Package 'rpyANTs'

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Title An Alternative Advanced Normalization Tools ('ANTs')

Version 0.0.7

Description Provides portable access from 'R' to biomedical image processing toolbox 'ANTs' by Avants et al. (2009) <doi:10.54294/uvnhin> via seamless integration with the 'Python' implementation 'ANTsPy'. Allows biomedical images to be processed in 'Python' and analyzed in 'R', and vice versa via shared memory. See 'citation(``rpyANTs'')' for more reference information.

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`ants` *Get 'ANTsPy' module*

Description

Get 'ANTsPy' module

Usage

```
ants

load_ants(force = FALSE, error_if_missing = TRUE)
```

Arguments

`force`	whether to force reloading `ants` module; default is false
`error_if_missing`	whether to raise errors when the module is unable to load; default is true.

Value

A 'Python' module if successfully loaded. If `error_if_missing` is set to false and module is unable to load, return `NULL`

See Also

`antspynet`

`antspynet` *Get 'ANTsPyNet' module*

Description

Get `'ANTsPyNet'` module

Usage

```
load_antspynet(force = FALSE, error_if_missing = TRUE)
```

Arguments

`force`	whether to force reloading `antspynet` module; default is false
`error_if_missing`	whether to raise errors when the module is unable to load; default is true.

Value

A 'Python' module if successfully loaded. If `error_if_missing` is set to false and module is unable to load, return `NULL`

See Also

`ants`

`antspynet_preprocess_brain_image` *Process brain image prior to segmentation*

Description

Strip skulls, normalize intensity, align and re-sample to template. This procedure is needed for many `antspynet` functions since the deep neural networks are trained in template spaces

Usage

```
antspynet_preprocess_brain_image(
  x,
  truncate_intensity = c(0.01, 0.99),
 brain_extraction_modality = c("none", "t1", "t1v0", "t1nobrainer", "t1combined",
    "flair", "t2", "bold", "fa", "t1infant", "t2infant"),
  template_transform_type = c("None", "Affine", "Rigid"),
  template = c("biobank", "croppedMni152"),
  do_bias_correction = TRUE,
  return_bias_field = FALSE,
  do_denoising = TRUE,
  intensity_matching_type = c("regression", "histogram"),
  reference_image = NULL,
  intensity_normalization_type = NULL,
  verbose = TRUE
)
```

Arguments

`x`	`'ANTsImage'` or path to image to process
`truncate_intensity`	defines the quantile threshold for truncating the image intensity
`brain_extraction_modality`	character of length 1, perform brain extraction modality
`template_transform_type`	either `'Rigid'` or `'Affine'` align to template brain
`template`	template image (not skull-stripped) or string, e.g. `'biobank'`, `'croppedMni152'`
`do_bias_correction`	whether to perform bias field correction
`return_bias_field`	return bias field as an additional output without bias correcting the image
`do_denoising`	whether to remove noises using non-local means
`intensity_matching_type`	either `'regression'` or `'histogram'`; only is performed if `reference_image` is not `NULL`.

reference_image
: 'ANTsImage' or path to image, or NULL

intensity_normalization_type
: either re-scale the intensities to c(0, 1) ('01'), or for zero-mean, unit variance ('0mean'); if NULL normalization is not performed

verbose
: print progress to the screen

Value

Dictionary with images after process. The images are registered and re-sampled into template.

See Also

antspynet$preprocess_brain_image

Examples

```
library(rpyANTs)
if(interactive() && ants_available("antspynet")) {
  image_path <- ants$get_ants_data('r30')
  preprocessed <- antspynet_preprocess_brain_image(
    image_path, verbose = FALSE
  )

  # Compare
  orig_img <- as_ANTsImage(image_path)
  new_img <- preprocessed$preprocessed_image
  pal <- grDevices::gray.colors(256, start = 0, end = 1)

  par(mfrow = c(1, 2), mar = c(0.1, 0.1, 0.1, 0.1),
      bg = "black", fg = "white")
  image(orig_img[], asp = 1, axes = FALSE,
        col = pal, ylim = c(1, 0))
  image(new_img[], asp = 1, axes = FALSE,
        col = pal, ylim = c(1, 0))

}
```

---

antspynet_segmentation

Imaging segmentation using antspynet

Description

Supports Desikan-Killiany-Tourville labeling and deep 'Atropos'.

