Package ‘freesurferformats’

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Type Package

Title Read and Write ‘FreeSurfer’ Neuroimaging File Formats

Version 0.1.8

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Description Provides functions to read and write data from neuroimaging files in ‘FreeSurfer’ <http://freesurfer.net/> binary formats. This includes the following file formats: 1) MGH/MGZ format files, which can contain multi-dimensional images or other data. Typically they contain time-series of three-dimensional brain scans acquired by magnetic resonance imaging (MRI). They can also contain vertex-wise measures of surface morphometry data. The MGH format is named after the Massachusetts General Hospital, and the MGZ format is a compressed version of the same format. 2) ‘FreeSurfer’ morphometry data files in binary ‘curv’ format. These contain vertex-wise surface measures, i.e., one scalar value for each vertex of a brain surface mesh. These are typically values like the cortical thickness or brain surface area at each vertex. 3) Annotation file format. This contains a brain surface parcellation derived from a cortical atlas. 4) Surface file format. Contains a brain surface mesh, given by a list of vertices and a list of faces.

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Encoding UTF-8

LazyData true

URL https://github.com/dfsp-spirit/freesurferformats

BugReports https://github.com/dfsp-spirit/freesurferformats/issues

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colortable.from.annot

Extract color lookup table (LUT) from annotation.

Description

Extract a colortable lookup table (LUT) from an annotation. Such a LUT can also be read from files like 'FREESURFER_HOME/FreeSurferColorLUT.txt' or saved as a file, check the 'See Also' section below.

Usage

colortable.from.annot(annot, compute_colorcode = FALSE)

Arguments

annot An annotation, as returned by \texttt{read.fs.annot}. If you want to assign specific indices, you can add a column named 'struct_index' to the data.frame \texttt{annot$colortable_df}. If there is no such columns, the indices will be created automatically in the order of the regions, starting at zero.

compute_colorcode logical, indicates whether the unique color codes should be computed and added to the returned data.frame as an extra integer column named 'code'. Defaults to FALSE.

Value

the colortable data.frame extracted from the annotation.

See Also

Other atlas functions: \texttt{read.fs.annot, read.fs.colortable, write.fs.annot, write.fs.colortable}

Other colorLUT functions: \texttt{read.fs.colortable, write.fs.colortable}
Examples

```r
annotfile = system.file("extdata", "lh.aparc.annot.gz");
package = "freesurferformats", mustWork = TRUE);
annot = read.fs.annot(annotfile);
colortable = colortable.from.annot(annot);
head(colortable);
```

---

download_optional_data

*Download optional data for the freesurferformats package.*

**Description**

Ensure that the optional data is available locally in the package cache. Will try to download the data only if it is not available. This data is not required for the package to work, but it is used in the examples, in the unit tests and also in the example code from the vignette. Downloading it is highly recommended.

**Usage**

download_optional_data()

**Value**

Named list. The list has entries: "available": vector of strings. The names of the files that are available in the local file cache. You can access them using get_optional_data_file(). "missing": vector of strings. The names of the files that this function was unable to retrieve.
### fs.get.morph.file.ext.for.format

Determine morphometry file extension from format

**Description**

Given a morphometry file format, derive the proper file extension.

**Usage**

```r
fs.get.morph.file.ext.for.format(format)
```

**Arguments**

- `format`, string. One of c("mgh", "mgz", "curv").

**Value**

`file.ext`, string. The standard file extension for the format. (May be an empty string for some formats.)

**See Also**

Other morphometry functions: `fs.get.morph.file.format.from.filename`, `read.fs.curv`, `read.fs.mgh`, `read.fs.morph`, `read.fs.weight`, `write.fs.curv`, `write.fs.mgh`, `write.fs.morph`, `write.fs.weight`

---

### fs.get.morph.file.format.from.filename

Determine morphometry file format from filename

**Description**

Given a morphometry file name, derive the proper file format, based on the end of the string. Case is ignored, i.e., cast to lowercase before checks. If the filepath ends with "mgh", returns format "mgh". For suffix "mgz", returns "mgz" format. For all others, returns "curv" format.

**Usage**

```r
fs.get.morph.file.format.from.filename(filepath)
```

**Arguments**

- `filepath`, string. A path to a file.

**Value**

`format`, string. The format, one of c("mgz", "mgh", "curv").
See Also

Other morphometry functions: `fs.get.morph.file.ext.for.format`, `read.fs.curv`, `read.fs.mgh`, `read.fs.morph`, `read.fs.weight`, `write.fs.curv`, `write.fs.mgh`, `write.fs.morph`, `write.fs.weight`

---

| fs.patch | Constructor for fs.patch |

Description

Constructor for fs.patch

Usage

```
fs.patch(vertices, faces = NULL)
```

Arguments

- **vertices**
  - numerical *n*x5 matrix (or *n*x7 matrix), see `read.fs.patch` for details. If it has 5 columns, columns 6-7 will be computed automatically from the first 5 columns (from column 1 and 5).

- **faces**
  - numerical *n*x5 matrix, see `read.fs.patch.asc` for details. Can be ‘NULL’.

Value

instance of class ‘fs.patch’

See Also

Other patch functions: `read.fs.patch.asc`, `read.fs.patch`, `write.fs.patch`

Examples

```
num_vertices = 6L;  # a tiny patch
vertices = matrix(rep(0., num_vertices*5), ncol=5);
vertices[,1] = seq.int(num_vertices);  # 1-based vertex indices
vertices[,2:4] = matrix(rnorm(num_vertices*3, 8, 2), ncol=3);  # vertex coords
vertices[,5] = rep(0L, num_vertices);  # is_border
vertices[3,5] = 1L;  # set a vertex to be a border vertex
patch = fs.patch(vertices);
patch;
```
get_optional_data_filepath

Access a single file from the package cache by its file name.

Description
Access a single file from the package cache by its file name.

Usage
get_optional_data_filepath(filename, mustWork = TRUE)

Arguments
filename, string. The filename of the file in the package cache.
mustWork, logical. Whether an error should be created if the file does not exist. If mustWork=FALSE and the file does not exist, the empty string is returned.

