Nordic PET-BIDS Onboarding and ezBIDS Workshop: 28-29 August 2025

PET-BIDS Tool Demonstrations and Tutorials: Image Analysis

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Agenda

- Common preprocessing choices for PET
- BIDS apps demo
    1. PETPrep head motion correction
    2. PETPrep extraction of time activity curves
    3. PETPrep (full pipeline)
    4. PETDeface

Demo here

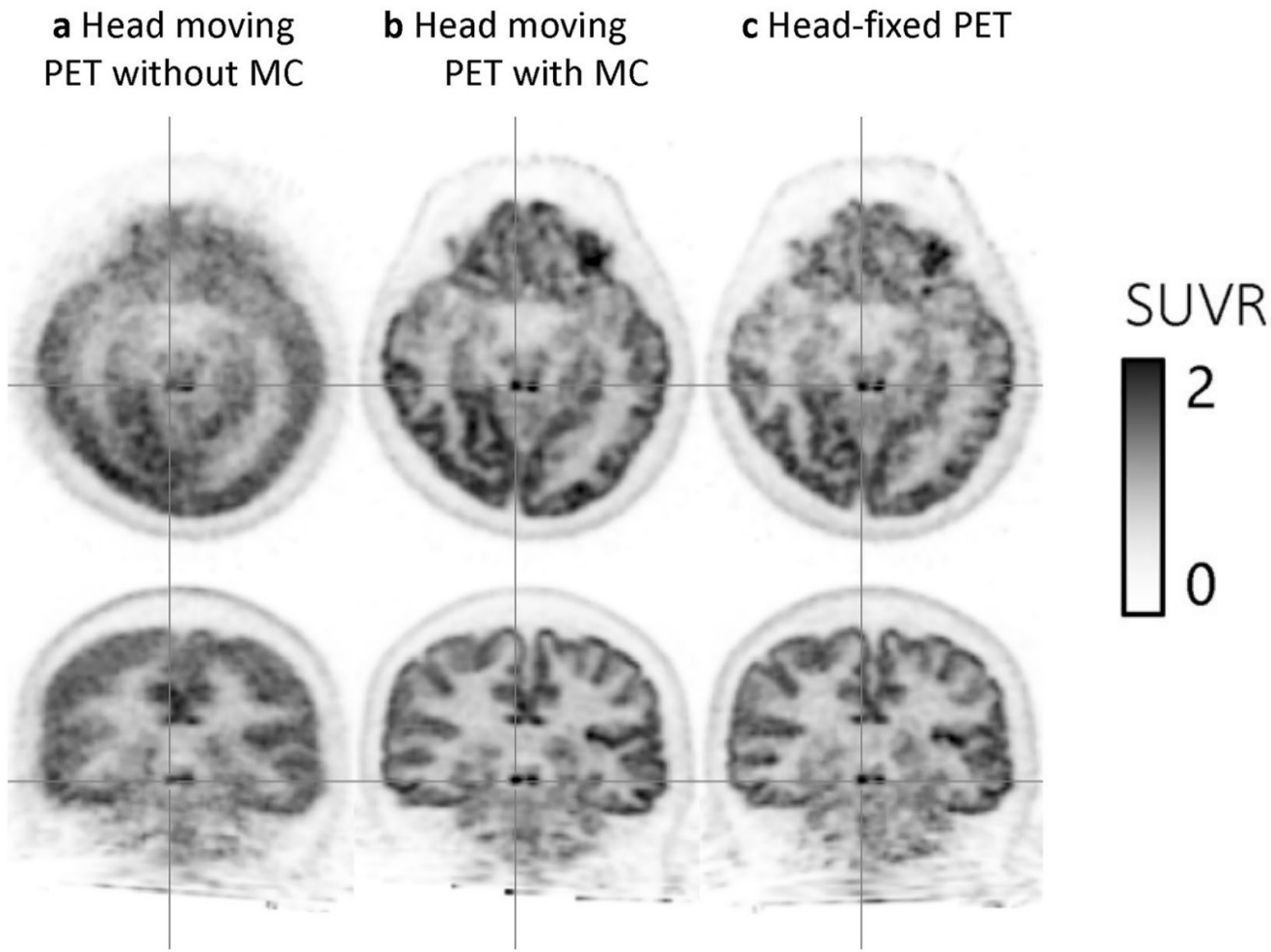
Short link:
https://shorturl.at/9UBOE

petprep_hmc:
github.com/mnoergaard/petprep_hmc

petprep_extract_tacs:
github.com/mnoergaard/petprep_extract_tacs

petprep:
https://github.com/nipreps/petprep

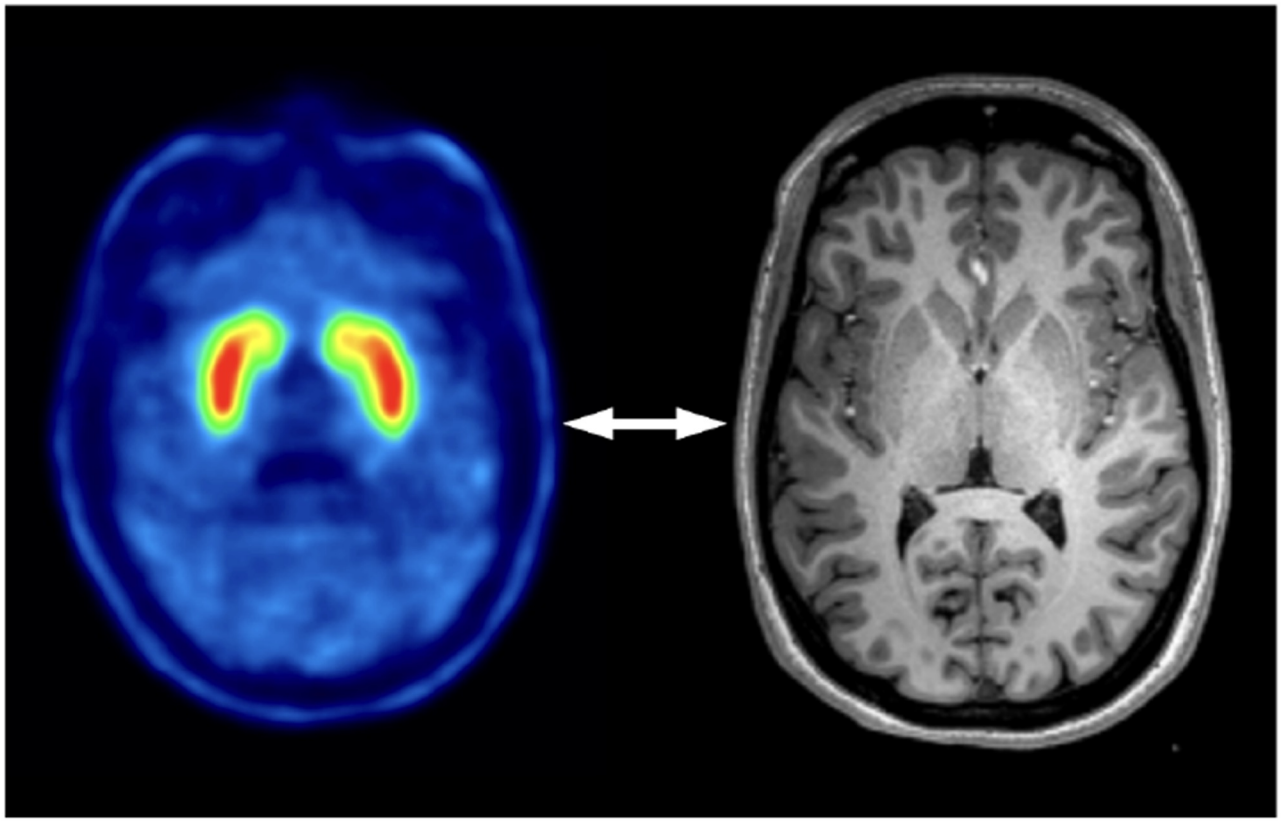
- Head motion renders PET data disturbed or even useless (Green et al. 1994).
- However, in the absence motion, motion correction may underestimate the true underlying signal (Orchard and Atkins 2003).



Iwao, Y., Akamatsu, G., Tashima, H. et al. Brain PET motion correction using 3D face-shape model: the first clinical study. Ann Nucl Med 36, 904–912 (2022).