Usage

```
antspynet_desikan_killiany_tourville_labeling(
  x,
  do_preprocessing = TRUE,
  return_probability_images = FALSE,
  do_lobar_parcellation = FALSE,
  verbose = TRUE
)

antspynet_deep_atropos(
  x,
  do_preprocessing = TRUE,
  use_spatial_priors = TRUE,
  aseg_only = TRUE,
  verbose = TRUE
)
```

Arguments

x	'NIfTI' image or path to the image that is to be segmented
do_preprocessing	whether x is in native space and needs the be registered to template brain before performing segmentation; default is true since the model is trained with template brain. If you want to manually process the image, see antspynet_preprocess_brain_image
return_probability_images	whether to return probability images
do_lobar_parcellation	whether to perform lobar 'parcellation'
verbose	whether to print out the messages
use_spatial_priors	whether to use 'MNI' partial tissue priors
aseg_only	whether to just return the segmented image

Value

One or a list of 'ANTsImage' image instances. Please print out antspynet$desikan_killiany_tourville_labeling or antspynet$deep_atropos to see the details.

See Also

antspynet$desikan_killiany_tourville_labeling, antspynet$deep_atropos

Examples

```
# Print Python documents
if(interactive() && ants_available("antspynet")) {
  antspynet <- load_antspynet()
```

```
  print(antspynet$deep_atropos)

  print(antspynet$desikan_killiany_tourville_labeling)
}
```

`ants_apply_transforms` *Apply a transform list to map an image from one domain to another*

Description

See `ants$apply_transforms` for more details.

Usage

```
ants_apply_transforms(
  fixed,
  moving,
  transformlist,
 interpolator = c("linear", "nearestNeighbor", "gaussian", "genericLabel", "bSpline",
    "cosineWindowedSinc", "welchWindowedSinc", "hammingWindowedSinc",
    "lanczosWindowedSinc"),
  imagetype = 0L,
  whichtoinvert = NULL,
  compose = NULL,
  defaultvalue = 0,
  verbose = FALSE,
  ...
)
```

Arguments

`fixed`	fixed image defining domain into which the moving image is transformed
`moving`	moving image to be mapped to fixed space
`transformlist`	list of strings (path to transforms) generated by `ants_registration` where each transform is a file name
`interpolator`	how to interpolate the image; see 'Usage'
`imagetype`	integer: 0 (scalar), 1 (vector), 2 (tensor), 3 (time-series), used when the fixed and moving images have different mode (dimensions)
`whichtoinvert`	either `NULL`, `None` ('Python'), or a vector of logical with same length as `transformlist`; print `ants$apply_transforms` to see detailed descriptions
`compose`	optional character pointing to a valid file location
`defaultvalue`	numerical value for mappings outside the image domain
`verbose`	whether to verbose application of transform
`...`	must be named arguments passing to further methods

Value

Transformed image. The image will share the same space as `fixed`.

See Also

```
print(ants$apply_transforms)
```

Examples

```
if(interactive() && ants_available()) {
  ants <- load_ants()
  fixed <- as_ANTsImage( ants$get_ants_data('r16') )
  moving <- as_ANTsImage( ants$get_ants_data('r64') )
  fixed <- ants_resample_image(fixed, c(64, 64), TRUE, "linear")
  moving <- ants_resample_image(moving, c(64,64), TRUE, "linear")

  mytx <- ants_registration(fixed = fixed,
                            moving = moving,
                            type_of_transform = 'SyN')
  mywarpedimage <- ants_apply_transforms(
    fixed = fixed,
    moving = moving,
    transformlist = mytx$fwdtransforms
  )

  par(mfrow = c(1,3), mar = c(0,0,3,0))
  pal <- gray.colors(256)
  image(fixed[], asp = 1, axes = FALSE, col = pal,
        ylim = c(1, 0), main = "Reference")
  image(moving[], asp = 1, axes = FALSE, col = pal,
        ylim = c(1, 0), main = "Moving")
  image(mywarpedimage[], asp = 1, axes = FALSE, col = pal,
        ylim = c(1, 0), main = "Moving reg+resamp into Reference")
}
```

`ants_apply_transforms_to_points`
Apply a transform list to map points from one domain to another

---

Description

See `ants$apply_transforms_to_points` for more details. Please note point mapping goes the opposite direction of image mapping (see `ants_apply_transforms`), for both reasons of convention and engineering.