Value
string. The full path to the file in the package cache or the empty string if there is no such file available. Use this in your application code to open the file.

is.fs.annot
Check whether object is an fs.annot

Description
Check whether object is an fs.annot

Usage
is.fs.annot(x)

Arguments
x any ‘R’ object

Value
TRUE if its argument is a brain surface annotation (that is, has "fs.annot" amongst its classes) and FALSE otherwise.
is.fs.label  
Check whether object is an fs.label

Description
Check whether object is an fs.label

Usage
is.fs.label(x)

Arguments
x  
any ‘R’ object

Value
TRUE if its argument is a brain surface label (that is, has ‘fs.label’ amongst its classes) and FALSE otherwise.

is.fs.surface  
Check whether object is an fs.surface

Description
Check whether object is an fs.surface

Usage
is.fs.surface(x)

Arguments
x  
any ‘R’ object

Value
TRUE if its argument is a brain surface (that is, has "fs.surface" amongst its classes) and FALSE otherwise.
is.fs.volume  Check whether object is an fs.volume

**Description**

Check whether object is an fs.volume

**Usage**

```r
is.fs.volume(x)
```

**Arguments**

- `x` any `R` object

**Value**

TRUE if its argument is a brain volume (that is, has "fs.volume" amongst its classes) and FALSE otherwise.

---

list_optional_data  Get file names available in package cache.

**Description**

Get file names of optional data files which are available in the local package cache. You can access these files with get_optional_data_file().

**Usage**

```r
list_optional_data()
```

**Value**

vector of strings. The file names available, relative to the package cache.
mghheader.crs.orientation

*Compute MGH volume orientation string.*

**Description**
Compute MGH volume orientation string.

**Usage**
mghheader.crs.orientation(header)

**Arguments**
header 
Header of the mgh datastructure, as returned by `read.fs.mgh`.

**Value**
character string of length 3, one uppercase letter per axis. Each of the three position is a letter from the alphabet: `LRISAP`. The meaning is ‘L’ for left, ‘R’ for right, ‘I’ for inferior, ‘S’ for superior, ‘P’ for posterior, ‘A’ for anterior. If the direction cannot be computed, all three characters are ‘¿’ for unknown. Of course, each axis (‘L/R’, ‘I/S’, ‘A/P’) is only represented once in the string.

mghheader.is.conformed

*Determine whether an MGH volume is conformed.*

**Description**
In the FreeSurfer sense, *conformed* means that the volume is in coronal primary slice direction, has dimensions 256x256x256 and a voxel size of 1 mm in all 3 directions. The slice direction can only be determined if the header contains RAS information, if it does not, the volume is not conformed.

**Usage**
mghheader.is.conformed(header)

**Arguments**
header 
Header of the mgh datastructure, as returned by `read.fs.mgh`.

**Value**
logical, whether the volume is *conformed*. 
mghheader.is.ras.valid

Check whether header contains valid ras information

**Description**

Check whether header contains valid ras information

**Usage**

mghheader.is.ras.valid(header)

**Arguments**

  header  mgh header or ‘fs.volume’ instance with header

**Value**

logical, whether header contains valid ras information (according to the ‘ras_good_flag’).

**See Also**

Other header coordinate space: mghheader.ras2vox.tkreg, mghheader.ras2vox, mghheader.scanner2tkreg, mghheader.tkreg2scanner, mghheader.vox2ras.tkreg, mghheader.vox2ras

**Examples**

```r
brain_image = system.file("extdata", "brain.mgz", package = "freesurferformats", mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.is.ras.valid(vdh$header);
```

mghheader.primary.slice.direction

Compute MGH primary slice direction

**Description**

Compute MGH primary slice direction

**Usage**

mghheader.primary.slice.direction(header)
mghheader.ras2vox

Arguments

header

Header of the mgh datastructure, as returned by read.fs.mgh.

Value

character string, the slice direction. One of 'sagittal', 'coronal', 'axial' or 'unknown'.

mghheader.ras2vox  Compute ras2vox matrix from basic MGH header fields.

Description

This is also known as the 'scanner' or 'native' ras2vox. It is the inverse of the respective vox2ras, see mghheader.vox2ras.

Usage

mghheader.ras2vox(header)

Arguments

header

the MGH header

Value

4x4 numerical matrix, the transformation matrix

See Also

Other header coordinate space: mghheader.is.ras.valid, mghheader.ras2vox.tkreg, mghheader.scanner2tkreg, mghheader.tkreg2scanner, mghheader.vox2ras.tkreg, mghheader.vox2ras

Examples

brain_image = system.file("extdata", "brain.mgz",
                          package = "freesurferformats",
                          mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.ras2vox(vdh$header);
**mghheader.ras2vox.tkreg**

Compute ras2vox-tkreg matrix from basic MGH header fields.

**Description**

This is also known as the 'tkreg' ras2vox. It is the inverse of the respective vox2ras, see `mghheader.vox2ras.tkreg`.

**Usage**

```r
mghheader.ras2vox.tkreg(header)
```

**Arguments**

- **header**
  - the MGH header

**Value**

4x4 numerical matrix, the transformation matrix

**See Also**

Other header coordinate space: `mghheader.is.ras.valid`, `mghheader.ras2vox`, `mghheader.scanner2tkreg`, `mghheader.tkreg2scanner`, `mghheader.vox2ras.tkreg`, `mghheader.vox2ras`

**Examples**

```r
brain_image = system.file("extdata", "brain.mgz", 
                        package = "freesurferformats", 
                        mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.ras2vox.tkreg(vdh$header);
```

**mghheader.scanner2tkreg**

Compute scanner-RAS 2 tkreg-RAS matrix from basic MGH header fields.

**Description**

This is also known as the 'scanner2tkreg' matrix. Note that this is a RAS-to-RAS matrix. It is the inverse of the 'tkreg2scanner' matrix, see `mghheader.tkreg2scanner`.

