

Package ‘ggseg’

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Title Plotting Tool for Brain Atlases

Version 1.6.8

Description Contains 'ggplot2' geom for plotting brain atlases using simple features. The largest component of the package is the data for the two built-in atlases. Mowinckel & Vidal-Piñero (2020) <[doi:10.1177/2515245920928009](https://doi.org/10.1177/2515245920928009)>.

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VignetteBuilder knitr

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adapt_scales	<i>Scale ggseg plot axes.</i>
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Description

adapt_scales returns a list of coordinate breaks and labels for axes or axes label manipulation of the ggseg brain atlases.

Usage

```
adapt_scales(geobrain, position = "dispersed", aesthetics = "labs")
```

Arguments

`geobrain` a data.frame containing atlas information.
`position` String choosing how to view the data. Either "dispersed"[default] or "stacked".
`aesthetics` String of which aesthetics to adapt scale of, either "x", "y", or "labs".

Value

nested list with coordinates for labels

`aseg`*Freesurfer automatic subcortical segmentation of a brain volume*

Description

Coordinate data for the subcortical parcellations implemented in Freesurfer.

Usage

```
data(aseg)
```

Format

An object of class `brain_atlas` of length 4.

Value

An object of class `'brain_atlas'` for plotting with `ggseg`

References

Fischl et al., (2002). Neuron, 33:341-355 ([PubMed](#))

See Also

Other `ggseg_atlases`: [dk](#)

Examples

```
data(aseg)
```

as_brain_atlas	Create brain atlas
----------------	--------------------

Description

Coerce object into an object of class 'brain_atlas'.

Usage

```
as_brain_atlas(x)
```

Arguments

x object to make into a brain_atlas

Value

an object of class 'brain_atlas'.

as_ggseg_atlas	Create ggseg atlas
----------------	--------------------

Description

Create ggseg atlas

Usage

```
as_ggseg_atlas(x)

## Default S3 method:
as_ggseg_atlas(x)

## S3 method for class 'data.frame'
as_ggseg_atlas(x)

## S3 method for class 'ggseg_atlas'
as_ggseg_atlas(x)

## S3 method for class 'brain_atlas'
as_ggseg_atlas(x)
```

Arguments

x object to make into a ggseg_atlas

Value

Object of class 'ggseg_atlas'

brain_atlas	<i>Constructor for brain atlas</i>
-------------	------------------------------------

Description

Creates an object of class 'brain_atlas' that is compatible for plotting using the ggseg-package plot functions

Usage

```
brain_atlas(atlas, type, data, palette = NULL)
```

Arguments

atlas	atlas short name, length one
type	atlas type, cortical or subcortical, length one
data	data.frame with atlas data
palette	named character vector of colours

Value

an object of class 'brain_atlas' containing information on atlas name, type, data and palette. To be used in plotting with [geom_brain](#).

brain_join	<i>Join atlas and data</i>
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Description

Joins data frame with a brain-atlas object.

Usage

```
brain_join(data, atlas, by = NULL)
```

Arguments

data	data.frame
atlas	atlas data
by	optional character vector of column to join by

Value

either an sf-object (if brain atlas) or a tibble (if ggseg-atlas) with merged atlas and data

Examples

```
someData = data.frame(
  region = c("transverse temporal", "insula",
            "precentral", "superior parietal"),
  p = sample(seq(0,.5,.001), 4),
  stringsAsFactors = FALSE)

brain_join(someData, dk)
brain_join(someData, dk, "region")
```

brain_labels	<i>Extract unique labels of brain regions</i>
--------------	---

Description

Convenience function to extract names of brain labels from a [brain_atlas](#). Brain labels are usually default naming obtained from the original atlas data.

Usage

```
brain_labels(x)

## S3 method for class 'ggseg_atlas'
brain_labels(x)

## S3 method for class 'brain_atlas'
brain_labels(x)
```

Arguments

x brain atlas

Value

Character vector of atlas region labels

brain_pal	<i>Generate palettes from the ggseg atlases</i>
-----------	---

Description

brain_pal return HEX colours for the different ggseg atlases.

