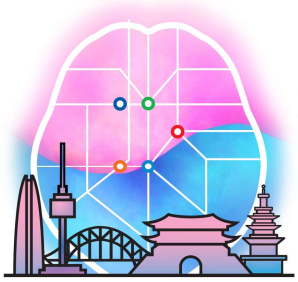

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JUNE 23~27, SEOUL, KOREA

FDG-PET: Data Processing and Analysis Using SPM

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New Jersey Institute of Technology

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I have no disclosures.

Code

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A brief introduction to FDG-PET

Access and checking data

Preprocessing

Data analysis

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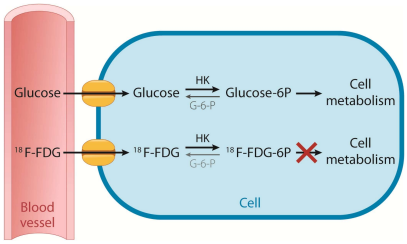
A brief introduction to FDG-PET

- [^{18}F]Fluorodeoxyglucose
- Half life of ^{18}F = 109.8 min
- Cerebral glucose consumptions
  - Neurons
  - Astrocytes



Rahman et al., 2019, in Biomed Pharmacother

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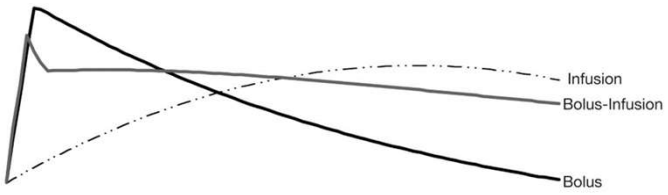
A brief introduction to FDG-PET

- Two aspects of PET imaging data
  - Static
  - Dynamic
- Radiotracer administration
  - Bolus
  - Constant infusion

Hypothesized plasma radioactivity curves



Jamadar et al., 2022, in GigaScience

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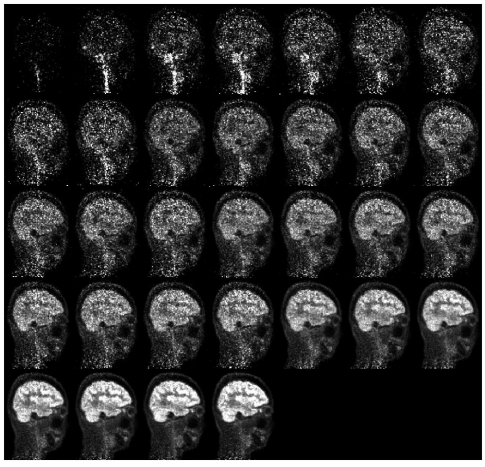
A brief introduction to FDG-PET



Quantifications

- Static image (average)
- Standardized uptake value (SUV)
- Regional cerebral metabolic rate of glucose consumption (rCMRGlc)
- Kinetic modeling

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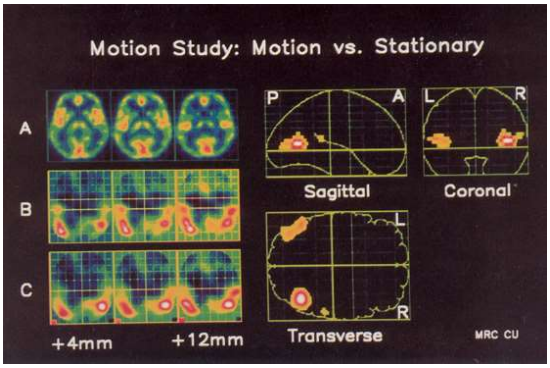
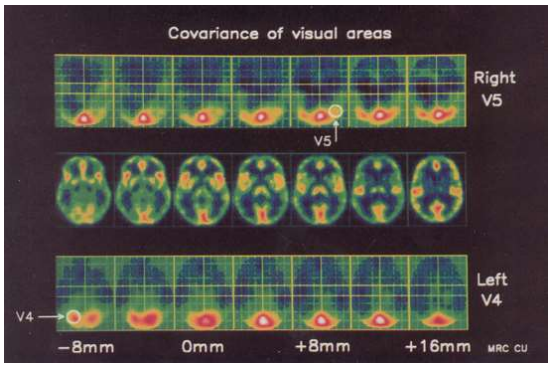
A brief introduction to FDG-PET

Activation analysis



Connectivity (covariance) analysis



Zeki et al., 1991, in J Neurosci.

