/tkkarjal/magia/wiki/4.-Preparing-your-data-for-MAGIA.

Installing Magia

Please first add the magia-directory to your MATLAB's path: `addpath('/installation/directory/magia')`

Magia requires the following environmental variables in MATLAB:

- DATA_DIR: The directory where the PET data are stored under, and where Magia will operate before archiving the results
- MRI_DIR: The directory where the MRI data are stored under
- SPM_DIR: The directory where SPM is installed in
- FREESURFER_HOME: The directory where FreeSurfer has been installed in

Pages 11

Find a Page...

Home
1. MAGIA pipeline for automated neuroimage analysis
10. How to add Magia specs to Aivo (Turku only)
2. List of the MAGIA functions
3. Overview of the pipeline
4. Preparing your data for MAGIA
5. Filling in the metadata to AIVO (Turku only)
6. Common problems
7. Installation
8. Usage

How do you use it?

Inputs:

- Study specifications
- Modelling specifications
- Magia preprocessing specifications
- PET (& MRI) dicom or nifti data stored in a predefined structure:
  - PETdatafolder / *ID* / PET / nii / pet_*ID*.nii
  - MRIdatafolder / *ID* / T1 / *ID*.nii

Study specifications

```
%study specs
specs.study.dose = 500; %MBq
specs.study.mri_code = 'nrm2018mri';
specs.study.scanner = 'siemens biograph mmr pet-mri';
specs.study.tracer = '[11c]ro15-4513';
specs.study.weight = 70; %Kg

specs.study.frames = [ 0 0.25;0.25 0.5;0.5 0.75;0.75 1;1 2;2 3;3 4;4 5; ...
    5 7.5;7.5 10;10 15;15 20;20 25;25 30;30 35;35 40;40 45;45 50; ...
    50 55;55 60;60 70;70 80;80 90];
```

Magia preprocessing specifications

```
%magia specs
specs.magia.mc_excluded_frames = '1,2';
specs.magia.mc_fwhm = 7;
specs.magia.mc_ref_frame = 10;
specs.magia.mc_rtm = 1;

specs.magia.norm_method = 'mri';
specs.magia.rc = 0;
specs.magia.roi_set = 'rs2';
specs.magia.roi_type = 'freesurfer';

specs.magia.dc = 1;
specs.magia.fwhm_pre = 2;
specs.magia.fwhm_post = 8;
specs.magia.fwhm_roi = 0;
```

Motion correction options

Modelling specs and options

```
%modelling options // SRTM
specs.magia.cpi = 1;
specs.magia.input_type = 'ref';
specs.magia.model = 'srtm';

modeling_options.lb = [0 0 0];          %[R1 k2 BPnd]
modeling_options.ub = [3 1 8];          %[R1 k2 BPnd]
modeling_options.theta3_lb = 0.06;
modeling_options.theta3_ub = 0.8;
modeling_options.nbases = 200;
```

Alternative way: metadata import to AIVO-database (Turku PET centre)

- Excel data sheet to be imported to database

patient_id	ID	ac_number	study_date	project	group_name	description	scanner	tracer	frames
26031988-1000	nrm2018baseline1	nrm2018baseline1	2018-03-26	NRM2018_	baseline	baseline	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1001	nrm2018baseline2	nrm2018baseline2	2018-03-26	NRM2018_	baseline	baseline	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1002	nrm2018baseline3	nrm2018baseline3	2018-03-26	NRM2018_	baseline	baseline	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1003	nrm2018baseline4	nrm2018baseline4	2018-03-26	NRM2018_	baseline	baseline	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1004	nrm2018baseline5	nrm2018baseline5	2018-03-26	NRM2018_	baseline	baseline	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1005	nrm2018displaced1	nrm2018displaced1	2018-03-26	NRM2018_	displaced	displaced	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1006	nrm2018displaced2	nrm2018displaced2	2018-03-26	NRM2018_	displaced	displaced	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1007	nrm2018displaced3	nrm2018displaced3	2018-03-26	NRM2018_	displaced	displaced	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1008	nrm2018displaced4	nrm2018displaced4	2018-03-26	NRM2018_	displaced	displaced	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1
26031988-1009	nrm2018displaced5	nrm2018displaced5	2018-03-26	NRM2018_	displaced	displaced	Siemens mMR PET-MRI	[11c]Ro15-4513	0 0.25; 0.25; 0.5 ; 0.5 0.75; 0.75 1; 1 2; 2 3; 3 4; 4 5; 5 7.5; 7.5 10; 1