Usage

```
brain_pal(name, n = "all", direction = 1, unname = FALSE, package = "ggseg")
```

Arguments

name	String name of atlas
n	Number of colours to return (or "all" [default])
direction	Direction of HEX, -1 reverses order Necessary if applying palette to other data than the brain atlas it comes from.
unname	return unnamed vector (default = FALSE)
package	package to get brain_pals data from (ggseg or ggsegExtra)

Value

vector of colours

Examples

```
brain_pal("dk")  
brain_pal("aseg")
```

brain_pals_info	<i>Get info on brain palettes</i>
-----------------	-----------------------------------

Description

Get info on brain palettes

Usage

```
brain_pals_info(package = "ggseg")
```

Arguments

package	package to get brain_pals data from (ggseg or ggsegExtra)
---------	---

Value

data.frame with palette information

Examples

```
brain_pals_info()
```

brain_regions	<i>Extract unique names of brain regions</i>
---------------	--

Description

Convenience function to extract names of brain regions from a [brain_atlas](#)

Usage

```
brain_regions(x)

## S3 method for class 'ggseg_atlas'
brain_regions(x)

## S3 method for class 'brain_atlas'
brain_regions(x)

## S3 method for class 'data.frame'
brain_regions(x)
```

Arguments

x brain atlas

Value

Character vector of brain region names

dk	<i>Desikan-Killiany Cortical Atlas</i>
----	--

Description

Coordinate data for the Desikan-Killiany Cortical atlas, with 40 regions in on the cortical surface of the brain.

Usage

```
data(dk)
```


Format

An object of class `brain_atlas` of length 4.

Value

An object of class `'brain_atlas'` for plotting with `ggseg`

References

Fischl et al. (2004) Cerebral Cortex 14:11-22 ([doi:10.1093/cercor/bhg087](https://doi.org/10.1093/cercor/bhg087))

See Also

Other `ggseg_atlas`s: [aseg](#)

Examples

```
data(dk)
```

<code>geom_brain</code>

<i>Brain geom</i>

Description

call to [geom_sf](#)

Usage

```
geom_brain(  
  mapping = aes(),  
  data = NULL,  
  atlas,  
  hemi = NULL,  
  side = NULL,  
  position = position_brain(),  
  show.legend = NA,  
  inherit.aes = TRUE,  
  ...  
)
```

Arguments

<code>mapping</code>	argument to pass to aes to map variables from the supplied data to the plot
<code>data</code>	data.frame with data to plot
<code>atlas</code>	object of type <code>brain_atlas</code> to plot
<code>hemi</code>	hemisphere to plot. Defaults to everything in the atlas.

side	slice to plot, as recorded in the "side" column in the atlas data. Defaults to all.
position	position of the data. Default is "identity" but can be changed by position_brain .
show.legend	logical. Should legend be added or not.
inherit.aes	logical. if aes should be inherited from the main ggplot call or not
...	arguments to geom_sf

Value

ggplot object

Examples

```
library(ggplot2)

ggplot() +
  geom_brain(atlas = dk)
```

ggseg_atlas	<i>'ggseg_atlas' class</i>
-------------	----------------------------

Description

The `'ggseg_atlas'` class is a subclass of `[data.frame][data.frame()]`, created in order to have different default behavior. It heavily relies on the "tibble" `[tbl_df][tibble()]`. [\[tidyverse\]\(https://www.tidyverse.org/packages/\)](#), including [\[dplyr\]\(http://dplyr.tidyverse.org/\)](#), [\[ggplot2\]\(http://ggplot2.tidyverse.org/\)](#), [\[tidyr\]\(http://tidyr.tidyverse.org/\)](#), and [\[readr\]\(http://readr.tidyverse.org/\)](#).

