

# Package: ggbrain (via r-universe)

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**Type** Package

**Title** Create Images of Volumetric Brain Data in NIfTI Format Using 'ggplot2' Syntax

**Version** 0.8.1

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**Description** A 'ggplot2'-consistent approach to generating 2D displays of volumetric brain imaging data. Display data from multiple NIfTI images using standard 'ggplot2' conventions such scales, limits, and themes to control the appearance of displays. The resulting plots are returned as 'patchwork' objects, inheriting from 'ggplot', allowing for any standard modifications of display aesthetics supported by 'ggplot2'.

**URL** <https://michaelhallquist.github.io/ggbrain/>

**BugReports** <https://github.com/michaelhallquist/ggbrain/issues>

**Depends** R (>= 3.5.0)

**Imports** Matrix, RNifti, checkmate, data.table, dplyr, ggplot2, ggnewscale, ggrepel, glue, imager, patchwork, rlang, tibble, tidyr, tidyselect, Rcpp

**Suggests** knitr, rmarkdown

**License** GPL (>= 3)

**Encoding** UTF-8

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**RoxygenNote** 7.2.3

**LinkingTo** Rcpp, RcppArmadillo

**VignetteBuilder** knitr

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

**RemoteUrl** <https://github.com/michaelhallquist/ggbrain>

**RemoteRef** HEAD

**RemoteSha** 3e85fdf43bd6d0c6f37f57cdc25ba0f57bb26641

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+.ggb                                    *addition operator for ggb object to support ggplot-like syntax*

---

**Description**

addition operator for ggb object to support ggplot-like syntax

**Usage**

```
## S3 method for class 'ggb'  
o1 + o2
```

**Arguments**

o1                    the first object inheriting the ggb class  
o2                    the second object inheriting the ggb class

**Details**

Note that the addition operator always clones the underlying o1 object rather than modifying it in place

**Value**

a modified version of the o1 object with o2 added to it

---

+.ggbrain\_images                    *addition operator for combining ggbrain\_images objects*

---

**Description**

addition operator for combining ggbrain\_images objects

**Usage**

```
## S3 method for class 'ggbrain_images'  
o1 + o2
```

**Arguments**

o1                    first ggbrain\_images object  
o2                    second ggbrain\_images object

**Details**

note that the addition does not modify either existing object. Rather, the first object is cloned and the second is added to it. If you want to add one `ggbrain_images` object to another in place (i.e., modifying the extant object), use the `$add()` method.

**Value**

combined `ggbrain_images` object

---

`annotate_coordinates` *Adds the coordinate labels to each panel based on the location of the slice along the slicing axis (e.g.,  $z = 15$ )*

---

**Description**

Adds the coordinate labels to each panel based on the location of the slice along the slicing axis (e.g.,  $z = 15$ )

**Usage**

```
annotate_coordinates(x = "right", y = "bottom", ...)
```

**Arguments**

<code>x</code>	the x position of the coordinate label. If numeric, it is assumed to be the pixel position along the x axis (e.g., 26). In addition, convenience values of "left", "right", or "q[1-100]" can be used to look up the left-most, right-most, or quantile-based positions along the x axis.
<code>y</code>	the y position of the coordinate label. If numeric, it is assumed to be the pixel position along the y axis (e.g., 26). In addition, convenience values of 'top', "bottom", or "q[1-100]" can be used to look up the top-most, bottom-most, or quantile-based positions along the y axis.
<code>...</code>	any other arguments to <code>ggplot2::annotate</code> , which will be passed through to each panel

**Value**

a `ggb` object with the action 'add\_annotatations', used in a `ggbrain` addition chain

annotate\_panel *Adds custom annotations to a single panel on the ggbrain plot*

**Description**

Adds custom annotations to a single panel on the ggbrain plot

**Usage**

```
annotate_panel(x = "middle", y = "middle", slice_index = NULL, ...)
```

**Arguments**

- x                    the x position of the annotation. If numeric, it is assumed to be the pixel position along the x axis (e.g., 26). In addition, convenience values of 'left', 'right', or 'q[1-100]' can be used to look up the left-most, right-most, or quantile-based positions along the x axis.
- y                    the y position of the annotation. If numeric, it is assumed to be the pixel position along the y axis (e.g., 26). In addition, convenience values of 'left', 'right', or 'q[1-100]' can be used to look up the left-most, right-most, or quantile-based positions along the x axis.
- slice\_index        the slice number to which this annotation is added. These are numbered in the wrapping order from patchwork::wrap\_plots, which will normally go from top-left to bottom-right.
- ...                  Additional parameters passed to ggplot2::annotate such as label or geom

**Details**

Note that this only handles a single annotation on a single panel!

**Value**

a ggb object with the relevant annotations field and an action of "add\_annotations"

count\_neighbors *This function counts the number of neighboring/touching pixels in a 2D binary image*

**Description**

This function counts the number of neighboring/touching pixels in a 2D binary image

**Arguments**

- im                    A boolean matrix representing a binary image
- diagonal            Whether to count diagonal elements as valid neighbors

**Details**

This is an internal function used by `geom_outline` to clean up outlines

**Value**

A matrix of the same size as `im` containing the number of neighboring pixels

**Author(s)**

Michael Hallquist

---

define	<i>Adds contrast definitions to the ggbrain plot</i>
--------	--

---

**Description**

Adds contrast definitions to the ggbrain plot

**Usage**

```
define(contrasts = NULL)
```

**Arguments**

`contrasts` a character vector or list containing contrasts to be computed as part of the ggbrain object definition.

**Details**

`contrasts` must take the form of `<name> := <value expression>` or must use a named vector. Note that defining a contrast does not directly impact the appearance of the plot unless the contrast is named in a `geom_*` layer.

Also note that contrasts can be specified in the definition of a layer. Thus, the `define` function has two primary virtues. First, it allows for the conceptual separation of contrast definition versus usage inside a `geom_*` layer, which is particularly useful if a contrast is used across several layers. Second, it allows downstream layers to further modify the contrast, such as when we compute a

**Value**

a `ggb` object with the relevant contrasts and an action of `'add_contrasts'`

**Examples**

```

# T1-weighted template
t1 <- system.file("extdata", "mni_template_2009c_3mm.nii.gz", package = "ggbrain")

# signed reward prediction error map
signed_pe <- system.file("extdata", "pe_ptfce_fwep_0.05.nii.gz", package = "ggbrain")

# unsigned (absolute value) prediction error map
abspe <- system.file("extdata", "abspe_ptfce_fwep_0.05.nii.gz", package = "ggbrain")

# simple example of a difference contrast, separating definition from usage in geom_brain
gg_obj <- ggbrain() +
  images(c(underlay = t1, signed_pe = signed_pe, abspe = abspe)) +
  slices(c("x = 25%", "x = 75%")) +
  define("signed_gt_abs := signed_pe - abspe") +
  geom_brain("signed_gt_abs")

# you can also use a named vector in define(), which is equivalent
gg_obj <- ggbrain() +
  images(c(underlay = t1, signed_pe = signed_pe, abspe = abspe)) +
  slices(c("x = 25%", "x = 75%")) +
  define(c(signed_gt_abs = "signed_pe - abspe")) +
  geom_brain("signed_gt_abs")

# contrast definitions can also occur inline, yielding equivalent plots
gg_obj <- ggbrain() +
  images(c(underlay = t1, signed_pe = signed_pe, abspe = abspe)) +
  slices(c("x = 25%", "x = 75%")) +
  geom_brain("signed_pe - abspe")

# The use of contrasts() is helpful when layers modify the contrast (e.g., subsetting)
gg_obj <- ggbrain() +
  images(c(underlay = t1, signed_pe = signed_pe, abspe = abspe)) +
  slices(c("x = 25%", "x = 75%")) +
  define(c(signed_gt_abs = "signed_pe - abspe")) +
  geom_brain(
    "signed_gt_abs[signed_gt_abs > 0]",
    fill_scale=ggplot2::scale_fill_distiller("Pos diff", palette = "Reds")
  )

```

---

fill\_from\_edge

*This function finds holes by flood filling TRUE into a 2D binary image, starting from the edge*


---

**Description**

This function finds holes by flood filling TRUE into a 2D binary image, starting from the edge

**Arguments**

im	A boolean matrix representing a binary image
nedges	An integer specifying how many starting points along the edge to use for filling TRUE. The starts are northwest (1), southwest (2), southeast (3), and northeast (4). The compute time increases with the number of starts.

