Package: threeBrain (via r-universe)

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Type Package

Title Your Advanced 3D Brain Visualization

Version 1.2.0.9000

Description A fast, interactive cross-platform, and easy to share 'WebGL'-based 3D brain viewer that visualizes 'FreeSurfer' and/or 'AFNI/SUMA' surfaces. The viewer widget can be either standalone or embedded into 'R-shiny' applications. The standalone version only require a web browser with 'WebGL2' support (for example, 'Chrome', 'Firefox', 'Safari'), and can be inserted into any websites. The 'R-shiny' support allows the 3D viewer to be dynamically generated from reactive user inputs. Please check the publication by Wang, Magnotti, Zhang, and Beauchamp (2023, <doi:10.1523/ENEURO.0328-23.2023>) for electrode localization. This viewer has been fully adopted by 'RAVE' <https://openwetware.org/wiki/RAVE>, an interactive toolbox to analyze 'iEEG' data by Magnotti, Wang, and Beauchamp (2020, <doi:10.1016/j.neuroimage.2020.117341>). Please check 'citation(``threeBrain'')' for details.

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URL https://dipterix.org/threeBrain/, https://github.com/dipterix/threeBrain

BugReports https://github.com/dipterix/threeBrain/issues

Imports utils, grDevices, graphics, dipsaus, xml2, servr, png, knitr, shiny (>= 1.2.0), digest (>= 0.6.22), freesurferformats (>= 0.1.7), jsonlite (>= 1.5), stringr (>= 1.3.1), htmlwidgets (>= 1.3), R6 (>= 2.3.0), gifti (>= 0.7.5), oro.nifti (>= 0.9.1)

Suggests rmarkdown, DT, ravetools, htmltools

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Repository https://rave-ieeg.r-universe.dev

RemoteUrl https://github.com/dipterix/threeBrain

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`AbstractGeom` *R6 Class - Abstract Class of Geometries*

Description

R6 Class - Abstract Class of Geometries

Author(s)

Zhengjia Wang

`BlankGeom` *A geometry that renders nothing*

Description

This is mainly used when you want to upload group data only

brain_proxy *Shiny Proxy for Viewer*

Description

Shiny Proxy for Viewer

Usage

```
brain_proxy(outputId, session = shiny::getDefaultReactiveDomain())
```

Arguments

outputId	shiny output ID
session	shiny session, default is current session (see domains)

Value

R6 class ViewerProxy

brain_setup *Setup Package, Install Environment*

Description

Setup Package, Install Environment

Usage

```
brain_setup(continued = FALSE, show_example = TRUE, ...)
```

Arguments

continued	logical, there are two phases of setting up environment. You probably need to restart R session after the first phase and continue setting up.
show_example	whether to show example of 'N27' subject at the end.
...	ignored

Author(s)

Zhengjia Wang

calculate_rotation *Calculate rotation matrix from non-zero vectors*

Description

Calculate rotation matrix from non-zero vectors

Usage

```
calculate_rotation(vec_from, vec_to)
```

Arguments

vec_from	original vector, length of 3
vec_to	vector after rotation, length of 3

Value

A four-by-four transform matrix

check_freesurfer_path *Function to check whether 'FreeSurfer' folder has everything we need*

Description

Function to check whether 'FreeSurfer' folder has everything we need

Usage

```
check_freesurfer_path(
  fs_subject_folder,
  autoinstall_template = FALSE,
  return_path = FALSE,
  check_volume = FALSE,
  check_surface = FALSE
)
```

Arguments

fs_subject_folder	character, path to 'fs' project directory or 'RAVE' subject directory
autoinstall_template	logical, whether 'N27' brain should be installed if missing
return_path	logical, whether to return 'FreeSurfer' path
check_volume	logical, whether to check volume data
check_surface	logical, whether to check surface data (not implemented yet)

Value

logical whether the directory is valid or, if `return_path` is true, return ‘FreeSurfer‘ path

---

`conform_volume` *Conform imaging data in* `'FreeSurfer'` *way*

Description

Reproduces conform algorithm used by `'FreeSurfer'` to conform `'NIfTI'` and `'MGH'` images.

Usage

```
conform_volume(x, save_to, dim = c(256, 256, 256))
```

Arguments

`x`	path to the image file
`save_to`	path where the conformed image will be saved, must ends with `'.mgz'`
`dim`	positive integers of length three, the conformed dimension; by default 'FreeSurfer' conform images to `1mm` volume cube with `256x256x256` dimension

Value

Nothing; the result will be save to `save_to`

`create_group` *Create a geometry group containing multiple geometries*

Description

Create a geometry group containing multiple geometries

Usage

```
create_group(name, position = c(0, 0, 0), layer = 1)
```

Arguments

`name`	string, name of the geometry
`position`	x,y,z location of the group
`layer`	layer of the group. reserved

Details

A geometry group is a container of multiple geometries. The geometries within the same group share the same shift and rotations (see example 1). In ECoG/iEEG world, you might have 'MRI', 'CT', 'FreeSurfer' that have different orientations. For example, if you want to align MRI to FreeSurfer, Instead of calculating the position of each geometries, you can just put all MRI components into a group, and then set transform of this group, making the group aligned to FreeSurfer.

GeomGroup also can be used to store large data. To generate 3D viewer, 'threeBrain' needs to dynamically serialize data into JSON format, which can be read by browsers. However, a FreeSurfer brain might be ~30 MB. This is a very large size and might take ~5 seconds to serialize. To solve this problem, GeomGroup supports cache in its 'set_group_data' method. This method supports caching static serialized data into a JSON file, and allows the files to be loaded as static data objects. By "static", I mean the data is not supposed to be dynamic, and it should be "read-only". In JavaScript code, I also optimized such that you don't need to load these large datasets repeatedly. And this allows you to load multiple subjects' brain in a short time.

