

# Package ‘ssbrain’

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**Type** Package

**Title** Take Brain Screenshots Using CIFTI And Border Files

**Version** 0.1.0

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**Description** This package allows you to provide CIFTI (dscalar/dlabel/dconn) and/or border files to take screenshots of brain surfaces, similar to what you would be able to produce in Connectome Workbench.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

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gplots,  
grDevices,  
magick,  
rgl,  
tidyr,  
viridisLite,  
xml2

**Depends** R (>= 4.1.1)

## R topics documented:

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+.ssbrain

*Overloaded Plus*

## Description

This is an overloaded function for '+' that allows for combining different ssbrain elements.

## Usage

```
## S3 method for class 'ssbrain'
obj1 + obj2
```

## Arguments

obj1	The existing ssbrain object
obj2	The new ssbrain object to add

## Value

A new ssbrain object with information from both previous objects.

---

.onAttach	<i>Message on Open</i>
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---

### Description

Present the start message when opening

### Usage

```
.onAttach(...)
```

### Arguments

...	Items passed to attach
-----	------------------------

---

add_border	<i>(Internal) Set a Border</i>
------------	--------------------------------

---

### Description

The internal function that calculates the result for [ss\\_border](#)

### Usage

```
add_border(obj1, obj2)
```

### Arguments

obj1	The existing ssbrain object
obj2	The new ssborder object to add

---

add_dconn	<i>(Internal) Set a Seed</i>
-----------	------------------------------

---

### Description

The internal function that calculates the result for [ss\\_seed](#)

### Usage

```
add_dconn(obj1, obj2)
```

### Arguments

obj1	The existing ssbrain object
obj2	The new ssdconn object to add

---

add_dlabel	<i>(Internal) Set a Dlabel</i>
------------	--------------------------------

---

**Description**

The internal function that calculates the result for [ss\\_dlabel](#)

**Usage**

```
add_dlabel(obj1, obj2)
```

**Arguments**

obj1	The existing ssbrain object
obj2	The new ssdlabel object to add

---

add_dscalar	<i>(Internal) Set a Dscalar</i>
-------------	---------------------------------

---

**Description**

The internal function that calculates the result for [ss\\_dscalar](#)

**Usage**

```
add_dscalar(obj1, obj2)
```

**Arguments**

obj1	The existing ssbrain object
obj2	The new ssdscalar object to add

---

add_view	<i>(Internal) Set a Viewpoint</i>
----------	-----------------------------------

---

**Description**

The internal function that calculates the result for [ss\\_view](#)

**Usage**

```
add_view(obj1, obj2)
```

**Arguments**

obj1	The existing ssbrain object
obj2	The new ssview object to add

captureBrain

*Capture a Visually-displayed Brain Surface***Description**

This function opens an rgl window and displays a brain surface, then saves a screenshot of it.

**Usage**

```
captureBrain(
  brain,
  hemisphere,
  filename,
  width = 800,
  height = 500,
  crop = TRUE,
  cropmargin = 10
)
```

**Arguments**

brain	An ssbrain object created by <a href="#">ss_surf</a> (and potentially modified by other functions)
hemisphere	Which brain hemisphere to display (either "left" or "right")
filename	A string with the full path to the PNG file you'd like to create
width	The width of the window. Default is 800.
height	The height of the window. Default is 500.
crop	Whether or not to crop the resulting image. Default is TRUE.
cropmargin	The margin of whitespace to leave around the brain when cropping. Default is 10.

**Examples**

```
## Not run:
my_brain = ss_surf(surf="fsaverage6") +
  ss_dscalar(dscalar_filename = "/path/to/my_file.dscalar.nii")

captureBrain(my_brain, hemisphere = "left", filename = "/path/to/my/output_image.png")

## End(Not run)
```

---

checkBin	<i>Check data bins</i>
----------	------------------------

---

### Description

Check to see which bin contains the value

### Usage

```
checkBin(x, y)
```

### Arguments

x	The levels (bins) of the output of the cut function
y	The value to check

### Value

TRUE or FALSE

---

closeBrainViewers	<i>Close All Open Brain Windows</i>
-------------------	-------------------------------------

---

### Description

Closes all currently-open brain windows

### Usage

```
closeBrainViewers()
```

### Examples

```
## Not run:
my_brain = ss_surf(surf="fsaverage6") +
  ss_dscalar(dscalar_filename = "/path/to/my_file.dscalar.nii")

showBrain(my_brain, hemisphere = "left")

closeBrainViewers()

## End(Not run)
```

