

Requirements

- FreeSurfer
- Connectome Workbench
- AFNI
- FSL with MSM (Multimodal Surface Matching)
- Ciftify
 - In Python3 environment with several libraries
 - Will be installed via script automatically with several packages (pip install ciftify)
 - NumPy, Pandas, SciPy, Nibabel, Matplotlib, Seaborn
- Provided files
 - 1) run_proc.sh, 2) ext_rsfc.py, 3) Gordon_352_parac.dlabel.nii

extract-rsfc-pipeline

Command for running the script

```
bash run_proc.sh <work_dir> <sub_id> <task> <n_cpus>
```

Arguments

<work_dir> : The directory with the input data (T1w, BOLD)

<sub_id> : subject id

<task> : It would be fixed “task-rest”

<n_cpus> : Number of cpu used for preprocessing

e.g. bash run_proc.sh /path/to/work_dir sub-01 task-rest 32

extract-rsfc-pipeline

Input

- 1) T1w image acquired from structure MRI
 - `<subject_id>_T1w.nii.gz`
 - e.g., `sub-01_T1w.nii.gz`
- 2) BOLD timeseries acquired from rs-fMRI
 - `<subject_id>_task-rest_bold.nii.gz`
 - e.g., `sub-01_task-rest_bold.nii.gz`
- Need to prepare two input data with the explicit directory structure and naming
- Three files (`ext_rsfc.py`, `Gordon_352_parcdlabel.nii`, `run_proc.sh`) should be included in `work_dir` at correct position

```
work_dir
├── data
│   ├── sub-01
│   │   ├── anat
│   │   │   └── sub-01_T1w.nii.gz
│   │   └── func
│   │       └── sub-01_task-rest_bold.nii.gz
├── ext_rsfc.py
├── Gordon_352_parcdlabel.nii
├── output
└── run_proc.sh
```

extract-rsfc-pipeline

Outputs

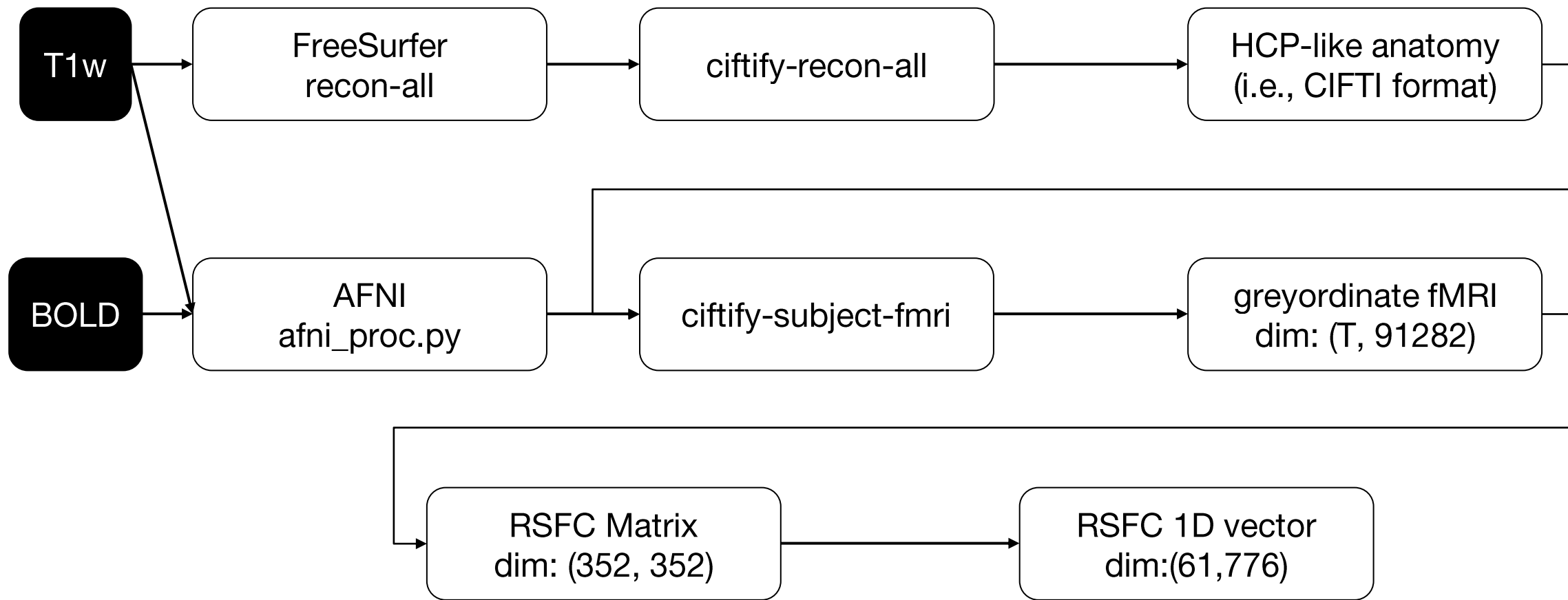
- **rsfc.npz**
 - Vectorized RSFC matrix with 61,776 dimensions
 - 352 x 352 RSFC matrix → only upper triangular matrix excluded diagonal components

```
work_dir
├── data
│   └── sub-01
│       ├── anat
│       │   └── sub-01_T1w.nii.gz
│       └── func
│           └── sub-01_task-rest_bold.nii.gz
├── ext_rsfc.py
├── Gordon_352_parcdlabel.nii
├── output
└── run_proc.sh
```

```
work_dir
├── data
│   └── sub-01
│       ├── freesurfer
│       │   └── outputs
│       ├── anat
│       │   └── sub-01.results
│       │       └── QC
│       └── func
├── output
│   ├── qc_recon_all
│   └── sub-01
│       ├── rsfc.npz
│       └── MNINonLinears
│           └── task-rest
│               └── task-
rest...
```