**Details**

This is an internal function used by geom\_outline to clean up outlines

**Value**

A matrix of the same size as im containing the number of neighboring pixels

**Author(s)**

Michael Hallquist

---

find_threads	<i>This function finds 'threads' hanging off of the edges of blobs in an image, allowing the user to trim them</i>
--------------	--

---

**Description**

This function finds 'threads' hanging off of the edges of blobs in an image, allowing the user to trim them

**Arguments**

im	A numeric matrix representing an image, with non-zero values representing pixels to display
min_neighbors	the minimum number of neighbors a pixel must have to be retained
maxit	the maximum number of iterations to run the thread trimming algorithm. Default: 15.
diagonal	Whether to count diagonal elements as valid neighbors

**Details**

This algorithm runs count\_neighbors iteratively until no pixel exceeds the trimming threshold min\_neighbors or the maximum number of iterations, maxit, is reached.

By running iteratively, long tails are trimmed sequentially by pruning the most disconnected voxels.

**Value**

A logical matrix matrix of the same size as im containing the number of neighboring pixels

**Author(s)**

Michael Hallquist

---

flood_fill	<i>This function flood fills a binary image with TRUE for any value of FALSE</i>
------------	--

---

**Description**

This function flood fills a binary image with TRUE for any value of FALSE

**Arguments**

im	A boolean matrix reference representing a binary image
x	the starting x position for fill
y	the starting y position for fill
r	the number of rows in im
c	the number of columns in im

**Details**

This is an internal function used by geom\_outline to clean up outlines

**Value**

Nothing. The matrix im is modified in place (by reference)

**Author(s)**

Michael Hallquist

---

geom_brain	<i>Adds a raster layer to the ggbrain plot, displaying pixels from the specified layer definition</i>
------------	---

---

**Description**

Adds a raster layer to the ggbrain plot, displaying pixels from the specified layer definition

**Usage**

```
geom_brain(
  definition = NULL,
  name = NULL,
  fill = NULL,
  fill_scale = NULL,
  mapping = NULL,
  limits = NULL,
  breaks = NULL,
  show_legend = TRUE,
  interpolate = FALSE,
  unify_scales = TRUE,
  alpha = NULL,
  blur_edge = NULL,
  fill_holes = NULL,
  remove_specks = NULL,
  trim_threads = NULL
)
```

**Arguments**

definition	a character string of the contrast or image definition used to define this layer. Can be a simple image name (e.g., 'underlay') or a contrast string (e.g., 'overlay[overlay > 5]')
name	the name of this layer, used for referencing in layer and panel modifications
fill	A character string indicating the color used to fill all non-NA pixels in this layer. This is used to set the fill color, in distinction to color mapping: <code>mapping=aes(fill=&lt;variable&gt;)</code> .
fill_scale	a <code>ggplot scale_fill_*</code> object used for mapping the fill column to the color of pixels in this layer.
mapping	the aesthetic mapping of the layer data to the display. Should be an <code>aes()</code> object and supports <code>fill</code> (color of filled pixels). Default is <code>aes(fill=value)</code> , which maps the numeric value of the layer data to the fill color of the squares at each spatial position. For labeled data, you might use <code>aes(fill=&lt;label_col_name&gt;)</code> .
limits	if provided, sets the upper and lower bounds on the scale
breaks	if provided, a function to draw the breaks on the fill scale
show_legend	if TRUE, show the fill scale in the plot legend
interpolate	passes to <code>geom_raster</code> and controls whether the fill is interpolated over continuous space
unify_scales	if TRUE, when this layer is reused across panels, unify the scales to match
alpha	a number between 0 and 1 that sets the alpha transparency of this layer. Default: 1
blur_edge	the standard deviation ( $\sigma$ ) of a Gaussian kernel applied to the edge of this layer to smooth it. This makes the layer less jagged in appearance and is akin to antialiasing.

fill_holes	An optional positive integer specifying the size of holes (in pixels) inside clusters to be filled by nearest neighbor imputation. Default: 0.
remove_specks	An optional positive integer specifying the size of specks (in pixels) to be removed from each slice prior to display. Specks are small clusters that may be distracting and contribute to a 'salt and pepper' appearance.
trim_threads	the minimum number of neighboring pixels (including diagonals) that must be present to keep a pixel.

### Details

Note that the fill\_scale and limits must be specified at the time of the geom\_brain creation in order for them to be mapped properly within ggplot. Because we overlay many raster layers in a ggplot object that all use the fill aesthetic mapping, it becomes hard to map the color scales after the layer is created using the typical + scale\_fill\_\* syntax, and similarly for scale limits.

### Value

a ggb object populated with the relevant geom\_brain and the action of 'add\_layers'

### Examples

```
# T1-weighted template
t1 <- system.file("extdata", "mni_template_2009c_3mm.nii.gz", package = "ggbrain")

# signed reward prediction error map
signed_pe <- system.file("extdata", "pe_ptfce_fwep_0.05.nii.gz", package = "ggbrain")

gg_obj <- ggbrain() +
  images(c(underlay = t1, overlay = signed_pe)) +
  slices(c("x = 25%", "x = 75%")) +
  geom_brain("underlay") +
  geom_brain(definition="overlay[overlay > 1]", fill_scale=ggplot2::scale_fill_viridis_c("pos z"))
```

---

geom_outline	<i>Adds an outline layer to the ggbrain plot, displaying outlines from the non-missing pixels in the specified layer definition</i>
--------------	---

---

### Description

Adds an outline layer to the ggbrain plot, displaying outlines from the non-missing pixels in the specified layer definition

### Usage

```
geom_outline(
  definition = NULL,
  name = NULL,
  outline = NULL,
```

```

outline_scale = NULL,
mapping = ggplot2::aes(outline = NULL, fill = NULL),
size = NULL,
limits = NULL,
breaks = integer_breaks(),
show_legend = TRUE,
interpolate = FALSE,
unify_scales = TRUE,
alpha = 1,
blur_edge = NULL,
fill_holes = NULL,
remove_specks = NULL,
trim_threads = NULL,
dil_ero = 0L
)

```

### Arguments

definition	a character string of the contrast or image definition used to define this layer. Can be a simple image name (e.g., 'underlay') or a contrast string (e.g., 'overlay[overlay > 5]')
name	the name of this layer, used for referencing in layer and panel modifications
outline	A character string indicating the color used to draw outlines in this layer. This is used to set the outline color, in distinction to outline color mapping: <code>mapping=aes(outline=&lt;variable&gt;</code>
outline_scale	a ggplot <code>scale_fill_*</code> object used for mapping the fill column to the color of pixels in this layer.
mapping	the aesthetic mapping of the layer data to the display. Should be an <code>aes()</code> object and supports <code>outline</code> (outline color of pixels). Default is <code>aes(outline=NULL)</code> , which uses a set outline color.
size	the size of outlines to be drawn in pixel units. Default: 1
limits	if provided, sets the upper and lower bounds on the scale
breaks	if provided, a function to draw the breaks on the fill scale
show_legend	if TRUE, show the fill scale in the plot legend
interpolate	passes to <code>geom_raster</code> and controls whether the fill is interpolated over continuous space
unify_scales	if TRUE, when this layer is reused across panels, unify the scales to match
alpha	a number between 0 and 1 that sets the alpha transparency of this layer. Default: 1
blur_edge	the standard deviation (sigma) of a Gaussian kernel applied to the edge of this layer to smooth it. This makes the layer less jagged in appearance and is akin to antialiasing.
fill_holes	An optional positive integer specifying the size of holes (in pixels) inside clusters to be filled by nearest neighbor imputation. Default: 0.

remove_specks	An optional positive integer specifying the size of specks (in pixels) to be removed from each slice prior to display. Specks are small clusters that may be distracting and contribute to a 'salt and pepper' appearance.
trim_threads	the minimum number of neighboring pixels (including diagonals) that must be present to keep a pixel.
dil_ero	the number of pixels to dilate (> 0) or erode (< 0) the outline for display purposes. Default: 0L

### Details

Note that the fill\_scale and limits must be specified at the time of the geom\_brain creation in order for them to be mapped properly within ggplot. Because we overlay many raster layers in a ggplot object that all use the fill aesthetic mapping, it becomes hard to map the color scales after the layer is created using the typical + scale\_fill\_\* syntax, and similarly for scale limits.

