

# Package ‘ciftiTools’

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**Type** Package

**Title** Tools for Reading, Writing, Viewing and Manipulating CIFTI Files

**Version** 0.12.2

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**Description** CIFTI files contain brain imaging data in “grayordinates,” which represent the gray matter as cortical surface vertices (left and right) and subcortical voxels (cerebellum, basal ganglia, and other deep gray matter). ‘ciftiTools’ provides a unified environment for reading, writing, visualizing and manipulating CIFTI-format data. It supports the “dscalar,” “dlabel,” and “dtseries” intents. Grayordinate data is read in as a “xifti” object, which is structured for convenient access to the data and metadata, and includes support for surface geometry files to enable spatially-dependent functionality such as static or interactive visualizations and smoothing.

**Depends** R (>= 3.5.0)

**License** GPL-3

**Encoding** UTF-8

**Imports** fields, gifti (> 0.7.5), grDevices, oro.nifti, RNifti,  
RColorBrewer, rgl, viridisLite, xml2

**Suggests** covr, ggplot2, ggpubr, grid, gridExtra, htmlwidgets,  
manipulateWidget, knitr, rmarkdown, png, testthat (>= 3.0.0)

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**URL** <https://github.com/mandymejia/ciftiTools>

**BugReports** <https://github.com/mandymejia/ciftiTools/issues>

**NeedsCompilation** no

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---

 add\_surf

*Add surface(s) to a "xifti"*


---

### Description

Add left or right cortical surface geometry to a "xifti" object.

### Usage

```
add_surf(xifti, surfL = NULL, surfR = NULL)
```

**Arguments**

|       |   |
|-------|---|
| xifti | A "xifti" object.   |
| surfL | (Optional) Left brain surface model. Can be a file path to a GIFTI surface geometry file (ends in "*.surf.gii"), a "gifti" object representing surface geometry, or a "surf" object.  |
| surfR | (Optional) Right brain surface model. Can be a file path to a GIFTI surface geometry file (ends in "*.surf.gii"), a "gifti" object representing surface geometry, or a "surf" object. |

**Details**

surfL will be added to `xifti$surf$cortex_left` and surfR will be added to `xifti$surf$cortex_right`. Any existing surfaces will be overwritten.

If the resolutions of the data and surfaces do not match, the surfaces will be resampled to match the resolution of the data. The barycentric resampling method, which is recommended for anatomical surfaces, will be used.

**Value**

the "xifti" object with added surface geometry components.

**See Also**

Other functions for manipulating 'xifti' objects: [apply\\_xifti\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [newdata\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [select\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

apply\_parc

*Apply function over locations in each parcel*

---

**Description**

Apply a function across all locations in each parcel. By default, the mean value in each parcel is calculated.

**Usage**

```
apply_parc(xii, parc, FUN = mean, mwall_value = NA, ...)
```

**Arguments**

|      |  |
|------|--|
| xii  | The "xifti" data to apply the function over, within each parcel.   |
| parc | The "xifti" "dlabel" parcellation. Each parcel is defined by a unique key in the label table. If there are multiple columns, only the first column will be used. Alternatively, parc can just be a vector of keys whose length is the number of data locations in "xii". |

|                          |  |
|--------------------------|--|
| FUN                      | A function that takes as input an $M \times N$ matrix ( $M$ locations in a given parcel, and $N$ measurements/columns in <code>xii</code> ) and outputs a constant-sized ( $Q$ ) numeric vector. |
| <code>mwall_value</code> | If there is a medial wall in <code>xii</code> , what should value should medial wall locations be replaced with prior to calculation? Default: NA.   |
| ...                      | Additional arguments to FUN.   |

**Value**

A  $P \times Q$  matrix, where  $P$  is the number of parcels and  $Q$  is the length of the output of FUN. (For mean,  $Q = 1$ ).

---

`apply_xifti`                      *Apply a function along the rows or columns of a "xifti"*

---

**Description**

Apply a many-to-N function (e.g. mean) to the rows or columns of a "xifti". If applied row-wise, a "xifti" with N data column(s) is returned. (If the "xifti" had the `dlabel` intent, and values that are not labels are created, then it is converted to `dscalar`.) If applied column-wise, a numeric matrix with N rows is returned.

For univariate functions, use [transform\\_xifti](#) instead.

**Usage**

```
apply_xifti(xifti, margin = c(1, 2), FUN, ...)
```

**Arguments**

|                     |  |
|---------------------|--|
| <code>xifti</code>  | A "xifti" object.  |
| <code>margin</code> | The dimension along which to apply FUN: 1 for rows (default) and 2 for columns.        |
| FUN                 | The function. It should take in a numeric vector and return a length-N numeric vector. |
| ...                 | Additional arguments to FUN  |

**Value**

A "xifti" if `margin == 1`, or a numeric matrix if `margin == 2`

**See Also**

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [newdata\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [select\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

|                 |                                      |
|-----------------|--------------------------------------|
| as.matrix.xifti | <i>Convert a "xifti" to a matrix</i> |
|-----------------|--------------------------------------|

---

**Description**

Converts a "xifti" to a matrix by concatenating the data from each brainstructure along the rows. Surfaces and metadata are discarded.

**Usage**

```
## S3 method for class 'xifti'
as.matrix(x, ...)
```

**Arguments**

|     |                   |
|-----|-------------------|
| x   | A "xifti" object. |
| ... | Unused            |

**Value**

The input as a matrix. Each brainstructure's data is concatenated.

---

|          |                                     |
|----------|-------------------------------------|
| as.xifti | <i>Assemble a "xifti" from data</i> |
|----------|-------------------------------------|

---

**Description**

Assembles cortical data, subcortical data, and/or surface geometry to form a "xifti". The inputs must be data objects (vectors, matrices or arrays, depending on the argument).