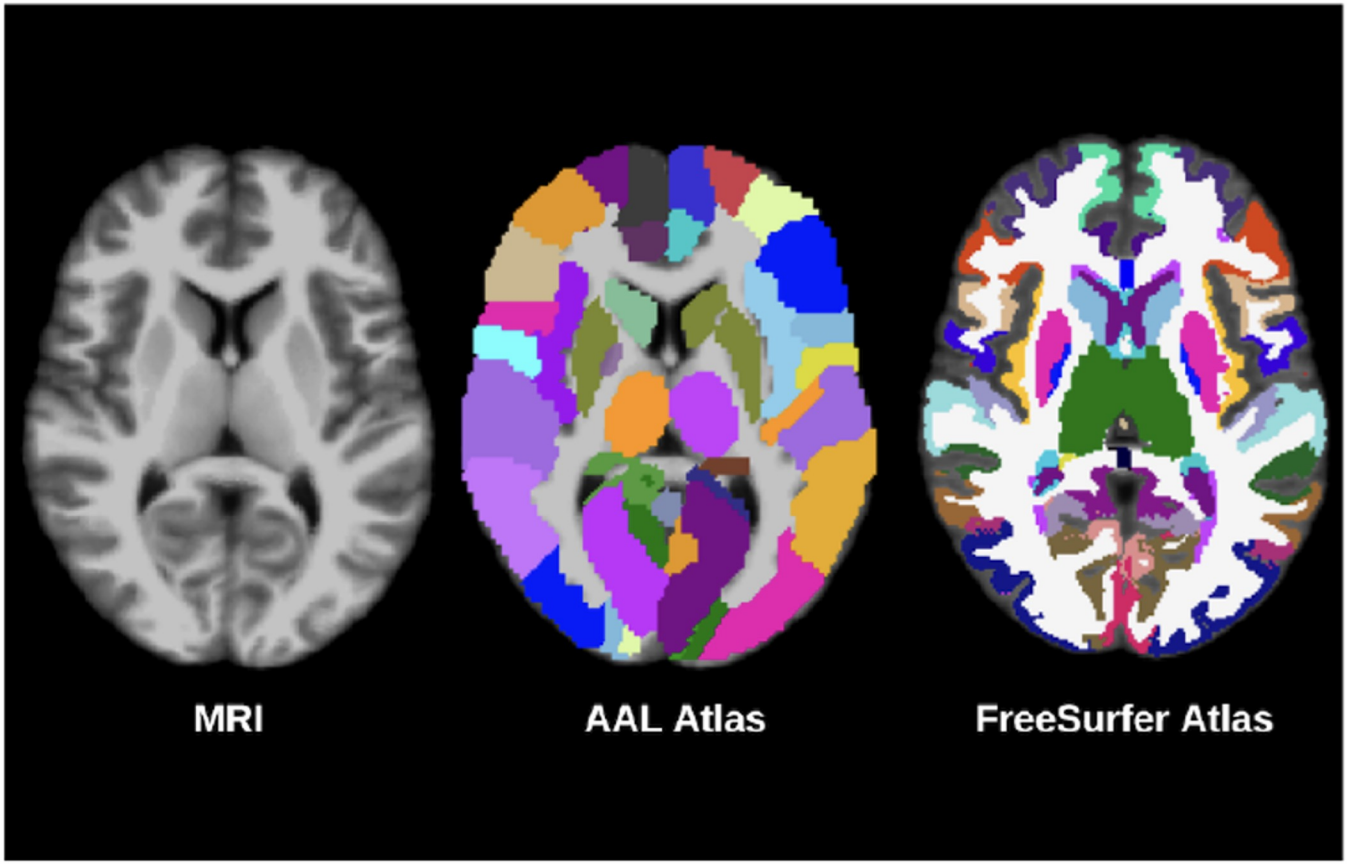
Co-registration

- A precise co-registration is needed, as voxels that move across tissue boundaries are prone to extreme signal changes (Schwarz et al. 2017).
- Resampling with spatial interpolation is carried out because PET and MRI have different resolutions, potentially biasing the signal (Strother 2004).

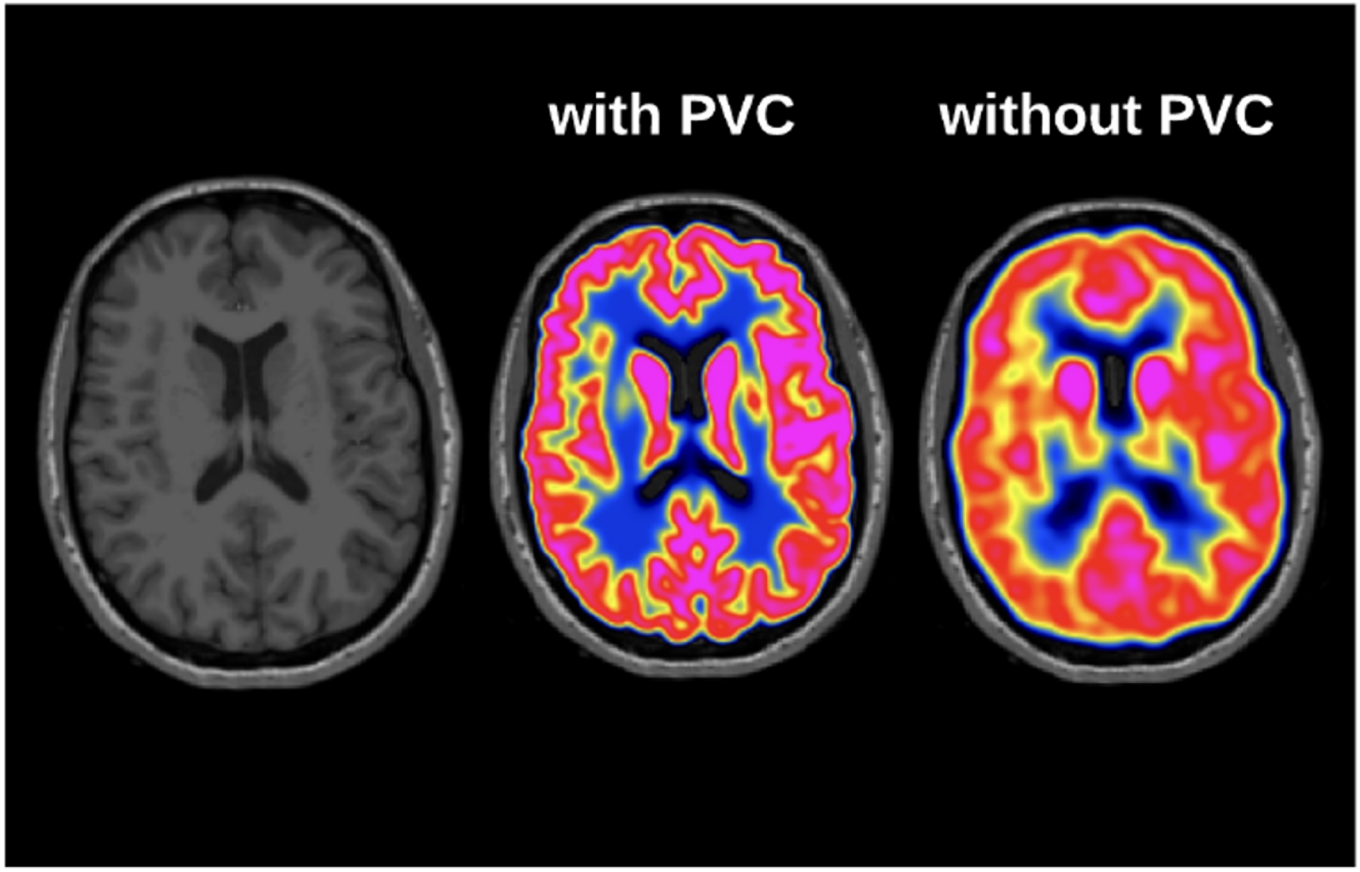


Delineation of volumes of interest

- PET studies are often interested in drawing inferences about specific anatomical brain structures.
- Different definitions of the same region may vary in size, location and delineation technique.