Value

a GeomGroup instance

Author(s)

Zhengjia Wang

Examples

```
# Example 1: relative position

# create group
g = create_group('Group A')

# create two spheres at 10,0,0, but s2 is relative to group A
s1 = geom_sphere('Sphere 1', radius = 2, position = c(10,0,0))
s2 = geom_sphere('Sphere 2', radius = 2, position = c(10,0,0), group = g)

# set transform (rotation)
g$set_transform(matrix(c(
  0,1,0,0,
  1,0,0,0,
  0,0,1,0,
  0,0,0,1
), byrow = TRUE, ncol = 4))

# global position for s2 is 0,10,0
if( interactive() ) { threejs_brain(s1, s2) }

# Example 2: cache

## Not run:

# download N27 brain
```

```
# Make sure you have N27 brain downloaded to `default_template_directory()`
# download_N27()

template_dir <- default_template_directory()

dat = freesurferformats::read.fs.surface(
  file.path(template_dir, 'N27/surf/lh.pial')
)
vertex = dat$vertices[,1:3]
face = dat$faces[,1:3]

# 1. dynamically serialize
mesh = geom_freemesh('lh', vertex = vertex, face = face, layer = 1)

# 2. cache
# Create group, all geometries in this group are relatively positioned
tmp_file = tempfile()
mesh = geom_freemesh('Left Hemisphere cached', vertex = vertex,
                     face = face, cache_file = tmp_file)


## End(Not run)
```

`cross_prod` *Calculate cross-product of two vectors in '3D'*

Description

Calculate cross-product of two vectors in '3D'

Usage

```
cross_prod(x, y)
```

Arguments

x, y	3-dimensional vectors

Value

A '3D' vector that is the cross-product of `x` and `y`

DataCubeGeom *R6 Class - Generate Data Cube Geometry*

Description

R6 Class - Generate Data Cube Geometry

Author(s)

Zhengjia Wang

DataCubeGeom2 *R6 Class - Generate Data Cube Geometry via 3D Volume Texture*

Description

R6 Class - Generate Data Cube Geometry via 3D Volume Texture

Author(s)

Zhengjia Wang

default_template_directory
Default Directory to Store Template Brain

Description

Default Directory to Store Template Brain

Usage

```
default_template_directory(check = FALSE)
```

Arguments

check	logical, check if the folder is missing, is so, create one. This option ensures the folder is always created.

Details

When `threeBrain.template_dir` is not set or invalid, the function checks 'RAVE' (R Analysis and Visualization for 'iEEG', https://openwetware.org/wiki/RAVE) folder at home directory. If this folder is missing, then returns results from `R_user_dir('threeBrain', 'data')`. To override the default behavior, use `options(threeBrain.template_dir=...)`.

Value

A directory path where template brain is stored at; see also download_N27

Examples

```
default_template_directory()
```

FreeGeom *R6 Class - Generate Geometry from Vertices and Face Indices*

Description

R6 Class - Generate Geometry from Vertices and Face Indices

---

freesurfer_brain *Read 'FreeSurfer' surface and volume files*

Description

Read 'FreeSurfer' surface and volume files

Usage

```
freesurfer_brain(
  fs_subject_folder,
  subject_name,
  additional_surfaces = NULL,
  aligned_ct = NULL,
  use_cache = TRUE,
  use_141 = getOption("threeBrain.use141", TRUE)
)

freesurfer_brain2(
  fs_subject_folder,
  subject_name,
  volume_types = "t1",
  surface_types = "pial",
  curvature = "sulc",
  atlas_types = c("aparc+aseg", "aparc.a2009s+aseg", "aparc.DKTatlas+aseg"),
  ct_path = NULL,
  use_cache = TRUE,
  use_141 = getOption("threeBrain.use141", TRUE),
  ...
)
```

Arguments

fs_subject_folder	character, 'FreeSurfer' subject folder, or 'RAVE' subject folder
subject_name	character, subject code to display with only letters and digits
additional_surfaces	character array, additional surface types to load, such as 'white', 'smoothwm'
aligned_ct	character, path to 'ct_aligned_mri.nii.gz', used for electrode localization
use_cache	logical, whether to use cached 'json' files or from raw 'FreeSurfer' files
use_141	logical, whether to use standard 141 brain for surface file, default is `getOption('threeBrain.use141', TRUE)`
volume_types	volume types, right now only support T1 image
surface_types	surface types to load
curvature	curvature data. Only support `"sulc"` for current version
atlas_types	atlas types to be loaded, choices are `'aparc+aseg'`, `'aparc.a2009s+aseg'`, `'aparc.DKTatlas+aseg'`, `'aseg'`
ct_path	an aligned CT file in 'Nifti' format
...	ignored

Details

This function is under FreeSurfer license. 1. Volumes: 3D viewer uses 'mri/T1.mgz' from 'FreeSurfer' to show the volume information. 'T1.mgz' results from step 1 to 5 in 'FreeSurfer' command 'recon-all -autorecon1', which aligns the original 'DICOM' image to 'RAS' coordinate system, resamples to volume with `256x256x256` voxels (tri-linear by default, check https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all for more information).

2. Surface: There are two options for surface files. The first choice is using 'std.141' brain generated by 'AFNI/SUMA'. This surface file re-calculates vertices from standard 141 space, which averages the "surface" of 141 subjects. If you want to map surface electrodes across different subjects, you might want to consider this case as it's especially designed for surface mapping. However, you'll need 'AFNI/SUMA' installed to generate the surface file. The details can be found via https://openwetware.org/wiki/Beauchamp:CorticalSurfaceHCP, and the 'AFNI/SUMA' command related is 'SurfToSurf'. Please generate the files to '[FREESURFER SUBJECT DIR]/SUMA/'. The file name follows the convention of 'std.141.[lr]h.[SURFACE TYPE].[POSTFIX]', where 'lh' means left hemisphere and 'rh' means right hemisphere; 'SURFACE TYPE' can be 'pial', 'white', 'smoothwm', and 'POSTFIX' can be 'asc', 'gii'. If multiple files for the same surface type exists, the search order will be 'asc > gii'. The other option is to use mesh files directly from 'FreeSurfer' output located at '[FREESURFER SUBJECT DIR]/surf'. If you want to use these surface, make sure they are converted to 'asc' or 'gii' format.

3. Electrode registration and transforms This package provides two ways to map electrodes to standard space. For surface electrodes, if standard 141 brain is provided, then the first option is to snap electrodes to the nearest vertices in subject space. The key is the vertex number matches across different subjects, hence the location of corresponding vertices at template brain are the mapped electrode coordinates. If standard 141 brain is missing, or the electrode type is 'stereo EEG', then the second option is volume mapping. The idea is to map electrodes to 'MNI305' brain. The

details can be found at https://surfer.nmr.mgh.harvard.edu/fswiki/CoordinateSystems. To perform volume mapping, we need 'FreeSurfer' folder 'mri/transforms'. Currently, only linear 'Talairach' transform matrix is supported (located at 'talairach.xfm').