Running Magia

```
%run magia
ID = 'nrm2018baseline1';
run_magia(ID,specs,modeling_options)
```

Running Magia with AIVO-data

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

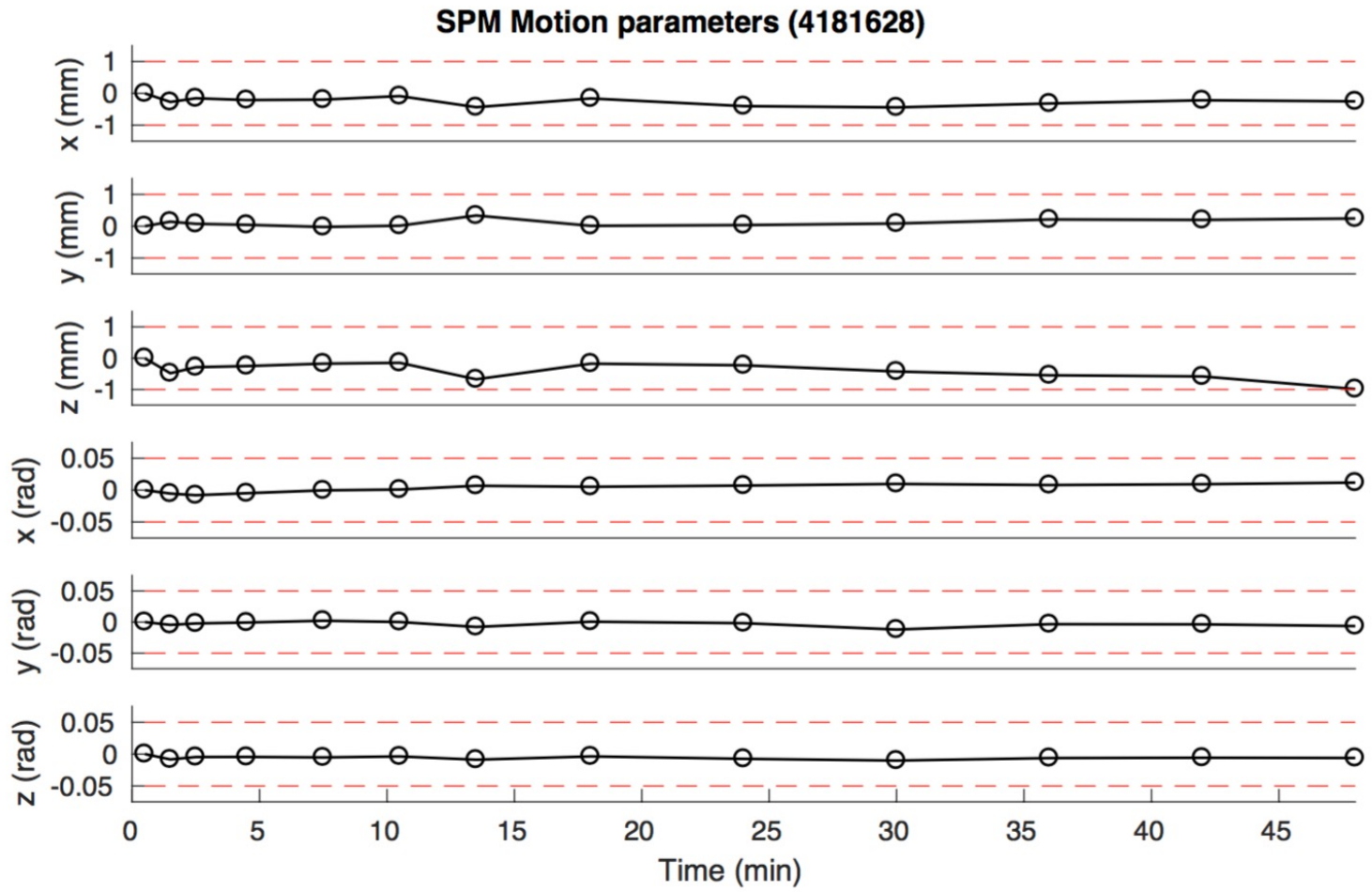
```
subjects = aivo_get_subjects('project','pleasure');

for i = 1:length(subjects)
     sub = subjects{i};
     run_magia(sub);
end
```

