1. Preprocessing MEG Python

Jupyter notebook with the **entire preprocessing and source reconstruction pipeline** for the SDMT dataset using the OSL Python library from the Oxford Centre for Human Brain Activity (OHBA) Ananalysis Group.

Reference: Quinn, A. J., van Es, M. W., Gohil, C., & Woolrich, M. W. (2023). OHBA Software Library in Python (OSL) (Version 0.2.0) [Computer software]. https://doi.org/10.5281/zenodo.6875060

Required input files/folders to run this Notebook:

- **raw_dataset_dir**: folder containing all raw. fif files for the SDMT data
- **T1_niifiles**: folder containing all the subjects' MRI scans (.nii files)
- **T1_MNI_niifiles**: folder containing all the subjects' already co-registered MRI scans in MATLAB (.nii.gz files)
- **parcellation file**: "fmri_d100_parcellation_with_PCC_reduced_2mm_ss5mm_ds8mm.nii.gz" **with 38 parcels** needs to be 4D (3 dimensions for spatial coordinates and 1 for each parcel) with sform_code = 1
- **Parcels_38_names.txt (extra)**: .txt file with the names of the 38 parcels of the parcellation file

Install necessary packages

In [1]:
```
#!pip install mne
#!pip install fieldtrip2mne
#!pip install fslpy
#!pip install osl                  #(from https://github.com/OHBA-analysis/os
#!pip install numpy --upgrade
#!pip install pymatreader
#!pip install trame
#!pip install ipywidgets
#!pip install numpy==1.22.4
#!pip install pandas~=1.3.5
#!pip install numba~=0.53.1
```

Import needed packages

In [8]:
```
import os
import glob
import mne
import numpy
import shutil
import osl
# opencv_python should be in same directory as the Jupyterlab Notebook
import opencv_python     # opencv_python is a manually edited package (conta
                         # stackoverflow.com/questions/68916893/typeerror-nu
                         # https://github.com/opencv/opencv/issues/23822
                         # should be fixed in release 4.9.x of opencv-pythor
```

Load in dataset - raw .fif files for all patients

In [4]:
```
raw_dataset_dir = "/home/data/vub_ms/MEGDATA_ANA/SDMT/DATA/"

all_fif_files = sorted(glob.glob(raw_dataset_dir + '*.fif'))
print(len(all_fif_files))
```

```
139
```

Remove subjects that should be excluded

In [5]:
```
# The subjects excluded in the preprocessing phase relate to prior findings
# - issues with MRI scan
# - issues in the headmodelling step
# - missing DIODE channel (in the event extraction)
subject_IDs_to_exclude = ['2304', '2180', '2202', '2357', '2371', '1035', '0
                          '1063', '2174',
                          '2412', '2413', '2233', '2234']
file_IDs = []
for filename in all_fif_files:
    file_IDs.append(filename[-21:-17])  #gets the 'code' Number per patient

# Function to quickly find matching elements between 2 lists
def find_matching_index(list1, list2):

    inverse_index = { element: index for index, element in enumerate(list1)

    return [index
        for index,element in enumerate(list2) if element in inverse_index]

# Use the function to find which subject IDs have to be removed from the tot
indices_to_remove = find_matching_index(subject_IDs_to_exclude,file_IDs)
print(indices_to_remove)
```

```
[2, 29, 55, 57, 63, 75, 76, 94, 112, 116, 121, 128, 129]
```

In [9]:
```
#Retained .fif files (filepaths)
fif_files = [ele for idx, ele in enumerate(all_fif_files) if idx not in indi

#Retained indices (subject ID
file_IDs_retained = [ele for idx, ele in enumerate(file_IDs) if idx not in i

print(len(fif_files))
```

```
126
```

In [10]:
```
# Quick example to see if a single .fif file can be loaded
parceled_data = mne.io.read_raw_fif(fif_files[0], preload=True)
```

```
Opening raw data file /home/data/vub_ms/MEGDATA_ANA/SDMT/DATA/meg_0922_SD
MT_tsss_mc.fif...
    Range : 56000 ... 1037999 =     56.000 ...  1037.999 secs
Ready.
Reading 0 ... 981999  =      0.000 ...   981.999 secs...
```

```
/tmp/ipykernel_2716435/3664972164.py:2: RuntimeWarning: This filename (/hom
e/data/vub_ms/MEGDATA_ANA/SDMT/DATA/meg_0922_SDMT_tsss_mc.fif) does not con
form to MNE naming conventions. All raw files should end with raw.fif, raw_
sss.fif, raw_tsss.fif, _meg.fif, _eeg.fif, _ieeg.fif, raw.fif.gz, raw_sss.f
if.gz, raw_tsss.fif.gz, _meg.fif.gz, _eeg.fif.gz or _ieeg.fif.gz
  parceled_data = mne.io.read_raw_fif(fif_files[0], preload=True)
```

Add MRI info/files

In [12]:
```
DIR_MRI_FILES = "/home/data/vub_ms/MEGNII/"
T1_niifiles = sorted(glob.glob(DIR_MRI_FILES + 'MEG_*_MRI_T1.nii'))
T1_MNI_niifiles = sorted(glob.glob(DIR_MRI_FILES + 'MEG_*_MRI_T1_MNI.nii.gz'

# We only retain subjects with existing T1_MNI.nii file:
file_IDs_MRI = []
for filename in T1_MNI_niifiles:
    file_IDs_MRI.append(filename[-22:-18])   # gets the 'code' from the .nii

# Match between the patients we want to keep (for preprocessing), and valid
indices_to_keep = find_matching_index(file_IDs_retained, file_IDs_MRI)

# Retained T1.nii files
T1_niifiles = [ele for idx, ele in enumerate(T1_niifiles) if idx in indices_

# Retained T1_MNI.nii.gz files
T1_MNI_niifiles = [ele for idx, ele in enumerate(T1_MNI_niifiles) if idx in

print(len(T1_niifiles), f'amount of T1.nii files for {len(fif_files)} patien
print(len(T1_MNI_niifiles), f'amount of T1_MNI.nii files for {len(fif_files)
```

```
126 amount of T1.nii files for 126 patients
126 amount of T1_MNI.nii files for 126 patients
```

Processing Pipeline - 1 subject

First, the Python package and all processing steps are tested for 1 single subject. This allows to learn how the package works, how each input needs to specified, and how to solve certain bugs/errors.

Step 1: Preprocessing

Preprocessing WITH removal of bad segments and channels

In [3]:
```
from osl import preprocessing, utils

# Directory in which we save the preprocessed data
PREPROC_DIR = "/home/olivierb/processed_data"

## Order of preprocessing steps actually matters in the list of dictionaries

# Settings
config = """
    preproc:
    - resample: {sfreq: 250}

    - filter: {l_freq: 0.01, h_freq: 70, method: iir, iir_params: {order: 5,
    - notch_filter: {freqs: 50, notch_widths: 2}

    - bad_segments: {segment_len: 500, picks: mag, significance_level: 0.1}
    - bad_segments: {segment_len: 500, picks: grad, significance_level: 0.1}
    - bad_segments: {segment_len: 500, picks: mag, mode: diff, significance_
    - bad_segments: {segment_len: 500, picks: grad, mode: diff, significance
    - bad_channels: {picks: mag, significance_level: 0.1}
    - bad_channels: {picks: grad, significance_level: 0.1}
    - ica_raw: {picks: meg, n_components: 64}
    - ica_autoreject: {apply: true}

    - interpolate_bads: {}
"""

# Main preprocessing
preprocessing.run_proc_batch(
    config,
    fif_files[0],
    outdir=PREPROC_DIR,
    overwrite=True,
)
```

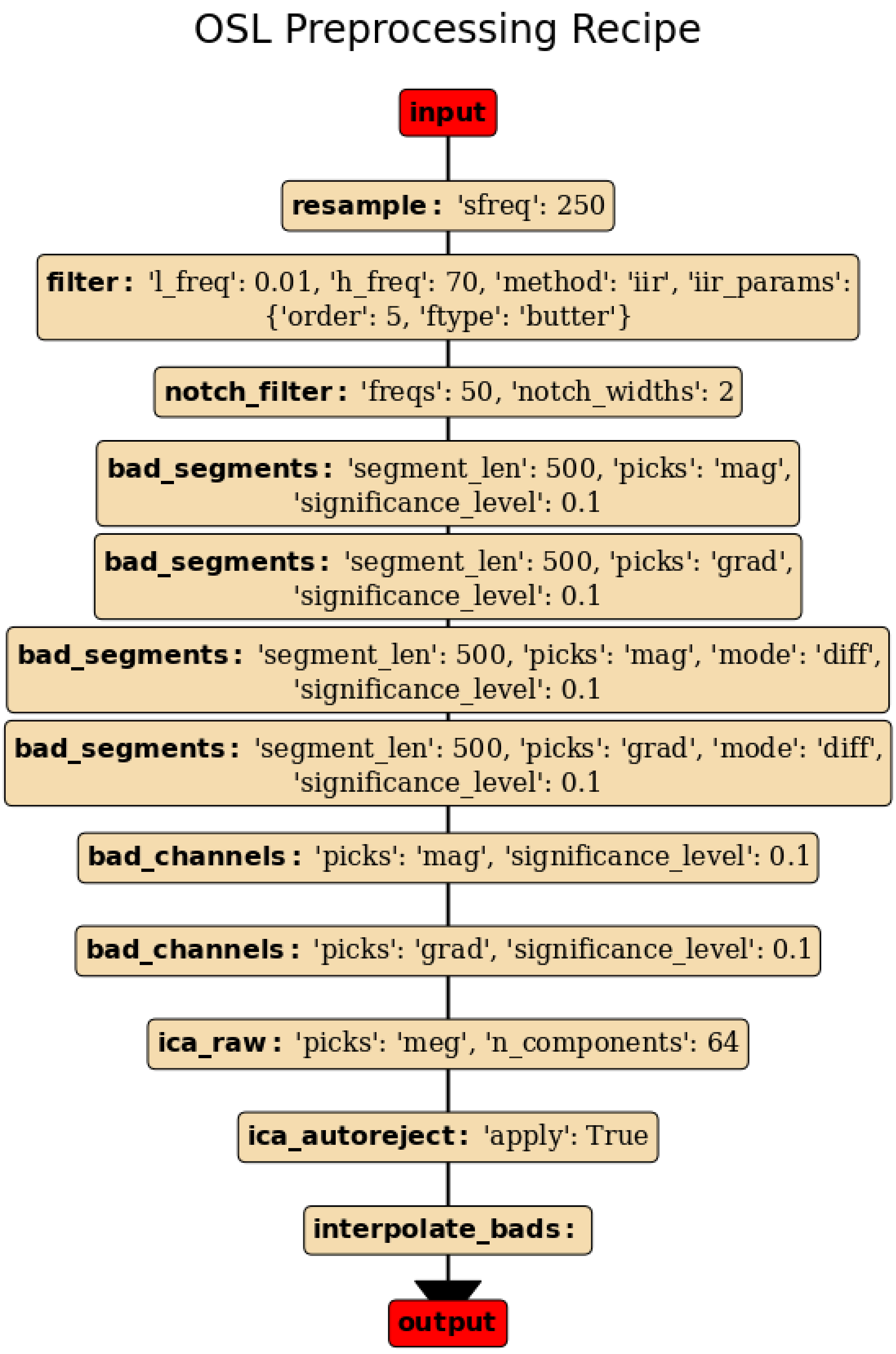
In [4]:

```
osl.preprocessing.plot_preproc_flowchart(config)
```

```
/home/olivierb/osl/preprocessing/batch.py:566: UserWarning: FigureCanvasA
gg is non-interactive, and thus cannot shown
  fig.show()
```

Out[4]:

```
(<Figure size 576x864 with 1 Axes>,
 <Axes: title={'center': 'OSL Preprocessing Recipe'}>)
```


OSL Preprocessing Recipe
input
resample : 'sfreq': 250
filter : 'l_freq': 0.01, 'h_freq': 70, 'method': 'iir', 'iir_params': {'order': 5, 'ftype': 'butter'}
notch_filter : 'freqs': 50, 'notch_widths': 2
bad_segments : 'segment_len': 500, 'picks': 'mag', 'significance_level': 0.1
bad_segments : 'segment_len': 500, 'picks': 'grad', 'significance_level': 0.1
bad_segments : 'segment_len': 500, 'picks': 'mag', 'mode': 'diff', 'significance_level': 0.1
bad_segments : 'segment_len': 500, 'picks': 'grad', 'mode': 'diff', 'significance_level': 0.1
bad_channels : 'picks': 'mag', 'significance_level': 0.1
bad_channels : 'picks': 'grad', 'significance_level': 0.1
ica_raw : 'picks': 'meg', 'n_components': 64
ica_autoreject : 'apply': True
interpolate_bads :
output

Step 2: Coregistration

In [5]:
```
#From: https://github.com/OHBA-analysis/osl/blob/main/examples/mrc_meguk/can

from osl import source_recon, utils

# Settings
config = """
    source_recon:
    - extract_fiducials_from_fif: {}     # ok
    - compute_surfaces:
        include_nose: False

    - coregister:
        use_nose: False
        use_headshape: True
        n_init: 50
"""


# Directories

subject = "/home/olivierb/test/meg_0925_SDMT_tsss_mc/meg_0925_SDMT_tsss_mc_p

# Directory in which we will save the coregistered data
COREG_DIR = "/home/olivierb/coreg"

# Directory to the FSL library, same as the one used in MATLAB, supported by
FSL_DIR = "/usr/lib/fsl/6.0"


# Run coregistration

source_recon.setup_fsl(FSL_DIR)
source_recon.run_src_batch(
    config,
    src_dir=COREG_DIR,
    subjects=['meg_0925_SDMT_tsss_mc_preproc_raw.fif'],   # name of the subj
    preproc_files=[subject],                              # path to preproce
    smri_files=[T1_MNI_niifiles[0]],                      # path to .nii fi
    )
```

Step 3: Source reconstruction (Forward Modelling/Beamforming/Parcellation/Orthogonalisation)