4. Coordinates The 3D viewer in this package uses the center of volume as the origin (0, 0, 0).

Author(s)

Zhengjia Wang

Examples

```
## Not run:
# Please run `download_N27()` if `N27` is not at `default_template_directory()`

# Import from `FreeSurfer` subject folder
brain = threeBrain::freesurfer_brain(
  fs_subject_folder = file.path(default_template_directory(), 'N27'),
  subject_name = 'N27',
  additional_surfaces = c('white', 'smoothwm')
)

# Visualize. Alternatively, you can use brain$plot(...)
plot( brain )

## End(Not run)
```

---

freesurfer_lut *Query the 'FreeSurfer' labels*

Description

Query the 'FreeSurfer' labels

Usage

```
freesurfer_lut
```

Format

An object of class `list` of length 3.

Details

The 'FreeSurfer' atlases use https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/AnatomicalROI/FreeSurferColorLUT look-up table to query indexes. The 'threeBrain' electrode localization also uses this table to export the `'FSLabel'` from electrode. If volume type is set to `'aparc_aseg'`, then please also use this table to filter.

Examples

```
freesurfer_lut$from_key(0:10)

freesurfer_lut$get_key("ctx-lh-supramarginal")
```

`generate_smooth_envelope` *Generate smooth envelope around surface*

Description

Alternative to 'Matlab' version of `'pial-outer-smoothed'`, use this function along with `fill_surface`.

Usage

```
generate_smooth_envelope(
  surface_path,
  save_as = NULL,
  inflate = 3,
  verbose = TRUE,
 save_format = c("auto", "bin", "asc", "vtk", "ply", "off", "obj", "gii", "mz3", "byu")
)
```

Arguments

`surface_path`	path to `'*h.pial'` surface in the 'FreeSurfer' folder, or a 3-dimensional mesh, see `read.fs.surface`
`save_as`	save final envelope to path, or `NULL` for dry-run
`inflate`	number of `'voxels'` to inflate before fitting envelope; must be a non-negative integer
`verbose`	whether to verbose the progress; default is true
`save_format`	format of saved file when `save_as` is not `NULL`; see `format` argument in function `write.fs.surface`

Value

A 3-dimensional mesh that contains vertices and face indices, the result is also saved to `save_as` is specified.

Examples

```
if(interactive() &&
   file.exists(file.path(default_template_directory(), "N27"))) {

library(threeBrain)

fs_path <- file.path(default_template_directory(), "N27")

# lh.pial-outer-smoothed
lh_pial <- file.path(fs_path, "surf", "lh.pial")
save_as <- file.path(fs_path, "surf", "lh.pial-outer-smoothed")
generate_smooth_envelope(lh_pial, save_as)

# rh.pial-outer-smoothed
rh_pial <- file.path(fs_path, "surf", "rh.pial")
save_as <- file.path(fs_path, "surf", "rh.pial-outer-smoothed")
generate_smooth_envelope(rh_pial, save_as)

brain <- threeBrain(
  path = fs_path, subject_code = "N27",
  surface_types = 'pial-outer-smoothed'
)
brain$plot(controllers = list(
  "Surface Type" = 'pial-outer-smoothed'
))

}
```

---

generate_subcortical_surface

Approximate 'sub-cortical' surfaces from 'parcellation'

Description

Superseded by volume_to_surf. Please do not use this function.

Usage

```
generate_subcortical_surface(
  atlas,
  index,
  save_prefix = NULL,
  label = NULL,
  IJK2RAS = NULL,
  grow = 1,
  remesh = TRUE,
  smooth = TRUE,
  smooth_delta = 3,
```

```
  ...
)
```

Arguments

`atlas`	path to imaging 'parcellation', can be `'nii'` or `'mgz'` formats
`index`	'parcellation' index, see 'FreeSurfer' look-up table
`save_prefix`	parent folder to save the resulting surface
`label`	character label or name of the 'sub-cortical' structure, usually automatically derived from `index`
`IJK2RAS`	an 'Affine' matrix from 'voxel' index to `'tkrRAS'`, usually automatically derived from `atlas`
`grow`	amount to grow (dilate) before generating mesh
`remesh, smooth, smooth_delta, ...`	passed to `mesh_from_volume`

Value

A surface mesh, containing 'atlas' index, label, surface nodes and face indices.

GeomGroup *R6 Class - Generate Group of Geometries*

Description

R6 Class - Generate Group of Geometries

Author(s)

Zhengjia Wang

---

geom_freemesh *Creates any mesh geometry given vertices and face indices*

Description

Creates any mesh geometry given vertices and face indices

Usage

```
geom_freemesh(
  name,
  vertex = NULL,
  face = NULL,
  position = c(0, 0, 0),
  layer = 1,
  cache_file = NULL,
  group = NULL
)
```

Arguments

name	unique string in a scene to tell apart from different objects
vertex	position of each vertices (3 columns)
face	face indices indicating which 3 vertices to be linked (3 columns)
position	x,y,z location of the geometry
layer	visibility of the geometry, used when there are multiple cameras 1 is visible for all cameras
cache_file	cache vertex and face data into group
group	a GeomGroup object, if null, then the group will be generated automatically

Details

When generating a free mesh internally, a group must be specified, therefore if group is NULL here, then a group will be generated. However, it's always recommended to pass a group to the free mesh.

Author(s)

Zhengjia Wang

Examples

```
## Not run:
# Make sure you have N27 brain downloaded to `default_template_directory()`
# threeBrain::download_N27()

n27_dir = file.path(default_template_directory(), "N27")
surf_type = 'pial'

# Locate mesh files
lh = read_fs_asc(file.path(n27_dir, sprintf('surf/lh.%s.asc', surf_type)))
rh = read_fs_asc(file.path(n27_dir, sprintf('surf/rh.%s.asc', surf_type)))

# Create groups
group = create_group(name = sprintf('Surface - %s (N27)', surf_type))

# create mesh
```

```
lh_mesh = geom_freemesh(
  name = sprintf('FreeSurfer Left Hemisphere - %s (N27)', surf_type),
  vertex = lh$vertices[,1:3],
  face = lh$faces[,1:3],
  group = group
)
rh_mesh = geom_freemesh(
  name = sprintf('FreeSurfer Right Hemisphere - %s (N27)', surf_type),
  vertex = rh$vertices[,1:3],
  face = rh$faces[,1:3],
  group = group
)


# Render
if( interactive() ) { threejs_brain(lh_mesh, rh_mesh) }




## End(Not run)
```

---

geom_sphere *Create sphere geometry*

Description

Create sphere geometry

Usage

```
geom_sphere(
  name,
  radius,
  position = c(0, 0, 0),
  layer = 1,
  group = NULL,
  value = NULL,
  time_stamp = NULL
)
```