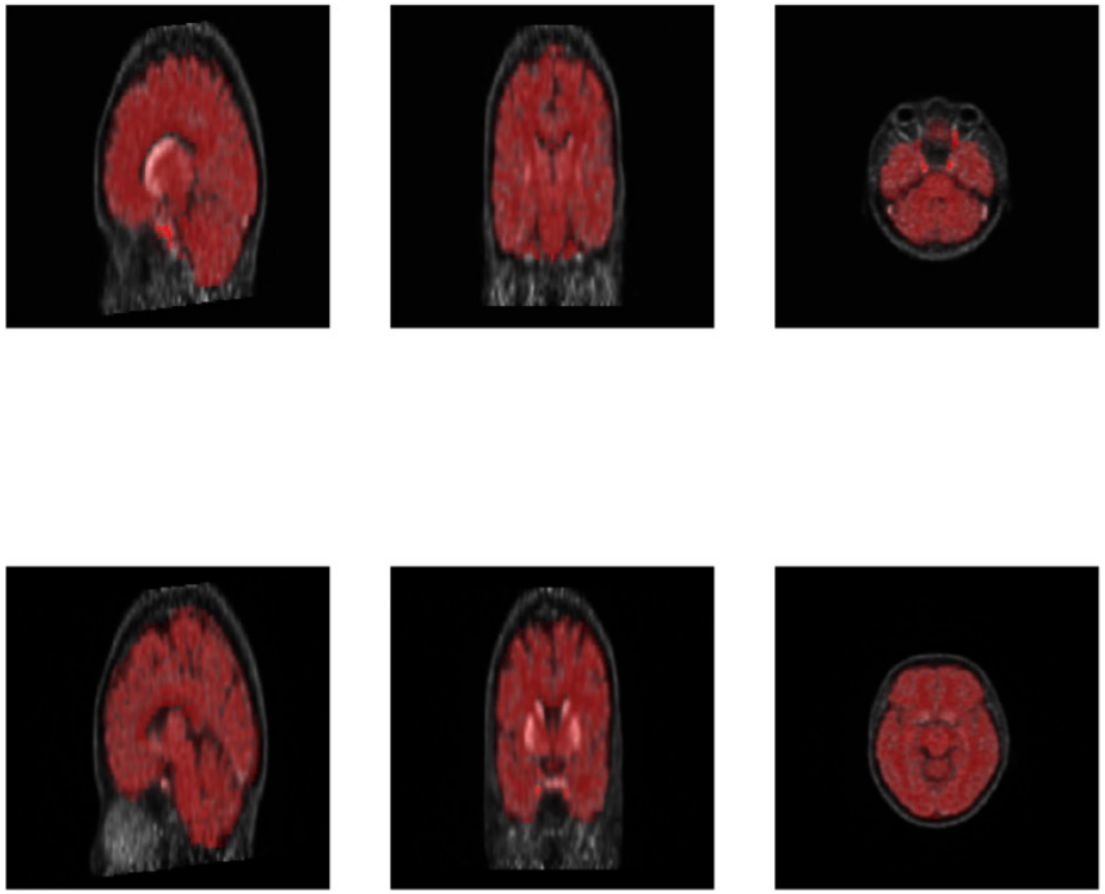
How long does it take?

- `run_magia` may take 10-20 hours to complete
  - FreeSurfer step only needs to be done once
  - Magia re-runs take only less than 1 hour