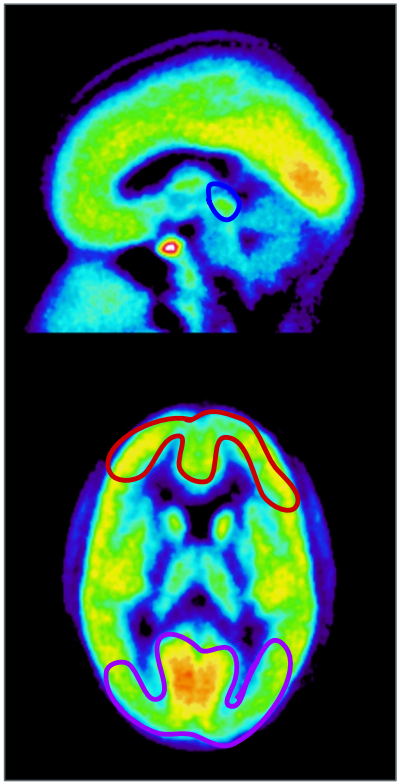


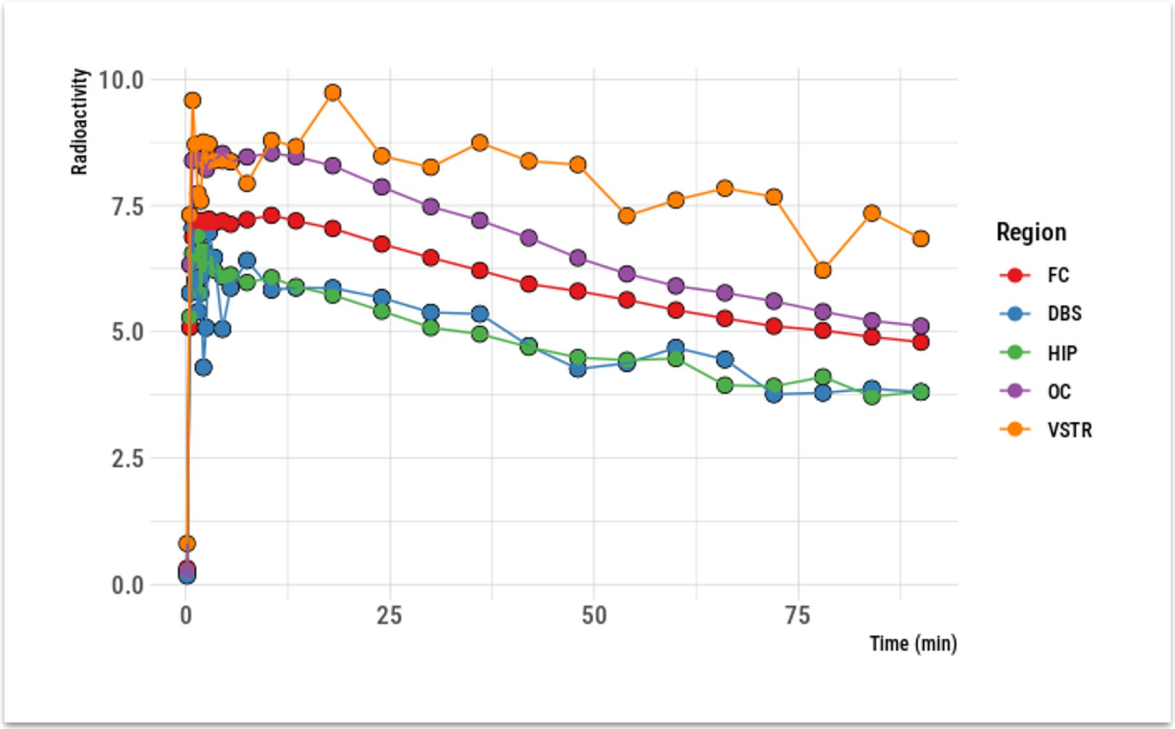
Partial Volume Correction (PVC)



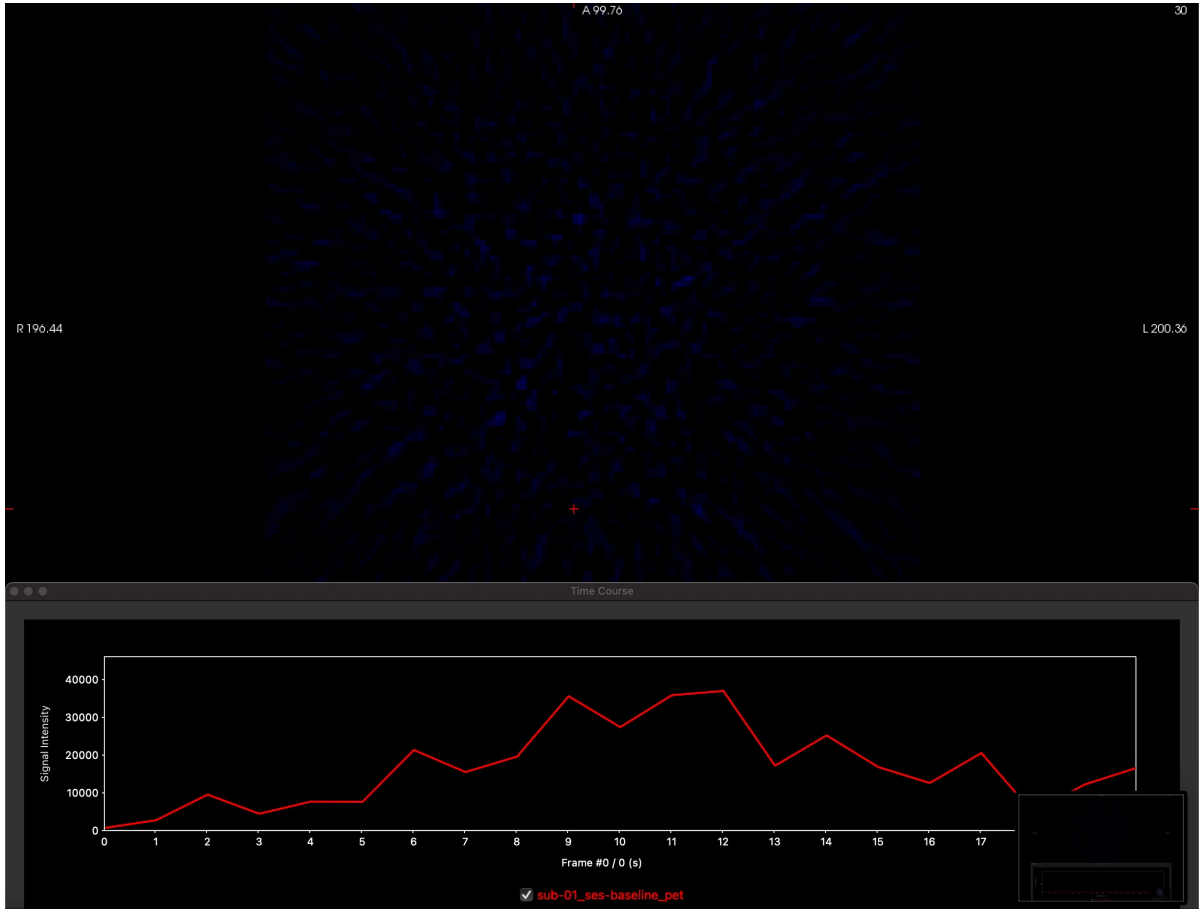
- Prerequisite in cases where brain anatomy may interact with an effect of interest (e.g. age or diagnosis).
- However, it may also cause noise amplification (Rousset 2007), and reflect differences in anatomy and not true radioligand uptake (Greve 2016).

Extraction of Time Activity Curves (TACs)