### Value

a ggb object populated with the geom\_outline layer and the action of 'add\_layers'

### Examples

```
# T1-weighted template
t1 <- system.file("extdata", "mni_template_2009c_3mm.nii.gz", package = "ggbrain")

# signed reward prediction error map
signed_pe <- system.file("extdata", "pe_ptfce_fwep_0.05.nii.gz", package = "ggbrain")

gg_obj <- ggbrain() +
  images(c(underlay = t1, overlay = signed_pe)) +
  slices(c("x = 25%", "x = 75%")) +
  geom_brain("underlay") +
  geom_outline(definition="overlay[overlay > 2]", outline="cyan")
```

---

geom\_region\_label      *Variant of geom\_label used for plotting region labels on slices*

---

### Description

Variant of geom\_label used for plotting region labels on slices

### Usage

```
geom_region_label(image, label_column = "label", min_px = 1L, ...)
```

**Arguments**

image	The name of the image within the underlying ggbrain_slices object that contains the labeled data positions
label_column	The column name name for the labels to use within the slice data
min_px	The minimum number of pixels present on a slice that will result in a text label. Default: 1
...	All other parameters passed through to geom_label

**Value**

a ggb object with the relevant ggbrain\_label field and an action of "add\_region\_labels"

---

geom\_region\_label\_repel

*Variant of geom\_label\_repel used for plotting region labels on slices with separation from other labels*

---

**Description**

Variant of geom\_label\_repel used for plotting region labels on slices with separation from other labels

**Usage**

```
geom_region_label_repel(image, label_column = "label", min_px = 1L, ...)
```

**Arguments**

image	The name of the image within the underlying ggbrain_slices object that contains the labeled data positions
label_column	The column name name for the labels to use within the slice data
min_px	The minimum number of pixels present on a slice that will result in a text label. Default: 1
...	All other parameters passed through to geom_label_repel

**Value**

a ggb object with the relevant ggbrain\_label field and an action of "add\_region\_labels"

---

geom\_region\_text      *Variant of geom\_text used for plotting region labels on slices*

---

**Description**

Variant of geom\_text used for plotting region labels on slices

**Usage**

```
geom_region_text(image, label_column = "label", min_px = 1L, ...)
```

**Arguments**

image	The name of the image within the underlying ggbrain_slices object that contains the labeled data positions
label_column	The column name name for the labels to use within the slice data
min_px	The minimum number of pixels present on a slice that will result in a text label. Default: 1
...	All other parameters passed through to geom_text

**Value**

a ggb object with the relevant ggbrain\_label field and an action of "add\_region\_labels"

---

geom\_region\_text\_repel      *Variant of geom\_text\_repel used for plotting region labels on slices with separation from other labels*

---

**Description**

Variant of geom\_text\_repel used for plotting region labels on slices with separation from other labels

**Usage**

```
geom_region_text_repel(image, label_column = "label", min_px = 1L, ...)
```

**Arguments**

image	The name of the image within the underlying ggbrain_slices object that contains the labeled data positions
label_column	The column name name for the labels to use within the slice data
min_px	The minimum number of pixels present on a slice that will result in a text label. Default: 1
...	All other parameters passed through to geom_text_repel

**Value**

a ggb object with the relevant ggbrain\_label field and an action of "add\_region\_labels"

---

ggbrain	<i>create ggb container object for a given plot</i>
---------	---

---

**Description**

create ggb container object for a given plot

**Usage**

```
ggbrain(  
  images = NULL,  
  slices = NULL,  
  title = NULL,  
  bg_color = "grey8",  
  text_color = "grey92",  
  base_size = 14  
)
```

**Arguments**

images	a character vector or existing ggbrain_images object defining which images should be included in this plot
slices	a set of slices to be added to the plot
title	the overall title to be added to the plot
bg_color	The background color of the overall plot
text_color	The default text color of the overall plot (passes through to panels)
base_size	The base size of fonts used in the plot (cf. theme_minimal)

**Value**

a ggb object containing basic information for a ggbrain plot such as background color, text color, and font size

---

`ggbrain_images`*R6 class for compiling images to render in ggplot*

---

**Description**

R6 class for compiling images to render in ggplot

R6 class for compiling images to render in ggplot

**Details**

Note that this class is exported only for power users and rarely needs to be called directly in typical use of the package. Instead, look at `images()`.

**Value**

a `ggbrain_images` R6 class containing fields related to a set of NIfTI images imported into R

**Active bindings**

`zero_tol` the (positive) numeric value that should be treated as indistinguishable from zero. This value is used to set small values in the images to exactly zero for proper masking. Default  $1e-6$

`slices` a character vector of cached slice specifications to be used in `$get_slices()`

`contrasts` a character vector of cached contrast specifications to be used in `$get_slices()`

**Methods****Public methods:**

- `ggbrain_images$new()`
- `ggbrain_images$add()`
- `ggbrain_images$add_labels()`
- `ggbrain_images$add_images()`
- `ggbrain_images$filter_images()`
- `ggbrain_images$dim()`
- `ggbrain_images$get_image_names()`
- `ggbrain_images$get_images()`
- `ggbrain_images$get_headers()`
- `ggbrain_images$remove_images()`
- `ggbrain_images$winsorize_images()`
- `ggbrain_images$na_images()`
- `ggbrain_images$summary()`
- `ggbrain_images$get_nz_indices()`
- `ggbrain_images$add_slices()`
- `ggbrain_images$add_contrasts()`

- `ggbrain_images$reset_slices()`
- `ggbrain_images$get_slices()`
- `ggbrain_images$get_slices_inplane()`
- `ggbrain_images$get_labels()`
- `ggbrain_images$lookup_slices()`
- `ggbrain_images$clone()`

**Method** `new()`: create `ggbrain_images` object consisting of one or more NIfTI images

*Usage:*

```
ggbrain_images$new(images = NULL, volumes = NULL, labels = NULL, filter = NULL)
```

*Arguments:*

`images` a character vector of file names containing NIfTI images to read

`volumes` the volumes to be read from each element of `images`. By default, this is 1, in which case the first volume is used, which is appropriate for all 3-D images. For 4-D images, `volumes` gives you more flexibility over the volume to display.

`labels` A named list of data.frames with labels that map to values in the integer-valued/atlas elements of `images`. If a single data.frame is passed, it will be accepted if only a single image is passed, too. These are then assumed to correspond

`filter` A named list of filter expressions to be applied to particular images. The names of the list correspond to the names of the `images` provided. Each element of the list can either be a character vector denoting a filtering expression (e.g., `'value < 100'`) or a numeric vector denoting values of the image that should be retained (e.g., `c(5, 10, 12)`).

**Method** `add()`: method to add another `ggbrain_images` object to this one

*Usage:*

```
ggbrain_images$add(obj)
```

*Arguments:*

`obj` the `ggbrain_images` object to combine with this one

**Method** `add_labels()`: add a labels data.frame that connects an integer-valued image with a set of labels

*Usage:*

```
ggbrain_images$add_labels(...)
```

*Arguments:*

`...` named arguments containing data.frame objects for each image to be labeled. The argument name should match the image name to be labeled and the value should be a data.frame containing value and label.

*Details:* As a result of `$add_labels`, the `$get_slices` method will always remap the numeric values for label images to the corresponding text-based labels in the label data. In addition, a new attribute will be returned called `"slice_labels"` that contains a row for each region represented in each slice.

**Method** `add_images()`: add one or more images to this `ggbrain_images` object

*Usage:*

```
ggbrain_images$add_images(images = NULL, volumes = NULL)
```

*Arguments:*

*images* a character vector of file names containing NIfTI images to read

*volumes* a number indicating the volume within the images to read. At present, this must be a single number – perhaps in the future, it could be a vector so that many timepoints in a 4-D image could be displayed.