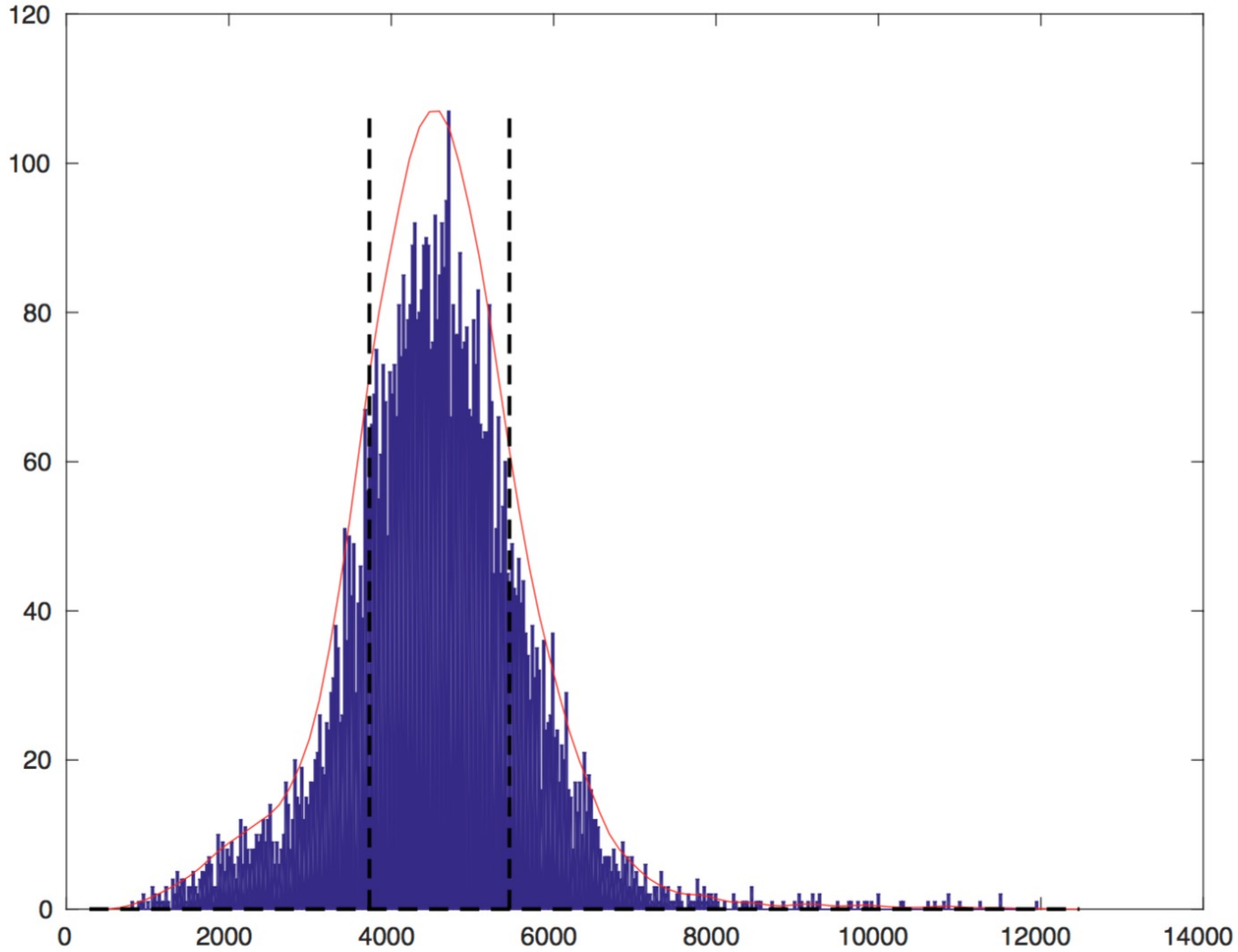
Magia outputs: motion correction QC



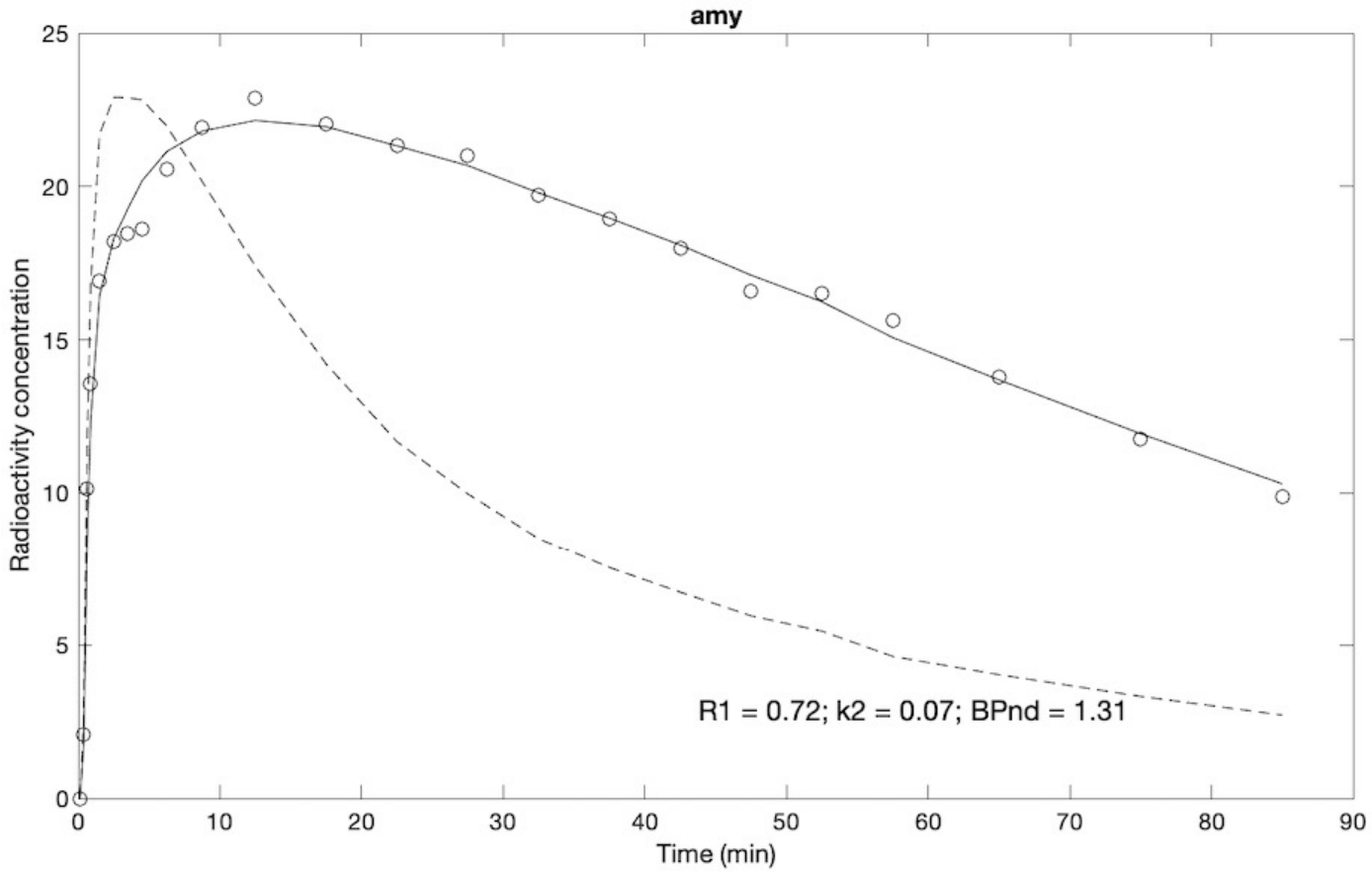
Magia outputs: coregistration QC



Magia outputs: reference tissue distribution

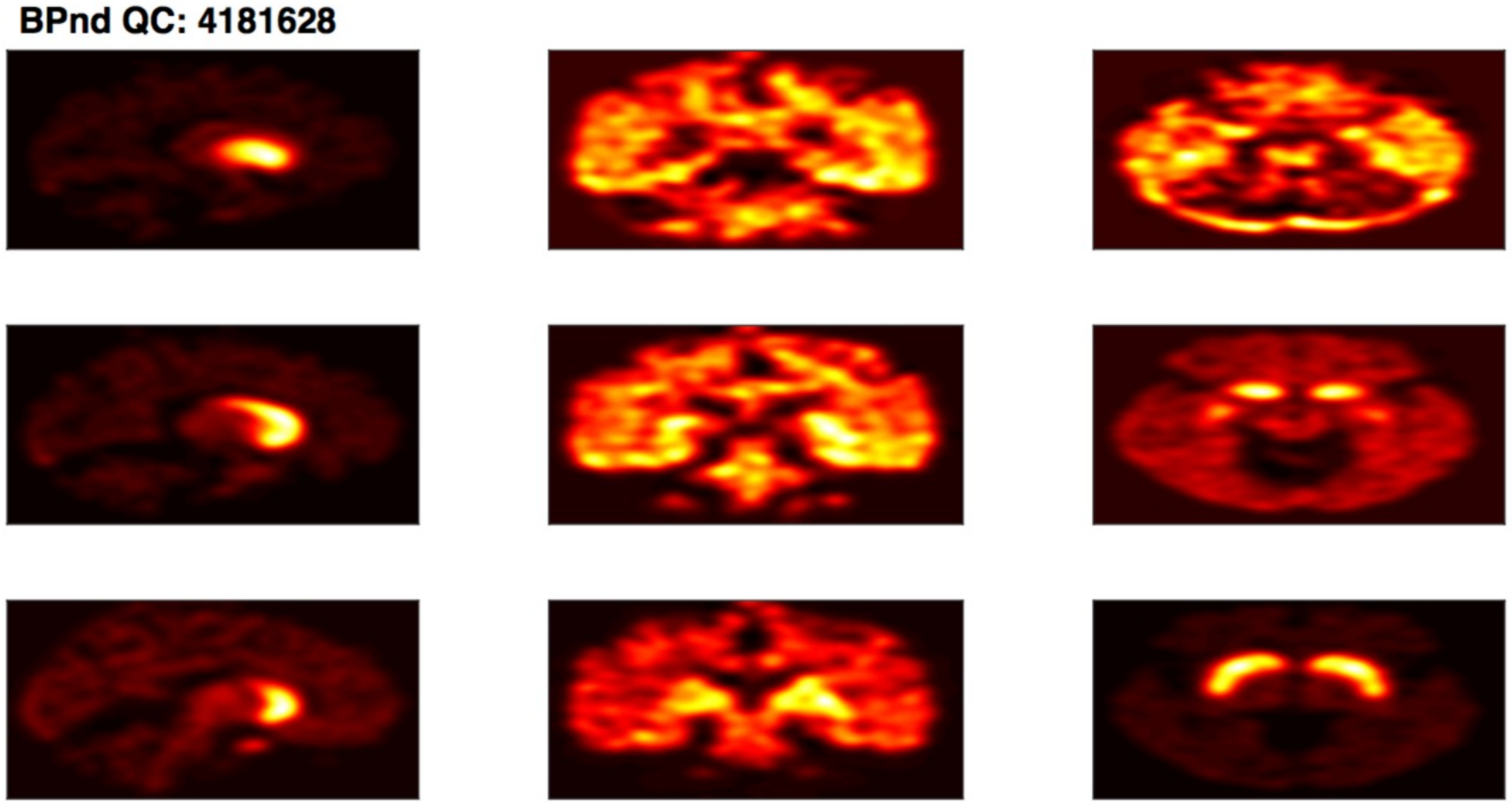


Magia outputs: ROI level fit & estimates



Row	R1	k2	BPnd	vol
amy	0.721	0.067	1.313	4181
cau	0.656	0.046	0.145	9316
amy	0.669	0.005	0.000	140267
dacc	0.880	0.081	1.044	5081
hip	0.672	0.062	1.037	10926
inftemp	0.888	0.080	0.774	27437
ins	1.048	0.088	1.342	16909
medul	0.346	0.007	0.005	5565
midbr	0.628	0.033	0.000	7915
midtemp	0.914	0.081	0.742	27802
nacc	0.849	0.079	1.518	1511
ofc	0.991	0.082	0.876	30532
parsop	1.082	0.083	0.691	11074
pcc	0.992	0.079	0.633	7530
pons	0.445	0.020	0.000	18316
put	0.957	0.062	0.537	12715
racc	1.061	0.104	1.679	5442
supfront	0.944	0.076	0.628	52053
suptemp	0.952	0.079	0.870	28373
tempol	0.670	0.067	1.090	5145
tha	0.808	0.052	0.028	21544

Magia outputs: parametric images



AIVO + Magia = 

- 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 to be used in the statistical analyses
2. Metadata is easily retrieved from the centralized AIVO-database
3. Allows analysis of massive (N >> 100) datasets easily
4. Quality control metrics are stored in AIVO