---

colorbarGenerator	<i>Generate Color Bar</i>
-------------------	---------------------------

---

**Description**

Given a name or color palette(s), generate the necessary information to use them in brain maps

**Usage**

```
colorbarGenerator(colorbar_name, neg_colorpalette, pos_colorpalette)
```

**Arguments**

colorbar_name	A string with the name of the color bar
neg_colorpalette	(Optional argument) A custom color palette created by colorRampPalette, to be used for negative values
pos_colorpalette	(Optional argument) A custom color palette created by colorRampPalette, to be used for positive values

---

createOutputList	<i>Create Color Maps</i>
------------------	--------------------------

---

**Description**

Creates the necessary outputs for colormaps used by ss\_dscalar and ss\_seed

**Usage**

```
createOutputList(colorbar_name, pos_list, neg_list)
```

**Arguments**

colorbar_name	A string with the name of the color bar
pos_list	The list of positive color values to create the palette
neg_list	The list of negative color values to create the palette

---

distill_dconn	<i>'Distill' a Connectivity Dconn File</i>
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---

### Description

This function "distills" a symmetrical .dconn.nii file containing connectivity information. It exports the correlation between each vertex and the specified vertex, resulting in a vector the length of the number of vertices. Functionally, it converts the dconn into a dscalar.

### Usage

```
distill_dconn(dconn_filepath, seed_value, num_verts)
```

### Arguments

dconn_filepath	A string with the full path to the .dconn.nii file
seed_value	A value for the seed (the row number, not vertex number)
num_verts	The number of vertices (row/columns) in your dconn file

### Value

An object of the same type returned by [importCifti](#) when used on a dscalar file.

### Examples

```
## Not run:
dconn_seed_data = distill_dconn(dconn_filepath = "/path/to/my/dconn/my_data.dconn.nii",
                                seed_value = 2214, num_verts = 81924)

## End(Not run)
```

---

exportCifti	<i>Export a CIFTI Data File or Border File</i>
-------------	------------------------------------------------

---

### Description

This function exports a CIFTI data file (or border file) from R, using a vector of data

### Usage

```
exportCifti(cifti_filename, data, luttpath)
```

### Arguments

cifti_filename	A string with the full path to the CIFTI data file you'd like to create
data	A vector of data values.
luttpath	(Optional argument) A path to a lut color file; used for dlabel and border files. Default is the Yeo 17-parcel color scheme.



## Details

This function currently only supports .dscalar.nii, .dlabel.nii, and .border files. For border files, outputs should be named filename.border. These will automatically be changed into left/right hemisphere files called filename\_lh.border and filename\_rh.border

## Examples

```
## Not run:
my_data = runif(81924, 1.0, 100.0) # a vector of 81,924 random values between 1 and 100
exportCifti("/path/to/my/output.dscalar.nii", my_data)

my_data = sample(1:15, 81924) # a vector of 81,924 random integers between 1 and 15
exportCifti("/path/to/my/output.dlabel.nii", my_data)

## End(Not run)
```

---

getSeedVector	<i>Get a Linear Vector of Seeds</i>
---------------	-------------------------------------

---

## Description

This function calculates the values of every seed that lie in a (relatively) straight line between the two seeds provided. It allows you to "draw" a series of seeds across the cortex, by looping through the resulting list with ss\_seed.

## Usage

```
getSeedVector(brain, seed_start, seed_end, dlabel)
```

## Arguments

brain	Any ss_surf object in the same mesh space that you plan to use for ss_seed (i.e. fsaverage6, fsaverage7)
seed_start	The value of the starting seed to draw from
seed_end	The value of the ending seed to draw toward
dlabel	(Optional argument)

## Value

A list with three items: vertices (Euclidean coordinates for each vertex), faces (the 3 vertex indices that make up each face), and num\_verts (the total number of vertices in the mesh)

## Examples

```
## Not run:
my_brain = ss_surf(surf = "fsaverage6")
my_seed_vector = getSeedVector(my_brain, 33424, 13264)

## End(Not run)
```

---

get_viewmatrix	<i>Calculation of View Matrix</i>
----------------	-----------------------------------

---

**Description**

This function calculates the coordinates that rgl needs to rotate a brain.

