

Visualisation of Brain Statistics with R-package ggseg

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ABSTRACT

There is an increasing emphasis on visualizing results from statistical analysis in more intuitive ways. Neuroimaging data already have, as a consequence of the source of the data, particular shapes and as such visualization of these data should reflect these same dimensional properties. The ggseg package makes it possible to visualize pre-defined brain segmentations of local/structural or connectivity features in both 2D polygons or 3D mesh. Presenting both relative position and size of segments in addition to statistical summary information aides interpretation and dissemination of results. In this tutorial, we present the data and functions in the ggseg and ggseg3d R-packages for brain atlas visualization. The tutorial highlights the main functions to create brain segmentation plots in R, and also introduces the accompanying package data that makes these visualizations possible.

1 INTRODUCTION

Visualization is increasingly important for accurate guidance and interpretation of neuroimaging results, as current research is able to generate a high amount of data and outcomes. For Magnetic Resonance Imaging (MRI), neuroimaging software provides whole-brain information by using many small units of space (>100,000). Nonetheless, this data is often grouped and summarized into a limited number of regions using predefined brain parcellation atlases. Brain parcellations segment the brain into a finite set of meaningful neurobiological components, which reflect one or more brain features either based on local/structural or on connectivity properties (Eickhoff et al. [2018]). The use of brain atlases is widespread as these facilitate interpretation and minimize the amount of data, hence reducing problems with multiple comparisons. This facilitates replicability and data sharing in otherwise computationally expensive analyses, which are often performed in specialized software environments such as R (R Core Team [2019]).

MRI data provides good spatial resolution and thus an optimal representation has to respect spatial relationships across regions. Results from brain atlas analyses are most meaningfully visualized when projected onto a representation of the brain, rather than on other types of graphs (e.g. bar charts) alone. The projection of data onto brain representations provides clear points of reference - especially when the reader is unfamiliar with the atlas - eases readability, guides interpretation, and conveys the spatial patterns of the data. Adopting the grammar of graphics implemented in ggplot2 (Wickham [2016]), one can plot neuroimaging data directly in R with several tools such as ggBrain (Fisher [2019]) and ggneuro (Muschelli [2017]; see neuroconductor [2018] for curated neuroimaging packages for R). Yet these tools display whole-brain image files and are not well-suited for representing brain atlas data.

In this tutorial, we introduce two packages for visualizing brain atlas data in R. The ggseg and ggseg3d – pluss the complimentary ggsegExtra – packages include pre-compiled data sets for different brain atlases that allow for 2D and 3D visualization. Two-dimensional functionality in ggseg is based on polygons and ggplot2-based grammar of graphics (Wickham [2016]), while the 3D functionality in ggseg3d is based on tri-surface mesh plots and plotly (Sievert [2018]).

Both packages present compiled data sets, tailored functions that allow brain data integration, and plotting, as well as other minor features such as custom colour palettes. The data featured in the

Table 1. Table of currently available atlases in the `ggseg`, `ggseg3d`, and the `ggsegExtra` R-packages. Polygon and mesh refer to 2D and 3D brain atlas representations, respectively

Title	Item	Mesh	Polygon	citation
Desikan-Killiany Cortical Atlas	dkt	ggseg3d	ggseg	Desikan et al. [2006]
Desterieux cortical parcellations	desterieux	ggsegExtra	None	Desterieux et al. [2010]
Freesurfer automatic subcortical segmentation of a brain volume	aseg	ggseg3d	ggseg	Fischl et al. [2002]
Genetic topography of brain area morphology	chenAr	None	ggsegExtra	Chen et al. [2013]
Genetic topography of brain thickness morphology	chenTh	None	ggsegExtra	Chen et al. [2013]
Harvard-Oxford Cortical atlas	hoCort	None	ggsegExtra	Makris et al. [2006]
Parcellation from a midsagittal slice	midsagittal	None	ggsegExtra	
Parcellation from JHU	jhu	ggsegExtra	ggsegExtra	Hua et al. [2008]
Parcellation from of white matter	icbm	ggsegExtra	None	Mori et al. [2005]
Parcellation from the Human Connectome Project	glasser	ggsegExtra	ggsegExtra	Glasser et al. [2016]
Schaefer 17 Resting-state Cortical Parcellations	schaefer17	ggsegExtra	None	Schaefer et al. [2017]
Schaefer 7 Resting-state Cortical Parcellations	schaefer7	ggsegExtra	None	Schaefer et al. [2017]
White matter tract parcellations	tracula	ggsegExtra	ggsegExtra	Yendiki et al. [2011]
Yeo 17 Resting-state Cortical Parcellations	yeo17	ggsegExtra	ggsegExtra	Yeo et al. [2011]
Yeo 7 Resting-state Cortical Parcellations	yeo7	ggsegExtra	ggsegExtra	Yeo et al. [2011]

packages are derived from two well-known parcellations: the Desikan-Killany cortical atlas (DKT; Desikan et al. [2006]), which covers the cortical surface of the brain, and the Automatic Segmentation of Subcortical Structures (aseg; Fischl et al. [2002]), which covers the subcortical structures. Both atlases are implemented in several neuroimaging softwares, such as FreeSurfer (Fischl et al. [1999], Dale et al. [1999], Fischl and Dale [2000]), and are commonly used in relation to developmental changes, disease biomarkers, genomic data, and cognition (Amlien et al. [2019], Walhovd et al. [2005], Pizzagalli et al. [2009]). The `ggsegExtra` package includes a library of precompiled atlases (currently including 13 additional atlases) and it is updated continuously. See Table 1 for a summary of the available atlases (as of November 2019).