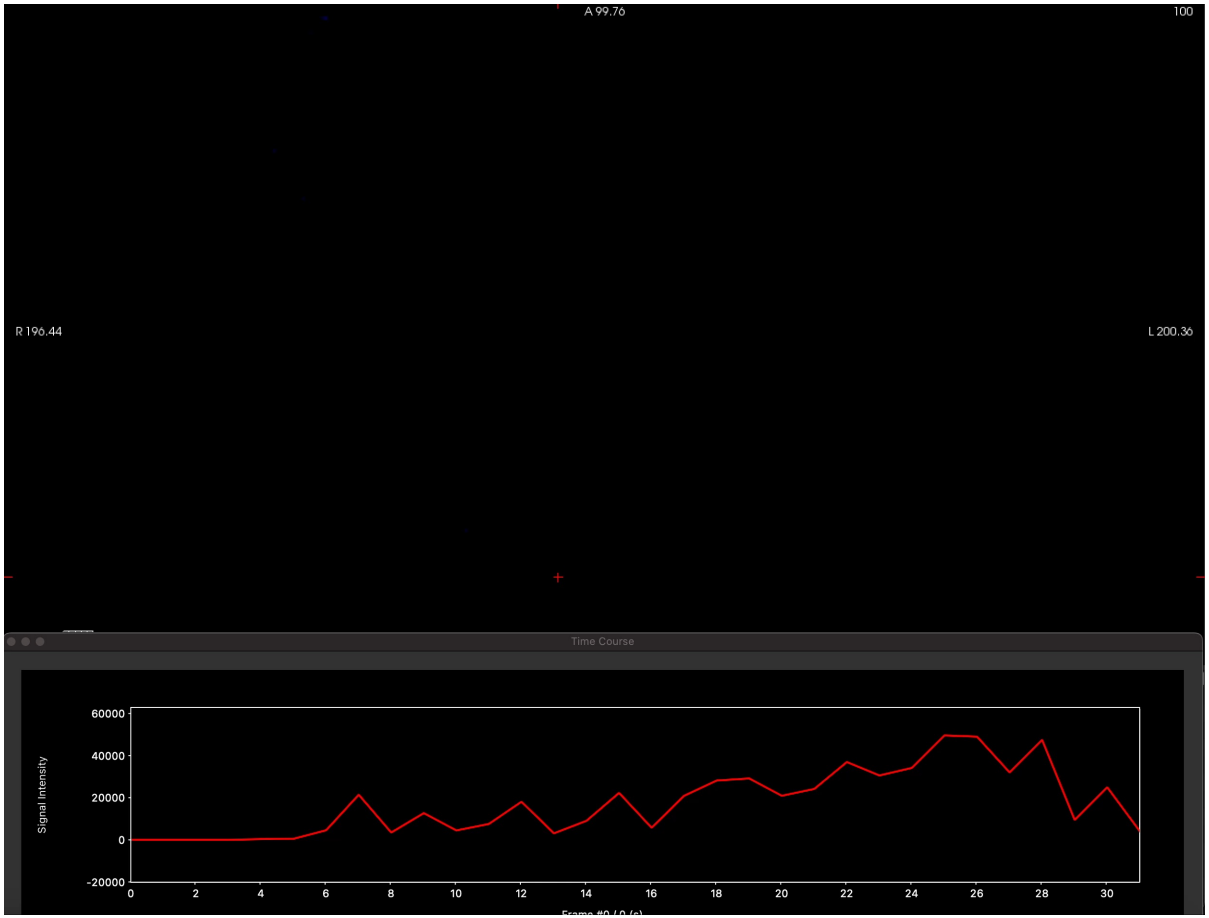




Quality of real PET data (example 1)



Quality of real PET data (example 2)



Differences between the two videos

Tracer	[11C]DASB (serotonin transporter)	[11C]DASB (serotonin transporter)
Scanner	Siemens HR+	Siemens High Resolution Research Tomograph
Resolution	5-8 mm	2-3 mm
Framing (s)	[3x20, 3x60, 3x120, 2x300, 10x600] (120min)	[6x5, 10x15, 4x30, 5x120, 5x300, 8x600] (90min)
Recon	Filtered Back Projection	Ordered Subset Expectation Maximization
High uptake	Thalamus, putamen, caudate	Thalamus, putamen, caudate

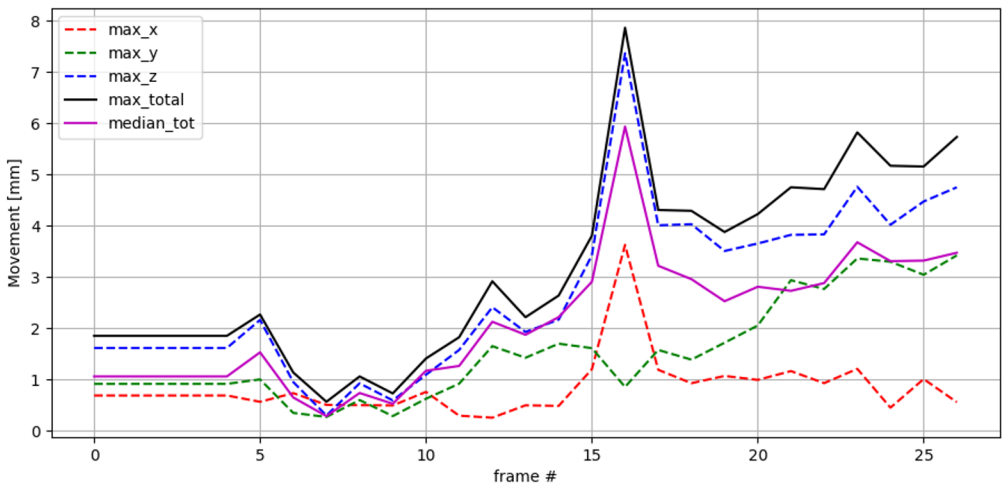
Note: Standard least-squares intensity cost function has been criticized, due to signal bias from task activation and outliers (Freire & Mangin, 2001; Orchard & Atkins, 2003).

1. Differences in resolution between frames (FIX: smoothing to boost SNR)
2. First frames have very little spatial information (FIX: assume motion to be similar for first frames < 2min)
3. Remove signal (noise) from outside of the brain (FIX: threshold individual frames)
4. What is a good reference frame? Mean across frames? Frame with high SNR?

Robust head motion correction using *petprep_hmc*

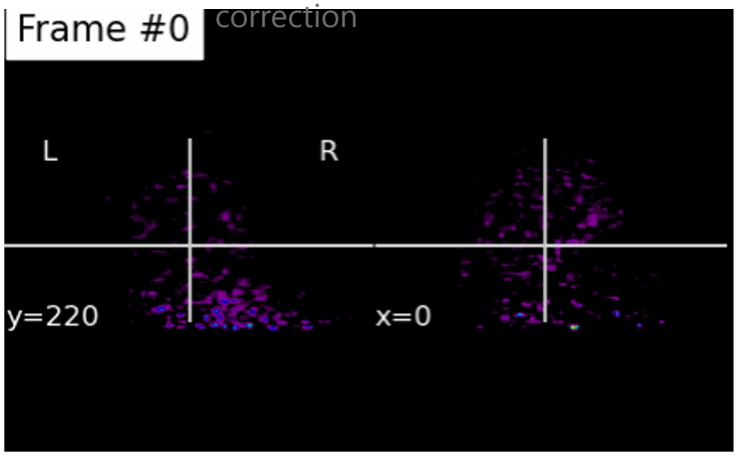
PETPrep Robust Head Motion Correction

```
docker run -it --rm \
      -v /path/to/bids_input:/data/input \
      -v /path/to/bids_output:/data/output \
      -v /path/to/freesurfer_license:/opt/freesurfer/license.txt \
      martinnoergaard/petprep_hmc:latest \
      --bids_dir /data/input \
      --output_dir /data/output \
```

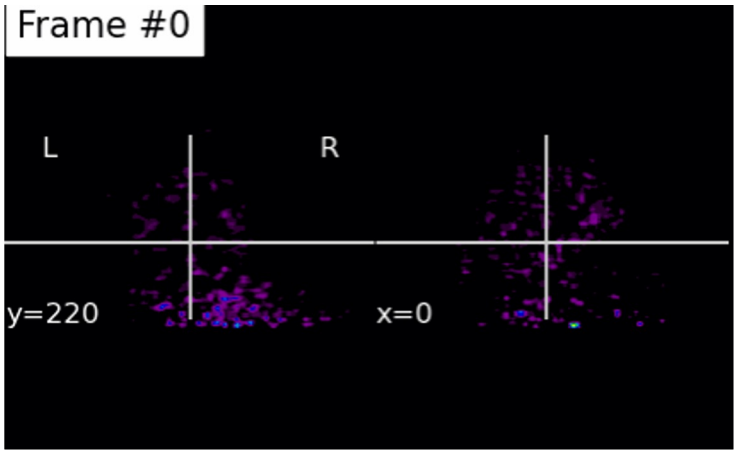


https://github.com/mnoergaard/petprep_hmc

Without motion correction



With motion correction



PETPrep Robust Head Motion Correction

Usage

To run the PETPrep Head Motion Correction BIDS App, use the following command:

```
python3 run.py --bids_dir /path/to/bids_input --output_dir /path/to/bids_output --analysis_level participant [--participant_label PARTICIPANT_LABEL]
```

- `--bids_dir`: Path to the input BIDS dataset
- `--output_dir`: Path to the output directory for preprocessed data
- `--analysis_level`: Level of the analysis that will be performed. Multiple participant level analyses can be run independently (in parallel) using the same output_dir.
- `--participant_label`: (Optional) A single participant label or a space-separated list of participant labels to process. If not provided, all participants in the dataset will be processed.
- `--mc_start_time`: (Optional) Start time for when to perform motion correction (subsequent frame will be chosen) in seconds (default = 120 seconds).
- `--mc_fwhm`: (Optional) FWHM for smoothing of frames prior to estimating motion (default = 10mm).
- `--mc_thresh`: (Optional) Threshold below the following percentage (0-100) of framewise ROBUST RANGE prior to estimating motion correction (default = 20).
- `--n_procs`: (Optional) Number of processors allocated to be used when running the workflow.
- `--no_resample`: (Optional) Whether or not to resample the motion corrected PET data to lowest x/y/z dim in original data (default = False).
- `--skip_bids_validator`: (Optional) Whether or not to perform BIDS dataset validation.