**Usage**

```
get_viewmatrix(hemisphere, side, wb_X, wb_Y, wb_Z)
```

**Arguments**

hemisphere	"left" or "right"
side	"lateral" or "medial"
wb_X	The x-axis rotation as shown in Connectome Workbench
wb_Y	The y-axis rotation as shown in Connectome Workbench
wb_Z	The z-axis rotation as shown in Connectome Workbench

**Value**

A view matrix that can be passed to rgl::view3d as a userMatrix.

---

importBorder	<i>Import a Border File</i>
--------------	-----------------------------

---

**Description**

This function imports a border file into R, providing information on vertices (and their ordering) used to form borders.

**Usage**

```
importBorder(border_name, border_surfname)
```

**Arguments**

border_name	A string with the full path to a border file
border_surfname	A string with the full path to the GIFTI surface used to create the border

**Value**

A gifti file containing border information

**Examples**

```
## Not run:
border_data = importBorder("/path/to/border/my_borderfile_lh.border",
                           border_surfname = "/path/to/surface/lh.pial_infl2.surf.gii")

## End(Not run)
```



---

importSurface	<i>Import a GIFTI Surface File</i>
---------------	------------------------------------

---

### Description

This function imports a GIFTI surface file into R, providing information for vertex coordinates in Euclidean space and the vertices used to draw triangular faces.

### Usage

```
importSurface(surface_name)
```

### Arguments

surface\_name     A string with the full path to a GIFTI surface file

### Value

A list with three items: vertices (Euclidean coordinates for each vertex), faces (the 3 vertex indices that make up each face), and num\_verts (the total number of vertices in the mesh)

### Examples

```
## Not run:
surface_data = importSurface("/path/to/surface/lh.pial_infl2.surf.gii")

## End(Not run)
```

---

is.border	<i>Check if Border</i>
-----------	------------------------

---

### Description

This function checks if an object is of the class ssborder.

### Usage

```
is.border(x)
```

### Arguments

x                     The object to check

### Value

TRUE or FALSE

**Examples**

```
## Not run:
new_border = ss_border(filename = "/path/to/my/datafile.dlabel.nii", hemisphere = "left")
is.dconn(new_border)

## End(Not run)
```

---

`is.dconn`*Check if Dconn*

---

**Description**

This function checks if an object is of the class `ssdconn`.

**Usage**

```
is.dconn(x)
```

**Arguments**

`x`                      The object to check

**Value**

TRUE or FALSE

**Examples**

```
## Not run:
new_dconn = ss_seed(filename = "/path/to/my/datafile.dconn.nii", seed_value = 2213)
is.dconn(new_dconn)

## End(Not run)
```

---

`is.dlabel`*Check if Dlabel*

---

**Description**

This function checks if an object is of the class `ssdlabel`.

**Usage**

```
is.dlabel(x)
```

**Arguments**

`x`                      The object to check

**Value**

TRUE or FALSE

**Examples**

```
## Not run:  
new_dlabel = ss_dlabel(filename = "/path/to/my/datafile.dlabel.nii")  
is.dlabel(new_dlabel)  
  
## End(Not run)
```

---

is.dscalar

*Check if Dscalar*

---

**Description**

This function checks if an object is of the class ssdscalar.

**Usage**

```
is.dscalar(x)
```

**Arguments**

x                      The object to check

**Value**

TRUE or FALSE

**Examples**

```
## Not run:  
new_dscalar = ss_dscalar(filename = "/path/to/my/datafile.dscalar.nii")  
is.dscalar(new_dscalar)  
  
## End(Not run)
```

---

is.view

*Check if View*

---

**Description**

This function checks if an object is of the class ssview.

**Usage**

```
is.view(x)
```

**Arguments**

x                      The object to check

**Value**

TRUE or FALSE

**Examples**

```
## Not run:
new_view = ss_view(side="lateral", rotation = "inferior_temporal")
is.view(new_view)

## End(Not run)
```

---

listColorbars	<i>List Available Colorbars</i>
---------------	---------------------------------

---

**Description**

This function lists the colorbars available in the ssbrain package for use with the [ss\\_dscalar](#) and [ss\\_seed](#) functions.

**Usage**

```
listColorbars()
```

---

listRotations	<i>List Available Rotations</i>
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---

**Description**

This function lists the pre-set rotations available in the ssbrain package for use with the [ss\\_view](#) function.