2 TUTORIAL

This tutorial will introduce the `ggseg`, `ggseg3d`, and `ggsegExtra` packages and familiarize the reader with the main functions and the general use of the packages. The tutorial will focus on the two main functions: `ggseg()` for plotting 2D polygons and `ggseg3d()` for plotting 3D brains based on tri-surface mesh plots.

2.1 Plotting polygon data (ggplot2)

`ggseg` is the main function for plotting 2D data. By default, the function automatically plots the DKT atlas (see Figure 1). The `ggseg` function is a wrapper for `geom_polygon` from `ggplot2`, and it can be built upon and combined like any `ggplot` object. The image plot consists of a simple brain representation containing no extra information. Hence, `ggseg` plots can be easily complemented with any of the available `ggplot` features and options. We recommend users to get familiarized with `ggplot2` grammar (Wickham [2016]). The package is currently only available through github, but we expect to submit to The Comprehensive R Archive Network (cra) some time during 2020.

```
# remotes::install_github("LCBC-UiO/ggseg")
library(ggseg)
library(tidyverse)

# Figure 1
ggseg()
```

In addition to the standard options for `ggplot` polygon geoms, the function also has several options for plotting the main brain representations. These options are atlas-specific. For cortical atlases, such as the 'dkt', one can stack the hemispheres, view only the medial or lateral side, choose either one or both hemispheres, or any combination of hemisphere and view. See Figure 2) for examples. For subcortical atlases, such as the 'aseg', the options are more limited but one can often choose between axial, sagittal, and coronal views.

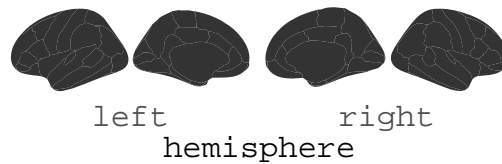


Figure 1. By default ggseg will plot the dkt atlas in grey shaded polygons.

```
# dkt dark theme
p1 <- ggseg(position = "stacked") +
  theme_dark() +
  labs(title=" ")

# dkt classic theme
p2 <- ggseg(position = "stacked") +
  theme_classic() +
  labs(title = " ")

# dkt medial view
med <- ggseg(view = "medial") +
  labs(title = " ")

# dkt left hemisphere
left <- ggseg(hemisphere = "left") +
  labs(title = " ")

# aseg default theme
p3 <- ggseg(atlas=aseg) +
  labs(title = " ")

# dkt left medial alone
combo <- ggseg(view = "medial",
  hemisphere = "left") +
  labs(title=" ")

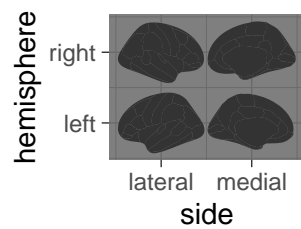
# Combine plots to Figure 2
cowplot::plot_grid(p1, med, combo, p2, left, p3,
  labels = c("A: dkt - dark", "B: dkt - medial",
    "C: dkt - combo", "D: dkt - classic",
    "E: dkt - left", "F: aseg"),
  hjust = -.05)
```

2.1.1 Using own data with fill and colour

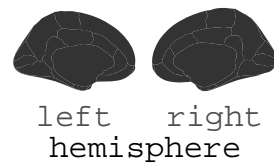
ggseg accepts any argument you can supply to `geom_polygon` and therefore is easy to work with for those familiar with ggplot functionality. Standard arguments like `fill` that floods the segments with a colour, or `colour` that colours the edges around the segments are typical arguments to provide to the function either as a single setting value or within the ggplot mapping function `aes`. To use color palettes corresponding to those used in the original neuroimaging softwares one can use atlas-specific ‘brain’ palette scales. See an example in Figure 3.

```
# Figure 3
ggseg(mapping=aes(fill = area), colour="black") +
```