**Usage**

```
as.xifti(
  cortexL = NULL,
  cortexL_mwall = NULL,
  cortexR = NULL,
  cortexR_mwall = NULL,
  mwall_values = c(NA, NaN),
  subcortVol = NULL,
  subcortLabs = NULL,
  subcortMask = NULL,
  surfL = NULL,
  surfR = NULL,
  col_names = NULL,
  HCP_32k_auto_mwall = TRUE,
```

```

    validate = TRUE
  )

as_xifti(
  cortexL = NULL,
  cortexL_mwall = NULL,
  cortexR = NULL,
  cortexR_mwall = NULL,
  mwall_values = c(NA, NaN),
  subcortVol = NULL,
  subcortLabs = NULL,
  subcortMask = NULL,
  surfL = NULL,
  surfR = NULL
)

as_cifti(
  cortexL = NULL,
  cortexL_mwall = NULL,
  cortexR = NULL,
  cortexR_mwall = NULL,
  mwall_values = c(NA, NaN),
  subcortVol = NULL,
  subcortLabs = NULL,
  subcortMask = NULL,
  surfL = NULL,
  surfR = NULL
)

as_cifti(
  cortexL = NULL,
  cortexL_mwall = NULL,
  cortexR = NULL,
  cortexR_mwall = NULL,
  mwall_values = c(NA, NaN),
  subcortVol = NULL,
  subcortLabs = NULL,
  subcortMask = NULL,
  surfL = NULL,
  surfR = NULL
)

```

### Arguments

cortexL, cortexL\_mwall

Left cortex data and ROI. Each must be a data matrix or vector.

If cortexL\_mwall is not provided, cortexL should have data for all vertices on the left cortical surface ( $V_L \times T$  data matrix). There will not be a mask for the medial wall. Not providing the medial wall mask is appropriate for ".dlabels.nii"

files where the medial wall may have its own label and therefore should not be treated as missing data.

If `cortexL_mwall` is provided, `cortexL` should either have data for all vertices on the left cortical surface ( $V_L \times T$  data matrix, with filler values e.g.  $\emptyset$  or NaN for medial wall vertices), or have data only for non-medial wall vertices ( $(V_L - mwall_L) \times T$  data matrix). The medial wall mask will be the  $\emptyset$  values in `cortexL_mwall`. The medial wall mask should be provided whenever the medial wall should be treated as missing data.

Since the unmasked cortices must have the same number of vertices, `V_L` should match `V_R`.

`cortexR`, `cortexR_mwall`

Right cortex data and ROI. Each must be a data matrix or vector.

If `cortexR_mwall` is not provided, `cortexR` should have data for all vertices on the right cortical surface ( $V_R \times T$  data matrix). `mwallR` will not be a mask for the medial wall. Not providing the medial wall mask is appropriate for ".dlabels.nii" files where the medial wall may have its own label and therefore should not be treated as missing data.

If `cortexR_mwall` is provided, `cortexR` should either have data for all vertices on the right cortical surface ( $V_R \times T$  data matrix, with filler values e.g.  $\emptyset$  or NaN for medial wall vertices), or have data only for non-medial wall vertices ( $(V_R - mwall_R) \times T$  data matrix). The medial wall mask will be the  $\emptyset$  values in `cortexR_mwall`. The medial wall mask should be provided whenever the medial wall should be treated as missing data.

Since the unmasked cortices must have the same number of vertices, `V_L` should match `V_R`.

`mwall_values`

If `cortex[L/R]_mwall` was not provided, or if it was invalid (i.e. bad length or all TRUE), the medial wall mask will be inferred from rows in `cortex[L/R]` that are constantly one of these values. Default: `c(NA, NaN)`. If NULL, do not attempt to infer the medial wall from the data values. NULL should be used if NA or NaN are legitimate values that non-medial wall vertices might take on.

`subcortVol`, `subcortLabs`, `subcortMask`

`subcortVol` represents the data values of the subcortex. It is either a 3D/4D numeric array ( $i \times j \times k \times T$ ), or a vectorized matrix ( $V_S$  voxels by  $T$  measurements). If it's vectorized, the voxels should be in spatial order ( $i$  index increasing fastest, then  $j$ , then  $k$ ).

`subcortLabs` represents the brainstructure labels of each voxel: see [substructure\\_table](#).

It is either a 3D data array ( $i \times j \times k$ ) of integer brainstructure indices, or a  $V_S$  length vector in spatial order with brainstructure names as factors or integer indices. The indices should be 3-21 (1 and 2 correspond to left and right cortex, respectively) or 1-19 (cortex labels omitted), with 0 representing out-of-mask voxels.

`subcortMask` is logical 3D data array ( $i \times j \times k$ ) where TRUE values indicate subcortical voxels (in-mask). If it is not provided, the mask will be inferred from voxels with labels  $\emptyset$ , NA, or NaN in `subcortLabs`. If `subcortLabs` are vectorized and `subcortMask` is not provided, the mask cannot be inferred so an error will occur.



|                    |   |
|--------------------|---|
| surfL, surfR       | (Optional) Surface geometries for the left or right cortex. Can be a surface GIFTI file path or "surf" object; see <a href="#">make_surf</a> for a full description of valid inputs.  |
| col_names          | Names of each measurement/column in the data.   |
| HCP_32k_auto_mwall | If left and/or right cortex data is provided, and the number of vertices matches that of the HCP 32k mesh (29696 on left, and 29716 on right), should the medial wall masks be added to the "xifti" if not provided? Default: TRUE. |
| validate           | Validate that the result is a "xifti"? Default: TRUE. If FALSE, the result may not be properly formatted if the inputs were invalid.  |

### Details

Each data or surface component is optional. Metadata components (cortex[L/R]\_mwall, subcortLabs, and subcortMask) will be ignored if its corresponding data component is not provided. If no data or surface components are provided, then the [template\\_xifti](#) will be returned.