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Access FDG-PET data

- Alzheimer's Disease Neuroimaging Initiative (ADNI)
- OpenNeuro PET
- Supplementary information By Sala et al., (2023) link

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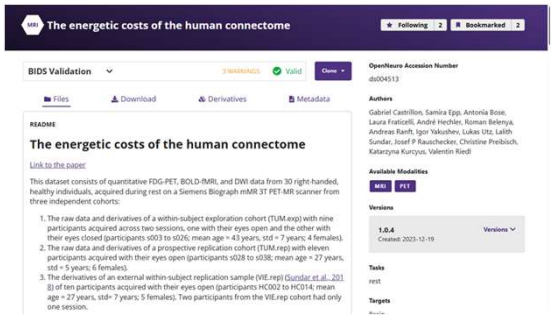
Access FDG-PET data

Demonstration dataset

- The Energetic Costs of the Human Connectome (ds003382)
- Total n = 20
- Eye open vs. eye closed: n = 9
  - FDG-PET
  - T1 MRI
  - fMRI
  - DWI
- 48.8 GB



https://openneuro.org/datasets/ds004513/

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Check data information

- Data integrity
- Number of images
- Frame duration
- Voxel dimension/size
- Brain coverage/origin

File types

- .json file
- .nii or .nii.gz files
- .tsv file

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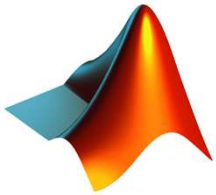

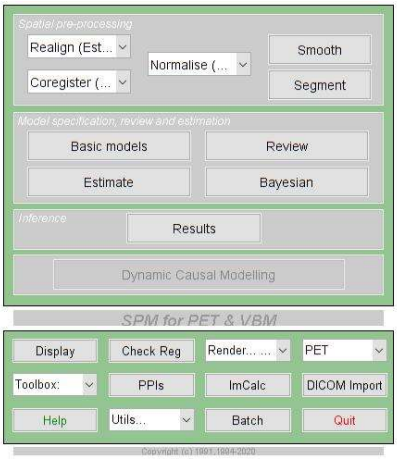

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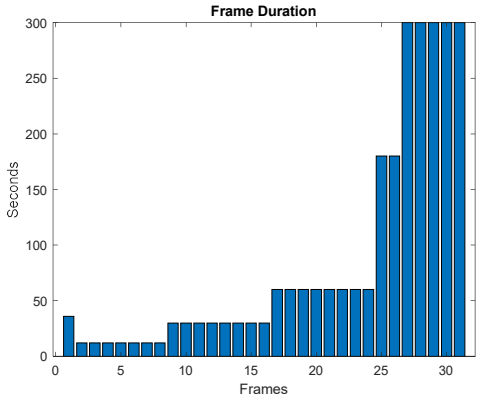
PET information json file

- % Read PET information json file
- fname = 'C:\PET_Munich\Data\sub-s003\ses-open\pet\sub-s003_ses-open_task-rest_pet.json';
- fid = fopen(fname);
- raw = fread(fid,inf);
- str = char(raw');
- fclose(fid);
- val = jsondecode(str);

- % Plot frame duration for each frame
- figure; bar(val.FrameDuration)
- title('Frame Duration')
- xlabel('Frames')
- ylabel('Seconds')



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PET header information

- % Read PET image header information
- METADATA = niftiinfo('C:\PET_Munich\Data\sub-s003\ses-open\pet\sub-s003_ses-open_task-rest_pet.nii.gz');

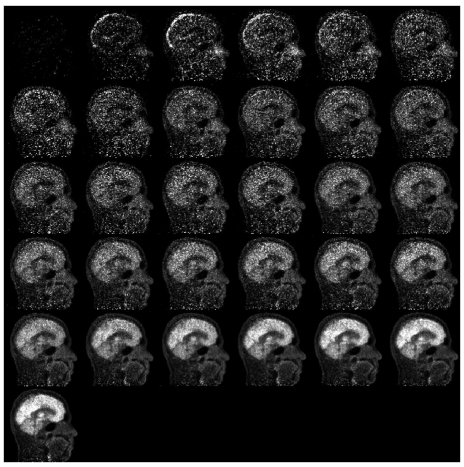
- ImageSize: [256 256 256 31]
- PixelDimensions: [1.0431 1.0431 1.0156 1]

