

Package ‘ggsegExtra’

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Title Extra Utilities for the 'ggseg' and 'ggseg3d' Plotting Tools

Version 1.6.0

Description Contains functions to create new data sets compatible with the 'ggseg' and 'ggseg3d' packages for plotting brain segmentations through R. Requires several external software to be installed on the system for atlas creations to work, and most of these are not available for windows. But atlas creation tools exist for 2d simple features data, and also 3d tri-surface mesh plots. Also has a list of compatible data sets and functions for easy installation of these.

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URL <https://github.com/ggseg/ggsegExtra>

BugReports <https://github.com/ggseg/ggsegExtra/issues>

Depends ggseg (>= 1.6.0), ggseg3d (>= 1.6.0), R (>= 4.1.0)

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ggsegExtra-package	<i>ggsegExtra: Extra Utilities for the 'ggseg' and 'ggseg3d' Plotting Tools</i>
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Description

Contains functions to create new data sets compatible with the 'ggseg' and 'ggseg3d' packages for plotting brain segmentations through R. Requires several external software to be installed on the system for atlas creations to work, and most of these are not available for windows. But atlas creation tools exist for 2d simple features data, and also 3d tri-surface mesh plots. Also has a list of compatible data sets and functions for easy installation of these.

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See Also

Useful links:

- <https://github.com/ggseg/ggsegExtra>
- Report bugs at <https://github.com/ggseg/ggsegExtra/issues>

aparc_2_mesh

Converts annotations to atlas

Description

This function will create an atlas ready data.frame for ggseg3d to plot with plotly.

Usage

```
aparc_2_mesh(
  subject = "fsaverage5",
  hemisphere = "rh",
  surface = "inflated",
  annot = "aparc",
  subjects_dir = freesurfer::fs_subj_dir(),
  annot_dir = file.path(subjects_dir, subject, "label"),
  output_dir = tempdir(),
  cleanup = TRUE,
  verbose = TRUE
)
```

Arguments

subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with \$SUBJECTS_DIR
hemisphere	hemisphere, either "rh" or "lh"
surface	surface from subjects surf-folder
annot	base-name of annot file
subjects_dir	Freesurfer subject directory
annot_dir	path to directory with annot-files
output_dir	output directory path
cleanup	logical to toggle removal of all intermediary files
verbose	logical indicating to be verbose or not

Details

Based on A. Winkler scripts

Value

data frame with one row per label

Examples

```
## Not run:
dt <- apar_2_mesh()
dt <- apar_2_mesh(surface = "white")
dt <- apar_2_mesh(hemisphere = "lh")
dt <- apar_2_mesh(annot = "apar.a2009s")

## End(Not run)
```

atlas_lab2ctab	<i>Label to ctab</i>
----------------	----------------------

Description

Create a FreeSurfer colortab based on labels. Calls FreeSurfer's mris_lab2ctab

Usage

```
atlas_lab2ctab(output_dir, verbose)
```

Arguments

- output_dir output directory path
- verbose logical indicating to be verbose or not

Value

returns nothing, creates files on the file system

atlas_vol2label	<i>Volume to label</i>
-----------------	------------------------

Description

Turn volumetric files into labels for use in annotations. Calls FreeSurfer's mri_vol2label.

Usage

```
atlas_vol2label(annot_lab, output_dir, verbose)
```

Arguments

annot_lab	annotation label
output_dir	output directory path
verbose	logical indicating to be verbose or not

Value

invisibly returns the list of labels.

atlas_vol2surf	<i>Nifti volume to surface</i>
----------------	--------------------------------

Description

Transform a Nifti volume to a surface file for FreeSurfer. Calls FreeSurfer's `mri_vol2surf` for the transformation.

Usage

```
atlas_vol2surf(input_file, output_dir, projfrac = 0.5)
```

Arguments

input_file	nifti volume
output_dir	output directory path
projfrac	value to freesurfer <code>mri_vol2surf -projfrac</code>

Value

nothing, creates surface files

change_meshes	<i>Change meshes to new system</i>
---------------	------------------------------------

Description

Change meshes to new system

Usage

```
change_meshes(mesh)
```

Arguments

mesh	mesh object
------	-------------

check_fs	<i>Check if FS can be run</i>
----------	-------------------------------

Description

Check if FS can be run

Usage

```
check_fs(msg = NULL, abort = FALSE)
```

Arguments

msg	message to print on error
abort	logical. If function should error if Freesurfer is not installed. Defaults to FALSE.

