Package ‘ggseg’

April 16, 2026

Title Plotting Tool for Brain Atlases

Version 2.1.1

Description Provides a 'ggplot2' geom and position for visualizing brain region data on cortical, subcortical, and white matter tract atlases. Brain atlas geometries are stored as simple features ('sf'), enabling seamless integration with the 'ggplot2' ecosystem including faceting, custom scales, and themes. Mowinckel & Vidal-Piñeiro (2020) <doi:10.1177/2515245920928009>.

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URL `https://ggsegverse.github.io/ggseg/`,
`https://github.com/ggsegverse/ggseg`

BugReports `https://github.com/ggsegverse/ggseg/issues`

Depends R (>= 4.1.0)

Imports cli, dplyr (>= 1.0.0), ggplot2 (>= 3.3), ggseg.formats, grid, lifecycle, sf, stats, tidyr (>= 1.0.0), utils

Suggests covr, devtools, here, knitr, rmarkdown, spelling, testthat (>= 3.0.0), vdiffr

VignetteBuilder knitr

Config/Needs/website ggsegverse/ggseg.docs

Config/testthat/edition 3

Config/testthat/parallel true

Encoding UTF-8

Language en-US

RoxygenNote 7.3.3

SystemRequirements C++17, GDAL (>= 2.0.1), GEOS (>= 3.4.0), PROJ (>= 4.8.0)

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-04-16 19:20:02 UTC

Contents

`annotate_brain` *Add view labels to brain atlas plots*

Description

Annotates each brain view with a text label positioned above the view's bounding box. For cortical atlases, labels show hemisphere and view (e.g., "left lateral"). For subcortical and tract atlases, labels show the view name directly (e.g., "axial_1", "sagittal").

Usage

```
annotate_brain(
  atlas,
  position = position_brain(),
  hemi = NULL,
  view = NULL,
  size = 3,
  colour = "grey30",
  family = "mono",
  nudge_y = 0,
```

```
  ...
)
```

Arguments

`atlas`	A ‘brain_atlas‘ object (e.g. ‘dk()‘, ‘aseg()‘).
`position`	A [position_brain()] object or position specification matching the one used in [geom_brain()].
`hemi`	Character vector of hemispheres to include. If ‘NULL‘ (default), all hemispheres are included.
`view`	Character vector of views to include. If ‘NULL‘ (default), all views are included.
`size`	Text size in mm (default: ‘3‘).
`colour`	Text colour (default: ‘"grey30"‘).
`family`	Font family (default: ‘"mono"‘).
`nudge_y`	Additional vertical offset for labels (default: ‘0‘).
`...`	Additional arguments passed to [ggplot2::annotate()].

Details

Labels respect the repositioning done by [position_brain()], so the same ‘position‘ argument should be passed to both [geom_brain()] and ‘annotate_brain()‘.

Value

A ggplot2 annotation layer.

Examples

```
library(ggplot2)

pos <- position_brain(hemi ~ view)
ggplot() +
  geom_brain(atlas = dk(), position = pos, show.legend = FALSE) +
  annotate_brain(atlas = dk(), position = pos)

ggplot() +
  geom_brain(atlas = dk(), show.legend = FALSE) +
  annotate_brain(atlas = dk())
```

`brain_join` *Join user data with a brain atlas*

Description

Performs a full join between user data and a brain atlas. Grouped data is handled automatically, producing one complete atlas per group.

Usage

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

Arguments

`data`	A data.frame with a column matching an atlas column (typically ‘"region"‘). Can be grouped with [dplyr::group_by()].
`atlas`	A ‘ggseg_atlas‘ object or data.frame containing atlas data.
`by`	Character vector of column names to join by. If ‘NULL‘ (default), columns are detected automatically.

Value

An ‘sf‘ object if the atlas contains geometry, otherwise a tibble.