Plot PET images

- % Read PET image
- v = spm_vol('C:\PET_Munich\Data\sub-s003\ses-open\pet\sub-s003_ses-open_task-rest_pet.nii.gz');
- y = spm_read_vols(v);

- % Select the middle sagittal slices for all the frames
- I = squeeze(y(size(y,1)/2,:,:,:));
- % Rotate the matrices for diaplay
- J = imrotate(I,90);

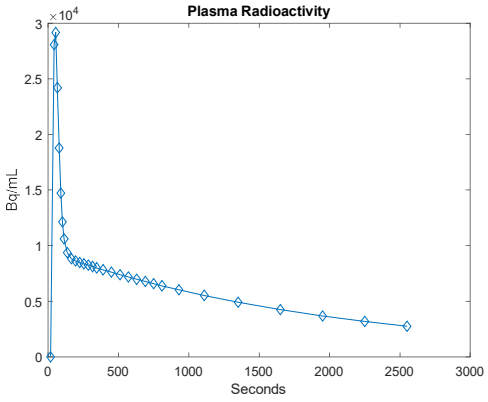
- % Plot all the frames using montage
- figure; montage(J,'DisplayRange',[0 20000])



Blood recording TSV file

- % Read blood sample recording data TSV file
- T_recording = readtable('C:\PET_Munich\Data\sub-s003\ses-open\pet\sub-s003_ses-open_task-rest_recording-autosampler_blood.tsv','FileType','text');

- % Plot plasma radioactivity data
- figure; plot(T_recording.time,T_recording.plasma_radioactivity,'-d');
- title('Plasma Radioactivity')
- xlabel('Seconds')
- ylabel('Bq/mL')



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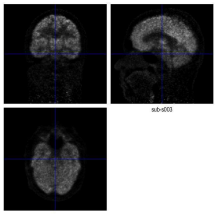
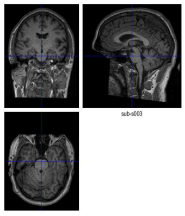
Check image initial position

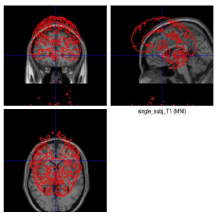
- 'Check Reg' button in SPM
- 'Contour'



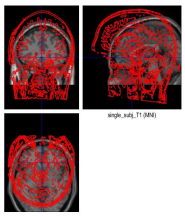
PET



T1 weighted MRI



MNI template



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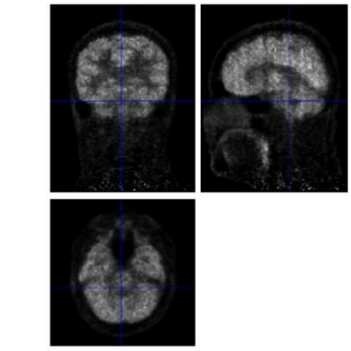
Set origin

- 'Display' button in SPM
- The origin of the image far from the anterior commissure may cause failures in image normalization and coregistration

Automated steps

- Place origin in the center
- Linear transformation



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Preprocessing of FDG-PET images

- Quality control
  - Check imaging parameters across participants
  - Check to make sure each preprocessing step finished successfully
- Motion correction and calculation of a static image
  - Realign
- Spatial normalization to a standard space
  - Segmentation of anatomical MRI image
  - Apply deformation field to normalize the mean PET image
- Spatial smoothing

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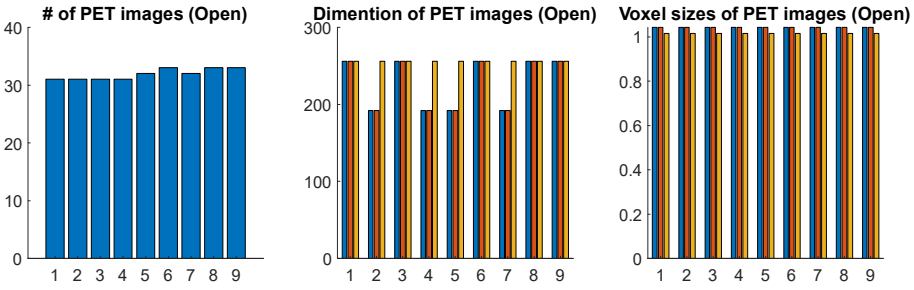
Checking image parameters