If cortical data are provided without a corresponding medial wall mask, or if the provided mask is invalid or empty, then the medial wall will be inferred from data rows that are constantly a value in mwall\_values. But if mwall\_values is NULL, no attempt to infer the medial wall will be made and the medial wall metadata entry will be NULL.

The total number of grayordinates will be  $G = (V_L - mwall_L) + (V_R - mwall_R) + V_S$ :  $V_L - mwall_L$  left vertices,  $V_R - mwall_R$  right vertices and  $V_S$  subcortical voxels.  $T$ , the total number of measurements (columns of data), must be the same for each brainstructure.

### Value

A "xifti"

### See Also

Other functions for reading in CIFTI or GIFTI data: [info\\_cifti\(\)](#), [load\\_parcs\(\)](#), [load\\_surf\(\)](#), [read\\_cifti\(\)](#), [read\\_surf\(\)](#), [read\\_xifti2\(\)](#)

---

boundary\_mask\_surf      *Boundary region of a mask*

---

### Description

Identify the vertices within boundary\_width edges of a vertex in the input mask on a triangular mesh. Returns a logical indicating if a vertex is within boundary\_width edges of the mask.

### Usage

```
boundary_mask_surf(faces, mask, boundary_width = 10)
```

**Arguments**

|                |   |
|----------------|---|
| faces          | An $F \times 3$ matrix, where each row contains the vertex indices for a given triangular face in the mesh. $F$ is the number of faces in the mesh.   |
| mask           | A length $V$ logical vector indicating if each vertex is within the input mask.   |
| boundary_width | A positive integer representing the width of the boundary to compute. The furthest vertices from the input mask will be this number of edges away from the closest vertex in the input mask. Default: 10. |

**Value**

A length- $V$  logical vector. Each entry corresponds to the vertex with the same index. The value is true if a vertex is within `boundary_width` edges of a vertex in the mesh, but is not within the mesh itself.

---

ciftiTools

*ciftiTools: Tools for Reading and Visualizing CIFTI Brain Files*


---

**Description**

Here are groups of commonly-used functions in `ciftiTools`:

**Details**

Functions for reading in CIFTI or GIFTI data:

- `read_xifti`: Read in a CIFTI file as a "xifti"
- `read_xifti2`: Read in GIFTI files as a "xifti"
- `as.xifti`: Combine numeric data to form a "xifti"
- `read_surf`: Read in a surface GIFTI file as a "surf"
- `info_cifti`: Read the metadata in a CIFTI file
- `load_surf`: Read in a surface included in `ciftiTools`
- `load_parcc`: Read in a parcellation included in `ciftiTools`

Functions for writing CIFTI or GIFTI data:

- `write_cifti`: Write a "xifti" to a CIFTI file
- `write_xifti2`: Write a "xifti" to GIFTI and NIFTI files
- `write_metric_gifti`: Write a numeric data matrix to a metric GIFTI file
- `write_surf_gifti`: Write a "surf" to a surface GIFTI file
- `write_subcort_nifti`: Write subcortical data to NIFTI files
- `separate_cifti`: Separate a CIFTI file into GIFTI and NIFTI files

Functions for manipulating "xifti"s:

- `apply_xifti`: Apply a function along the rows or columns of the "xifti" data matrix
- `combine_xifti`: Combine multiple "xifti"s with non-overlapping brain structures
- `convert_xifti`: Convert the intent of a "xifti"
- `merge_xifti`: Concatenate data matrices from multiple "xifti"s
- `newdata_xifti`: Replace the data matrix in a "xifti"
- `remove_xifti`: Remove a brain structure or surface from a "xifti"
- `select_xifti`: Select data matrix columns of a "xifti"
- `transform_xifti`: Apply a univariate transformation to a "xifti" or pair of "xifti"s
- `add_surf`: Add surfaces to a "xifti"
- `move_from_mwall`: Move medial wall vertices back into the "xifti" data matrix
- `move_to_mwall`: Move rows with a certain value into the "xifti" medial wall mask

S3 methods for "xifti"s:

- `summary` and `print`: Summarize the contents.
- `as.matrix`: Convert data to a locations by measurements numeric matrix.
- `dim`: Obtain number of locations and number of measurements.
- `plot`: Visualize the cortical surface and/or subcortical data.
- `+`, `-`, `*`, `/`, `^`, `%%`, `%/%`: Operation between a "xifti" and a scalar, or between two "xifti"s.
- `abs`, `ceiling`, `exp`, `floor`, `log`, `round`, `sign`, and `sqrt`: Univariate transformation of "xifti" data.

Functions for working with surfaces:

- `read_surf`: Read in a surface GIFTI file as a "surf"
- `is_surf`: Verify a "surf"
- `write_surf_gifti`: Write a "surf" to a surface GIFTI file
- `view_surf`: Visualize a "surf"
- `resample_surf`: Resample a "surf"
- `rotate_surf`: Rotate the geometry of a "surf"

---

|                  |                  |
|------------------|------------------|
| ciftiTools.files | ciftiTools.files |
|------------------|------------------|

---

**Description**

CIFTI and surface GIFTI files included in the ciftiTools package

**Usage**

```
ciftiTools.files()
```

**Details**

The CIFTI files are from NITRC: cifti-2\_test\_data-1.2.zip at [https://www.nitrc.org/frs/?group\\_id=454](https://www.nitrc.org/frs/?group_id=454)

The surfaces are from the HCP and are included according to these data use terms: Data were provided [in part] by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University.

