

Parameter	Options	Purpose	When to choose it
--bids_filter	JSON	Select a specific subset of data (anatomical or functional) according to BIDS criteria.	When you need to analyze only certain image types or specific conditions.
--bold_only	true, false	Run preprocessing using only functional (EPI) images.	When you do not have structural images and want a quick analysis using only functional images.
--anat_autobox	true, false	Automatically crop extra space in anatomical images.	When there is too much empty space around the brain and you want to optimize processing time and storage.
--bold_autobox	true, false	Automatically crop extra space in functional (EPI) images.	Same as above, but applied to functional images.
--oblique2card	none, affine, 3dWarp	Correct oblique coordinates in structural and functional images.	Use only if images have oblique (non-cardinal) coordinates. 'affine' corrects the matrix; '3dWarp' resamples. 'none' is recommended by default.
--apply_despiking	true, false	Apply a despiking filter to remove extreme intensity spikes from the signal.	Useful for images with impulsive artifacts or transient noise.
--HMC_option	intraSubjectBOLD, 0, 1, 2, 3, optim	Define a preset strategy for motion correction realignment.	'optim' (default) is customized for accuracy. Other presets depending on specific needs (see ANTs documentation).
--isotropic_HMC	true, false	Resample the image to isotropic resolution to improve motion estimation.	Useful with low-resolution images or when motion estimation quality is limited. Increases processing time.
--voxelwise_motion	true, false	Generate voxelwise maps of absolute and relative displacement.	For detailed inspection and advanced analyses of motion at each voxel.
--apply_slice_mc	true, false	Correct slice-specific (within-TR) motion.	For fast within-TR motion that causes inter-slice misalignment; improves accuracy at the cost of longer runtime.
--detect_dummy	true, false	Detect and remove initial 'dummy' EPI volumes.	Useful if acquisition included initial volumes before signal stabilization.
--data_type	int16, int32, float32, float64	Set output numeric format, affecting file size.	Use float32 (default) for a balance between precision and size. Integer types reduce size but lower precision.
--anat_inho_cor — --bold_inho_cor	method: Rigid, Affine, SyN, no_reg, N4_reg, disable; otsu_thresh: 0–	Correct intensity inhomogeneity in anatomical and functional images.	Use method=SyN for highest accuracy (default for anatomy). Choose simpler methods (Rigid/Affine) for speed or limited image

	4; multiotsu: true, false		quality. An otsu_thresh=2 is a balanced default. Use multiotsu=true in difficult cases with strong intensity gradients.
--anat_robust_inho_cor — --bold_robust_inho_cor	apply: true, false; masking: true, false; brain_extraction: true, false; keep_mask_after_extract: true, false; template_registration: Rigid, Affine, SyN, no_reg	Robust inhomogeneity correction using a dataset-generated template.	Enable apply=true to improve quality in challenging datasets; masking=true and brain_extraction=true for higher precision when masks are reliable. Use SyN registration for best quality.
--commonspace_reg	Same as previous options + fast_commonspace: true, false	Control alignment to a common space (registration to an external template).	Use SyN (default) for highest accuracy. fast_commonspace=true performs direct fast registration (lower accuracy). Use masks when their quality is high.
--inherit_unbiased_template	Path to a previous RABIES results folder	Reuse a previously generated unbiased template for a new preprocessing run.	When reprocessing the same or a similar dataset, to avoid regenerating templates.
--bold2anat_coreg	masking: true, false; brain_extraction: true, false; registration: Rigid, Affine, SyN, no_reg	Non-linear correction of susceptibility distortions by aligning EPI to the anatomical image.	SyN is recommended by default for best quality. Use masks and brain extraction if reliable to further improve the correction.
--nativespace_resampling — -- commonspace_resampling — -- anatomical_resampling	Dimensions (dim1xdim2xdim3), inputs_defined	Specify the voxel resolution (in mm) of the output after resampling.	Use inputs_defined to preserve the original resolution; specify dimensions to standardize or reduce file size. Smaller voxel size yields higher precision and larger files.
--apply_STC	true, false	Apply Slice Timing Correction (STC).	Useful when TR is long; important for dynamic studies requiring precise temporal synchronization.
--TR	Number in seconds, or auto	Repetition Time (TR).	Set it manually in seconds if it is not correctly specified in the NIfTI file.
--tpattern	alt-z, alt-z2, seq-z, alt+z, alt+z2, seq+z	Specify the slice acquisition pattern for STC.	Depends on the scanner protocol; the scanner documentation indicates the exact type (interleaved/sequential and direction). Default: alt-z.
--stc_axis	X, Y, Z	Anatomical axis over which STC is applied.	Usually Y (default, anteroposterior). Use another axis if your acquisition differs.
--interp_method	linear, cubic, quintic,	Interpolation method for STC.	fourier (default) is recommended to avoid