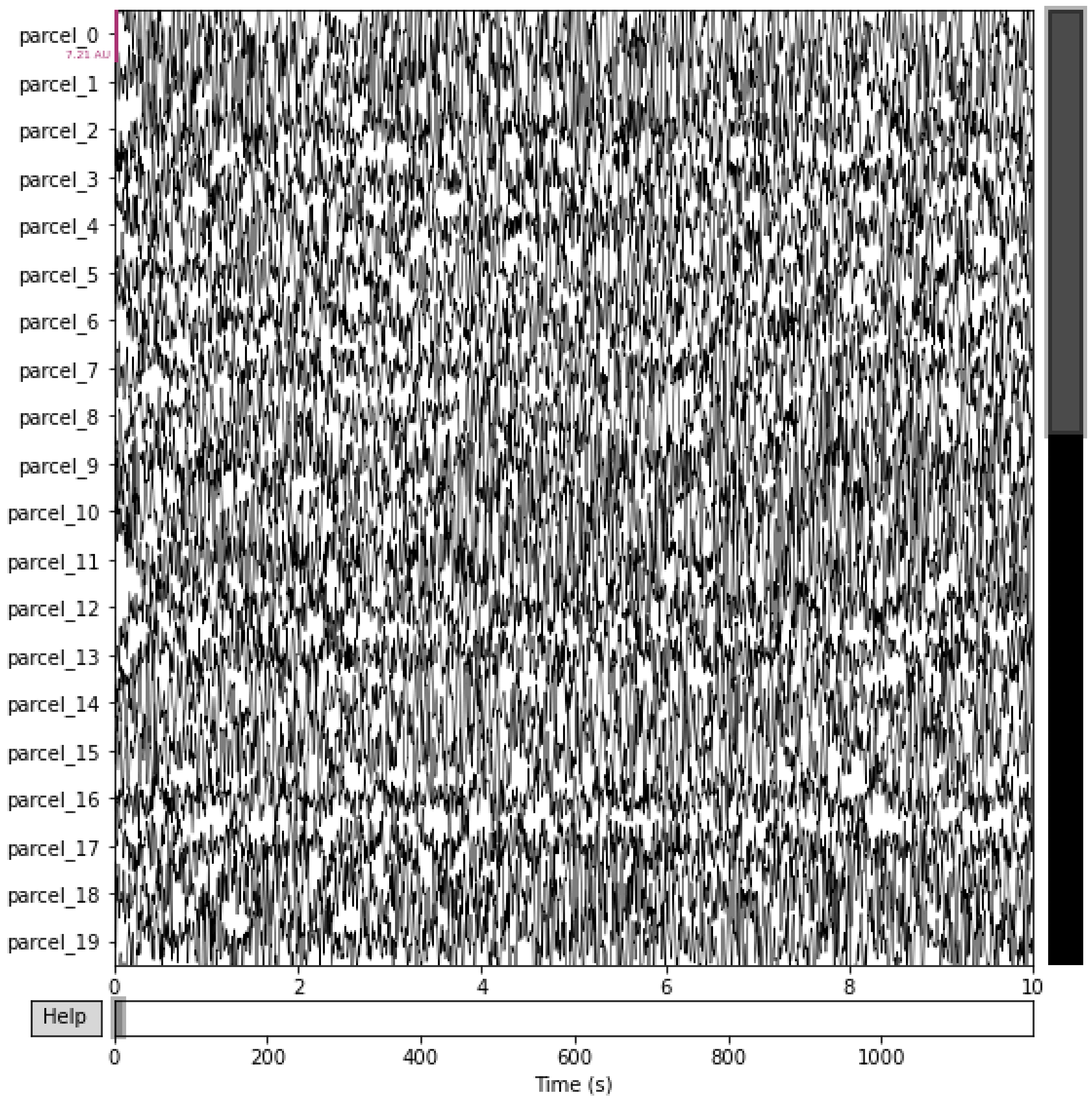
In [ ]:

```
from osl import source_recon
# '/home/olivierb/38_parcels.nii' => 38 parcels / sform_code=1

# Settings
config = """
    source_recon:
    - forward_model:
        model: Single Layer                      # ok: Single Shell in MA
    - beamform_and_parcellate:
        freq_range: [1, 80]
        chantypes: [mag, grad]                   # standard for MEG
        rank: {meg: 60}
        parcellation_file: '/home/olivierb/38_parcels.nii'
        method: spatial_basis                    # ok => spatial_basis or
        orthogonalisation: symmetric             # ok
"""

# Run beamforming and parcellation
FSL_DIR = "/usr/lib/fsl/6.0"
COREG_DIR = "/home/olivierb/coreg"
SUBJECT = subject = "/home/olivierb/processed_data/meg_0925_SDMT_tsss_mc/meg

source_recon.setup_fsl(FSL_DIR)
source_recon.run_src_batch(
    config,
    src_dir=COREG_DIR,                                     # path to all the
    subjects=['meg_0925_SDMT_tsss_mc_preproc_raw.fif'],    # name of the sub
    preproc_files=[subject]                             # path to preproc
)
```

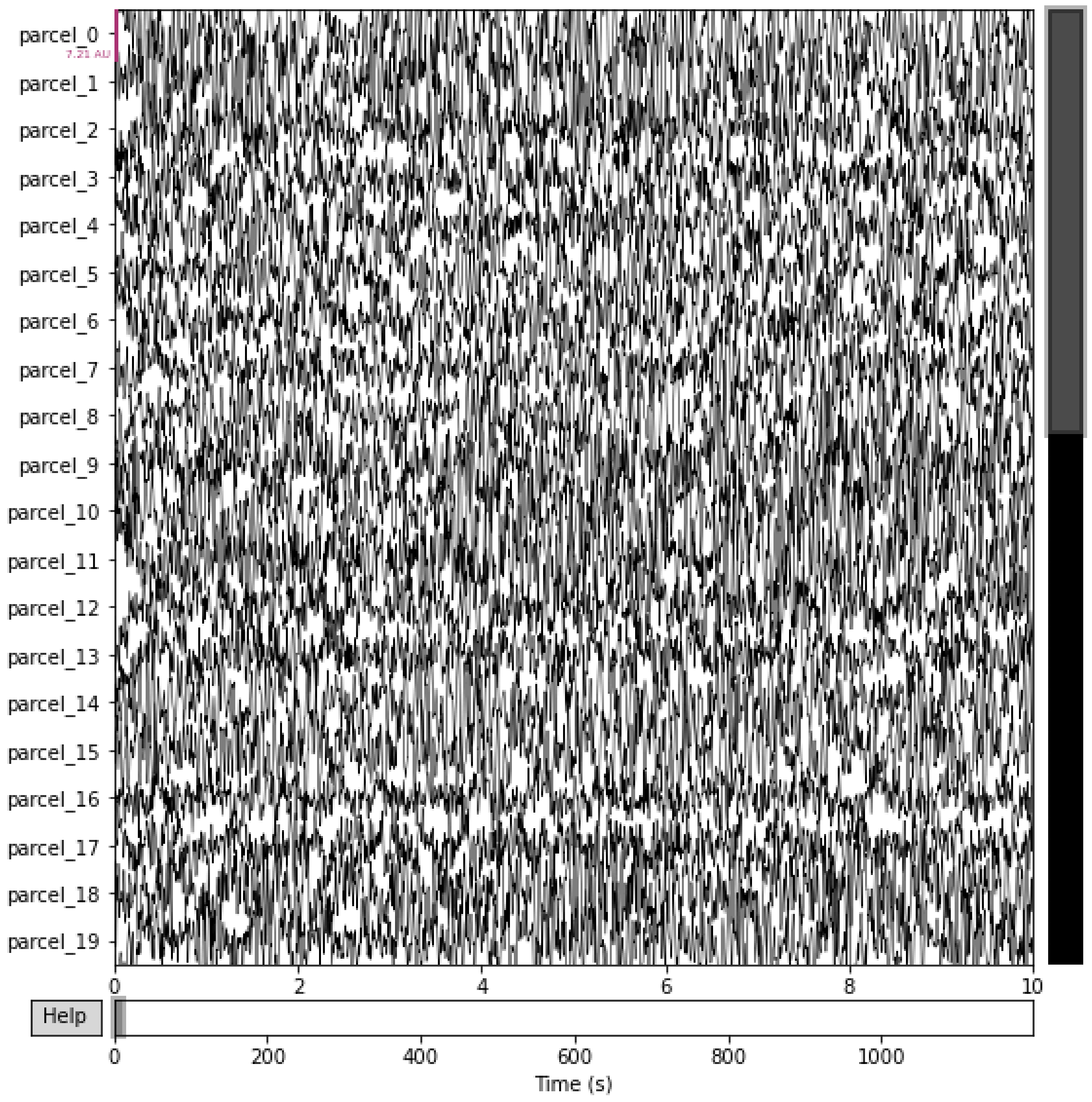
Plot result of one of parcelated file

In [47]:
```
raw = mne.io.read_raw_fif("/home/olivierb/coreg/meg_0925_SDMT_tsss_mc_prepro
```

In [48]:
```
raw.plot()
```



Out[48]:



Processing Pipeline - different subject groups in Parallel processing

Here the entire pipeline is ran for a larger amount of subjects at once. The goal is to process all subject files. I avoid processing all subjects in a single run, in case that an unexpected error occurs.

Several CPU cores can be allocated at the same time to perform the processing of several subjects in parallel (faster).

Select subject group to perform analysis on:

In [15]:

```
from dask.distributed import Client

## To check for correct .fif/.nii pairs
#for i in range(len(fif_files)):
    #print(i, fif_files[i][-21:-17], T1_MNI_niifiles[i][-22:-18])

## 1. index 0-59
#idx_start = 18
#idx_end = 60
#input_fif_files = fif_files[idx_start:idx_end]
```

```
## 2. index 60-115
#idx_start = 60
#idx_end = len(fif_files)
#input_fif_files = fif_files[idx_start:idx_end]

## 3. index 90-115
idx_start = 90
idx_end = len(fif_files)
input_fif_files = fif_files[idx_start:idx_end]
```

Step 1: Preprocessing

In [ ]:
```
from osl import preprocessing, utils

# Directory in which we save the preprocessed data
PREPROC_DIR = "/home/olivierb/processed_data"
inputs = input_fif_files

## Order of preprocessing steps actually matters in the list of dictionaries

# Settings
config = """
    preproc:
    - resample: {sfreq: 250}

    - filter: {l_freq: 0.01, h_freq: 70, method: iir, iir_params: {order: 5,
    - notch_filter: {freqs: 50, notch_widths: 2}

    - bad_segments: {segment_len: 500, picks: mag, significance_level: 0.1}
    - bad_segments: {segment_len: 500, picks: grad, significance_level: 0.1}
    - bad_segments: {segment_len: 500, picks: mag, mode: diff, significance_
    - bad_segments: {segment_len: 500, picks: grad, mode: diff, significance
    - bad_channels: {picks: mag, significance_level: 0.1}
    - bad_channels: {picks: grad, significance_level: 0.1}

    - ica_raw: {picks: meg, n_components: 64}
    - ica_autoreject: {apply: true}

    - interpolate_bads: {}
"""
# Setup parallel processing
client = Client(n_workers=4, threads_per_worker=1)

# Main preprocessing
preprocessing.run_proc_batch(
    config,
    inputs,
    outdir=PREPROC_DIR,
    overwrite=True,
    dask_client = True
)
```

In [18]:
```
# Prepare subjects and subject names for the remaining steps in the pipeline

# Get the group of preprocessed files
DIR_processed = "/home/olivierb/processed_data/"
all_processed = sorted(glob.glob(DIR_processed + 'meg_*_SDMT_tsss_mc/'))

#get the actual fif files for the current group of subjects
group_processed_fif = []
for i in range(idx_end - idx_start):
    group_processed_fif.append(sorted(glob.glob(all_processed[idx_start + i]

# Get the names of the subjects of each preprocessed file (the last of part
group_processed_names = []
for i in range(idx_end - idx_start):
    group_processed_names.append(os.path.basename(group_processed_fif[i]))

# Get the group of T1_MNI.nii files
group_smri = T1_MNI_niifiles[idx_start:idx_end]
print(len(group_smri))
```

```
126
```

Step 2: Coregistration

In [ ]:
```
from osl import source_recon, utils
import numpy as np

# Settings
config = """
    source_recon:
    - extract_fiducials_from_fif: {}     # ok
    - fix_headshape_points: {}           # ok
    - compute_surfaces:
        include_nose: False

    - coregister:
        use_nose: False
        use_headshape: True
        n_init: 50
"""

# Directories

# Directory in which we will save the coregistered data
COREG_DIR = "/home/olivierb/coreg"
# Directory to the FSL library, same as the one used in MATLAB, supported by
FSL_DIR = "/usr/lib/fsl/6.0"

# Setup parallel processing
client = Client(n_workers=4, threads_per_worker=1)

# Run coregistration
source_recon.setup_fsl(FSL_DIR)
source_recon.run_src_batch(
    config,
    src_dir=COREG_DIR,
    subjects=group_processed_names,                # name of the subject (pr
    preproc_files=group_processed_fif,             # path to preprocessed fi
    smri_files=group_smri,                         # path to .nii file of th
    dask_client=True
    )
```

Step 3: Source reconstruction (Forward Modelling/Beamforming/Parcellation/Orthogonalisation)

In [ ]:
```
from osl import source_recon
#'/home/olivierb/38_parcels.nii' => 38 parcels / sform_code=1

# Settings
config = """
```

```
    source_recon:
    - forward_model:
        model: Single Layer                                      # ok: Single
    - beamform_and_parcellate:
        freq_range: [1, 80]
        chantypes: [mag, grad]                                   # standard f
        rank: {meg: 60}
        parcellation_file: '/home/olivierb/38_parcels.nii'
        method: spatial_basis                                    # ok => spat
        orthogonalisation: None                                  # ok (if you
"""

# Run beamforming and parcellation
FSL_DIR = "/usr/lib/fsl/6.0"
COREG_DIR = "/home/olivierb/coreg"

# Setup parallel processing
client = Client(n_workers=4, threads_per_worker=1)

## !!!!!!!!!!!!! Parallel processing fails for source reconstruction for som

source_recon.setup_fsl(FSL_DIR)
source_recon.run_src_batch(
    config,
    src_dir=COREG_DIR,                                       # path to all the
    subjects=group_processed_names,                          # name of the sub
    preproc_files=group_processed_fif,                       # path to preproc
    #dask_client=True
)
```

Before we can do the Sign-Flipping (Step 4):

1 subject (ID 0995) is missing ECG/EOG channels, the automated ICA artifact rejection can not be executed

For the single subject that did not have EOG/ECG channels

In [ ]:
```
from osl import preprocessing, utils

# Directory in which we save the preprocessed data
PREPROC_DIR = "/home/olivierb/processed_data"

## Order of preprocessing steps actually matters in the list of dictionaries

# Settings
config = """
    preproc:
    - resample: {sfreq: 250}

    - filter: {l_freq: 0.01, h_freq: 70, method: iir, iir_params: {order: 5,
    - notch_filter: {freqs: 50, notch_widths: 2}

    - bad_segments: {segment_len: 500, picks: mag, significance_level: 0.1}
    - bad_segments: {segment_len: 500, picks: grad, significance_level: 0.1}
    - bad_segments: {segment_len: 500, picks: mag, mode: diff, significance_
    - bad_segments: {segment_len: 500, picks: grad, mode: diff, significance
    - bad_channels: {picks: mag, significance_level: 0.1}
    - bad_channels: {picks: grad, significance_level: 0.1}

    - interpolate_bads: {}
    # NO ICA FOR SUBJECT 0995 => NO EOG CHANNELS FOUND
    #- ica_raw: {picks: meg, n_components: 64}
    #- ica_autoreject: {apply: true}

"""

# Main preprocessing
preprocessing.run_proc_batch(
    config,
    fif_files[7],
    outdir=PREPROC_DIR,
    overwrite=True,
)
```

Manual ICA - subject 0995

be careful! ICA should be performed on the .fif file after filtering/referencing etc. (Don't accidentally select the file with the already applied manual ICA on it)