**Usage**

```
listRotations()
```

---

openNewBrainViewer	<i>Open a New Brain Window</i>
--------------------	--------------------------------

---

### Description

Forces a new brain window to open. All new instances of `showBrain` and `captureBrain` will use this window. This can be useful if you've already opened a brain window and don't want to overwrite/close it (e.g. to look at two brains at once).

### Usage

```
openNewBrainViewer(width = 800, height = 500)
```

### Arguments

width	The width of the window. Default is 800.
height	The height of the window. Default is 500.

### Examples

```
## Not run:
my_brain1 = ss_surf(surf="fsaverage6") +
  ss_dscalar(dscalar_filename = "/path/to/my_file1.dscalar.nii")

my_brain2 = ss_surf(surf="fsaverage6") +
  ss_dscalar(dscalar_filename = "/path/to/my_file2.dscalar.nii")

# To show my_brain1, then replace it with my_brain2:
showBrain(my_brain1, hemisphere = "left")
showBrain(my_brain2, hemisphere = "left")

# To show my_brain1, then to open my_brain2 in a second window:
showBrain(my_brain1, hemisphere = "left")
openNewBrainViewer()
showBrain(my_brain2, hemisphere = "left")

## End(Not run)
```

---

rgb_fun1	<i>Create a Color Code</i>
----------	----------------------------

---

### Description

Create a color HEX code from an RGB triple in a vector

### Usage

```
rgb_fun1(x)
```

### Arguments

x	A vector with three RGB values
---	--------------------------------



---

`set_wbpath`*Set Workbench Directory*

---

**Description**

This allows you to set the path to your Workbench executable file.

**Usage**

```
set_wbpath(value)
```

**Arguments**

value	A string with the full filepath to your Workbench executable. It should end with "wb_command"
-------	-----------------------------------------------------------------------------------------------

**Details**

This sets a global option for your R environment. It only needs to be run the first time you start R. It is advised that you put this function at the top of every ssbrain script.

**Examples**

```
## Not run:  
set_wbpath("/path/to/directory/for/workbench/wb_command")  
  
## End(Not run)
```

---

`showBrain`*Visually Display Brain Surface*

---

**Description**

This function opens an rgl window and displays a brain surface.

**Usage**

```
showBrain(brain, hemisphere, width = 800, height = 500)
```

**Arguments**

brain	An ssbrain object created by <a href="#">ss_surf</a> (and potentially modified by other functions)
hemisphere	Which brain hemisphere to display (either "left" or "right")
width	The width of the window. Default is 800.
height	The height of the window. Default is 500.

## Examples

```
## Not run:
my_brain = ss_surf(surf="fsaverage6") +
  ss_dscalar(dscalar_filename = "/path/to/my_file.dscalar.nii")

showBrain(my_brain, hemisphere = "left")

## End(Not run)
```

---

ss\_border

*Set a Border*


---

## Description

This function sets a border data file on the surface of the brain

## Usage

```
ss_border(
  filename,
  hemisphere,
  borders = NULL,
  width = 5,
  colors = NULL,
  offset = TRUE
)
```

## Arguments

filename	A string with the full filepath to a border file
hemisphere	The hemisphere of the border file, either "left" or "right"
borders	A single border, either an integer corresponding to the border number in the file (e.g. 5) or the name in the file (e.g. "LANG"). Can also be a vector of integers/names if multiple borders should be displayed. If omitted, all borders in the file will be plotted.
width	The width of the borders to be plotted. Defaults to 5.
colors	A list of colors the same length as borders; colors can be R color names (e.g. "red"), hex codes (e.g. "#FF0000"), or RGB triples (e.g. c(255,0,0)). If omitted, the default colors of the file will be used.
offset	Whether the border should be slightly raised up (offset) above the brain (TRUE) or not (FALSE). Defaults to TRUE.

## Details

Note: Adding multiple ss\_border items to the same object will cause overlapping brain maps, with the most recently-added on top.