	heptic, wsinc5, wsinc9, fourier		artificial autocorrelation. Polynomial methods (linear, cubic) are faster but increase autocorrelation.
--anat_template — --brain_mask — --WM_mask — --CSF_mask — --vascular_mask — --labels	Path to NIfTI files	Specify the anatomical atlas, tissue masks, and anatomical labels for registration and analysis.	By default DSURQE (mouse) is used; change them if working with a different atlas or species (e.g., rat).

To view all this information, use the --help command. For example, in Windows PowerShell using Docker, simply type:

```
docker run --rm --privileged ` ghcr.io/cobralab/rabies:latest ` preprocess ` --help
```

Documentation obtained using the `preprocess --help` command

```
docker run --rm --privileged ` ghcr.io/cobralab/rabies:latest ` preprocess ` --help
```

```
usage: rabies preprocess [-h] [--bids_filter BIDS_FILTER] [--bold_only]
                        [--anat_autobox] [--bold_autobox]
                        [--oblique2card {none,affine,3dWarp}]
                        [--apply_despiking]
                        [--HMC_option {intraSubjectBOLD,0,1,2,3,optim}]
                        [--isotropic_HMC] [--voxelwise_motion]
                        [--apply_slice_mc] [--detect_dummy]
                        [--data_type {int16,int32,float32,float64}]
                        [--anat_inho_cor ANAT_INHO_COR]
                        [--anat_robust_inho_cor ANAT_ROBUST_INHO_COR]
                        [--bold_inho_cor BOLD_INHO_COR]
                        [--bold_robust_inho_cor BOLD_ROBUST_INHO_COR]
                        [--commonspace_reg COMMONSPACE_REG]
                        [--inherit_unbiased_template INHERIT_UNBIASED_TEMPLATE]
                        [--bold2anat_coreg BOLD2ANAT_COREG]
                        [--nativespace_resampling NATIVESPACE_RESAMPLING]
                        [--commonspace_resampling COMMONSPACE_RESAMPLING]
                        [--anatomical_resampling ANATOMICAL_RESAMPLING]
                        [--apply_STC] [--TR TR]
                        [--tpattern {alt-z,alt-z2,seq-z,alt+z,alt+z2,seq+z}]
```

```

[--stc_axis {X,Y,Z}]
[--interp_method {linear,cubic,quintic,heptic,wsinc5,wsinc9,fourier}]
[--anat_template ANAT_TEMPLATE]
[--brain_mask BRAIN_MASK] [--WM_mask WM_MASK]
[--CSF_mask CSF_MASK] [--vascular_mask VASCULAR_MASK]
[--labels LABELS]
bids_dir output_dir

```

positional arguments:

```

bids_dir      The root folder of the BIDS-formated input data directory.
output_dir    the output path to drop outputs from major preprocessing steps.