Usage

```
ggseg_atlas(x)
```

Arguments

x data.frame to be made a ggseg-atlas

Value

a tibble with polygon coordinates for plotting brain regions

Properties of `'ggseg_atlas'`

Objects of class `'ggseg_atlas'` have: * A `'class'` attribute of `c("ggseg_atlas", "tbl_df", "tbl", "data.frame")`. * A base type of `"list"`, where each element of the list has the same `[NROW()]`. * A lot of this script and its functions are taken from the `[tibble][tibble()]`-package

is_brain_atlas	<i>Validate brain atlas</i>
----------------	-----------------------------

Description

Validate brain atlas

Usage

```
is_brain_atlas(x)
```

Arguments

x an object

Value

logical if object is of class 'brain_atlas'

is_ggseg_atlas	<i>Validate ggseg_atlas</i>
----------------	-----------------------------

Description

Validate ggseg_atlas

Usage

```
is_ggseg_atlas(x)
```

Arguments

x an object

Value

logical if object is of class 'ggseg_atlas'

position_brain	<i>Alter brain atlas position</i>
----------------	-----------------------------------

Description

Function to be used in the position argument in geom_brain to alter the position of the brain slice/views.

Usage

```
position_brain(position = "horizontal")
```

Arguments

position formula describing the rows ~ columns organization.

Value

a ggproto object

Examples

```
library(ggplot2)
ggplot() +
  geom_brain(atlas = dk, aes(fill = region),
             position = position_brain(. ~ side + hemi ),
             show.legend = FALSE)

ggplot() +
  geom_brain(atlas = dk, aes(fill = region),
             position = position_brain(side ~ hemi ),
             show.legend = FALSE)
```

read_atlas_files	<i>Read in atlas data from all subjects</i>
------------------	---

Description

Recursively reads in all stats files for an atlas (given a unique character string), for all subjects in the subjects directory. Will add hemisphere and subject id to the data.

Usage

```
read_atlas_files(subjects_dir, atlas)
```

Arguments

subjects_dir	FreeSurfer subject directory
atlas	unique character combination identifying the atlas

Value

tibble with stats information for subjects from FreeSurfer

Examples

```
## Not run:
subj_dir <- "/path/to/freesurfer/7.2.0/subjects/"
read_atlas_files(subj_dir, "aseg.stats")

read_atlas_files(subj_dir, "lh.aparc.stats")

## End(Not run)
```

read_freesurfer_stats *Read in raw FreeSurfer stats file*

Description

FreeSurfer atlas stats files have a format that can be difficult to easily read in to R. This function takes a raw stats-file from the subjects directory and reads it in as a data.frame.

Usage

```
read_freesurfer_stats(path, rename = TRUE)
```

Arguments

path	path to stats file
rename	logical. rename headers for ggseg compatibility

Value

tibble with stats information for subjects from FreeSurfer

Examples

```
## Not run:
subj_dir <- "/path/to/freesurfer/7.2.0/subjects/"
aseg_stats <- file.path(subj_dir, "bert/stats/aseg.stats")
read_freesurfer_stats(aseg_stats)

## End(Not run)
```

`read_freesurfer_table` *Read in stats table from FreeSurfer*

Description

FreeSurfer has functions to create tables from raw stats files. If you have data already merged using the `aparcstats2table` or `asegstats2table` from FreeSurfer, this function will read in the data and prepare it for `ggseg`.

Usage

```
read_freesurfer_table(path, measure = NULL, ...)
```

Arguments

<code>path</code>	path to the table file
<code>measure</code>	which measure is the table of
<code>...</code>	additional arguments to <code>read.table</code>

Value

tibble with stats information for subjects from FreeSurfer

Examples

```
## Not run:
file_path <- "all_subj_aseg.txt"
read_freesurfer_table(file_path)

## End(Not run)
```

`reposition_brain` *Reposition brain slices*

Description

Function for repositioning pre-joined atlas data (i.e. data and atlas already joined to a single data frame). This makes it possible for users to reposition the geometry data for the atlas for control over final plot layout. For even more detailed control over the positioning, the "hemi" and "side" columns should be converted into factors and ordered by wanted order of appearance.

Usage

```
reposition_brain(data, position = "horizontal")
```

Arguments

data	sf-data.frame of joined brain atlas and data
position	position formula for slices

Value

sf-data.frame with repositioned slices

Examples

```
reposition_brain(dk, hemi ~ side)
reposition_brain(dk, side ~ hemi)
reposition_brain(dk, hemi + side ~ .)
reposition_brain(dk, . ~ hemi + side)
```

scale_brain	<i>Colour and fill scales from the ggseg atlases</i>
-------------	--

Description

The 'brain' palette scales provides scales for the different atlases in the package. Colours are according to the colours used in the papers where the atlases were first introduced.

