Parámetro	Opciones	¿Para qué sirve?	¿Cuándo elegirlo?
--bids_filter	JSON	Seleccionar un subconjunto específico de datos (anatómicos o funcionales) según criterios BIDS.	Cuando quieras analizar sólo ciertos tipos de imágenes o condiciones específicas.
--bold_only	true, false	Realiza el procesamiento sólo con imágenes funcionales (EPI).	Cuando no dispongas de imágenes estructurales y quieras realizar un análisis rápido usando únicamente imágenes funcionales.
--anat_autobox	true, false	Recorta automáticamente espacio adicional en las imágenes anatómicas.	Cuando haya demasiado espacio vacío alrededor del cerebro y quieras optimizar el tiempo de procesamiento y almacenamiento.
--bold_autobox	true, false	Recorta automáticamente espacio adicional en las imágenes funcionales (EPI).	Idem al anterior, pero aplicado a imágenes funcionales.
--oblique2card	none, affine, 3dWarp	Corrige coordenadas oblicuas en imágenes estructurales y funcionales.	Usa sólo si las imágenes tienen coordenadas oblicuas (no cardinales). affine corrige matriz, 3dWarp resamplea. none recomendado por defecto.

--apply_despiking	true, false	Aplica un filtro de "despiking" para eliminar picos de intensidad extrema en la señal.	Útil para imágenes con artefactos puntuales o ruido transitorio.
--HMC_option	intraSubjectBOLD, 0, 1, 2, 3, optim	Define estrategia preestablecida de realineación para corrección de movimiento.	optim (por defecto) es personalizado para precisión. Otras opciones preestablecidas según necesidades particulares (ver documentación de ANTs).
--isotropic_HMC	true, false	Resamplea la imagen a resolución isotrópica para mejor estimación de movimientos.	Útil en imágenes con baja resolución o problemas de calidad en la estimación de movimiento. Aumenta el tiempo de procesamiento.
--voxelwise_motion	true, false	Genera mapas voxel por voxel del desplazamiento absoluto y relativo.	Para inspección detallada y análisis avanzado de movimiento cerebral en cada voxel.
--apply_slice_mc	true, false	Corrige movimientos específicos por cada rebanada (slice-specific).	Para movimientos rápidos intra-TR que producen desalineación entre rebanadas, aumenta precisión con mayor tiempo de procesamiento.
--detect_dummy	true, false	Detecta y elimina volúmenes iniciales ("dummy") del EPI.	Útil si la adquisición incluyó volúmenes iniciales no válidos (sin estabilizar la señal).

--data_type	int16, int32, float32, float64	Define formato numérico de salida, afectando tamaño del archivo.	Usa float32 (por defecto) para equilibrio entre precisión y tamaño. Opciones enteras reducen tamaño pero bajan precisión.
--anat_inho_cor-- bold_inho_cor	method: Rigid, Affine, SyN, no_reg, N4_reg, disableotsu_thresh: 0– 4multiotsu: true, false	Corrige inhomogeneidades de intensidad en imágenes anatómicas y funcionales.	Usa método SyN para máxima precisión (por defecto anatómico), método más simple (Rigid o Affine) si necesitas rapidez o la imagen tiene calidad limitada. otsu_thresh=2 es valor balanceado predeterminado. Usa multiotsu=true en casos difíciles con fuertes gradientes de intensidad.
--anat_robust_inho_cor-- bold_robust_inho_cor	apply: true, falsemasking: true, falsebrain_extraction: true, falsekeep_mask_after_extract: true, falsetemplate_registration: Rigid, Affine, SyN, no_reg	Corrección robusta de inhomogeneidad usando plantilla generada del dataset.	Activa apply=true para mejorar la calidad en datasets difíciles, masking=true y brain_extraction=true para mejor precisión si las máscaras cerebrales son fiables. Usa registro SyN para mejor calidad.
--commonspace_reg	Igual a parámetros anteriores + fast_commonspace: true, false	Controla alineación al espacio común (registro a plantilla externa).	Usa SyN (por defecto) para máxima precisión. fast_commonspace=true para registro rápido directo (menor precisión). Usa máscaras si la calidad de estas es alta.
--inherit_unbiased_template	Ruta a carpeta anterior de resultados RABIES	Reutiliza plantilla generada previamente (unbiased template)	Cuando re-procesas el mismo conjunto o uno similar, para evitar regenerar plantillas.

		para nuevo procesamiento.	
--bold2anat_coreg	masking: true, falsebrain_extraction: true, falseregistration: Rigid, Affine, SyN, no_reg	Corrección no-lineal de distorsiones de susceptibilidad alineando EPI a anatómica.	SyN recomendado por defecto para máxima calidad. Usa máscaras y extracción cerebral si estas son precisas, para mejorar aún más la corrección.
--nativespace_resampling-- commonspace_resampling-- anatomical_resampling	Dimensiones (dim1xdim2xdim3), inputs_defined	Especifica resolución voxel (en mm) del resultado tras el resampling.	Usa inputs_defined para conservar resolución original, define dimensiones específicas para estandarizar o reducir tamaño archivos. A menor dimensión, mayor precisión y tamaño.
--apply_STC	true, false	Aplica corrección por tiempos de adquisición de slices (Slice Timing Correction).	Útil cuando TR largo, importante para estudios dinámicos con sincronización temporal precisa.
--TR	Número en segundos, o auto	Tiempo de repetición (TR).	Define manualmente el TR en segundos si no está correctamente especificado en el archivo NIfTI.
--tpattern	alt-z, alt-z2, seq-z, alt+z, alt+z2, seq+z	Especifica patrón de adquisición de rebanadas para corrección temporal.	Depende del protocolo del escáner; la documentación del escáner indica el tipo exacto (interleaved/secuencial y dirección). Por defecto: alt-z.

--stc_axis	X, Y, Z	Eje anatómico sobre el que se aplica STC.	Usualmente Y (por defecto, eje anterior-posterior). Usa otro eje si adquisición es diferente.
--interp_method	linear, cubic, quintic, heptic, wsinc5, wsinc9, fourier	Método de interpolación para corrección temporal.	fourier (por defecto) recomendado para no introducir autocorrelaciones artificiales. Usa interpolación polinómica (linear, cubic) para rapidez (con mayor autocorrelación).
--anat_template--brain_mask--WM_mask--CSF_mask--vascular_mask--labels	Ruta a archivos NIfTI	Especifica atlas anatómico, máscaras de tejidos cerebrales y etiquetas anatómicas para registro y análisis.	Por defecto usa DSURQE (ratón), cámbialos si trabajas con otro atlas específico o especie distinta (ej. ratas).

Para ver toda esta información utiliza el comando --help. Por ejemplo, en Powershell en Windows utilizando Docker sólo hay que escribir:

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

Documentación obtenida al usar el comando ` preprocess ` --help

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-formatted 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)

--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)

--commonspace_reg COMMONSPACE_REG

Specify registration options for the commonspace 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 commonspace 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 commonspace 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 overriden to enforce

consistency with the previous run: --anatomical_resampling, --commonspace_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), follwing 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)