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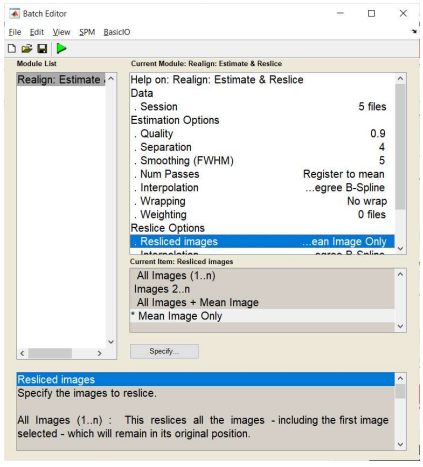
Realign of PET images

- Realign the last five PET images to correct for head motion
- Calculate a mean image



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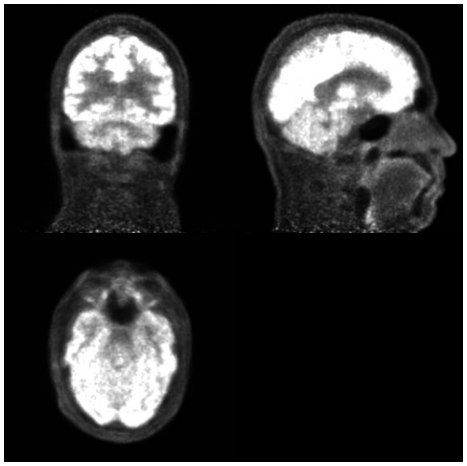
Realign of PET images

- Realign the last five PET images to correct for head motion
- Calculate a mean image



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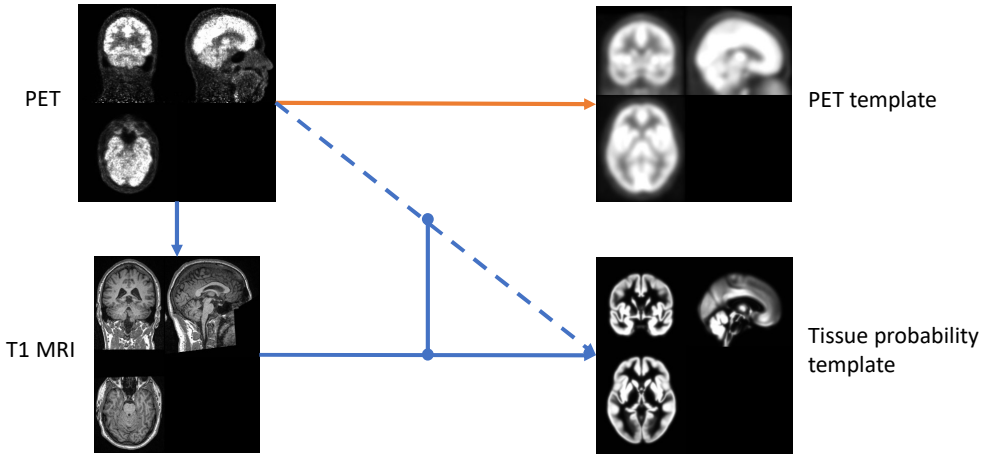
Spatial normalization



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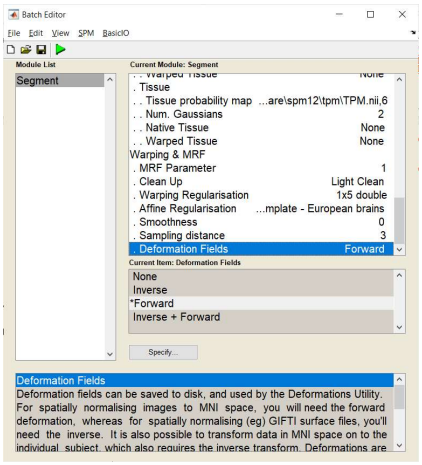
Segmentation of T1 weighted image

- Segment the T1 weighted MRI image into GM, WM, CSF, and so on.
- Obtain a deformation field map that maps native space to MNI space.