Only the inflated surfaces are available as GIFTI files. To access the other surfaces included in the package (very inflated and midthickness), see [load\\_surf](#).

**Value**

a list of file paths

---

|                      |                                |
|----------------------|--------------------------------|
| ciftiTools.getOption | <i>Get a ciftiTools option</i> |
|----------------------|--------------------------------|

---

**Description**

Gets an R option (with prefix "ciftiTools\_") value. See [ciftiTools.listOptions](#).

**Usage**

```
ciftiTools.getOption(opt)
```

**Arguments**

|     |             |
|-----|-------------|
| opt | The option. |
|-----|-------------|

**Value**

The value, val

---

`ciftiTools.listOptions`  
*List ciftiTools options*

---

**Description**

List ciftiTools options

**Usage**

`ciftiTools.listOptions()`

**Value**

data.frame describing the options

---

`ciftiTools.setOption` *Set a ciftiTools option*

---

**Description**

Sets an R option (with prefix "ciftiTools\_"). See [ciftiTools.listOptions](#).

**Usage**

`ciftiTools.setOption(opt, val)`

**Arguments**

|                  |                                 |
|------------------|---------------------------------|
| <code>opt</code> | The option.                     |
| <code>val</code> | The value to set the option as. |

**Value**

The new value, `val`

---

|               |   |
|---------------|---|
| combine_xifti | <i>Combine "xifti"s with non-overlapping brain structures</i> |
|---------------|---|

---

### Description

Combine two to three "xifti"s with non-overlapping brain structures into a single "xifti". The names, intent, and surfaces of the first will be used, if present. To add more surfaces to the result, use [add\\_surf](#).

### Usage

```
combine_xifti(..., xii_list = NULL, meta = c("first", "all"))
```

### Arguments

|          |   |
|----------|---|
| ...      | The "xifti" objects   |
| xii_list | Alternatively, a list of "xifti" objects. If specified, will ignore ...   |
| meta     | "first" (default) to just use the metadata from the first argument, or "all" to include the other metadata in a list. |

### Value

A "xifti" with data from the inputs

### See Also

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [apply\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [newdata\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [select\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

|           |                                |
|-----------|--------------------------------|
| dim.xifti | <i>Dimensions of a "xifti"</i> |
|-----------|--------------------------------|

---

### Description

Returns the number of rows (vertices + voxels) and columns (measurements) in the "xifti" data.

### Usage

```
## S3 method for class 'xifti'
dim(x)
```

### Arguments

|   |                   |
|---|-------------------|
| x | A "xifti" object. |
|---|-------------------|

### Value

The number of rows and columns in the "xifti" data.

---

|                |                             |
|----------------|-----------------------------|
| edit_mask_surf | <i>Edit mask on surface</i> |
|----------------|-----------------------------|

---

**Description**

Erode, dilate, or get the borders of a mask along the cortical surface

**Usage**

```
edit_mask_surf(
  x,
  mwall = NULL,
  surf = NULL,
  hemisphere = c("left", "right"),
  do = c("erode", "dilate", "borders"),
  depth = 1
)

erode_mask_surf(
  x,
  mwall = NULL,
  surf = NULL,
  hemisphere = c("left", "right"),
  depth = 1
)

dilate_mask_surf(
  x,
  mwall = NULL,
  surf = NULL,
  hemisphere = c("left", "right"),
  depth = 1
)
```

**Arguments**

**x, mwall** Vector of the data mask to edit, and the medial wall mask. These can be specified in two ways. First, `mwall` can be a logical vector with each entry corresponding to a vertex as the cortical surface, and using `FALSE` values to indicate medial wall vertices. In this first case, `x` should then be a logical vector with each entry corresponding to a `TRUE` value in `mwall`. `TRUE` values in `x` should indicate the mask to be edited.

Second, `mwall` can be `NULL` (default) in which case `x` should then be a logical vector with each entry corresponding to a vertex on the cortical surface. `TRUE` values in `x` should indicate the mask to be edited.

In either case, `xii$data$cortex_left[,1]` and `xii$meta$cortex$medial_wall_mask$left` should work.

|                  |  |
|------------------|--|
| surf, hemisphere | Provide one: the surface in the same resolution as the data, or the name of the hemisphere of the surface to resample and use (default: resample the left surface).  |
| do               | "erode" (default), "dilate", or "borders". "erode" removes faces with at least one vertex not inside the mask. "dilate" adds faces with at least one vertex inside the mask. "borders" obtains the vertices inside the mask which share a face with at least one vertex not inside the mask. |
| depth            | How many iterations of the edit? Default: 1. Does not apply to "borders".  |

### Details

The depth of the edit is determined by the number of edges between the vertices. To erode or dilate based on spatial distance (mm), see `-cifti-dilate` and `-cifti-erode`.

### Value

x after erosion or dilation.

---

|                |                                       |
|----------------|---------------------------------------|
| even_vert_samp | <i>Evenly sample vertices of mesh</i> |
|----------------|---------------------------------------|

---

### Description

Get a subset of the mesh vertices that are spatially evenly-sampled, by resampling the mesh and choosing the original vertices closest (Euclidian distance) to the new vertices.

### Usage

```
even_vert_samp(surf, n_vert)
```

### Arguments

|        |  |
|--------|--|
| surf   | A "surf" object  |
| n_vert | The desired number of vertices in the evenly-spaced sample. Note that the actual size of the subset will likely be close to but not exactly <code>n_vert</code> because it depends on the size of the resampled surface. |

### Value

An integer vector giving the indices of the vertices in the subset.