Value

logical

curv2ply	<i>Convert Freesurfer curvature file to ply</i>
----------	---

Description

Function to convert Freesurfer curvature file into .ply

Usage

```
curv2ply(input_file, output_file = paste(input_file, ".ply"), verbose = TRUE)
```

Arguments

input_file	path to Freesurfer curvature file
output_file	path to output file
verbose	logical indicating to be verbose or not

Value

.ply text

fs_curvatures	<i>Available Freesurfer curvatures</i>
---------------	--

Description

Available Freesurfer curvatures

Usage

```
fs_curvatures()
```

Value

character

Examples

```
fs_curvatures()
```

fs_nofixcurv	<i>Available Freesurfer no fix curvatures</i>
--------------	---

Description

Available Freesurfer no fix curvatures

Usage

```
fs_nofixcurv()
```

Value

character

Examples

```
fs_nofixcurv()
```

fs_surfaces	<i>Available Freesurfer surfaces</i>
-------------	--------------------------------------

Description

Available Freesurfer surfaces

Usage

```
fs_surfaces()
```

Value

character

Examples

```
fs_surfaces()
```

get_mesh	<i>Extract mesh data from ply</i>
----------	-----------------------------------

Description

.ply files contain a lot of information. for ggseg3d, we only need information on the vertices and faces of the mesh. This function opens a ply file, and organises the meshes and faces into a single list.

Usage

```
get_mesh(ply, ...)
```

Arguments

ply	path to ply-file
...	arguments to <code>geomorph::read.ply()</code>

Value

list of meshes and faces

Examples

```
## Not run:
get_mesh("path/to/surface.ply")

# Turn off showing the ply when reading
get_mesh("path/to/surface.ply", ShowSpecimen = FALSE)

## End(Not run)
```

ggseg_atlas_repos	<i>List all online repositories with ggseg-atlases</i>
-------------------	--

Description

Function to easily find all online repositories that contain ggseg atlases

Usage

```
ggseg_atlas_repos(pattern = NULL, ...)
```

Arguments

pattern	string pattern to search repos
...	additional arguments to <code>base::grep()</code>

Value

data frame of online repositories with ggseg-atlases

Examples

```
## Not run:
ggseg_atlas_repos()

ggseg_atlas_repos("yeo")

## End(Not run)
```

install_ggseg_atlas	<i>Install ggseg-atlas from repo</i>
---------------------	--------------------------------------

Description

installs ggseg-atlas library from the ggseg r-universe <https://ggseg.r-universe.dev/ui#builds>.

Usage

```
install_ggseg_atlas(
  package,
  repos = c(ggseg = "https://ggseg.r-universe.dev", getOption("repos")),
  ...
)
```

Arguments

package	package name
repos	vector of repositories to install from. Defaults to ggseg r-universe and CRAN.
...	additional arguments to <code>install.packages</code> .

Details

To install, will temporarily alter your install repo settings to also use the ggseg r-universe build as source for packages. These settings will be restored when the function exits.

Examples

```
## Not run:
ggseg_atlas_repos("yeo")
install_ggseg_atlas("ggsegYeo2011")

## End(Not run)
```

```
install_ggseg_atlas_all
```

Install all registered ggseg-atlases

Description

Calls [ggseg_atlas_repos\(\)](#), and installs all libraries listed. Be careful calling this function, this will likely take quite some time to complete, and also will contain a lot of heavy data. We recommend only installing atlases you are likely to use and on demand.

Usage

```
install_ggseg_atlas_all(
  repos = c(ggseg = "https://ggseg.r-universe.dev", getOption("repos")),
  ...
)
```

Arguments

repos	repositories to install from. Defaults to ggseg r-universe and a CRAN mirror.
...	additional arguments to <code>install.packages</code> .