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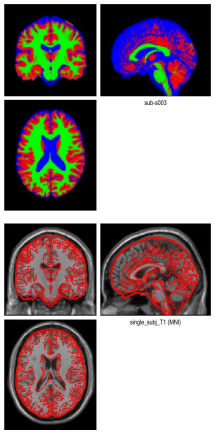
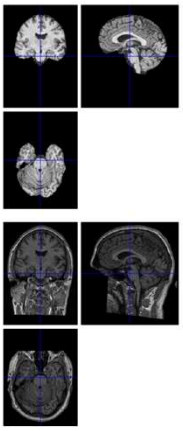


Coregistration of mean PET image to T1 weighted image

- Skull striping
  - Image calculator
  - i1.*((i2+i3+i4)>0.5)
- Setting origin if necessary



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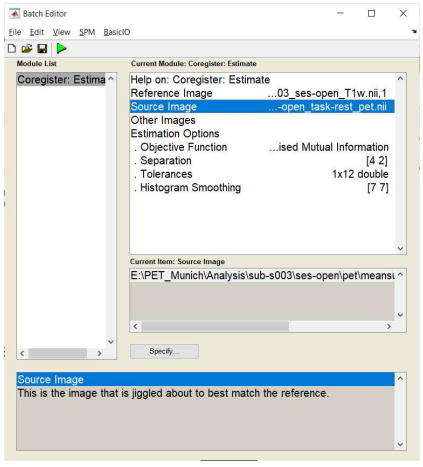
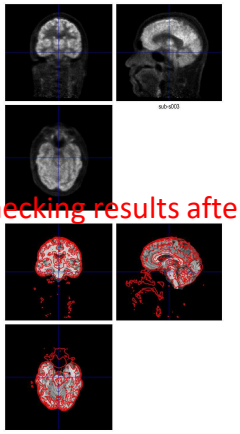
Coregistration of mean PET image to T1 weighted image





Always checking results after this step!

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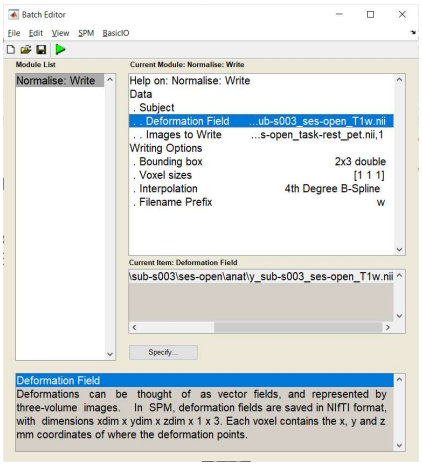
Spatial Normalize

- Apply the deformation field maps to the mean PET data
- Voxel sizes



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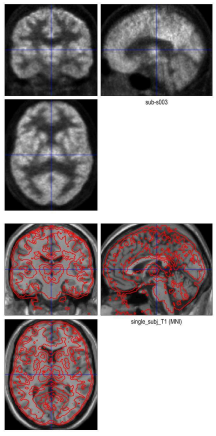
Spatial Normalize

- Apply the deformation field maps to the mean PET data
- Voxel sizes



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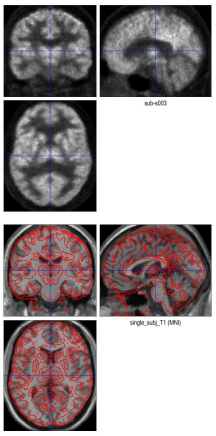
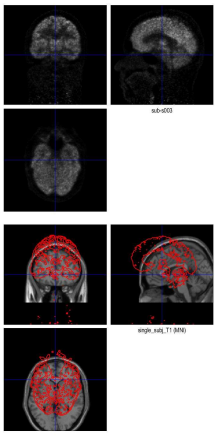
Spatial Normalize

- Apply the deformation field maps to the mean PET data
- Voxel sizes





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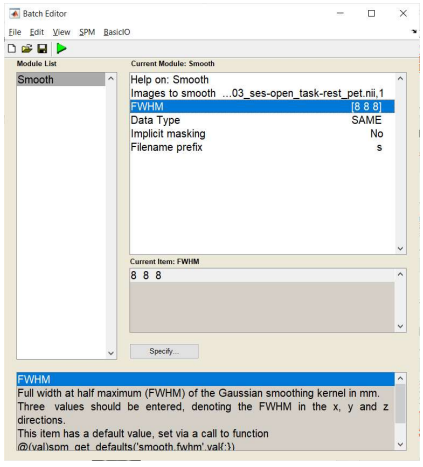
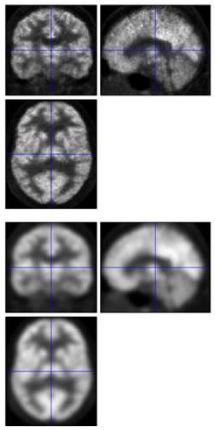
Smoothing