Usage

```
ants_apply_transforms_to_points(
  dim,
  points,
  transformlist,
  whichtoinvert = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

dim	dimensions of the transformation
points	data frame containing columns 'x', 'y', 'z', 't' (depending on dim)
transformlist	list of strings (path to transforms) generated by ants_registration where each transform is a file name
whichtoinvert	either NULL, None ('Python'), or a vector of logical with same length as transformlist; print ants$apply_transforms_to_points to see detailed descriptions
verbose	whether to verbose application of transform
...	ignored

Value

Transformed points in data frame (R object)

See Also

```
print(ants$apply_transforms_to_points)
```

Examples

```
if(interactive() && ants_available()) {
  ants <- load_ants()
  fixed <- as_ANTsImage( ants$get_ants_data('r16') )
  moving <- as_ANTsImage( ants$get_ants_data('r27') )

  reg <- ants_registration(
    fixed = fixed, moving = moving,
    type_of_transform = "antsRegistrationSyNRepro[a]")

  pts <- data.frame(
    x = c(128, 127),
    y = c(101, 111)
  )

  ptsw = ants_apply_transforms_to_points(2, pts, reg$fwdtransforms)
  ptsw
}
```

ants_available *Check if 'ANTs' is available*

Description

Check if 'ANTs' is available

Usage

```
ants_available(module = c("ants", "antspynet"))
```

Arguments

module	either 'ants' or 'antspynet'; default is 'ants'

Value

Logical, whether 'ANTs' or 'ANTsPyNet' is available

See Also

install_ants

ants_motion_correction *Motion correction*

Description

Print ants$motion_correction to see the original document

Usage

```
ants_motion_correction(
  x,
  fixed = NULL,
  type_of_transform = "BOLDRigid",
  mask = NULL,
  fdOffset = 50,
  outprefix = "",
  verbose = FALSE,
  ...
)
```

Arguments

x	input image, usually 'fMRI' series
fixed	fixed image to register all timepoints to
type_of_transform	see ants_registration
mask	mask for image
fdOffset	offset value to use in frame-wise displacement calculation
outprefix	save path
verbose	whether to verbose the messages
...	passed to registration methods

Value

Motion-corrected image

Examples

```
if(interactive() && ants_available()) {
  fi <- as_ANTsImage(ants$get_ants_data('ch2'))
  mytx <- ants_motion_correction( fi )

  par(mfrow = c(1, 2), mar = c(1,1,1,1))
  image(fi[,,91], asp = 1, axes = FALSE)
  image(mytx$motion_corrected[,,91], asp = 1, axes = FALSE)
}
```

---

ants_plot *Plot single* 'ANTsImage'

Description

Plot single 'ANTsImage'

Usage

```
ants_plot(
  image,
  overlay = NULL,
  blend = FALSE,
  alpha = 1,
  cmap = "Greys_r",
  overlay_cmap = "turbo",
  overlay_alpha = 0.9,
  vminol = NULL,
```

```
  vmaxol = NULL,
  cbar = FALSE,
  cbar_length = 0.8,
  cbar_dx = 0,
  cbar_vertical = TRUE,
  axis = 0,
  nslices = 12,
  slices = NULL,
  ncol = NULL,
  slice_buffer = NULL,
  black_bg = TRUE,
  bg_thresh_quant = 0.01,
  bg_val_quant = 0.99,
  domain_image_map = NULL,
  crop = FALSE,
  scale = FALSE,
  reverse = FALSE,
  title = "",
  title_fontsize = 20,
  title_dx = 0,
  title_dy = 0,
  filename = NULL,
  dpi = 500,
  figsize = 1.5,
  reorient = TRUE,
  resample = TRUE,
  force_agg = FALSE,
  close_figure = TRUE
)
```

Arguments

`image`	`'ANTsImage'`, or something can be converted to `'ANTsImage'`
`overlay`	overlay `'ANTsImage'`, can be `NULL`, optional
`blend`	whether to blend image with overlay; default is false
`cmap`, `alpha`	image color map and transparency
`overlay_cmap`, `overlay_alpha`	overlay color map and transparency
`vminol`, `vmaxol`	I could not find its usage
`cbar`	whether to draw color legend
`cbar_length`, `cbar_dx`, `cbar_vertical`	legend position and size
`axis`	see 'Details'
`nslices`, `slices`, `ncol`	controls slice to show
`slice_buffer`	performance

`black_bg`, `bg_thresh_quant`, `bg_val_quant`
: controls background

`domain_image_map`
: optional `'ANTsImage'`

`crop`, `scale`, `reverse`
: whether to crop, scale, or reverse the image according to background

`title`, `title_fontsize`, `title_dx`, `title_dy`
: image title

`filename`, `dpi`, `figsize`
: needed when saving to file

`reorient`
: whether to reorient to `'LAI'` before plotting; default is true

`resample`
: whether to resample

`force_agg`
: whether to force graphic engine to use `'agg'` device; default is false

`close_figure`
: whether to close figure when returning the function

Details

By default, images will be reoriented to `'LAI'` orientation before plotting. So, if `axis=0`, the images will be ordered from the left side of the brain to the right side of the brain. If `axis=1`, the images will be ordered from the anterior (front) of the brain to the posterior (back) of the brain. And if `axis=2`, the images will be ordered from the inferior (bottom) of the brain to the superior (top) of the brain.

Value

Nothing

Examples