**Method** `filter_images()`: filters an image based on an expression such as a subsetting operation

*Usage:*

```
ggbrain_images$filter_images(filter = NULL)
```

*Arguments:*

*filter* a character string or numeric vector of the filter to apply

*Details:* if *expr* is a numeric vector, only values in this set will be retained. If a character string expression is used, it should use the variable name 'value' to refer to the numeric values to be filtered, such as 'value > 10'.

**Method** `dim()`: return the 3D dimensions of the images contained in this object

*Usage:*

```
ggbrain_images$dim()
```

**Method** `get_image_names()`: return the names of the images contained in this object

*Usage:*

```
ggbrain_images$get_image_names()
```

**Method** `get_images()`: return the RNifti objects of one or more images contained in this object

*Usage:*

```
ggbrain_images$get_images(img_names = NULL, drop = TRUE)
```

*Arguments:*

*img\_names* The names of images to return. Use `$get_image_names()` if you're uncertain about what is available.

*drop* If TRUE, a single image is returned as an RNifti object, rather than a single-element list containing that object.

**Method** `get_headers()`: return the NIfTI headers for one or more images contained in this object

*Usage:*

```
ggbrain_images$get_headers(img_names = NULL, drop = TRUE)
```

*Arguments:*

*img\_names* The names of images whose header are returned. Use `$get_image_names()` if you're uncertain about what is available.

*drop* If TRUE, a single header is returned as an niftiHeader object, rather than a single-element list containing that object.

**Method** `remove_images()`: method for removing one or more images from the `ggbrain_images` object

*Usage:*

```
ggbrain_images$remove_images(img_names)
```

*Arguments:*

`img_names` names of images to remove from object

**Method** `winsorize_images()`: winsorize the tails of a set of images to pull in extreme values

*Usage:*

```
ggbrain_images$winsorize_images(img_names, quantiles = c(0.001, 0.999))
```

*Arguments:*

`img_names` The names of images in the `ggbrain_images` object to be winsorized

`quantiles` The lower and upper quantiles used to define the thresholds for winsorizing.

**Method** `na_images()`: method to set values less than threshold to NA

*Usage:*

```
ggbrain_images$na_images(img_names, threshold = NULL)
```

*Arguments:*

`img_names` The names of images in the `ggbrain_images` object whose values should be set to NA

`threshold` The threshold value whose absolute value used to determine which voxels to set to NA. If NULL, use the `pvt_zero_tol` field (default 1e-6).

**Method** `summary()`: print a summary of the `ggbrain_images` object

*Usage:*

```
ggbrain_images$summary()
```

**Method** `get_nz_indices()`: return the indices of non-zero voxels

*Usage:*

```
ggbrain_images$get_nz_indices(img_names = NULL)
```

*Arguments:*

`img_names` The names of images in the `ggbrain_images` object whose non-zero indices should be looked up

*Details:* Note that this function looks for non-zero voxels in any of the images specified by `img_names`.

**Method** `add_slices()`: adds one or more slices to the cached slices that will be retrieved by `$get_slices()` when no `slices` argument is passed.

*Usage:*

```
ggbrain_images$add_slices(slices = NULL)
```

*Arguments:*

`slices` a character vector containing one or more slices to be extracted by `$get_slices`. Uses the syntax "`<xyz>=<number>`". Example: `c("x=10", "y=50%")`

**Method** `add_contrasts()`: adds one or more contrasts to the cached contrasts that will be retrieved by `$get_slices()` when no contrasts argument is passed.

*Usage:*

```
ggbrain_images$add_contrasts(contrasts = NULL)
```

*Arguments:*

`contrasts` a character vector containing one or more contrasts to be extracted by `$get_slices`.  
Uses the syntax "`<img_name>[subset_expression] + <img_name>`".

**Method** `reset_slices()`: remove all cached slice settings

*Usage:*

```
ggbrain_images$reset_slices()
```

**Method** `get_slices()`: get slice data for one or more slices based on their coordinates

*Usage:*

```
ggbrain_images$get_slices(  
  slices = NULL,  
  img_names = NULL,  
  contrasts = NULL,  
  fill_labels = FALSE,  
  make_square = TRUE,  
  remove_null_space = TRUE  
)
```

*Arguments:*

`slices` a vector of slice positions

`img_names` a character vector of images contained in the `ggbrain_images` object to be sliced

`contrasts` a named character vector of contrasts to be calculated for each slice

`fill_labels` if TRUE, the numeric value of the image will be used for any value that does not have a corresponding label in the `labels.data.frame`. Default: FALSE

`make_square` If TRUE, make all images square and of the same size

`remove_null_space` If TRUE, remove slices where all values are approximately zero

*Details:* This function always returns a data.frame where each row represents a slice requested by the user. The `$slice_data` element is a list-column where each element is itself a list of slice data for a given layer/image (e.g., underlay or overlay) . The `$slice_matrix` is a list-column where each element is a list of 2-D matrices, one per layer/image. @return a `ggbrain_slices` object containing the requested slices and contrasts

**Method** `get_slices_inplane()`: `get_slices_inplane` is mostly an internal function for getting one or more slices from a given plane

*Usage:*

```
ggbrain_images$get_slices_inplane(  
  imgs = NULL,  
  slice_numbers,  
  plane,  
  drop = FALSE  
)
```

*Arguments:*

`imgs` The names of images to slice  
`slice_numbers` The numbers of slices in the specified plant to grab  
`plane` The image plane to slice. Must be "coronal", "sagittal", or "axial"  
`drop` if TRUE, a single slice is returned as a 2D matrix instead of a 3D matrix with a singleton first dimension

*Returns:* A 3D matrix of slices x dim1 x dim2

**Method** `get_labels()`: return a list of data.frames containing labels for a given image

*Usage:*

```
ggbrain_images$get_labels()
```

*Details:* the names of the list correspond directly with the names of the images

**Method** `lookup_slices()`: internal function to lookup which slices to display along each axis based on their quantile, xyz coordinate, or ijk coordinate

*Usage:*

```
ggbrain_images$lookup_slices(slices, ignore_null_space = TRUE)
```

*Arguments:*

`slices` A character vector of coordinates for slices to display  
`ignore_null_space` If TRUE, any coordinates specified as quantiles (e.g., `x = 50%`) use the quantiles of only the non-zero slices (ignoring blank slices)

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_images$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

---

ggbrain\_label

*R6 class for adding labels to a ggbrain\_panel*

---

**Description**

R6 class for adding labels to a ggbrain\_panel

R6 class for adding labels to a ggbrain\_panel

**Value**

a ggbrain\_label R6 class containing fields related to ggbrain plot labels

**Public fields**

`addl_args` a named list of additional argument to be passed to `geom_text/geom_label` at render

**Active bindings**

**data** a data.frame containing labels to be printed on the panel. Must contain dim1, dim2, and label as columns. The dim1 and dim2 columns control where the labels will appear on the panel

**image** A character string specifying the image to which these labels pertain

**label\_column** A character string indicating which data.frame column should be used for drawing labels

**min\_px** A positive integer indicating the minimum number of pixels present on slice that will generate a label

**Methods****Public methods:**

- `ggbrain_label$new()`
- `ggbrain_label$add_to_gg()`
- `ggbrain_label$clone()`

**Method** `new()`: create a new `ggbrain_label` object

*Usage:*

```
ggbrain_label$new(
  data = NULL,
  geom = "text",
  image = NULL,
  label_column = NULL,
  min_px = NULL,
  ...
)
```

*Arguments:*

**data** a data.frame containing labels to be printed on the panel. Must contain dim1, dim2, and label as columns. The dim1 and dim2 columns control where the labels will appear on the panel

**geom** The geom type to be plotted. Must be "text" or "label", corresponding to `geom_text` and `geom_label`, respectively.