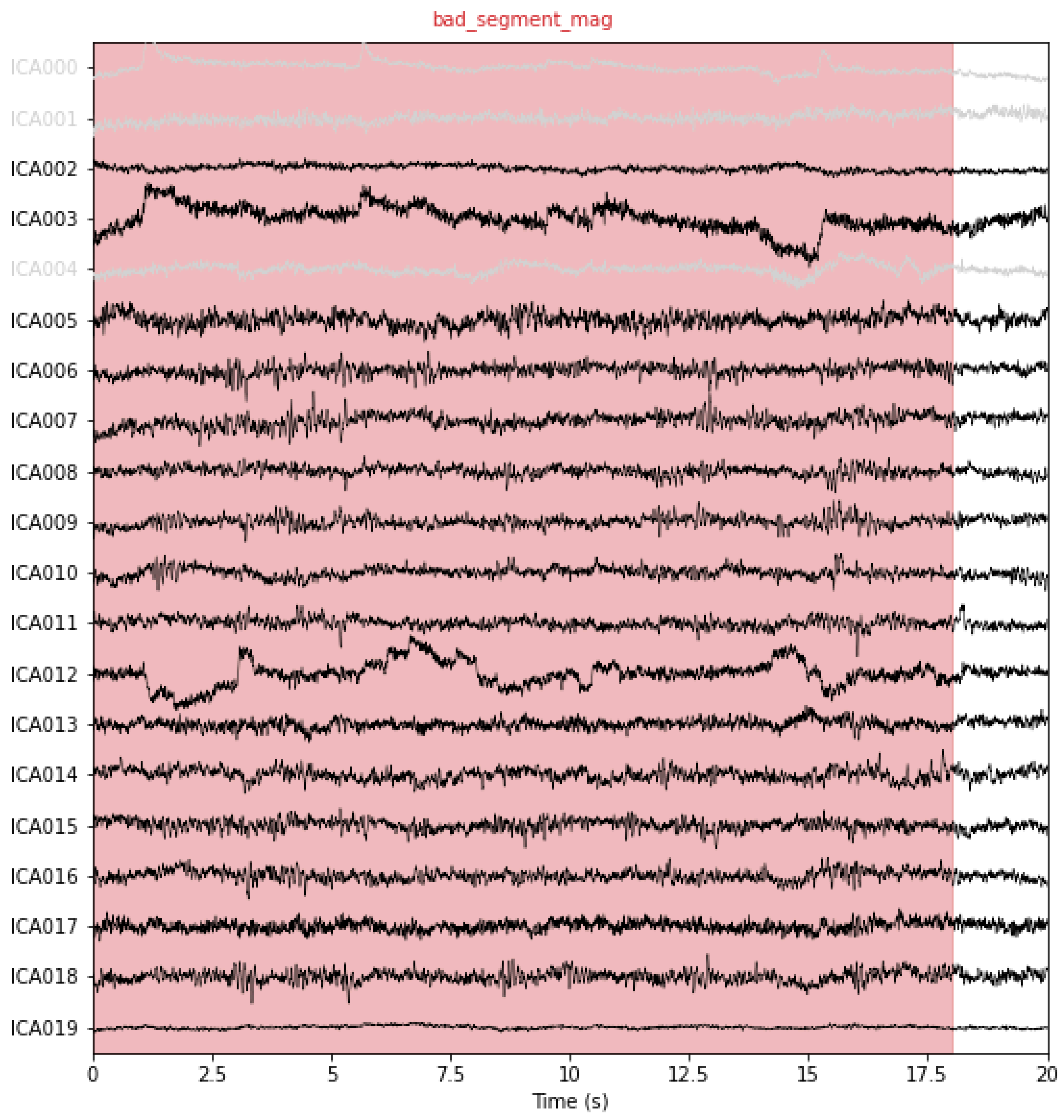
In [9]:
```
# Load the sinlge subject
raw = mne.io.read_raw_fif('/home/olivierb/processed_data/meg_0995_SDMT_tsss_
```

In [10]:
```
ica = mne.preprocessing.ICA(n_components=64, random_state = 0)
raw_ica = raw.copy()
ica.fit(raw_ica)
```

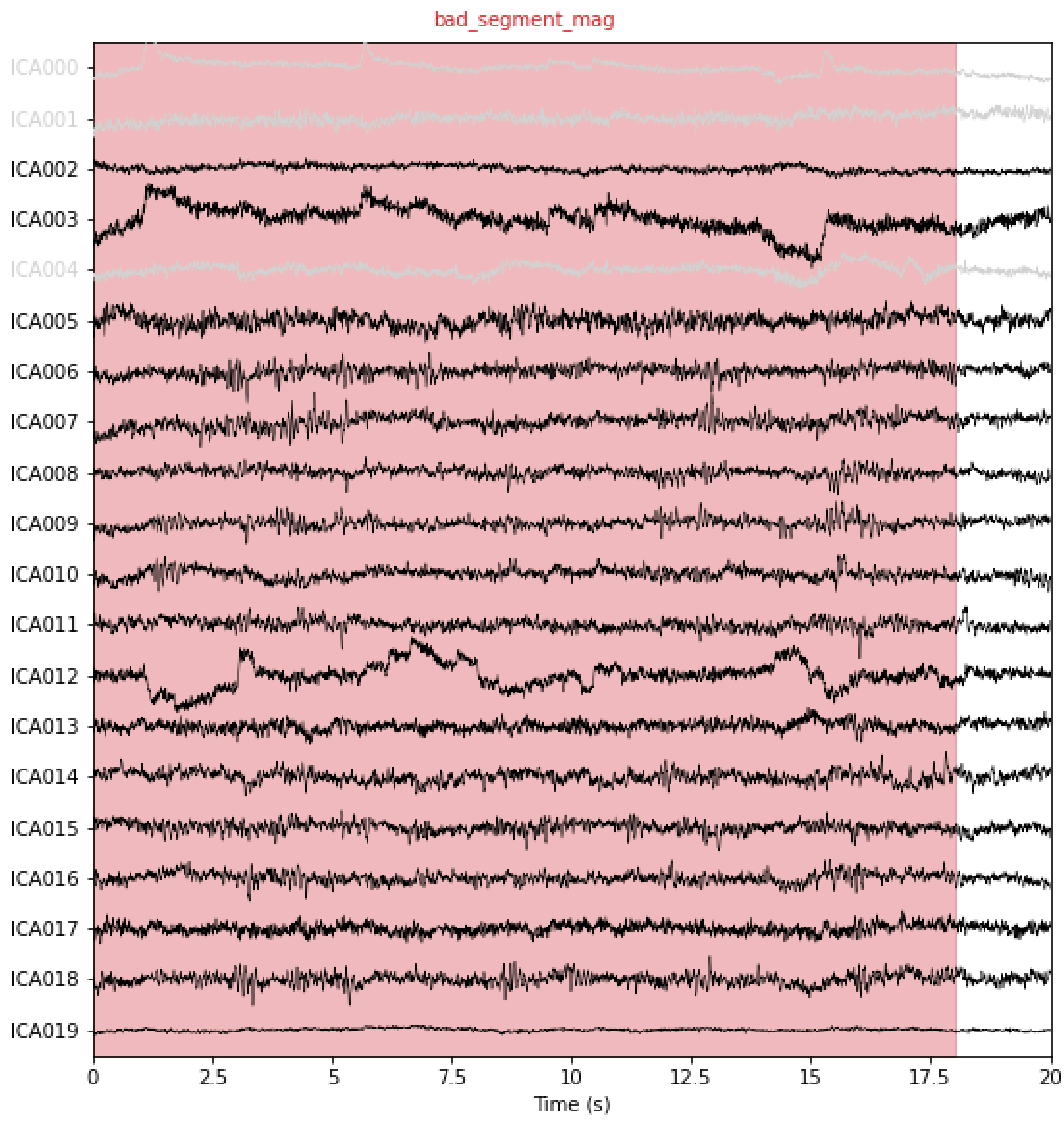
Out[10]:

Method	fastica
Fit	76 iterations on raw data (239001 samples)
ICA components	64
Available PCA components	306
Channel types	mag, grad
ICA components marked for exclusion	—

In [17]:
```
ica.plot_sources(raw_ica, show_scrollbars=False)
```


bad_segment_mag
ICA000
ICA001
ICA002
ICA003
ICA004
ICA005
ICA006
ICA007
ICA008
ICA009
ICA010
ICA011
ICA012
ICA013
ICA014
ICA015
ICA016
ICA017
ICA018
ICA019
0
2.5
5
7.5
10
12.5
15
17.5
20
Time (s)

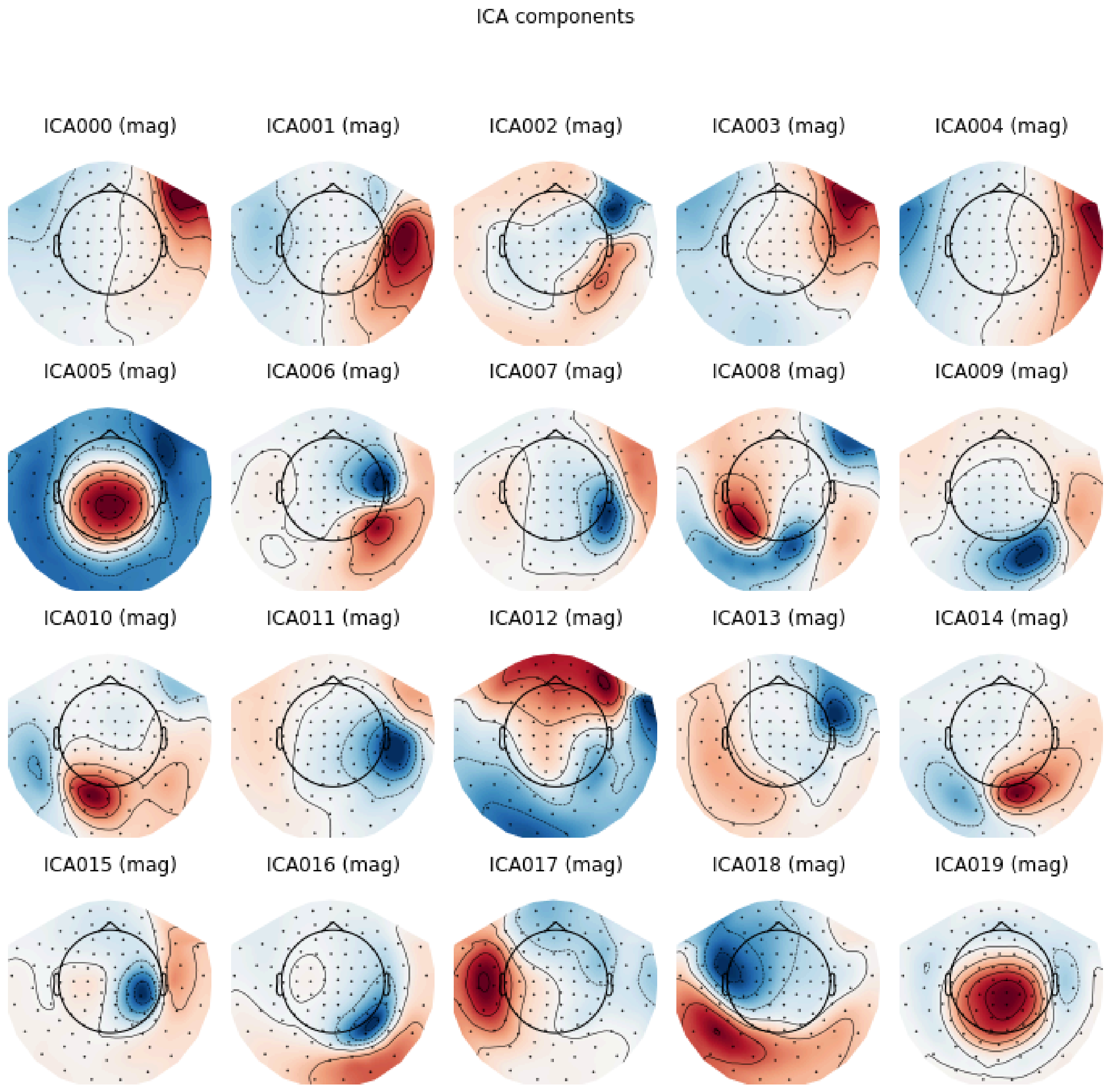
Out[17]:

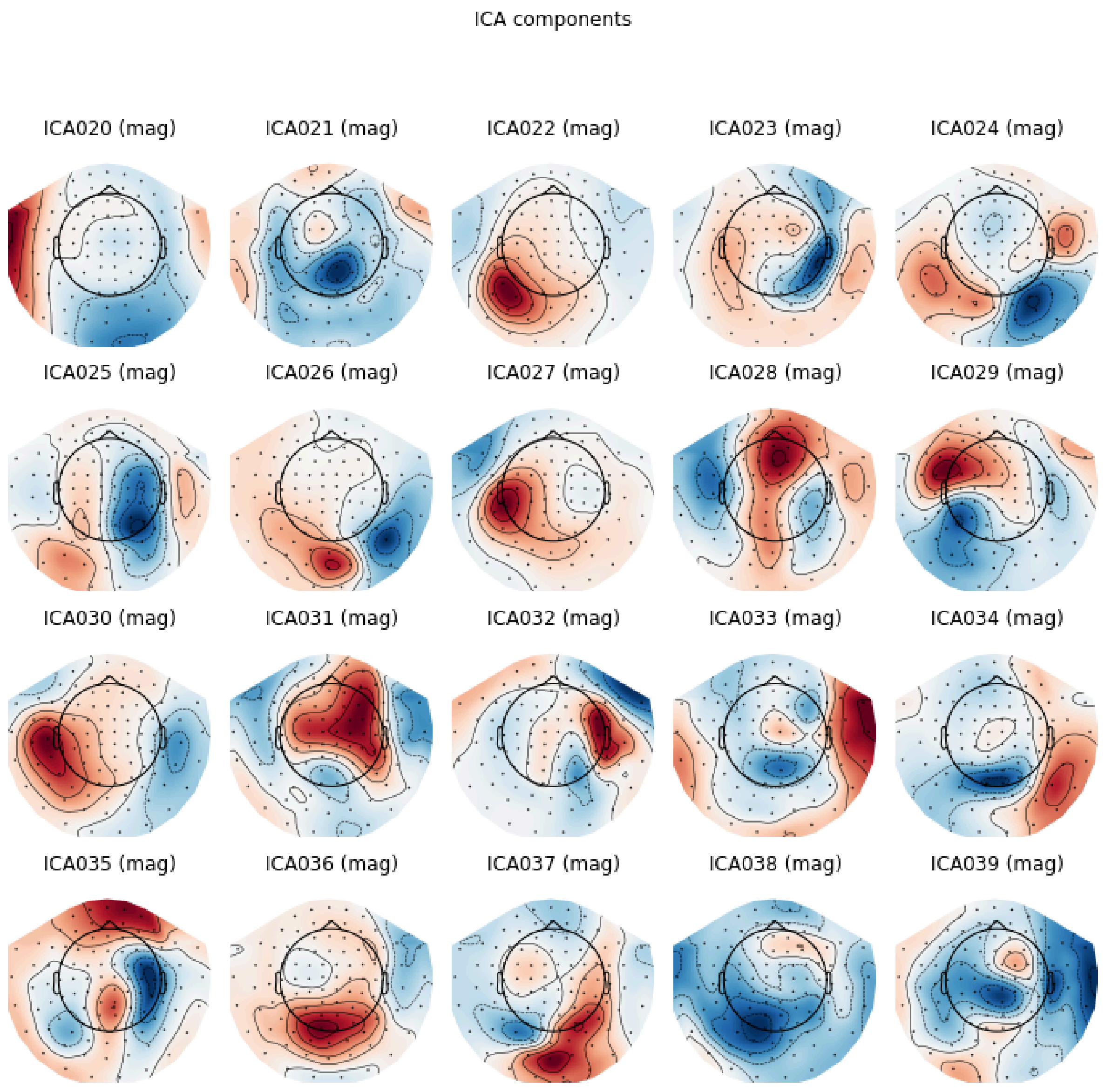


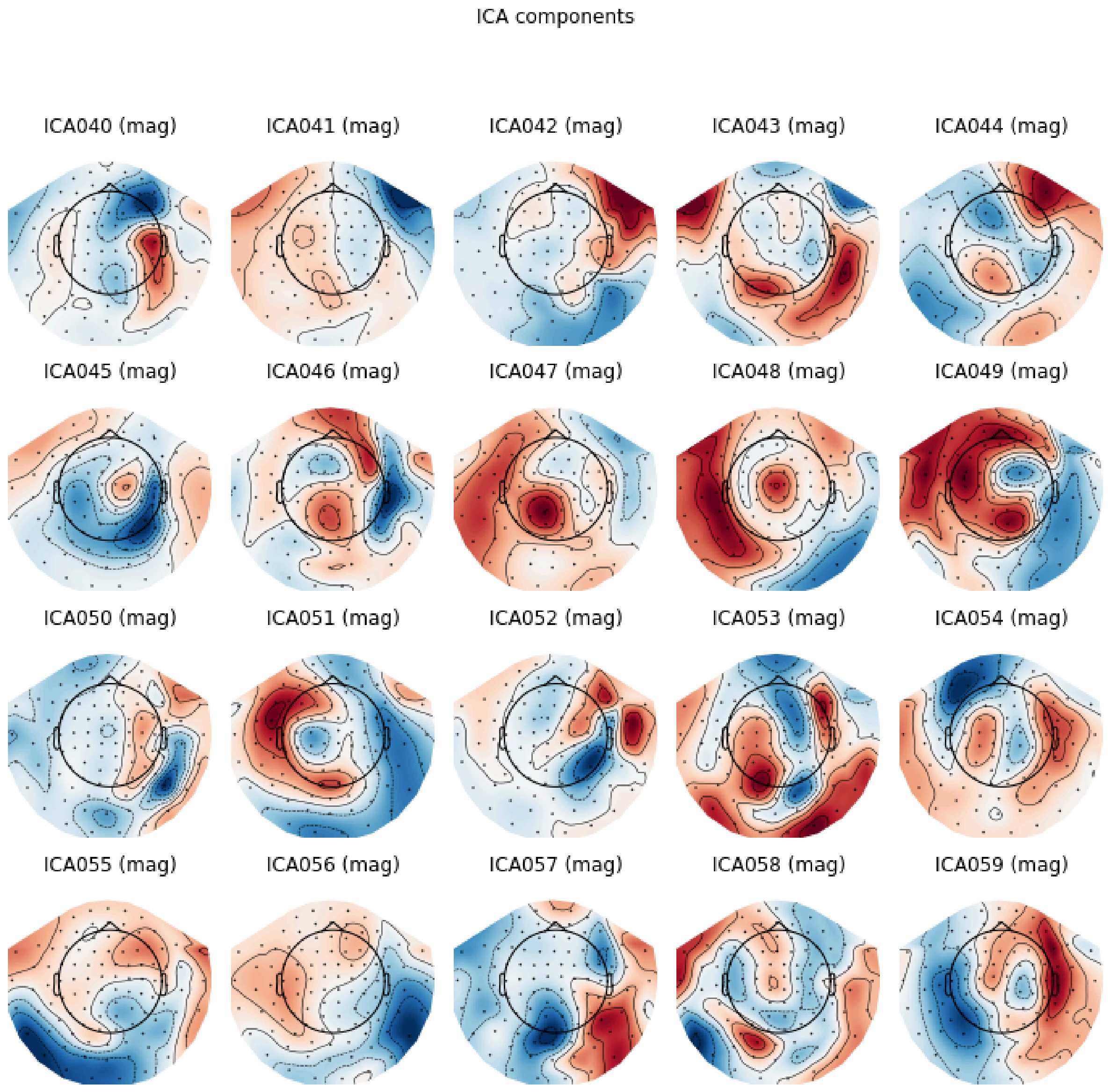
In [15]:

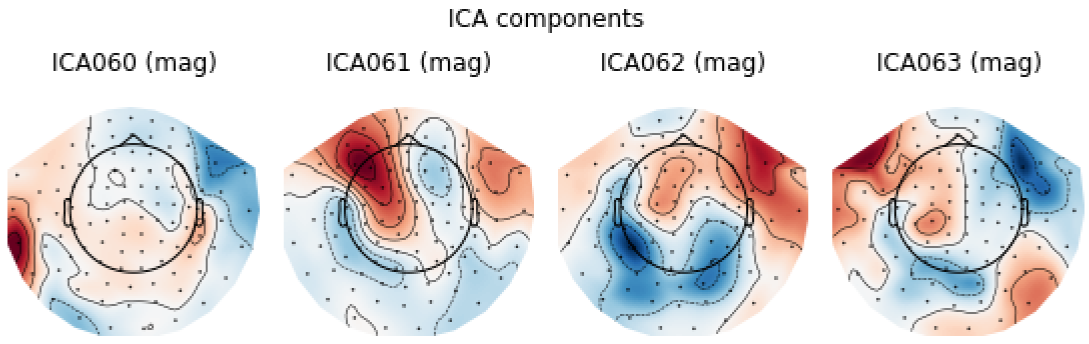
```
%matplotlib inline
ica.plot_components()
```

```
/tmp/ipykernel_945248/150138342.py:2: RuntimeWarning: (X, Y) fit (3.1, 2
0.1) more than 20 mm from head frame origin
  ica.plot_components()
```


ICA components
ICA000 (mag)
ICA001 (mag)
ICA002 (mag)
ICA003 (mag)
ICA004 (mag)
ICA005 (mag)
ICA006 (mag)
ICA007 (mag)
ICA008 (mag)
ICA009 (mag)
ICA010 (mag)
ICA011 (mag)
ICA012 (mag)
ICA013 (mag)
ICA014 (mag)
ICA015 (mag)
ICA016 (mag)
ICA017 (mag)
ICA018 (mag)
ICA019 (mag)


ICA components
ICA020 (mag)
ICA021 (mag)
ICA022 (mag)
ICA023 (mag)
ICA024 (mag)
ICA025 (mag)
ICA026 (mag)
ICA027 (mag)
ICA028 (mag)
ICA029 (mag)
ICA030 (mag)
ICA031 (mag)
ICA032 (mag)
ICA033 (mag)
ICA034 (mag)
ICA035 (mag)
ICA036 (mag)
ICA037 (mag)
ICA038 (mag)
ICA039 (mag)

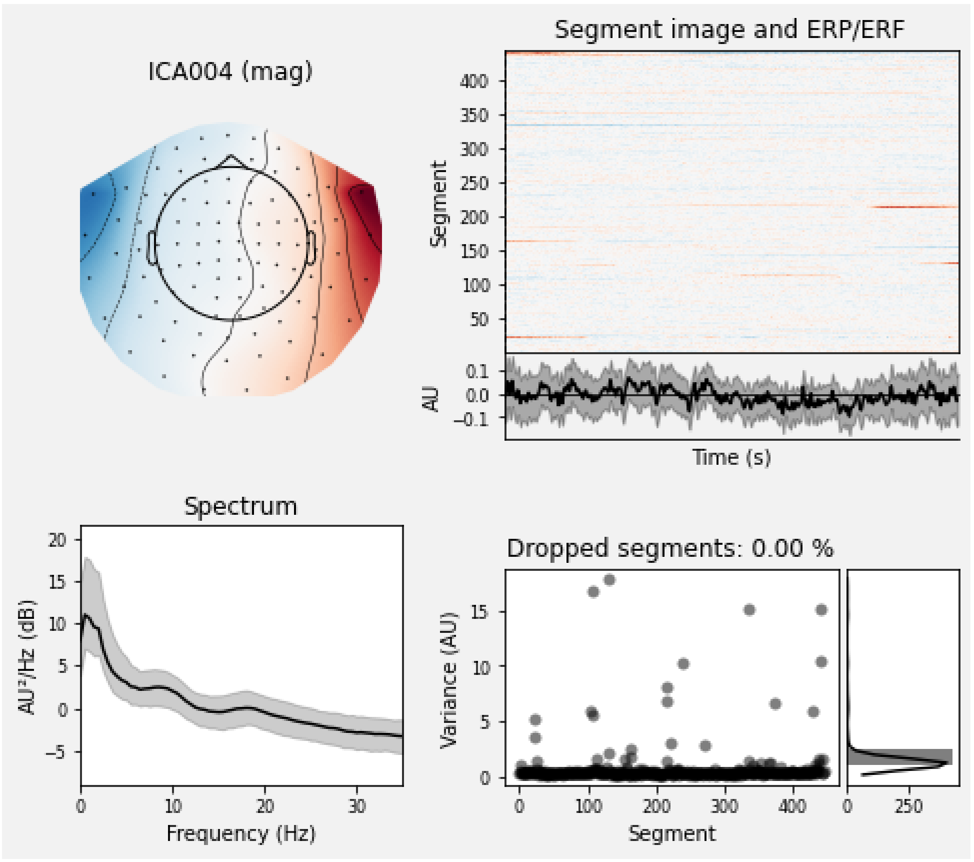




```
Out[15]: [<MNEFigure size 702x696.24 with 20 Axes>,
          <MNEFigure size 702x696.24 with 20 Axes>,
          <MNEFigure size 702x696.24 with 20 Axes>,
          <MNEFigure size 561.6x187.56 with 4 Axes>]
```

```
In [45]: %matplotlib inline
         ica.plot_properties(raw, picks=4, psd_args={'fmax': 35.})
```

```
/tmp/ipykernel_945248/2658260692.py:2: RuntimeWarning: (X, Y) fit (3.1, 2
0.1) more than 20 mm from head frame origin
  ica.plot_properties(raw, picks=4, psd_args={'fmax': 35.})
```



Out[45]:
```
[<Figure size 504x432 with 6 Axes>]
```

In [46]:
```
#ICA000, ICA001, ICA003, ICA004
artifact_picks = 0,1,3,4

#Removing the ICA components containing eyeblinks and eyemovements
ica.exclude = artifact_picks  # indices chosen based on various plots above

reconst_raw_1 = raw.copy()
ica.apply(reconst_raw_1)
```

Out[46]:

Measurement date	August 26, 2015 11:01:12 GMT
Experimenter	neuromag
Participant	
Digitized points	299 points
Good channels	204 Gradiometers, 102 Magnetometers, 3 Stimulus, 12 misc, 9 CHPI
Bad channels	None
EOG channels	Not available
ECG channels	Not available
Sampling frequency	250.00 Hz
Highpass	0.10 Hz
Lowpass	70.00 Hz
Filenames	meg_0995_SDMT_tsss_mc_preproc_raw.fif
Duration	00:18:18 (HH:MM:SS)

In [47]:
```
reconst_raw_1.save('/home/olivierb/processed_data/meg_0995_SDMT_tsss_mc/meg_
```

In [5]:
```
from osl import source_recon, utils

# Settings
config = """
    source_recon:
    - extract_fiducials_from_fif: {}     # ok
    - compute_surfaces:
        include_nose: False

    - coregister:
        use_nose: False
        use_headshape: True
        n_init: 50
"""

# Directories

subject = "/home/olivierb/test/meg_0995_SDMT_tsss_mc/meg_0995_SDMT_tsss_mc_p

# Directory in which we will save the coregistered data
COREG_DIR = "/home/olivierb/coreg"

# Directory to the FSL library, same as the one used in MATLAB, supported by
FSL_DIR = "/usr/lib/fsl/6.0"


# Run coregistration

source_recon.setup_fsl(FSL_DIR)
source_recon.run_src_batch(
    config,
    src_dir=COREG_DIR,
    subjects=['meg_0995_SDMT_tsss_mc_preproc_raw.fif'],   # name of the subj
    preproc_files=[subject],                              # path to preproce
    smri_files=[T1_MNI_niifiles[7]],                      # path to .nii fil
    )
```

In [ ]:
```
from osl import source_recon
# '/home/olivierb/38_parcels.nii' => 38 parcels / sform_code=1

# Settings
config = """
    source_recon:
    - forward_model:
        model: Single Layer                        # ok: Single Shell in MA
    - beamform_and_parcellate:
        freq_range: [1, 80]
        chantypes: [mag, grad]                     # standard for MEG
        rank: {meg: 60}
        parcellation_file: '/home/olivierb/38_parcels.nii'
        method: spatial_basis                      # ok => spatial_basis or
        orthogonalisation: symmetric               # ok
"""

# Run beamforming and parcellation
FSL_DIR = "/usr/lib/fsl/6.0"
COREG_DIR = "/home/olivierb/coreg"
SUBJECT = subject = "/home/olivierb/processed_data/meg_0995_SDMT_tsss_mc/meg

source_recon.setup_fsl(FSL_DIR)
source_recon.run_src_batch(
    config,
    src_dir=COREG_DIR,                                     # path to all the
    subjects=['meg_0995_SDMT_tsss_mc_preproc_raw.fif'],     # name of the sub
    preproc_files=[subject]                                 # path to preproc
)
```

Step 4: Sign-flipping (all files together)

In [ ]:
```
# To fix dipole sign amiguity.

from dask.distributed import Client
from osl import utils
from osl.source_recon import find_template_subject, run_src_batch, setup_fsl

# Directories
SRC_DIR = "/home/olivierb/coreg"
FSL_DIR = "/usr/lib/fsl/6.0"

# Get the parceled data
DIR_parceled = "/home/olivierb/coreg/"
all_parceled = sorted(glob.glob(DIR_parceled + 'meg_*_SDMT_tsss_mc_preproc_r
subjects = all_parceled

setup_fsl(FSL_DIR)

# Find a good template subject to align other subjects to
template = find_template_subject(SRC_DIR, subjects, n_embeddings=15, standar
```

Get the subject names for all processed files

In [ ]:
```
all_succesful_parceled = sorted(glob.glob('/home/olivierb/coreg/' + 'meg_*_S

names_subjects = []

# Gets you all the subject names for which the data was succesfully parceled
for file_path in all_succesful_parceled:
    # Split the string by '/'
    parts = file_path.split('/')
    # Extract the desired part (second-to-last element)
    desired_part = parts[-3]
    names_subjects.append(desired_part)
```