```
if(interactive() && ants_available()) {
  ants <- load_ants()
  img <- ants$image_read(ants$get_ants_data('mni'))

  ants_plot(
    img, nslices = 12, black_bg = FALSE,
    bg_thresh_quant = 0.05, bg_val_quant = 1.0, axis = 2,
    cbar = TRUE, crop = TRUE, reverse = TRUE, cbar_vertical = FALSE,
    ncol = 4, title = "Axial view of MNI brain"
  )
}
```

ants_plot_grid *Plot multiple* 'ANTsImage'

Description

R-friendly wrapper function for ants$plot_grid

Usage

```
ants_plot_grid(
  images,
  shape = NULL,
  slices = 0,
  axes = 2,
  figsize = 1,
  rpad = 0,
  cpad = 0,
  vmin = NULL,
  vmax = NULL,
  colorbar = TRUE,
  cmap = "Greys_r",
  title = "",
  tfontsize = 20,
  title_dx = 0,
  title_dy = 0,
  rlabels = NULL,
  rfontsize = 14,
  rfontcolor = "black",
  rfacecolor = "white",
  clabels = NULL,
  cfontsize = 14,
  cfontcolor = "black",
  cfacecolor = "white",
  filename = NULL,
  dpi = 400,
  transparent = TRUE,
  ...,
  force_agg = FALSE,
  close_figure = TRUE
)
```

Arguments

images	a single 'ANTsImage', list, or nested list of 'ANTsImage'
shape	shape of grid, default is using dimensions of images
slices	length of one or equaling to length of slices, slice number to plot

axes	0 for 'sagittal', 1 for 'coronal', 2 for 'axial'; default is 2
figsize, rpad, cpad, colorbar, cmap, transparent	graphical parameters
vmin, vmax	value threshold for the image
title	title of figure
title_dx, title_dy, tfontsize	controls title margin and size
rlabels, clabels	row and column labels
rfontsize, rfontcolor, rfacecolor, cfontsize, cfontcolor, cfacecolor	row and column font size, color, and background color
filename, dpi	parameters to save figures
...	passed to ants$plot_grid; make sure all entries are named
force_agg	whether to force graphic engine to use 'agg' device; default is false
close_figure	whether to close figure when returning the function

Value

Nothing

Examples

```
if(interactive() && ants_available()) {
  ants <- load_ants()
  image1 <- ants$image_read(ants$get_ants_data('mni'))
  image2 <- image1$smooth_image(1.0)
  image3 <- image1$smooth_image(2.0)
  image4 <- image1$smooth_image(3.0)

  ants_plot_grid(
    list(image1, image2, image3, image4),
    slices = 100, title = "4x1 Grid"
  )

  ants_plot_grid(
    list(image1, image2, image3, image4),
    shape = c(2, 2),
    slices = 100, title = "2x2 Grid"
  )
  ants_plot_grid(
    list(image1, image2, image3, image4),
    shape = c(2, 2), axes = c(0,1,2,1),
    slices = 100, title = "2x2 Grid (diff. anatomical slices)"
  )

}
```

`ants_registration` *Register two images using 'ANTs'*

Description

Register two images using 'ANTs'

Usage