**Usage**

```r
mghheader.scanner2tkreg(header)
```
mghheader.tkreg2scanner

Arguments

header the MGH header

Value

4x4 numerical matrix, the transformation matrix

See Also

Other header coordinate space: mghheader.is.ras.valid, mghheader.ras2vox.tkreg, mghheader.ras2vox, mghheader.tkreg2scanner, mghheader.vox2ras.tkreg, mghheader.vox2ras

Examples

brain_image = system.file("extdata", "brain.mgz", 
  package = "freesurferformats", 
  mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.scanner2tkreg(vdh$header); 

mghheader.tkreg2scanner

Compute tkreg-RAS to scanner-RAS matrix from basic MGH header fields.

Description

This is also known as the 'tkreg2scanner' matrix. Note that this is a RAS-to-RAS matrix. It is the inverse of the 'scanner2tkreg' matrix, see mghheader.scanner2tkreg.

Usage

mghheader.tkreg2scanner(header)

Arguments

header the MGH header

Value

4x4 numerical matrix, the transformation matrix

See Also

Other header coordinate space: mghheader.is.ras.valid, mghheader.ras2vox.tkreg, mghheader.ras2vox, mghheader.scanner2tkreg, mghheader.vox2ras.tkreg, mghheader.vox2ras
Examples

```r
brain_image = system.file("extdata", "brain.mgz", package = "freesurferformats", mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.tkreg2scanner(vdh$header);
```

---

**mghheader.vox2ras** *Compute vox2ras matrix from basic MGH header fields.*

**Description**

This is also known as the 'scanner' or 'native' vox2ras. It is the inverse of the respective ras2vox, see **mghheader.ras2vox**.

**Usage**

```r
mghheader.vox2ras(header)
```

**Arguments**

- **header** the MGH header

**Value**

4x4 numerical matrix, the transformation matrix

**See Also**

Other header coordinate space: mghheader.is.ras.valid, mghheader.ras2vox.tkreg, mghheader.ras2vox, mghheader.scanner2tkreg, mghheader.tkreg2scanner, mghheader.vox2ras.tkreg

**Examples**

```r
brain_image = system.file("extdata", "brain.mgz", package = "freesurferformats", mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.vox2ras(vdh$header);
```
mghheader.vox2ras.tkreg

Compute vox2ras-tkreg matrix from basic MGH header fields.

Description

This is also known as the 'tkreg' vox2ras. It is the inverse of the respective ras2vox, see mghheader.ras2vox.tkreg.

Usage

mghheader.vox2ras.tkreg(header)

Arguments

header the MGH header

Value

4x4 numerical matrix, the transformation matrix

See Also

Other header coordinate space: mghheader.is.ras.valid, mghheader.ras2vox.tkreg, mghheader.ras2vox, mghheader.scanner2tkreg, mghheader.tkreg2scanner, mghheader.vox2ras

Examples

brain_image = system.file("extdata", "brain.mgz", package = "freesurferformats", mustWork = TRUE);
vdh = read.fs.mgh(brain_image, with_header = TRUE);
mghheader.vox2ras.tkreg(vdh$header);

mghheader.vox2vox

Compute vox2vox matrix between two volumes.

Description

Compute vox2vox matrix between two volumes.

Usage

mghheader.vox2vox(header_from, header_to)
print.fs.annot

Arguments

header_from the MGH header of the source volume
header_to the MGH header of the target volume

Value

4x4 numerical matrix, the transformation matrix

print.fs.annot  Print description of a brain atlas or annotation.

Description

Print description of a brain atlas or annotation.

Usage

## S3 method for class 'fs.annot'
print(x, ...)

Arguments

x brain surface annotation or atlas with class ‘fs.annot’.
...

print.fs.label  Print description of a brain surface label.

Description

Print description of a brain surface label.

Usage

## S3 method for class 'fs.label'
print(x, ...)

Arguments

x brain surface label with class ‘fs.label’.
...

Further arguments passed to or from other methods
print.fs.patch  Print description of a brain surface patch.

Description

Print description of a brain surface patch.

Usage

## S3 method for class 'fs.patch'
print(x, ...)

Arguments

x  brain surface patch with class 'fs.patch'.
...
  further arguments passed to or from other methods

print.fs.surface  Print description of a brain surface.

Description

Print description of a brain surface.

Usage

## S3 method for class 'fs.surface'
print(x, ...)

Arguments

x  brain surface with class 'fs.surface'.
...
  further arguments passed to or from other methods
print.fs.volume  

**Print description of a brain volume.**

**Description**

Print description of a brain volume.

**Usage**

```r
## S3 method for class 'fs.volume'
print(x, ...)
```

**Arguments**

- `x`  
  brain volume with class ‘fs.volume’.
- `...`  
  further arguments passed to or from other methods

---

read.fs.annot  

**Read file in FreeSurfer annotation format**

**Description**

Read a data annotation file in FreeSurfer format. Such a file assigns a label and a color to each vertex of a brain surface. The assignment of labels to vertices is based on at atlas or brain parcellation file. Typically the atlas is available for some standard template subject, and the labels are assigned to another subject by registering it to the template. For a subject (MRI image pre-processed with FreeSurfer) named ‘bert’, an example file would be ‘bert/label/lh.aparc.annot’, which contains the annotation based on the Desikan-Killiany Atlas for the left hemisphere of bert.

**Usage**

```r
read.fs.annot(filepath, empty_label_name = "unknown",
               metadata = list())
```

**Arguments**

- `filepath`  
  string. Full path to the input annotation file. Note: gzipped files are supported and gz format is assumed if the filepath ends with " .gz ".
- `empty_label_name`  
  string. The region name to assign to regions with empty name. Defaults to 'unknown'. Set to NULL if you want to keep the empty region name.
- `metadata`  
  named list of arbitrary metadata to store in the instance.
Value

named list, entries are: "vertices" vector of n vertex indices, starting with 0. "label_codes": vector of n integers, each entry is a color code, i.e., a value from the 5th column in the table structure included in the "colortable" entry (see below). "label_names": the n brain structure names for the vertices, already retrieved from the colortable using the code. "hex_colors_rgb": Vector of hex color for each vertex. The "colortable" is another named list with 3 entries: "num_entries": int, number of brain structures. "struct_names": vector of strings, the brain structure names. "table": numeric matrix with num_entries rows and 5 columns. The 5 columns are: 1=color red channel, 2=color blue channel, 3=color green channel, 4=color alpha channel, 5=unique color code. "colortable_df": The same information as a dataframe. Contains the extra columns "hex_color_string_rgb" and "hex_color_string_rgba" that hold the color as an RGB(A) hex string, like "#rrggbbaa".