## Examples

```
## Not run:
# Here, all borders will be plotted and the file's colorscheme will be used
my_brain = ss_surf(surf="fsaverage6") +
  ss_border(filename = "/path/to/my/datafile_lh.border", hemisphere = "left")

# Here, only borders 1 and 5 from the file will be used, and they are colored "red" and "green"
my_brain = ss_surf(surf="fsaverage6")

my_brain_new = my_brain +
  ss_border(filename = "/path/to/my/datafile_lh.border",
            hemisphere = "left",
            borders = c(1,5),
            colors = list("red", "green"))

# Here, labels 8 through 10 will be plotted, with different
# color specifications used for each
my_brain = ss_surf(surf="fsaverage6") +
  ss_border(filename = "/path/to/my/datafile_lh.border",
            hemisphere = "left",
            borders = 8:10,
            colors = list("#FF00FF", c(212,118,97), "palegreen"))

# Here, three borders are plotted by name, and all are black
my_brain = ss_surf(surf="fsaverage6") +
  ss_border(filename = "/path/to/my/datafile_lh.border",
            hemisphere = "left",
            borders = c("LANG", "VIS", "AUD"),
            colors = "black")

## End(Not run)
```

---

ss\_dlabel

Set a Dlabel

---

## Description

This function sets a dlabel data file on the surface of the brain

## Usage

```
ss_dlabel(filename, labels = NULL, colors = NULL)
```

## Arguments

filename	A string with the full filepath to a dlabel file
labels	A single label, either an integer corresponding to the label number in the file (e.g. 5) or the name in the file (e.g. "LANG"). Can also be a vector of integers/names if multiple labels should be displayed. If omitted, all labels in the file will be plotted.
colors	A list of colors the same length as labels; colors can be R color names (e.g. "red"), hex codes (e.g. "#FF0000"), or RGB triples (e.g. c(255,0,0)). If omitted, the default colors of the file will be used.

## Details

Note: Adding multiple ss\_dlabel items to the same object will cause overlapping brain maps, with the most recently-added on top.

## Examples

```
## Not run:
# Here, all labels will be plotted and the file's colorscheme will be used
my_brain = ss_surf(surf="fsaverage6") +
  ss_dlabel(filename = "/path/to/my/datafile.dlabel.nii")

# Here, only labels 1 and 5 from the file will be used, and they are colored "red" and "green"
my_brain = ss_surf(surf="fsaverage6")

my_brain_new = my_brain +
  ss_dlabel(filename = "/path/to/my/datafile.dlabel.nii",
            labels = c(1,5),
            colors = list("red", "green"))

# Here, labels 8 through 10 will be plotted, with different
# color specifications used for each
my_brain = ss_surf(surf="fsaverage6") +
  ss_dlabel(filename = "/path/to/my/datafile.dlabel.nii",
            labels = 8:10,
            colors = list("#FF00FF", c(212,118,97), "palegreen"))

## End(Not run)
```

---

ss\_dscalar

*Set a Dscalar*


---

## Description

This function sets a dscalar data file on the surface of the brain

## Usage

```
ss_dscalar(
  filename,
  colorbar = "FSL",
  show = "all",
  pos_thresh = 1,
  neg_thresh = -1,
  pos_colorrage = c(1, 3),
  neg_colorrage = c(-1, -3),
  pos_palette,
  neg_palette
)
```

## Arguments

filename	A string with the full filepath to a dscalar file
colorbar	A string containing the name of a colorbar to use (same names as Connectome Workbench)
show	Whether to show positive data, negative data, or all data. Options are "all", "pos", or "neg". Defaults to "all".
pos_thresh	The threshold below which to hide positive data. Defaults to 1.
neg_thresh	The option above which to hide negative data. Defaults to -1.
pos_colorrangle	The positive range in which to spread the colorbar's colors. Defaults to c(1,3)
neg_colorrangle	The negative range in which to spread the colorbar's colors. Defaults to c(-1,-3)
pos_palette	(Experimental) A color palette created by colorRampPalette; overrides colorbar for positive colors.
neg_palette	(Experimental) A color palette created by colorRampPalette; overrides colorbar for negative colors.

## Details

Note: Adding multiple ss\_dscalar items to the same object will cause overlapping brain maps, with the most recently-added on top.

## Examples

```
## Not run:
my_brain = ss_surf(surf="fsaverage6") +
  ss_dscalar(filename = "/path/to/my/datafile.dscalar.nii")

my_brain = ss_surf(surf="fsaverage6")

my_brain_new = my_brain +
  ss_dscalar(filename = "/path/to/my/datafile.dscalar.nii",
             colorbar = "ROY-BIG-BL",
             show= "pos",
             pos_thresh = 10,
             pos_colorrangle = c(10,50))

## End(Not run)
```

---

ss\_seed

*Set a Seed*


---

## Description

This function sets a seed (based on a vertex row number) and then creates a map from a corresponding dconn file containing a functional connectivity matrix.