```

optional arguments:

```

-h, --help      show this help message and exit
--bids_filter BIDS_FILTER
                Allows to provide additional BIDS specifications (found within the input BIDS directory)
                for selected a subset of functional and/or anatomical images. Takes as input a JSON file
                containing the set of parameters for functional image under 'func' and under 'anat' for the
                anatomical image. See online documentation for an example.
                (default: {'func': {'suffix': ['bold', 'cbv']}, 'anat': {'suffix': ['T1w', 'T2w']}})

--bold_only      Apply preprocessing with only EPI scans. Commonspace registration is executed directly using
                the corrected EPI 3D reference images. The commonspace registration simultaneously applies
                distortion correction, this option will produce only commonspace outputs.
                (default: False)

--anat_autobox   Crops out extra space around the brain on the structural image using AFNI's 3dAutobox
                https://afni.nimh.nih.gov/pub/dist/doc/program\_help/3dAutobox.html.
                (default: False)

--bold_autobox   Crops out extra space around the brain on the EPI image using AFNI's 3dAutobox
                https://afni.nimh.nih.gov/pub/dist/doc/program\_help/3dAutobox.html.
                (default: False)

--oblique2card {none,affine,3dWarp}
                Correct for oblique coordinates on all structural and functional data.
                WARNING: these corrections are suboptimal, and may alter the data. Only apply if necessary.
                affine: only the affine matrix is changed to cardinal axes.
                3dWarp: Applies AFNI's 3dWarp -oblique2card. This involves resampling the data on a new isotropic grid.
                (default: none)

```

--apply_despiking Applies AFNI's 3dDespike https://afni.nimh.nih.gov/pub/dist/doc/program_help/3dDespike.html.
(default: False)

--HMC_option {intraSubjectBOLD,0,1,2,3,optim}
Select a pre-built option for registration during head motion realignment. 'optim' was customized as documented in <https://github.com/CoBrALab/RABIES/discussions/259>. Other options were taken from https://github.com/ANTsX/ANTsR/blob/master/R/ants_motion_estimation.R.
(default: optim)

--isotropic_HMC Whether to resample the EPI to isotropic resolution (taking the size of the axis with highest resolution) for the estimation of motion parameters. This should greatly mitigating registration 'noise' which arise from partial volume effects, or poor image resolution (see online post on this topic <https://github.com/CoBrALab/RABIES/discussions/288>). This option will increase computational time, given the higher image resolution.
(default: False)

--voxelwise_motion Whether to output estimates of absolute displacement and framewise displacement at each voxel. This will generate 4D nifti files representing motion timeseries derived from the 6 motion parameters. This is handled by antsMotionCorrStats.
(default: False)

--apply_slice_mc Whether to apply a slice-specific motion correction after initial volumetric HMC. This can correct for interslice misalignment resulting from within-TR motion. With this option, motion corrections and the subsequent resampling from registration are applied sequentially since the 2D slice registrations cannot be concatenate with 3D transforms.
(default: False)

--detect_dummy Detect and remove initial dummy volumes from the EPI, and generate a reference EPI based on these volumes if detected. Dummy volumes will be removed from the output preprocessed EPI.
(default: False)

--data_type {int16,int32,float32,float64}
Specify data format outputs to control for file size.
(default: float32)

Registration Options:

Customize registration operations and troubleshoot registration failures.

--anat_inho_cor ANAT_INHO_COR
Select options for the inhomogeneity correction of the structural image.
* method: specify which registration strategy is employed for providing a brain mask.

*** Rigid: conducts only rigid registration.
 *** Affine: conducts Rigid then Affine registration.
 *** SyN: conducts Rigid, Affine then non-linear registration.
 *** no_reg: skip registration.
 *** N4_reg: previous correction script prior to version 0.3.1.
 *** disable: disables the inhomogeneity correction.
 * otsu_thresh: The inhomogeneity correction script necessitates an initial correction with a Otsu masking strategy (prior to registration of an anatomical mask). This option sets the Otsu threshold level to capture the right intensity distribution.
 *** Specify an integer among [0,1,2,3,4].
 * multiotsu: Select this option to perform a staged inhomogeneity correction, where only lower intensities are initially corrected, then higher intensities are iteratively included to eventually correct the whole image. This technique may help with images with particularly strong inhomogeneity gradients and very low intensities.
 *** Specify 'true' or 'false'.
 (default: method=SyN,otsu_thresh=2,multiotsu=false)