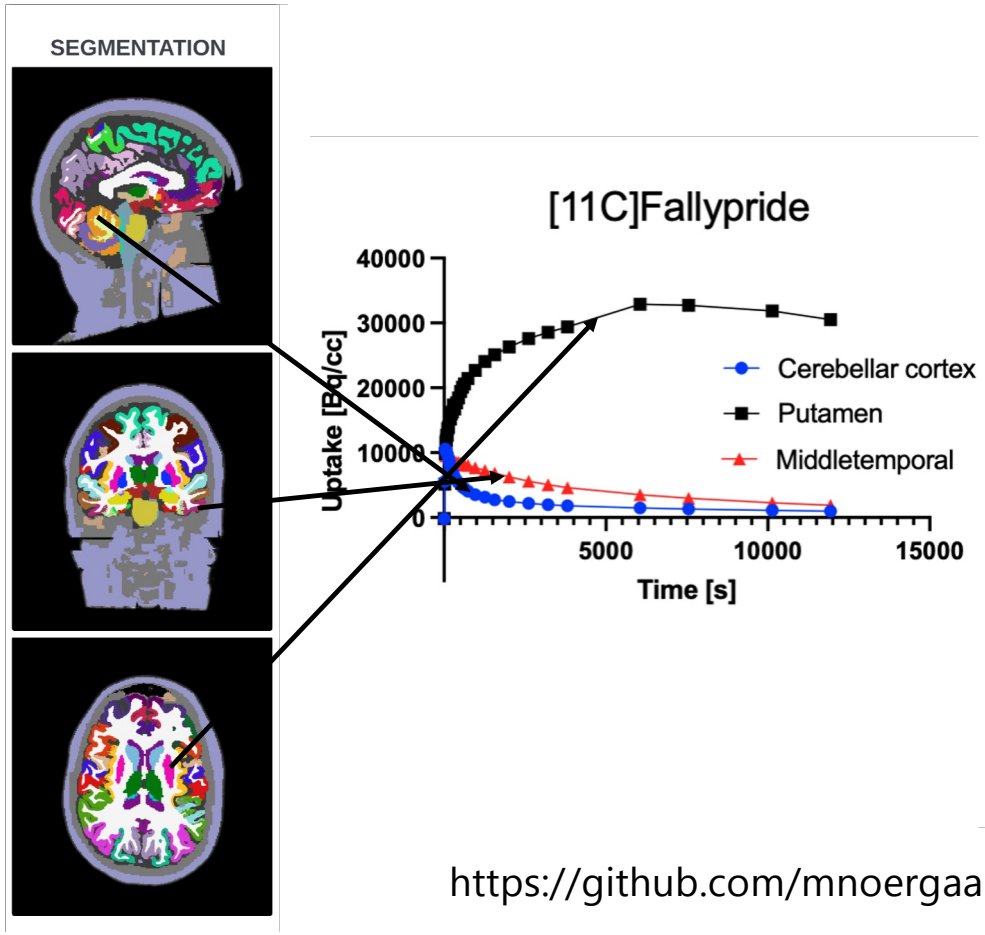
For example, to process participant `sub-01`, use the following command:

```
python3 run.py --bids_dir /data/bids_input --output_dir /data/bids_output --participant_label 01
```

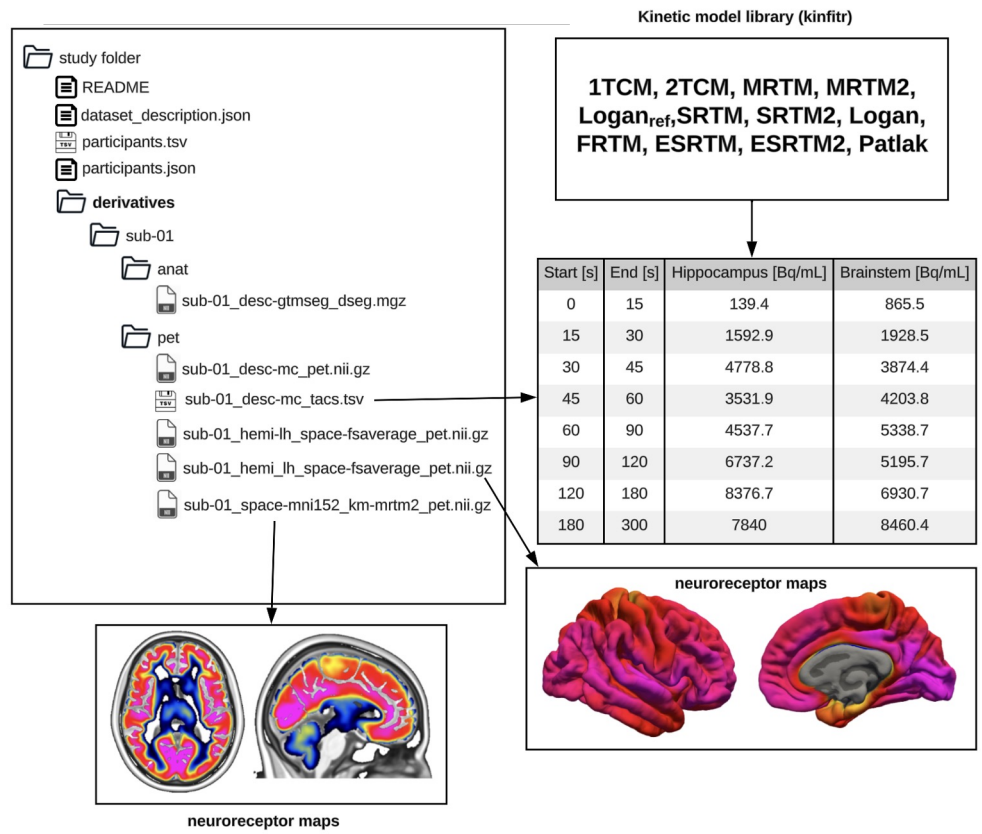
https://github.com/mnoergaard/petprep_hmc

Extraction of time activity curves using *petprep_extract_tacs*

Preprocessing of PET Data



PET-BIDS Derivatives



Start [s]	End [s]	Hippocampus [Bq/mL]	Brainstem [Bq/mL]
0	15	139.4	865.5
15	30	1592.9	1928.5
30	45	4778.8	3874.4
45	60	3531.9	4203.8
60	90	4537.7	5338.7
90	120	6737.2	5195.7
120	180	8376.7	6930.7
180	300	7840	8460.4

https://github.com/mnoergaard/petprep_extract_tacs

PETPrep Extraction of Time Activity Curves

Overview

This BIDS App is designed to extract time activity curves (TACs) from PET data. The workflow has options to extract TACs from different regions of the brain, and it uses the Brain Imaging Data Structure (BIDS) standard for organizing and describing the data. This README will guide you through how to use the app and the various options available.

Features

- BIDS compliant PET data input and output
- Time Activity Curve extraction from various brain regions

Requirements

- Python 3.9+
- FreeSurfer v. 7.3.2
- MATLAB RUNTIME (`sudo fs_install_mcr R2019b` when FreeSurfer is installed)

Quickstart

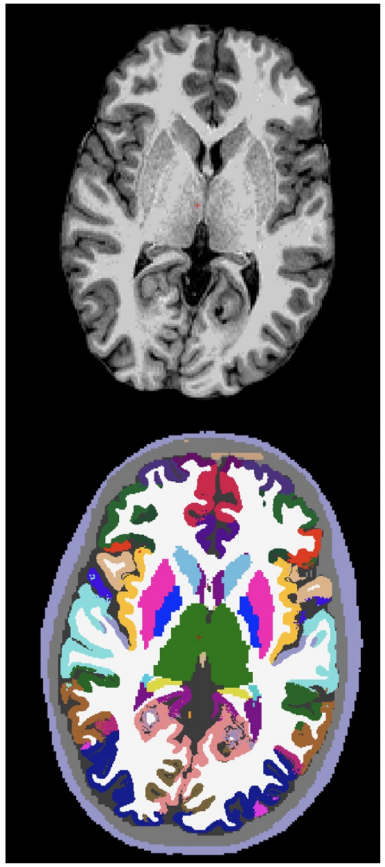
To get started, you'll need to have your data organized according to the BIDS standard. Once that's in place, you can run the app like this:

```
python3 run.py --bids_dir /path/to/your/bids/dataset --output_dir /path/to/output/dir --n_proc
```

This will run the app on your BIDS dataset and save the output to the specified directory.