Arguments

name	unique string in a scene to tell apart from different objects
radius	size of sphere
position	x,y,z location of the sphere
layer	visibility of the geometry, used when there are multiple cameras 1 is visible for all cameras

group a GeomGroup object

value, time_stamp
color of the sphere, used for animation/color rendering

Author(s)

Zhengjia Wang

Examples

```
# Create a sphere with animation
g = lapply(1:10, function(ii){
  v = rep(ii, 10)
  v[1:ii] = 1:ii
 geom_sphere(paste0('s', ii), ii, value = v, position = c(11 * ii, 0,0), time_stamp = (1:10)/10)
})
if( interactive() ) { threejs_brain(.list = g) }
```

---

get_digest_header *Function to read digest header*

Description

Function to read digest header

Usage

```
get_digest_header(file, key, if_error = NULL, .list = NULL)
```

Arguments

file	file path to a 'JSON' file
key	character, key to extract
if_error	value to return if key not found or read error occurs
.list	alternative list to supply if file is missing

get_ijk2ras *Get 'voxel' to world matrix*

Description

Get 'voxel' to world matrix

Usage

```
get_ijk2ras(x, type = c("scanner", "tkr"))
```

Arguments

x	path to imaging files
type	world space type; choices are 'scanner' (same as 'sform' or 'qform' in) or 'NIfTI' file headers; or 'tkr' (used to shared surface nodes)

Value

A four by four matrix

import-fs-suma *Import 'FreeSurfer' or 'SUMA' files into the viewer structure*

Description

Import 'T1-MRI', surface files, curvature/'sulcus', atlas, and 'Talairach' transform matrix into 'json' format. These functions are not intended to be called directly, use import_from_freesurfer instead.

Usage

```
import_fs(
  subject_name,
  fs_path,
  quiet = FALSE,
  dtype = c("T1", "surface", "curv", "atlas_volume", "atlas_surface", "xform"),
  sub_type = NULL,
  hemisphere = c("l", "r"),
  ...
)

import_suma(
  subject_name,
  fs_path,
```

```
  quiet = FALSE,
  dtype = c("T1", "surface", "curv", "atlas_volume", "atlas_surface", "xform"),
  sub_type = NULL,
  hemisphere = c("l", "r"),
  ...
)
```

Arguments

subject_name	character, subject code
fs_path	path to 'FreeSurfer' folder
quiet, ...	passed from or to other methods.
dtype	data type to import, choices are 'T1', 'surface', 'curv', 'atlas_volume', 'atlas_surface', 'xform'
sub_type	detailed files to import. 'atlas_surface' is not supported for now
hemisphere	which hemisphere to import, ignored when dtype is in 'T1', 'atlas_volume', 'atlas_surface', 'xform'.

Value

logical, TRUE if the file is or has been cached, or FALSE if the file is missing.

---

import_from_freesurfer

Import from 'FreeSurfer' and create 'JSON' cache for 3D viewer

---

Description

Import from 'FreeSurfer' and create 'JSON' cache for 3D viewer

Usage

```
import_from_freesurfer(fs_path, subject_name, quiet = FALSE)
```

Arguments

fs_path	'FreeSurfer' subject directory
subject_name	subject code
quiet	whether to suppress message or not

Value

None.

LineSegmentsGeom *R6 Class - Generate Line Segments*

Description

R6 Class - Generate Line Segments

Author(s)

Zhengjia Wang

list_electrode_prototypes *List or load all electrode prototypes*

Description

List all built-in and user-customized electrode prototypes. User paths will be searched first, if multiple prototype configuration files are found for the same type.

Usage

```
list_electrode_prototypes()

load_prototype(type)
```

Arguments

type	electrode type, character

Value

`list_electrode_prototypes` returns a named list, names are the prototype types and values are the prototype configuration paths; `load_prototype` returns the prototype instance if `type` exists, or throw an error.

Examples

```
availables <- list_electrode_prototypes()
if( "sEEG-16" %in% names(availables) ) {
  proto <- load_prototype( "sEEG-16" )

  print(proto, details = FALSE)
}
```

`localization_module` *Launch a 'shiny' application to localize electrodes*

Description

If 'RAVE' has been installed, please use 'RAVE' modules. This function is purely for demonstration purposes.

Usage

```
localization_module(
  subject_code,
  fs_path,
  ct_path = NULL,
  surfaces = "pial",
  use_141 = TRUE,
  shiny_options = list(launch.browser = TRUE),
  save_path = tempfile(pattern = "electrode", fileext = ".csv"),
  ...,
  control_presets = NULL,
  side_display = FALSE,
  controllers = list()
)
```

Arguments

`subject_code`	subject code
`fs_path`	the subject's 'FreeSurfer' path
`ct_path`	the file path of 'CT' scans that have already been aligned to 'T1'; must be in 'NIFTI' format
`surfaces`	which surfaces to load
`use_141`	whether to try 'SUMA' standard 141 surface; default is true
`shiny_options`	shiny application options; see `options` in `shinyApp`
`save_path`	a temporary file where the electrode table should be cached; this file will be used to keep track of changes in case the application is crashed or shutdown
`...`	other parameters to pass into `freesurfer_brain2`
`control_presets`, `side_display`, `controllers`	passed to `threejs_brain`

Value

A list of `'ui'` elements, `'server'` function, and a stand-alone `'app'`

Examples

```
# This example require N27 template brain to be installed
# see `?download_N27` for details

# using N27 to localize
fs_path <- file.path(default_template_directory(), "N27")
if(interactive() && dir.exists(fs_path)){
  module <- localization_module("N27", fs_path)

  print(module$app)
}
```

`merge_brain` *Create Multi-subject Template*

Description

Create Multi-subject Template

Usage

```
merge_brain(
  ...,
  .list = NULL,
  template_surface_types = NULL,
  template_subject = unname(getOption("threeBrain.template_subject", "N27")),
  template_dir = default_template_directory()
)
```

Arguments

`..., .list`	`Brain2` objects
`template_surface_types`	which template surface types to load, default is auto-guess
`template_subject`	character, subject code to be treated as template, default is 'N27'
`template_dir`	the parent directory where template subject is stored in

Author(s)

Zhengjia Wang

new_electrode_prototype *Create or load new electrode prototype from existing configurations*