```
ants_registration(
  fixed,
  moving,
  type_of_transform = "SyN",
  initial_transform = NULL,
  outprefix = tempfile(),
  mask = NULL,
  grad_step = 0.2,
  flow_sigma = 3,
  total_sigma = 0,
  aff_metric = c("mattes", "GC", "meansquares"),
  aff_sampling = 32,
  aff_random_sampling_rate = 0.2,
  syn_metric = c("mattes", "CC", "meansquares", "demons"),
  syn_sampling = 32,
  reg_iterations = c(40, 20, 0),
  aff_iterations = c(2100, 1200, 1200, 10),
  aff_shrink_factors = c(6, 4, 2, 1),
  aff_smoothing_sigmas = c(3, 2, 1, 0),
  write_composite_transform = FALSE,
  verbose = FALSE,
  smoothing_in_mm = FALSE,
  ...
)
```

Arguments

`fixed`	fixed image to which we register the moving image, can be character path to 'NIfTI' image, or `'ANTsImage'` instance, `'oro.nifti'` object, `'niftiImage'` from package `'RNifti'`, or `'threeBrain.nii'` from package `'threeBrain'`; see also `as_ANTsImage`
`moving`	moving image to be mapped to fixed space; see also `as_ANTsImage`
`type_of_transform`	a linear or non-linear registration type; print `ants$registration` to see details
`initial_transform`	optional list of strings; transforms to apply prior to registration
`outprefix`	output file to save results

`mask` image mask; see also `as_ANTsImage`

`grad_step`, `flow_sigma`, `total_sigma`
optimization parameters

`aff_metric` the metric for the 'affine' transformation, choices are `'GC'`, `'mattes'`, `'meansquares'`

`aff_sampling`, `aff_random_sampling_rate`, `aff_iterations`, `aff_shrink_factors`, `aff_smoothing_sigmas`
controls 'affine' transform

`syn_metric` the metric for the `'SyN'` transformation, choices are `'GC'`, `'mattes'`, `'meansquares'`, `'demons'`

`syn_sampling`, `reg_iterations`
controls the `'SyN'` transform

`write_composite_transform`
whether the composite transform (and its inverse, if it exists) should be written to an 'HDF5' composite file; default is false

`verbose` verbose the progress

`smoothing_in_mm`
logical, currently only impacts low dimensional registration

`...` others passed to `ants$registration`

Details

Function family `ants_registration*` align images (specified by `moving`) to `fixed`. Here are descriptions of the variations:

`ants_registration` Simple wrapper function for 'Python' implementation `ants.registration`, providing various of registration options

`ants_registration_halpern1` Rigid-body registration designed for 'Casey-Halpern' lab, mainly used for aligning 'MRI' to 'CT' (or the other way around)

Value

A 'Python' dictionary of aligned images and transform files.

Examples

```
if(interactive() && ants_available()) {

  ants <- load_ants()

  # check the python documentation here for detailed explanation
  print(ants$registration)

  # example to register
  fi <- ants$image_read(ants$get_ants_data('r16'))
  mo <- ants$image_read(ants$get_ants_data('r64'))

  # resample to speed up this example
  fi <- ants$resample_image(fi, list(60L,60L), TRUE, 0L)
```

```
  mo <- ants$resample_image(mo, list(60L,60L), TRUE, 0L)

  # SDR transform
  transform <- ants_registration(
    fixed=fi, moving=mo, type_of_transform = 'SyN' )

  ants$plot(fi, overlay = transform$warpedmovout, overlay_alpha = 0.3)


}
```

`ants_resample_image` *Resample image*

Description

See `ants$resample_image` for more details

Usage

```
ants_resample_image(
  x,
  resample_params,
  use_voxels = FALSE,
  interp_type = c("linear", "nn", "guassian", "sinc", "bspline")
)
```

Arguments

`x`	input image
`resample_params`	either relative number or absolute integers
`use_voxels`	whether the `resample_params` should be treated as new dimension `use_voxels=TRUE`, or the new dimension should be calculated based on current dimension and `resample_params` combined (`use_voxels=FALSE` then `resample_params` will be treated as relative number); default is `FALSE`
`interp_type`	interpolation type; either integer or character; see 'Usage' for available options

Value

Resampled image

Examples