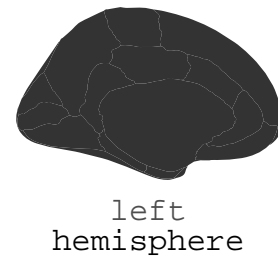
A: dkt – dark



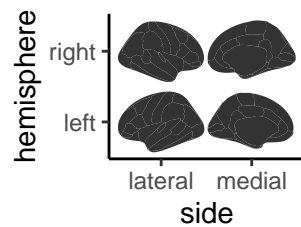
B: dkt – medial



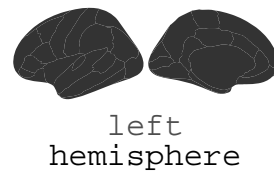
C: dkt – combo



D: dkt – classic



E: dkt – left



F: aseg

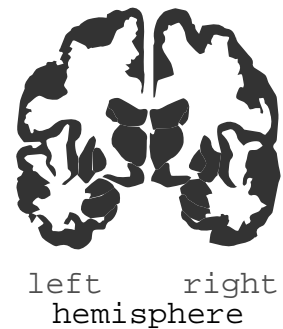


Figure 2. ggseg plots can be used with any ggplot feasture such as standard scales and themes. For cortical atlases, one can supply special ggseg options to determine hemisphere or view, and control how the plots looks like and is organised. **A:** dkt atlas, stacked with dark theme ; **B:** dkt with medial view only; **C:** dkt atlas with only left medial display; **D:** dkt atlas, stacked, with classic theme; **E:** dkt atlas with left hemisphere only; **F:** complete aseg atlas

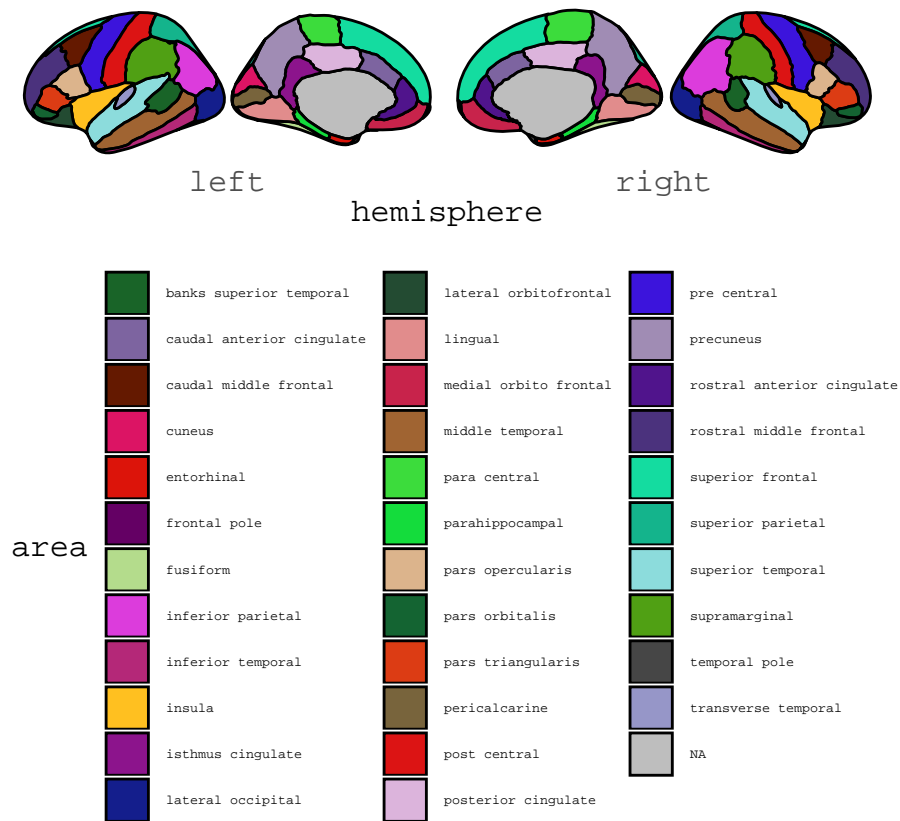


Figure 3. Supplying ‘area’ to the fill option in ggseg, will use the column ‘area’ from the accompanying dataset to create a discrete colour palette over the segments in the atlas. The ‘dkt’ atlas default palette corresponds to the FreeSurferColorLut scheme.

```
scale_fill_brain("dkt") +
theme(legend.justification=c(1,0),
      legend.position="bottom",
      legend.text = element_text(size = 5)) +
guides(fill = guide_legend(ncol = 3))
```

Most users will use ggseg to display - using a color scale - some descriptive or inferential statistics, such as mean thickness or brain-cognition relationships across the different brain regions. Yet, before projecting the statistics onto the segments, we need to explore the structure of the atlas data sets. The atlas data set structure will help us understand what incoming statistical data needs to look like. Note that each atlas corresponds to a unique data set. All data sets have a similar structure and contain key information regarding the atlas, the region names, and the coordinates for the segment polygons.

```
head(dkt, 5)
## # A tibble: 5 x 6
##   atlas area             hemi side label             ggseg
##   <chr> <chr>             <chr> <chr> <chr>             <list>
## 1 dkt superior temporal left lateral lh_superiortempor~ <tibble [1,494~
## 2 dkt pre central      left lateral lh_precentral   <tibble [1,314~
## 3 dkt post central     left lateral lh_postcentral  <tibble [1,164~
## 4 dkt rostral middle fr~ left lateral lh_rostralmiddlef~ <tibble [1,194~
## 5 dkt insula           left lateral lh_insula      <tibble [870 x~
```