extract-rsfc-pipeline

Workflow of script



Useful reference link

- **Ciftify**

- GitHub page: <https://edickie.github.io/ciftify/#/>
- Paper: Dickie, E. W., Anticevic, A., Smith, D. E., Coalson, T. S., Manogaran, M., Calarco, N., ... & Voineskos, A. N. (2019). Ciftify: A framework for surface-based analysis of legacy MR acquisitions. *Neuroimage*, 197, 818-826.

- **AFNI**

- Web page for afni_proc.py:

https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/programs/afni_proc.py_sphx.html

- **Connectome Workbench**

- Website: <https://www.humanconnectome.org/software/connectome-workbench>

extract-rsfc-pipeline

Processing blocks in script

1. FreeSurfer recon-all

```
# 1. Run FreeSurfer's recon-all for surface-based analysis
echo "-----"
echo "1. Freesurfer recon-all"
echo "-----"
recon-all -s ${sub} -i ${ant_dir}/${sub}_T1w.nii -all -qcache
```

1. ciftify-recon-all

```
# 2. Run ciftify-recon-all to make CIFTI format surface-based T1w
echo "-----"
echo "2. ciftify recon-all"
echo "-----"
ciftify_recon_all --ciftify-work-dir ${work_dir}/output \
--fs-subjects-dir $SUBJECTS_DIR \
-v --n_cpus ${n_cpus} ${sub}
```

3. AFNI afni_proc.py

```
# 3. Run AFNI's afni_proc.py to preprocess 4D rs-fMRI volume
echo "-----"
echo "3. afni_proc.py"
echo "-----"
✓ afni_proc.py -subj_id ${sub} \
-script ${top_dir}/proc.${sub} -scr_overwrite \
-blocks despike tshift align volreg mask scale regress \
-copy_anat ${ant_dir}/${sub}_T1w.nii \
-dsets ${epi_dir}/${sub}_${tsk}_bold.nii \
-align_opts_aea -cost lpc+ZZ -giant_move -check_flip \
-volreg_align_to MIN_OUTLIER \
-volreg_align_e2a \
-mask_epi_anat yes \
-mask_segment_anat yes \
-mask_apply anat \
-regress_censor_motion 0.3 \
-regress_censor_outliers 0.1 \
-regress_bandpass 0.008 0.09 \
-regress_apply_mot_types demean deriv \
-html_review_style pythonic
```

extract-rsfc-pipeline

Processing blocks in script

4. ciftify-subject-fmri

```
# 4. Run ciftify-subject-fmri to register preprocessed fMRI to surface
echo "-----"
echo "4. ciftify-subject-fmri.py"
echo "-----"
ciftify_subject_fmri ${epi_dir}/proc_bold.nii.gz \
    ${sub} ${tsk} --SmoothingFWHM 2 --n_cpus ${n_cpus} \
    -v --debug
```

5. ext_rsfc.py

```
# 5. Run extract_rsfc.py to extract RSFC
echo "-----"
echo "5. Running extract_rsfc.py"
echo "-----"
bold_path=${mni_dir}/Results/${tsk}/${tsk}_Atlas_s8.dtseries.nii
parc_path=${work_dir}/Gordon_352_parcdlabel.nii
save_path=${work_dir}/output/${sub}

python3 ${work_dir}/ext_rsfc.py ${bold_path} ${parc_path} ${save_path}
```


extract-rsfc-pipeline

QC files

- **index.html**
 - Produced from AFNI processing
- **qc.html**
 - Produced from ciftify-recon-all processing

```
work_dir
├── data
│   ├── sub-01
│   │   ├── sub-01.results
│   │   │   ├── QC_sub-01
│   │   │   │   └── index.html
│   └── output
│       ├── qc_recon_all
│       │   ├── sub-01
│       │   │   └── qc.html
│       └── sub-01
│           ├── rsfc.npz
│           ├── MNINonLinears
│           │   └── task-rest
│           └── task-rest...
```