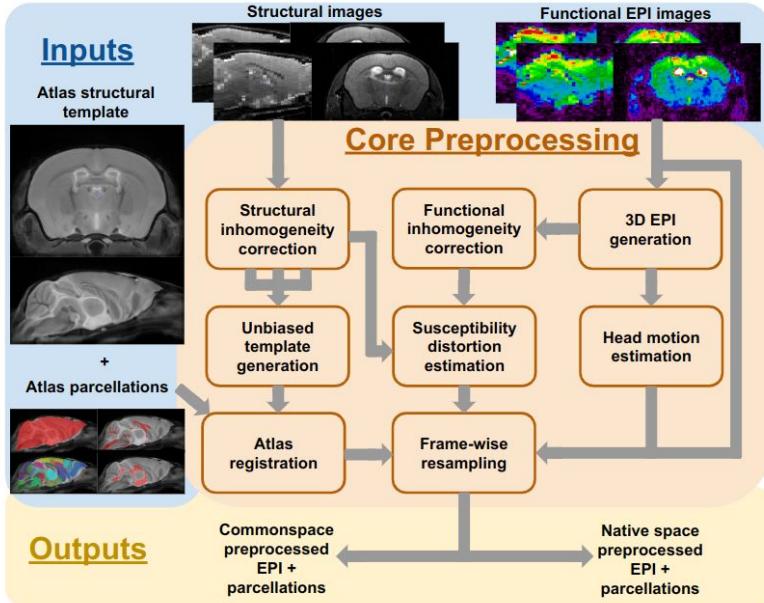


RABIES: Rodent Automated Bold Improvement of EPI Sequences. (overview)

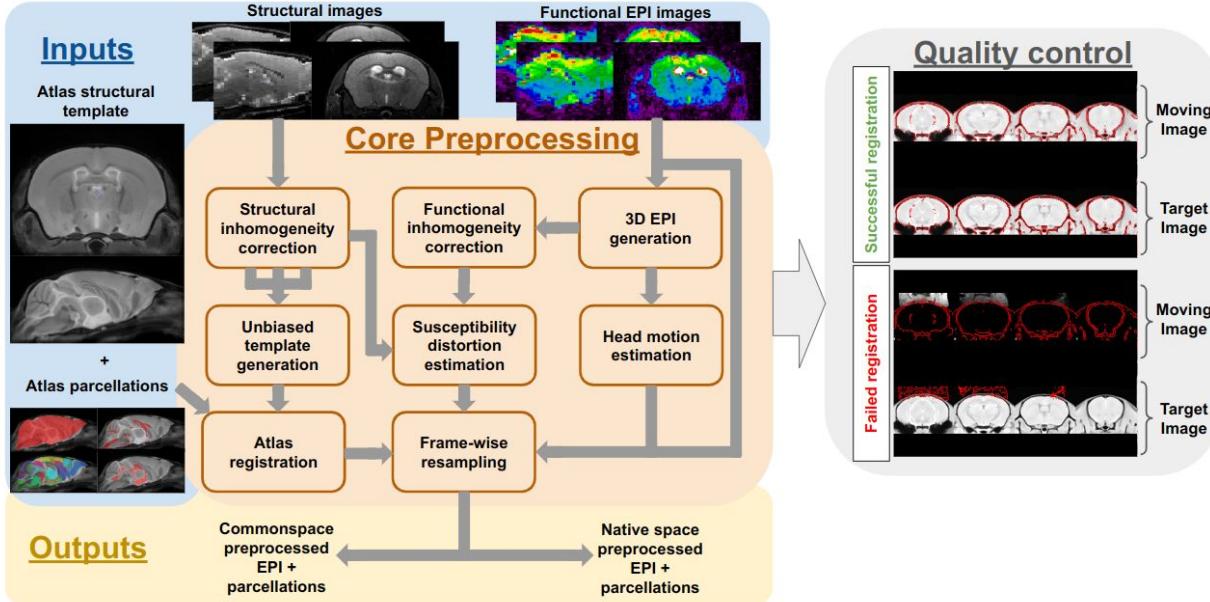
INCF Neuroinformatics Assembly 2023

Presented by Gabriel Desrosiers-Gregoire
McGill University

RABIES: Rodent Automated Bold Improvement of EPI Sequences

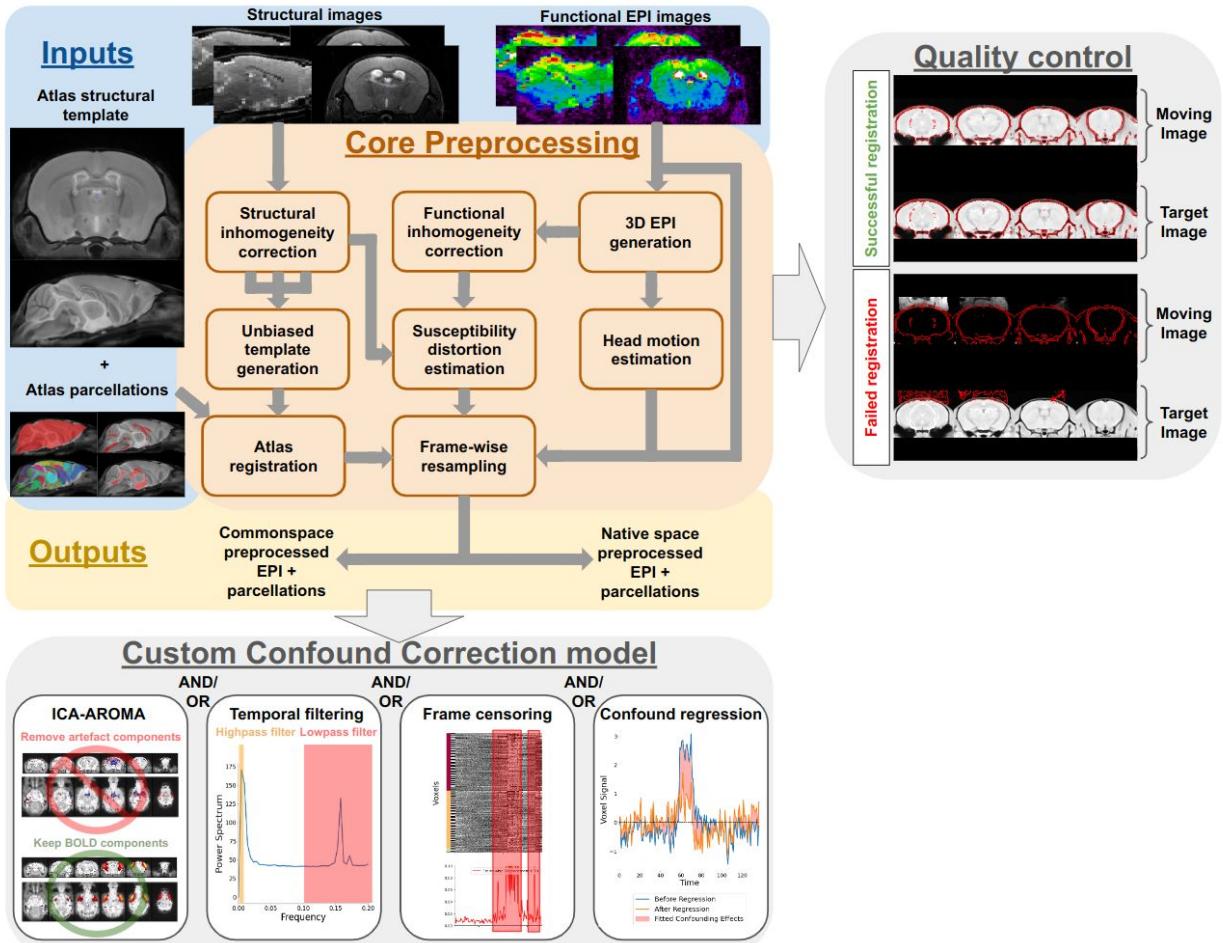


RABIES: Rodent Automated Bold Improvement of EPI Sequences

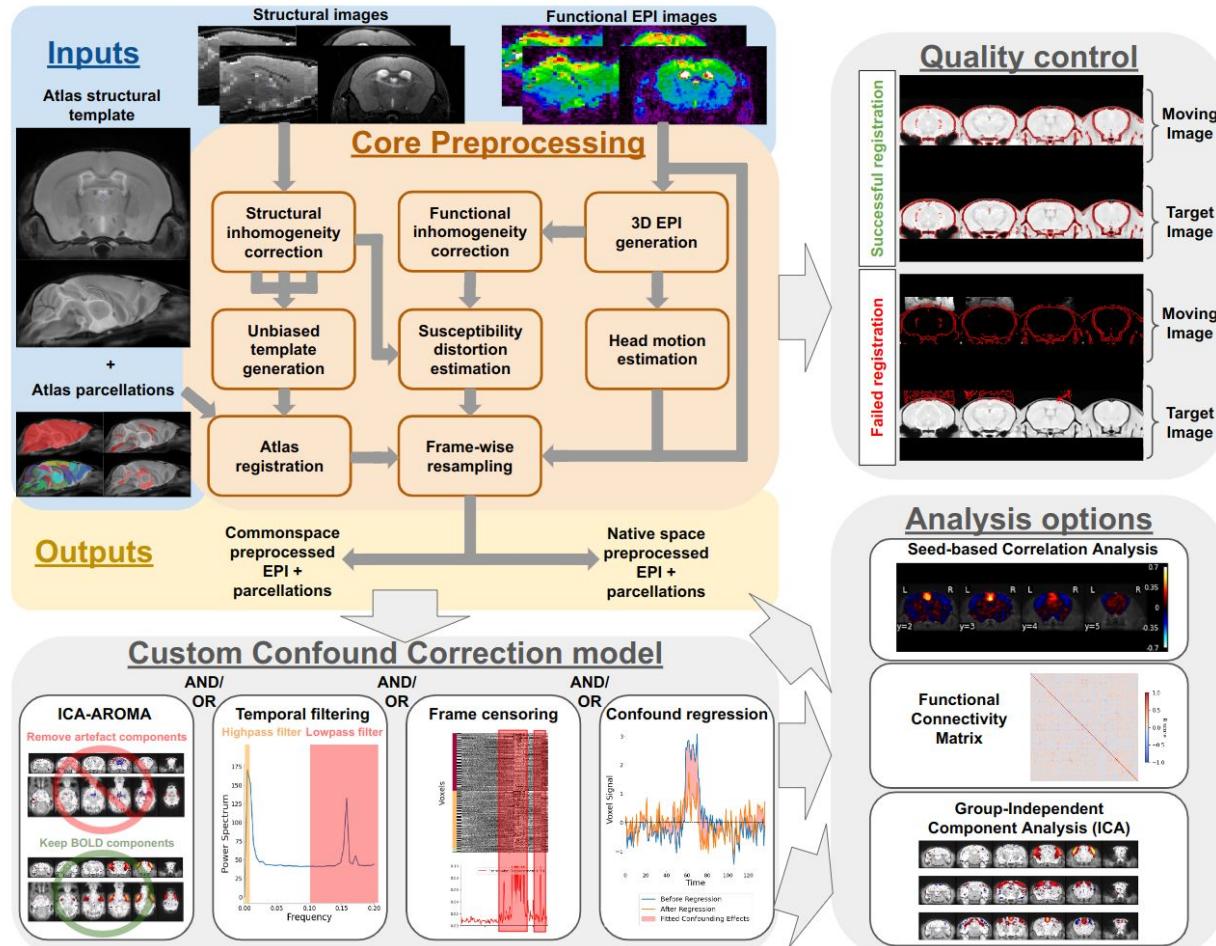


~99% success rate for preprocessing registration across 23 datasets (including both mice and rats)
(Desrosiers-Gregoire et al. (2022), BioRxiv) + **43 rat fMRI sites**
(Grandjean et al. (2022), BioRxiv)

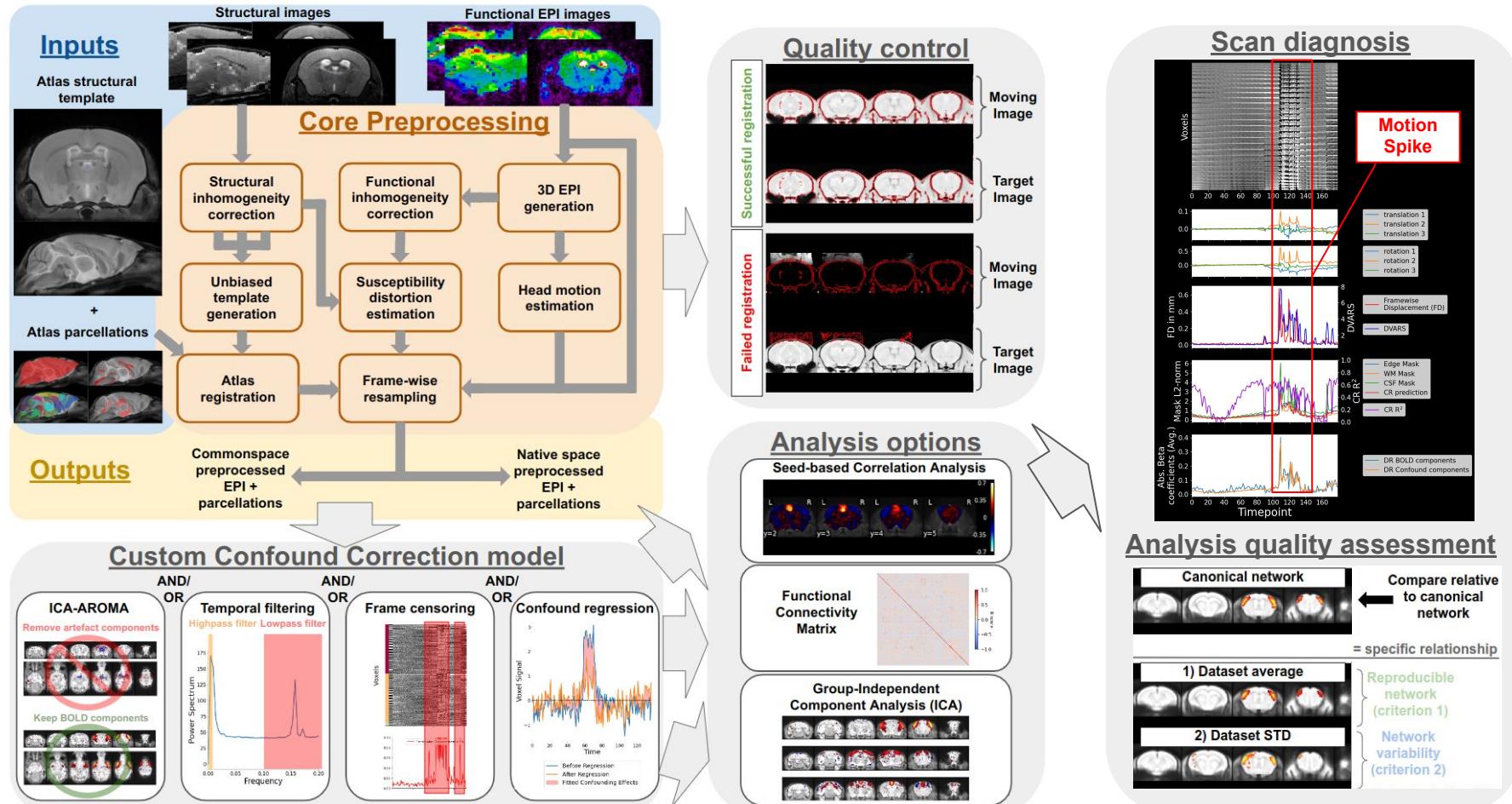
RABIES: Rodent Automated Bold Improvement of EPI Sequences



RABIES: Rodent Automated Bold Improvement of EPI Sequences

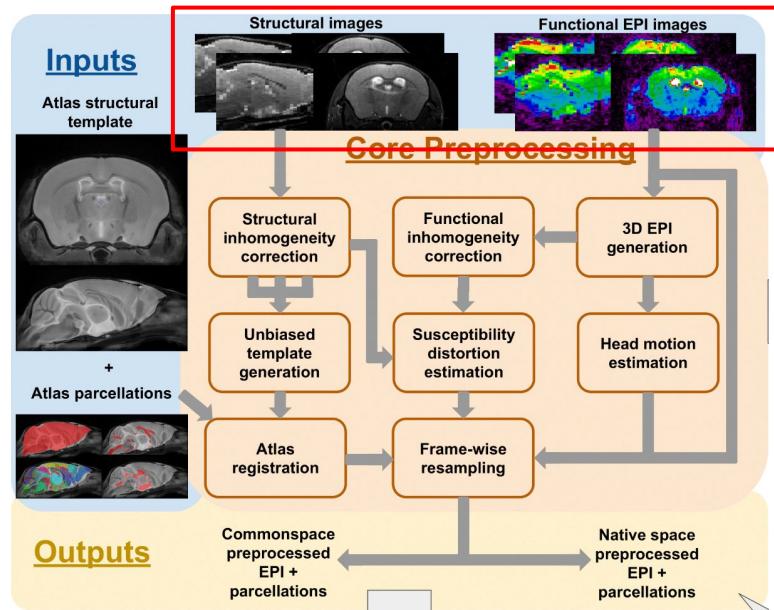


RABIES: Rodent Automated Bold Improvement of EPI Sequences



Preprocessing

Inputs: BIDS dataset



Input dataset following BIDS format:

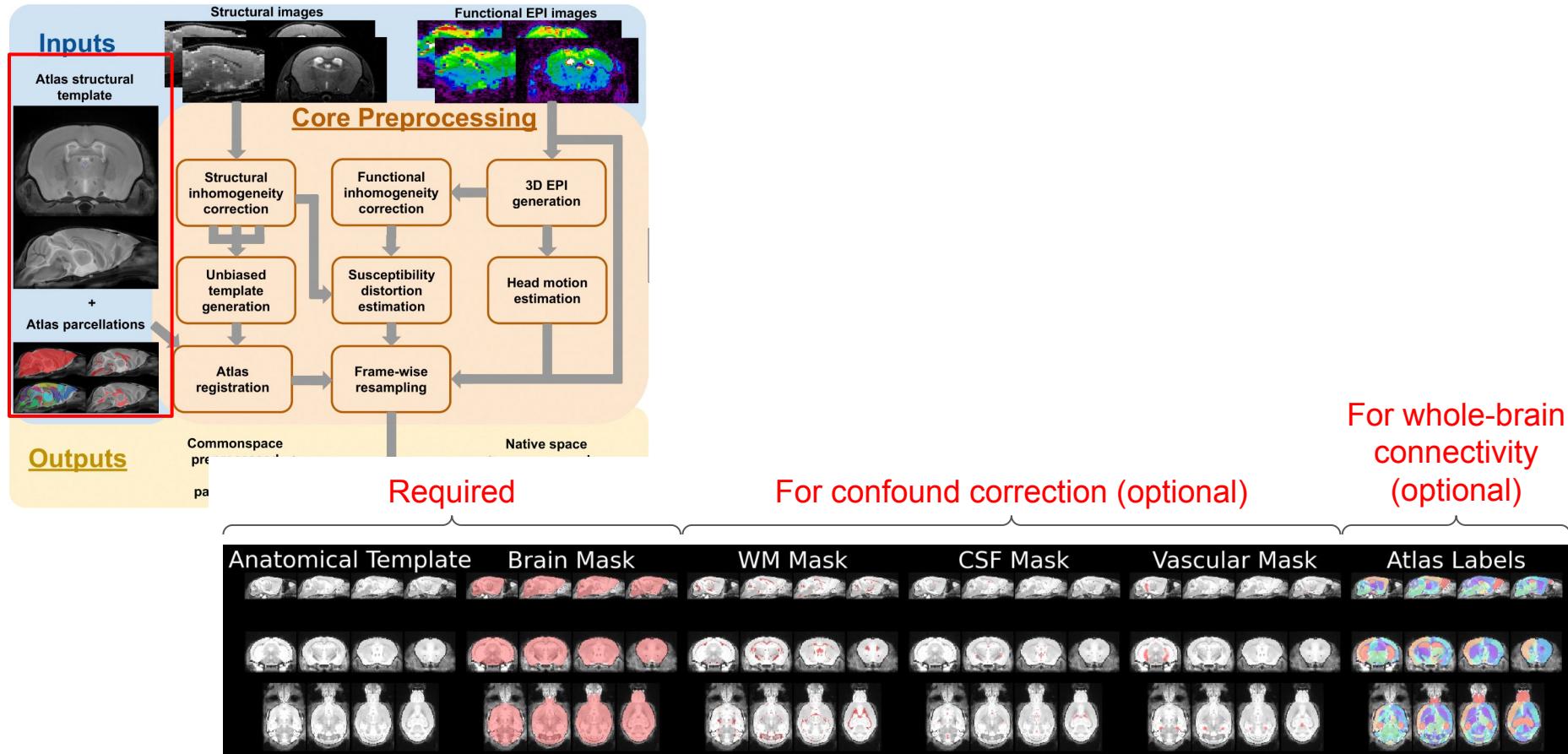
```
test_dataset
└── sub-MFC067
    └── ses-1
        ├── anat
        │   └── sub-MFC067_ses-1_acq-FLASH_T1w.nii.gz
        └── func
            └── sub-MFC067_ses-1_task-rest_acq-EPI_run-1_bold.nii.gz
└── sub-MFC068
    └── ses-1
        ├── anat
        │   └── sub-MFC068_ses-1_acq-FLASH_T1w.nii.gz
        └── func
            └── sub-MFC068_ses-1_task-rest_acq-EPI_run-1_bold.nii.gz
```

Bruker to Nifti conversion: <https://brkraw.github.io/>

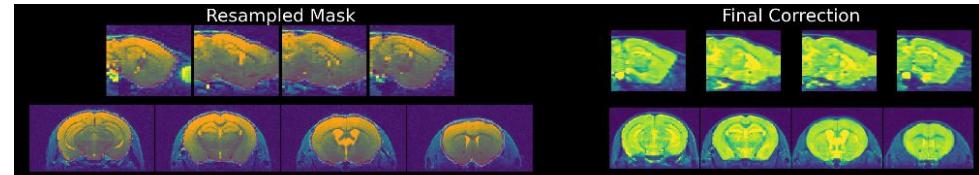
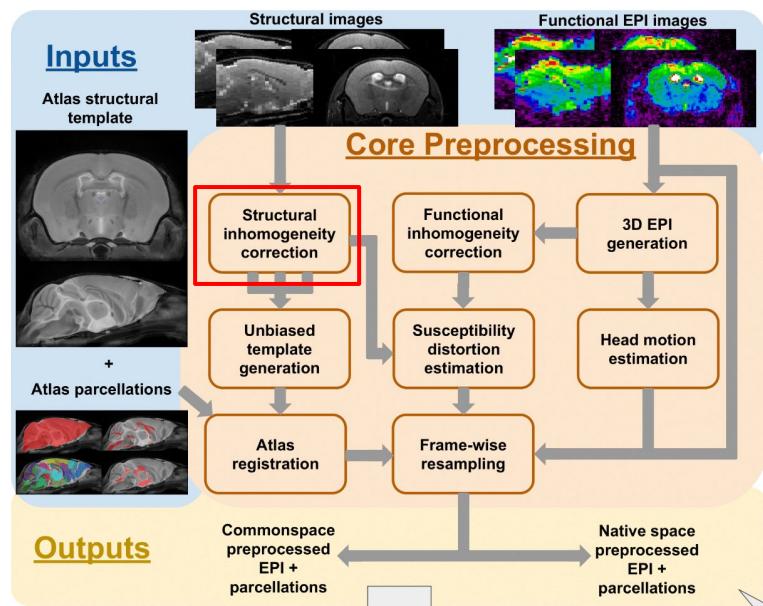
*may also handle direct conversion to BIDS format

CoBrA lab wiki: <https://github.com/CoBrALab/documentation/wiki/bruker2nifti-conversion>

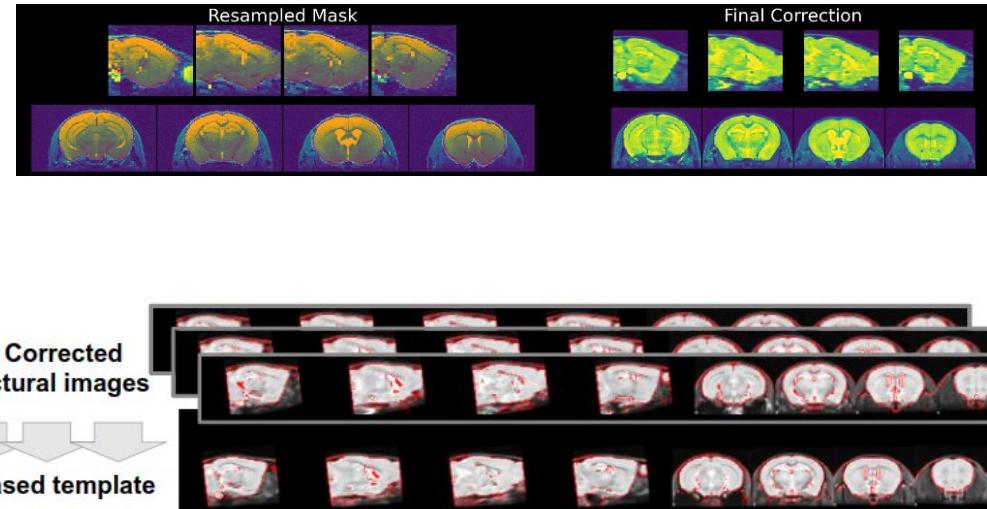
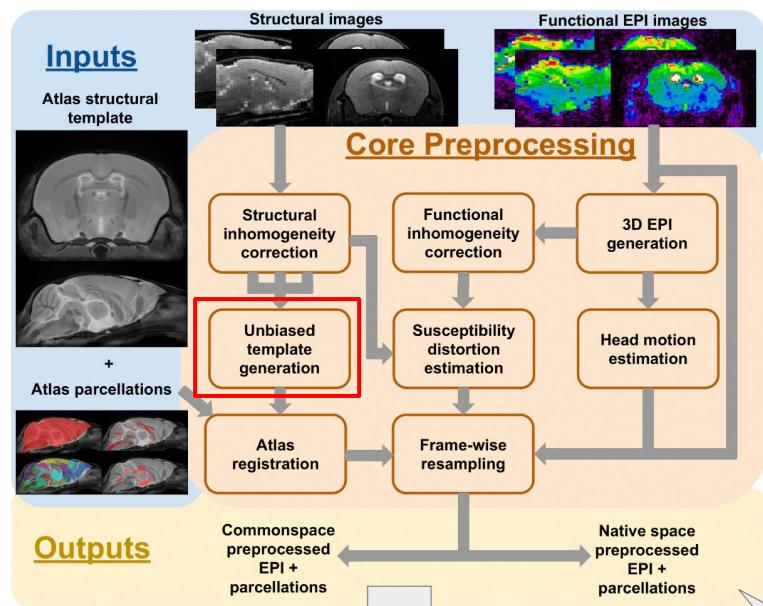
Inputs: template files



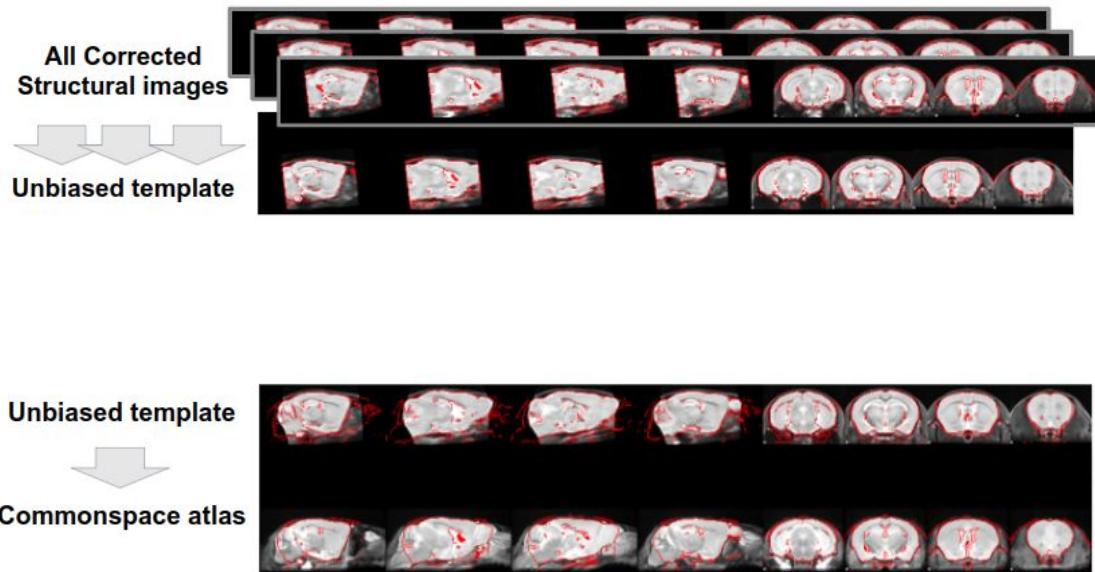
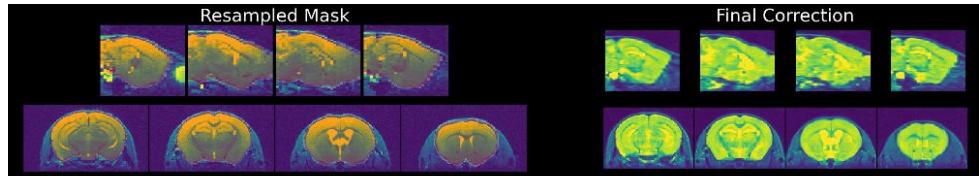
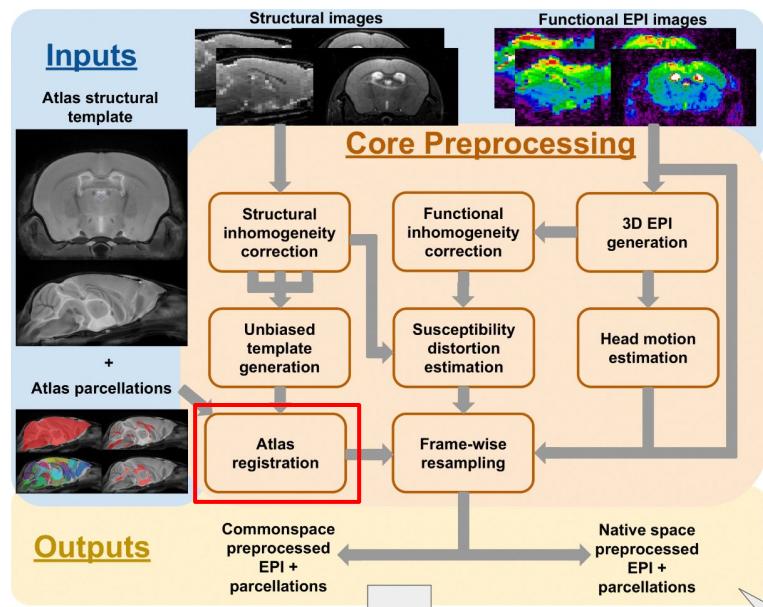
Preprocessing: commonspace alignment