**image** A string specifying the image to which these labels pertain

**label\_column** the column in data that should be drawn as labels on the plot

**min\_px** the minimum number of pixels

... All other arguments that will be passed directly to `geom_text` or `geom_label` such as `hjust`, `size`, and `color`

**Method** `add_to_gg()`: add this text layer to an existing ggplot object

*Usage:*

```
ggbrain_label$add_to_gg(base_gg)
```

*Arguments:*

**base\_gg** the ggplot object to which we add the layer

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_label$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

 ggbrain\_layer

*R6 class for a single layer of a ggbrain panel*


---

**Description**

R6 class for a single layer of a ggbrain panel

R6 class for a single layer of a ggbrain panel

**Details**

Note that this class is exported only for power users and rarely needs to be called directly in typical use of the package. Instead, look at `geom_brain()` and `geom_outline()`.

**Value**

a ggbrain\_layer R6 class containing fields related to a visual layer on the ggbrain plot

**Active bindings**

`name` the name of this layer, used for referencing in layer and panel modifications

`all_na` whether all values for this layer are NA in the data field

`definition` a character string specifying the image name or contrast that defines this layer

`source` a character string specifying the layer source within a relevant ggbrain\_slices object. This is used to lookup the right layer information when combining slices and layers together Note that multiple layers can potentially have the same source, which is why a 1:1 mapping to name does not work

`data` the data.frame containing relevant data for this layer.

`show_legend` a logical indicating whether to show or hide the fill/color scale

`unify_scales` a logical indicating whether to unify scale limits and levels when this layer is added across many panels

`bisided` read-only access to whether this layer uses a bisided color scale

`categorical_fill` read-only access to whether this layer has a categorical fill scale

`fill_column` read-only access to layer fill column

`fill_scale` a `scale_fill_*` object containing the ggplot2 fill scale for this layer

`alpha` sets the alpha transparency of this layer.

`blur_edge` controls the standard deviation (sigma) of a Gaussian blur applied to the layer at the edge

`trim_threads` iteratively trim any pixels that have fewer than this number of neighboring pixels

`fill_holes` controls the size of holes to be filled for display (in pixels)

`remove_specks` controls the size of specks to be removed (in pixels)

**Methods****Public methods:**

- ggbrain\_layer\$new()
- ggbrain\_layer\$set\_limits()
- ggbrain\_layer\$set\_pos\_limits()
- ggbrain\_layer\$set\_neg\_limits()
- ggbrain\_layer\$set\_breaks()
- ggbrain\_layer\$set\_pos\_breaks()
- ggbrain\_layer\$set\_neg\_breaks()
- ggbrain\_layer\$plot()
- ggbrain\_layer\$add\_to\_gg()
- ggbrain\_layer\$get\_data()
- ggbrain\_layer\$is\_empty()
- ggbrain\_layer\$clone()

**Method** `new()`: create a new ggbrain\_layer object

*Usage:*

```
ggbrain_layer$new(
  name = NULL,
  definition = NULL,
  limits = NULL,
  breaks = integer_breaks(),
  show_legend = TRUE,
  interpolate = NULL,
  unify_scales = TRUE,
  alpha = NULL,
  blur_edge = NULL,
  fill_holes = NULL,
  remove_specks = NULL,
  trim_threads = NULL,
  data = NULL
)
```

*Arguments:*

`name` the name of this layer, used for referencing in layer and panel modifications

`definition` an optional character string defining the image or contrast that should be used to lookup data from a ggbrain\_slices object. This is mostly used internally by the ggbrain + syntax to allow layers to be defined without data in advance of the plot.

`limits` if provided, sets the upper and lower bounds on the scale

`breaks` if provided, a function to draw the breaks on the color scale

`show_legend` if TRUE, show the scale on the plot legend

`interpolate` passes to geom\_raster and controls whether the fill is interpolated over continuous space

`unify_scales` if TRUE, when this layer is reused across panels, unify the scales to match

`alpha` fixed alpha transparency of this layer (use mapping for alpha mapping)

`blur_edge` the standard deviation (sigma) of a Gaussian kernel applied to the edge of this layer to smooth it. This makes the layer less jagged in appearance and is akin to antialiasing.

`fill_holes` the size of holes (in pixels) inside clusters to be filled by nearest neighbor imputation prior to display

`remove_specks` the size of specks (in pixels) to be removed from each slice prior to display

`trim_threads` the minimum number of neighboring pixels (including diagonals) that must be present to keep a pixel

`data` the data.frame containing image data for this layer. Must contain "dim1", "dim2", and "value" as columns

**Method** `set_limits()`: set the limits for this layer's scale

*Usage:*

```
ggbrain_layer$set_limits(limits)
```

*Arguments:*

`limits` a 2-element numeric vector setting the lower and upper limits on the layer's scale

**Method** `set_pos_limits()`: set the limits for this layer's positive scale (only relevant to bisided)

*Usage:*

```
ggbrain_layer$set_pos_limits(limits)
```

*Arguments:*

`limits` a 2-element numeric vector setting the lower and upper limits on the layer's positive scale

**Method** `set_neg_limits()`: set the limits for this layer's positive scale (only relevant to bisided)

*Usage:*

```
ggbrain_layer$set_neg_limits(limits)
```

*Arguments:*

`limits` a 2-element numeric vector setting the lower and upper limits on the layer's positive scale

**Method** `set_breaks()`: set the breaks element of this layer's scale

*Usage:*

```
ggbrain_layer$set_breaks(breaks)
```

*Arguments:*

`breaks` a function used to label the breaks

**Method** `set_pos_breaks()`: set the breaks element of this layer's positive scale (only relevant to bisided)

*Usage:*

```
ggbrain_layer$set_pos_breaks(breaks)
```

*Arguments:*

`breaks` a function used to label the positive breaks

**Method** `set_neg_breaks()`: set the breaks element of this layer's negative scale (only relevant to bisided)

*Usage:*

```
ggbrain_layer$set_neg_breaks(breaks)
```

*Arguments:*

`breaks` a function used to label the negative breaks

**Method** `plot()`: plot this layer alone (mostly for debugging)

*Usage:*

```
ggbrain_layer$plot()
```

**Method** `add_to_gg()`: method to add this layer to an existing ggplot object

*Usage:*

```
ggbrain_layer$add_to_gg(base_gg)
```

*Arguments:*

`base_gg` the ggplot object to which we add the layer

**Method** `get_data()`: return the data.frame associated with this layer

*Usage:*

```
ggbrain_layer$get_data(add_layer_name = FALSE)
```

*Arguments:*

`add_layer_name` if TRUE, adds a `layer_name` column to the data.frame for record-keeping.  
Default: FALSE.

**Method** `is_empty()`: returns TRUE if all values are NA or if the data has 0 rows

*Usage:*

```
ggbrain_layer$is_empty()
```

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_layer$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

---

ggbrain\_layer\_brain *R6 class for a single layer of a ggbrain panel using fill geom*

---

### Description

R6 class for a single layer of a ggbrain panel using fill geom

R6 class for a single layer of a ggbrain panel using fill geom

### Details

Note that this class is exported only for power users and rarely needs to be called directly in typical use of the package. Instead, look at `geom_brain()`.

### Value

a `ggbrain_layer_brain` R6 class with fields related to a brain visual layer (relates to `geom_brain`)

### Super class

`ggbrain::ggbrain_layer` -> `ggbrain_layer_brain`

### Active bindings

`fill` controls color of the filled in pixels for non-NA (valid) voxels. Note that this **sets** the fill color, while the `mapping=aes(fill=<value>)` would **map** the fill to a column in the data, consistent with ggplot2 logic.

`mapping` the ggplot2 aesthetic mapping between the data columns and the display

### Methods

#### Public methods:

- `ggbrain_layer_brain$new()`
- `ggbrain_layer_brain$clone()`

**Method** `new()`: create a new `ggbrain_layer` object

*Usage:*

```
ggbrain_layer_brain$new(  
  name = NULL,  
  definition = NULL,  
  limits = NULL,  
  breaks = integer_breaks(),  
  show_legend = TRUE,  
  interpolate = NULL,  
  unify_scales = TRUE,  
  alpha = NULL,  
  mapping = ggplot2::aes(fill = value),
```

```

    fill = NULL,
    fill_scale = NULL,
    blur_edge = NULL,
    fill_holes = NULL,
    remove_specks = NULL,
    trim_threads = NULL,
    data = NULL
  )

```

*Arguments:*

**name** the name of this layer, used for referencing in layer and panel modifications

**definition** an optional character string defining the image or contrast that should be used to lookup data from a ggbrain\_slices object. This is mostly used internally by the ggbrain + syntax to allow layers to be defined without data in advance of the plot.