```
if(interactive() && ants_available()) {

  sample_fpath <- as.character(ants$get_ants_data("r16"))

  if (file.exists(sample_fpath)) {

    try(silent = TRUE, {

      ants <- load_ants()
      fi <- as_ANTsImage(ants$get_ants_data("r16"))

      # linear (interp_type = 0 or "linear)
      filin <- ants_resample_image(fi, c(50, 60), TRUE, "linear")

      # nearest neighbor (interp_type = 1 or "nn)
      finn <- ants_resample_image(fi, c(50, 60), TRUE, "nn")

      par(mfrow = c(1, 3), mar = c(0, 0, 0, 0))
      pal <- gray.colors(256, start = 0)

      image(fi[], asp = 1, axes = FALSE,
            ylim = c(1,0), col = pal)
      image(filin[], asp = 1, axes = FALSE,
            ylim = c(1,0), col = pal)
      image(finn[], asp = 1, axes = FALSE,
            ylim = c(1,0), col = pal)

    })

  }

}
```

`as_ANTsImage` *Load data as 'ANTsImage' class*

Description

Load data as 'ANTsImage' class

Usage

```
as_ANTsImage(x, strict = FALSE)
```

Arguments

x	data to be converted; this can be an 'ANTsImage' instance, character, 'oro.nifti' object, 'niftiImage' from package 'RNifti', or 'threeBrain.nii' from package 'threeBrain'
strict	whether x should not be NULL

Value

An 'ANTsImage' instance; use ants$ANTsImage to see the 'Python' documentation

Examples

```
if(interactive() && ants_available()) {

  ants <- load_ants()

  # Python string
  x1 <- ants$get_ants_data('r16')
  as_ANTsImage( x1 )

  # R character
  nii_path <- system.file(package = "RNifti",
                          "extdata", "example.nii.gz")
  as_ANTsImage( nii_path )

  # niftiImage object
  x2 <- RNifti::readNifti(nii_path)
  as_ANTsImage( x2 )

}
```

---

as_ANTsTransform *Convert to 'ANTsTransform'*

Description

Convert to 'ANTsTransform'

Usage

```
as_ANTsTransform(x, ...)

## Default S3 method:
as_ANTsTransform(x, dimension = 3, ...)

## S3 method for class 'ants.core.ants_transform.ANTsTransform'
as_ANTsTransform(x, ...)
```

```
## S3 method for class 'ants.core.ants_image.ANTsImage'
as_ANTsTransform(x, ...)

## S3 method for class 'numpy.ndarray'
as_ANTsTransform(x, ...)

## S3 method for class 'character'
as_ANTsTransform(x, ...)
```

Arguments

x	'affine' matrix or 'numpy' array, character path to the matrix, 'ANTsTransform', 'ANTsImage' as displacement field.
...	passed to other methods
dimension	expected transform space dimension; default is 3

Value

An 'ANTsTransform' object

Examples

```
if(interactive() && ants_available()) {

  mat <- matrix(c(
    0, -1, 0, 128,
    1, 0, 0, -128,
    0, 0, -1, 128,
    0, 0,  0,   1
  ), ncol = 4, byrow = TRUE)

  trans <- as_ANTsTransform(mat)
  trans

  # apply transform
  trans$apply_to_point(c(120, 400, 1))

  # same results
  mat %*% c(120, 400, 1, 1)

  trans[] == mat

}
```

`brain_extraction` *Extract brain and strip skull*

Description

Function `brain_mask` and `brain_extraction` use the `ants` base package. Function `antspynet_brain_extraction` uses `antspynet` to extract the brain using deep neural network. This requires additional configuration. Print `antspynet$brain_extraction` to see the original documentation.

Usage

```
antspynet_brain_extraction(
  x,
 modality = c("t1", "t1nobrainer", "t1combined", "flair", "t2", "t2star", "bold", "fa",
    "t1t2infant", "t1infant", "t2infant"),
  verbose = FALSE
)

brain_mask(
  x,
  work_path = tempfile(pattern = "rpyant_brain_extraction_"),
  verbose = TRUE,
  auto_clean = TRUE
)