In [ ]:
```
# Settings for batch processing
config = f"""
        source_recon:
        - fix_sign_ambiguity:
            template: {template}
            n_embeddings: 15
            standardize: True
            n_init: 5
            n_iter: 500
            max_flips: 20
"""

# Setup parallel processing
DIR_parceled = "/home/olivierb/coreg/"

# Do the sign flipping - Apply the template
run_src_batch(config, SRC_DIR, names_subjects) #dask_client=True)
```

Extra: Function to overwrite sform_code of a .nii file (can be used on both MRI scans & parcelation files)

This is required due to a mismatch in sform_code for the **parcellation file** (gives an error in osl python):

- Original sform_code = 4 (normalized coordinates)
- Required sform_code = 1 (scanner)based anatomical coordinates)

Meaning of the sform codes: https://nifti.nimh.nih.gov/nifti-1/documentation/nifti1fields/nifti1fields_pages/qsform.html/document_view

In [20]:
```
import nibabel as nib
import numpy as np
import pandas as pd

## Parcellation files
#(original_file_path = "/home/olivierb/osl/source_recon/parcellation/files/1

# Function to overwrite the sform_code of an existing .nii file
def overwrite_sformcode(original_file_path, output_file_path):

    # Load the NIfTI image
    nii_img = nib.load(original_file_path)

    # Get the image data and affine matrix
    data = nii_img.get_fdata()
    affine = nii_img.affine

    # Create a new NIfTI image with the modified sform_code
    new_sformcode = 1  # Set to the desired value
    new_header = nii_img.header.copy()
    new_header.set_sform(affine, code=new_sformcode)

    # Create a new image using the modified data and header
    nii_img_with_modified_header = nib.Nifti1Image(data, affine, header=new_

    # Save the new image to a file
    nib.save(nii_img_with_modified_header, output_file_path)

    # Reload the saved image
    loaded_img = nib.load(output_file_path)

    # Check the sform_code of the loaded image
    print(loaded_img.header['sform_code'])

    return
```

Extra: Explore and visualise parcellation file

Plot parcellation for visualisation

In [50]:
```
from nilearn import image

nii_img = image.load_img("/home/fahimeha/PhD/preprocessing/parcellation/fmri

print(nii_img.shape)

one_volume = image.index_img(nii_img, 3)
print(one_volume.shape)
```

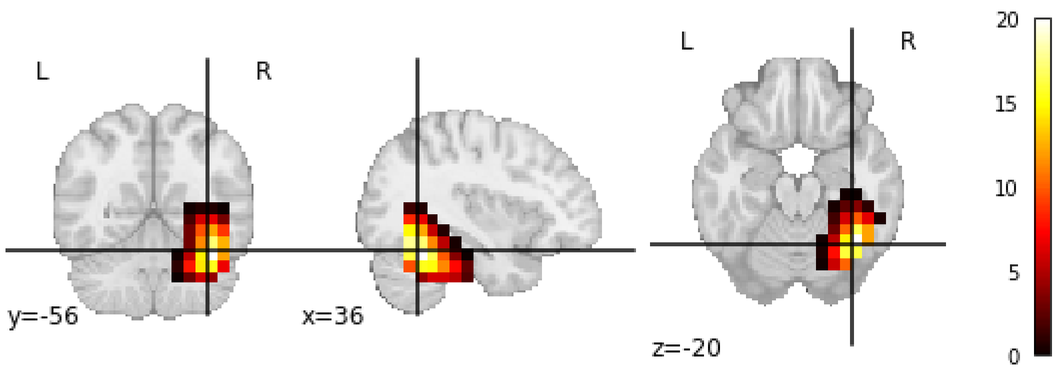
```
(23, 27, 23, 42)
(23, 27, 23)
```

In [51]:
```python
from nilearn import image
path_parcel = "/home/olivierb/osl/source_recon/parcellation/files/fmri_d100_
nii_img = image.load_img(path_parcel)
print(nii_img.shape)
```

```
(23, 27, 23, 38)
```

In [52]:
```python
from nilearn import plotting

plotting.plot_stat_map(one_volume)
```

Out[52]:
```
<nilearn.plotting.displays._slicers.OrthoSlicer at 0x7f6ed5594640>
```



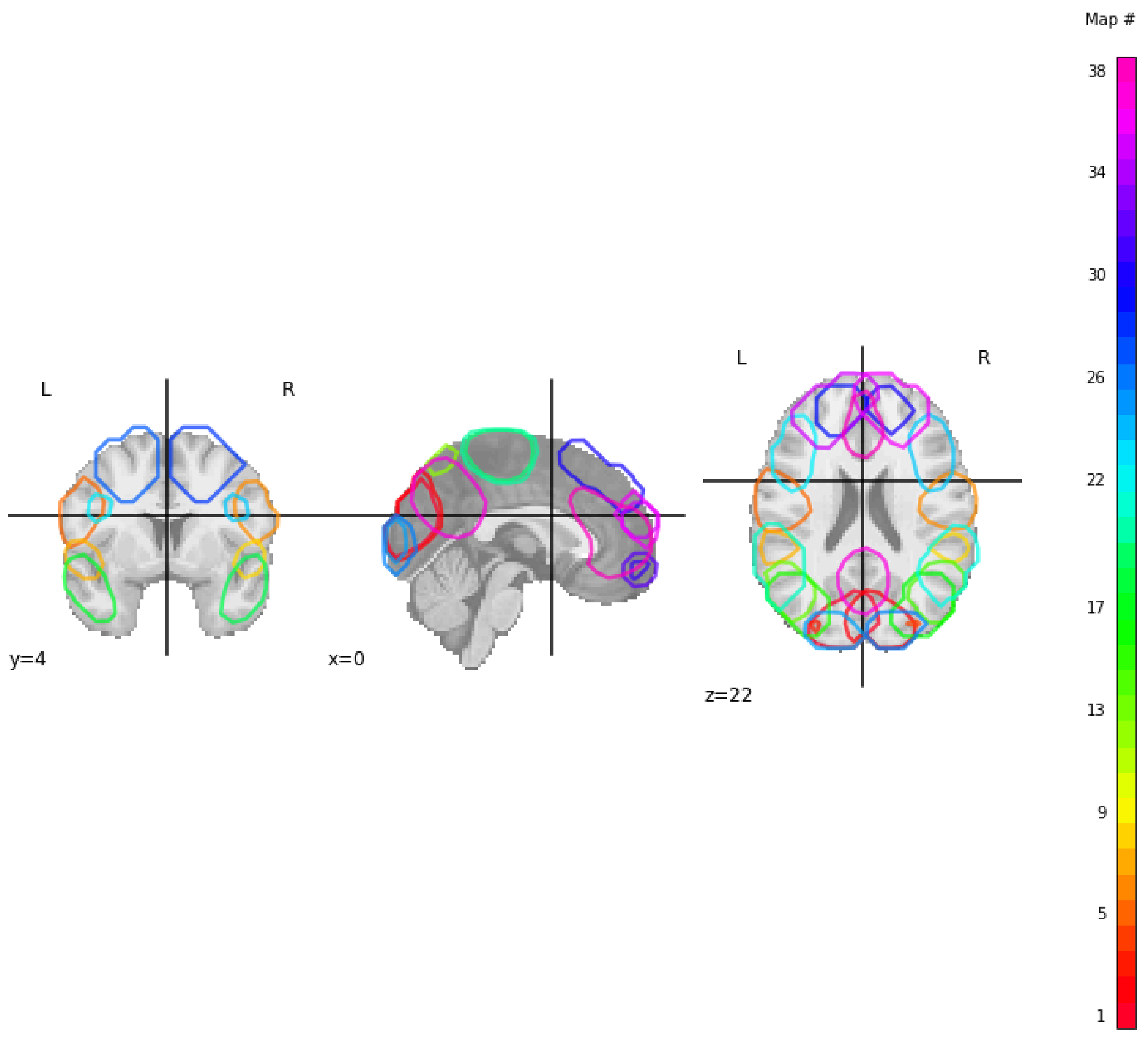
In [21]:
```python
import nilearn
```

In [22]:
```python
from nilearn.regions import connected_regions
from nilearn import datasets, plotting
import nibabel as nib
atlas = nib.load("/home/olivierb/38_parcels.nii")
```

In [23]:
```python
region_labels = connected_regions(atlas)
```

In [24]:
```python
import matplotlib.pyplot as plt
nilearn.plotting.plot_prob_atlas(atlas, figure=plt.figure(figsize=(10,10)),
```

Out[24]:
```
<nilearn.plotting.displays._slicers.OrthoSlicer at 0x7f695e0115e0>
```



Extract parcel names for the parcellation file

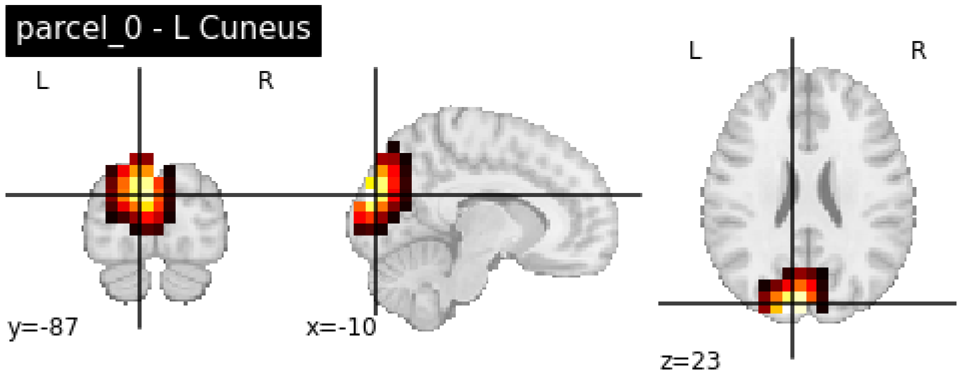
In [25]:
```
## Parcel names extract

# Open the .txt file for reading
file_path = "/home/olivierb/Downloads/Parcels_38_names.txt"
with open(file_path, 'r') as file:
    lines = file.readlines()

# Strip any leading/trailing whitespace and create a list of strings
parcel_names = [line.strip() for line in lines]

# Print the list of strings
print(parcel_names)

# Parcel indices (how the channel names are stored in the Python parceled .1
parcel_idx= []
for i in range(len(parcel_names)):        # 38 parcels
    parcel_idx.append('parcel_' + str(i))
print(parcel_idx)
```

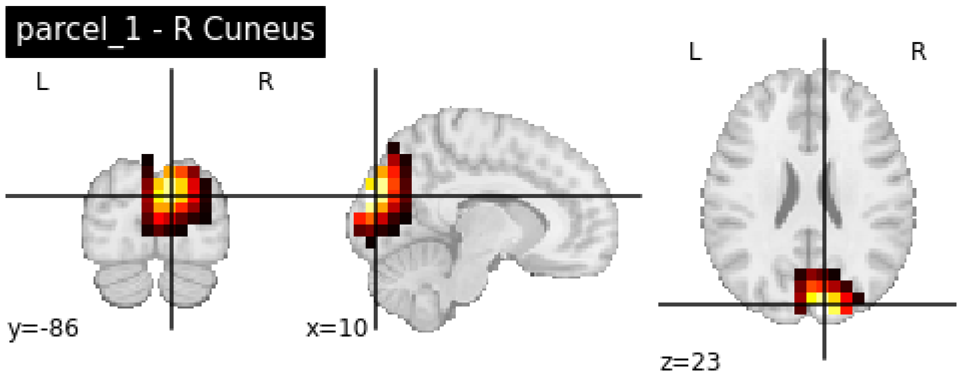
```
['L Cuneus', 'R Cuneus', 'L Inf Occ', 'R Inf Occ', 'L Supramarginal', 'R
Supramarginal', 'L Sup Temp', 'R Sup Temp', 'L Lat SMC', 'R Lat SMC', 'L
Sup Parietal', 'R Sup Parietal', 'L Middle Occ', 'R Middle Occ', 'L Sup O
cc', 'R Sup Occ', 'L Ant Temp', 'R Ant Temp', 'L Medial SMC', 'R Medial S
MC', 'L Angular', 'R Angular', 'L VL PFC', 'R VL PFC', 'L Occ pole', 'R O
cc pole', 'L Sup PFC', 'R Sup PFC', 'L Sup Dorsal PFC', 'R Sup Dorsal PF
C', 'L Orbitofrontal', 'R Orbitofrontal', 'L Post Temp', 'R Post Temp',
'L Inf Dorsal PFC', 'R Inf Dorsal PFC', 'Medial PFC', 'Posterior Cingulat
e Cortex']
['parcel_0', 'parcel_1', 'parcel_2', 'parcel_3', 'parcel_4', 'parcel_5',
'parcel_6', 'parcel_7', 'parcel_8', 'parcel_9', 'parcel_10', 'parcel_11',
'parcel_12', 'parcel_13', 'parcel_14', 'parcel_15', 'parcel_16', 'parcel_
17', 'parcel_18', 'parcel_19', 'parcel_20', 'parcel_21', 'parcel_22', 'pa
rcel_23', 'parcel_24', 'parcel_25', 'parcel_26', 'parcel_27', 'parcel_2
8', 'parcel_29', 'parcel_30', 'parcel_31', 'parcel_32', 'parcel_33', 'par
cel_34', 'parcel_35', 'parcel_36', 'parcel_37']
```

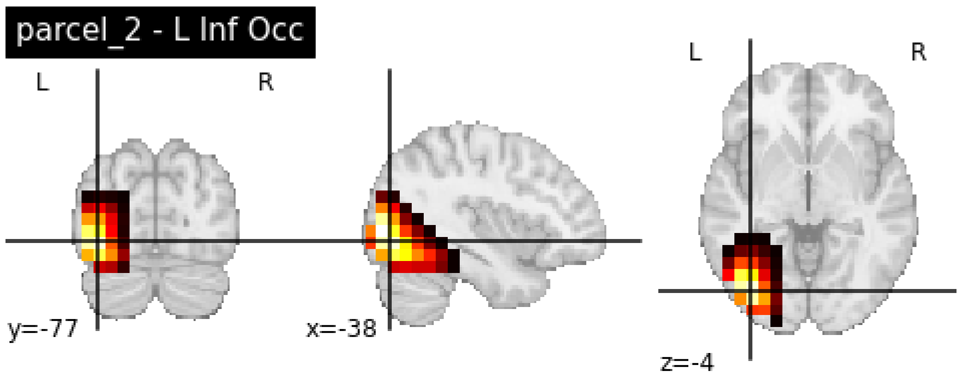
In [26]:

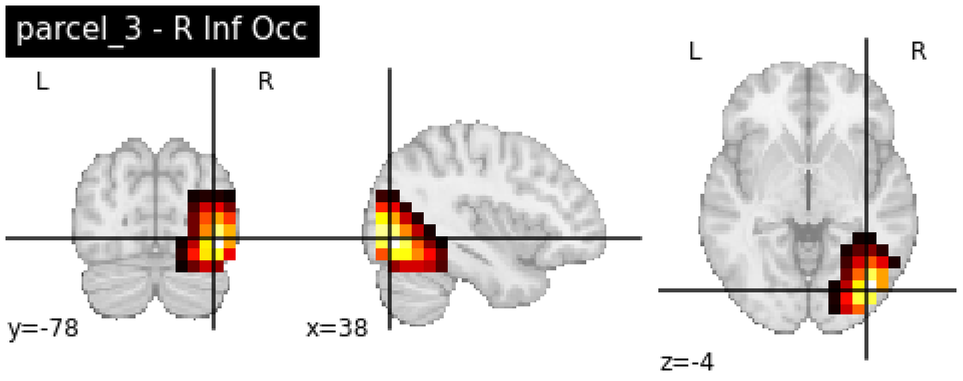
```python
from nilearn.image import iter_img
from nilearn.plotting import plot_stat_map, show

for i, cur_img in enumerate(iter_img(atlas)):
    plot_stat_map(
        cur_img,
        title=f"{parcel_idx[i]} - {parcel_names[i]}",
        colorbar=False,
    )

# takes a little while to plot everything
```

