Carpet Plot Documentation

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1   Directory Structure

All the code related to carpet plot is located in the dir:

`/projects/jbyambadorj/matlab_code`

The overall structure follows the same format as the directory layout in Dr. Jonathan Power's `plotdemo.zip`, available at `https://www.jonathanpower.net/2017-ni-the-plot.html`. As a result, many files and directories such as `libraries` are identical.

Inside the `matlab_code` directory, data are organized by subject. Within each subject directory, all necessary files for constructing carpet plots are stored.

Taking `sub-CMH00000012_data` as an example, its structure is shown below:

```
aparc+aseg.atlas.CSFMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.CSFMASK_ero0.nii.gz
aparc+aseg.atlas.CSFMASK_ero1_EPI.nii.gz
aparc+aseg.atlas.CSFMASK_ero1.nii.gz
aparc+aseg.atlas.CSFMASK_ero2_EPI.nii.gz
aparc+aseg.atlas.CSFMASK_ero2.nii.gz
aparc+aseg.atlas.CSFMASK_ero3_EPI.nii.gz
aparc+aseg.atlas.CSFMASK_ero3.nii.gz
aparc+aseg.atlas.CSFMASK_ero4_EPI.nii.gz
aparc+aseg.atlas.CSFMASK_ero4.nii.gz
aparc+aseg.atlas.GM_ALLMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.GM_ALLMASK_ero0.nii.gz
aparc+aseg.atlas.GM_CBLMMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.GM_CBLMMASK_ero0.nii.gz
aparc+aseg.atlas.GM_CBLMMASK_ero1_EPI.nii.gz
aparc+aseg.atlas.GM_CBLMMASK_ero1.nii.gz
aparc+aseg.atlas.GM_CBLMMASK_ero2_EPI.nii.gz
aparc+aseg.atlas.GM_CBLMMASK_ero2.nii.gz
aparc+aseg.atlas.GM_RIBBONMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.GM_RIBBONMASK_ero0.nii.gz
aparc+aseg.atlas.GM_SCMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.GM_SCMASK_ero0.nii.gz
aparc+aseg.atlas.GM_SCMASK_ero1_EPI.nii.gz
aparc+aseg.atlas.GM_SCMASK_ero1.nii.gz
```

```
aparc+aseg.atlas.GM_SCMASK_ero2_EPI.nii.gz
aparc+aseg.atlas.GM_SCMASK_ero2.nii.gz
aparc+aseg.atlas.INBRAINMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.INBRAINMASK_ero0.nii.gz
aparc+aseg.atlas.nii.gz
aparc+aseg.atlas.WMMASK_ero0_EPI.nii.gz
aparc+aseg.atlas.WMMASK_ero0.nii.gz
aparc+aseg.atlas.WMMASK_ero1_EPI.nii.gz
aparc+aseg.atlas.WMMASK_ero1.nii.gz
aparc+aseg.atlas.WMMASK_ero2_EPI.nii.gz
aparc+aseg.atlas.WMMASK_ero2.nii.gz
aparc+aseg.atlas.WMMASK_ero3_EPI.nii.gz
aparc+aseg.atlas.WMMASK_ero3.nii.gz
aparc+aseg.atlas.WMMASK_ero4_EPI.nii.gz
aparc+aseg.atlas.WMMASK_ero4.nii.gz
aparc+aseg.nii.gz
fd_sub-CMH00000012_ses-0*_run-0*.txt
ses0*
smoothened_sub-CMH00000012_ses-0*_task-rest_run-0*_space-
    MNI152NLin6Asym_res-2_desc-preproc_bold.nii.gz
sub-CMH00000012_ses-0*_task-rest_run-0*_space-MNI152NLin6Asym_res-2_desc
    -preproc_bold.nii.gz
sub-CMH00000012_space-MNI152NLin6Asym_res-2_desc-preproc_T1w.nii.gz
```

1.1   Organization of the files

- Physiological traces are located in session subdirectories `ses-*`

- aparc+aseg.nii.gz is the input file used for generating aparc+aseg.atlas.nii.gz file (details are in next section).

- fd_sub*.txt are framewise displacement fMRIprep outputs.