--anat_robust_inho_cor ANAT_ROBUST_INHO_COR

When selecting this option, inhomogeneity correction is executed twice to optimize outcomes. After completing an initial inhomogeneity correction step, the corrected outputs are co-registered to generate an unbiased template, using the same method as the commonspace registration. This template is then masked, and is used as a new target for masking during a second iteration of inhomogeneity correction. Using this dataset-specific template should improve the robustness of masking for inhomogeneity correction.
 * apply: select 'true' to apply this option.
 *** Specify 'true' or 'false'.
 * masking: Combine masks derived from the inhomogeneity correction step to support registration during the generation of the unbiased template, and then during template registration.
 *** Specify 'true' or 'false'.
 * brain_extraction: conducts brain extraction prior to template registration based on the combined masks from inhomogeneity correction. This will enhance brain edge-matching, but requires good quality masks. This must be selected along the 'masking' option.
 *** Specify 'true' or 'false'.
 * template_registration: Specify a registration script for the alignment of the dataset-generated unbiased template to a reference template for masking.
 *** Rigid: conducts only rigid registration.
 *** Affine: conducts Rigid then Affine registration.
 *** SyN: conducts Rigid, Affine then non-linear registration.
 *** no_reg: skip registration.
 (default: apply=false,masking=false,brain_extraction=false,template_registration=SyN)

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--bold_inho_cor BOLD_INHO_COR
    Same as --anat_inho_cor, but for the EPI images.
    (default: method=Rigid,otsu_thresh=2,multiotsu=false)

--bold_robust_inho_cor BOLD_ROBUST_INHO_COR
    Same as --anat_robust_inho_cor, but for the EPI images.
    (default: apply=false,masking=false,brain_extraction=false,template_registration=SyN)

--commonsense_reg COMMONSPACE_REG
    Specify registration options for the commonsense registration.
    * masking: Combine masks derived from the inhomogeneity correction step to support
      registration during the generation of the unbiased template, and then during template
      registration.
    *** Specify 'true' or 'false'.
    * brain_extraction: conducts brain extraction prior to template registration based on the
      combined masks from inhomogeneity correction. This will enhance brain edge-matching, but
      requires good quality masks. This must be selected along the 'masking' option.
    *** Specify 'true' or 'false'.
    * template_registration: Specify a registration script for the alignment of the
      dataset-generated unbiased template to the commonsense atlas.
    *** Rigid: conducts only rigid registration.
    *** Affine: conducts Rigid then Affine registration.
    *** SyN: conducts Rigid, Affine then non-linear registration.
    *** no_reg: skip registration.
    * fast_commonspace: Skip the generation of a dataset-generated unbiased template, and
      instead, register each scan independently directly onto the commonsense atlas, using the
      template_registration. This option can be faster, but may decrease the quality of
      alignment between subjects.
    *** Specify 'true' or 'false'.
    (default: masking=false,brain_extraction=false,template_registration=SyN,fast_commonspace=false)