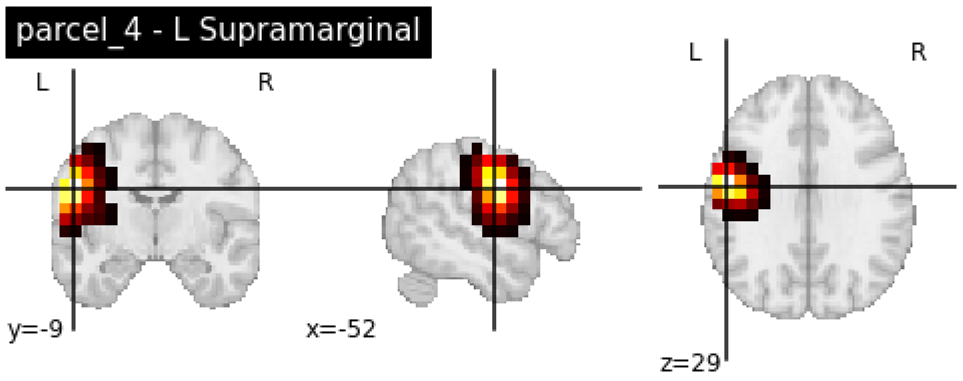
```
/home/olivierb/.local/lib/python3.9/site-packages/nilearn/plotting/displa
ys/_slicers.py:144: RuntimeWarning: More than 20 figures have been opene
d. Figures created through the pyplot interface (`matplotlib.pyplot.figur
e`) are retained until explicitly closed and may consume too much memory.
(To control this warning, see the rcParam `figure.max_open_warning`). Con
sider using `matplotlib.pyplot.close()`.
  figure = plt.figure(figure, figsize=figsize,
```