---

|                  |   |
|------------------|---|
| expand_color_pal | <i>Interpolates between entries in the input palette to make a larger palette with COLOR_RES entries.</i> |
|------------------|---|

---

**Description**

Interpolates between entries in the input palette to make a larger palette with COLOR\_RES entries.

**Usage**

```
expand_color_pal(pal, COLOR_RES = 255)
```

**Arguments**

|           |  |
|-----------|--|
| pal       | The color palette to expand, as a data.frame with two columns: "color" (character: color hex codes) and "value" (numeric). |
| COLOR_RES | The number of entries to have in the output palette.   |

**Value**

A data.frame with two columns: "color" (character: color hex codes) and "value" (numeric)

---

|             |              |
|-------------|--------------|
| faces_Param | <i>faces</i> |
|-------------|--------------|

---

**Description**

faces

**Arguments**

|       |   |
|-------|---|
| faces | An $F \times 3$ matrix, where each row contains the vertex indices for a given triangular face in the mesh. $F$ is the number of faces in the mesh. |
|-------|---|

---

|           |                      |
|-----------|----------------------|
| fix_xifti | <i>Fix a "xifti"</i> |
|-----------|----------------------|

---

**Description**

Make adjustments to a putative "xifti" so that it is valid. Each adjustment is reported.

**Usage**

```
fix_xifti(xifti, verbose = TRUE)
```

**Arguments**

|         |                                       |
|---------|---------------------------------------|
| xifti   | A "xifti" object.                     |
| verbose | Report each adjustment? Default: TRUE |

**Details**

Right now it only coerces the data to numeric matrices.

**Value**

The fixed "xifti"

---

|                 |  |
|-----------------|--|
| get_wb_cmd_path | <i>Get the Connectome Workbench command path</i> |
|-----------------|--|

---

**Description**

Retrieves the path to the Connectome Workbench executable from a file path that may point to the executable itself, or to the Workbench folder which contains it (i.e., "path/to/workbench/bin\_linux64/wb\_command" or "path/to/workbench".)

**Usage**

```
get_wb_cmd_path(wb_path)
```

**Arguments**

|         |   |
|---------|---|
| wb_path | (Optional) Path to the Connectome Workbench folder or executable. |
|---------|---|

**Value**

The path to the Connectome Workbench executable

---

|                  |   |
|------------------|---|
| infer_resolution | <i>Infer resolution from "xifti" and surfaces</i> |
|------------------|---|

---

### Description

Infer the numbers of vertices on each cortex of a "xifti" object. Also supports the result of [info\\_cifti](#).

### Usage

```
infer_resolution(xifti, surfL = NULL, surfR = NULL)
```

### Arguments

|       |                   |
|-------|-------------------|
| xifti | A "xifti" object. |
| surfL | Left surface      |
| surfR | Right surface     |

### Value

The inferred resolution

---

|            |                           |
|------------|---------------------------|
| info_cifti | <i>Get CIFTI metadata</i> |
|------------|---------------------------|

---

### Description

Get CIFTI metadata from the NIFTI header and XML using the Connectome Workbench command `-nifti-information`. The information is formatted as the meta component in a "xifti" object (see [template\\_xifti](#)), and includes:

1. medial wall masks for the left and right cortex
2. the subcortical labels (ordered spatially)
3. the subcortical mask
4. other NIFTI intent-specific metadata

### Usage

```
info_cifti(cifti_fname)
```

```
infoCIfTI(cifti_fname)
```

```
infocii(cifti_fname)
```

**Arguments**

cifti\_fname      File path to a CIFTI file (ending in ".d\*.nii").

**Details**

Additional metadata depends on the type of CIFTI file:

1. "dtseries"
  - (a) time\_start: Start time
  - (b) time\_step: The TR
  - (c) time\_unit: Unit of time
2. "dscalar"
  - (a) names: Name of each data column
3. "dlabels"
  - (a) names:( Names of each data column.)
  - (b) labels:( List of  $L \times 5$  data.frames. Row names are the label names. Column names are Key, Red, Green, Blue, and Alpha. List entry names are the names of each data column.)

**Value**

The metadata component of a "xifti" for the input CIFTI file

**Connectome Workbench**

This function interfaces with the "-nifti-information" Workbench command.

**Label Levels**

xifti\$meta\$subcort\$labels is a factor with the following levels:

1. Cortex-L
2. Cortex-R
3. Accumbens-L
4. Accumbens-R
5. Amygdala-L
6. Amygdala-R
7. Brain Stem
8. Caudate-L
9. Caudate-R
10. Cerebellum-L
11. Cerebellum-R
12. Diencephalon-L
13. Diencephalon-R

14. Hippocampus-L
15. Hippocampus-R
16. Pallidum-L
17. Pallidum-R
18. Putamen-L
19. Putamen-R
20. Thalamus-L
21. Thalamus-R

These correspond to the same structures as given by `ft_read_cifti` in the `cifti-matlab` MATLAB toolbox. Note that the first two levels (left and right cortex) are not used.

### See Also

Other functions for reading in CIFTI or GIFTI data: `as.xifti()`, `load_parcs()`, `load_surf()`, `read_cifti()`, `read_surf()`, `read_xifti2()`

---

|                       |                                  |
|-----------------------|----------------------------------|
| <code>is.cifti</code> | <i>Validate a "xifti" object</i> |
|-----------------------|----------------------------------|

---

### Description

Check if object is valid for a "xifti". This alias for `is.xifti` is offered as a convenience, and a message will warn the user. We recommend using `is.xifti` instead.