--inherit_unbiased_template INHERIT_UNBIASED_TEMPLATE
    Provide a path to a previous RABIES preprocessing output folder to inherit the unbiased template
    generated in that previous run, as well as the registration to the external atlas. In place of
    conducting unbiased template generation, each scan is registered to this pre-generated template
    with registration parameters that are consistent with that of the previous run. The atlas registration
    is also inherited, and won't be conducted again.
    By selecting this option, the following preprocessing parameters will be overridden to enforce
    consistency with the previous run: --anatomical_resampling, --commonsense_reg, --anat_template,
    --brain_mask, --WM_mask, --CSF_mask, --vascular_mask, --labels

```

(default: none)

--bold2anat_coreg BOLD2ANAT_COREG

Specify the registration script for cross-modal alignment between the EPI and structural images. This operation is responsible for correcting EPI susceptibility distortions.

* masking: With this option, the brain masks obtained from the EPI inhomogeneity correction step are used to support registration.

*** Specify 'true' or 'false'.

* brain_extraction: conducts brain extraction prior to registration using the EPI masks from inhomogeneity correction. This will enhance brain edge-matching, but requires good quality masks. This must be selected along the 'masking' option.

*** Specify 'true' or 'false'.

* registration: Specify a registration script.

*** Rigid: conducts only rigid registration.

*** Affine: conducts Rigid then Affine registration.

*** SyN: conducts Rigid, Affine then non-linear registration.

*** no_reg: skip registration.

(default: masking=false,brain_extraction=false,registration=SyN)

Resampling Options:

The following options allow to resample the voxel dimensions for the preprocessed EPIs or for the anatomical images during registration.

The resampling syntax must be 'dim1xdim2xdim3' (in mm), following the RAS axis convention (dim1=Right-Left, dim2=Anterior-Posterior, dim3=Superior-Inferior). If 'inputs_defined' is provided instead of axis dimensions, the original dimensions are preserved.

--nativespace_resampling NATIVESPACE_RESAMPLING

Can specify a resampling dimension for the nativespace fMRI outputs.

(default: inputs_defined)

--commonspace_resampling COMMONSPACE_RESAMPLING

Can specify a resampling dimension for the commonspace fMRI outputs.

(default: inputs_defined)

--anatomical_resampling ANATOMICAL_RESAMPLING

This specifies resampling dimensions for the anatomical registration targets. By default, images are resampled to isotropic resolution based on the smallest dimension among the provided anatomical images (EPI images instead if --bold_only is True). Increasing voxel resampling size will increase registration speed at the cost of accuracy.

(default: inputs_defined)

STC Options:

Specify Slice Timing Correction (STC) info that is fed to AFNI's 3dTshift (https://afni.nimh.nih.gov/pub/dist/doc/program_help/3dTshift.html). The STC is applied in the anterior-posterior orientation, and thus RABIES assumes slices were acquired in this direction.

--apply_STC Select this option to apply the STC step.
 (default: False)

--TR TR Specify repetition time (TR) in seconds. (e.g. --TR 1.2). 'auto' will read the TR from the nifti header.
 (default: auto)

--tpattern {alt-z,alt-z2,seq-z,alt+z,alt+z2,seq+z}
 Specify if interleaved ('alt') or sequential ('seq') acquisition, and specify in which direction (- or +) to apply the correction. If slices were acquired from front to back, the correction should be in the negative (-) direction. If slices were collected in an interleaved order starting with the second or (second-to-last) slice, use 'alt+z2' or 'alt-z2'. Refer to this discussion on the
topic for more information <https://github.com/CoBrALab/RABIES/discussions/217>.
 (default: alt-z)

--stc_axis {X,Y,Z} Can specify over which axis of the image the STC must be applied. Generally, the correction should be over the Y axis, which corresponds to the anteroposterior axis in RAS convention.
 (default: Y)

--interp_method {linear,cubic,quintic,heptic,wsinc5,wsinc9,fourier}
 Can specify the interpolation method used for STC. Polynomial methods (e.g., linear, cubic, etc.) will introduce greater autocorrelation to the interpolated timeseries, while wsinc and fourier methods will introduce less (or none). Refer to this discussion on the topic for more information <https://github.com/CoBrALab/RABIES/discussions/267>.
 (default: fourier)

Template Files:

Specify commonspace template and associated mask/label files. By default, RABIES provides the mouse DSURQE atlas
<https://wiki.mouseimaging.ca/display/MICePub/Mouse+Brain+Atlases>.

--anat_template ANAT_TEMPLATE
 Anatomical file for the commonspace atlas.

(default: /home/mambauser/.local/share/rabies/DSURQE_40micron_average.nii.gz)

--brain_mask BRAIN_MASK

Brain mask aligned with the template.

(default: /home/mambauser/.local/share/rabies/DSURQE_40micron_mask.nii.gz)

--WM_mask WM_MASK

White matter mask aligned with the template.

(default: /home/mambauser/.local/share/rabies/DSURQE_40micron_eroded_WM_mask.nii.gz)

--CSF_mask CSF_MASK

CSF mask aligned with the template.

(default: /home/mambauser/.local/share/rabies/DSURQE_40micron_eroded_CSF_mask.nii.gz)

--vascular_mask VASCULAR_MASK

Can provide a mask of major blood vessels to compute associated nuisance timeseries.

The default mask was generated by applying MELODIC ICA and selecting the resulting component mapping onto major brain vessels.

(default: /home/mambauser/.local/share/rabies/vascular_mask.nii.gz)

--labels LABELS

Labels file providing the atlas anatomical annotations.

(default: /home/mambauser/.local/share/rabies/DSURQE_40micron_labels.nii.gz)