In any atlas, the column ‘label’ is particularly useful for combining the data of interest with the ggseg-polygons. The column ‘label’ contains the label (region) names as in the original neuroimaging

software. For example, the DKT atlas label column matches the region names from Freesurfer statistics table outputs. Yet the data in `ggseg` is in a long format - that is each region has its own row - and any data of interest needs to be in this same format. Often data sets are organized in wide format, in which subjects are represented by rows and each different data variable is represented in a separate column, and thus need to be rearranged in order to work with `ggseg`. See below an example of wide-to-long conversion.

```
freesurfer_stats <- data.frame(
  id = c(10:12),
  lh_superiortemporal = c(3.32, 4.1, 3.5),
  lh_precentral = c(2.3, 2.5, 2.1),
  lh_rostralmiddlefrontal = c(3.3, 3.2, 3.1)
)
freesurfer_stats
##   id lh_superiortemporal lh_precentral lh_rostralmiddlefrontal
## 1 10                3.32           2.3                3.3
## 2 11                4.10           2.5                3.2
## 3 12                3.50           2.1                3.1

freesurfer_long <- freesurfer_stats %>%
  gather(label, thickness, -id)
freesurfer_long
##   id          label thickness
## 1 10 lh_superiortemporal    3.32
## 2 11 lh_superiortemporal    4.10
## 3 12 lh_superiortemporal    3.50
## 4 10 lh_precentral        2.30
## 5 11 lh_precentral        2.50
## 6 12 lh_precentral        2.10
## 7 10 lh_rostralmiddlefrontal 3.30
## 8 11 lh_rostralmiddlefrontal 3.20
## 9 12 lh_rostralmiddlefrontal 3.10
```

Data in long format can then be used directly with the `ggseg` function, as the `label` column corresponds in name and content with the `label` column in the atlas data of `dkd`. The data **must** include a column that has the same name and at least *some* data matching the values in the corresponding column in the atlas data. In the next example we create some data with 4 rows, and an ‘area’ and ‘p’ column, representing the results of a hypothetical analysis. The `ggseg` function will recognise the matching column ‘area’, and merge the supplied data into the atlas using `dplyr` joins. We use the `p` column as the column flooding the segment with colour. The appearance of the plot can then be modified similarly to any other `ggplot` graph using functions such as `scales`, `labs`, `themes`, etc.

```
someData = data.frame(
  area = c("transverse temporal", "insula",
           "pre central", "superior parietal"),
  p = sample(seq(0, .5, .001), 4),
  stringsAsFactors = FALSE)

# Figure 4
ggseg(.data=someData, mapping=aes(fill=p)) +
  labs(title="A nice plot title", fill="p-value") +
  scale_fill_gradient(low="firebrick", high="goldenrod")
```

If the results are only in one hemisphere, but you still want to plot both of them, make sure your `data.frame` includes the column `hemi` with either ‘right’ or ‘left’ for this to happen. In this case, data will be merged into the atlas both by ‘area’ and by ‘hemi’.

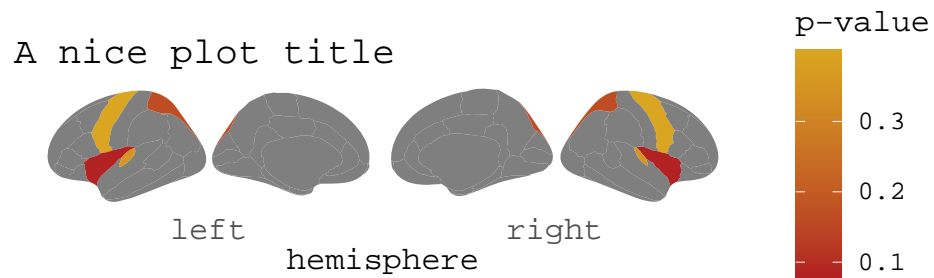


Figure 4. Supplying data through the `.data` option in `ggseg` will make it possible to use columns in the supplied data to aesthetics (such as fill) in `ggseg`. The `ggseg` object can be used with any other polygon compatible function from `ggplot` or `ggplot` extensions, like here adding title, changing the legend name and the colour scheme with standard `ggplot2` functions.