Examples

```
## Not run:
install_ggseg_atlas_all()

## End(Not run)
```

is_ctab	<i>Check if object is colourtable</i>
---------	---------------------------------------

Description

Check if object is colourtable

Usage

```
is_ctab(colourtable)
```

Arguments

colourtable data frame with colour table

Value

logical

lcbc_surf2surf	<i>Convert LCBC surface file to other subjects</i>
----------------	--

Description

Convert LCBC surface file to other subjects

Usage

```
lcbc_surf2surf(
  input_volume,
  source_subject = "fsaverage",
  target_subject = "fsaverage5",
  hemisphere = "rh",
  subjects_dir = fs_subj_dir(),
  output_dir = file.path(subjects_dir, target_subject, "surf"),
  cortex = TRUE,
  verbose = TRUE
)
```

Arguments

input_volume	path to input volume
source_subject	source subject
target_subject	target subject
hemisphere	hemisphere, either "rh" or "lh"
subjects_dir	Freesurfer subject directory
output_dir	output directory path
cortex	toggle "--cortex" (TRUE) or "--no-cortex" (FALSE)
verbose	logical indicating to be verbose or not

make_aparc_2_3datlas *Create cortical ggseg3d-atlas from annot-file*

Description

Function loops through hemispheres and surfaces to create a data frame that is ready to use with ggseg3d.

Usage

```
make_aparc_2_3datlas(
  annot,
  subject = "fsaverage5",
  hemisphere = c("rh", "lh"),
  surface = c("inflated", "LCBC"),
  subjects_dir = freesurfer::fs_subj_dir(),
  annot_dir = file.path(subjects_dir, subject, "label"),
  output_dir = tempdir(),
  cleanup = TRUE,
  verbose = TRUE
)
```

Arguments

annot	annotation file, with name without the hemisphere information or the .annot extension, and be in annot_dir
subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with \$SUBJECTS_DIR
hemisphere	hemisphere, either "rh" or "lh"
surface	Freesurfer surface
subjects_dir	Freesurfer subject directory
annot_dir	path to directory with annot-files
output_dir	output directory path
cleanup	logical to toggle removal of all intermediary files
verbose	logical indicating to be verbose or not

Details

It is recommended that you change the region names for the atlas, and the atlas name to something shorter. See the dk_3d atlas for examples.

Value

nested data frame as ggseg3d-atlas

Examples

```
## Not run:
dt <- aparc_2_3datlas(annot = "aparc.a2009s")
dt <- aparc_2_3datlas(annot = "aparc.a2009s",
                      surface = "sphere")

## End(Not run)
```

make_ggseg3d_2_ggseg *Turn ggseg3d-atlas to ggseg*

Description

Function will create a data.frame based on a ggseg3d atlas, based on the contours of each segment.

Usage

```
make_ggseg3d_2_ggseg(
  ggseg3d_atlas,
  steps = 1:7,
  output_dir = tempdir(),
  view = c("medial", "lateral"),
  tolerance = 0,
  smoothness = 5,
  cleanup = FALSE
)
```

Arguments

ggseg3d_atlas	object of class ggseg3d-atlas
steps	numeric vector of steps to run
output_dir	output directory path
view	which sides of the brain to be snapshotted
tolerance	tolerance during vertex reduction st_simplify
smoothness	smoothing factor, argument to smooth
cleanup	logical to toggle removal of all intermediary files

Value

data.frame ready for manual cleaning before turning into a proper ggseg3d-atlas

Examples

```
## Not run:

# Create the DKT atlas as found in the FreeSurfer Subjects directory
# And output the temporary files to the Desktop.
dkt_3d <- make_aparc_2_3datlas(annot = "aparc.DKTatlas",
                              output_dir = "~/Desktop/")

## End(Not run)
```

make_palette_ggseg	<i>Create ggseg palette from ggseg3d-atlas</i>
--------------------	--

Description

atlases in ggseg have palettes based on colours from the paper originally introducing the atlas. These colours are hard-coded into ggseg3d-atlases. This function extracts those and makes a object ready for incorporation to a ggseg-atlas repository

Usage

```
make_palette_ggseg(ggseg3d_atlas)
```

Arguments

```
ggseg3d_atlas  ggseg3d-atlas
```

Value

list with a colour palette

Examples

```
make_palette_ggseg(dk_3d)
```

make_volumetric_2_3datlas	<i>Volumetric segmentation to 3d-atlas</i>
---------------------------	--

Description

Function to create a ggseg3d-atlas from a volumetric parcellation. Currently only tested using .mgz extension images. Will call command-line tools to complete the process.