See Also

Other atlas functions: colortable.from.annot, read.fs.colortable, write.fs.annot, write.fs.colortable

Examples

annot_file = system.file("extdata", "lh.aparc.annot.gz", package = "freesurferformats", mustWork = TRUE);
annot = read.fs.annot(annot_file);
print(annot);

read.fs.colortable  

Read colortable file in FreeSurfer ASCII LUT format.

Description

Read a colortable from a text file in FreeSurfer ASCII colortable lookup table (LUT) format. An example file is 'FREESURFER_HOME/FreeSurferColorLUT.txt'.

Usage

read.fs.colortable(filepath, compute_colorcode = FALSE)

Arguments

filepath,  

string. Full path to the output colormap file.

compute_colorcode  

logical, indicates whether the unique color codes should be computed and added to the returned data.frame as an extra integer column named 'code'. Defaults to FALSE.
Value

the data.frame that was read from the LUT file. It contains the following columns that were read from the file: 'struct_index': integer, index of the struct entry. 'struct_name': character string, the label name. 'r': integer in range 0-255, the RGBA color value for the red channel. 'g': same for green channel. 'b': same for blue channel. 'a': same for alpha (transparency) channel. If 'compute_colorcode' is TRUE, it also contains the following columns which were computed from the color values: 'code': integer, unique color identifier computed from the RGBA values.

See Also

Other atlas functions: colortable.from.annot, read.fs.annot, write.fs.annot, write.fs.colortable
Other colorLUT functions: colortable.from.annot, write.fs.colortable

Examples

lutfile = system.file("extdata", "colorlut.txt", package = "freesurferformats", mustWork = TRUE);
colortable = read.fs.colortable(lutfile, compute_colorcode=TRUE);
head(colortable);

---

**read.fs.curv**  
**Read file in FreeSurfer curv format**

**Description**

Read vertex-wise brain morphometry data from a file in FreeSurfer 'curv' format. Both binary and ASCII versions are supported. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/surf/lh.thickness', which contains n values. Each value represents the cortical thickness at the respective vertex in the brain surface mesh of bert.

**Usage**

read.fs.curv(filepath, format = "auto")

**Arguments**

filepath  
string. Full path to the input curv file. Note: gzipped binary curv files are supported and gz binary format is assumed if the filepath ends with ".gz".

format  
one of 'auto', 'asc', or 'bin'. The format to assume. If set to 'auto' (the default), binary format will be used unless the filepath ends with ".asc".

**Value**

data vector of floats. The brain morphometry data, one value per vertex.
read.fs.label

Read file in FreeSurfer label format

Description

Read a mask in FreeSurfer label format. A label defines a list of vertices (of an associated surface or morphometry file) which are part of it. All others are not. You can think of it as binary mask. Label files are ASCII text files, which have 5 columns (vertex index, coord1, coord2, coord3, value), but only the vertex indices are of interest.

Usage

read.fs.label(filepath, return_one_based_indices = TRUE, full = FALSE, metadata = list())

Arguments

filepath 
string. Full path to the input label file.

return_one_based_indices 
logical. Whether the indices should be 1-based. Indices are stored zero-based in the file, but R uses 1-based indices. Defaults to TRUE, which means that 1 will be added to all indices read from the file before returning them.

full 
logical, whether to return a full object of class ‘fs.label’ instead of only a vector containing the vertex indices. If TRUE, a named list with the following two entries is returned: ‘one_based_indices’: logical, whether the vertex indices are one-based, ‘vertexdata’: a data.frame with the following columns: ‘vertex_index’: integer, see parameter ‘return_one_based_indices’, ‘coord1’, ‘coord2’, ‘coord3’: float coordinates, ‘value’: float, scalar data for the vertex, can mean anything. This parameter defaults to FALSE.

metadata 
named list of arbitrary metadata to store in the instance, ignored unless the parameter ‘full’ is TRUE.
**Value**

vector of integers or `fs.label` instance (see parameter `full`). The vertex indices from the label file. See the parameter `return_one_based_indices` for important information regarding the start index.

**See Also**

Other label functions: `write.fs.label`

**Examples**

```r
labelfile = system.file("extdata", "lh.entorhinal_exvivo.label", 
    package = "freesurferformats", mustWork = TRUE); 
label = read.fs.label(labelfile);
```

---

**read.fs.mgh**

**Description**

Read multi-dimensional brain imaging data from a file in FreeSurfer binary MGH or MGZ format. The MGZ format is just a gzipped version of the MGH format. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/mri/T1.mgz', which contains a 3D brain scan of bert.

**Usage**

```r
read.fs.mgh(filepath, is_gzipped = "AUTO", flatten = FALSE, 
    with_header = FALSE, drop_empty_dims = FALSE)
```

**Arguments**

- **filepath** string. Full path to the input MGZ or MGH file.
- **is_gzipped** a logical value (TRUE or FALSE) or the string 'AUTO'. Whether to treat the input file as gzipped, i.e., MGZ instead of MGH format. Defaults to 'AUTO', which tries to determine this from the last three characters of the `filepath` parameter. Files with extensions 'mgz' and '.gz' (in arbitrary case) are treated as MGZ format, all other files are treated as MGH. In the special case that `filepath` has less than three characters, MGH is assumed.
- **flatten** logical. Whether to flatten the return volume to a 1D vector. Useful if you know that this file contains 1D morphometry data.
- **with_header** logical. Whether to return the header as well. If TRUE, return an instance of class `fs.volume` for data with at least 3 dimensions, a named list with entries 'data' and 'header'. The latter is another named list which contains the header data. These header entries exist: "dtype": int, one of: 0=MRI_UCHAR; 1=MRI_INT; 3=MRI_FLOAT; 4=MRI_SHORT. "voldim": integer vector. The
volume (=data) dimensions. E.g., c(256, 256, 256, 1). These header entries may exist: "vox2ras_matrix" (exists if "ras_good_flag" is 1), "mr_params" (exists if "has_mr_params" is 1). See the ‘mghheader.*’ functions, like mghheader.vox2ras.tkreg, to compute more information from the header fields.