2.1.2 Creating subplots

There is often the need to plot a statistic of interest in different groups (e.g. thickness or brain - cognition relationships in young or older adults). This may be obtained also with `ggseg`, using `ggplot`'s `facet_wrap` or `facet_grid`, using two guiding rules: **1)** as before, data needs to be in long format (group data should appear in separate rows, not in separate columns). **2)** The data needs to be grouped using `dplyr`'s `group_by` function *before* providing the data to the `ggseg` function. The `ggseg` function will detect grouped data, and adapt it to `facet`'s requirements.

```
someData = data.frame(
  area = rep(c("transverse temporal", "insula",
              "pre central", "superior parietal"), 2),
  p = sample(seq(0, .5, .001), 8),
  AgeG = c(rep("Young", 4), rep("Old", 4)),
  stringsAsFactors = FALSE) %>%
  group_by(AgeG)

# Figure 5
ggseg(.data=someData, colour="white", position = "stacked",
      mapping=aes(fill=p)) +
  facet_wrap(~AgeG, ncol=2) +
  theme(legend.position = "bottom")
```

All the concepts described above also work with the 'aseg' atlas for subcortical structures, with the exception of 'hemisphere' and 'view' arguments that are superfluous in subcortical atlases such as `aseg`. Again, inspecting the atlas data directly will be of aid when preparing data to use with the atlas. Note the equivalent structures between 'aseg' and the 'dkt' atlases.

```
head(aseg, 5)
## # A tibble: 5 x 6
##   atlas area          hemi side label          ggseg
##   <chr> <chr>          <chr> <chr> <fct>          <list>
## 1 aseg <NA>          right axial <NA>          <tibble [808 x 5]>
## 2 aseg <NA>          left  axial <NA>          <tibble [1,014 x 5]>
## 3 aseg thalamus proper left  axial Left-Thalamus-Proper <tibble [56 x 5]>
## 4 aseg thalamus proper right axial Right-Thalamus-Prop~ <tibble [61 x 5]>
## 5 aseg lateral ventric~ right axial Right-Lateral-Ventr~ <tibble [66 x 5]>
```

```
# Figure 6
ggseg(atlas="aseg", mapping=aes(fill=area))
```

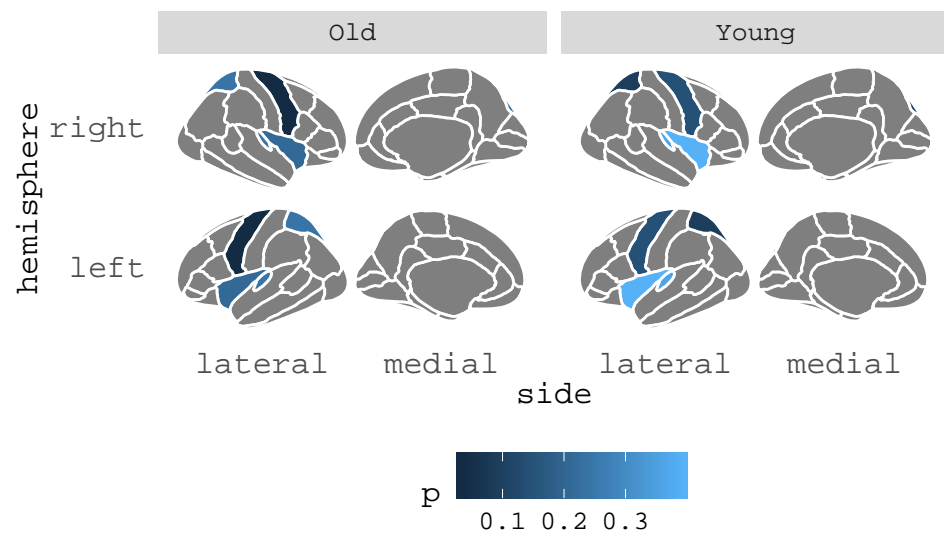


Figure 5. Data with different groups need the data to be grouped_by before providing the data to ggseg

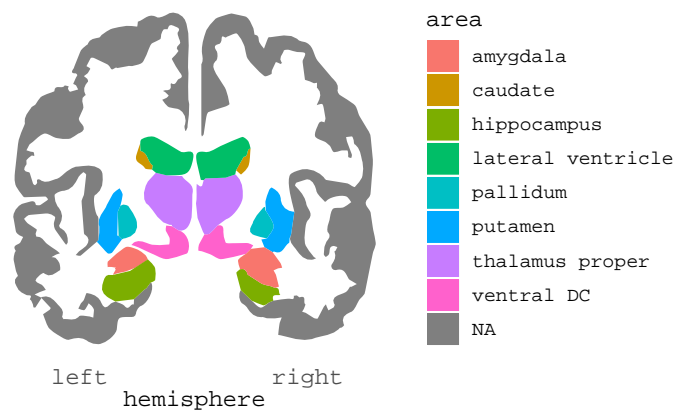


Figure 6. The first 10 rows of the 'aseg' dataset, that has some specific differences from the dkt, like missing the option to not view both hemispheres, as the plot would be hard to understand that way.

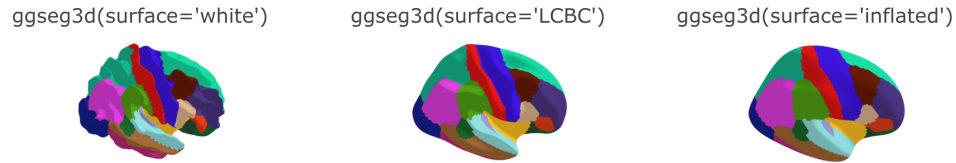


Figure 7. The three surface options provided in ggseg 3d atlases. From left: the 'white' surface is the white matter surface, 'LCBC' surface is the semi-inflated white matter surface (inflated over 10 iterations), and the 'inflated' surface is a fully inflated grey matter cortical surface.