Usage

```
make_volumetric_2_3datlas(
  template,
  color_lut = NULL,
  subject = "fsaverage5",
  subjects_dir = freesurfer::fs_subj_dir(),
  steps = 1:5,
  output_dir = tempdir(),
  verbose = TRUE,
  cleanup = TRUE
)
```

Arguments

template	template volume.mgz file path
color_lut	Freesurfer colour look-up-table. Either as a path or a data.frame that <code>is_ctab()</code>
subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with <code>\$SUBJECTS_DIR</code>
subjects_dir	Freesurfer subject directory
steps	if cleanup is disabled, all files are saved, and steps can be re-run individually
output_dir	output directory path
verbose	logical indicating to be verbose or not
cleanup	logical to toggle removal of all intermediary files

Value

returns a ggseg3d-atlas ready object. Might need manual cleaning to become a good atlas.

Examples

```
## Not run:

fs_subject_dir <- freesurfer::fs_dir()
aseg_temp <- file.path(fs_subject_dir, "fsaverage5/mri/aseg.mgz")
colorlut <- file.path(fs_subject_dir, "ASegStatsLUT.txt")

make_volumetric_2_3datlas(aseg_temp, colorlut)

## End(Not run)
```

make_volumetric_ggseg *Make ggseg atlas from volumetric template*

Description

If making an atlas from a non-cortical atlas, volumetric atlases are the best options. Instead of snapshotting images of inflated brain, will snapshot brain slices given x, y, z coordinates for the slices through the slices argument.

Usage

```
make_volumetric_ggseg(
  label_file,
  subject = "fsaverage5",
  subjects_dir = fs_subj_dir(),
  output_dir = tempdir(),
  color_lut = NULL,
  steps = 1:8,
  skip_existing = TRUE,
  slices = data.frame(x = c(130, 122, 122), y = c(130, 235, 112), z = c(130, 100, 106),
    view = c("axial", "sagittal", "coronal"), stringsAsFactors = FALSE),
  vertex_size_limits = NULL,
```

```

    dilate = NULL,
    tolerance = 0,
    smoothness = 5,
    verbose = TRUE,
    cleanup = FALSE
  )

```

Arguments

label_file	a volumetric image containing the labels
subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with \$SUBJECTS_DIR
subjects_dir	Freesurfer subject directory
output_dir	output directory path
color_lut	a file containing color information for the labels
steps	numeric vector of steps to run
skip_existing	logical. If slice snapshots already exist, should these be skipped.
slices	a data.frame with columns x, y, z, and view specifying coordinates and view of slice snapshots.
vertex_size_limits	numeric vector of two, setting the minimum and maximum vector size of polygons. Defaults to NULL, which sets no limits.
dilate	numeric. Dilation factor for polygons. Default NULL applies no dilation.
tolerance	tolerance during vertex reduction st_simplify
smoothness	smoothing factor, argument to smooth
verbose	logical indicating to be verbose or not
cleanup	logical to toggle removal of all intermediary files

Value

brain-atlas class

Examples

```

## Not run:

label_file <- file.path(fs_subj_dir(), subject, "mri/aseg.mgz")
slices = data.frame(x=130, y=130, z=130, view="axial", stringsAsFactors = FALSE)

aseg2 <- make_volumetric_ggseg(
  label_file = label_file,
  slices = slices
)

# Have a look at the atlas
plot(aseg2)

## End(Not run)

```

mri_annotation2label *Convert annotation to label*

Description

Calls FreeSurfer's mri_annotation2label to split an annotation file into several labels.

Usage

```
mri_annotation2label(
  annot_name,
  subject = "fsaverage5",
  hemisphere = "rh",
  output_dir = fs_subj_dir(),
  verbose = TRUE,
  opts = NULL
)
```

Arguments

annot_name	annotation name. File should exist in subjects label directory
subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with \$SUBJECTS_DIR
hemisphere	hemisphere, either "rh" or "lh"
output_dir	output directory path
verbose	logical indicating to be verbose or not
opts	other arguments to freesurfer command

Value

nothing. Runs command line to write label files

Examples

```
# for freesurfer help see:
freesurfer::fs_help("mri_annotation2label")
mri_annotation2label(annot_name = "aparc")

mri_annotation2label(annot_name = "aparc.a2009s")

mri_annotation2label(subject = "fsaverage", annot_name = "aparc.a2009s")
```

mri_surf2surf_rereg	<i>Re-register an annotation file</i>
---------------------	---------------------------------------

Description

Annotation files are subject specific. Most are registered for fsaverage, but we recommend using fsaverage5 for the mesh plots in ggseg3d, as these contain a decent balance in number of vertices for detailed rendering and speed.