Description

Create or load new electrode prototype from existing configurations

Usage

```
new_electrode_prototype(base_prototype, modifier = NULL)
```

Arguments

base_prototype	base prototype, this can be a string of prototype type (see list_electrode_prototypes), path to the prototype configuration file, configuration in 'json' format, or an electrode prototype instance
modifier	internally used

Value

An electrode prototype instance

Examples

```
available_prototypes <- list_electrode_prototypes()
if("Precision33x31" %in% names(available_prototypes)) {

  # Load by type name
  new_electrode_prototype("Precision33x31")

  # load by path
  path <- available_prototypes[["Precision33x31"]]
  new_electrode_prototype(path)

  # load by json string
  json <- readLines(path)
  new_electrode_prototype(json)

}
```

plot_slices *Plot slices of volume*

Description

Plot slices of volume

Usage

```
plot_slices(
  volume,
  overlays = NULL,
  transform = NULL,
  positions = NULL,
  zoom = 1,
  pixel_width = 0.5,
  col = c("black", "white"),
  normalize = NULL,
  zclip = NULL,
  overlay_alpha = 0.3,
  zlim = normalize,
  main = "",
  title_position = c("left", "top"),
  fun = NULL,
  nc = NA,
  which = NULL,
  ...
)
```

Arguments

volume	path to volume (underlay)
overlays	images to overlay on top of the underlay, can be either a vector of paths to the overlay volume images, or a sequence of named lists. Each list item has 'volume' (path to the volume) and 'color' (color of the overlay)
transform	rotation of the volume in scanner 'RAS' space
positions	vector of length 3 or matrix of 3 columns, the 'RAS' position of cross-hairs
zoom	zoom-in radio, default is 1
pixel_width	output image pixel resolution; default is 0.5, one pixel is 0.5 millimeters wide
col	color palette, can be a sequence of colors
normalize	range for volume data to be normalized; either NULL (no normalize) or a numeric vector of length two
zclip	clip image densities; if specified, values outside of this range will be clipped into this range

overlay_alpha	transparency of the overlay; default is 0.3
zlim	image plot value range, default is identical to normalize
main	image titles
title_position	title position; choices are "left" or "top"
fun	function with two arguments that will be executed after each image is drawn; can be used to draw cross-hairs or annotate each image
nc	number of "columns" in the plot when there are too many positions, must be positive integer; default is NA (automatically determined)
which	which plane to plot; default is NULL, which will trigger new plots and add titles; set to 1 for 'Axial' plane, 2 for 'Sagittal', and 3 for 'Coronal'.
...	additional arguments passing into image

Value

Nothing

---

read_fs_asc *Read 'FreeSurfer' ascii file*

Description

Read 'FreeSurfer' ascii file

Usage

```
read_fs_asc(file)
```

Arguments

file	file location

Value

a list of vertices and face indices

read_fs_labels *Read FreeSurfer Annotations*

Description

Read FreeSurfer Annotations

Usage

```
read_fs_labels(path, vertex_number)
```

Arguments

path	label path
vertex_number	force to reset vertex number if raw file is incorrect

read_fs_m3z *Read 'FreeSurfer' m3z file*

Description

Read 'FreeSurfer' m3z file

Usage

```
read_fs_m3z(filename)
```

Arguments

filename	file location, usually located at 'mri/transforms/talairach.m3z'

Details

An 'm3z' file is a 'gzip' binary file containing a dense vector field that describes a 3D registration between two volumes/images. This implementation follows the 'Matlab' implementation from the 'FreeSurfer'. This function is released under the 'FreeSurfer' license: https://surfer.nmr.mgh.harvard.edu/fswiki/FreeSurferSoftwareLicense.

Value

registration data

`read_fs_mgh_mgz` *Read 'FreeSurfer' 'mgz/mgh' file*

Description

Read 'FreeSurfer' 'mgz/mgh' file

Usage

```
read_fs_mgh_mgz(filename)
```

Arguments

`filename`	file location

Value

list contains coordinate transforms and volume data

`read_gii2` *Function to load surface data from 'Gifti' files*

Description

The function 'read_gii2' is a dynamic wrapper of Python 'nibabel' loader. If no Python is detected, it will switch to 'gifti::readgii'.

Usage

```
read_gii2(path)
```

Arguments

`path`	'Gifti' file path

Format

An R function acting as safe wrapper for `nibabel.load`.

read_mgz *Function to load 'FreeSurfer' 'mgz/mgh' file*

Description

The function 'read_mgz' is a dynamic wrapper of Python 'nibabel' loader. If no Python is detected, it will switch to built-in function 'read_fs_mgh_mgz', which has limited features.

Usage

```
read_mgz(path)
```

Arguments

path	'mgz/mgh' file path

Format

An R function acting as safe wrapper for `nibabel.load`.

read_volume *Read volume file in 'MGH' or 'Nifti' formats*

Description

Read volume file in `'MGH'` or `'Nifti'` formats

Usage

```
read_volume(file, format = c("auto", "mgh", "nii"), header_only = FALSE)
```

Arguments

file	file path
format	the file format
header_only	whether only read headers; default is false

Value

A list of volume data and transform matrices; if `header_only=TRUE`, then volume data will be substituted by the header.

renderBrain *Shiny Renderer for threeBrain Widgets*

Description

Shiny Renderer for threeBrain Widgets

Arguments

expr	R expression that calls three_brain function or Brain object
env	environment of expression to be evaluated
quoted	is expr quoted? Default is false.

Author(s)

Zhengjia Wang

reorient_volume *Function to reshape data to 'RAS' order*

Description

Function to reshape data to 'RAS' order

Usage

```
reorient_volume(volume, Torig)
```

Arguments

volume	3-mode tensor (voxels), usually from 'mgz', 'nii', or 'BRIK' files
Torig	a 4x4 transform matrix mapping volume ('CRS') to 'RAS'

Value

Reshaped tensor with dimensions corresponding to 'R', 'A', and 'S'

save_brain *Save threeBrain widgets to local file system*

Description

Save threeBrain widgets to local file system

Usage

```
save_brain(widget, path, title = "3D Viewer", as_zip = FALSE, ...)
```

Arguments

widget	generated from function 'threejs_brain'
path	path to save the brain widget
title	widget title.
as_zip	whether to create zip file "compressed.zip".
...	ignored, used for backward compatibility

Author(s)

Zhengjia Wang

seeg_prototype *Create 'sEEG' shaft geometry prototype*

Description

Intended for creating/editing geometry prototype, please see load_prototype to load existing prototype