drop_empty_dims
logical, whether to drop empty dimensions of the returned data

Value
data, multi-dimensional array. The brain imaging data, one value per voxel. The data type and the dimensions depend on the data in the file, they are read from the header. If the parameter flatten is ‘TRUE’, a numeric vector is returned instead. Note: The return value changes if the parameter with_header is ‘TRUE’, see parameter description.

See Also
To derive more information from the header, see the ‘mghheader.*’ functions, like mghheader.vox2ras.tkreg.
Other morphometry functions: fs.get.morph.file.ext.for.format, fs.get.morph.file.format.from.filename, read.fs.curv, read.fs.morph, read.fs.weight, write.fs.curv, write.fs.mgh, write.fs.morph, write.fs.weight

Examples
brain_image = system.file("extdata", "brain.mgz",
package = "freesurferformats",
mustWork = TRUE);
vd = read.fs.mgh(brain_image);
cat(sprintf("Read voxel data with dimensions %s. Values: min=%d, mean=%f, max=%d.\n", pastedim(vd), collapse = ' '), min(vd), mean(vd), max(vd)));
# Read it again with full header data:
vdh = read.fs.mgh(brain_image, with_header = TRUE);
# Use the vox2ras matrix from the header to compute RAS coordinates at CRS voxel (0, 0, 0):
vdh$header$vox2ras_matrix %*% c(0,0,0,1);

read.fs.morph
Read morphometry data file in any FreeSurfer format.

Description
Read vertex-wise brain surface data from a file. The file can be in any of the supported formats, and the format will be determined from the file extension.

Usage
read.fs.morph(filepath)
read.fs.patch

Arguments

filepath, string. Full path to the input file. The suffix determines the expected format as follows: ".mgz" and ".mgh" will be read with the read.fs.mgh function, all other file extensions will be read with the read.fs.curv function.

Value
data, vector of floats. The brain morphometry data, one value per vertex.

See Also

Other morphometry functions: fs.get.morph.file.ext.for.format, fs.get.morph.file.format.from.filename, read.fs.curv, read.fs.mgh, read.fs.weight, write.fs.curv, write.fs.mgh, write.fs.morph, write.fs.weight

Examples

curvfile = system.file("extdata", "lh.thickness", package = "freesurferformats", mustWork = TRUE);
c = read.fs.morph(curvfile);
cat(sprintf("Read data for %d vertices. Values: min=%f, mean=%f, max=%f.\n", length(c), min(c), mean(c), max(c)));

mghfile = system.file("extdata", "lh.curv.fwhm10.fsaverage.mgz", package = "freesurferformats", mustWork = TRUE);
curv = read.fs.morph(mghfile);
cat(sprintf("Read data for %d vertices. Values: min=%f, mean=%f, max=%f.\n", length(c), min(c), mean(c), max(c)));

read.fs.patch

Read FreeSurfer binary or ASCII patch file.

Description

A patch is a subset of a surface. Note that the contents of ASCII and binary patch format files is different. A binary format patch contains vertices only, without connection (face) information. ASCII patch files can also contain face data. See the return value description for details.

Usage

read.fs.patch(filepath, format = "auto")

Arguments

filepath string. Full path to the input patch file. An example file is ‘FREESURFER_HOME/subjects/fsaverage/surf/lh.cortex.patch.3d’.

format one of ‘auto’, ‘asc’, or ‘bin’. The format to assume. If set to ‘auto’ (the default), binary format will be used unless the filepath ends with ‘.asc’.
Value

named list with 2 entries: "faces": can be NULL, only available if the format is ASCII, see return value of `read.fs.patch.asc`. "vertices": numerical *n*×7 matrix. The columns are named, and appear in the following order: 'vert_index1': the one-based (R-style) vertex index. 'x', 'y', 'z': float vertex coordinates. 'is_border': integer, 1 if the vertex lies on the patch border, 0 otherwise (treat as logical). 'raw_vtx': integer, the raw vtx value encoding index and border. 'vert_index0': the zero-based (C-style) vertex index.

See Also

Other patch functions: `fs.patch`, `read.fs.patch.asc`, `write.fs.patch`
Description

Read a brain surface mesh consisting of vertex and face data from a file in FreeSurfer binary or ASCII surface format. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/surf/lh.white'.

Usage

read.fs.surface(filepath, format = "auto")

Arguments

filepath string. Full path to the input surface file. Note: gzipped files are supported and gz format is assumed if the filepath ends with ".gz".

format one of 'auto', 'asc', or 'bin'. The format to assume. If set to 'auto' (the default), binary format will be used unless the filepath ends with '.asc'.

Value

named list. The list has the following named entries: "vertices": nx3 double matrix, where n is the number of vertices. Each row contains the x,y,z coordinates of a single vertex. "faces": nx3 integer matrix. Each row contains the vertex indices of the 3 vertices defining the face. WARNING: The indices are returned starting with index 1 (as used in GNU R). Keep in mind that you need to adjust the index (by subtracting 1) to compare with data from other software.

See Also

Other mesh functions: read.fs.surface.asc, read_nisurfacefile, read_nisurface, write.fs.surface.asc, write.fs.surface

Examples

surface_file = system.file("extdata", "lh.tinysurface", package = "freesurferformats", mustWork = TRUE);
mesh = read.fs.surface(surface_file);
cat(sprintf("Read data for %d vertices and %d faces. \n", nrow(mesh$vertices), nrow(mesh$faces)));
**read.fs.surface.asc**  
*Read FreeSurfer ASCII format surface.*

**Description**

Read FreeSurfer ASCII format surface.