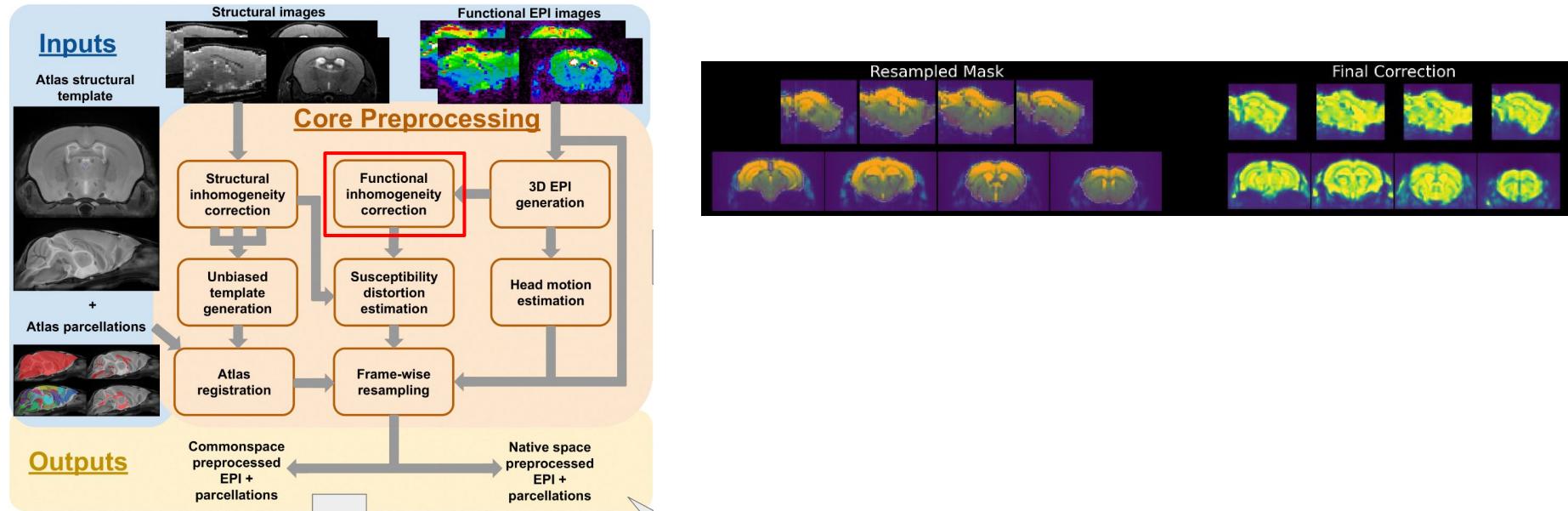
Preprocessing: commonspace alignment



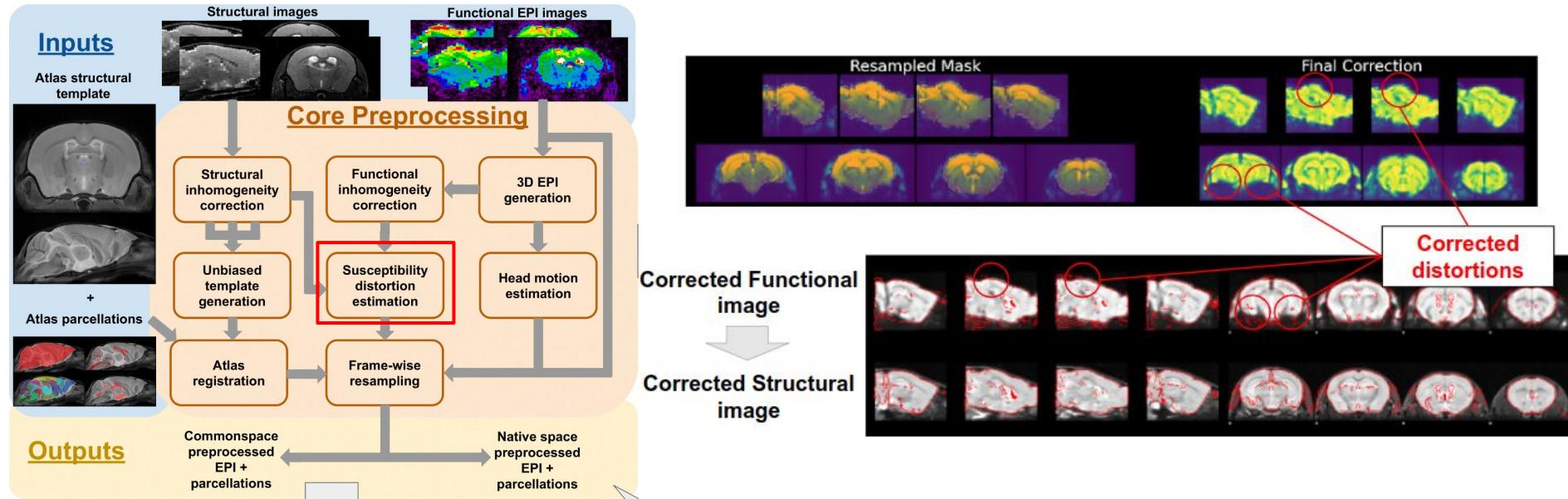
Preprocessing: commonspace alignment



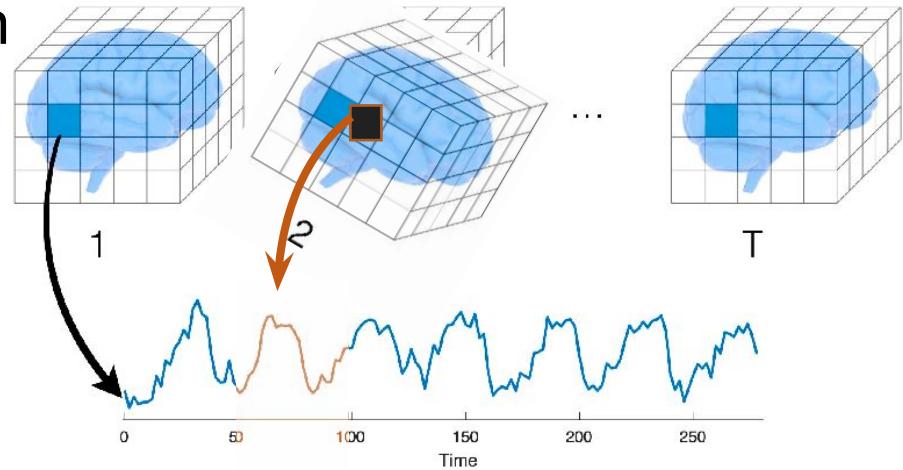
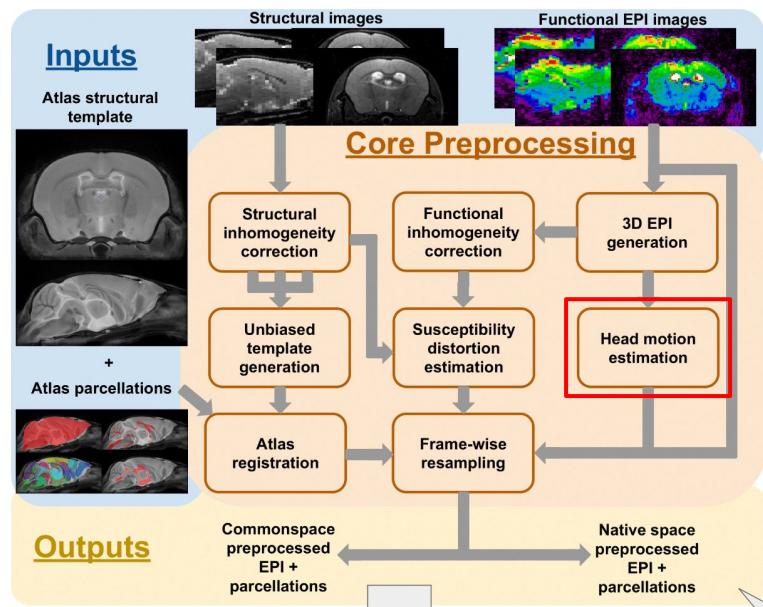
Preprocessing: EPI distortion correction



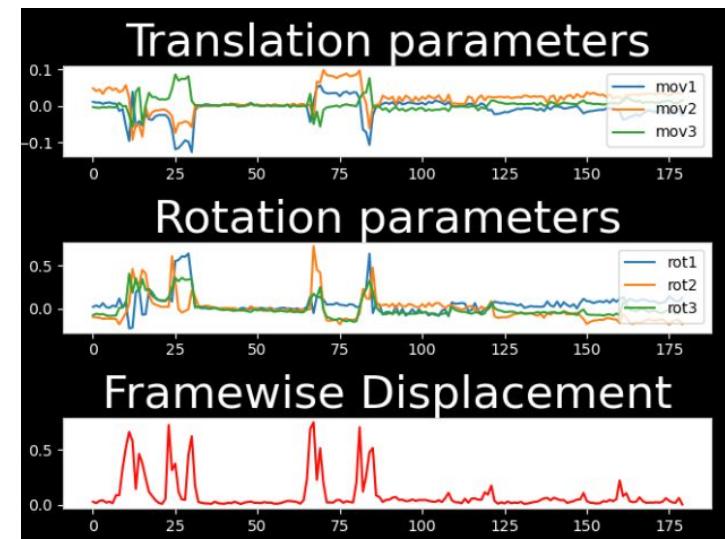
Preprocessing: EPI distortion correction



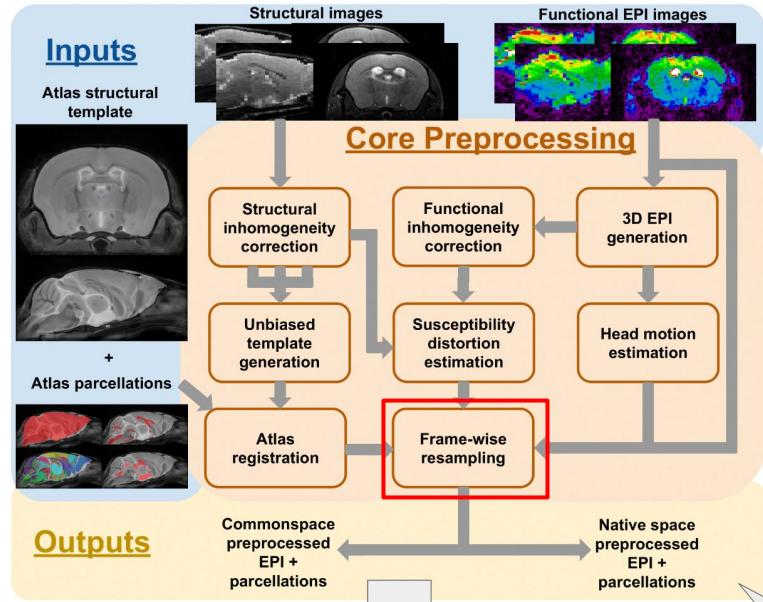
Preprocessing: motion correction



Siden, 2020



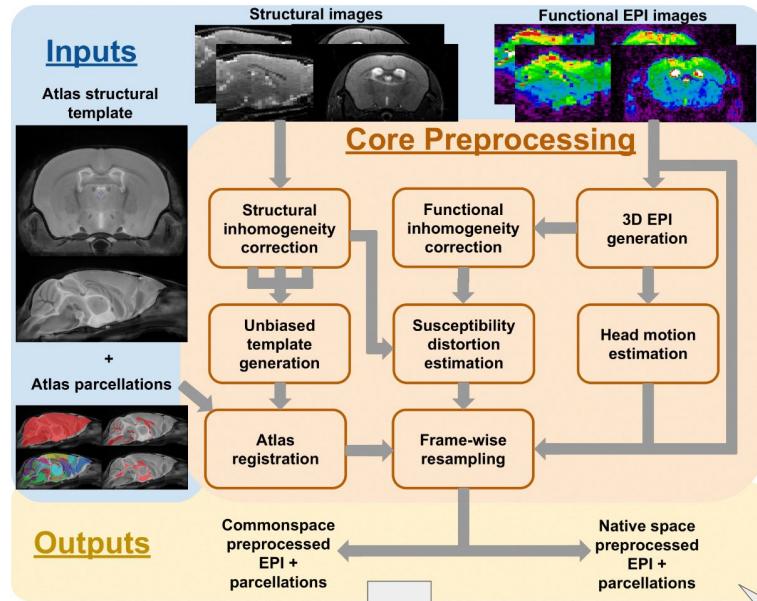
Preprocessing: “one-shot” resampling



Combine and apply transforms in one interpolation for each frame:

1. head motion realignment
2. distortion correction
3. resampling to common/native space

Preprocessing: additional options



- Slice-timing correction (AFNI)
- Despiking (AFNI)
- Autobox (AFNI)
- Customize resampling resolution (common or native space)

See complete command line interface at

https://rabies.readthedocs.io/en/stable/running_the_software.html#command-line-interface

Preprocessing: Execution (https://rabies.readthedocs.io/en/stable/running_the_software.html#)

PyPi installation:

```
pip install rabies
```

RABIES command line syntax:

```
(base) gabriel@gabriel-XPS-13-7390:~$ rabies -p MultiProc preprocess input_BIDS/ preprocess_outputs/ --apply_STC --TR 1.2
```

Containerized installation:

- Install Singularity .sif file:

```
singularity build rabies.sif docker://gabdesgreg/rabies:tagname
```

```
#!/bin/bash
#SBATCH --time=24:00:00
#SBATCH --nodes=1
#SBATCH --account=rrg-mchakrav-ab
singularity run -B /scratch/m/mchakrav/desgab/data/multicenter/inputs/7_Cryo_mediso_v:/nii_inputs:ro \
-B /scratch/m/mchakrav/desgab/data_preprocess/multicenter/rabies_7_cryo_mediso_v_20221024:/rabies_out \
-B /home/m/mchakrav/desgab/atlasses:/atlasses:ro /home/m/mchakrav/desgab/singularity_images/rabies-0.4.7.sif \
-p MultiProc preprocess /nii_inputs/rabies_out --labels /atlasses/hierarchical_downsample/EPI_template_DSURQE_downsample.nii.gz \
--bold_only --commonspace_resampling 0.2x0.2x0.2 \
--commonspace_reg masking=true,brain_extraction=false,template_registration=SyN,fast_commonspace=false
preprocess_call/preprocess_7_Cryo_mediso_v.sh (END)
```

Managing computing resources

```
Execution Options:
  Options for parallel execution and memory management.

  -p {Linear,MultiProc,SGE,SGEGraph,PBS,LSF,SLURM,SLURMGraph}, --plugin {Linear,MultiProc,SGE,SGEGraph,PBS,LSF,SLURM,SLURMGraph}
    Specify the nipype plugin for workflow execution.
    Consult https://nipype.readthedocs.io/en/0.11.0/users/plugins.html for details.
    (default: Linear)

  --local_threads LOCAL_THREADS
    For --plugin MultiProc, set the maximum number of processors run in parallel.
    Defaults to number of CPUs.
    (default: 12)

  --scale_min_memory SCALE_MIN_MEMORY
    For --plugin MultiProc, set the memory scaling factor attributed to nodes during
    execution. Increase the scaling if memory crashes are reported.
    (default: 1.0)

  --min_proc MIN_PROC  For --plugin SGE/SGEGraph, scale the number of nodes attributed to jobs to
    avoid memory crashes.
    (default: 1)

  --verbose VERBOSE    Set the verbose level. 0=WARNING, 1=INFO, 2 or above=DEBUG.
    (default: 1)
```

Outputs

```
rabies_7_Cryo_mediso_v_20221024
├── boilerplate.txt
├── bold_datasink
├── confounds_datasink
├── main_wf
├── preprocess_QC_report
├── rabies_preprocess.log
├── rabies_preprocess.pkl
├── rabies_preprocess_workflow.pkl
├── transforms_datasink
└── unbiased_template_datasink
```

- Preprocessed images and label files
- Nuisance timecourses
- Internal files from execution
- Quality control report
- Log report
- Transform files for various registration steps

Outputs

```
rabies_7_Cryo_mediso_v_20221024
├── boilerplate.txt
└── bold_datasink
├── confounds_datasink
├── main_wf
├── preprocess_QC_report
├── rabies_preprocess.log
├── rabies_preprocess.pkl
├── rabies_preprocess_workflow.pkl
└── transforms_datasink
└── unbiased_template_datasink
```

```
bold_datasink/
├── commonspace_bold
├── commonspace_CSF_mask
├── commonspace_labels
├── commonspace_mask
├── commonspace_resampled_template
├── commonspace_vascular_mask
├── commonspace_WM_mask
├── inho_cor_bold
├── initial_bold_ref
├── input_bold
├── raw_brain_mask
├── std_map_preprocess
└── tSNR_map_preprocess
```