https://github.com/mnoergaard/petprep_extract_tacs

PETPrep Extraction of Time Activity Curves



A	B	C	D	E	F	G	H
frame_start	frame_end	Left-Cerebra	Left-Cerebell	Left-Cerebell	Left-Thalam	Left-Caudate	Left-Putame
0	30	6866.52539	7235.44873	8969.10156	9735.34668	8669.91406	11645.9854
30	60	13811.9033	14901.3398	17751.4023	18644.668	17031.3867	22109.6504
60	90	20499.3574	21455.3691	26245.1621	27601.4766	26851.1777	32925.0625
90	120	23324.3906	25101.5078	30721.8594	31450.2871	29055.1387	37790.4922
120	150	23012.5625	24511.457	30327.9531	31907.2344	29424.7578	38484.6484
150	180	22583.6953	23887.7949	29040.2891	30596.5215	28588.4609	35319.0586
180	240	21920.5078	23092.6621	28177.375	30316.7148	26556.3223	34635.6836
240	300	21264.5898	22498.9141	26931.8555	28885.8203	26385.748	33001.4883
300	360	20591.5059	22225.1855	25665.7324	28628.6074	23686.5215	31514.9082
360	480	19826.3145	21095.0605	24489.5352	27689.3379	22836.1699	30335.8203
480	600	19140.0547	20643.0879	23034.6289	26379.2676	21410.5684	27782.6289
600	900	18197.5605	19615.7695	21048.1074	24872.5566	19252.1289	25828.6895
900	1200	17103.1348	18642.3789	18713.6113	22844.4023	16763.9766	22610.5859
1200	1500	16238.7354	17576.0762	16855.5391	21207.2676	15096.3691	20343.1836
1500	1800	15554.3008	16921.4766	15346.9375	20047.4824	13649.3164	18766.2363
1800	2100	14981.748	16038.3965	14192.249	18693.3496	13339.0029	17638.5566
2100	2400	14400.5654	15329.2148	13186.4043	17651.9375	12062.5557	16014.2148
2400	2700	13912.416	14271.0635	12196.5059	16132.6172	11287.1133	15143.123
2700	3000	13359.9053	13994.5146	11341.1719	15533.9941	10319.9619	14722.2334
3000	3300	12783.9551	13390.7637	10728.9131	14353.1494	9781.65234	12956.96
3300	3600	12233.8984	12523.6553	9733.04297	13791.1279	9580.76953	12535.2705
3600	3900	11801.665	12096.9326	9276.30566	12831.8213	9058.38477	11513.748
3900	4200	11478.7266	11764.1572	8873.22656	12073.3232	8916.43848	11422.7646
4200	4500	11047.7393	11474.3057	8453.29395	11052.2646	8203.42285	10289.8643
4500	4800	10904.3496	11254.168	8032.7749	11055.085	7901.18262	10351.2354
4800	5100	10510.7881	10504.1016	7652.05273	10762.8164	8110.64209	9596.25977
5100	5400	10287.3877	10612.5967	7399.45557	10249.3252	7968.80029	9226.31738

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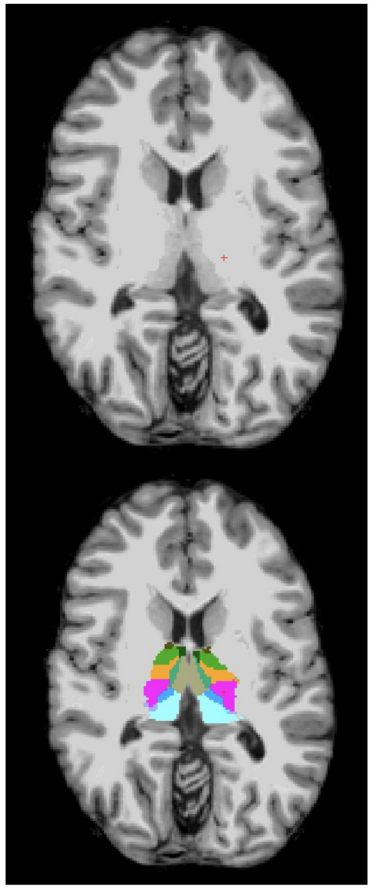
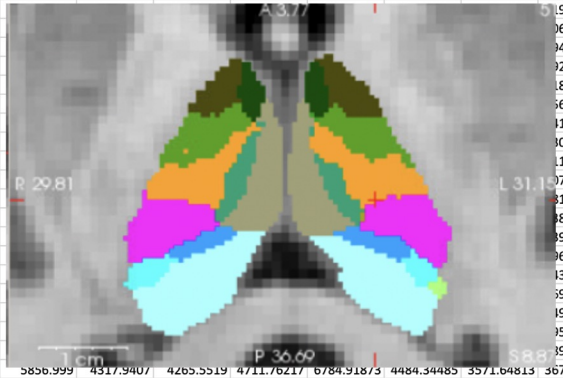
100 regions … can be loaded into PMOD

https://github.com/mnoergaard/petprep_extract_tacs

PETPrep Extraction of Time Activity Curves



frame_end	Left-AV	Left-CeM	Left-CL	Left-CM	Left-LD	Left-LGN	Left-LP	Left-L-Sg	Left-MDl	Left-MDm
30	924.10314	755.48742	1228.4917	851.85205	1128.11679	807.56117	1031.19504	1223.91374	1553.38888	1165.77388
60	6964.59568	6309.43481	8876.7825	8018.03385	8562.11513	6597.14932	8951.58631	6530.66815	8615.94954	8285.445
90	15983.8605	13118.0883	15903.6639	18820.7154	17810.6749	13350.4055	17043.836	13162.797	18026.6885	17476.067
120	17311.1167	17271.7293	20593.2117	20412.6289	21225.1969	16598.4185	22966.5788	16353.7261	23204.3899	21374.3827
150	16561.7634	15455.6863	18958.3328	21007.0464	18381.9736	15390.3019	21257.302	16399.1815	24151.6317	21069.053
180	15572.6997	15702.9911	19689.5085	20231.1212	18178.6207	16333.5196	18412.0863	16527.7171	20986.0768	19355.2579
240	16194.7632								1945.2264	19914.9366
300	15503.5284								0638.4622	19244.2811
360	16576.0746								9450.3049	18715.3896
480	15121.0364								9247.3277	18451.324
600	14230.2501								18150.084	17347.7373
900	13845.5678								5633.4907	15428.6331
1200	13013.2979								4109.2408	13266.8968
1500	12157.3877								3001.2864	12446.1414
1800	10572.4056								11696.631	11100.529
2100	9929.0722								0762.2253	10224.4189
2400	8540.37555								818.25763	8559.30564
2700	8120.67656								385.15877	7539.92628
3000	6933.76045								398.54783	7257.30906
3300	7164.78405								960.81256	6380.957
3600	6492.35381								437.50391	6079.15175
3900	5933.94285								593.82821	5611.74029
4200	5946.77444								4946.2176	5306.23098
4500	6160.58829								955.00899	5312.69464
4800	4405.09401								395.98844	4537.39134
5100	6439.44251	5856.999	4317.9407	4265.5519	4711.76217	6784.91873	4484.34485	3571.64813	3671.24396	3724.30202
5400	4088.88164	3492.21756	4528.4413	5019.42741	4222.64551	7242.74568	5074.50936	5981.66939	4250.34629	3984.313
5700	4152.55165	5910.69894	3569.12763	3428.48366	3392.69013	6158.82263	4043.26329	4105.51152	3040.34892	3491.37593
6000	3858.36083	4620.11983	4584.57322	4432.66323	5001.18193	5127.15948	6026.60181	4221.01025	3857.86595	3698.31579
6300	4538.76678	3857.51747	3398.89541	4518.14567	3627.36381	5368.05895	4627.05056	3918.0229	3959.25099	3742.06842
6600	3288.46676	3428.9226	3102.01222	3730.65384	3651.47774	4291.62641	3862.18486	2223.93636	3520.97784	3316.02736
6900	2797.70798	2941.69222	3095.69485	2922.11639	2966.80033	4124.31469	5713.70519	3413.63056	2083.49731	2551.8519
7200	3476.93997	3581.50033	4444.30979	3352.90479	5359.56468	5198.63621	4842.92414	3163.69292	3400.45961	3193.9343