### Usage

```
is.cifti(x, messages = TRUE)
```

```
is_cifti(x, messages = TRUE)
```

```
isCIFTI(x, messages = TRUE)
```

### Arguments

|                       |   |
|-----------------------|---|
| <code>x</code>        | The putative "xifti".   |
| <code>messages</code> | If <code>x</code> is not a "xifti", print messages explaining the problem? Default is TRUE. |

### Details

Requirements: it is a list with the same structure as `template_xifti`. The size of each data entry must be compatible with its corresponding mask (medial wall for the cortex and volumetric mask for the subcortex). Metadata should be present if and only if the corresponding data is also present. The surfaces can be present whether or not the cortex data are present.

See the "Label Levels" section for the requirements of `xifti$meta$subcort$labels`.

**Value**

Logical. Is `x` a valid "xifti"?

**Label Levels**

`xifti$meta$subcort$labels` is a factor with the following levels:

1. Cortex-L
2. Cortex-R
3. Accumbens-L
4. Accumbens-R
5. Amygdala-L
6. Amygdala-R
7. Brain Stem
8. Caudate-L
9. Caudate-R
10. Cerebellum-L
11. Cerebellum-R
12. Diencephalon-L
13. Diencephalon-R
14. Hippocampus-L
15. Hippocampus-R
16. Pallidum-L
17. Pallidum-R
18. Putamen-L
19. Putamen-R
20. Thalamus-L
21. Thalamus-R

These correspond to the same structures as given by `ft_read_cifti` in the `cifti-matlab` MATLAB toolbox. Note that the first two levels (left and right cortex) are not used.

**See Also**

Other commonly-used functions: [read\\_cifti\(\)](#), [resample\\_cifti\(\)](#), [smooth\\_cifti\(\)](#), [view\\_xifti\\_surface\(\)](#), [view\\_xifti\\_volume\(\)](#), [write\\_cifti\(\)](#)

---

|         |  |
|---------|--|
| is.surf | <i>Validate a "surf" object (vertices + faces)</i> |
|---------|--|

---

### Description

Check if object is valid for `xifti$surf$cortex_left` or `xifti$surf$cortex_right`, where `xifti` is a "xifti" object.

### Usage

```
is.surf(x)
```

### Arguments

`x` The putative "surf".

### Details

This is a helper function for [is.xifti](#).

Requirements: the "surf" must be a list of three components: "vertices", "faces", and "hemisphere". The first two should each be a numeric matrix with three columns. The values in "vertices" represent spatial coordinates whereas the values in "faces" represent vertex indices defining the face. Thus, values in "faces" should be integers between 1 and the number of vertices. The last list entry, "hemisphere", should be "left", "right", or NULL indicating the brain hemisphere which the surface represents.

### Value

Logical. Is `x` a valid "surf"?

### See Also

Other functions for working with GIFTI surface geometry data: [read\\_surf\(\)](#), [resample\\_surf\(\)](#), [rotate\\_surf\(\)](#), [view\\_surf\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

|          |                                   |
|----------|-----------------------------------|
| is.xifti | <i>Validate a "xifti" object.</i> |
|----------|-----------------------------------|

---

### Description

Check if object is valid for a "xifti" object.

### Usage

```
is.xifti(x, messages = TRUE)
```

```
is_xifti(x, messages = TRUE)
```

**Arguments**

|          |   |
|----------|---|
| x        | The putative "xifti" object.  |
| messages | If x is not a "xifti" object, print messages explaining the problem? Default is TRUE. |

**Details**

Requirements: it is a list with the same structure as [template\\_xifti](#). The size of each data entry must be compatible with its corresponding mask (medial wall for the cortex and volumetric mask for the subcortex). Metadata should be present if and only if the corresponding data is also present. The surfaces can be present whether or not the cortex data are present.

See the "Label Levels" section for the requirements of `xifti$meta$subcort$labels`.

**Value**

Logical. Is x a valid "xifti" object?

**Label Levels**

`xifti$meta$subcort$labels` is a factor with the following levels:

1. Cortex-L
2. Cortex-R
3. Accumbens-L
4. Accumbens-R
5. Amygdala-L
6. Amygdala-R
7. Brain Stem
8. Caudate-L
9. Caudate-R
10. Cerebellum-L
11. Cerebellum-R
12. Diencephalon-L
13. Diencephalon-R
14. Hippocampus-L
15. Hippocampus-R
16. Pallidum-L
17. Pallidum-R
18. Putamen-L
19. Putamen-R
20. Thalamus-L
21. Thalamus-R

These correspond to the same structures as given by `ft_read_cifti` in the `cifti-matlab` MATLAB toolbox. Note that the first two levels (left and right cortex) are not used.



---

|           |   |
|-----------|---|
| load_parc | <i>Load a parcellation included in ciftiTools</i> |
|-----------|---|

---

### Description

Load a parcellation included in ciftiTools.

### Usage

```
load_parc(
  name = c("Schaefer_100", "Schaefer_400", "Schaefer_1000", "Yeo_7", "Yeo_17")
)
```

### Arguments

|      |   |
|------|---|
| name | The name of the parcellation to load: <ul style="list-style-type: none"> <li>"Schaefer_100": (2018) 100 parcels based on the "local-global" approach.</li> <li>"Schaefer_400": (2018) 400 parcels based on the "local-global" approach.</li> <li>"Schaefer_1000": (2018) 1000 parcels based on the "local-global" approach.</li> <li>"Yeo_7": (2011) 7 networks based on fcMRI clustering. Networks are further divided into 51 components.</li> <li>"Yeo_17": (2011) 17 networks based on fcMRI clustering. Networks are further divided into 114 components.</li> </ul> |
|------|---|

NULL (default) will load the first choice, where applicable. This argument will affect the indices, colors, and names of each parcel, but not the parcel boundaries.