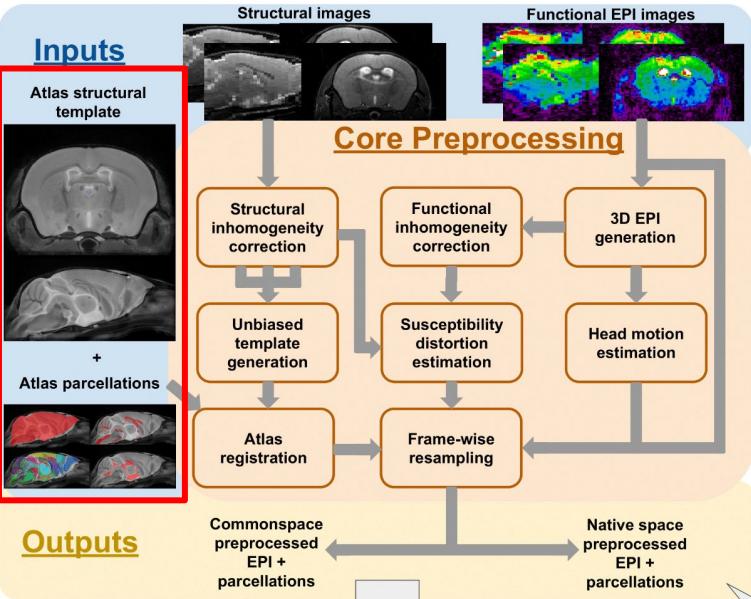
```
commonspace_bold
├── scan_info_subject_id001.session1.runNone_split_name_sub-001_ses-1_task-rest_acq-EPI_bold
│   └── sub-001_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id002.session1.runNone_split_name_sub-002_ses-1_task-rest_acq-EPI_bold
│   └── sub-002_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id003.session1.runNone_split_name_sub-003_ses-1_task-rest_acq-EPI_bold
│   └── sub-003_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id004.session1.runNone_split_name_sub-004_ses-1_task-rest_acq-EPI_bold
│   └── sub-004_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id005.session1.runNone_split_name_sub-005_ses-1_task-rest_acq-EPI_bold
│   └── sub-005_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id006.session1.runNone_split_name_sub-006_ses-1_task-rest_acq-EPI_bold
│   └── sub-006_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id007.session1.runNone_split_name_sub-007_ses-1_task-rest_acq-EPI_bold
│   └── sub-007_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id008.session1.runNone_split_name_sub-008_ses-1_task-rest_acq-EPI_bold
│   └── sub-008_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id009.session1.runNone_split_name_sub-009_ses-1_task-rest_acq-EPI_bold
│   └── sub-009_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id010.session1.runNone_split_name_sub-010_ses-1_task-rest_acq-EPI_bold
│   └── sub-010_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id011.session1.runNone_split_name_sub-011_ses-1_task-rest_acq-EPI_bold
│   └── sub-011_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id012.session1.runNone_split_name_sub-012_ses-1_task-rest_acq-EPI_bold
│   └── sub-012_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id013.session1.runNone_split_name_sub-013_ses-1_task-rest_acq-EPI_bold
│   └── sub-013_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
├── scan_info_subject_id014.session1.runNone_split_name_sub-014_ses-1_task-rest_acq-EPI_bold
│   └── sub-014_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
└── scan_info_subject_id015.session1.runNone_split_name_sub-015_ses-1_task-rest_acq-EPI_bold
    └── sub-015_ses-1_task-rest_acq-EPI_bold_combined.nii.gz
```

Quality control

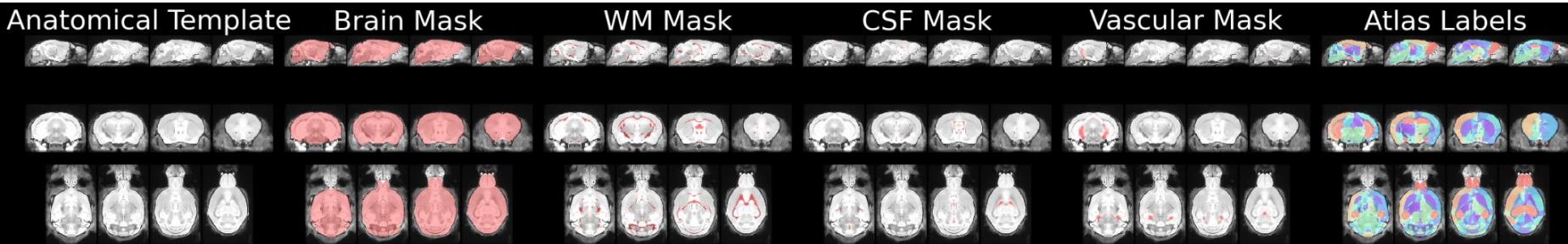
```
rabies_7_Cryo_mediso_v_20221024
├── boilerplate.txt
├── bold_datasink
├── confounds_datasink
├── main_wf
└── preprocess_QC_report
    └── rabies_preprocess.log
    └── rabies_preprocess.pkl
    └── rabies_preprocess_workflow.pkl
    └── transforms_datasink
    └── unbiased_template_datasink
```

```
preprocess_QC_report/
├── anat_inho_cor
├── bold_inho_cor
├── commonspace_reg_wf.Native2Unbiased
├── commonspace_reg_wf.Unbiased2Atlas
├── EPI2Anat
└── template_files
    └── temporal_features
```

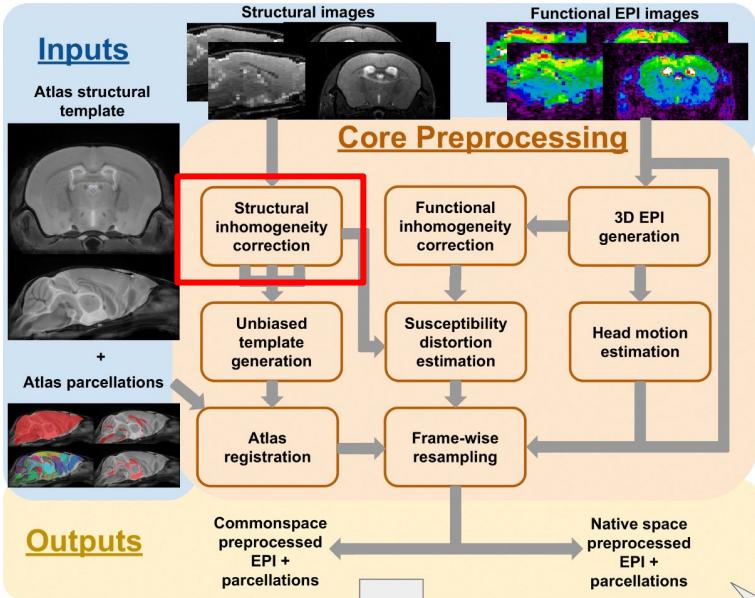
Quality control



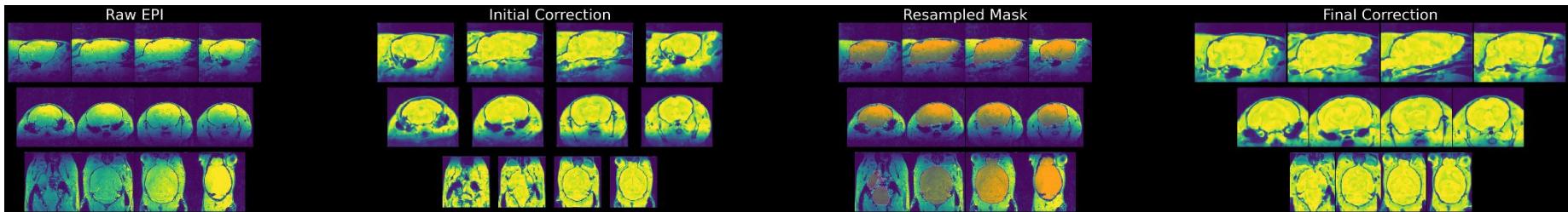
```
preprocess_QC_report/
  anat_inho_cor
  bold_inho_cor
  commonspace_reg_wf.Native2Unbiased
  commonspace_reg_wf.Unbiased2Atlas
  FPT2Anat
  template_files
  temporal_features
```



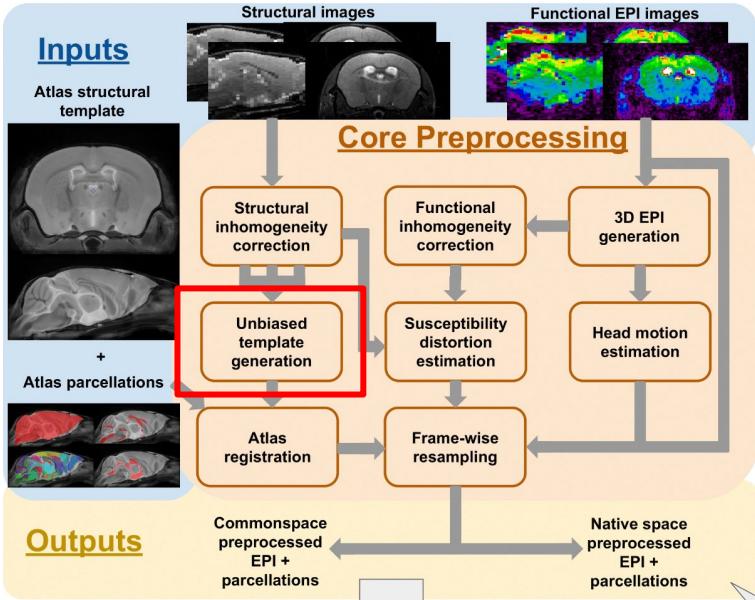
Quality control



```
preprocess QC report/
  anat_inho_cor
  bold_inho_cor
  commonspace_reg_wf.Native2Unbiased
  commonspace_reg_wf.Unbiased2Atlas
  EPI2Anat
  template_files
  temporal_features
```

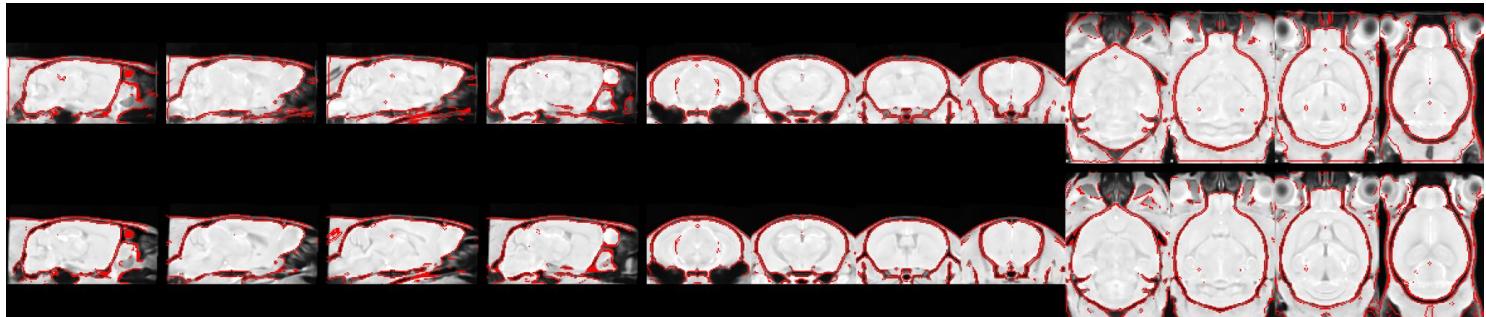


Quality control



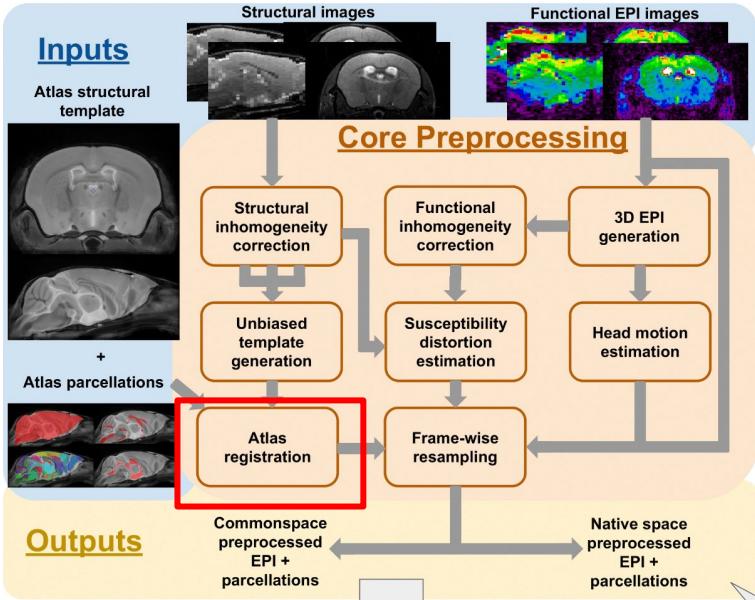
```
preprocess_QC_report/
└── anat_inho_cor
└── bold_inho_cor
└── commonspace_reg_wf.Native2Unbiased
└── commonspace_reg_wf.Unbiased2Atlas
└── EPI2Anat
└── template_files
└── temporal_features
```

Single anatomical scan



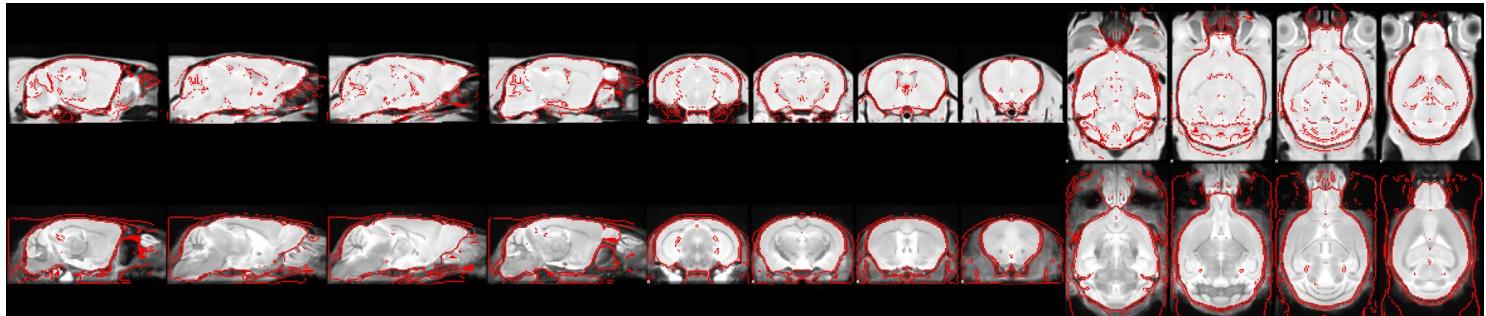
Generated template

Quality control



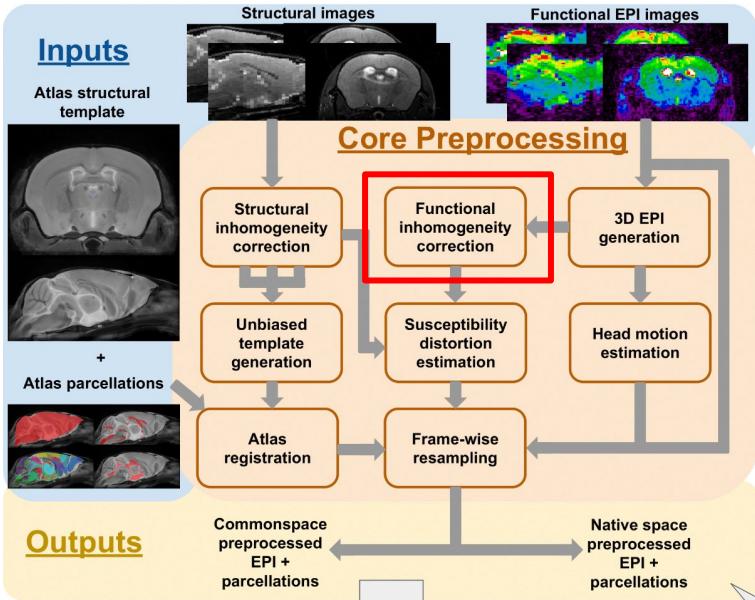
```
preprocess_QC_report/
  anat_inho_cor
  bold_inho_cor
  commonspace_reg_wf.Native2Unbiased
  commonspace_reg_wf.Unbiased2Atlas
  EPI2Anat
  template_files
  temporal_features
```

Generated template

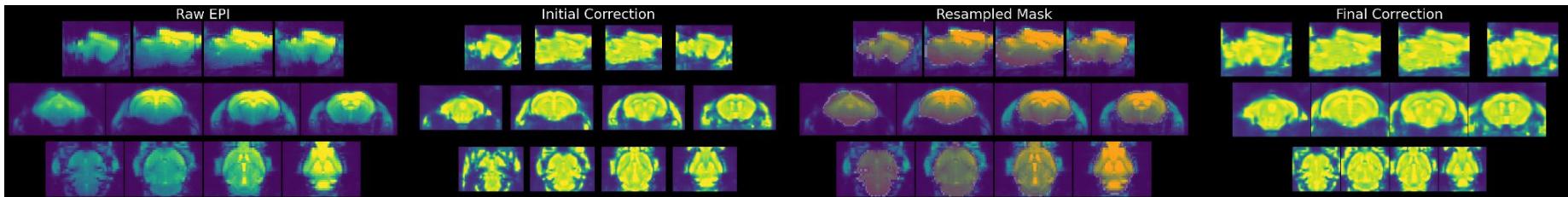


External template

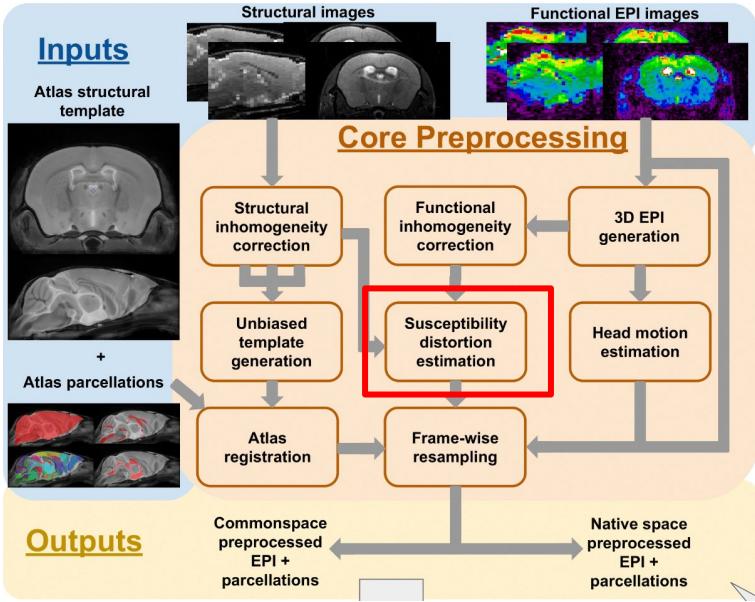
Quality control



```
preprocess_QC_report/
  anat_inho_cor
  bold_inho_cor
  commonspace_reg_wf.Native2Unbiased
  commonspace_reg_wf.Unbiased2Atlas
  EPI2Anat
  template_files
  temporal_features
```