Usage

```
seeg_prototype(
  type,
  center_position,
  contact_widths,
  diameter = 1,
  channel_order = seq_along(center_position),
  fix_contact = 1,
  overall_length = 200,
  description = NULL,
  dry_run = FALSE,
  default_interpolation = NULL,
  viewer_options = NULL,
  overwrite = FALSE
)
```

Arguments

type	type string and unique identifier of the prototype
center_position	numerical vector, contact center positions
contact_widths	numerical vector or length of one, width or widths of the contacts
diameter	probe diameter
channel_order	the channel order of the contacts; default is a sequence along the number
fix_contact	NULL or integer in channel_order, indicating which contact is the most important and should be fixed during the localization, default is 1 (inner-most target contact)
overall_length	probe length, default is 200
description	prototype description
dry_run	whether not to save the prototype configurations
default_interpolation	default interpolation string for electrode localization
viewer_options	list of viewer options; this should be a list of key-value pairs where the keys are the controller names and values are the corresponding values when users switch to localizing the electrode group
overwrite	whether to overwrite existing configuration file; default is false, which throws a warning when duplicated

Value

A electrode shaft geometry prototype; the configuration file is saved to 'RAVE' 3rd-party repository.

Examples

```
probe_head <- 2
n_contacts <- 12
width <- 2.41
contact_spacing <- 5
overall_length <- 400
diameter <- 1.12

contacts <- probe_head + width / 2 + 0:(n_contacts-1) * contact_spacing
proto <- seeg_prototype(
  type = "AdTech-sEEG-SD12R-SP05X-000",
  description = c(
    "AdTech sEEG - 12 contacts",
    "Contact length   : 2.41 mm",
    "Central spacing  : 5    mm",
    "Tip size         : 2    mm",
    "Diameter         : 1.12 mm"
  ),
  center_position = contacts,
  contact_widths = width,
  diameter = diameter,
```

```
  overall_length = overall_length,
  dry_run = TRUE
)

print(proto, details = FALSE)
```

SphereGeom *R6 Class - Generate Sphere Geometry*

Description

R6 Class - Generate Sphere Geometry

Author(s)

Zhengjia Wang

SpriteGeom *R6 Class - Generate Sphere Geometry*

Description

R6 Class - Generate Sphere Geometry

Author(s)

Zhengjia Wang

---

template_subject *Download and Manage Template Subjects*

Description

Download and Manage Template Subjects

Usage

```
download_template_subject(
  subject_code = "N27",
  url,
  template_dir = default_template_directory()
)

download_N27(make_default = FALSE, ...)

set_default_template(
  subject_code,
  view = TRUE,
  template_dir = default_template_directory()
)

threebrain_finalize_installation(
  upgrade = c("ask", "always", "never", "data-only", "config-only"),
  async = TRUE
)

available_templates()
```

Arguments

subject_code	character with only letters and numbers (Important); default is 'N27'
url	zip file address; must be specified if subject_code is not from the followings: 'bert', 'cvs_avg35', 'cvs_avg35_inMNI152', 'fsaverage', 'fsaverage_sym', or 'N27'
template_dir	parent directory where subject's 'FreeSurfer' folder should be stored
make_default	logical, whether to make 'N27' default subject
...	more to pass to download_template_subject
view	whether to view the subject
upgrade	whether to check and download 'N27' brain interactively. Choices are 'ask', 'always', and 'never'
async	whether to run the job in parallel to others; default is true

Details

To view electrodes implanted in multiple subjects, it's highly recommended to view them in a template space The detail mapping method is discussed in function freesurfer_brain.

To map to a template space, one idea is to find someone whose brain is normal. In our case, the choice is subject 'N27', also known as 'Colin 27'. function download_N27 provides a simple and easy way to download a partial version from the Internet.

If you have any other ideas about template brain, you can use function set_default_template(subject_code, template_dir) to redirect to your choice. If your template brain is a 'Zip' file on the Internet, we provide function download_template_subject to automatically install it.

Author(s)

Zhengjia Wang

`threeBrain` *Create a brain object*

Description

Create a brain object

Usage

```
threeBrain(
  path,
  subject_code,
  surface_types = "pial",
  atlas_types,
  ...,
  template_subject = unname(getOption("threeBrain.template_subject", "N27")),
  backward_compatible = getOption("threeBrain.compatible", FALSE)
)
```

Arguments

`path`	path to 'FreeSurfer' directory, or 'RAVE' subject directory containing 'FreeSurfer' files, or simply a 'RAVE' subject
`subject_code`	subject code, characters
`surface_types`	surface types to load; default is `'pial'`, other common types are `'white'`, `'smoothwm'`
`atlas_types`	brain atlas to load; default is `'wmparc'`, or if not exists, `'aparc+aseg'`, other choices are `'aparc.a2009s+aseg'`, `'aparc.DKTatlas+aseg'`, depending on the atlas files in `'fs/mri'` folder
`...`	reserved for future use
`template_subject`	template subject to refer to; used for group template mapping
`backward_compatible`	whether to support old format; default is false

threejsBrainOutput *Shiny Output for threeBrain Widgets*

Description

Shiny Output for threeBrain Widgets

Arguments

outputId	unique identifier for the widget
width, height	width and height of the widget. By default width="100 and height="500px".
reportSize	whether to report widget size in shiny session$clientData

Author(s)

Zhengjia Wang

threejs_brain *Create a Threejs Brain and View it in Browsers*

Description

Create a Threejs Brain and View it in Browsers

Usage

```
threejs_brain(
  ...,
  .list = list(),
  width = NULL,
  height = NULL,
  background = "#FFFFFF",
  cex = 1,
  timestamp = TRUE,
  title = "",
  side_canvas = FALSE,
  side_zoom = 1,
  side_width = 250,
  side_shift = c(0, 0),
  side_display = TRUE,
  control_panel = TRUE,
  control_presets = NULL,
  control_display = TRUE,
  camera_center = c(0, 0, 0),
  camera_pos = c(500, 0, 0),
```

```
  start_zoom = 1,
  symmetric = 0,
  default_colormap = "Value",
  palettes = NULL,
  value_ranges = NULL,
  value_alias = NULL,
  show_inactive_electrodes = TRUE,
 surface_colormap = system.file("palettes", "surface", "ContinuousSample.json", package
    = "threeBrain"),
 voxel_colormap = system.file("palettes", "datacube2", "FreeSurferColorLUT.json",
    package = "threeBrain"),
  videos = list(),
  widget_id = "threebrain_data",
  tmp_dirname = NULL,
  debug = FALSE,
  enable_cache = FALSE,
  token = NULL,
  controllers = list(),
  browser_external = TRUE,
  global_data = list(),
  global_files = list(),
  qrcode = NULL,
  custom_javascript = NULL,
  show_modal = "auto",
  embed = FALSE
)
```

