Package ‘ggseg’

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adapt_scales

Scale ggseg plot axes.

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

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
**brain_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**

```r
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**

```r
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

```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_labels**

*Extract unique labels of brain regions*

**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**

```r
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  

*Generate palettes from the *ggseg* atlases*

**Description**

brain_pal return HEX colours for the different *ggseg* atlases.

**Usage**

```r
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**

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

brain_pals_info  

*Get info on brain palettes*

**Description**

Get info on brain palettes

**Usage**

```r
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)

geom_brain Brain geom

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
  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/).

### 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/).

### Usage

```r
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

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**

```r
library(ggplot2)

# Two examples of using position_brain

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

# Another example

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)
```
read_freesurfer_stats

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**

```r
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**

```r
## 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**

```r
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**

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

`scale_brain` *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 were first introduced.

**Usage**

```r
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")
)
```

```r
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

```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")
)
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

```r
## 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

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

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

```r
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
theme_brain

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)

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See Also

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

Examples

library(ggplot2)

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

  geom_brain(atlas = dk) +
  theme_darkbrain()
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