Further details & Magia reference

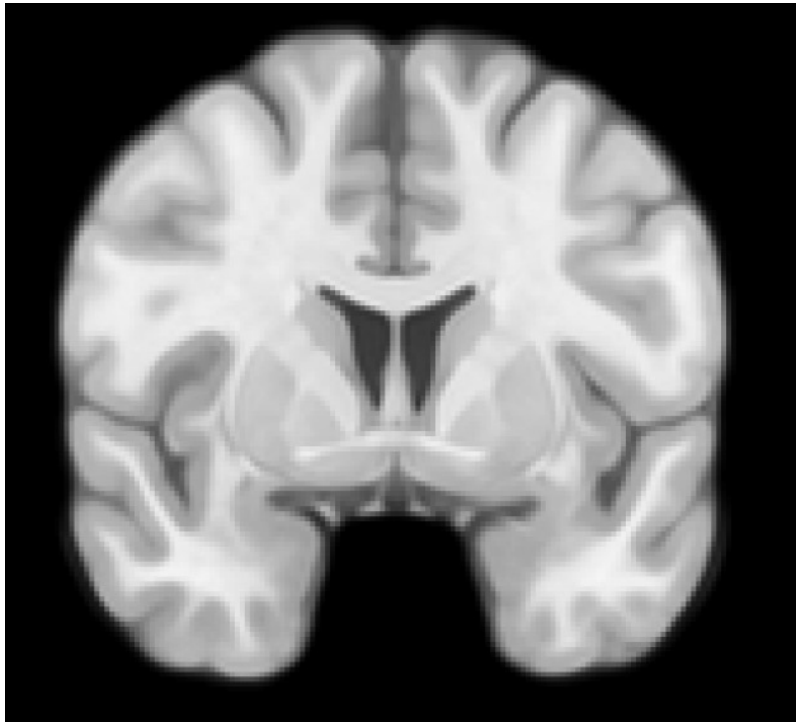
Front. Neuroinform., 04 February 2020 | https://doi.org/10.3389/fninf.2020.00003

Magia: Robust Automated Image Processing and Kinetic Modeling Toolbox for PET Neuroinformatics

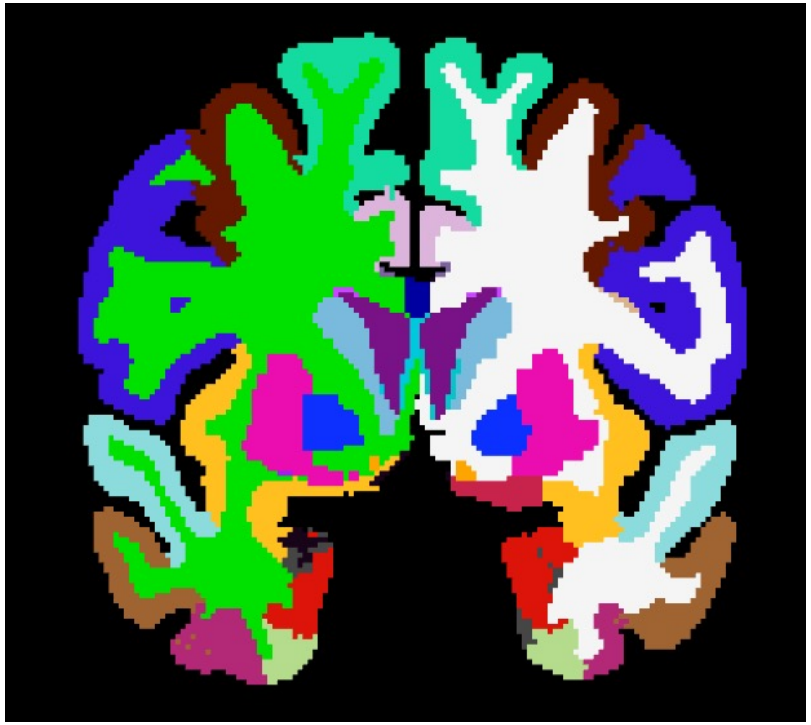
Tomi Karjalainen[1*], Jouni Tuisku[1], Severi Santavirta[1], Tatu Kantonen[1],  Marco Bucci[1], Lauri Tuominen[2],  Jussi Hirvonen[1,3], Jarmo Hietala[1,4], Juha O. Rinne[1,5] and  Lauri Nummenmaa[1,6]

ROI parcellation (FreeSurfer)

Input: T1w MRI



Output: FreeSurfer parcellation



Reference region extraction (FreeSurfer)

- Magia/FreeSurfer ROIs compare well with the manually drawn ROIs

Example [^{11}C]raclopride cerebellum TAC