- sub*MNI152NLin6Asym_res-2_desc-preproc_bold.nii.gz are the BOLD func images

- smoothened_sub*MNI152NLin6Asym_res-2_desc-preproc_bold.nii.gz are smoothened images from using the above as inputs

- sub*MNI152NLin6Asym_res-2_desc-preproc_T1w.nii.gz are the anatomical T1W image

Note that all the nifti image files are in the MNI152NLin6Asym space

Currently, carpet plot data are fully organized and functional for subjects 10, 11, and 12. These subjects can be identified by their directory names, which use full subject identifiers (e.g., `sub-CMH00000010`). In contrast, for directories following a shorter naming format, such as `sub0i_data`, the data inside them need to be organized to be fully ready for running the matlab carpet plot script.

1.2 Outputs and Scripts

In the base dir, **matlab_code**, carpet plot outputs are stored in **output_images** and **output_video**.

The scripts needed for preparing the stage for running the matlab code (carpetplot.m) are stored in the directory: **/projects/jbyambadorj/matlab_code/scripts**

2 Preparing the data

To generate carpet plots, you need the following fMRIprep outputs for each subject:

- BOLD run

- aparc+aseg.mgz from freesurfer (inside fMRIprep output)

- T1W anatomical image

- fd file

- sub*res-2_boldref.nii.gz file

- sub*_from-fsnative_to-T1w_mode-image_xfm.txt

- sub*_from-T1w_to-MNI152NLin6Asym_mode-image_xfm.h5

The general workflow is as follows:

- 1) Convert the aparc+aseg.mgz into aparc+aseg.nii.gz file using freesurfer's **mri_convert** command.

- 2) Then, convert this aparc+aseg.nii.gz file into same space (MNI152NLin6Asym) as the rest of the T1W and BOLD func images by using ANTS **antsApplyTransforms** command. This command requires the following 3 files as inputs:

  - sub*res-2_boldref.nii.gz file
  - sub*_from-fsnative_to-T1w_mode-image_xfm.txt
  - sub*_from-T1w_to-MNI152NLin6Asym_mode-image_xfm.h5

  Once the command finishes running, you will have the aparc+aseg.nii.gz image in the same space (MNI152NLin6Asym in this example) as the rest of the functional and anatomical files. The naming convention used here follows the format `aparc+aseg.atlas.nii.gz`, consistent with Dr. Jonathan Power's original carpet plot scripts. However, you may modify the filename—for instance, by including subject identifiers—by adjusting the **-o** parameter in the **antsApplyTransforms** command.

- 3) Once you have the aparc+aseg.atlas.nii.gz file and T1W image in the same space, call generate_masks.csh by typing ./generate_masks.csh on shell in the matlab_code dir. (Make sure you change the top line of the script where subject ID is declared for the appropriate subject).

```
#!/bin/tcsh -xf

# You need to have AFNI installed for this script to work.

set sub = "11"    <------- Edit this part by correct sub identifier!

set pdir = `pwd`
set masterimg = ${pdir}/sub-CMH000000${sub}_data/sub-
CMH000000${sub}_space-MNI152NLin6Asym_res-2_desc-preproc_T1w.nii.gz

echo ------------------------------------------------------------
echo ------------------------------------------------------------
echo CLEARING OUT OLD MASKS IF PRESENT
echo ------------------------------------------------------------
echo ------------------------------------------------------------
....... script continues......
```

- 4) Once you have changed all the imaging data into a same space, all that is left is to run the matlab scripts carpetplot.m for generating carpet plots and qcPeaks.m for generating zoomed-in PPG traces with identified peaks.

- 5) After you have all the necessary png and mp4 (or avi) outputs from running carpetplot.m and qcPeaks.m, you can call the python scripts generate_group_images.py and generate_group_videos.py to generate a html page that overlays and organizes all the outputs together for a given subject.

You can find the scripts used for generating these in:
/projects/jbyambadorj/matlab_code/scripts

2.1   File structure in scripts dir

- mri_convert.sh - For converting aparc+aseg.dseg to aparc+aseg.nii.gz

- ants.sh - For converting aparc+aseg.nii.gz into same space as func and anat images (MNI152NLin6 space). Output is named aparc+aseg.atlas.nii.gz

- fd_extract.sh - Populate subject dirs with fd outputs from the fMRIprep sub/ses/func

- import_physio.sh - Populate subject dirs with physiological traces

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- rename.py - Rename the imported physiological file names to appropriate names

- smoothen.sh - For applying 3dmerge command from AFNI and smoothen the BOLD images.