### Details

When using these parcellations, please cite the corresponding paper(s):

1. Yeo, B. T. T. et al. The organization of the human cerebral cortex estimated by intrinsic functional connectivity. *J Neurophysiol* 106, 1125-1165 (2011).
2. Schaefer, A. et al. Local-Global Parcellation of the Human Cerebral Cortex from Intrinsic Functional Connectivity MRI. *Cereb Cortex* 28, 3095-3114 (2018).
3. Kong, R. et al. Individual-Specific Areal-Level Parcellations Improve Functional Connectivity Prediction of Behavior. *Cerebral Cortex* (2021+) doi:10.1093/cercor/bhab101.

Note that the Schaefer parcels have been matched to networks from Kong (2021+).

### Value

The parcellation as a dlabel "xifti" with one column. Each key represents one unique parcel.

**See Also**

Other functions for reading in CIFTI or GIFTI data: [as.xifti\(\)](#), [info\\_cifti\(\)](#), [load\\_surf\(\)](#), [read\\_cifti\(\)](#), [read\\_surf\(\)](#), [read\\_xifti2\(\)](#)

---

|           |   |
|-----------|---|
| load_surf | <i>Load a "surf" included in ciftiTools</i> |
|-----------|---|

---

**Description**

Load a "surf" object from one of the three 32k anatomical surfaces included in ciftiTools.

**Usage**

```
load_surf(
  hemisphere = c("left", "right"),
  name = c("inflated", "very inflated", "midthickness"),
  resamp_res = NULL
)
```

**Arguments**

|            |   |
|------------|---|
| hemisphere | "left" (default) or "right"   |
| name       | The name of the surface geometry to load: "inflated" (default), "very inflated", and "midthickness".  |
| resamp_res | The resolution to resample the surfaces to. If NULL (default) or 32492, do not resample. Note that the barycentric resampling method, which is recommended for anatomical surfaces, will be used. |

**Details**

The surfaces are from the HCP and are included according to these data use terms: Data were provided [in part] by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University.

**Value**

The "surf" object

**See Also**

Other functions for reading in CIFTI or GIFTI data: [as.xifti\(\)](#), [info\\_cifti\(\)](#), [load\\_parcc\(\)](#), [read\\_cifti\(\)](#), [read\\_surf\(\)](#), [read\\_xifti2\(\)](#)

---

|                |                              |
|----------------|------------------------------|
| make_color_pal | <i>Make a color palette.</i> |
|----------------|------------------------------|

---

## Description

Control the mapping of values to colors with `colors`, `color_mode`, and `zlim`.

## Usage

```
make_color_pal(
  colors = NULL,
  color_mode = c("sequential", "qualitative", "diverging"),
  zlim = NULL
)
```

## Arguments

|                         |   |
|-------------------------|---|
| <code>colors</code>     | (Optional) "ROY_BIG_BL", the name of a ColorBrewer palette (see <code>RColorBrewer::brewer.pal.info</code> and <code>colorbrewer2.org</code> ), the name of a viridisLite palette, or a character vector of colors. NULL (default) will use "ROY_BIG_BL" if <code>color_mode</code> is "sequential" or "diverging", and "Set2" if <code>color_mode</code> is "qualitative". See the description for more details. |
| <code>color_mode</code> | (Optional) "sequential", "qualitative", or "diverging". Default: "sequential". See the description for more details.  |
| <code>zlim</code>       | (Optional) Controls the mapping of values to each color in <code>colors</code> . See the description for more details.  |

## Details

There are three kinds of arguments for `colors`: "ROY\_BIG\_BL", the name of a ColorBrewer palette (see `RColorBrewer::brewer.pal.info` and `colorbrewer2.org`), the name of a viridisLite palette, or a character vector of color names.

If `colors=="ROY_BIG_BL"`, the "ROY\_BIG\_BL" palette will be used. It is the same palette as the default for the Connectome Workbench application (<https://github.com/Washington-University/workbench/blob/master/src/F>). The midpoint will be colored black. From the midpoint toward the upper bound, colors will proceed from black to red to yellow. From the midpoint toward the lower bound, colors will proceed from black to blue to purple to green to aqua. Here is how each color mode behaves if `colors=="ROY_BIG_BL"`:

`color_mode=="sequential"` Only half of the palette will be used. If `zlim` is length 2, the higher value will be the maximum and the lower value will be the minimum. Set `zlim[1] > zlim[2]` to reverse the color scale. (Note that the second half, black → red → yellow, is used by default. To use the negative half specify `colors=="ROY_BIG_BL_neg"` instead. It will also be used automatically by `xifti_read_surface` when the data range is negative.) `zlim` can also be length 10, in which case each value corresponds to the position of an individual color in the half palette.

color\_mode=="qualitative" "ROY\_BIG\_BL" is not recommended for qualitative data, so a warning will be issued. Palette colors will be selected from the landmark "ROY\_BIG\_BL" colors, with interpolated colors added if the number of colors in the palette (18) is less than this range. zlim should be a single number: the number of unique colors to get.

color\_mode=="diverging" If zlim is length 2 or 3, the lowest number will be the lower bound and the highest number will be the upper bound. If zlim is length 3, the middle number will be the midpoint (black). The lower and upper bounds will be aqua and yellow, respectively, except if zlim is in descending order, in which case the color scale will be reversed (lowest is yellow; highest is aqua). zlim can also be length 19, in which case each value corresponds to the position of an individual color in the palette.