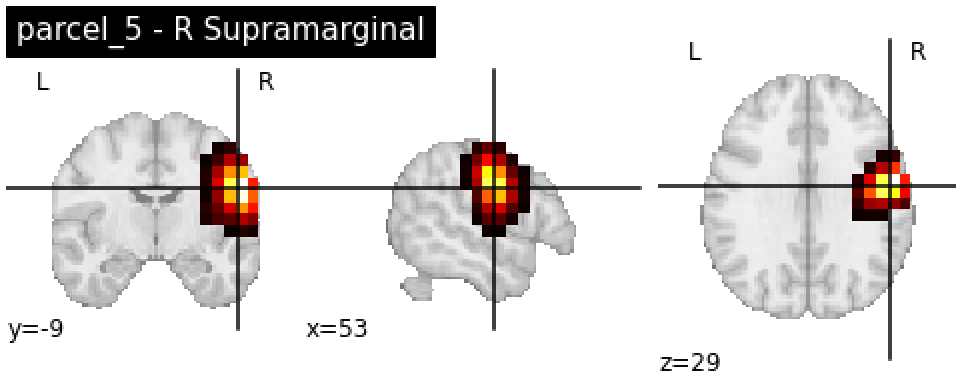


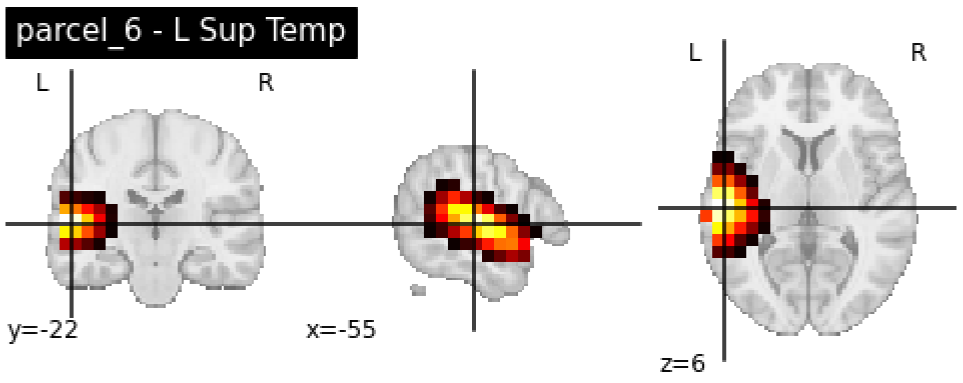


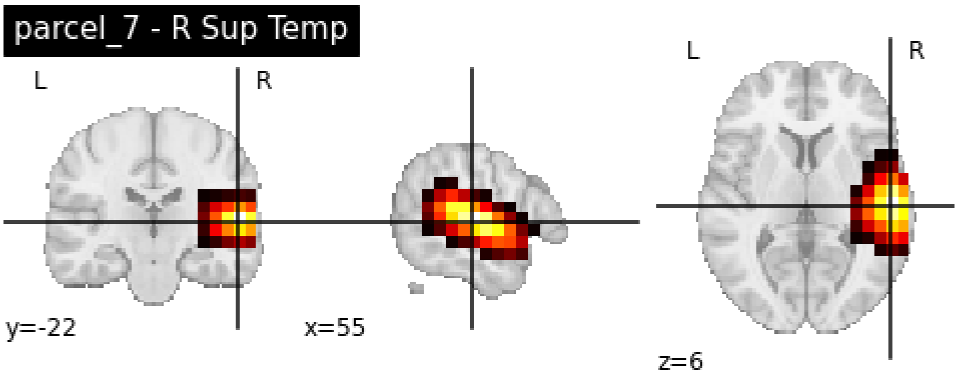

parcel_2 - L Inf Occ
L
R
y=-77
x=-38
L
R
z=-4

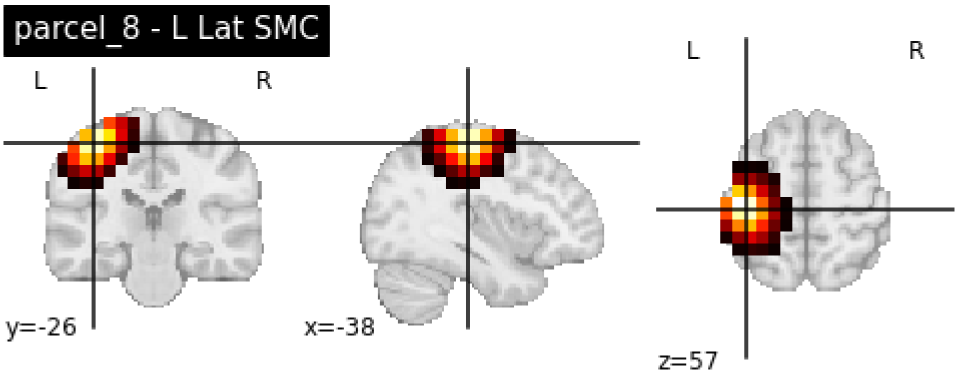

parcel_3 - R Inf Occ
L
R
y=-78
x=38
L
R
z=-4

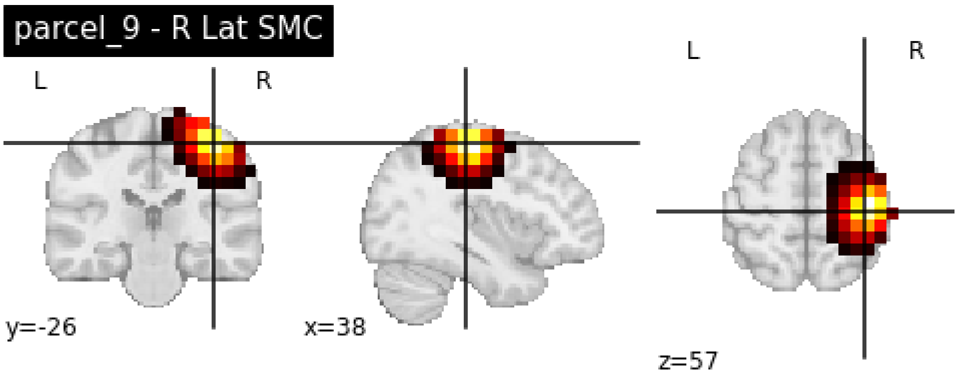

parcel_4 - L Supramarginal
L
R
y=-9
x=-52
L
R
z=29

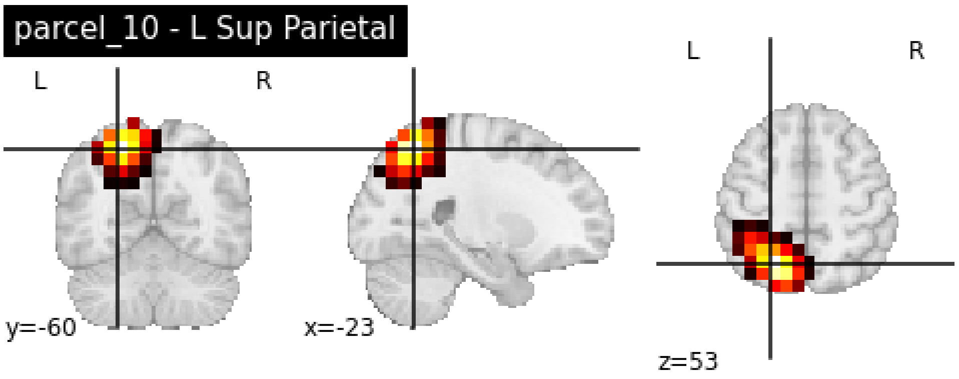

parcel_5 - R Supramarginal
L
R
y=-9
x=53
L
R
z=29

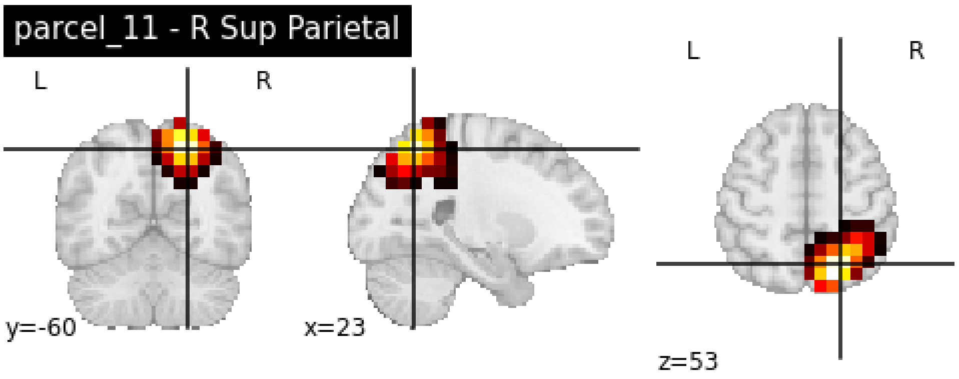

parcel_6 - L Sup Temp
L
R
y=-22
x=-55
L
R
z=6

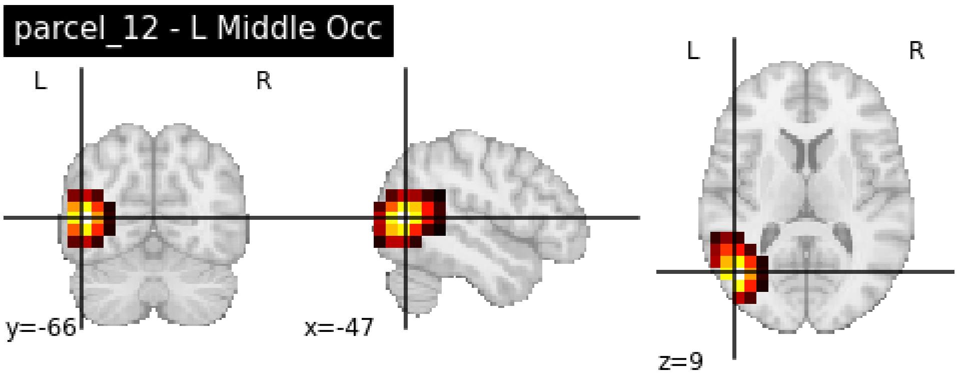

parcel_7 - R Sup Temp
L
R
y=-22
x=55
L
R
z=6

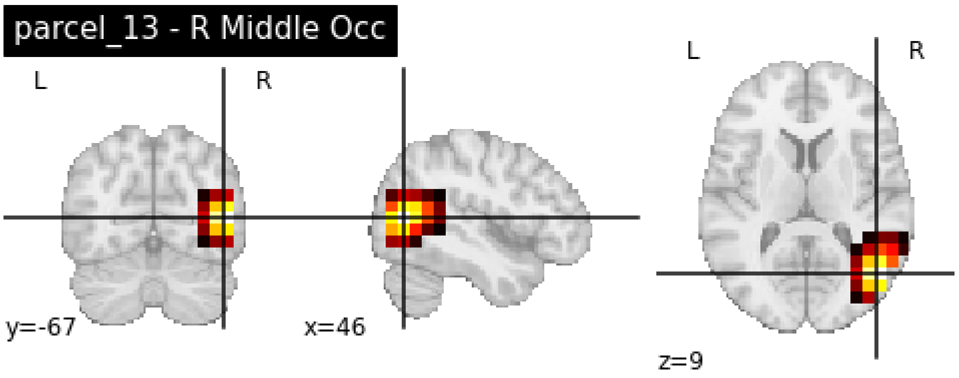

parcel_8 - L Lat SMC
L
R
y=-26
x=-38
L
R
z=57

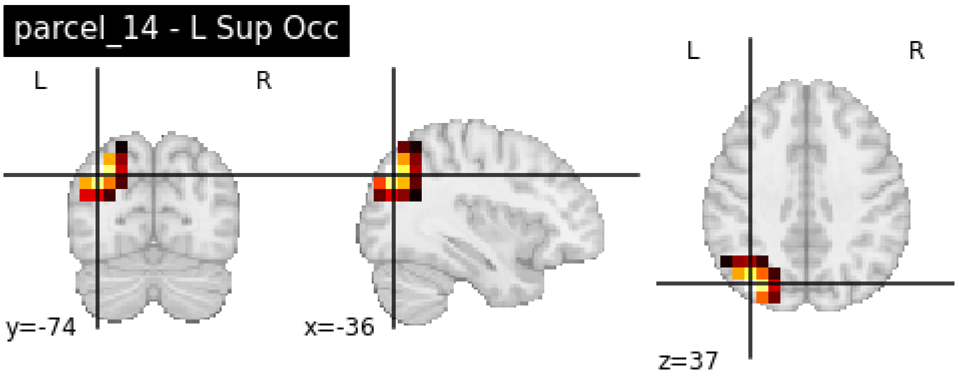

parcel_9 - R Lat SMC
L
R
y=-26
x=38
L
R
z=57

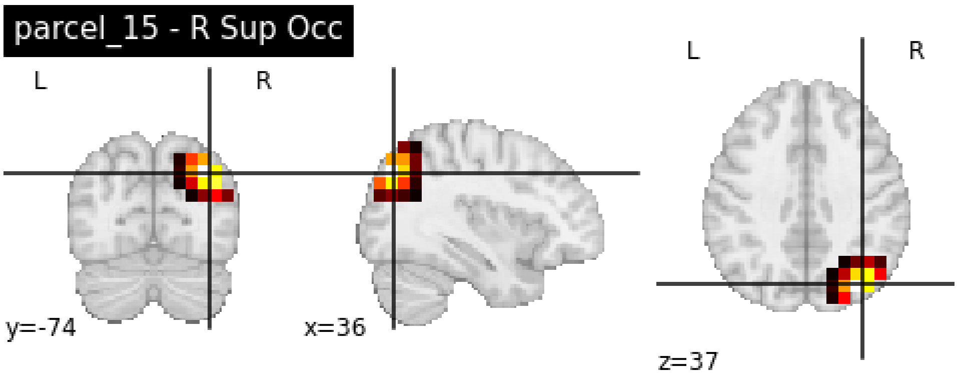

parcel_10 - L Sup Parietal
L
R
y=-60
x=-23
L
R
z=53

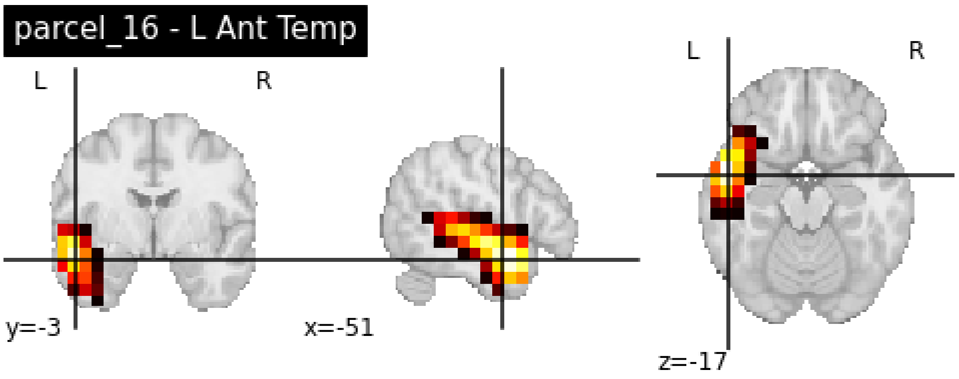

parcel_11 - R Sup Parietal
L
R
y=-60
x=23
L
R
z=53

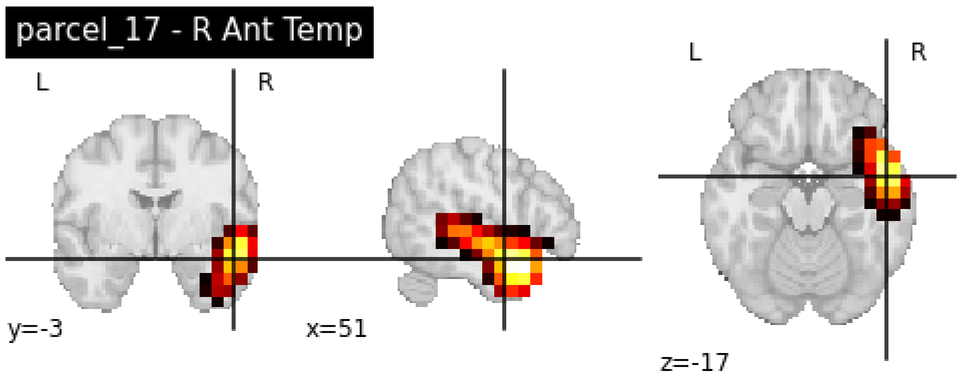

parcel_12 - L Middle Occ
L
R
y=-66
x=-47
L
R
z=9

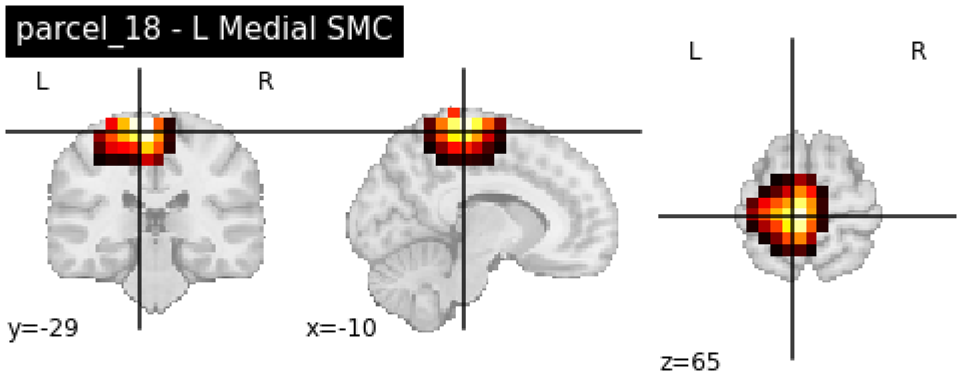

parcel_13 - R Middle Occ
L
R
y=-67
x=46
L
R
z=9

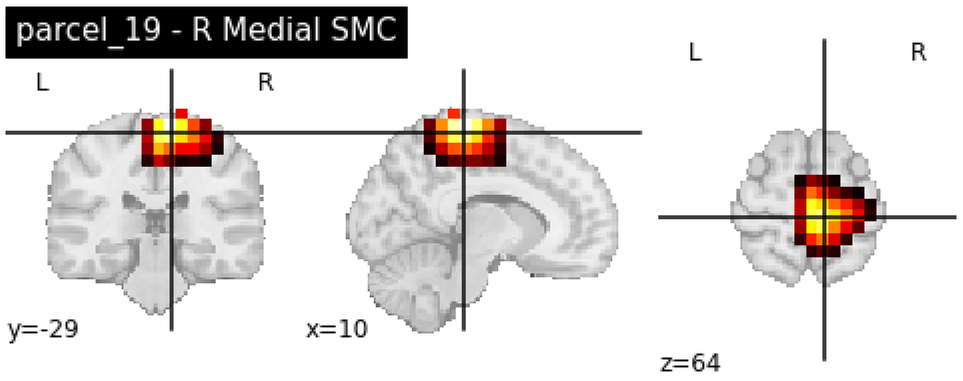

parcel_14 - L Sup Occ
L
R
y=-74
x=-36
L
R
z=37

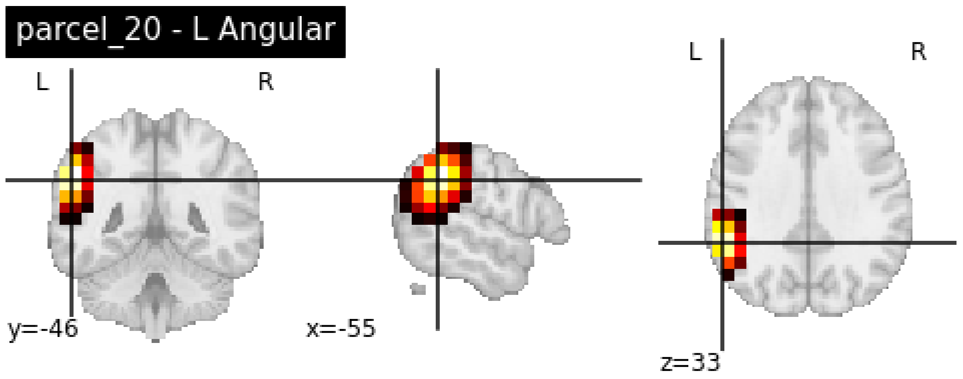

parcel_15 - R Sup Occ
L
R
y=-74
x=36
L
R
z=37

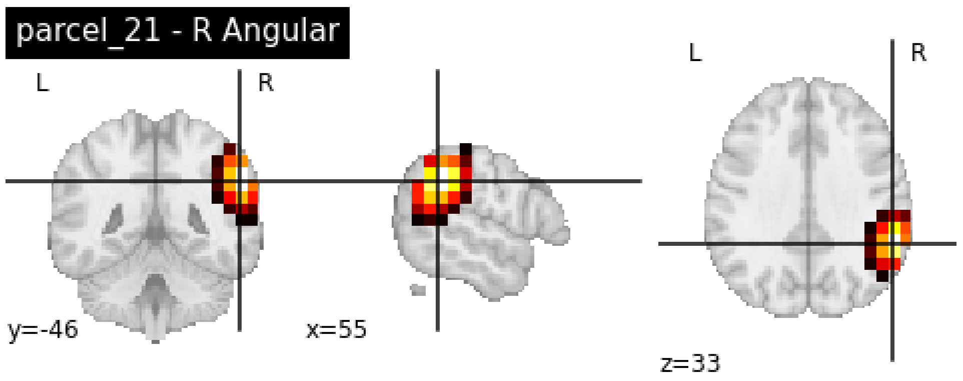

parcel_16 - L Ant Temp
L
R
y=-3
x=-51
L
R
z=-17

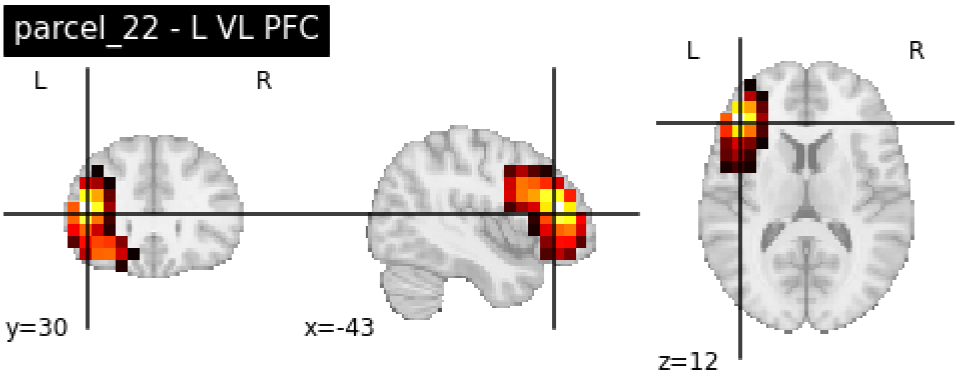

parcel_17 - R Ant Temp
L
R
y=-3
x=51
L
R
z=-17

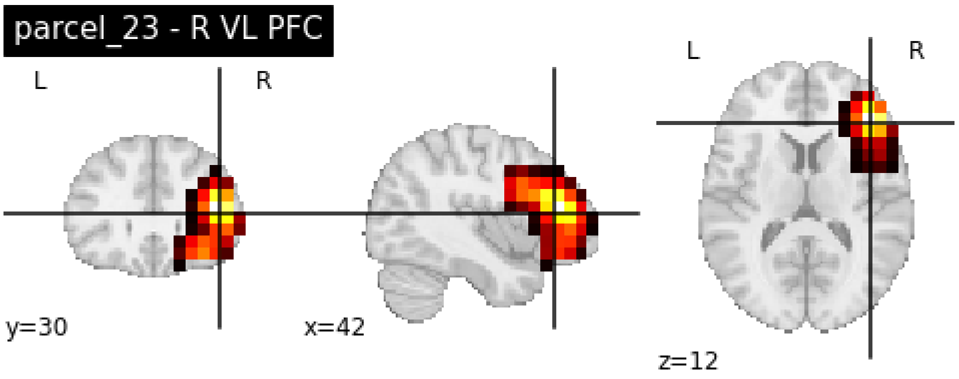