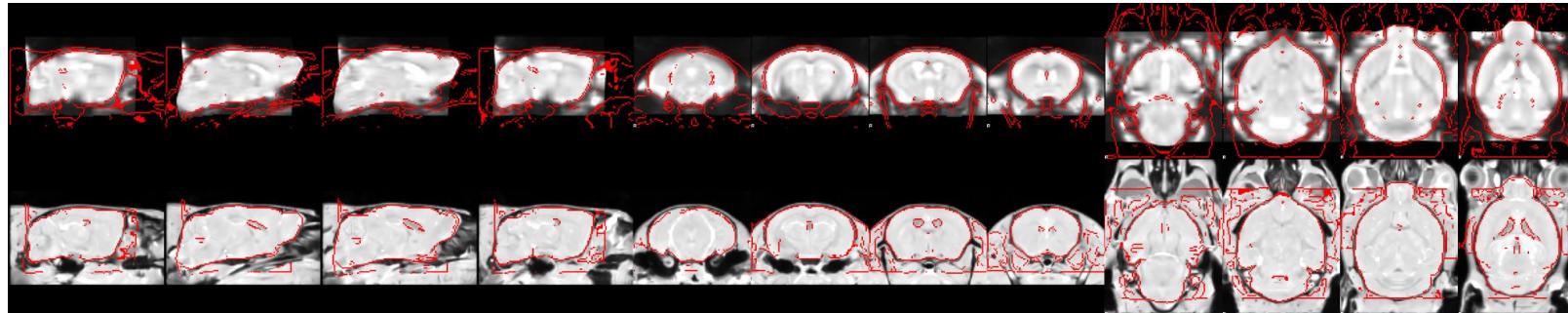


Quality control



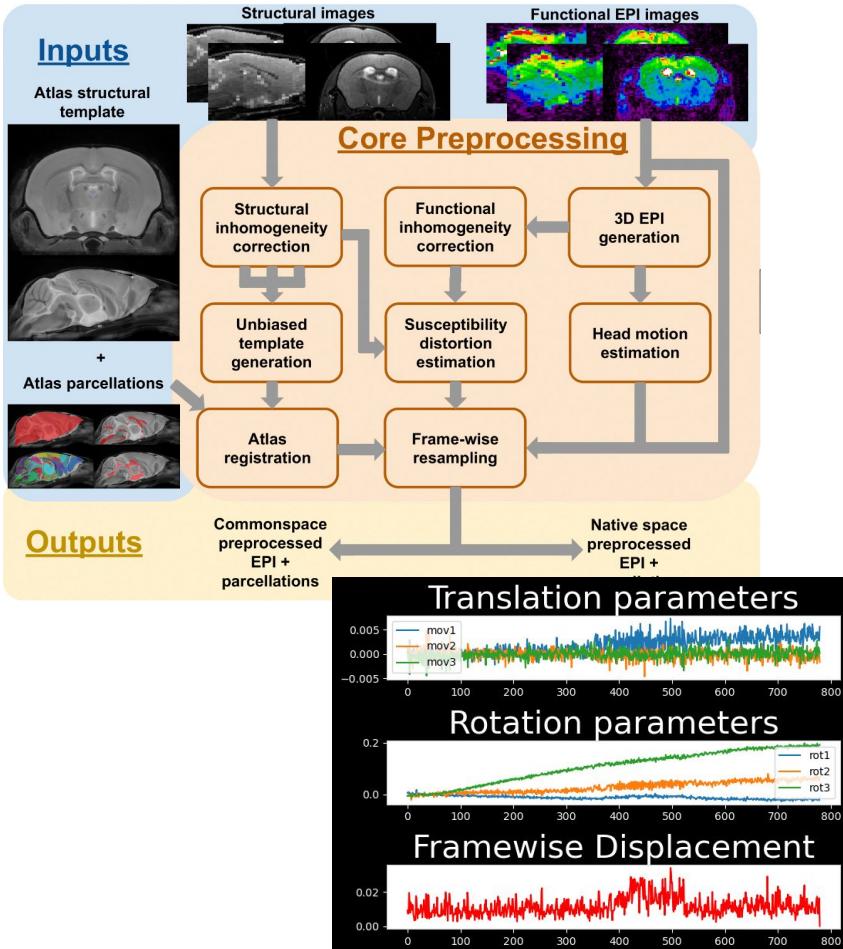
```
preprocess_QC_report/
  anat_inho_cor
  bold_inho_cor
  commonspace_reg_wf.Native2Unbiased
  commonspace_reg_wf.Unbiased2Atlas
  EPI2Anat
  template_files
  temporal_features
```

EPI scan

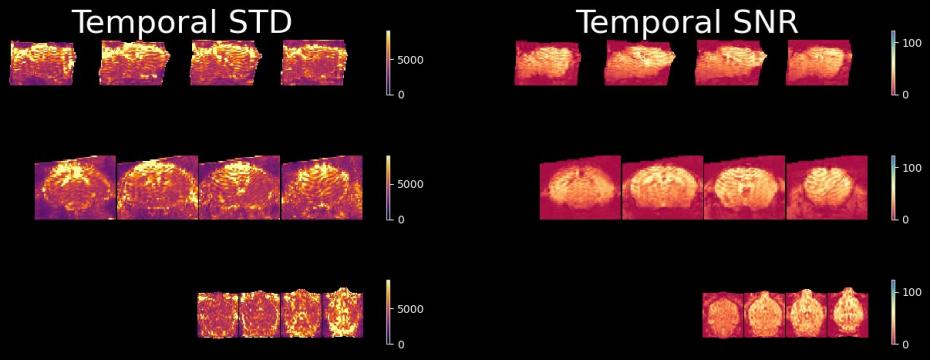


Same session anatomical scan

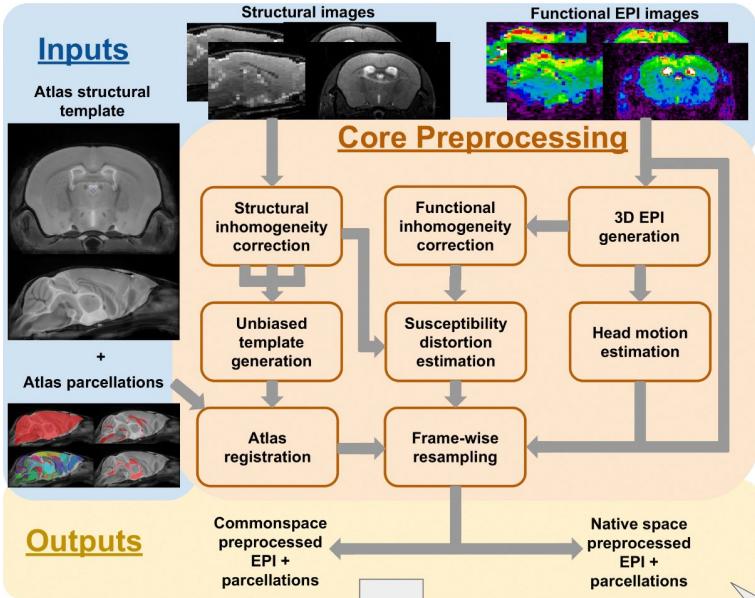
Quality control



```
preprocess_QC_report/
  anat_inho_cor
  bold_inho_cor
  commonspace_reg_wf.Native2Unbiased
  commonspace_reg_wf.Unbiased2Atlas
  EPI2Anat
  template_files
  temporal_features
```

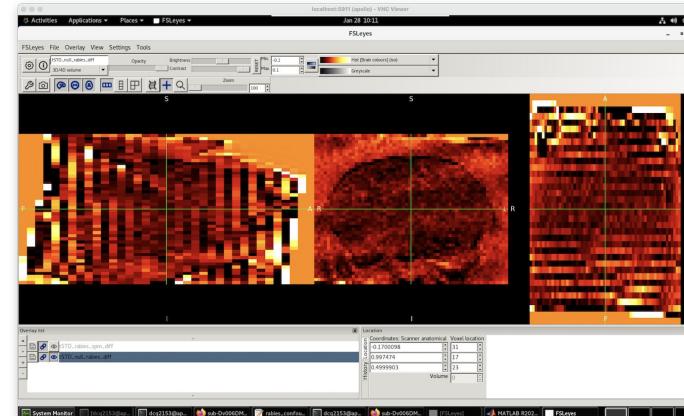


Quality control



```
preprocess_QC_report/
├── anat_inho_cor
├── bold_inho_cor
├── commonspace_reg_wf.Native2Unbiased
├── commonspace_reg_wf.Unbiased2Atlas
└── EPI2Anat
    └── template_files
        └── temporal_features
```

User detected grating artefact from slice timing correction (<https://github.com/CoBrALab/RABIES/discussions/270>):

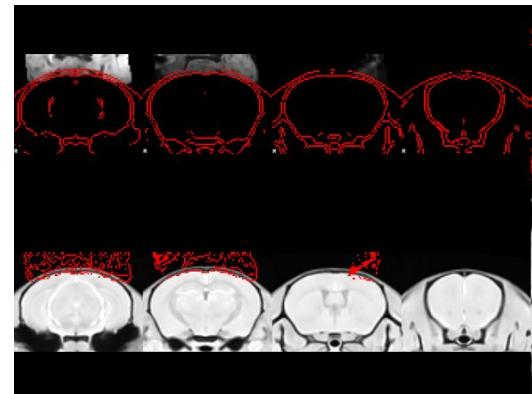


Registration troubleshooting

- Inhomogeneity correction (`--anat_inho_cor` or `--bold_inho_cor`):
 - Incomplete bias field correction (despite accurate brain mask): `multiotsu=true`
 - There a subset of masking failure, or mask is partially misregistered:
`--anat_robust_inho_cor`/`--bold_robust_inho_cor`
 - Registration is impacted by tissue outside the brain: consider `--anat_autobox`/`--bold_autobox` to crop the image, or increase `otsu_thresh` to ignore voxels with lower intensity
 - There remains many masking failures: reduce the registration method from `SyN` -> `Affine` -> `Rigid` -> `no_reg`
- Commonspace or EPI2Anat registration (`--commonspace_reg` or `--bold2anat_coreg`)
 - `masking=true` : rely on the pre-computed brain mask during inhomogeneity correction
 - `brain_extraction=true` : ignore voxels outside the brain; effective for matching brain edges, or for incomplete brain coverage

More details at

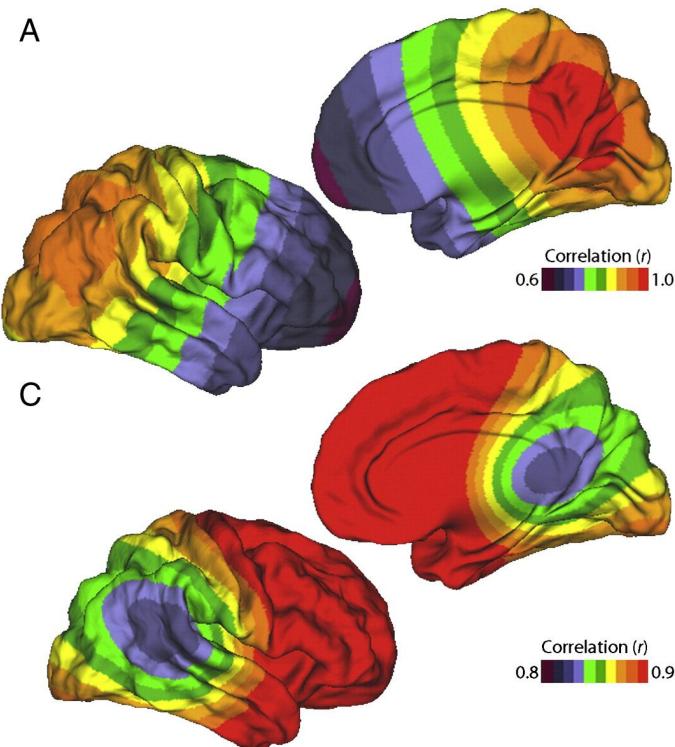
https://rabies.readthedocs.io/en/latest/registration_troubleshoot.html



Confound correction

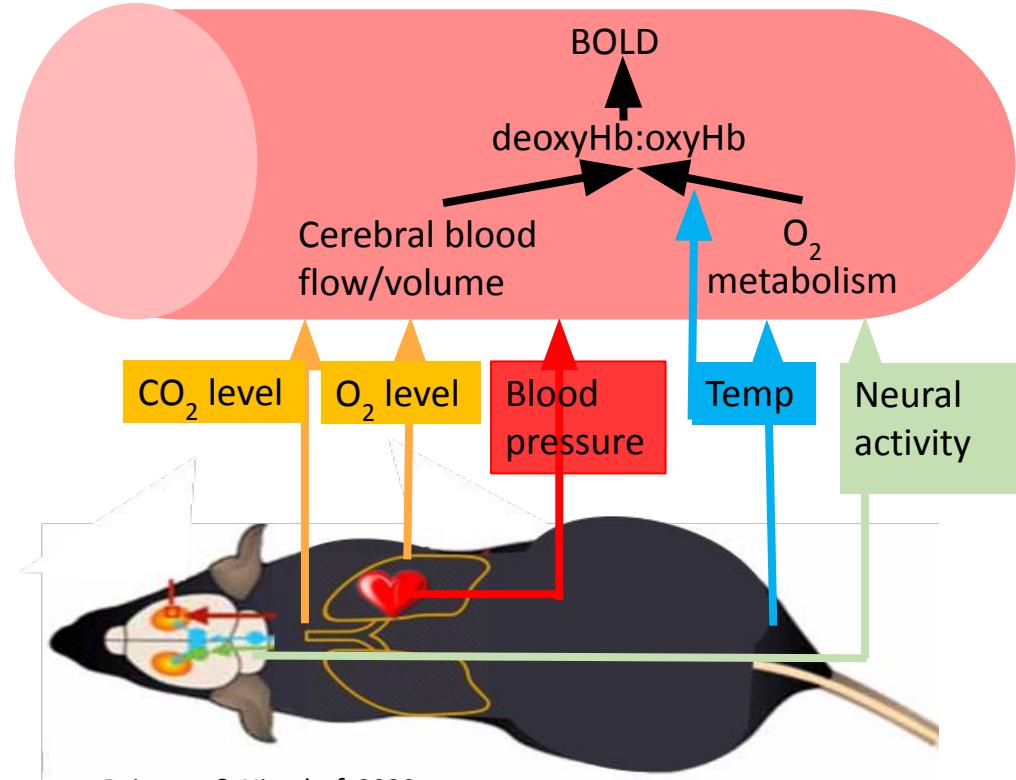
BOLD confounds

Motion causes global correlations



Satterthwaite, T. D., et al. (2013). *Neuroimage*, 64, 240-256.