brain_extraction(
  x,
  skull_alpha = 0,
  threshold_quantile = 0.85,
  ...,
  verbose = TRUE
)
```

Arguments

`x`	input image or image path
`modality`	modality type, used by `antspynet_brain_extraction` only
`verbose`	whether to print out process to the screen
`work_path`	working directory; default is temporary path
`auto_clean`	whether to automatically clean the working path if the path is temporary; default is true
`skull_alpha`	used by `brain_extraction`, the opacity of the skull in the final image; default is 0 (completely strip the skull); set to values between 0 to 1 to add skulls (in such case, the background noises will be set to 0)
`threshold_quantile`	used only when `skull_alpha` is positive to remove the noises

... see work_path and auto_clean

Value

brain_mask Brain mask image

brain_extraction extracted brain

antspynet_brain_extraction Brain mask image

---

correct_intensity *Truncate and correct 'MRI' intensity*

Description

Uses ants.abp_n4 to truncate and correct intensity

Usage

```
correct_intensity(image, mask = NULL, intensity_truncation = c(0.025, 0.975))
```

Arguments

image	'MRI' image to be corrected, will be passed to as_ANTsImage
mask	binary mask image
intensity_truncation	numerical length of two, quantile probabilities to truncate.

Value

An 'ANTsImage' instance

Examples

```
if(interactive() && ants_available()) {
  ants <- load_ants()
  scale <- (0.1 + outer(
    seq(0, 1, length.out = 256)^6,
    seq(0, 1, length.out = 256)^2,
    FUN = "+"
  )) / 6
  img = ants$image_read(ants$get_ants_data('r16')) * scale

  corrected <- correct_intensity(img)

  pal <- gray.colors(255, start = 0)
  par(mfrow = c(1, 2), mar = c(0.1, 0.1, 2.1, 0.1),
      bg = "black", fg = "white")
  image(img[], asp = 1, axes = FALSE,
        col = pal, ylim = c(1, 0),
```

```
      main = "Original", col.main = "white")
  image(corrected[], asp = 1, axes = FALSE,
      col = pal, ylim = c(1, 0),
      main = "Corrected", col.main = "white")

}
```

---

ensure_template *Ensure the template directory is downloaded*

Description

Ensure the template directory is downloaded

Usage

```
ensure_template(name = BUILTIN_TEMPLATES)
```

Arguments

name	name of the template, commonly known as 'MNI152' templates; choices are "mni_icbm152_nlin_asym_09a", "mni_icbm152_nlin_asym_09b", and "mni_icbm152_nlin_asym_09

Value

The downloaded template path

Examples

```
# Do not run for testing as this will download the template
if(FALSE) {

# Default is `mni_icbm152_nlin_asym_09a`
ensure_template()
ensure_template("mni_icbm152_nlin_asym_09a")

# Using MNI152b
ensure_template("mni_icbm152_nlin_asym_09b")

}
```

extract_coregistration *Extract transform in right-anterior-superior coordinate system*

Description

Extract transform from 'ANTs' and moving image, save the transform matrices.

Usage

```
extract_coregistration(transform_path, moving_img, outprefix = NULL)
```

Arguments

transform_path	path to the transform ('ANTs_0GenericAffine.mat' matrix) file
moving_img	path to the moving image, for example, if 'CT' is aligned to 'T1w', then 'CT' is the moving image
outprefix	output prefix, where the matrices are saved to; default is at the same folder as transform_path

Value

A list of two matrices: new_sform is the new index to image transform (see 'sform' in 'NIfTI' header definition). This is a four-by-four matrix transforming from the voxel index (moving image) to the fixed image 'RAS' coordinates. ras_transform is a four-by-four matrix from the moving image to the fixed image in 'RAS' coordinates.

halpern_preprocess *'ANTs' functions for 'Halpern' lab*

Description

'ANTs' functions for 'Halpern' lab

Usage

```
halpern_register_ct_mri(
  fixed,
  moving,
  outprefix,
  fixed_is_ct = TRUE,
  verbose = TRUE
)

halpern_register_template_mri(
```

```
  fixed,
  moving,
  outprefix,
  mask = NULL,
  verbose = TRUE
)

halpern_apply_transform_template_mri(roi_folder, outprefix, verbose = TRUE)
```

Arguments

`fixed`	fixed image as template
`moving`	moving image that is to be registered into `fixed`
`outprefix`	output prefix, needs to be absolute path prefix
`fixed_is_ct`	whether `fixed` is 'CT'
`verbose`	whether to verbose the progress; default is true
`mask`	mask file for template (skull-stripped)
`roi_folder`	template 'ROI' or atlas folder in which the image atlases or masks will be transformed into subject's native brain

Value

A list of result configurations

`install_ants` *Install 'ANTs' via 'ANTsPy'*

Description

Install 'ANTs' via 'ANTsPy'

Usage

