Package ‘ggseg’

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Author Athanasia Mo Mowinckel [aut, cre] (<https://orcid.org/0000-0002-5756-0223>), Didac Vidal-Piñeiro [aut] (<https://orcid.org/0000-0001-9997-9156>)

Maintainer Athanasia Mo Mowinckel <a.m.mowinckel@psykologi.uio.no>

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adapt_scales

Scale ggseg plot axes.

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".
aseg

Value

nested list with coordinates for labels

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


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**

*Constructor for brain atlas*

**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**

*Join atlas and data*

**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
brain_labels

Value

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

Examples

```r
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_pal**

Generate palettes from the ggseg atlases

**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**

Get info on brain palettes

**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
Extract unique names of brain regions

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 Desikan-Killiany Cortical Atlas

Description

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

Usage

data(dk)
**geom_brain**

**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 (PubMed)

**See Also**

Other ggseg_atlases: `aseg`

**Examples**

data(dk)

---

**call to geom_sf**

**Usage**

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

**Arguments**

- `mapping`: argument to pass to `aes` to map variables from the supplied data to the plot
- `data`: data.frame with data to plot
- `atlas`: object of type `brain_atlas` to plot
- `hemi`: hemisphere to plot. Defaults to everything in the atlas.
The 'ggseg_atlas' class is a subclass of ['data.frame'][data.frame()], created in order to have different default behaviour. 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

**Value**

ggplot object

**Examples**

```r
library(ggplot2)

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

---

<table>
<thead>
<tr>
<th>ggseg_atlas</th>
<th>'ggseg_atlas' class</th>
</tr>
</thead>
</table>

**Description**

The 'ggseg_atlas' class is a subclass of ['data.frame'][data.frame()], created in order to have different default behaviour. 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/).
is_brain_atlas

Validate brain atlas

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

Validate ggseg_atlas

Description
Validate ggseg_atlas

Usage
is_ggseg_atlas(x)

Arguments
x an object

Value
logical if object is of class 'ggseg_atlas'
position_brain

Alter brain atlas position

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 organisation.

Value

a ggproto object

Examples

library(ggplot2)

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

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

read_atlas_files

Read in atlas data from all subjects

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 <- freesurfer::fs_subj_dir()
  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 <- freesurfer::fs_subj_dir()
  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
path  path to the table file
measure which measure is the table of
...  additional arguments to read.table

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")
**scale_brain**

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)

---

**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

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

---

**scale_brain2**  
*Colour and fill scales from the ggseg atlases*

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 where first introduced.

Usage

```r
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").
scale_continuous_brain

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

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

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

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

```r
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
theme_brain

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)

<table>
<thead>
<tr>
<th>theme_brain</th>
<th>ggseg plot theme</th>
</tr>
</thead>
</table>

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 customisation of the brain themes.

Value

function that alters the themeing of a ggplot object

Author(s)

Athanasia Mo Mowinckel

See Also

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

Examples

```r
library(ggplot2)

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

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