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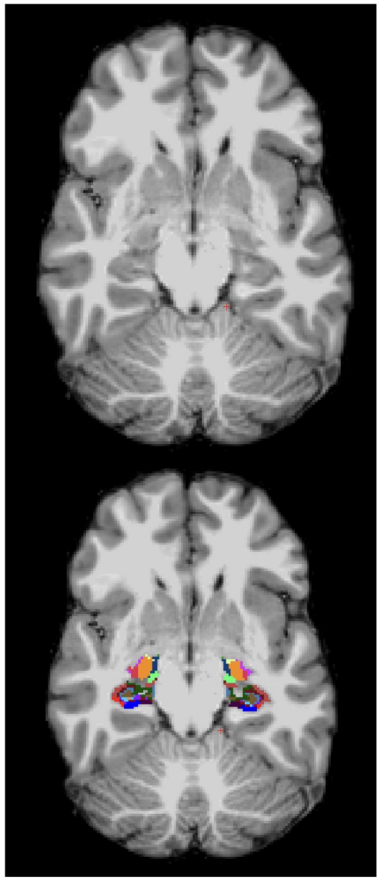
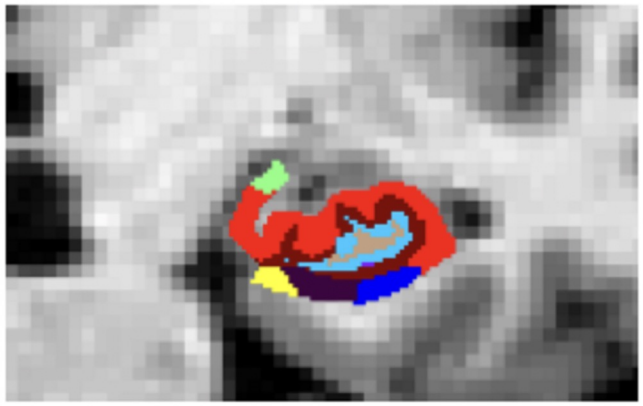
Thalamic nuclei segmentation
… can be loaded into PMOD

https://github.com/mnoergaard/petprep_extract_tacs

PETPrep Extraction of Time Activity Curves



frame_start	frame_end	parasubiculu	HATA	fimbria	hippocampal	HP_tail	presubiculun	presubiculun	subiculum-h	subiculum-b	CA1-head
0	30	1359.41676	1228.4442	707.89168	711.24002	469.61735	807.13934	1201.59903	541.8428	729.18917	753.14863
30	60	8402.13469	6254.27994	6743.58771	6994.46347	7010.16601	6128.14272	7591.81911	5632.88781	6111.60894	6553.61414
60	90	13010.3606	12622.7505	13843.9442	13421.1659	14128.5604	12872.6501	15167.5452	11533.0093	12845.9076	11641.1683
90	120	13611.1434	13520.4583	15404.4834	14856.7554	15152.9464	15353.2763	16590.3397	14497.4124	15107.3024	13117.9386
120	150	13855.1398	13409.2589	17292.7389	15512.1132	15118.1907	15121.5778	17121.3254	14679.2107	16138.8761	13864.6947
150	180									211	14043.0433
180	240									531	12944.7553
240	300									755	13315.8946
300	360									819	12885.0729
360	480									428	13407.0663
480	600									847	13235.8927
600	900									084	12786.6531
900	1200									607	12331.0375
1200	1500									969	11722.8282
1500	1800									847	11536.0907
1800	2100									223	10547.6759
2100	2400									176	10641.1285
2400	2700									169	10228.8567
2700	3000									634	9527.94731
3000	3300									737	9160.4078
3300	3600									008	9251.86316
3600	3900									921	9043.84839
3900	4200									442	8467.31074
4200	4500									093	8236.97648
4500	4800									232	8541.01916
4800	5100									406	7612.24576
5100	5400									366	7521.1453
5400	5700									608	8427.61926
5700	6000	4418.47934	4827.5171	7143.54901	7494.28443	6902.4194	6262.39788	5575.06016	6630.42056	8258.37626	6423.66427
6000	6300	3347.76947	4147.25118	8585.09866	9476.68181	7094.39084	6258.82982	5025.00388	7127.48184	8610.13313	7097.98345
6300	6600	3558.96539	5406.19575	7419.77883	8417.52027	6642.86431	5644.14231	3266.12633	8294.44682	7343.55935	8136.29844
6600	6900	2965.69008	3221.49416	7512.40002	7899.54264	5305.19955	5857.25574	3488.20896	6655.38887	7292.95277	5667.49007
6900	7200	4745.82858	6901.9147	7568.17933	7473.79328	4767.19221	5485.80564	5252.3231	6476.88921	8134.16927	6338.15665

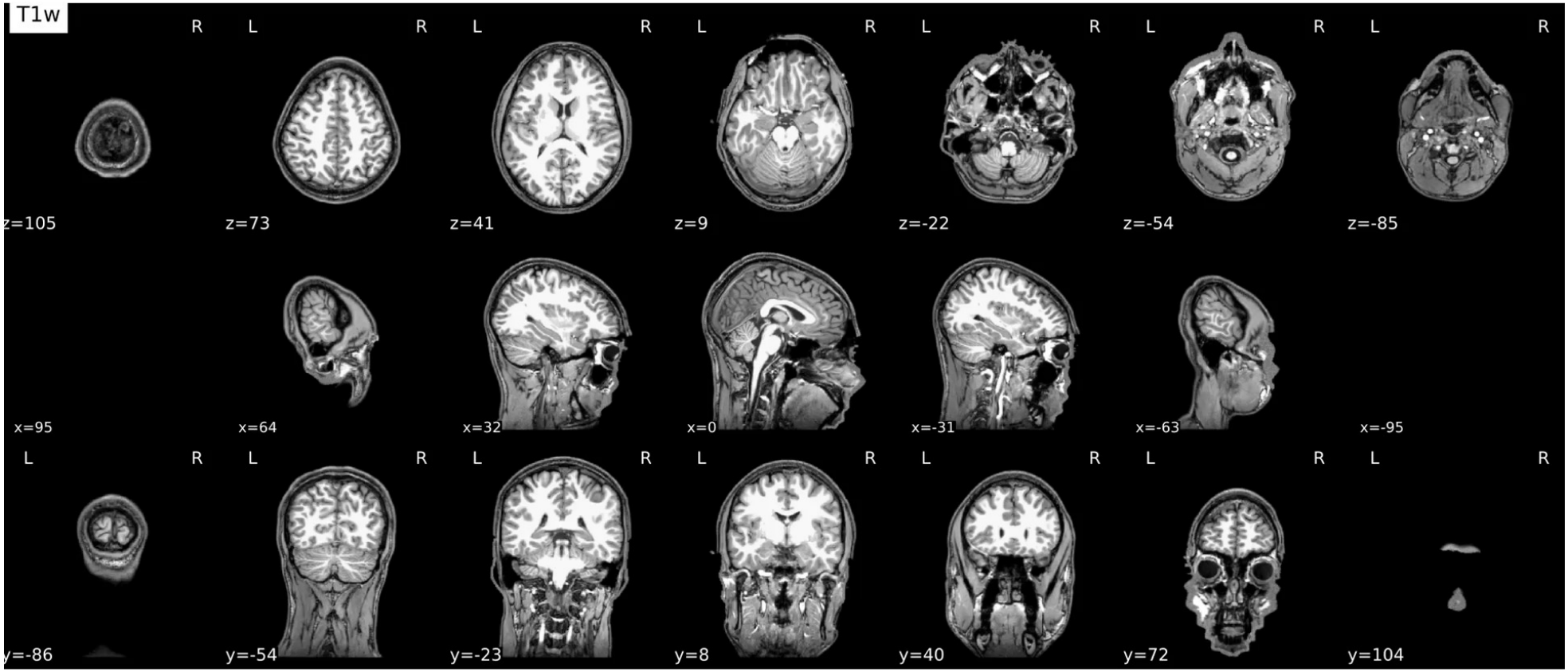


…

Hippocampal subfield segmentation
… can be loaded into PMOD

https://github.com/mnoergaard/petprep_extract_tacs

Co-registration diagnostics



https://github.com/mnoergaard/petprep_extract_tacs

Derivatives data pushed to OpenNeuro

Positron emission tomography (PET) quantification in healthy humans of cyclooxygenase-2 (COX-2), a potential biomarker of neuroinflammation Files: 275 Size: 7.79GB

- CHANGES
- LICENSE
- README
- dataset_description.json
- participants.json
- participants.tsv
- derivatives
  - petprep_extract_tacs
    - sub-01
      - ses-01
        - sub-01_ses-01_desc-gtmseg_dseg.nii.gz
        - sub-01_ses-01_desc-gtmseg_dseg.tsv
        - sub-01_ses-01_desc-gtmseg_morph.tsv
        - sub-01_ses-01_desc-gtmseg_tacs.tsv
        - sub-01_ses-01_desc-hippocampusAmygdala_dseg.nii.gz
        - sub-01_ses-01_desc-hippocampusAmygdala_dseg.tsv
        - sub-01_ses-01_desc-hippocampusAmygdala_morph.tsv
        - sub-01_ses-01_desc-hippocampusAmygdala_tacs.tsv
        - sub-01_ses-01_desc-whiteMatter_dseg.nii.gz
        - sub-01_ses-01_desc-whiteMatter_dseg.tsv
        - sub-01_ses-01_desc-whiteMatter_morph.tsv
        - sub-01_ses-01_desc-whiteMatter_tacs.tsv