**limits** if provided, sets the upper and lower bounds on the scale

**breaks** if provided, a function to draw the breaks on the color scale

**show\_legend** if TRUE, show the scale on the plot legend

**interpolate** passes to geom\_raster and controls whether the fill is interpolated over continuous space

**unify\_scales** if TRUE, when this layer is reused across panels, unify the scales to match

**alpha** a number between 0 and 1 that sets the alpha transparency of this layer. Default: 1

**mapping** the aesthetic mapping of the layer data to the display. Should be an aes() object and supports fill (color of filled pixels). Default is aes(fill=value), which maps the numeric value of the layer data to the fill color of the squares at each spatial position. For labeled data, you might use aes(fill=<label\_col\_name>).

**fill** A character string indicating the color used to fill all non-NA pixels in this layer. This is used in distinction to mapping=aes(fill=<variable>).

**fill\_scale** a ggplot scale object used for mapping the value column as the fill color for the layer.

**blur\_edge** the standard deviation (sigma) of a Gaussian kernel applied to the edge of this layer to smooth it. This makes the layer less jagged in appearance and is akin to antialiasing.

**fill\_holes** the size of holes (in pixels) inside clusters to be filled by nearest neighbor imputation prior to display

**remove\_specks** the size of specks (in pixels) to be removed from each slice prior to display

**trim\_threads** the minimum number of neighboring pixels (including diagonals) that must be present to keep a pixel

**data** the data.frame containing image data for this layer. Must contain "dim1", "dim2", and "value" as columns

*Details:* To set mapping, you must provide a ggplot2 aes() object. A geom\_brain() layer requires a fill aesthetic mapping, which controls the fill color of regions.

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_layer_brain$clone(deep = FALSE)
```

*Arguments:*

**deep** Whether to make a deep clone.

---

ggbrain\_layer\_outline *R6 class for a single layer of a ggbrain panel using outline geom*

---

### Description

R6 class for a single layer of a ggbrain panel using outline geom

R6 class for a single layer of a ggbrain panel using outline geom

### Details

Note that this class is exported only for power users and rarely needs to be called directly in typical use of the package. Instead, look at `geom_outline()`.

### Value

a ggbrain\_layer\_outline R6 class with fields related to a brain visual layer (relates to geom\_outline)

### Super class

`ggbrain::ggbrain_layer` -> ggbrain\_layer\_outline

### Active bindings

mapping the ggplot2 aesthetic mapping between the data columns and the display

outline controls color of outline draw around non-NA (valid) voxels

outline\_scale a scale\_fill\_\* object containing the ggplot2 outline color scale for this layer

size controls size of outline drawn around non-NA (valid) voxels

dil\_ero controls the number of pixels to dilate (> 0) or erode (< 0) the outline

### Methods

#### Public methods:

- `ggbrain_layer_outline$new()`
- `ggbrain_layer_outline$clone()`

**Method** `new()`: create a new ggbrain\_layer object

*Usage:*

```
ggbrain_layer_outline$new(  
  name = NULL,  
  definition = NULL,  
  limits = NULL,  
  breaks = integer_breaks(),  
  show_legend = TRUE,  
  interpolate = NULL,  
  unify_scales = TRUE,
```

```

alpha = NULL,
mapping = ggplot2::aes(outline = NULL, fill = NULL),
outline = NULL,
outline_scale = NULL,
size = NULL,
blur_edge = NULL,
fill_holes = NULL,
remove_specks = NULL,
trim_threads = NULL,
dil_ero = NULL,
data = NULL
)

```

*Arguments:*

**name** the name of this layer, used for referencing in layer and panel modifications

**definition** an optional character string defining the image or contrast that should be used to lookup data from a ggbrain\_slices object. This is mostly used internally by the ggbrain + syntax to allow layers to be defined without data in advance of the plot.

**limits** if provided, sets the upper and lower bounds on the scale

**breaks** if provided, a function to draw the breaks on the color scale

**show\_legend** if TRUE, show the scale on the plot legend

**interpolate** passes to geom\_raster and controls whether the fill is interpolated over continuous space

**unify\_scales** if TRUE, when this layer is reused across panels, unify the scales to match

**alpha** a number between 0 and 1 that sets the alpha transparency of this layer. Default: 1

**mapping** the aesthetic mapping of the layer data to the display. Should be an aes() object and supports outline (color of outline around clusters). Default is aes(outline=value), which maps the numeric value of the layer data to the outline color of the squares at around spatial regions. For labeled data, you might use aes(fill=<label\_col\_name>).

**outline** A character string indicating the color used to outline all non-NA pixels in this layer. This is used in distinction to mapping=aes(outline=<variable>).

**outline\_scale** a ggplot scale object used for mapping the value column as the outline color for the layer.

**size** controls the thickness of outlines

**blur\_edge** the standard deviation (sigma) of a Gaussian kernel applied to the edge of this layer to smooth it. This makes the layer less jagged in appearance and is akin to antialiasing.

**fill\_holes** the size of holes (in pixels) inside clusters to be filled by nearest neighbor imputation prior to display

**remove\_specks** the size of specks (in pixels) to be removed from each slice prior to display

**trim\_threads** the minimum number of neighboring pixels (including diagonals) that must be present to keep a pixel

**dil\_ero** the number of pixels to dilate (> 0) or erode (<0) the outline.

**data** the data.frame containing image data for this layer. Must contain "dim1", "dim2", and "value" as columns

*Details:* To set mapping, you must provide a ggplot2 aes() object. A geom\_outline() layer requires an outline aesthetic mapping, which controls the color of outlines drawn around regions.

note that the ggbrain\_layer\_outline class maps onto \*\_fill fields

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_layer_outline$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

---

ggbrain\_panel

*R6 class for a single panel of a ggbrain image*

---

## Description

R6 class for a single panel of a ggbrain image

R6 class for a single panel of a ggbrain image

## Details

Note that this class is exported only for power users and rarely needs to be called directly in typical use of the package. Instead, look at slices().

## Value

a ggbrain\_panel R6 class with fields related to a panel on the ggbrain plot

## Public fields

gg The ggplot object that contains the panel

## Methods

### Public methods:

- ggbrain\_panel\$new()
- ggbrain\_panel\$reset\_limits()
- ggbrain\_panel\$plot()
- ggbrain\_panel\$add\_to\_gg()
- ggbrain\_panel\$add\_layer()
- ggbrain\_panel\$remove\_layers()
- ggbrain\_panel\$get\_data()
- ggbrain\_panel\$get\_layer\_names()
- ggbrain\_panel\$get\_layers()
- ggbrain\_panel\$set\_layer\_order()
- ggbrain\_panel\$clone()

**Method** new(): create a new ggbrain\_panel object

*Usage:*

```
ggbrain_panel$new(
  layers = NULL,
  title = NULL,
  bg_color = NULL,
  text_color = NULL,
  border_color = NULL,
  border_size = NULL,
  xlab = NULL,
  ylab = NULL,
  theme_custom = NULL,
  annotations = NULL,
  region_labels = NULL
)
```

*Arguments:*

**layers** a list of ggbrain\_layer objects to form the panel

**title** a title for the panel added to the ggplot object using ggtitle()

**bg\_color** the color used for the background of the plot. Default: 'gray10' (nearly black)

**text\_color** the color used for text displayed on the plot. Default: 'white'.

**border\_color** the color used for drawing a border around on the plot. Default: 'gray50' (though borders are not drawn by default).

**border\_size** the size of the border line drawn around the panel. Default: NULL. If this value is greater than zero, a border of this size and with color border\_color will be drawn around the panel

**xlab** The label to place on x axis. Default is NULL.

**ylab** The label to place on y axis. Default is NULL.

**theme\_custom** Any custom theme() settings to be added to the plot

**annotations** a data.frame containing all annotations to be added to this plot. Each row is cleaned up and passed to ggplot2::annotate()

**region\_labels** a list of ggbrain\_label objects with data for plotting region labels on this panel

**Method** reset\_limits(): Reset the scale limits for the specified layers

*Usage:*