2.2 Plotting 3D mesh data

Representing brains as 2D polygons is a good solution for fast, efficient, and flexible plotting, and can be easily combined with interactive apps such as Shiny (Chang et al. [2019]). Yet, brains are intrinsically 3-dimensional and it can be challenging to recognize the location of a region as a flattened image. This problem is exacerbated in atlases that represent subcortical features – after all, cortical surfaces are 2-dimensional – such as grey matter structures or white matter tracts. Hence, here we also provide the ggseg3d package to plot, view, and print 3D-atlases in R. ggseg3d is based on tri-surface mesh plots using plotly (Sievert [2018]). The data structure is somewhat more complex than the ggplot polygons, and includes additional options for brain inflation, glass brains, camera locations, etc. As ggseg3d is based on plotly, the resulting brain atlases are interactive, which guides interpretation, and is useful for public dissemination. We recommend users to familiarize themselves with plotly (Sievert [2018]) when using this function.

Out-of-the-box, ggseg3d() plots the dkt_3d atlas in 'LCBC' surface. The 'LCBC' surface consists on a semi-inflated white matter surface based on the *fsaverage* template subject. See *SI SCRIPT* for reproducibility. All [...]_3d atlases have a built in colour column for default colour plotting of the regions, based on the color scheme used in the neuroimaging software.

The 3D-atlas data is stored in nested tibbles. Each cortical atlas has data sets for three different surfaces (see Figure 7) and the two hemispheres. Only one surface is available for subcortical atlases as inflation procedures do not yield better representations. The 'ggseg_3d' column includes all necessary information for ggseg3d() to create a 3D mesh-plot, but that the user should not attempt to alter. The additional 3D-atlases in ggsegExtra have the same data structure. It is important to note that the coordinates in the plot (X, Y, Z) are **not** any type of radiological coordinate system, but rather Cartesian plot coordinates without further meaning.

```
# remotes::install_github("LCBC-UiO/ggseg")
library(ggseg3d)
dkt_3d
## # A tibble: 6 x 4
##   atlas surf      hemi ggseg_3d
##   <chr> <chr>    <chr> <list>
## 1 dkt_3d inflated left  <tibble [36 x 8]>
## 2 dkt_3d inflated right <tibble [36 x 8]>
## 3 dkt_3d LCBC    left  <tibble [36 x 8]>
## 4 dkt_3d LCBC    right <tibble [36 x 8]>
## 5 dkt_3d white   left  <tibble [36 x 8]>
## 6 dkt_3d white   right <tibble [36 x 8]>
```

2.2.1 External data supply

Similarly as in the 2D-atlas, the user will use ggseg3d to display through a colour scale some descriptive or inferential statistics. If the data is not already in the correct long format, or uses similar naming as the atlas, one needs to grab the data for a specific surface (and hemisphere, if desired) and then unnest (ggseg_3d) it to see what the atlas expects.

```

dkt_3d %>%
  filter(surf == "inflated" & hemi == "right") %>%
  unnest(ggseg_3d) %>%
  select(-lobe, -acronym, -roi, -annot) %>%
  head(5)
## # A tibble: 5 x 7
##   atlas surf hemi area colour mesh label
##   <chr> <chr> <chr> <chr> <chr> <list> <chr>
## 1 dkt_3d inflat~ right <NA> <NA> <named li~ rh_medialwall
## 2 dkt_3d inflat~ right banks superior ~ #196428 <named li~
rh_bankssts
## 3 dkt_3d inflat~ right caudal anterior~ #7D64A0 <named li~
rh_caudalanteri~
## 4 dkt_3d inflat~ right caudal middle f~ #641900 <named li~
rh_caudalmiddle~
## 5 dkt_3d inflat~ right corpus callosum <NA> <named li~
rh_corpuscallos~

```

Note the `mesh` column, which contains lists. Each list corresponds to a region and contains 6 vectors required to create the mesh of the tri-surface plot. It should also be noted that the ‘label’, ‘annot’ and ‘area’ columns could provide matching values for your own data. Similarly to the `ggseg`-function, the ‘label’ column should match the region names used in the original neuroimaging software while ‘area’ and ‘annot’ provide alternative/secondary names. It is thus important to match your regional identifiers with those used in the atlas. A warning will be issued in case of any mismatch. The column you want to use for colour, needs to be supplied to the `colour` option, and you’ll likely want to supply it to the `text` option, as this will add another line to the plot’s hover information.

```

someData = dkt_3d %>%
  filter(surf == "inflated" &
         hemi == "right") %>%
  unnest(ggseg_3d) %>%
  select(area) %>%
  na.omit() %>%
  mutate(p = sample(seq(0,.5, length.out = 100), nrow(.)) %>%
         round(2))
# Figure 8
ggseg3d(.data = someData, atlas = dkt_3d, colour = "p", text = "p")