**Usage**

```
read.fs.surface.asc(filepath)
```

**Arguments**

- `filepath`  
  - string. Full path to the input surface file in ASCII surface format.

**Value**

named list. The list has the following named entries:  
"vertices": nx3 double matrix, where n is the number of vertices. Each row contains the x,y,z coordinates of a single vertex.  
"faces": nx3 integer matrix. Each row contains the vertex indices of the 3 vertices defining the face.  
WARNING: The indices are returned starting with index 1 (as used in GNU R). Keep in mind that you need to adjust the index (by subtracting 1) to compare with data from other software.

**See Also**

Other mesh functions:  
`read.fs.surface`, `read_nisurfacefile`, `read_nisurface`, `write.fs.surface.asc`, `write.fs.surface`

---

**read.fs.weight**  
*Read file in FreeSurfer weight or w format*

**Description**

Read morphometry data in weight format (aka ‘w‘ files). A weight format file contains morphometry data for a set of vertices, defined by their index in a surface. This can be only a *subset* of the surface vertices.

**Usage**

```
read.fs.weight(filepath, format = "auto")
```

**Arguments**

- `filepath`  
  - string. Full path to the input weight file. Weight files typically have the file extension '.w', but that is not enforced.
- `format`  
  - one of ‘auto’, ‘asc’, or ‘bin’. The format to assume. If set to ‘auto’ (the default), binary format will be used unless the filepath ends with ‘.w.asc’.
Value

the indices and weight data, as a named list. Entries: "vertex_indices": vector of *n* vertex indices. They are stored zero-based in the file, but are returned one-based (R-style). "value": double vector of length *n*, the morphometry data for the vertices. The data can be whatever you want.

See Also

Other morphometry functions: `fs.get.morph.file.ext.for.format`, `fs.get.morph.file.format.from.filename`, `read.fs.curv`, `read.fs.mgh`, `read.fs.morph`, `write.fs.curv`, `write.fs.mgh`, `write.fs.morph`, `write.fs.weight`

---

**read_nisurface**  
*Read a surface, based on the file path without extension.*

Description

Tries to read all files which can be constructed from the base path and the given extensions.

Usage

```r
read_nisurface(filepath_noext, extensions = c("", ".asc", ".gii"), ...)
```

Arguments

- `filepath_noext` character string, the full path to the input surface file without file extension.
- `extensions` vector of character strings, the file extensions to try.
- `...` parameters passed on to `read_nisurfacefile`. Allows you to set the 'methods'.

Value

an instance of ‘fs.surface’, read from the file. See `read.fs.surface` for details. If none of the reader methods succeed, an error is raised.

See Also

Other mesh functions: `read.fs.surface.asc`, `read.fs.surface`, `read_nisurfacefile`, `write.fs.surface.asc`, `write.fs.surface`

Examples

```r
surface_filepath_noext = paste(get_optional_data_filepath("subjects_dir/subject1/surf/"), 'lh.white', sep="");
mesh = read_nisurface(surface_filepath_noext);
```

read_nisurfacefile

S3 method to read a neuroimaging surface file.

Description

Tries to read the file with all implemented surface format reader methods. The file must exist. With the default settings, one can read files in the following surface formats: 1) FreeSurfer binary surface format (e.g., 'surf/lh.white'). 2) FreeSurfer ASCII surface format (e.g., 'surf/lh.white,asc'). 3) GIFTI surface format, only if package 'gifti' is installed. See read_gifti for details. Feel free to implement additional methods. Hint: keep in mind that they should return one-based indices.

Usage

read_nisurfacefile(filepath, methods = c("fsnative", "fsascii", "gifti"),
...)

Arguments

filepath character string, the full path to the input surface file.
methods list of character strings, the formats to try. Each of these must have a function called read_nisurface.<method>, which must return an 'fs.surface' instance on success.
... parameters passed on to the individual methods

Value

an instance of 'fs.surface', read from the file. See read.fs.surface for details. If none of the reader methods succeed, an error is raised.

See Also

Other mesh functions: read.fs.surface.asc, read.fs.surface, read_nisurface, write.fs.surface.asc, write.fs.surface

Examples

surface_file = system.file("extdata", "lh.tinysurface",
                          package = "freesurferformats", mustWork = TRUE);
mesh = read_nisurface(surface_file);
mesh;
read_nisurfacefile.fsascii

Read a FreeSurfer ASCII surface file.

Description
Read a FreeSurfer ASCII surface file.

Usage
## S3 method for class 'fsascii'
read_nisurfacefile(filepath, ...)

Arguments

filepath character string, the full path to the input surface file.
...

parameters passed to read.fs.surface.asc.

Value
an instance of 'fs.surface', read from the file. See read.fs.surface for details. If none of the reader methods succeed, an error is raised.

read_nisurfacefile.fsnative

Read a FreeSurfer ASCII surface file.

Description
Read a FreeSurfer ASCII surface file.

Usage
## S3 method for class 'fsnative'
read_nisurfacefile(filepath, ...)

Arguments

filepath character string, the full path to the input surface file.
...

parameters passed to read.fs.surface.

Value
an instance of 'fs.surface', read from the file. See read.fs.surface for details. If none of the reader methods succeed, an error is raised.
read_nisurfacefile.gifti

*Read a gifti file as a surface.*

Description

Read a gifti file as a surface.

Usage

```
## S3 method for class 'gifti'
read_nisurfacefile(filepath, ...)
```

Arguments

- `filepath` character string, the full path to the input surface file.
- `...` ignored

Value

an instance of `fs.surface`, read from the file. See `read.fs.surface` for details. If none of the reader methods succeed, an error is raised.

write.fs.annot

*Write annotation to binary file.*

Description

Write an annotation to a FreeSurfer binary format annotation file in the new format (v2). An annotation (or brain parcellation) assigns each vertex to a label (or region). One of the regions is often called 'unknown' or similar and all vertices which are not relevant for the parcellation are assigned this label.