Arguments

`...`, `.list`	geometries inherit from AbstractGeom
`width`, `height`	positive integers. Width and height of the widget. By default width='100%', and height varies.
`background`	character, background color such as `"#FFFFFF"` or `"white"`
`cex`	positive number, relative text magnification level
`timestamp`	logical, whether to show time-stamp at the beginning
`title`	viewer title
`side_canvas`	logical, enable side cameras to view objects from fixed perspective
`side_zoom`	numerical, if side camera is enabled, zoom-in level, from 1 to 5
`side_width`	positive integer, side panel size in pixels
`side_shift`	integer of length two, side panel shift in pixels ('CSS style': top, left)
`side_display`	logical, show/hide side panels at beginning
`control_panel`	logical, enable control panels for the widget
`control_presets`	characters, presets to be shown in control panels

`control_display`
: logical, whether to expand/collapse control UI at the beginning

`camera_center`
: numerical, length of three, XYZ position where camera should focus at

`camera_pos`
: XYZ position of camera itself, default (0, 0, 500)

`start_zoom`
: numerical, positive number indicating camera zoom level

`symmetric`
: numerical, default 0, color center will be mapped to this value

`default_colormap`
: character, which color map name to display at startup

`palettes`
: named list, names corresponds to color-map names if you want to change color palettes

`value_ranges`
: named list, similar to `palettes`, value range for each values

`value_alias`
: named list, legend title for corresponding variable

`show_inactive_electrodes`
: logical, whether to show electrodes with no values

`surface_colormap`
: a color map or its path generated by `create_colormap(gtype="surface")` to render surfaces vertices; see `create_colormap` for details.

`voxel_colormap`
: a color map or its path generated by `create_colormap(gtype="volume")` to render volume such as atlases; see `create_colormap` for details.

`videos`
: named list, names corresponds to color-map names, and items are generated from `video_content`

`widget_id`
: character, internally used as unique identifiers for widgets; only use it when you have multiple widgets in one website

`tmp_dirname`
: character path, internally used, where to store temporary files

`debug`
: logical, internally used for debugging

`enable_cache`
: whether to enable cache, useful when rendering the viewers repeatedly in shiny applications

`token`
: unique character, internally used to identify widgets in 'JavaScript' `'localStorage'`

`controllers`
: list to override the settings, for example `proxy$get_controllers()`

`browser_external`
: logical, use system default browser (default) or built-in one.

`global_data`, `global_files`
: internally use, mainly to store orientation matrices and files.

`qrcode`
: 'URL' to show in the 'QR' code; can be a character string or a named list of `'url'` and `'text'` (hyper-reference text)

`custom_javascript`
: customized temporary 'JavaScript' code that runs after ready state; available 'JavaScript' variables are:

  `'groups'` input information about each group

  `'geoms'` input information about each geometry

  `'settings'` input information about canvas settings

  `'scene'` 'threejs' scene object

	`'canvas'` canvas object
	`'gui'` controls data panel
	`'presets'` preset `'gui'` methods
`show_modal`	logical or `"auto"`, whether to show a modal instead of direct rendering the viewers; designed for users who do not have `'WebGL'` support; only used in shiny applications
`embed`	whether to try embedding the viewer in current run-time; default is false (will launch default web browser); set to true if running in `'rmarkdown'` or `'quarto'`, or to see the viewer in `'RStudio'` default panel.

Author(s)

Zhengjia Wang

Examples

```
if( interactive() ) {
library(threeBrain)

# Please use `download_N27` to download N27 Collins template brain
n27_path <- file.path(default_template_directory(), "N27")
if( dir.exists(n27_path) ) {

  brain <- threeBrain(path = n27_path, subject_code = "N27",
                              surface_types = c('pial', 'smoothwm'))
  print(brain)

  brain$plot(
    background = "#000000",
    controllers = list(
      'Voxel Type' = 'aparc_aseg',
      'Surface Type' = 'smoothwm',
      'Blend Factor' = 1,
      'Right Opacity' = 0.3,
      'Overlay Sagittal' = TRUE
    ),
    show_modal = TRUE
  )

}
}
```

`TubeGeom` *R6 Class - Generate Tube Geometry*

Description

R6 Class - Generate Tube Geometry

Author(s)

Zhengjia Wang

`video_content` *Add video content to the viewer*

Description

Add video content to the viewer

Usage

```
video_content(
  path,
  duration = Inf,
  time_start = 0,
  asp_ratio = 16/9,
  local = TRUE
)
```

Arguments

`path`	local file path or 'URL'
`duration`	duration of the video
`time_start`	start time relative to the stimuli onset
`asp_ratio`	aspect ratio; default is `16/9`
`local`	used only when `path` is a 'URL': whether to download the video before generating the viewer; see 'Details'

Details

The video path can be either local file path or a 'URL' from websites. When path is from the internet, there are two options: download the video before generating the viewer, or directly use the 'URL'.

If download happens before a viewer is generated (`local=TRUE`), then the video content is local. The viewer will be self-contained. However, the distribution will contain the video, and the archive size might be large.

If raw 'URL' is used (`local=FALSE`), then viewer is not self-contained as the video link might break anytime. The 'screenshot' and 'record' function might be limited if the 'URL' has different domain than yours. However, the distribution will not contain the video, hence smaller. This works in the scenarios when it is preferred not to share video files or they are licensed, or simply distribution is limited. Besides, this method is slightly faster than the local alternatives.

volume_to_surf *Generate surface file from 'nii' or 'mgz' volume files*

Description

Generate surface file from 'nii' or 'mgz' volume files

Usage

```
volume_to_surf(
  volume,
  save_to = NA,
  lambda = 0.2,
  degree = 2,
  threshold_lb = 0.5,
  threshold_ub = NA,
  format = "auto"
)
```

Arguments

volume	path to the volume file, or object from read_volume.
save_to	where to save the surface file; default is NA (no save).
lambda	'Laplacian' smooth, the higher the smoother
degree	'Laplacian' degree; default is 2
threshold_lb	lower threshold of the volume (to create mask); default is 0.5
threshold_ub	upper threshold of the volume; default is NA (no upper bound)
format	The format of the file if save_to is a valid path, choices include 'auto' Default, supports 'FreeSurfer' binary format and 'ASCII' text format, based on file name suffix 'bin' 'FreeSurfer' binary format 'asc' 'ASCII' text format 'ply' 'Stanford' 'PLY' format 'off' Object file format 'obj' 'Wavefront' object format 'gii' 'GIfTI' format. Please avoid using 'gii.gz' as the file suffix 'mz3' 'Surf-Ice' format 'byu' 'BYU' mesh format 'vtk' Legacy 'VTK' format 'gii', otherwise 'FreeSurfer' format. Please do not use 'gii.gz' suffix.