```
ggbrain_panel$reset_limits(layer_names)
```

*Arguments:*

**layer\_names** not implemented yet

**Method** plot(): plot the panel

*Usage:*

```
ggbrain_panel$plot(use_global_limits = TRUE)
```

*Arguments:*

**use\_global\_limits** Not implemented at present

**Method** add\_to\_gg(): add one or more custom ggplot settings to the panel

*Usage:*

```
ggbrain_panel$add_to_gg(list_args)
```

*Arguments:*

`list_args` A list containing elements to add to the ggplot object

*Details:* Note that passing in an expression such as `theme_bw() + ggtitle("hello")` will not work because it creates an object that cannot be added sequentially to the ggplot. As noted in ggplot2's documentation (<https://ggplot2.tidyverse.org/reference/gg-add.html>), to programmatically add elements to a ggplot, pass in a list where each element is added sequentially

**Method** `add_layer()`: adds a `ggplot_layer` object to the panel

*Usage:*

```
ggbrain_panel$add_layer(layer_obj)
```

*Arguments:*

`layer_obj` a `ggbrain_layer` object to add to the panel

**Method** `remove_layers()`: removes one or more layers by name

*Usage:*

```
ggbrain_panel$remove_layers(layer_names)
```

*Arguments:*

`layer_names` a character string of the layers to remove from the panel

**Method** `get_data()`: returns the data for all layers in the object

*Usage:*

```
ggbrain_panel$get_data()
```

**Method** `get_layer_names()`: returns the names of the layers in this panel, ordered from bottom to top

*Usage:*

```
ggbrain_panel$get_layer_names()
```

**Method** `get_layers()`: returns a list of `ggbrain_layer` objects that comprise this panel

*Usage:*

```
ggbrain_panel$get_layers()
```

**Method** `set_layer_order()`: sets the order of layers from bottom to top based on the layer names provided

*Usage:*

```
ggbrain_panel$set_layer_order(ordered_names = NULL)
```

*Arguments:*

`ordered_names` the names of the layers in the desired order from bottom to top. All layer names must be provided, not just a subset

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_panel$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

---

ggbrain_plot	<i>An R6 class for constructing a ggbrain plot from a ggbrain_slices object</i>
--------------	---

---

### Description

An R6 class for constructing a ggbrain plot from a ggbrain\_slices object

An R6 class for constructing a ggbrain plot from a ggbrain\_slices object

### Details

Note that this class is exported only for power users and rarely needs to be called directly in typical use of the package. Instead, look at ggbrain().

### Value

a ggbrain\_plot R6 class containing fields related to a ggbrain plot object

### Active bindings

slices a ggbrain\_slices object containing all slice data for this plot

layers a list of ggbrain\_layer objects for this plot. Note that in assignment, the input can be a list of ggbrain\_layer objects, or a list of lists where each inner element specifies the settings for that layer. Example: `list(list(name='hello', fill_scale=scale_fill_distiller()))`

annotations a list of annotations to be added to this plot

region\_labels a list of region\_labels to be added to this plot

panel\_settings a list of panel settings (aesthetics) to be added to this plot

title overall plot title, added to composite plot by patchwork: `:plot_annotation()`

bg\_color background color of plot

text\_color the color of text use across panels (can be overridden by panel settings)

base\_size the base size of text used in ggplot theming

### Methods

#### Public methods:

- `ggbrain_plot$new()`
- `ggbrain_plot$add_layers()`
- `ggbrain_plot$reset_layers()`
- `ggbrain_plot$generate_plot()`
- `ggbrain_plot$plot()`
- `ggbrain_plot$clone()`

**Method** `new()`: instantiate a new instance of a ggbrain\_plot object

*Usage:*

```
ggbrain_plot$new(
  title = NULL,
  bg_color = NULL,
  text_color = NULL,
  base_size = NULL,
  slice_data = NULL
)
```

*Arguments:*

`title` overall plot title  
`bg_color` background color of plot  
`text_color` text color of plot  
`base_size` base size of text used in ggplot theming  
`slice_data` a ggbrain\_slices object generated by ggbrain\_images\$get\_slices()

**Method** `add_layers()`: adds one or more ggbrain\_layer objects to this plot

*Usage:*

```
ggbrain_plot$add_layers(layers = NULL)
```

*Arguments:*

`layers` a list of ggbrain\_layer objects (can also be a list that just specifies names, definitions, etc.)

**Method** `reset_layers()`: removes all existing layers from this ggbrain\_plot object

*Usage:*

```
ggbrain_plot$reset_layers()
```

**Method** `generate_plot()`: generate the plot

*Usage:*

```
ggbrain_plot$generate_plot(layers = NULL, slice_indices = NULL)
```

*Arguments:*

`layers` a list of layers to be displayed on each panel, the order of which yields the bottom-to-to drawing order within ggplot2. Each element of `layers` should be a list that follows the approximate structure of the ggbrain\_layer class, minimally including the layer name, which is used to lookup data of images or contrasts within the slice\_data object. If NULL, all layers in the slices object will be plotted. If only a character string is passed, then those layers will be plotted with default scales.

`slice_indices` An optional subset of slice indices to display from the stored slice data

*Details:* In addition to name, the elements of a layer can include `fill_scale` a ggplot2 scale object for coloring the layer. Should be a `scale_fill_*` object. `limits` the numeric limits to use for the color scale of this layer `breaks` the scale breaks to use for the color scale of this layer `show_legend` if FALSE, the color scale will not appear in the legend

**Method** `plot()`: return a plot of all panels as a patchwork object

*Usage:*

```
ggbrain_plot$plot(guides = "collect")
```

*Arguments:*

`guides` Passes through to `patchwork::plot_layout` to control how legends are combined across plots. The default is "collect", which collects legends within a given nesting level (removes duplicates).

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
ggbrain_plot$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

---

```
ggplot_add.ggbrain_label
```

*S3 method to support adding ggbrain\_label objects to an existing ggplot object*

---

## Description

S3 method to support adding ggbrain\_label objects to an existing ggplot object

## Usage

```
## S3 method for class 'ggbrain_label'
ggplot_add(object, plot, object_name)
```

## Arguments

<code>object</code>	the ggbrain_layer object to be added to an existing ggplot
<code>plot</code>	the ggplot object
<code>object_name</code>	not used, but required by ggplot_add

---

```
ggplot_add.ggbrain_layer
```

*S3 method to support adding ggbrain\_layer objects to an existing ggplot object*

---

## Description

S3 method to support adding ggbrain\_layer objects to an existing ggplot object

**Usage**

```
## S3 method for class 'ggbrain_layer'
ggplot_add(object, plot, object_name)
```

**Arguments**

object	the ggbrain_layer object to be added to an existing ggplot
plot	the ggplot object
object_name	not used, but required by ggplot_add

---

```
ggplot_add.ggbrain_panel
```

*S3 method to support adding ggbrain\_layer objects to an existing ggplot object*

---

**Description**

S3 method to support adding ggbrain\_layer objects to an existing ggplot object

**Usage**

```
## S3 method for class 'ggbrain_panel'
ggplot_add(object, plot, object_name)
```

**Arguments**

object	the ggbrain_layer object to be added to an existing ggplot
plot	the ggplot object
object_name	not used, but required by ggplot_add

---

```
images
```

*Add images to a ggbrain object*

---

**Description**

Add images to a ggbrain object

**Usage**

```
images(images = NULL, volumes = NULL, labels = NULL, filter = NULL)
```

**Arguments**

images	a character vector or ggbrain_images object containing NIFTI images to add to this plot
volumes	a number indicating the volume within the images to display. At present, this must be a single number – perhaps in the future, it could be a vector so that many timepoints in a 4-D image could be displayed.
labels	a data.frame or named list of data.frame objects corresponding to images that should be labeled. You can only provide a data.frame if there is a single image being added. If multiple images are added, the names of the labels list are used to align the labels with a given matching image.
filter	a named list or character string specifying an expression of values to retain in the image, or a numeric vector of values to retain. Calls ggbrain_images\$filter_image()

**Value**

a ggb object with the relevant images and an action of 'add\_images'

**Examples**