## Usage

```
ss_seed(
  filename,
  seed_value,
  colorbar = "JET256",
  thresh = 0.2,
  colorrange = c(0.2, 0.6),
  show_seed_sphere = TRUE,
  seed_sphere_size = 2,
  seed_sphere_color = "white",
  seed_data,
  palette
)
```

## Arguments

filename	A string with the full filepath to a dconn file
seed_value	The number of the seed (row number, not vertex number)
colorbar	A string containing the name of a colorbar to use (same names as Connectome Workbench)
thresh	The option above which to hide data. Defaults to 0.2.
colorrange	The range in which to spread the colorbar's colors. Defaults to c(0.2, 0.6)
show_seed_sphere	Whether or not to draw a sphere where the seed is (TRUE) or not (FALSE). Defaults to TRUE.
seed_sphere_size	If show_seed_sphere is TRUE, the radius of the sphere. Defaults to 2.
seed_sphere_color	If show_seed_sphere is TRUE, the color of the sphere. Defaults to "white".
seed_data	(Optional argument) Rather than passing a dconn file, you can directly pass in an R matrix containing the functional connectivity data. This can save time if you want to draw multiple seeds from the same dconn matrix. This overrides dconne_filename.
palette	(Experimental) A color palette created by colorRampPalette; overrides colorbar.

## Details

Note: Adding multiple ss\_seed items to the same object will cause overlapping brain maps, with the most recently-added on top.

## Examples

```
## Not run:
my_brain = ss_surf(surf="fsaverage6") +
  ss_seed(filename = "/path/to/my/datafile.dconn.nii", seed_value = 31272)

my_brain = ss_surf(surf="fsaverage6")

my_brain_new = my_brain +
  ss_dscalar(filename = "/path/to/my/datafile.dconn.nii",
    seed_value = 2213,
```

```

        colorbar = "TURBO",
        thresh = 0.3,
        colorrange = c(0.3, 0.8),
        seed_sphere_size = 4,
        seed_sphere_color = "red")

# Warning: this may take a while (especially for fsaverage7),
# and will likely require a lot of memory!
dconn_data = importCifti(cifti_name = "/path/to/my/datafile.dconn.nii", data_only = TRUE)
my_brain = ss_surf(surf="fsaverage6") +
  ss_seed(seed_data = dconn_data, seed_value = 31272)

## End(Not run)

```

ss\_surf

*Set a Surface Mesh*

## Description

This is the core function of the ssbrain package. It creates an object that will store all of the surface information you want to display. It sets which surface mesh you plan to use.

## Usage

```
ss_surf(surf = NULL, surfL = NULL, surfR = NULL)
```

## Arguments

surf	A string with the surface mesh you wish to use. Options are "fsaverage6" and "fsaverage7".
surfL	(Optional argument) If you don't want to use fs6/fs7, you can provide the full path to a surface GIFTI file for the left hemisphere.
surfR	(Optional argument) If you don't want to use fs6/fs7, you can provide the full path to a surface GIFTI file for the right hemisphere.

## Value

An ssbrain object with the specified surface mesh(es).

## Examples

```

## Not run:
my_brain = ss_surf(surf="fsaverage6")

my_brain = ss_surf(surfL = "/path/to/surface/lh.pial_infl2.surf.gii")

## End(Not run)

```

---

ss\_view

*Set a Viewpoint*


---

### Description

This function sets the view of the brain in the viewer window. It determines if a lateral or medial view is used, and the x/y/z axis rotation of the brain.

### Usage

```
ss_view(side = "lateral", rotation = c(0, 90, 90))
```

### Arguments

side	Which side of the brain to show, either "lateral" or "medial". Defaults to "lateral".
rotation	The rotation applied to the side chosen. Either a pre-defined rotation (e.g. "orbitofrontal"), or a vector of x/y/z angles (e.g. c(90,120,90)).

### Details

Note: ss\_view is the only ss\_\* function that **overwrites** any preexisting view, rather than adding on additional elements.

### Examples

```
## Not run:
my_brain = ss_surf(surf="fsaverage6") +
  ss_view(side="lateral", rotation = "inferior_temporal")

my_brain = ss_surf(surf="fsaverage6")

my_brain_new = my_brain +
  ss_view(side="medial", rotation = c(30,90,90))

## End(Not run)
```

---

start\_msg

*Start Message*


---

### Description

The start message to present when opening

### Usage

```
start_msg()
```



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