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")
```

`geom_brain` *Plot brain atlas regions*

Description

A ggplot2 geom for rendering brain atlas regions as filled polygons, built on top of [ggplot2::geom_sf()]. Accepts a ‘brain_atlas‘ object and automatically joins user data to atlas geometry for visualisation.

Usage

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

Arguments

`mapping`	Set of aesthetic mappings created by [ggplot2::aes()].
`data`	A data.frame containing variables to map. If ‘NULL‘, the atlas is plotted without user data.
`atlas`	A ‘ggseg_atlas‘ object (e.g. ‘dk()‘, ‘aseg()‘, ‘tracula()‘).
`hemi`	Character vector of hemispheres to include (e.g. ‘"left"‘, ‘"right"‘). Defaults to all hemispheres in the atlas.
`view`	Character vector of views to include, as recorded in the atlas data. For cortical atlases: ‘"lateral"‘, ‘"medial"‘. For subcortical/tract atlases: slice identifiers like ‘"axial_3"‘. Defaults to all views.
`position`	Position adjustment, either as a string or the result of a call to [position_brain()].
`show.legend`	Logical. Should this layer be included in the legends?
`inherit.aes`	Logical. If ‘FALSE‘, overrides the default aesthetics rather than combining with them.
`...`	Additional arguments passed to [ggplot2::geom_sf()].

Value

A list of ggplot2 layer and coord objects.

GeomBrain ggproto

‘GeomBrain‘ is a [ggplot2::Geom] ggproto object that handles rendering of brain atlas polygons. It is used internally by [geom_brain()] and should not typically be called directly.

Examples

```
library(ggplot2)

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

`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", nrow = NULL, ncol = NULL, views = NULL)
```

Arguments

`position`	Formula describing the rows ~ columns organisation for cortical atlases (e.g., ‘hemi ~ view‘). For subcortical/tract atlases, can be "horizontal", "vertical", or a formula with ‘type ~ .‘ where type is extracted from view names like "axial_1" -> "axial".
`nrow`	Number of rows for grid layout. If NULL (default), calculated automatically. Only used for subcortical/tract atlases when position is not a formula.
`ncol`	Number of columns for grid layout. If NULL (default), calculated automatically. Only used for subcortical/tract atlases when position is not a formula.
`views`	Character vector specifying which views to include and their order. If NULL (default), all views are included in their original order. Only applies to subcortical/tract atlases.

Value

a ggproto object

Examples

```
library(ggplot2)

# Cortical atlas with formula
ggplot() +
  geom_brain(
    atlas = dk(), aes(fill = region),
    position = position_brain(. ~ view + hemi),
    show.legend = FALSE
  )

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


ggplot() +
  geom_brain(
    atlas = aseg(), aes(fill = region),
    position = position_brain(nrow = 2)
  )

ggplot() +
  geom_brain(
    atlas = aseg(), aes(fill = region),
    position = position_brain(
      views = c("sagittal", "axial_3", "coronal_2"),
      nrow = 1
    )
  )

ggplot() +
  geom_brain(
    atlas = aseg(), aes(fill = region),
    position = position_brain(type ~ .)
  )
```

`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 "view" columns should be converted into factors and ordered by wanted order of appearance.

Usage

```
reposition_brain(
  data,
  position = "horizontal",
  nrow = NULL,
  ncol = NULL,
  views = NULL
)
```

Arguments

`data`	sf-data.frame of joined brain atlas and data
`position`	Position formula for slices. For cortical atlases, use formulas like ‘hemi ~ view‘. For subcortical/tract atlases, use "horizontal", "vertical", or ‘type ~ .‘ for type-based layout.
`nrow`	Number of rows for grid layout (subcortical/tract only)
`ncol`	Number of columns for grid layout (subcortical/tract only)
`views`	Character vector specifying view order (subcortical/tract only)

Value

sf-data.frame with re-positioned slices

Examples

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


reposition_brain(aseg(), nrow = 2)
reposition_brain(aseg(), views = c("sagittal", "axial_3"))
```

`scale_brain` *Colour and fill scales from brain atlas palettes*

Description

‘r lifecycle::badge("deprecated")‘

Atlas palettes are now applied automatically by [geom_brain()]. Use [scale_fill_brain_manual()] for custom palettes.