Many physiological influences

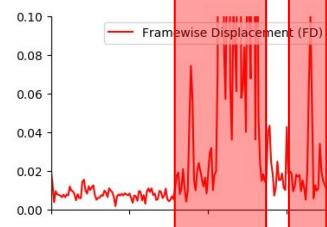
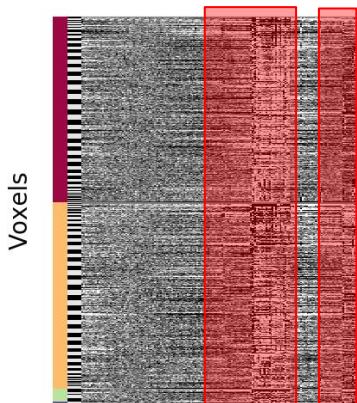


Reimann & Niendorf, 2020

Slide credit: Mila Urosevic

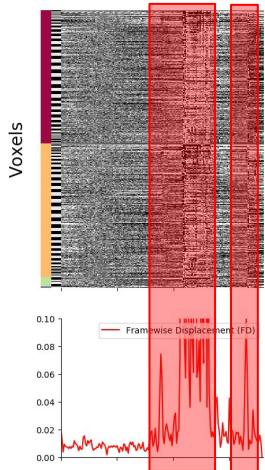
Confound correction

Spike censoring ("scrubbing")

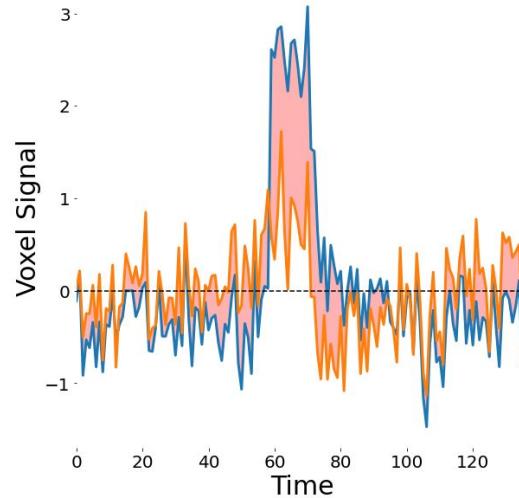


Confound correction

Spike censoring

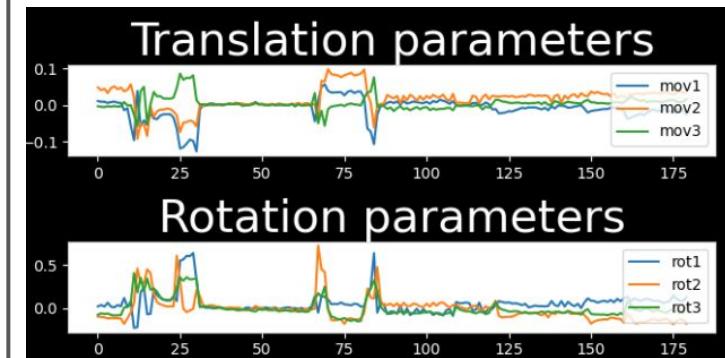


Confound regression



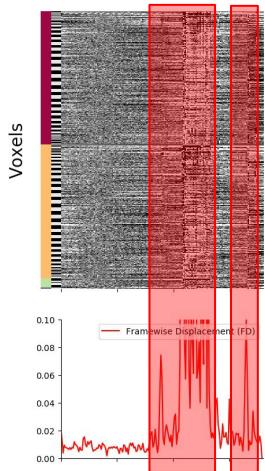
Before Regression
After Regression
Fitted Confounding Effects

Confound regressors: e.g. 6 motion parameters

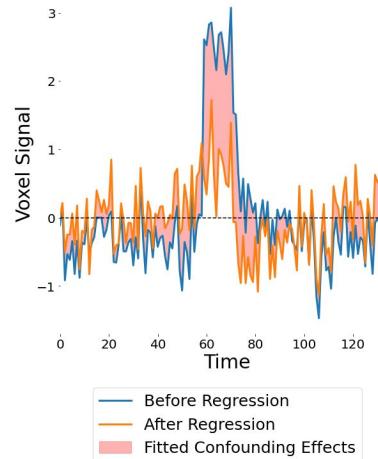


Confound correction

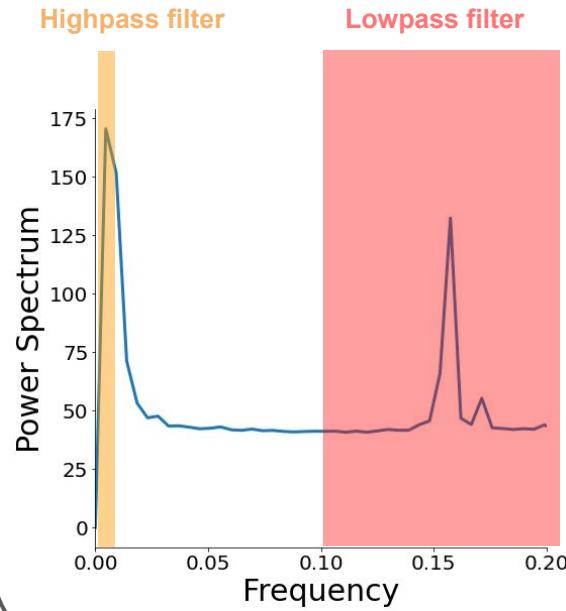
Spike censoring



Confound regression

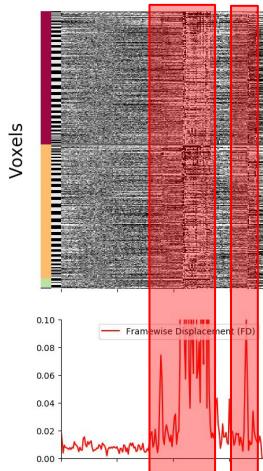


Temporal filtering

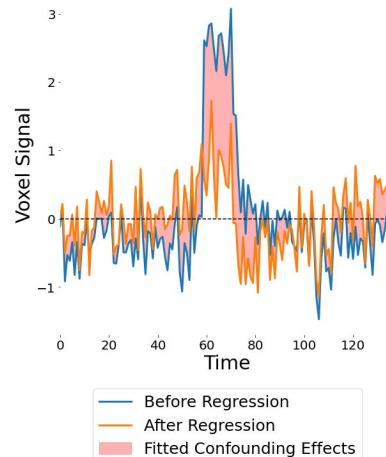


Confounding correction

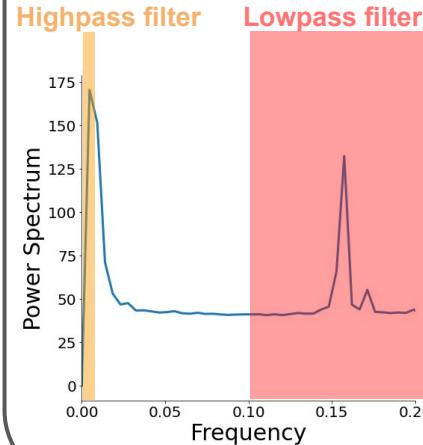
Spike censoring



Confound regression

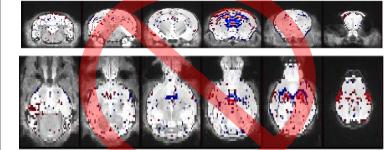


Temporal filtering

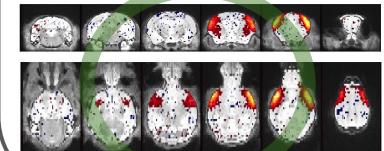


ICA-AROMA

Remove artefact components



Keep BOLD components



Confound correction: implementation within RABIES

Execution step	Custom Options	Comments on implementation
#1 Frame censoring <code>--frame_censoring</code>	<ul style="list-style-type: none">• framewise displacement threshold• remove DVARS spikes• Define minimum # of frames to retain a scan	
#2 Detrending <code>--detrending_order</code>	Linear or Quadratic	Applied after censoring to avoid influence of spikes on trend calculations.
#3 ICA AROMA <code>--ica_aroma</code>	Specify # of components for ICA, or automatic estimation	Applied after spike censoring, before filtering to reduce ringing
#4 Frequency filtering <code>--TR</code> / <code>--highpass</code> / <code>--lowpass</code>	Specify highpass and/or lowpass filters	<ul style="list-style-type: none">• Applied post-censoring to avoid ringing (Carp (2013), Neuroimage)• Missing frames are handled by simulations using Lomb-Scargle periodogram (Power et al. (2014), Neuroimage)

Confound correction: implementation within RABIES

Execution step	Custom Options	Comments on implementation
#5 Confound regression <small>--conf_list</small>	<ul style="list-style-type: none">• 6 or 24 (Friston et al. (1996), Magnetic Resonance in Medicine) motion parameters• WM or CSF or vascular mask• Global signal• aCompCorr (Muschelli et al. (2014), Neuroimage)	Nuisance regressors are also censored, detrended and filtering before regression to avoid re-introduction of confounds (Power et al. (2014), Neuroimage; Lindquist et al. (2019), Human Brain Mapping)
#6 Image scaling <small>--image_scaling</small>	<ul style="list-style-type: none">• Grand mean• Total variance• Voxelwise variance standardization• Voxelwise mean scaling	
#7 Smoothing <small>--smo</small>	<p>***only detrending is always applied, every other option needs to be manually specified!</p>	
Additional options:	<ul style="list-style-type: none">• <small>--edge_cutoff</small> : remove X seconds at each end of the timeseries after frequency filtering to avoid artefact (Power et al. (2014), Neuroimage)• <small>--match_number_timepoints</small> : keep same # of frames post-censoring• <small>--nativespace_analysis</small> : select this if conducting analysis in native space	

Confound correction: implementation within RABIES

Execution step	Custom Options	Comments on implementation
#5 Confound regression <small>--conf_list</small>	<ul style="list-style-type: none">• 6 or 24 (Friston et al. (1996), Magnetic Resonance in Medicine) motion parameters• WM or CSF or vascular mask• Global signal• aCompCorr (Muschelli et al. (2014), Neuroimage)	Nuisance regressors are also censored, detrended and filtering before regression to avoid re-introduction of confounds (Power et al. (2014), Neuroimage; Lindquist et al. (2019), Human Brain Mapping)
#6 Image scaling <small>--image_scaling</small>	<ul style="list-style-type: none">• Grand mean• Total variance• Voxelwise variance standardization• Voxelwise mean scaling	
#7 Smoothing <small>--smoothing</small>	<p>***only detrending is always applied, every other option needs to be manually specified!</p>	

RABIES command line syntax:

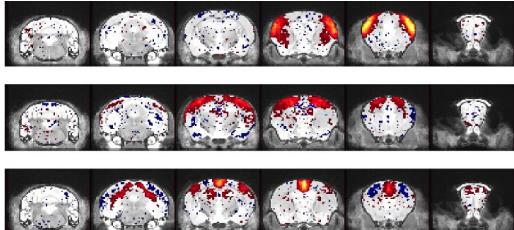
```
(base) gabriel@gabriel-XPS-13-7390:~$ rabies -p MultiProc confound_correction preprocess_outputs/ confound_correction_outputs/ --conf_list WM_signal CSF_ signal vascular_signal mot_6 --smoothing_filter 0.3 --highpass 0.01 --FD_censoring
```

```
confound_correction_datasink/
└── cleaned_timeseries
    ├── frame_censoring_mask
    └── plot_CR_overfit
```

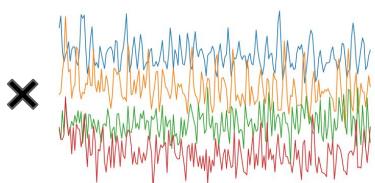
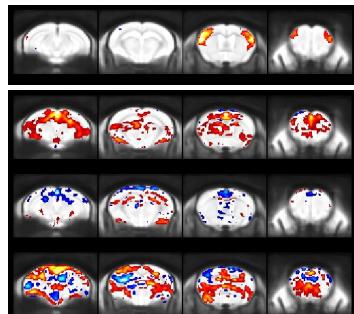
Analysis

Analysis: computing resting-state connectivity

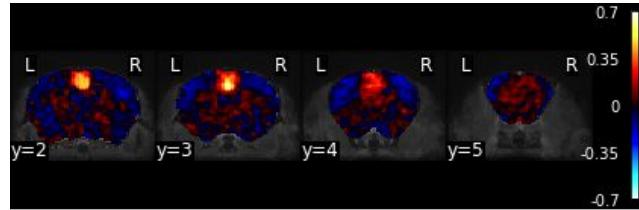
Group-Independent Component Analysis (ICA)



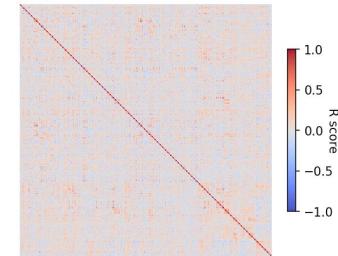
Dual regression



Seed-based Correlation Analysis



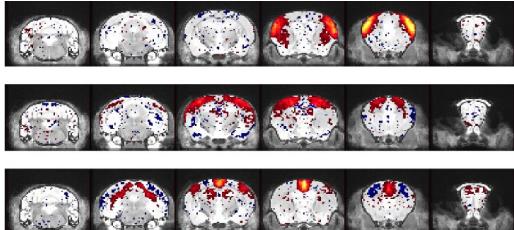
Whole-brain connectivity matrix



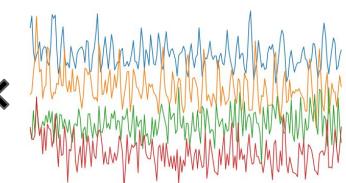
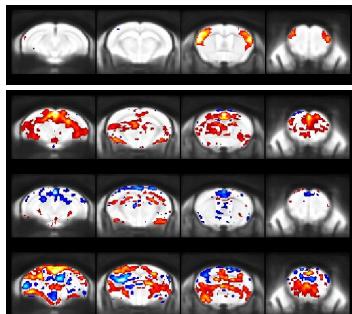
- Group-level: MELODIC ICA
- Connectivity map for every scan:
 - Dual regression
 - Seed connectivity
 - Connectivity matrix

Analysis: computing resting-state connectivity

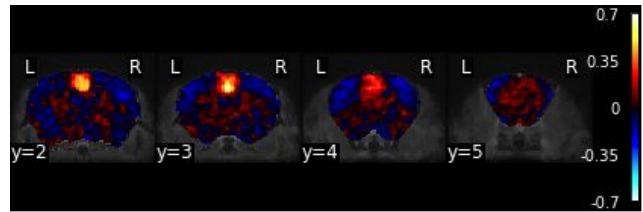
Group-Independent Component Analysis (ICA)



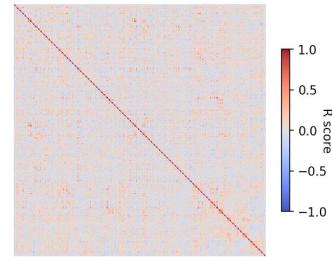
Dual regression



Seed-based Correlation Analysis



Whole-brain connectivity matrix



```
analysis_datasink/
└── dual_regression_nii
└── dual_regression_timecourse_csv
└── seed_correlation_maps
└── seed_timecourse_csv
```

Data quality assessment

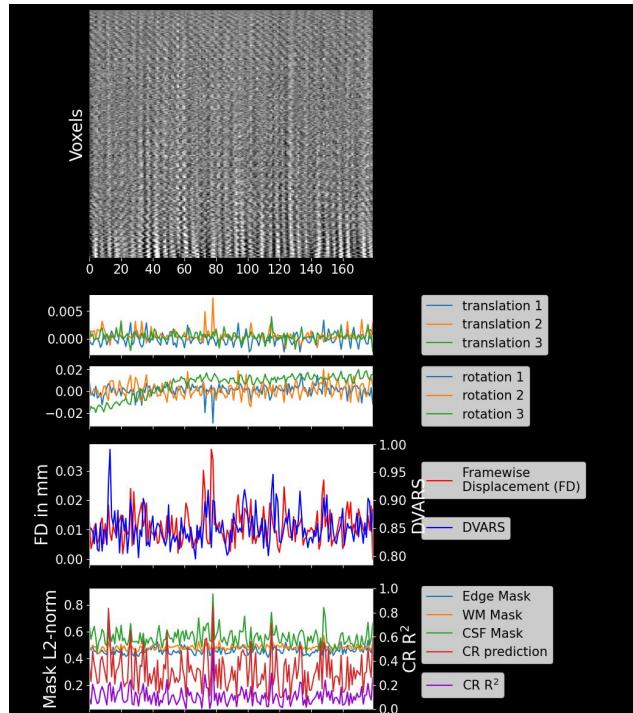
https://rabies.readthedocs.io/en/latest/nested_docs/scan_diagnosis.html