parcel_18 - L Medial SMC
L
R
y=-29
x=-10
L
R
z=65

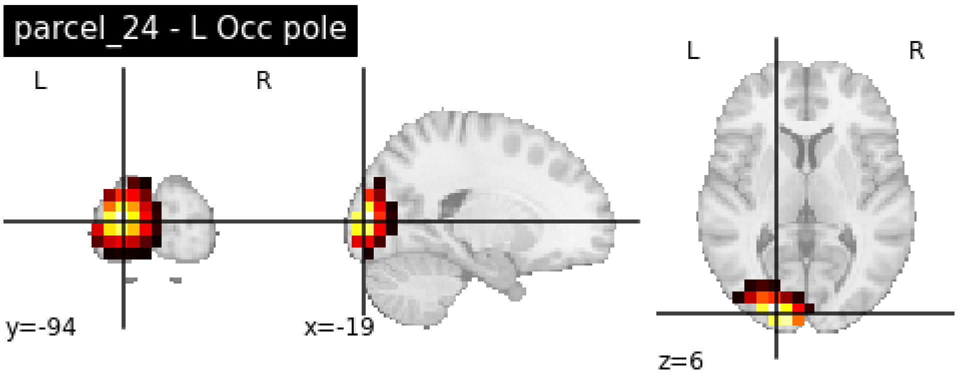

parcel_19 - R Medial SMC
L
R
y=-29
x=10
L
R
z=64

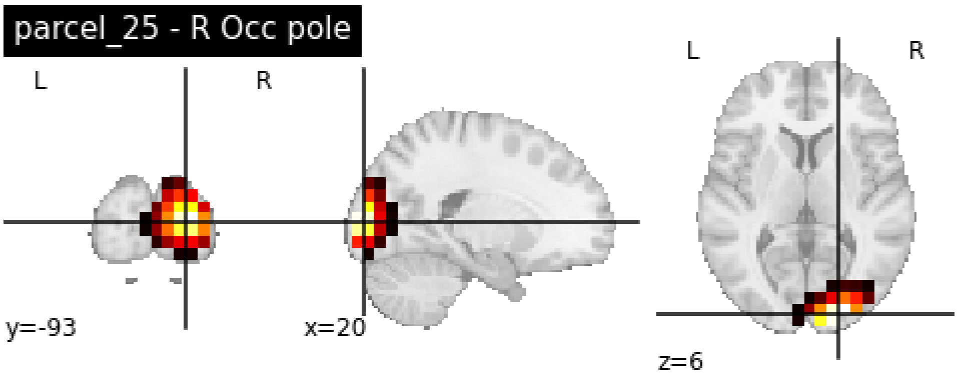

parcel_20 - L Angular
L
R
y=-46
x=-55
L
R
z=33

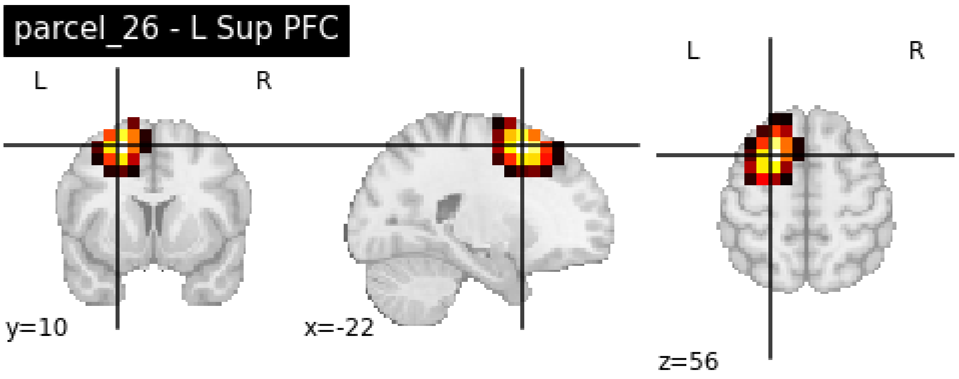

parcel_21 - R Angular
L
R
y=-46
x=55
L
R
z=33

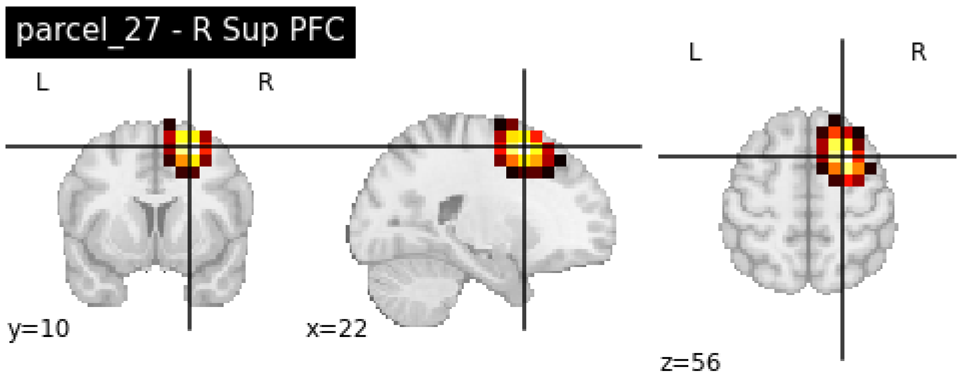

parcel_22 - L VL PFC
L
R
y=30
x=-43
L
R
z=12

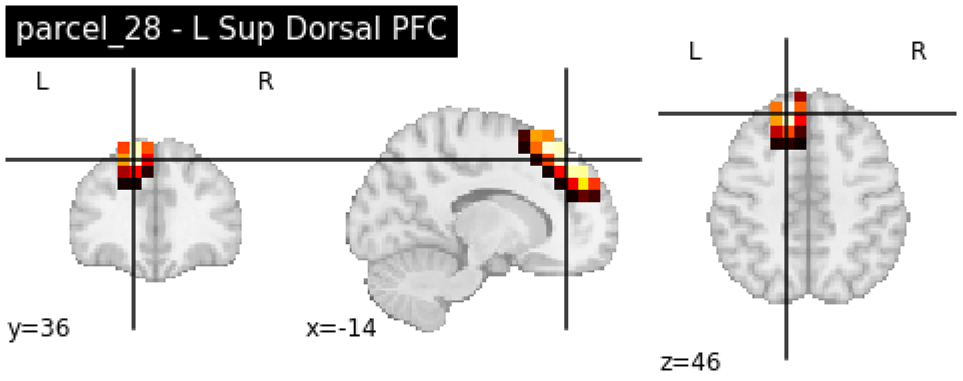

parcel_23 - R VL PFC
L
R
y=30
x=42
L
R
z=12

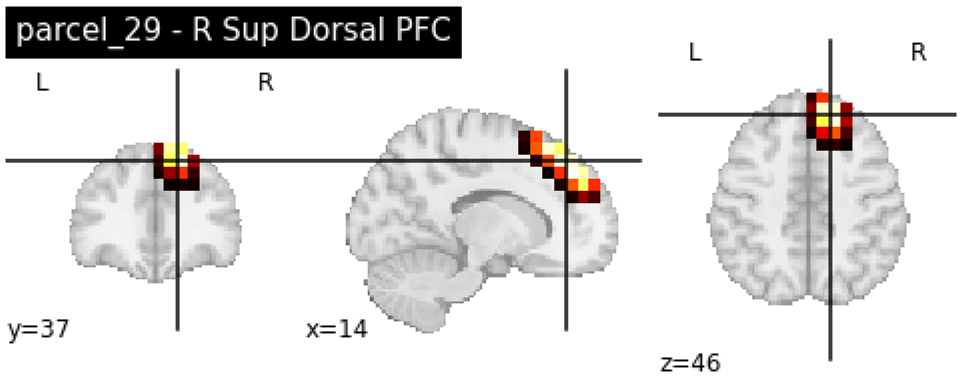

parcel_24 - L Occ pole
L
R
y=-94
x=-19
L
R
z=6

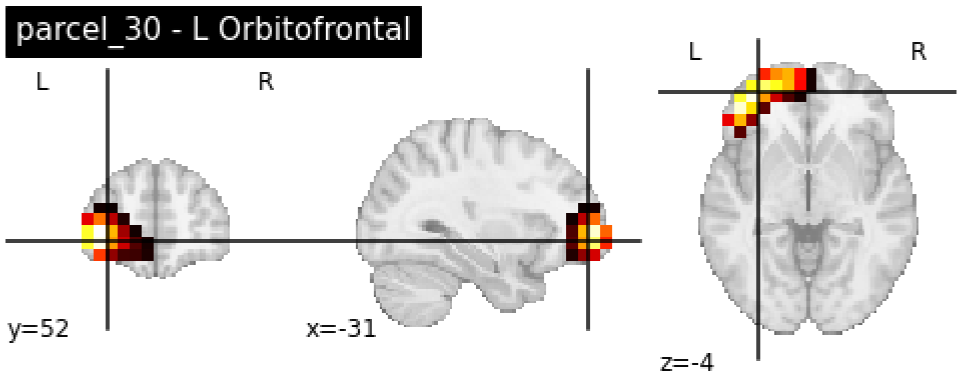

parcel_25 - R Occ pole
L
R
y=-93
x=20
L
R
z=6

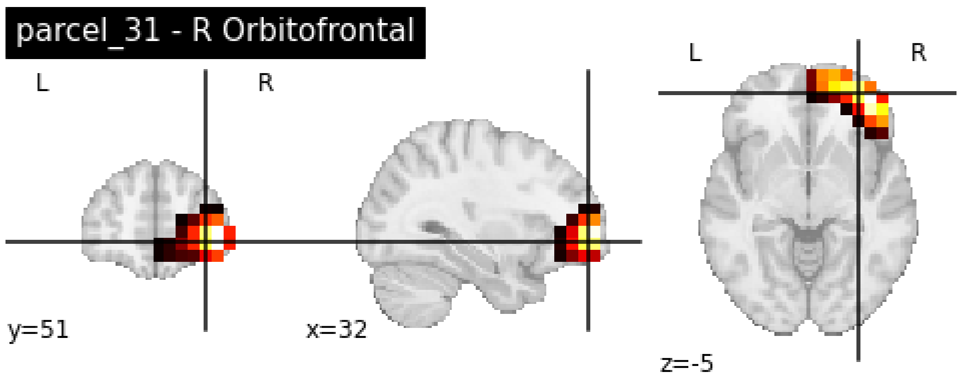

parcel_26 - L Sup PFC
L
R
y=10
x=-22
L
R
z=56

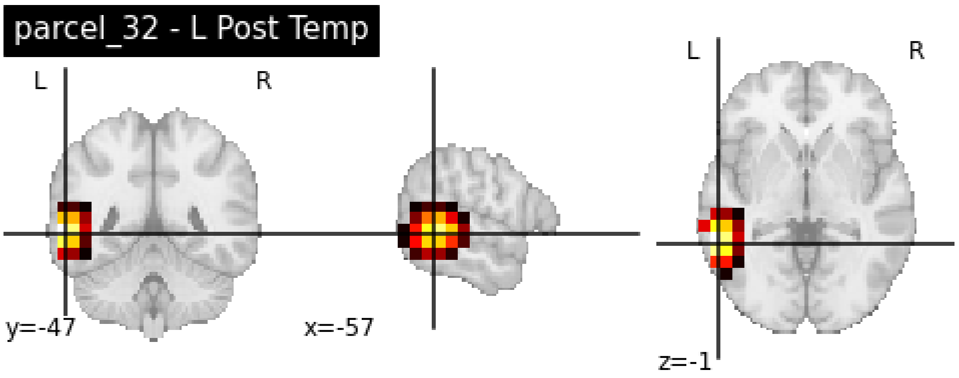

parcel_27 - R Sup PFC
L
R
y=10
x=22
L
R
z=56

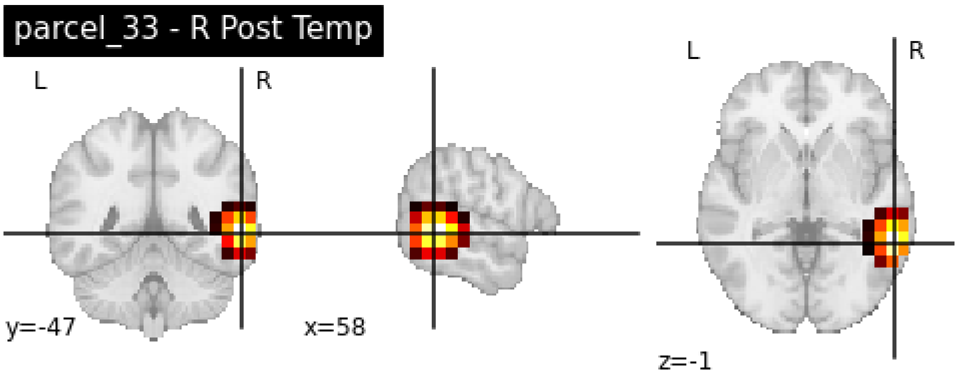

parcel_28 - L Sup Dorsal PFC
L
R
y=36
x=-14
L
R
z=46

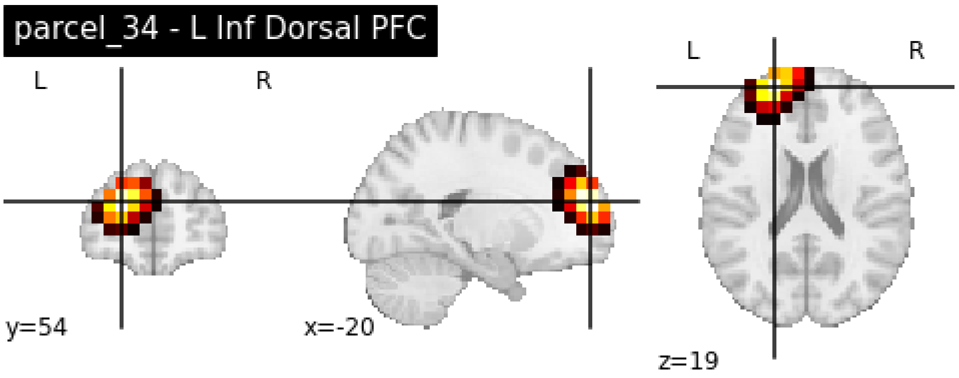

parcel_29 - R Sup Dorsal PFC
L
R
y=37
x=14
L
R
z=46

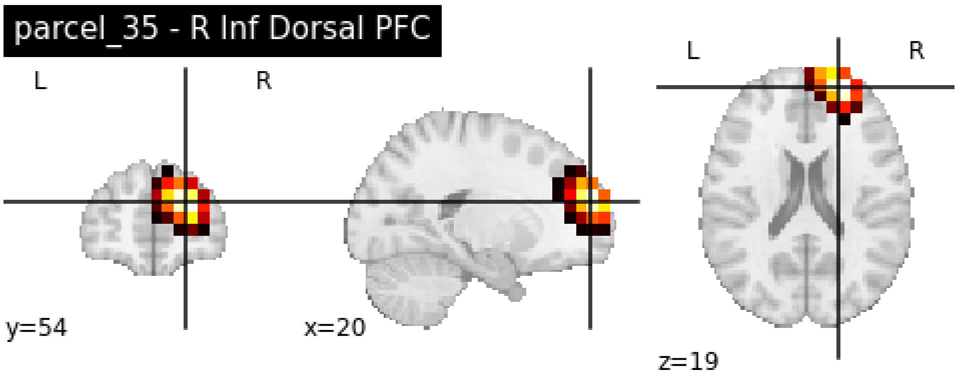

parcel_30 - L Orbitofrontal
L
R
y=52
x=-31
L
R
z=-4

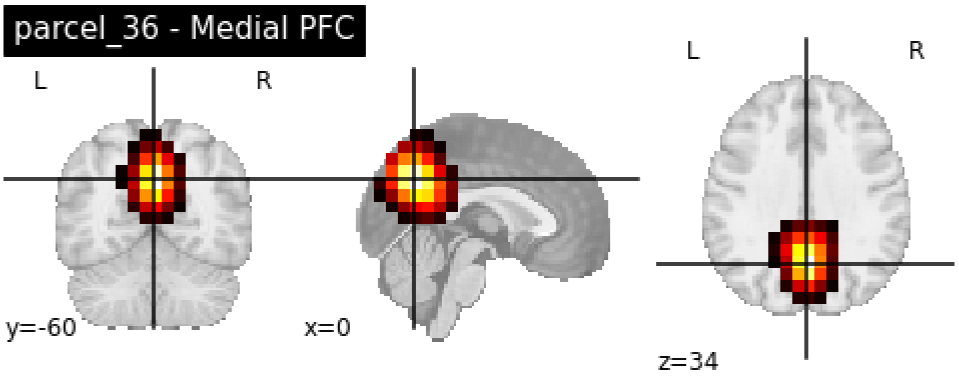

parcel_31 - R Orbitofrontal
L
R
y=51
x=32
L
R
z=-5

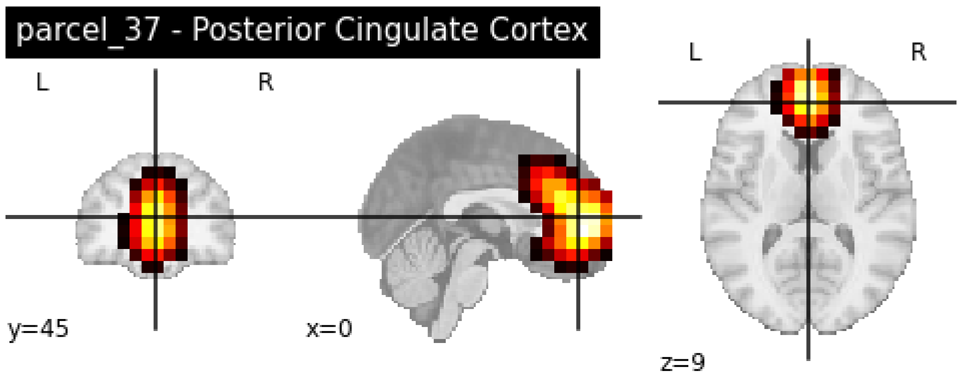

parcel_32 - L Post Temp
L
R
y=-47
x=-57
L
R
z=-1


parcel_33 - R Post Temp
L
R
y=-47
x=58
L
R
z=-1


parcel_34 - L Inf Dorsal PFC
L
R
y=54
x=-20
L
R
z=19


parcel_35 - R Inf Dorsal PFC
L
R
y=54
x=20
L
R
z=19


parcel_36 - Medial PFC
L
R
y=-60
x=0
L
R
z=34


parcel_37 - Posterior Cingulate Cortex
L
R
y=45
x=0
L
R
z=9