Package ‘ggseg’

June 13, 2022

**Title**  Plotting Tool for Brain Atlases

**Version**  1.6.5

**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-Piñeiro (2020) <doi:10.1177/2515245920928009>.

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**LazyDataCompression**  xz

**Imports**  ggplot2 (>= 3.3), dplyr (>= 1.0.0), tidyr (>= 1.0.0), sf (>= 0.9-2), stats, grid, utils, vctrs

**Suggests**  knitr, here, rmarkdown, covr, vdiffr, devtools, testthat (>= 2.1.0), spelling

**VignetteBuilder**  knitr

**URL**  https://github.com/ggseg/ggseg

**BugReports**  https://github.com/ggseg/ggseg/issues

**Language**  en-US

**SystemRequirements**  C++11, GDAL (>= 2.0.1), GEOS (>= 3.4.0), PROJ (>= 4.8.0)

**NeedsCompilation**  no

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**Repository**  CRAN

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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

ggeobrain 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
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
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
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

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

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()

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**


**See Also**

Other ggseg_atlases: [aseg](#)

**Examples**

```r
data(dk)
```

---

**geom_brain**  
*Brain geom*

**Description**

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.
ggseg_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

x: data.frame to be made a ggseg-atlas

Value

ggplot object

Examples

library(ggplot2)

ggplot() + geom_brain(atlas = dk)

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

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**

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

**Arguments**

- `position`: formula describing the rows ~ columns organisation.

**Value**

a ggproto object

**Examples**

```r
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

**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**

```r
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*

```r
## 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**

```r
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*

```r
## 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
- 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")
**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(...)**
- **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

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

scale_continous_brain(
atlas = dk,
position = "dispersed",
aesthetics = c("y", "x")
)
scale_x_brain(...)nscale_y_brain(...)nscale_labs_brain(atlas = dk, position = "dispersed", aesthetics = "labs")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>atlas</td>
<td>data.frame containing the atlas</td>
</tr>
<tr>
<td>position</td>
<td>Character of either &quot;dispersed&quot; or &quot;stacked&quot;.</td>
</tr>
<tr>
<td>aesthetics</td>
<td>String vector of which aesthetics to scale &quot;x&quot;, &quot;y&quot;, or &quot;labs&quot;.</td>
</tr>
<tr>
<td>...</td>
<td>additional arguments to pass to adapt_scales</td>
</tr>
</tbody>
</table>
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

```
theme_brain

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
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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