Usage

```
mri_surf2surf_rereg(
  subject,
  annot,
  hemi = c("lh", "rh"),
  target_subject = "fsaverage5",
  output_dir = file.path(fs_subj_dir(), subject, "label"),
  verbose = TRUE
)
```

Arguments

subject	subject the original annotation file is registered to
annot	annotation file name (as found in subjects_dir)
hemi	hemisphere (one of "lh" or "rh")
target_subject	subject to re-register the annotation (default fsaverage5)
output_dir	output directory path
verbose	logical indicating to be verbose or not

Value

nothing

Examples

```
# For help see:
freesurfer::fs_help("mri_surf2surf")

mri_surf2surf_rereg(subject = "bert",
  annot = "aparc.DKTatlas",
  target_subject = "fsaverage5")
```

mri_vol2label	<i>Convert volume to label</i>
---------------	--------------------------------

Description

Converts values in a volume or surface overlay to a label. The program searches the input for values equal to labelid. The xyz values for each point are then computed based on the tkregister voxel-to-RAS matrix (volume) or from the xyz of the specified surface. The xyz values are then stored in labelfile in the label file format. The statistic value is set to 0. While this program can be used with any mri volume, it was designed to convert parcellation volumes, which happen to be stored in mri format. Calls FreeSurfer's mri_vol2label.

Usage

```
mri_vol2label(
  input_file,
  label_id,
  hemisphere = "rh",
  output_dir,
  surface = NULL,
  subject = "fsaverage5",
  subjects_dir = fs_subj_dir(),
  opts = NULL,
  verbose = TRUE
)
```

Arguments

input_file	input volume
label_id	label to run
hemisphere	hemisphere, either "rh" or "lh"
output_dir	output directory path
surface	output surface
subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with \$SUBJECTS_DIR
subjects_dir	Freesurfer subject directory
opts	other arguments to freesurfer command
verbose	logical indicating to be verbose or not

Value

returns nothing. Writes a label file.

Examples

```
# for freesurfer help see:
freesurfer::fs_help("mri_vol2label")

out_dir <- tempdir()
```

```

vol <- file.path(freesurfer::fs_subj_dir(),
                 "fsaverage5/mri/aseg.mgz")

mri_vol2label(vol,
              label_id = 2,
              hemisphere = "rh",
              output_dir = out_dir)

# delete output dir when not needed
unlink(out_dir)

```

mris_ca_label

MRI ca label

Description

For a single subject, produces an annotation file, in which each cortical surface vertex is assigned a neuroanatomical label. This automatic procedure employs data from a previously-prepared atlas file. An atlas file is created from a training set, capturing region data manually drawn by neuroanatomists combined with statistics on variability correlated to geometric information derived from the cortical model (sulcus and curvature). Besides the atlases provided with FreeSurfer, new ones can be prepared using `mris_ca_train`).

Usage

```

mris_ca_label(
  subject = "fsaverage5",
  hemisphere = "lh",
  canonsurf = "sphere.reg",
  classifier = file.path(fs_dir(), "average/lh.DKTatlas40.gcs"),
  output_file,
  subjects_dir = fs_subj_dir(),
  opts = NULL
)

```

Arguments

subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with <code>\$\$SUBJECTS_DIR</code>
hemisphere	hemisphere, either "rh" or "lh"
canonsurf	canonical surface file. Ie: the name of the spherical surface file which describes the registration of a subject's vertices to the reference "average" surface. Example: sphere.reg
classifier	specify classifier array input file (atlas file)
output_file	path to output file
subjects_dir	Freesurfer subject directory
opts	other arguments to freesurfer command

Examples

```
# for freesurfer help see:
freesurfer::fs_help("mris_ca_label")
mris_ca_label(output_file = "test.lh.annot")

mris_ca_label(hemisphere = "rh", output_file = "test.rh.annot")
```

mris_label2annot	<i>Convert Label to Annotation</i>
------------------	------------------------------------

Description

If you have labels rather than a full annotation file, these can be combined with FreeSurfer's `mris_label2annot`.