N/A

Targets

Scanner Manufacturers
Siemens

Scanner Models
petmct2petmct1PET petmct2

Radionuclides
11CC11

Radiotracers
MC1Mc1

Uploaded by
Martin Nørgaard on 2023-12-04 - 6 months ago

Last Updated
2024-06-10 - 4 days ago

Sessions
4

Participants
27

Dataset DOI
doi:10.18112/openneuro.ds004869.v1.0.1

License
CC0

How To Cite

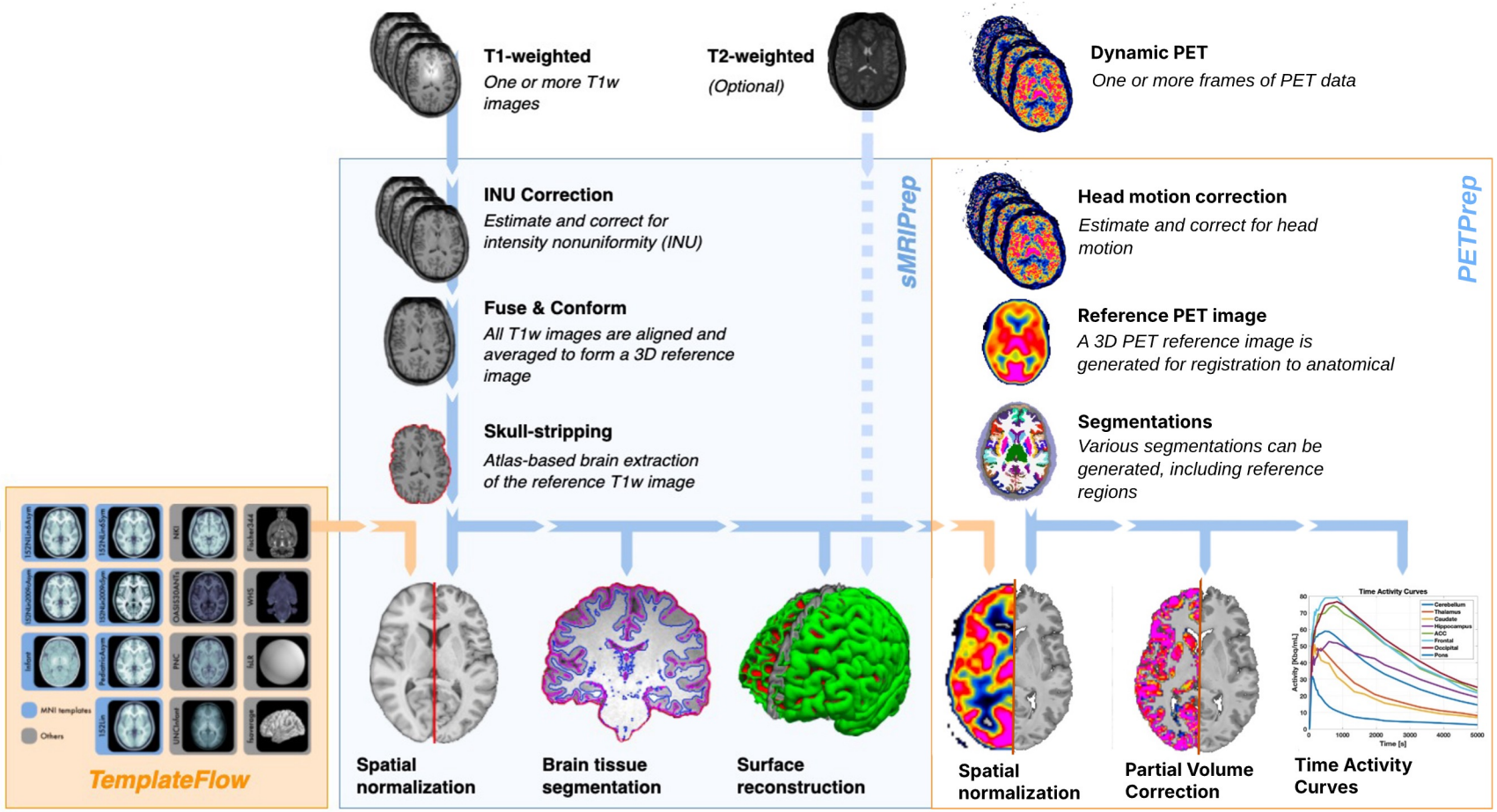
https://openneuro.org/datasets/ds004869/versions/1.0.1

To the demo…

Short link:
https://shorturl.at/9UBOE

BIDS Applications | PETPrep

https://github.com/nipreps/petprep



BIDS Applications | PETPrep

https://github.com/nipreps/petprep

Documentation (https://petprep.readthedocs.io/en/latest/)

petprep

latest

Search docs

- Installation
- Usage Notes
- Processing pipeline details
- Outputs of *PETPrep*
- Performance benchmarks
- Defining standard and nonstandard spaces where data will be resampled

/ *PETPrep*: A Robust Preprocessing Pipeline for PET Data

View page source

PETPrep: A Robust Preprocessing Pipeline for PET Data

PETPrep is a *NiPreps (NeuroImaging PREProcessing toolS)* application (www.nipreps.org) for the preprocessing of positron emission tomography (PET) imaging.

Stable tests passing | docs passing | EOSS

About

BIDS Applications | PETDeface

v.0.3.0 released on July 17, 2025

petdeface.readthedocs.io/en/latest/

petdeface

latest

Search docs

CONTENTS:

Installation

PETdeface

Usage

MongoDB

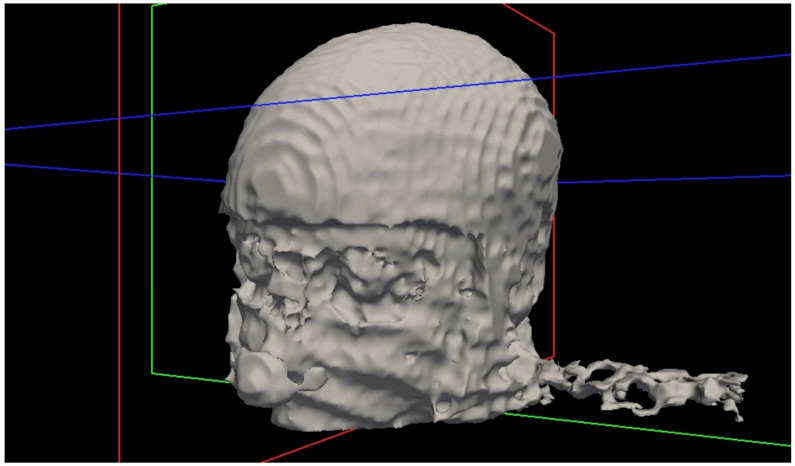
Simplify infrastructure with MongoDB Atlas, the leading developer data platform

Ad by EthicalAds

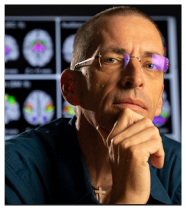
/ Welcome to petdeface's documentation! View page source

Welcome to petdeface's documentation!

petdeface is a nipype implementation of an anatomical MR and PET defacing pipeline for BIDS datasets. This is a working prototype, in active development denoted by the 0.x.x version number.

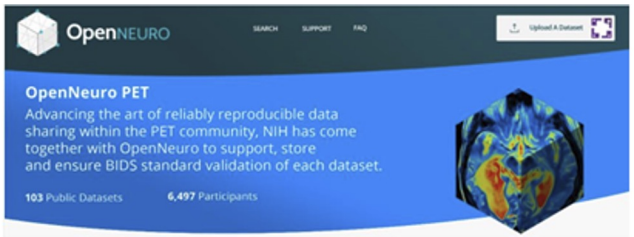


Petdface can be used to deface PET and MR data as well as co-register the two modalities. Use is encouraged and feedback via Github issues or email to openneuropet@gmail.com is more than welcome. As is often the case, this medical research software is constrained to testing on data that its developers have access to.



Georgia State University

Thank you for your attention



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NIH National Institute of Mental Health

Athinoula A. Martinos Center For Biomedical Imaging

Harvard–MIT Health Sciences & Technology

MASSACHUSETTS GENERAL HOSPITAL

Stanford University

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