

Package: sulcimap (via r-universe)

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Title Mapping Cortical Folding Patterns

Version 1.0.6

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Description Visualizes sulcal morphometry data derived from 'BrainVisa' <<https://brainvisa.info/>> including width, depth, surface area, and length. The package enables mapping of statistical group results or subject-level values onto cortical surface maps, with options to focus on all sulci or only selected regions of interest. Users can display all four measures simultaneously or restrict plots to chosen measures, creating composite, publication-quality brain visualizations in R to support the analysis and interpretation of sulcal morphology.

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Encoding UTF-8

RoxygenNote 7.3.3

Depends R (>= 4.0)

Imports utils, tools, magick, ggplot2, viridisLite, scales, patchwork, cowplot, grid, grDevices

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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Repository <https://cran.r-universe.dev>

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Contents

clear_sulcimap_cache	2
get_assets_light	2
get_sulcimap_assets_dir	3
get_sulcus_image	3
list_sulci_images	4
plot_sulci	4
Index	7

clear_sulcimap_cache	<i>Clear sulcimap cached assets</i>
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Description

Clear sulcimap cached assets

Usage

```
clear_sulcimap_cache()
```

Value

Logical TRUE if cache removed or did not exist

get_assets_light	<i>Lightweight assets for light example Unzips a tiny assets bundle and returns the directory path.</i>
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Description

Lightweight assets for light example Unzips a tiny assets bundle and returns the directory path.

Usage

```
get_assets_light()
```

Value

A character scalar: path to the unzipped assets directory.

`get_sulcimap_assets_dir`
Path to sulcimap extracted asset directory

Description

Unzips the bundled assets into a cache (persistent for users, temporary under checks)

Usage

`get_sulcimap_assets_dir()`

Value

Character scalar: full path to the root of extracted assets

`get_sulcus_image` *Full path to a bundled PNG (after extraction)*

Description

Full path to a bundled PNG (after extraction)

Usage

`get_sulcus_image(name)`

Arguments

name Relative path inside the assets (e.g. "leftlat/S.C._left.png")

Value

Character scalar: full path

list_sulci_images	<i>List bundled PNGs (after extraction)</i>
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Description

List bundled PNGs (after extraction)

Usage

```
list_sulci_images()
```

Value

Character vector of relative PNG paths

plot_sulci	<i>Plot sulcal measures on brain</i>
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Description

Generates composite brain figures (left/right lateral/medial) by mapping sulcal values.

Usage

```
plot_sulci(
  sulcus_values,
  palette = "gyr",
  value_range = NULL,
  save_dir = NULL,
  measure = c("all", "opening", "depth", "surface", "length"),
  show_colorbar = TRUE,
  caption = expression(-log[10](p)),
  ...
)
```

Arguments

sulcus_values	data.frame or path/to/csv Either (1) a two-column dataframe with Sulcus and Value, or (2) a path to a CSV file containing those columns. Sulcus must use BrainVISA-style tags (left/right, 4 types) and include all expected names. Missing sulcus should have Value = 0 (see README and data samples).
palette	character Color palette for mapping values and the colorbar. Options include "viridis", "magma", "plasma", "inferno", "cividis", "heat", "gyr".
value_range	numeric length-2 or NULL (default NULL) Controls the color scale. <ul style="list-style-type: none"> • NULL: auto-scale from the min/max of the provided values.

	<ul style="list-style-type: none"> • <code>c(min, max)</code>: fix the scale across plots/conditions for comparability.
<code>save_dir</code>	character or NULL (default NULL) Directory where the plot image(s) are saved. If it does not exist, it will be created. Set to NULL to skip saving and only return the plot object.
<code>measure</code>	character What to plot: <ul style="list-style-type: none"> • "all": generate all four measures in one figure. • "opening", "depth", "surface", "length": generate a single-measure plot.
<code>show_colorbar</code>	logical Show or hide the color bar on the figure.
<code>caption</code>	character or expression Label displayed with the color bar. For math, use e.g. <code>expression(-log[10](p))</code> .
<code>...</code>	Advanced options: <code>base_dir</code> (path to assets), <code>scale_width</code> (magick scale, default "1000x"), <code>file_prefix</code> (default "sulci"), <code>width_in</code> , <code>height_in</code> (inches; defaults 14, 8), <code>dpi</code> (default 300).

Value

If `save_dir = NULL`, returns a ggplot (or patchwork) object representing the brain figure, which can be further modified and saved. If `save_dir` is not NULL, the plot image(s) are automatically saved in that directory and the function (invisibly) returns a character vector with the path(s) to the saved file(s).

Examples

```
# Minimal executable example using assets_light
ex <- data.frame(
  Sulcus = c("S.C._left.opening", "S.C._right.opening",
            "S.F.int._left.opening", "S.F.int._right.opening"),
  Value = c(1, 0.5, 0.8, 0.4)
)
assets_light <- sulcimaps::get_assets_light()
p <- plot_sulci(
  sulcus_values = ex,
  measure       = "opening",
  palette       = "gyr",
  show_colorbar = FALSE,
  base_dir      = assets_light,
  save_dir      = NULL
)
# p is a ggplot/patchwork object; printing it will draw the figure.

# Full example
# df should have columns: Sulcus (BrainVISA-style names with suffixes), Value
# plot_out <- plot_sulci(
#   sulcus_values = df,
#   palette       = "gyr",
#   value_range   = NULL,
#   save_dir      = NULL,
```

```
# measure      = "opening",
# show_colorbar = TRUE,
# caption      = expression(-log[10](p))
# )
```

Index

`clear_sulcimap_cache`, 2

`get_assets_light`, 2

`get_sulcimap_assets_dir`, 3

`get_sulcus_image`, 3

`list_sulci_images`, 4

`plot_sulci`, 4