```
install_ants(python_ver = "3.11", verbose = TRUE)
```

Arguments

`python_ver`	'Python' version, see `configure_conda`; default is `"3.11"` since `'ANTsPy'` is compiled for all platforms under this version
`verbose`	whether to print the installation messages

Value

This function returns nothing.

`is_affine3D` *Check if an object is a 3D 'affine' transform matrix*

Description

Check if an object is a 3D 'affine' transform matrix

Usage

```
is_affine3D(x, ...)

## Default S3 method:
is_affine3D(x, strict = TRUE, ...)

## S3 method for class 'ants.core.ants_transform.ANTsTransform'
is_affine3D(x, ...)
```

Arguments

`x`	R or Python object, accepted forms are numeric `matrix`, `'ANTsTransform'`, or `character` (path to transform matrix)
`...`	passed to other methods
`strict`	whether the last element should be always 1

Value

A logical value whether the object can be loaded as a 4-by-4 matrix.

Examples

```
# not affine
is_affine3D(1)

# 3x3 matrix is not as it is treated as 2D transform
is_affine3D(matrix(rnorm(9), nrow = 3))

# 3x4 matrix
x <- matrix(rnorm(12), nrow = 3)
is_affine3D(x)

# 4x4 matrix
x <- rbind(x, c(0,0,0,1))
is_affine3D(x)

if(interactive() && ants_available()) {

  ants <- load_ants()
  x <- ants$new_ants_transform(dimension = 3L)
```

```
  is_affine3D(x)

  # save the parameters
  f <- tempfile(fileext = ".mat")
  ants$write_transform(x, f)
  is_affine3D(f)

}
```

---

py *Get 'Python' main process environment*

Description

Get 'Python' main process environment

Usage

```
py
```

Format

An object of class `NULL` of length 0.

Value

The 'Python' main process as a module

---

py_builtin *Get 'Python' built-in object*

Description

Get 'Python' built-in object

Usage

```
py_builtin(name, convert = TRUE)
```

Arguments

`name`	object name
`convert`	see `import_builtins`

Value

A python built-in object specified by name

Examples

```
if(interactive() && ants_available()) {


# ------ Basic case: use python `int` as an R function ---------
py_int <- py_builtin("int")

# a is an R object now
a <- py_int(9)
print(a)
class(a)

# ------ Use python `int` as a Python function -----------------
py_int2 <- py_builtin("int", convert = FALSE)

# b in a python object
b <- py_int2(9)

# There is no '[1] ' when printing
print(b)
class(b)

# convert to R object
py_to_r(b)



}
```

`py_list` *List in 'Python'*

Description

List in 'Python'

Usage

```
py_list(..., convert = FALSE)
```

Arguments

`...`	passing to `list` ('Python')
`convert`	whether to convert the results back into R; default is no

Value

List instance, or an R vector if converted

Examples

```
if(interactive() && ants_available()) {

  py_list(list(1,2,3))
  py_list(c(1,2,3))

  py_list(array(1:9, c(3,3)))
  py_list(list(list(1:3), letters[1:3]))

}
```

`py_slice` *Slice index in 'Python' arrays*

Description

Slice index in 'Python' arrays

Usage

```
py_slice(...)
```

Arguments

`...`	passing to `slice` ('Python')

Value

Index slice instance

Examples

```
if(interactive() && ants_available()) {

  x <- np_array(array(seq(20), c(4, 5)))

  # equivalent to x[::2]
  x[py_slice(NULL, NULL, 2L)]

}
```

`t1_preprocess` *Process 'T1' image*

Description

Process 'MRI' and align with template brains

Usage

```
t1_preprocess(
  t1_path,
  templates = "mni_icbm152_nlin_asym_09a",
  work_path = ".",
  verbose = TRUE
)
```

Arguments

`t1_path`	path to a 'T1' image
`templates`	template to use; default is `'mni_icbm152_nlin_asym_09a'`,
`work_path`	working path, must be a directory
`verbose`	whether to verbose the progress

Value

Nothing will be returned. Please check `work_path` for results.

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