Usage

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

scale_colour_brain(name = "dk", na.value = "grey", ...)

scale_color_brain(name = "dk", na.value = "grey", ...)

scale_fill_brain(name = "dk", na.value = "grey", ...)
```

Arguments

`name`	String name of the atlas palette (e.g. ‘"dk"‘, ‘"aseg"‘).
`na.value`	Colour for ‘NA‘ entries (default: ‘"grey"‘).
`...`	Additional arguments passed to [ggseg.formats::atlas_palette()].
`aesthetics`	Which aesthetic to scale: ‘"fill"‘, ‘"colour"‘, or ‘"color"‘.

Value

A ggplot2 scale object.

Examples

```
## Not run:
library(ggplot2)
ggplot() +
  geom_brain(atlas = dk(), aes(fill = region), show.legend = FALSE) +
  scale_brain("dk")

## End(Not run)
```

`scale_brain2` *Deprecated scale functions*

Description

‘r lifecycle::badge("deprecated")‘

These functions have been renamed for clarity: - ‘scale_brain2()‘ -> [scale_brain_manual()] - ‘scale_fill_brain2()‘ -> [scale_fill_brain_manual()] - ‘scale_colour_brain2()‘ -> [scale_colour_brain_manual()] - ‘scale_color_brain2()‘ -> [scale_color_brain_manual()]

Usage

```
scale_brain2(...)

scale_colour_brain2(...)

scale_color_brain2(...)

scale_fill_brain2(...)
```

Arguments

`...`	Arguments passed to the replacement function.

Value

A ggplot2 scale object.

Examples

```
pal <- c("transverse temporal" = "#FF0000", "insula" = "#00FF00")
suppressWarnings(scale_fill_brain_manual(palette = pal))
```

`scale_brain_manual` *Manual colour and fill scales for brain plots*

Description

Apply a custom named colour palette to brain atlas plots. Use this when you want to override the atlas default colours with your own colour mapping.

Usage

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

scale_colour_brain_manual(...)

scale_color_brain_manual(...)

scale_fill_brain_manual(...)
```

Arguments

`palette`	Named character vector mapping region names to colours.
`na.value`	Colour for ‘NA‘ entries (default: ‘"grey"‘).
`...`	Additional arguments (unused).
`aesthetics`	Which aesthetic to scale: ‘"fill"‘, ‘"colour"‘, or ‘"color"‘.

Value

A ggplot2 scale object.

Examples

```
library(ggplot2)

pal <- c("insula" = "red", "precentral" = "blue")
ggplot() +
  geom_brain(atlas = dk(), aes(fill = region), show.legend = FALSE) +
  scale_fill_brain_manual(palette = pal)
```

`scale_continous_brain` *Axis and label scales for brain atlas plots*

Description

Add axis labels and tick labels corresponding to brain atlas regions. These scales add hemisphere or view labels to the x and y axes based on the atlas layout.

Usage

```
scale_continous_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`	A ‘ggseg_atlas‘ object or data.frame containing atlas data.
`position`	Layout style: ‘"dispersed"‘ (default) or ‘"stacked"‘.
`aesthetics`	Which axis to scale: ‘"x"‘, ‘"y"‘, or ‘"labs"‘.
`...`	Additional arguments passed to [adapt_scales()].

Value

A ggplot2 scale or labs object.

Examples

```
library(ggplot2)

ggplot() +
  geom_brain(atlas = dk()) +
  scale_x_brain() +
  scale_y_brain() +
  scale_labs_brain()
```

`theme_brain` *Themes for brain atlas plots*

Description

A set of ggplot2 themes designed for brain atlas visualisations. All themes remove axis ticks and grid lines for a clean presentation.

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`	Text size in points (default: ‘12‘).
`text.family`	Font family (default: ‘"mono"‘).

`plot.background`	Background fill colour (‘theme_custombrain‘ and ‘theme_brain2‘ only).
`text.colour`	Text colour (‘theme_custombrain‘ and ‘theme_brain2‘ only).

Details

‘theme_brain‘ Default theme. Transparent background, no axes, no grid.

‘theme_darkbrain‘ Dark theme with black background and light text.

‘theme_custombrain‘ Fully customisable background, text colour, size, and font.

‘theme_brain2‘ Like ‘theme_custombrain‘ but with axis text removed entirely.

Value

A [ggplot2::theme] object.

See Also

[geom_brain()], [ggplot2::theme()]

Examples

```
library(ggplot2)

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

p +
  theme_brain()

p +
  theme_darkbrain()
```

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