Scan-level spatiotemporal diagnosis

**SD: standard deviation

**CR: confound regression

**DR: dual regression

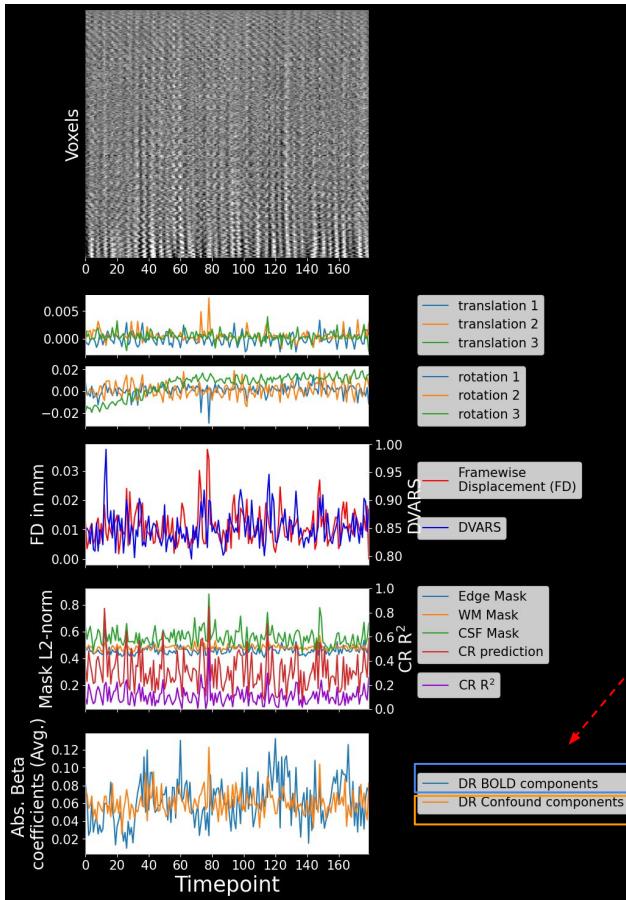


Scan-level spatiotemporal diagnosis

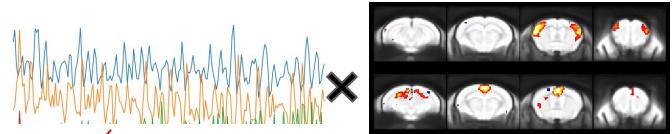
**SD: standard deviation

**CR: confound regression

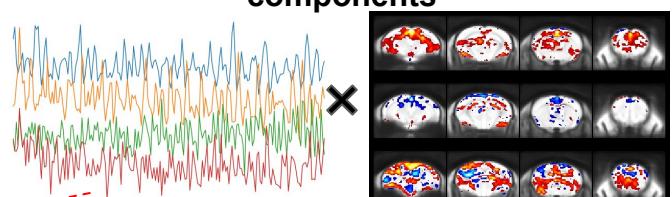
**DR: dual regression



DR outputs: network components



DR outputs: confound components



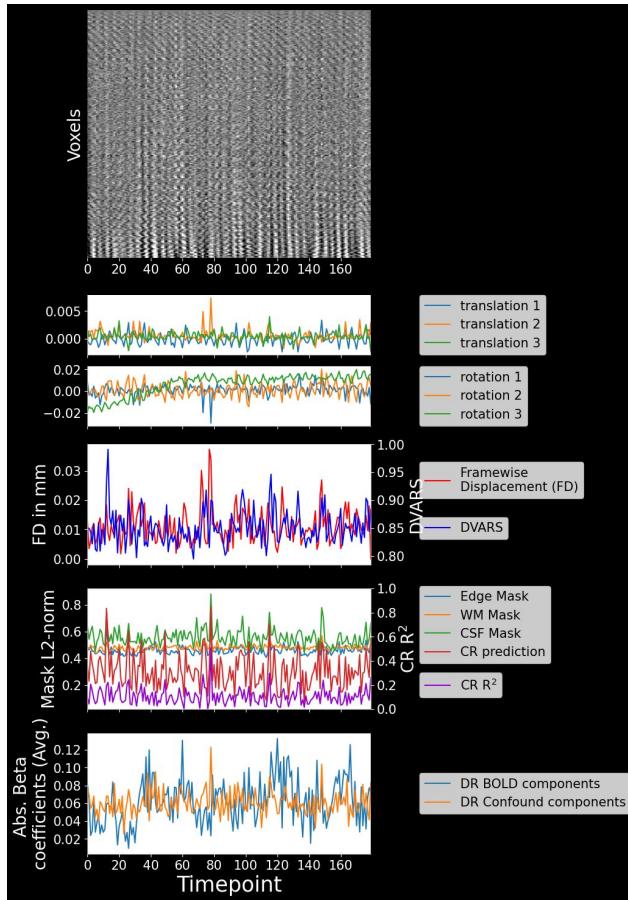
Mean amplitude
across components

Scan-level spatiotemporal diagnosis

**SD: standard deviation

**CR: confound regression

**DR: dual regression



Computed from
preprocessing

From cleaned timeseries

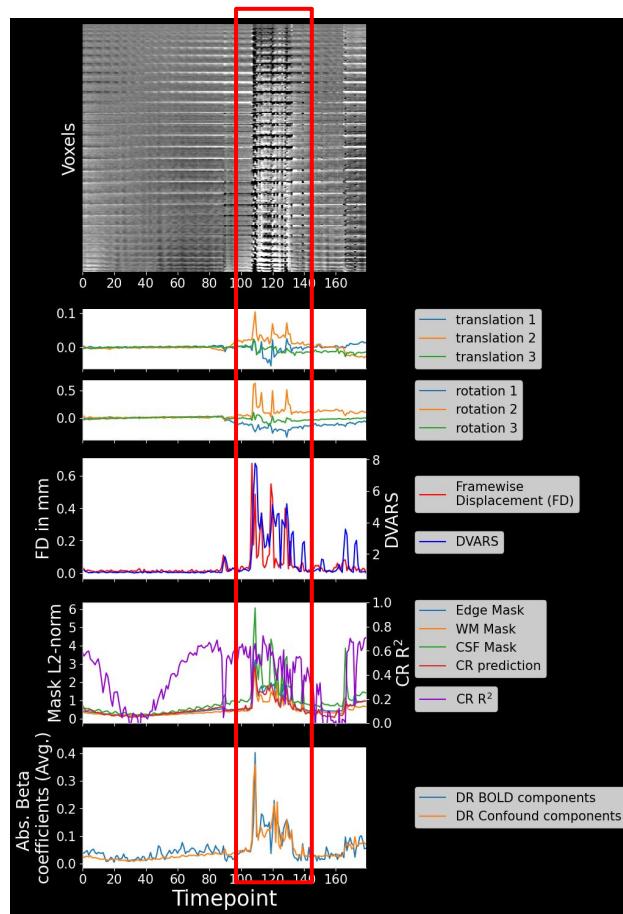
***If CR not applied,
computed with 6 motion
parameters (but no
regression applied)

Scan-level spatiotemporal diagnosis

**SD: standard deviation

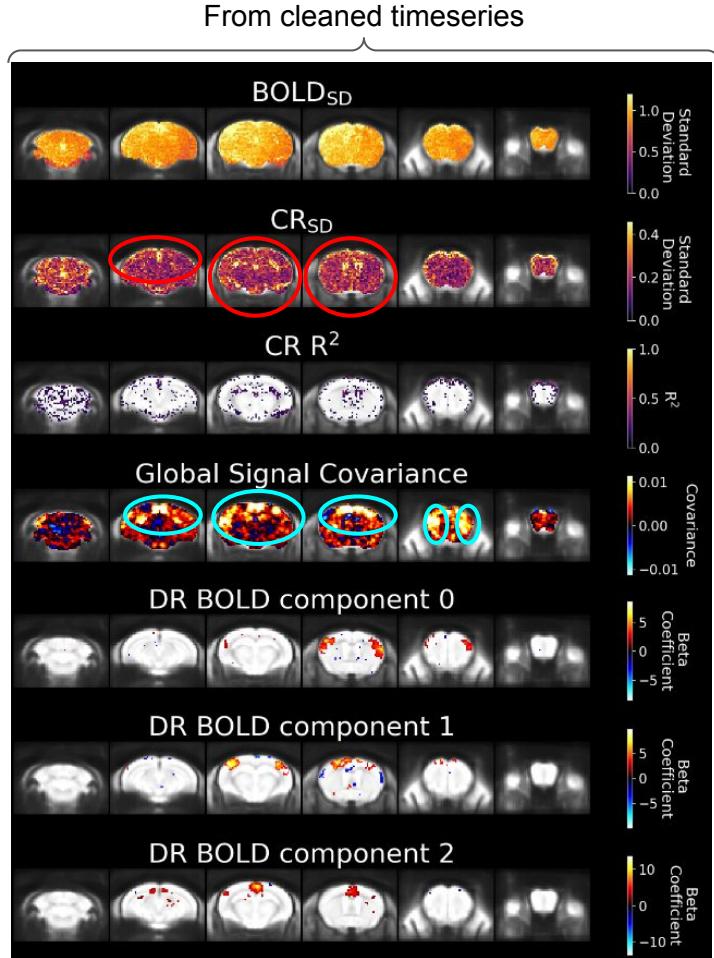
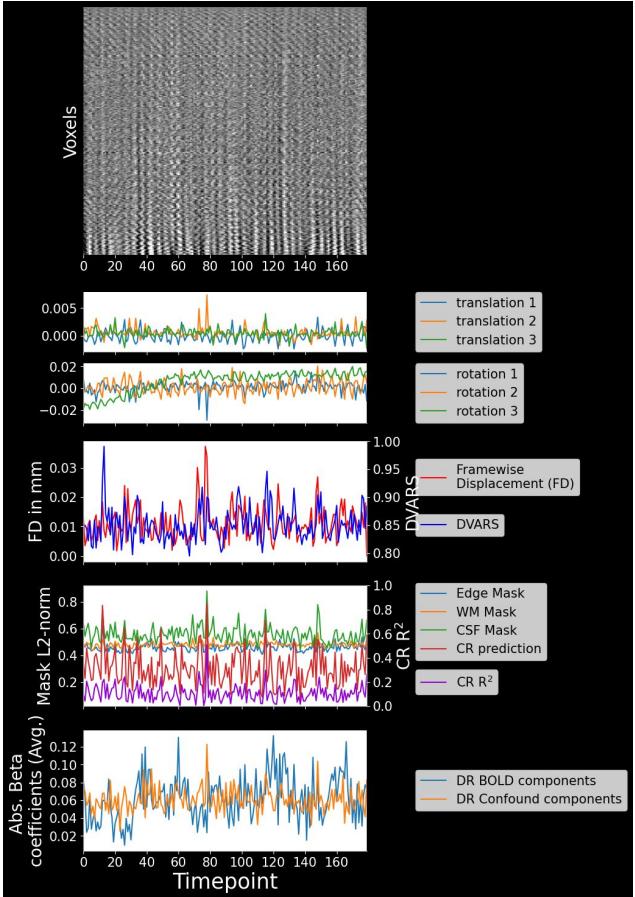
**CR: confound regression

**DR: dual regression



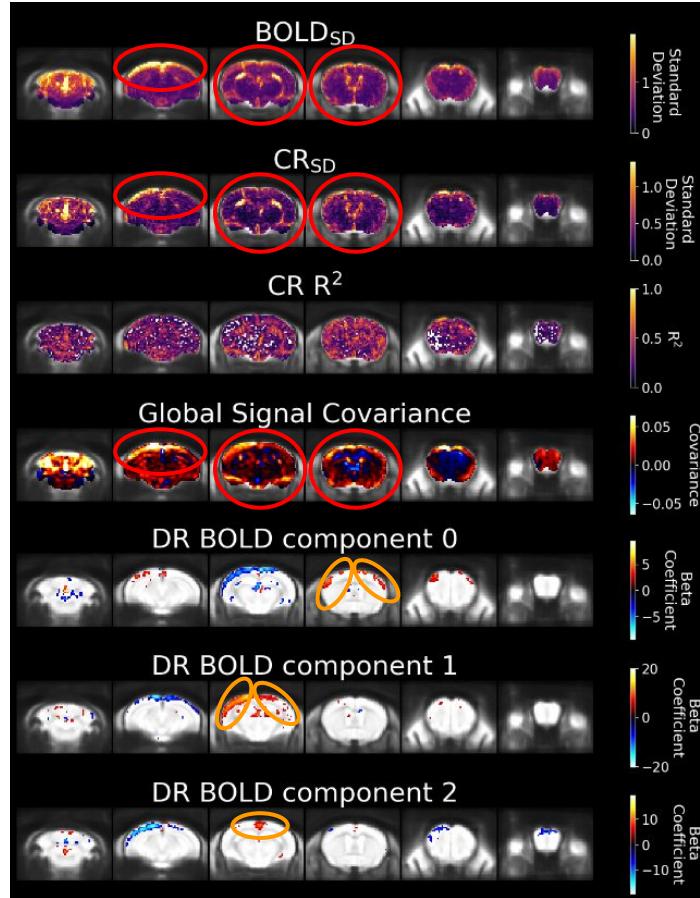
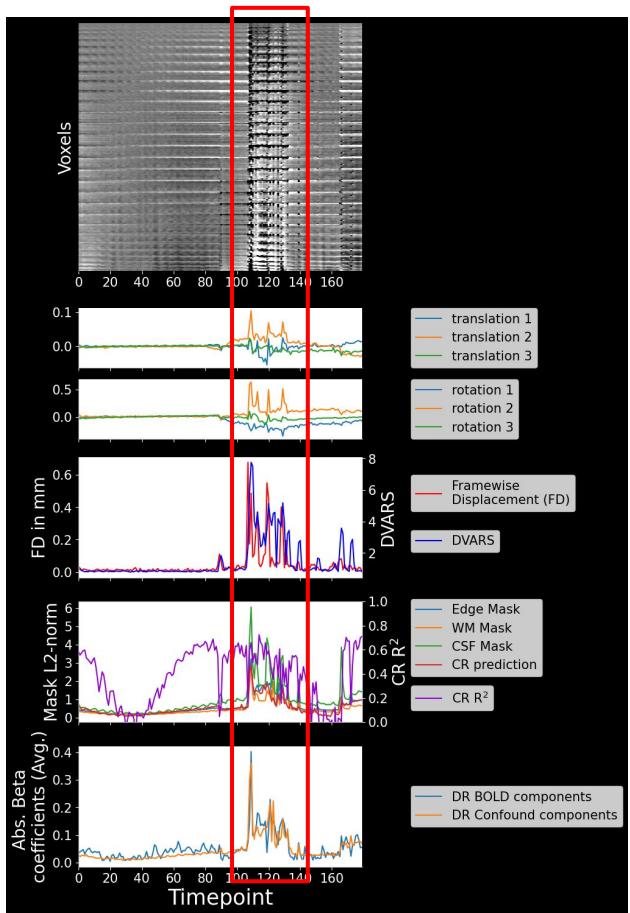
Scan-level spatiotemporal diagnosis