Usage

```
mris_label2annot(
  labels,
  hemisphere = "rh",
  ctab,
  subject = "fsaverage5",
  subjects_dir = fs_subj_dir(),
  output_dir = subjects_dir,
  opts = NULL,
  verbose = TRUE
)
```

Arguments

labels	label file path vector
hemisphere	hemisphere, either "rh" or "lh"
ctab	colourtable file
subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with <code>\$SUBJECTS_DIR</code>
subjects_dir	Freesurfer subject directory
output_dir	output directory path
opts	other arguments to freesurfer command
verbose	logical indicating to be verbose or not

Examples

```
## Not run:
# for freesurfer help see:
freesurfer::fs_help("mris_label2annot")

subj_dir <- freesurfer::fs_subj_dir()
# Split up aparc annot into labels
mri_annotation2label(annot_name = "aparc")
```

```

# get annot for colour labels
annot <- freesurfer::read_annotation(
  file.path(subj_dir,
    "fsaverage5/label/rh.aparc.annot"))

labels <- list.files(
  file.path(subj_dir, "fsaverage5/label/aparc"),
  full.names = TRUE)

# Write colortable to file
ctab_file <- tempfile(fileext = ".ctab")
write_ctab(annot$colortable, ctab_file)

# Combine labels back into annotation
mris_label2annot(labels, hemisphere = "rh", ctab = ctab_file)

## End(Not run)

```

read_ctab	<i>Read colourtat</i>
-----------	-----------------------

Description

Read in a FreeSurfer colortab file.

Usage

```
read_ctab(path)
```

Arguments

path	path to read from
------	-------------------

Value

a data.frame with index, label name and RGBA colours

restruct_old_3datlas	<i>Change old atlas setup to new</i>
----------------------	--------------------------------------

Description

Change old atlas setup to new

Usage

```
restruct_old_3datlas(atlas_data)
```

Arguments

atlas_data	ggseg3d-atlas object
------------	----------------------

smooth2srf	<i>Turn smooth file to ascii</i>
------------	----------------------------------

Description

Turn smooth file to ascii

Usage

```
smooth2srf(input_file, output_file, verbose)
```

Arguments

input_file	input file path
output_file	path to output file
verbose	logical indicating to be verbose or not

subject_2_ascii	<i>Convert subject surface files to ascii</i>
-----------------	---

Description

This function goes through all specified subject, per hemisphere, surface, curvature and no fix curvature specified and turns them into ascii files.

Usage

```
subject_2_ascii(
  subject = "fsaverage5",
  hemisphere = c("rh", "lh"),
  surfaces = fs_surfaces(),
  curvatures = fs_curvatures(),
  nofix_curv = fs_nofixcurv(),
  subjects_dir = freesurfer::fs_subj_dir(),
  output_dir = subjects_dir,
  verbose = TRUE
)
```

Arguments

subject	Freesurfer subject, must exist in whatever subject directory specified or set in the environment with \$SUBJECTS_DIR
hemisphere	hemisphere, either "rh" or "lh"
surfaces	string vector of surfaces
curvatures	string vector of curvatures
nofix_curv	string vector of nofix curvatures
subjects_dir	Freesurfer subject directory
output_dir	output directory path
verbose	logical indicating to be verbose or not

Value

no return. Writes files.

Examples

```
## Not run:
subject_2_ascii()
subject_2_ascii("fsaverage")
subject_2_ascii("bert")

## End(Not run)
```

surf2ply

Convert Freesurfer surface file into ply

Description

Function to convert Freesurfer surface file into .ply

Usage

```
surf2ply(input_file, output_file = paste(input_file, ".ply"), verbose = TRUE)
```

Arguments

input_file	path to Freesurfer surface file
output_file	path to output file
verbose	logical indicating to be verbose or not

Value

ply text

surfsplit

Split surface file into separate plys

Description

Function to split up a surface ply into several ply's based on a freesurfer label file.

Usage

```
surfsplit(
  srf_ply,
  label_path,
  prefix = "test",
  output_dir = dirname(label_path),
  verbose = TRUE
)
```


Arguments

srf_ply	Surface ply path
label_path	label dpv file
prefix	output prefix
output_dir	output directory path
verbose	logical indicating to be verbose or not

Details

Script adapted to R and ggseg based on scripts from Anderson M. Winkler: <http://brainder.org>

Value

list of ply meshes. Will also write ply meshes to files.

write_ctab	<i>Write colourtab</i>
------------	------------------------

Description

write a colortab to file, will be in a format that is accessible by FreeSurfer.

Usage

```
write_ctab(x, path)
```

Arguments

x	colourtab data
path	path to write to

Value

returns nothing, writes file

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