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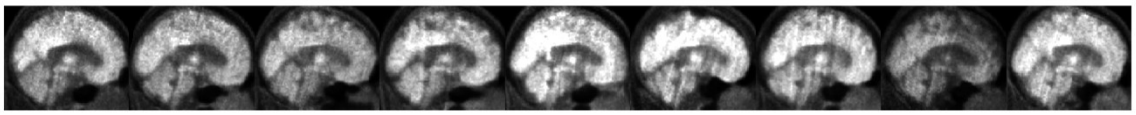
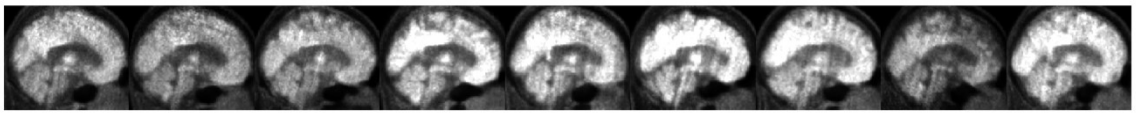
Statistical analysis

Eye open



Eye closed



Participants

- Where in the brain is there higher glucose metabolism when the eyes are open compared to when they are closed?

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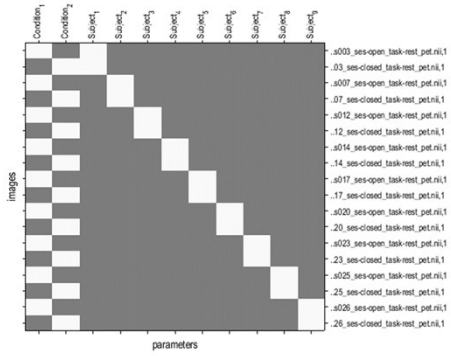
Statistical analysis

- Voxel-wise generalized linear model (GLM)
- Global Normalization
  - Proportional
  - ANCOVA (additive)
- Global Calculation
- Mask



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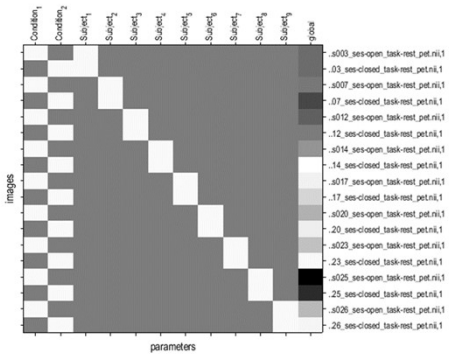
Statistical analysis

- Voxel-wise generalized linear model (GLM)
- Global Normalization
  - Proportional
  - ANCOVA (additive)
- Global Calculation
- Mask

ANCOVA model



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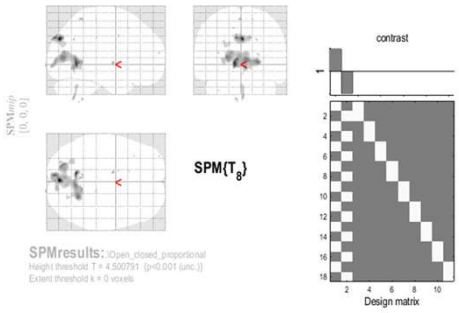
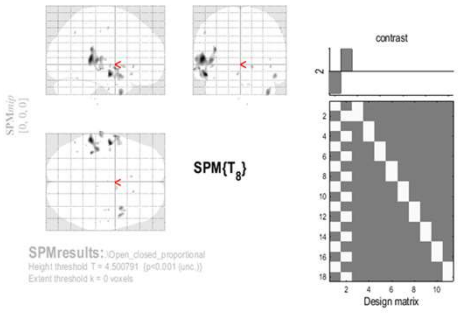
Statistical analysis

open - closed



closed - open



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Acknowledgements

- Lab members
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  - Pratik Jain
  - Le Gao
- Open access datasets
  Castrillon et al. (2023)

  OpenNEURO
- Funding

  NIH

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