Usage

```
write.fs.annot(filepath, num_vertices = NULL, colortable = NULL,
               labels_as_colorcodes = NULL,
               labels_as_indices_into_colortable = NULL, fs.annot = NULL)
```
Arguments

filepath  
string, path to the output file

num_vertices  
integer, the number of vertices of the surface. Must be given unless parameter
'fs.annot' is not NULL.

colortable  
dataframe that contains one region per row. Required columns are: 'struct_name':
character string, the region name. 'r': integer in range 0-255, the RGB color
value for the red channel. 'g': same for the green channel. 'b': same for the
blue channel. 'a': the alpha (transparency) channel value. Optional columns
are: 'code': the color code. Will be computed if not set. Note that you can pass
the dataframe returned by read.fs.annot as 'colortable_df'. Only required if
'labels_as_indices_into_colortable' is used.

labels_as_colorcodes  
vector of *n* integers. The first way to specify the labels. Each integer is a
colorcode, that has been computed from the RGBA color values of the regions
in the colortable as $r + g \times 2^8 + b \times 2^16 + a \times 2^24$. If you do not already have
these color codes, it is way easier to set this to NULL and define the labels as
indices into the colortable, see parameter 'labels_as_indices_into_colortable'.

labels_as_indices_into_colortable  
vector of *n* integers, the second way to specify the labels. Each integer is an
index into the rows of the colortable. Indices start with 1. This parameter and
'labels_as_colorcodes' are mutually exclusive, but required.

fs.annot  
instance of class 'fs.annot'. If passed, this takes precedence over all other pa-
rameters and they should all be NULL (with the exception of 'filepath').

See Also

Other atlas functions: colortable.from.annot, read.fs.annot, read.fs.colortable, write.fs.colortable

Examples

# Load annotation
annot_file = system.file("extdata", "lh.aparc.annot.gz", 
package = "freesurferformats", 
mustWork = TRUE);
annot = read.fs.annot(annot_file);

# New method: write the annotation instance:
write.fs.annot(tempfile(fileext=".annot"), fs.annot=annot);

# Old method: write it from its parts:
write.fs.annot(tempfile(fileext=".annot"), length(annot$vertices), 
annot$colortable_df, labels_as_colorcodes=annot$label_codes);
write.fs.colortable  Write colortable file in FreeSurfer ASCII LUT format.

Description
Write the colortable to a text file in FreeSurfer ASCII colortable lookup table (LUT) format. An example file is ‘FREESURFER_HOME/FreeSurferColorLUT.txt’.

Usage
write.fs.colortable(filepath, colortable)

Arguments
filepath, string. Full path to the output colormap file.
colortable data.frame, a colortable as read by read.fs.colortable. Must contain the following columns: 'struct_name': character string, the label name. 'r': integer in range 0-255, the RGBA color value for the red channel. 'g': same for green channel. 'b': same for blue channel. 'a': same for alpha (transparency) channel. Can contain the following column: 'struct_index': integer, index of the struct entry. If this column does not exist, sequential indices starting at zero are created.

Value
the written dataframe, invisible. Note that this is will contain a column named 'struct_index’, no matter whether the input colortable contained it or not.

See Also
Other atlas functions: colortable.from.annot, read.fs.annot, read.fs.colortable, write.fs.annot
Other colorLUT functions: colortable.from.annot, read.fs.colortable

write.fs.curv  Write file in FreeSurfer curv format

Description
Write vertex-wise brain surface data to a file in FreeSurfer binary 'curv' format. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/surf/lh.thickness', which contains n values. Each value represents the cortical thickness at the respective vertex in the brain surface mesh of bert.

Usage
write.fs.curv(filepath, data)
write.fs.label

Arguments

filepath, string. Full path to the output curv file. If it ends with ".gz", the file is written in gzipped format. Note that this is not common, and that other software may not handle this transparently.
data vector of floats. The brain morphometry data to write, one value per vertex.

See Also

Other morphometry functions: fs.get.morph.file.ext.for.format, fs.get.morph.file.format.from.filename, read.fs.curv, read.fs.mgh, read.fs.morph, read.fs.weight, write.fs.mgh, write.fs.morph, write.fs.weight

write.fs.label Write vertex indices to file in FreeSurfer label format

Description

Write vertex coordinates and vertex indices defining faces to a file in FreeSurfer binary surface format. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/label/lh.cortex'.

Usage

write.fs.label(filepath, vertex_indices, vertex_coords = NULL, vertex_data = NULL, indices_are_one_based = TRUE)

Arguments

filepath string. Full path to the output label file. If it ends with ".gz", the file is written in gzipped format. Note that this is not common, and that other software may not handle this transparently.
vertex_indices instance of class ‘fs.label’ or an integer vector, the label. The vertex indices included in the label. As returned by read.fs.label.
vertex_coords an *n* x 3 float matrix of vertex coordinates, where *n* is the number of 'vertex_indices'. Optional, defaults to NULL, which will write placeholder data. The vertex coordinates are not used by any software I know (you should get them from the surface file). Will be used from ‘fs.label’ instance if given.
vertex_data a numerical vector of length *n*, where *n* is the number of 'vertex_indices'. Optional, defaults to NULL, which will write placeholder data. The vertex data are not used by any software I know (you should get them from a morphometry file). Will be used from ‘fs.label’ instance if given.
indices_are_one_based logical, whether the given indices are one-based, as is standard in R. Indices are stored zero-based in label files, so if this is TRUE, all indices will be incremented by one before writing them to the file. Defaults to TRUE. If FALSE, it is assumed that they are zero-based and they are written to the file as-is. Will be used from ‘fs.label’ instance if given.
write.fs.mgh

Write file in FreeSurfer MGH or MGZ format

Description
Write brain data to a file in FreeSurfer binary MGH or MGZ format.