Usage

```
scale_brain(
  name = "dk",
  na.value = "grey",
  ...,
  aesthetics = c("fill", "colour", "color")
)

scale_colour_brain(...)

scale_color_brain(...)

scale_fill_brain(...)
```

Arguments

name	String name of atlas
na.value	String name or hex for the colour of NA entries
...	additional arguments to pass to brain_pal
aesthetics	String vector of which aesthetics to scale c("colour", "color", "fill").

Value

scaling function for altering colour of ggplot aesthetics

Palettes

The following palettes are available for use with these scales:

ggseg - dk, aseg

ggsegExtra - tracula, jhu, yeo7, yeo17, glasser, chenAr, chenTh,

Examples

```
scale_brain()
scale_colour_brain()
scale_fill_brain()
```

scale_brain2	<i>Colour and fill scales from the ggseg atlases</i>
--------------	--

Description

The 'brain' palette scales provides scales for the different atlases in the package. Colours are according to the colours used in the papers where the atlases were first introduced.

Usage

```
scale_brain2(
  palette,
  na.value = "grey",
  ...,
  aesthetics = c("fill", "colour", "color")
)

scale_colour_brain2(...)

scale_color_brain2(...)

scale_fill_brain2(...)
```

Arguments

palette	named character vector of regions and colours
na.value	String name or hex for the colour of NA entries
...	additional arguments to pass to brain_pal
aesthetics	String vector of which aesthetics to scale c("colour", "color", "fill").

Value

scaling function for altering colour of ggplot aesthetics

Palettes

The following palettes are available for use with these scales:

ggseg - dk, aseg

ggsegExtra - tracula, jhu, yeo7, yeo17, glasser, chenAr, chenTh,

Examples

```
scale_brain()
scale_colour_brain()
scale_fill_brain()
```

scale_continuous_brain *Axis and label scales from the ggseg atlases*

Description

The 'brain' axis and label scales provides scales for the different atlases in the package. These add axis labels and tick labels corresponding to the different atlases.

Usage

```
scale_continuous_brain(
  atlas = dk,
  position = "dispersed",
  aesthetics = c("y", "x")
)

scale_x_brain(...)

scale_y_brain(...)

scale_labs_brain(atlas = dk, position = "dispersed", aesthetics = "labs")
```

Arguments

atlas	data.frame containing the atlas
position	Character of either "dispersed" or "stacked".
aesthetics	String vector of which aesthetics to scale "x", "y", or "labs".
...	additional arguments to pass to adapt_scales

Value

a scaling function to alter continuous axes labels in ggplot2

Examples

```
## Not run:
scale_x_brain()
scale_y_brain()
scale_labs_brain()

## End(Not run)
```

 theme_brain

ggseg plot theme

Description

a set of themes created for the ggseg plots. Use theme() to tweak.

Usage

```
theme_brain(text.size = 12, text.family = "mono")

theme_darkbrain(text.size = 12, text.family = "mono")

theme_custombrain(
  plot.background = "white",
  text.colour = "darkgrey",
  text.size = 12,
  text.family = "mono"
)

theme_brain2(
  plot.background = "white",
  text.colour = "darkgrey",
  text.size = 12,
  text.family = "mono"
)
```

Arguments

text.size	Specify size of plot text
text.family	Specify font family
plot.background	Specify fill of plot background ('theme_custombrain' only)
text.colour	Specify colour of plot text

Details

‘theme_brain’ Default theme for ggseg. Transparent background, no axis lines, and no grid.

‘theme_darkbrain’ Dark equivalent to theme_brain, with black background, and light text.

‘theme_custombrain’ Theme for easy customization of the brain themes.

Value

function that alters the themeing of a ggplot object

Author(s)

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See Also

[ggplot()], [aes()], [geom_polygon()], [coord_fixed()] from the ggplot2 package

Examples

```
library(ggplot2)

p <- ggplot() +
  geom_brain(atlas = dk)

p +
  theme_brain()

p +
  theme_darkbrain()
```

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