

# Package: ggseg (via r-universe)

August 22, 2024

**Title** Plotting Tool for Brain Atlases

**Version** 1.6.6

**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](https://doi.org/10.1177/2515245920928009)>.

**License** MIT + file LICENSE

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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)

**Repository** <https://lifebrain.r-universe.dev>

**RemoteUrl** <https://github.com/ggseg/ggseg>

**RemoteRef** HEAD

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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

*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	<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 ([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**

<code>mapping</code>	argument to pass to <a href="#">aes</a> to map variables from the supplied data to the plot
<code>data</code>	<code>data.frame</code> 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 <a href="#">position_brain</a> .
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 <a href="#">geom_sf</a>

**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 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

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

### Arguments

position      formula describing the rows ~ columns organisation.

### 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      *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 <- "/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                      *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**

```
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

*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**

```
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 <a href="#">brain_pal</a>
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 <a href="#">adapt_scales</a>

**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	<i>ggseg plot theme</i>
-------------	-------------------------

---

**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

```
library(ggplot2)

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

p +
  theme_brain()

p +
  theme_darkbrain()
```

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