```
t1 <- system.file("extdata", "mni_template_2009c_3mm.nii.gz", package = "ggbrain")
gg_obj <- ggbrain() +
  images(c(underlay = t1))
```

---

integer_breaks	<i>breaks function to encourage integer-valued breaks, based on input from pretty</i>
----------------	---

---

**Description**

breaks function to encourage integer-valued breaks, based on input from pretty

**Usage**

```
integer_breaks(n = 5, ...)
```

**Arguments**

n	number of breaks (default = 5)
...	Additional arguments passed to the pretty() function

**Details**

Code from here: <https://joshuacook.netlify.app/post/integer-values-ggplot-axis/>

**Value**

a function for generating integer-valued breaks on a continuous scale

---

montage	<i>Convenience function to add many slices in a montage along one of the 3D planes</i>
---------	--

---

## Description

Convenience function to add many slices in a montage along one of the 3D planes

## Usage

```
montage(
  plane = NULL,
  n = 12,
  min = 0.1,
  max = 0.9,
  min_coord = NULL,
  max_coord = NULL
)
```

## Arguments

plane	a character string specifying the 3D plane: "sagittal", "axial", "coronal", "x", "y", or "z"
n	number of slices to add in this plane. Default: 12
min	the lowest quantile to be included in the montage (between 0 and 1). Default: 0.1
max	the highest quantile to be included in the montage (between 0 and 1). Default: 0.9
min_coord	the lowest spatial position (in image coordinate space) to be included in the montage.
max_coord	the highest spatial position (in image coordinate space) to be included in the montage.

## Details

This can be used with `slices` to make a quick montage, such as `slices(montage("axial", 10))`.

Also note that use of standardized coordinates (in quantiles, using `min` and `max`) is mutually exclusive with the the image coordinate specifications `min_coord` and `max_coord`.

## Value

a character string containing the slice positions along the requested axis

**Examples**

```
t1 <- system.file("extdata", "mni_template_2009c_3mm.nii.gz", package = "ggbrain")
gg_obj <- ggbrain() +
  images(c(underlay = t1)) +
  slices(montage("sagittal", 15))
```

---

nn_impute	<i>Imputes missing values in a 2D matrix based on the nearest non-missing neighbors in a given radius</i>
-----------	---

---

**Description**

Imputes missing values in a 2D matrix based on the nearest non-missing neighbors in a given radius

**Arguments**

in_mat	a 2D matrix to fill using nearest neighbors
neighbors	the number of closest non-NA neighboring values to return within in_mat. Default is 4.
radius	the radius (in pixels) around each missing value to search for non-missing neighbors. Default is 8.
aggfun	the function used to aggregate the neighbors in imputation. Supports "mean", "median", and "mode."
ignore_zeros	if TRUE, then zero is not a valid imputation value (since these are not data in NIFTIs)

**Details**

The "mode" aggfun should only be used when the matrix in\_mat can be converted to integers without loss of information (i.e., the data are integerish values already).

**Value**

A copy of the matrix with NA values imputed by their nearest neighbors

---

plot.ggb	<i>S3 method to allow for plot() syntax with ggbrain (ggb) objects</i>
----------	--

---

**Description**

S3 method to allow for plot() syntax with ggbrain (ggb) objects

**Usage**

```
## S3 method for class 'ggb'  
plot(x, ...)
```

**Arguments**

x	the ggb object to be plotted
...	additional argument passed to the plot method

---

plot.ggbrain_panel	<i>S3 method to allow for plot() syntax with ggbrain_panel objects</i>
--------------------	--

---

**Description**

S3 method to allow for plot() syntax with ggbrain\_panel objects

**Usage**

```
## S3 method for class 'ggbrain_panel'  
plot(x, ...)
```

**Arguments**

x	the ggbrain_panel object to be plotted
...	additional argument passed to the plot method

---

plot.ggbrain\_plot      *S3 method to allow for plot() syntax with ggbrain\_panel objects*

---

**Description**

S3 method to allow for plot() syntax with ggbrain\_panel objects

**Usage**

```
## S3 method for class 'ggbrain_plot'
plot(x, ...)
```

**Arguments**

x                      the ggbrain\_plot object to be plotted  
 ...                    additional argument passed to the plot method

---

range\_breaks            *breaks function for including min + max with labels, and a few unlabeled ticks in between*

---

**Description**

breaks function for including min + max with labels, and a few unlabeled ticks in between

**Usage**

```
range_breaks(n = 3, digits = 2)
```

**Arguments**

n                      number of breaks added within the min-max range  
 digits                number of decimal places to display

**Value**

a function for generating breaks on a continuous scale with the min and max labeled

---

render	<i>Function to convert ggb object to ggplot/patchwork object</i>
--------	--

---

**Description**

Function to convert ggb object to ggplot/patchwork object

**Usage**

```
render()
```

**Value**

a ggb object with the action 'render', used in a ggbrain addition chain

---

scale_fill_bisided	<i>scale for plotting separate color gradients for positive and negative values</i>
--------------------	---

---

**Description**

scale for plotting separate color gradients for positive and negative values

**Usage**

```
scale_fill_bisided(
  name = ggplot2::waiver(),
  neg_scale = scale_fill_distiller(palette = "Blues", direction = 1),
  pos_scale = scale_fill_distiller(palette = "Reds"),
  symmetric = TRUE
)
```

**Arguments**

name	the scale name to be printed in the legend (above positive scale)
neg_scale	a scale_fill_* object used for negative values
pos_scale	a scale_fill_* object used for positive values
symmetric	if TRUE, the limits of the positive scale will equal the inverse limits of the negative scale. Said differently, this makes the positive and negative scales symmetric

**Details**

Note that this will absolutely not work as a general purpose ggplot2 scale! The positive/negative combination is achieved by adding two layers/geoms behind the scenes with different color scale.

**Value**

a ggplot2 scale of type ScaleContinuous that includes negative and positive fill scales internally in the \$neg\_scale and \$pos\_scale elements

---

slices	<i>Adds slices to the ggbrain plot, including additional panel aesthetics</i>
--------	---

---

**Description**

Adds slices to the ggbrain plot, including additional panel aesthetics

**Usage**

```
slices(
  coordinates = NULL,
  title = NULL,
  bg_color = NULL,
  text_color = NULL,
  border_color = NULL,
  border_size = NULL,
  xlab = NULL,
  ylab = NULL,
  theme_custom = NULL
)
```

**Arguments**

coordinates	a character vector specifying the x, y, or z coordinates of the slices to be added.
title	a title for the slice panels added to the ggplot object using ggtitle()
bg_color	the color used for the background of the panels. Default: 'gray10' (nearly black)
text_color	the color used for text displayed on the panels. Default: 'white'.
border_color	the color used for drawing a border around on the panels. Default: 'gray50' (though borders are not drawn by default).
border_size	the size of the border line drawn around the panels. Default: NULL. If this value is greater than zero, a border of this size and with color border_color will be drawn around the panels.
xlab	The label to place on x axis. Default is NULL.
ylab	The label to place on y axis. Default is NULL.
theme_custom	Any custom theme() settings to be added to the panels.

**Details**

note that if you pass in multiple coordinates (as a vector), the `title`, `bg_color`, and other attributes will be reused for all slices added by this operation. Thus, if you want to customize specific slices or groups of slices, use multiple addition operations, as in `slices(c('x=10', 'y=15'), bg_color='white') + slices(c('x=18', 'y=22'), bg_color='black')`.

**Value**

a `ggb` object with the relevant slices and an action of `'add_slices'`

**Examples**

```
t1 <- system.file("extdata", "mni_template_2009c_3mm.nii.gz", package = "ggbrain")
gg_obj <- ggbrain() +
  images(c(underlay = t1)) +
  slices(c("x = 25%", "x = 75%"), border_color = "blue")
```

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