**SD: standard deviation
**CR: confound regression
**DR: dual regression



Scan-level spatiotemporal diagnosis

**SD: standard deviation
**CR: confound regression
**DR: dual regression

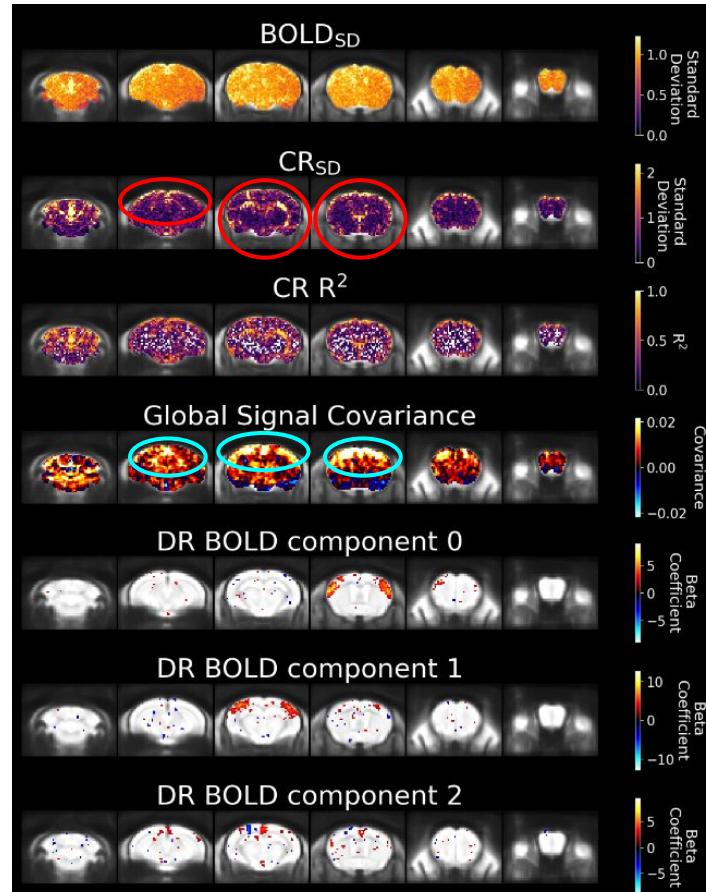
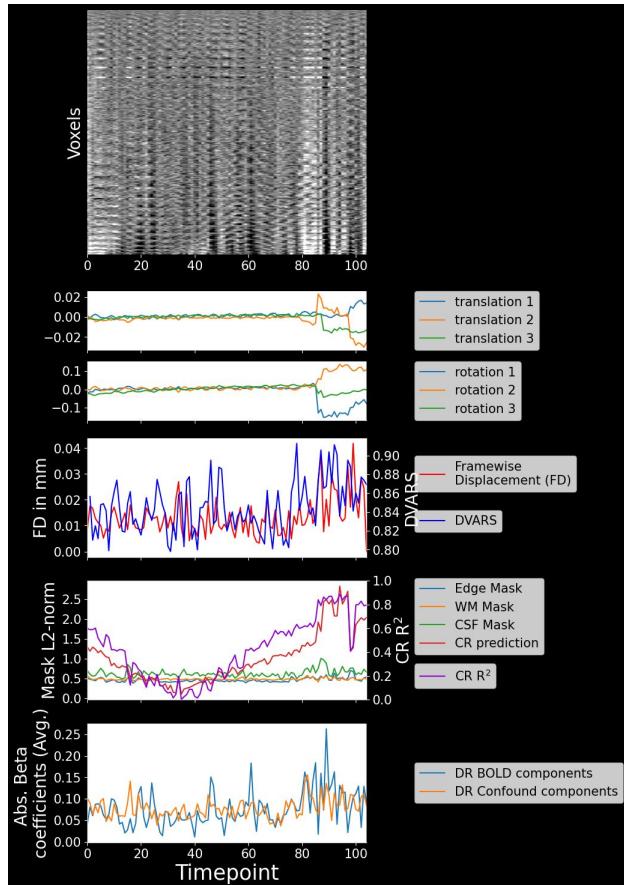


Scan-level spatiotemporal diagnosis

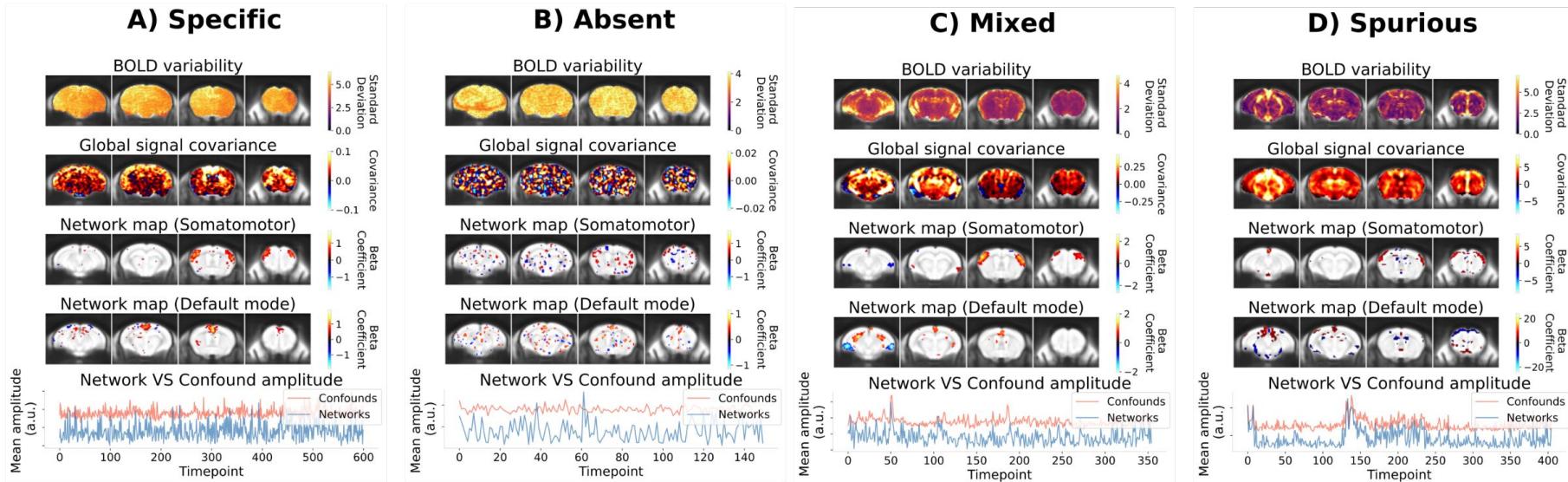
**SD: standard deviation

**CR: confound regression

**DR: dual regression



Categories of scan quality outcomes



Scan-level spatiotemporal diagnosis: inform confound correction strategy

- Physiological confounds -> regression of WM/CSF/vascular signals, bandpass
- Motion -> FD censoring, mot6/mot24, ICA-AROMA
- Suspicious DVARS spikes -> DVARS censoring
- Low-frequency drifts -> highpass
- Last resort “remove everything” solution -> global signal regression

Over-correction: extra regression can remove network signal, in particular global signal regression and lowpass (see RABIES preprint/Bright and Murphy (2015), Neuroimage))

Execution

Specify ICA components for dual regression

```
--scan_list [SCAN_LIST ...]
    This option offers to run the analysis on a subset of the scans. The scans are selected by providing the full path to the corresponding EPI file in the input BIDS folder. The list of scan can be specified manually as a list of file name '--scan_list scan1.nii.gz scan2.nii.gz ...' or the files can be imbedded into a .txt file with one filename per row. By default, 'all' will use all the scans previously processed.
    (default: ['all'])

--prior_maps PRIOR_MAPS
    Provide a 4D nifti image with a series of spatial priors representing common sources of signal (e.g. ICA components from a group-ICA run). This 4D prior map file will be used for Dual regression, Dual ICA and --data_diagnosis. The RABIES default corresponds to a MELODIC run on a combined group of anesthetized-ventilated and awake mice. Confound correction consisted of highpass at 0.01 Hz, FD censoring at 0.03mm, DVARS censoring, and mot_6_WM_signal,CSF_signal as regressors.
    (default: /home/gabriel/.local/share/rabies/melodic_IC.nii.gz)

--prior_bold_idx [PRIOR_BOLD_IDX ...]
    Specify the indices for the priors corresponding to BOLD sources from --prior_maps. These will be fitted during Dual ICA and provide the BOLD components during --data_diagnosis.
    (default: [5, 12, 19])

--prior_confound_idx [PRIOR_CONFOUND_IDX ...]
    Specify the indices for the confound components from --prior_maps. This is pertinent for the --data_diagnosis outputs.
    (default: [0, 1, 2, 6, 7, 8, 9, 10, 11, 13, 14, 21, 22, 24, 26, 28, 29])

--data_diagnosis
    This option carries out the spatiotemporal diagnosis as described in Desrosiers-Gregoire et al. The diagnosis generates key temporal and spatial features both at the scan level and the group level, allowing the identification of sources of confounds and data quality issues. We recommend using this data diagnosis workflow, more detailed in the publication, to improve the control for data quality issues and prevent the corruptions of analysis outputs.
    (default: False)

--outlier_threshold OUTLIER_THRESHOLD
    The modified Z-score threshold for detecting outliers during dataset QC when using --data_diagnosis. The default of 3.5 is recommended in https://www.itl.nist.gov/div898/handbook/eda/section3/eda35h.htm.
    (default: 3.5)

--seed_list [SEED_LIST ...]
    Can provide a list of Nifti files providing a mask for an anatomical seed, which will be used to evaluate seed-based connectivity maps using on Pearson's r. Each seed must consist of a binary mask representing the ROI in commonspace.
    (default: [])

--seed_prior_list [SEED_PRIOR_LIST ...]
    For analysis QC of seed-based FC during --data_diagnosis, prior network maps are required for each seed provided in --seed_list. Provide the list of prior files in matching order of the --seed_list arguments to match corresponding seed maps.
    (default: [])
```

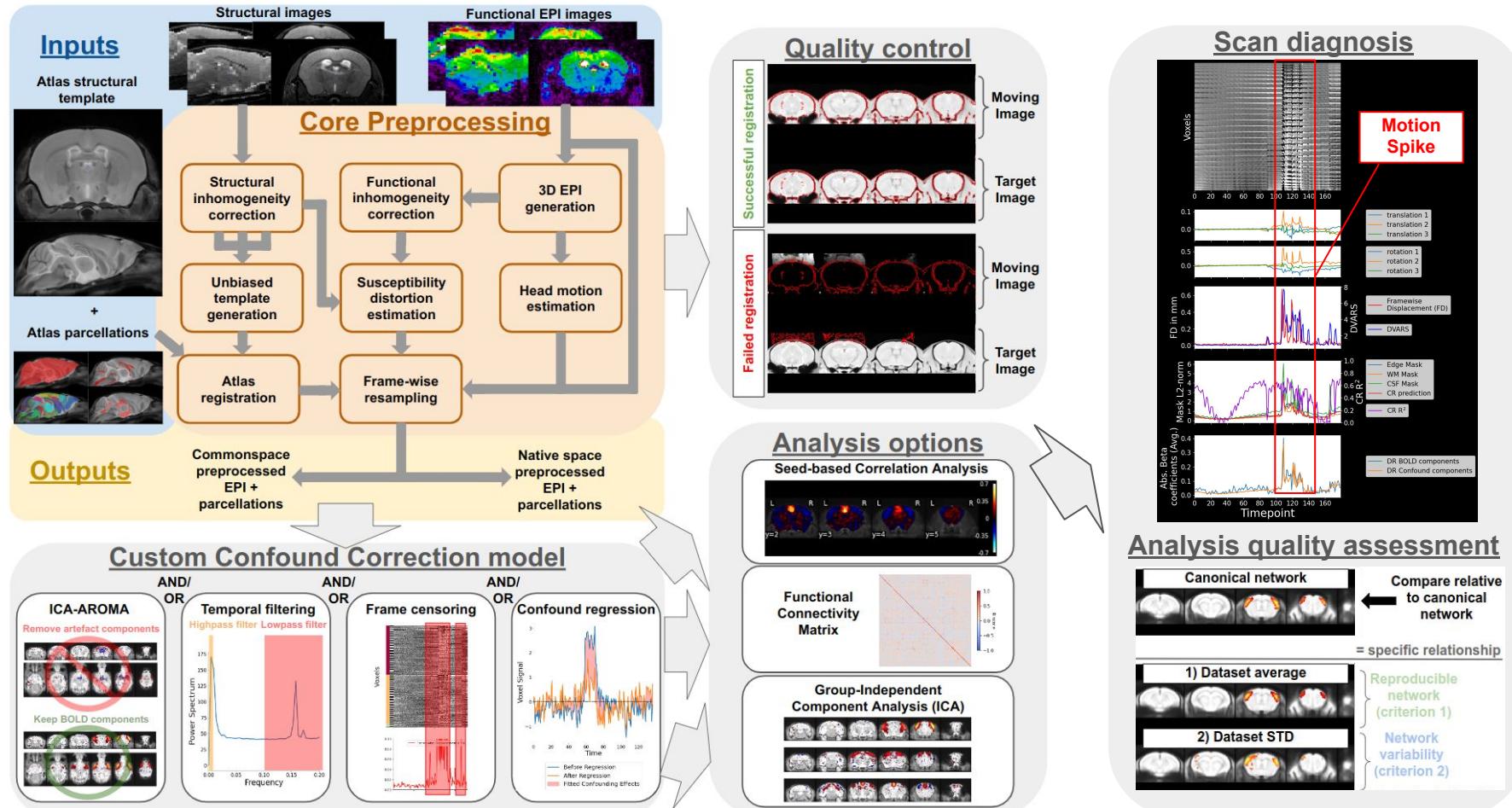
Provide prior network maps for seed connectivity

Outputs

```
data_diagnosis_datasink/
└── analysis_QC
    ├── corrected_CR_std.nii
    └── CR_prediction_std.nii
    └── figure_spatial_diagnosis
    └── figure_temporal_diagnosis
    └── GS_cov.nii
    └── random_CR_std.nii
    └── spatial_VE.nii
    └── temporal_info_csv
    └── temporal_std.nii
```

```
data_diagnosis_datasink/figure_spatial_diagnosis/
└── split_name_sub-001_ses-1_task-rest_acq-EPI_bold
    └── sub-001_ses-1_task-rest_acq-EPI_bold_spatial_diagnosis.png
    └── split_name_sub-002_ses-1_task-rest_acq-EPI_bold_spatial_diagnosis.png
    └── split_name_sub-003_ses-1_task-rest_acq-EPI_bold_spatial_diagnosis.png
    └── split_name_sub-004_ses-1_task-rest_acq-EPI_bold_spatial_diagnosis.png
    └── split_name_sub-005_ses-1_task-rest_acq-EPI_bold_spatial_diagnosis.png
    └── sub-005_ses-1_task-rest_acq-EPI_bold_spatial_diagnosis.png
    └── split_name_sub-006_ses-1_data_diagnosis_datasink/figure_temporal_diagnosis/
        └── sub-006_ses-1_task-rest_acq-EPI_bold
            └── split_name_sub-001_ses-1_task-rest_acq-EPI_bold
                └── sub-001_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-002_ses-1_task-rest_acq-EPI_bold
                └── sub-002_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-003_ses-1_task-rest_acq-EPI_bold
                └── sub-003_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-004_ses-1_task-rest_acq-EPI_bold
                └── sub-004_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-005_ses-1_task-rest_acq-EPI_bold
                └── sub-005_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-006_ses-1_task-rest_acq-EPI_bold
                └── sub-006_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-007_ses-1_task-rest_acq-EPI_bold
                └── sub-007_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-008_ses-1_task-rest_acq-EPI_bold
                └── sub-008_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-009_ses-1_task-rest_acq-EPI_bold
                └── sub-009_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
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                └── sub-010_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
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                └── sub-011_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
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                └── sub-013_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-014_ses-1_task-rest_acq-EPI_bold
                └── sub-014_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── split_name_sub-015_ses-1_task-rest_acq-EPI_bold
                └── sub-015_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
            └── sub-015_ses-1_task-rest_acq-EPI_bold_temporal_diagnosis.png
```

RABIES: Rodent Automated Bold Improvement of EPI Sequences



Resources

Rodent Automated Bold Improvement of EPI Sequences (RABIES): A standardized image processing and data quality platform for rodent fMRI

Gabriel Desrosiers-Gregoire, Gabriel A. Devenyi, Joanes Grandjean, M. Mallar Chakravarty

doi: <https://doi.org/10.1101/2022.08.20.504597>

Preprint: <https://doi.org/10.1101/2022.08.20.504597>

master ▾ 2 branches 20 tags

Go to file Add file ▾ Code ▾

Gab-D-G Merge pull request #250 from CoBrALab/outliers_QC ... 4425a7f 22 days ago 747 commits

.github/ISSUE_TEMPLATE Added new template for b

docs Version 0.4.7 - the FD calc

minc-toolkit-extras @ 037d97e Added an option in inho_c

optimized_antsMultivariateTempla... Changed the template generation to using median with a tempor... 17 months ago

patch A patch is added to nu_estimate_np_and_em to correct for a sporad... 14 months ago

rabies One more error catch was necessary 20 days ago

GitHub: <https://github.com/CoBrALab/RABIES>



gabdesgreg/rabies ☆

By [gabdesgreg](#) • Updated a month ago

Docker image for RABIES <https://github.com/CoBrALab/RABIES>

Image

Docker Pull Command

`docker pull gabdesgreg/rabies`

Docker distribution:

<https://hub.docker.com/r/gabdesgreg/rabies>

RABIES Documentation stable Search docs

CONTENT

- Installation
- Running The Software
- Preprocessing Pipeline
 - Preprocessing quality control (QC)
- Recommendations for registration troubleshooting
 - Confound Correction pipeline
- Analysis
- Understanding the Outputs
- Bibliography

Documentation:

<https://rabies.readthedocs.io/en/stable/>

The team



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Twitter/X [@GabrielDesrosi2](https://twitter.com/GabrielDesrosi2)



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Radboud university, The Netherlands

Github github.com/grandjeanlab



Dr. Gabriel A. Devenyi

McGill University, Canada

Github github.com/gdevenyi



Dr. Mallar Chakravarty

McGill University, Canada

Github github.com/CoBrALab