```

2.2.2 Colours

You can provide custom colour palettes either in hex or R-names. Colours will be evenly spaced when creating the colour-scale, and you may provide as many colours as you wish. If you want to alter the colour of NA regions, supply `na.colour`, either as HEX colour or colour name. This option only takes a single colour.

```

# Figure 9 left
ggseg3d(.data = someData, atlas = dkt_3d,
        colour = "p", text = "p",
        palette = c("#ff0000", "#00ff00", "#0000ff")) %>%
  pan_camera("lateral") %>%
  remove_axes()

# Figure 9 right
ggseg3d(.data = someData, atlas = dkt_3d,
        colour = "p", text = "p",
        na.colour = "black") %>%
  pan_camera("lateral") %>%
  remove_axes()

```

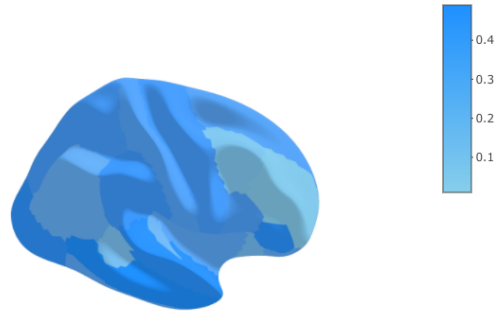


Figure 8. Supplying data so `ggseg3d` works in much the same way as for `ggseg`. Since `ggseg3d` is based on `plotly` rather than `ggplot`, much adaptation of the plots aesthetics must be done immediately in the main function. Here we set the parcellation colours with `'colour'` and accompanying mouse-hover text with `'text'`.

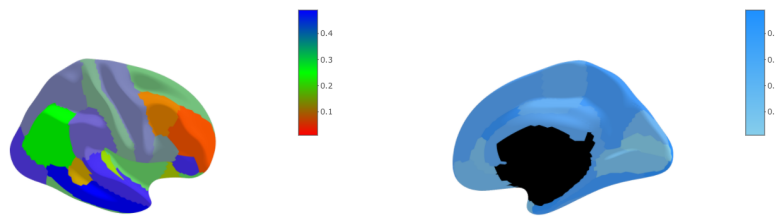


Figure 9. Left: Specifying the palette for `ggseg3d` must be done directly in the main call to the plot, rather than a separate function later like in `ggseg`. The `'palette'` option takes vectors of colours either as HEX-codes or R-colour names, but not a combination of these. Right: The colour of the `'NA'` values can also be changed through the option `'na.colour'`. Here the medial wall (which is `'NA'`), has been coloured black using this option.

2.3 Glass brain

Subcortical atlases include cortical surfaces and other landmark structures for visualization purposes only. One can control the opacity of these NA structures, to improve visualization. Additionally, one can add the `glassbrain` option, which provides a frame of reference for the subcortical structures. Glass brains can be added with the function `add_glassbrain()` which takes three extra arguments: hemisphere, colour, and opacity.

```
# Figure 10
ggseg3d(atlas = aseg_3d,
        na.alpha= .5) %>%
  add_glassbrain("left") %>%
  pan_camera("lateral") %>%
  remove_axes()
```

`ggseg3d()` is based on `plotly` and thus additional `plotly` functionalities can be used to modify and improve the 3D atlas representations. In addition to Carson Sievert's book on `plotly` in R ([2018]), we recommend resources for modifying axes in 3D plots (unknown [unknowna]), the basic introduction to tri-surface plots (unknown [unknownb]), and this tutorial on tri-surface plots with `plotly` in R (Riddihiman

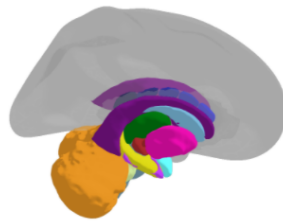


Figure 10. When visualising subcortical structures, it might be an idea to add a glassbrain to the plot. This will help with understanding structure locations in the brain and make the plot easier to interpret. The glassbrain is controlled by three options: opacity:0-1, hemisphere left, right or both, and colour.

[2016]). Finally, we recommend orca command line tool to save ggseg3d atlas snapshots.