Usage
write.fs.mgh(filepath, data, vox2ras_matrix = NULL, mr_params = c(0, 0, 0, 0), mri_dtype = "auto")

Arguments
filepath
    string. Full path to the output curv file. If this ends with ".mgz", the file will be written gzipped (i.e., in MGZ instead of MGH format).

data
    matrix of numerical values. The brain data to write. Must be integers or doubles. (The data type is set automatically to MRI_INT for integers and MRI_FLOAT for doubles in the MGH header).

vox2ras_matrix
    4x4 matrix. An affine transformation matrix for the RAS transform that maps voxel indices in the volume to coordinates, such that for y(i1,i2,i3) (i.e., a voxel defined by 3 indices in the volume), the xyz coordinates are vox2ras_matrix*[i1 i2 i3 1]. If no matrix is given (or a NULL value), the ras_good flag will be 0 in the file. Defaults to NULL.
**mr_params**

double vector of length four (without fov) or five. The acquisition parameters, in order: tr, flipangle, te, ti, fov. Spelled out: repetition time, flip angle, echo time, inversion time, field-of-view. The unit for the three times is ms, the angle unit is radians. Defaults to c(0., 0., 0., 0., 0.) if omitted. Pass NULL if you do not want to write them at all.

**mri_dtype**

character string representing an MRI data type code or `auto`. Valid strings are 'MRI_UCHAR' (1 byte unsigned integer), 'MRI_SHORT' (2 byte signed integer), 'MRI_INT' (4 byte signed integer) and 'MRI_FLOAT' (4 byte signed floating point). The default value `auto` will determine the data type from the type of the 'data' parameter. Leave this alone if in doubt.

**See Also**

Other morphometry functions:
- `fs.get.morph.file.ext.for.format`
- `fs.get.morph.file.format.from.filename`
- `read.fs.curv`
- `read.fs.mgh`
- `read.fs.morph`
- `read.fs.weight`
- `write.fs.curv`
- `write.fs.morph`
- `write.fs.weight`

---

**write.fs.morph**

Write morphometry data in a format derived from the given file name (the file extension).

**Description**

Given data and a morphometry file name, derive the proper format and write the file.

**Usage**

```
write.fs.morph(filepath, data)
```

**Arguments**

- `filepath`, string. The full file name. The format to use will be derived from the last characters, the suffix. Supported suffixes are "mgh" for MGH format, "mgz" for MGZ format, everything else will be treated as curv format.
- `data`, numerical vector. The data to write.

**Value**

`format`, string. The format that was used to write the data. One of c("mgh", "mgz", "curv").

**See Also**

Other morphometry functions:
- `fs.get.morph.file.ext.for.format`
- `fs.get.morph.file.format.from.filename`
- `read.fs.curv`
- `read.fs.mgh`
- `read.fs.morph`
- `read.fs.weight`
- `write.fs.curv`
- `write.fs.morph`
- `write.fs.weight`
write.fs.patch Write a surface patch

Description
Write a surface patch, i.e. a set of vertices and patch border information, to a binary patch file.

Usage
write.fs.patch(filepath, patch)

Arguments
- filepath: string. Full path to the output patch file. If it ends with ".gz", the file is written in gzipped format. Note that this is not common, and that other software may not handle this transparently.
- patch: an instance of class 'fs.patch', see read.fs.patch.

Value
the patch, invisible

See Also
Other patch functions: fs.patch, read.fs.patch.asc, read.fs.patch

write.fs.surface Write mesh to file in FreeSurfer binary surface format

Description
Write vertex coordinates and vertex indices defining faces to a file in FreeSurfer binary surface format. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/surf/lh.white'. This function writes the triangle version of the surface file format.

Usage
write.fs.surface(filepath, vertex_coords, faces)
**write.fs.surface.asc**

**Arguments**

- `filepath` string. Full path to the output curv file. If it ends with ".gz", the file is written in gzipped format. Note that this is not common, and that other software may not handle this transparently.
- `vertex_coords` n x 3 matrix of doubles. Each row defined the x,y,z coords for a vertex.
- `faces` n x 3 matrix of integers. Each row defined the 3 vertex indices that make up the face. WARNING: Vertex indices should be given in R-style, i.e., the index of the first vertex is 1. However, they will be written in FreeSurfer style, i.e., all indices will have 1 subtracted, so that the index of the first vertex will be zero.

**Value**

string the format that was written. One of "tris" or "quads". Currently only triangular meshes are supported, so always 'tris'.

**See Also**

Other mesh functions: read.fs.surface.asc, read.fs.surface, read_nisurfacefile, read_nisurface, write.fs.surface.asc

**Examples**

```r
# Read a surface from a file:
surface_file = system.file("extdata", "lh.tinysurface",
   package = "freesurferformats", mustWork = TRUE);
mesh = read.fs.surface(surface_file);

# Now save it:
write.fs.surface(tempfile(), mesh$vertices, mesh$faces);
```

---

**write.fs.surface.asc**  
Write mesh to file in FreeSurfer ASCII surface format

**Description**

Write vertex coordinates and vertex indices defining faces to a file in FreeSurfer ASCII surface format. For a subject (MRI image pre-processed with FreeSurfer) named 'bert', an example file would be 'bert/surf/lh.white.asc'.

**Usage**

`write.fs.surface.asc(filepath, vertex_coords, faces)`
write.fs.weight

Write file in FreeSurfer weight format

Description

Write vertex-wise brain data for a set of vertices to a binary file in *weight* format. This format is also known as *paint* format or simply as *w* format.

Usage

write.fs.weight(filepath, vertex_indices, values)
**write.fs.weight**

**Arguments**

- filepath, string. Full path to the output weight file.
- vertex_indices vector of integers, the vertex indices. Must be one-based (R-style). This function will subtract 1, as they need to be stored zero-based in the file.
- values vector of floats. The brain morphometry data to write, one value per vertex.

**See Also**

Other morphometry functions: `fs.get.morph.file.ext.for.format`, `fs.get.morph.file.format.from.filename`, `read.fs.curv`, `read.fs.mgh`, `read.fs.morph`, `read.fs.weight`, `write.fs.curv`, `write.fs.mgh`, `write.fs.morph`
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