Value

Triangle 'rgl' mesh (vertex positions in native 'RAS'). If save_to is a valid path, then the mesh will be saved to this location.

See Also

read_volume, vcg_isosurface, vcg_smooth_implicit

Examples

```
library(threeBrain)
N27_path <- file.path(default_template_directory(), "N27")
if(dir.exists(N27_path)) {
  aseg <- file.path(N27_path, "mri", "aparc+aseg.mgz")

  # generate surface for left-hemisphere insula
  mesh <- volume_to_surf(aseg, threshold_lb = 1034,
                         threshold_ub = 1036)

  if(interactive()) {
    ravetools::rgl_view({
      ravetools::rgl_call("shade3d", mesh, color = "yellow")
    })
  }
}
```

---

voxel_colormap *Color maps for volume or surface data*

Description

Color maps for volume or surface data

Usage

```
create_colormap(
  gtype = c("surface", "volume"),
  dtype = c("continuous", "discrete"),
  key,
  color,
  value,
  alpha = FALSE,
  con = NULL,
  auto_rescale = FALSE,
  ...
)

save_colormap(cmap, con)

freeserfer_colormap(con)

load_colormap(con)
```

Arguments

gtype	geometry type, choices are "surface", "volume"
dtype	data type, "continuous" or "discrete"
key	non-negative integer vector corresponding to color values; its length must exceed 1; see 'Details'
color	characters, corresponding to color strings for each key
value	actual value for each key
alpha	whether to respect transparency
con	a file path to write results to or to read from. The file path can be passed as voxel_colormap into threejs_brain.
auto_rescale	automatically scale the color according to image values; only valid for continuous color maps
...	used by continuous color maps, passed to colorRampPalette
cmap	color map object

Details

Internal 'JavaScript' shader implementation uses integer color keys to connect color palettes and corresponding values. The keys must be non-negative.

Zero key is a special color key reserved by system. Please avoid using it for valid values.

Value

A list of color map information

Examples

```
# Creates a symmetric continuous colormap with 3 keys
# The color range is -10 to 10
# The colors are 'blue','white','red' for these keys

pal <- create_colormap(
  gtype = "volume", dtype = "continuous",
  key = c(1,2,3), value = c(-10,0,10),
  color = c('blue','white','red'))

print( pal )

# ---------------- Get colormap key from a value ------------

# returns key index starting from
pal$get_key( -10 )

# nearest value
pal$get_key( 2 )

# set threshold, key is now 0 (no color)
```

```
pal$get_key( 2, max_delta = 1 )


# ---------------- Save and load ----------------
f <- tempfile( fileext = '.json' )
save_colormap( pal, f )
cat(readLines(f), sep = '\n')

load_colormap(f)
```

---

voxel_cube *Generate volume data from 'MNI' coordinates*

Description

Generate volume data from 'MNI' coordinates

Usage

```
add_voxel_cube(
  brain,
  name,
  cube,
  size = c(256, 256, 256),
  trans_mat = NULL,
  trans_space_from = c("model", "scannerRAS"),
  color_format = c("RGBAFormat", "RedFormat")
)

add_nifti(
  brain,
  name,
  path,
  trans_mat = NULL,
  color_format = c("RGBAFormat", "RedFormat"),
  trans_space_from = c("model", "scannerRAS")
)

create_voxel_cube(
  mni_ras,
  value,
  colormap,
  keys = colormap$get_key(value),
  dimension = c(256, 256, 256)
)
```

Arguments

brain	a 'threeBrain' brain object generated from freesurfer_brain2 or merge_brain. If you have 'rave' package installed, the brain can be generated from rave::rave_brain2
name	the name of voxel cube, only letters, digits and '_' are allowed; other characters will be replaced by '_'
cube	a 3-mode array; see the following example
size	the actual size of the volume, usually dot multiplication of the dimension and voxel size
trans_mat	the transform matrix of the volume. For add_voxel_cube, this matrix should be from data cube geometry model center to world ('tkrRAS') transform. For add_nifti, this matrix is the 'Nifti' 'RAS' to world ('tkrRAS') transform.
trans_space_from	where does trans_mat transform begin; default is from object 'model' space; alternative space is 'scannerRAS', meaning the matrix only transform volume cube from its own 'scannerRAS' to the world space.
color_format	color format for the internal texture. Default is 4-channel 'RGBAFormat'; alternative choice is 'RedFormat', which saves volume data with single red-channel to save space
path	'Nifti' data path
mni_ras	'MNI' 'RAS' coordinates, should be a n-by-3 matrix
value	data values (length n); used if keys is missing
colormap	a color map generated from create_colormap; see voxel_colormap for details
keys	integer color-keys generated from a color map with length of n; alternatively, you could specify value and colormap to generate keys automatically
dimension	volume dimension; default is a 256 x 256 x 256 array cube; must be integers and have length of 3

Value

create_voxel_cube returns a list of cube data and other informations; add_voxel_cube returns the brain object

Examples

```
# requires N27 brain to be installed
# use `download_N27()` to download template Collins brain


# sample MNI coords
tbl <- read.csv(system.file(
  'sample_data/example_cube.csv', package = 'threeBrain'
))
head(tbl)

# load colormap
cmap <- load_colormap(system.file(
```

```
  'palettes/datacube2/Mixed.json', package = 'threeBrain'
))

x <- create_voxel_cube(
  mni_ras = tbl[, c('x', 'y', 'z')],
  keys = tbl$key,
  dimension = c(128, 128, 128)
)


n27_path <- file.path(default_template_directory(), "N27")
if( interactive() && dir.exists(n27_path) ) {
  brain <- merge_brain()

  # or add_voxel_cube(brain, 'example', x$cube)
  x$add_to_brain(brain, 'example')

  brain$plot(controllers = list(
    "Voxel Type" = 'example',
    'Right Opacity' = 0.3,
    'Left Opacity' = 0.3,
    'Background Color' = '#000000'
  ), voxel_colormap = cmap)
}
```

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