3 DISCUSSION

The main aim of the ggseg, ggseg3d, and ggsegExtra packages is to ease and streamline visualization of brain atlas data in R, by gathering a collection of atlases from several scientific sources and providing plotting functions adapted to these atlases. In this tutorial, we introduce the packages to the readers by presenting some use examples and highlighting the main functions and options that are available. As a visualization tool, this package adds up to manifold functionalities such as ggBrain (Fisher [2019]) and ggneuro (Muschelli [2017]) in R, and software-specific image viewers such as FSLeves (McCarthy [2019]) and Freeview (Dale et al. [1999]). In this regard, we do not aim to compete with software-specific visualizations or advocate for the superiority of the ggseg-packages as visualization tools. After all, flattened 2D polygons do not rely on a meaningful brain coordinate system and the units of information in 3D meshes are limited to the number of parcellations. On the contrary, we believe the ggseg niche among visualization tools resides in its simplicity and its ability to be combined with statistical analysis pipelines. The possibility to serve as an interactive tool for dissemination and reproducibility when combined with other technologies, such as Binder (et al. [2018]) or Shiny (Chang et al. [2019]), is an added benefit. An example of this is in the online supplementary information of Vidal-Piñero et al. ([2019]).

The ggseg, ggseg3d, and ggsegExtra packages contain three main features: **1)** a collection of 2D-polygon and 3D mesh brain parcellation atlases. The atlas data are necessary to create the coordinate system for the brain atlas plotting, but are made in such a way to make it easy to use for ones own purposes. **2)** ggseg() and ggseg3d() functions for visualization. ggseg() is a wrapper function for geom_polygon from ggplot2 and it can be built upon like any ggplot object. ggseg3d() is a plotly wrapper function for tri-surface mesh plots which prints 3D atlases. Both functions are flexible and well-adapted to their environment and can be combined with any additional argument from ggplot and plotly, respectively. **3)** Complimentary features – e.g. color scales - and functions such as as_ggseg_atlas() and as_ggseg3d_atlas() to convert data in the correct atlas format. These function should provide users with the possibility of adapting their plots to their wishes, and also to make it possible to create and contribute to the atlas repository in ggsegExtra.

The foundations of the ggseg-packages trace back to the necessity of visualizing and exploring the lifespan trajectories of cortical thickness across different brain regions (see supporting information in Vidal-Piñero et al. ([2019])). That is, ggseg appears with the need to inspect and display brain information over time - that is, including a spatial dimension and a time-varying factor - overcoming the constrains of printed journals and classical 2D plots (e.g. bar plots). The current state of science requires researches to share the results of studies in both high detail and in an intuitive manner, as it permits communication

to wide audiences and facilitates reproducibility. Hence, we believe this tool conforms to the essence of open science and invite users to improve the code, provide examples, or tutorials, and contribute to the atlas collection according to their own interest and needs via the public ggseg GitHub repository, ggseg3d GitHub repository, and ggsegExtra GitHub repository.

Finally - while the ggseg-packages are circumscribed to brain parcellations - we believe that the structure and functions of the package can be easily applied to any scientific field that benefits from data being displayed across the spatial dimension. We encourage readers to borrow the package functionalities and adapt it to their respective fields and structures of interest, such as has already been done with the gganatogram-package (Maag [2018]).

4 PLANNED PACKAGE IMPROVEMENTS

In the package github wiki, we offer a pipeline to create and supply atlases for 2D plotting. However, the current way to do this is convoluted and difficult, and we are putting efforts into improving the way atlases can be made more easily. The aim is to create a set of functions that will call specialized tools like FSL(Woolrich et al. [2009]), Freesurfer(Fischl et al. [1999], Dale et al. [1999], Fischl and Dale [2000]) and Imagemagick(Ooms [2019]) to detect the polygon vectors or the mesh segments given an MRI image containing a parcellation specification, and organize these into valid ggseg atlases. We encourage users to contribute to the ggsegExtra brain atlas repository by including additional brain atlases.

5 CONCLUSION

Visualization is a fundamental aspect of neuroimaging to explore and understand data, guide interpretation and, communicate with colleagues and general audience. In this tutorial, we have introduced the ggseg-package, a tool for visualizing brain statistics through brain parcellation atlases in R. This visualization tool easily combines with interactive routines as well as with diverse statistical analysis pipelines. We hope this tool and tutorial proves useful to neuroscientists and inspires others to apply the functions in a wide variety of fields and structures.

6 AUTHOR CONTRIBUTIONS

Didac Vidal-Piñeiro generated the idea for the tool, and the initial scripts that made the plots. He has also been responsible for converting images from neuroimaging software into the type of data necessary for plotting polygons and mesh plots in R. Athanasia M. Mowinckel adapted the initial scripts and made the functions into package format and has continued developing the functions with the aim of increasing user-friendliness. She is also responsible for conceiving and adding the mesh-plot functionality through plotly, and developing the pipeline for making that possible. A. M. Mowinckel wrote the first draft of the paper, and both have since critically edited it.

7 CONFLICTS OF INTEREST

The authors declare that there were no conflicts of interest with respect to the authorship or the publication of this article.

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10 PRIOR VERSIONS

Some of the content presented here also appears in the package vignette of `ggseg` and `ggseg3d`, which may be accessed through R or in the package websites (Mowinckel and Piñeiro [2019a], Mowinckel and Piñeiro [2019b]). Athanasia Monika Mowinckel also has several tutorials on her blog regarding `ggseg` creation and functionality (Mowinckel [2018a], Mowinckel [2018b]).

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