If colors is the name of an RColorBrewer palette (see RColorBrewer::brewer.pal.info) or viridisLite palette, the colors in that palette will be used, and the following behavior applies. If colors is a character vector of color names (hex codes or standard R color names), the following behavior applies directly:

color\_mode=="sequential" If zlim is length 2, the higher value will be the maximum and the lower value will be the minimum. Set zlim[1] > zlim[2] to reverse the color scale. zlim can also be the same length as the palette, in which case each value corresponds to the position of an individual color in the palette.

color\_mode=="qualitative" zlim should be a single number: the number of unique colors to get. Color interpolation will be used if the number of colors in the palette is less than this range. If length(zlim)==length(colors), each color will be mapped to each corresponding value.

color\_mode=="diverging" If zlim is length 2 or 3, the lowest number will be the lower bound and the highest number will be the upper bound. If zlim is length 3, the middle number will be the midpoint. Set zlim in descending order to reverse the color scale. zlim can also be the same length as the palette, in which case each value corresponds to the position of an individual color in the palette.

## Value

A data.frame with two columns: "color" (character: color hex codes) and "value" (numeric)

---

mask\_Param\_vertices    *mask: vertices*

---

## Description

mask: vertices

## Arguments

mask                    A length  $V$  logical vector indicating if each vertex is within the input mask.

---

|           |                     |
|-----------|---------------------|
| mask_surf | <i>Mask surface</i> |
|-----------|---------------------|

---

**Description**

Mask a surface mesh.

**Usage**

```
mask_surf(surf, mask)
```

**Arguments**

|      |   |
|------|---|
| surf | A "surf" object   |
| mask | A length $V$ logical vector indicating if each vertex is within the input mask. |

**Details**

Apply a binary mask to a "surf" object (list of vertices and corresponding faces). Vertices not in the mask are removed, and faces (triangles) with any vertices not in the mask are removed. Finally, vertex numbering for the new faces matrix is corrected.

**Value**

The masked "surf" object.

---

|             |                             |
|-------------|-----------------------------|
| merge_xifti | <i>Concatenate "xifti"s</i> |
|-------------|-----------------------------|

---

**Description**

Concatenate "xifti" objects along the columns. They must have the same brainstructures and resolutions. The first "xifti"'s metadata will be retained, including its intent.

**Usage**

```
merge_xifti(..., xifti_list = NULL)
```

**Arguments**

|                 |   |
|-----------------|---|
| ..., xifti_list | Provide as arguments the "xifti"s to concatenate, OR the single argument xifti_list which should be a list of "xifti"s. (If xifti_list is provided all other inputs will be ignored.) |
|-----------------|---|

**Value**

The concatenated "xifti"

**See Also**

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [apply\\_xifti\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [newdata\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [select\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

|                 |   |
|-----------------|---|
| move_from_mwall | <i>Move data locations from medial wall</i> |
|-----------------|---|

---

**Description**

Move all medial wall locations into the cortical data matrices by assigning them a specific value (e.g. NA).

**Usage**

```
move_from_mwall(xifti, value = NA, name = "Medial_Wall", RGBA = c(1, 1, 1, 0))
```

**Arguments**

|            |   |
|------------|---|
| xifti      | A "xifti" object.   |
| value      | The value to assign the medial wall locations. Default: NA.   |
| name, RGBA | Only used if the "xifti" has the dlabel intent and value is not an already-existing Key. This is the name to assign to the new key for the medial wall locations, as well as a length-four numeric vector indicating the red, green, blue, and alpha values for the color to assign to the new key. These will be reflected in the updated label table. Note that RGBA values must all be in [0, 1].<br>Currently, only one name and set of RGBA values are supported, meaning that the medial wall locations will have the same Key, name, and color across all data columns in the "xifti". An error will occur if the Key already exists for some columns but not others.<br>Defaults: "Medial_Wall" for "name" and white with 0 alpha for RGBA. |

**Value**

The "xifti" with re-organized data and medial wall masks

**See Also**

[move\\_to\\_mwall](#)  
[unmask\\_cortex](#)

---

|               |   |
|---------------|---|
| move_to_mwall | <i>Move data locations to the medial wall</i> |
|---------------|---|

---

### Description

Move cortical data locations with a specific value(s) to the medial wall mask. For example, dlabel CIFTIs often have medial wall vertices set to a specific key value, rather than a medial wall mask. This function can move those data locations from the data matrix to the medial wall mask in the metadata.

### Usage

```
move_to_mwall(xifti, values = c(NA, NaN), drop = FALSE)
```

### Arguments

|        |   |
|--------|---|
| xifti  | A "xifti" object.   |
| values | Medial wall values. Default: NA and NaN. Data locations in the left and right cortex that are one of these values (across all columns) will be moved to the medial wall mask in the metadata. |
| drop   | Only used if the "xifti" has the dlabel intent. Drop the key(s) in values from the label tables, for columns in which they no longer exist? Default: FALSE.                                   |

### Value

The "xifti" with re-organized data and medial wall masks

### See Also

move\_from\_mwall

---

|               |                                      |
|---------------|--------------------------------------|
| newdata_xifti | <i>Replace the data in a "xifti"</i> |
|---------------|--------------------------------------|

---

### Description

Replace the data in a "xifti" with new data from a data matrix.

### Usage

```
newdata_xifti(xifti, newdata, newnames = NULL)
```

**Arguments**

|          |   |
|----------|---|
| xifti    | A "xifti" object.   |
| newdata  | The $V \times T$ matrix of data values to replace those in xifti with. The left cortex vertices should be at the top, right cortex vertices in the middle, and subcortex vertices at the bottom (when present).<br>If newdata is instead a $V \times Q$ matrix where $Q$ is not $T$ , then any column names or label tables will be removed. (A "dlabel" will be converted to a "dscalar".)<br>Can also be a length-one vector to set all values equally. |
| newnames | Replaces the names in the xifti. If NULL (default), keep the original names, except if the number of columns in newdata doesn't match that of xifti, in which case no names will be used.   |

**Details**

If the "xifti" has  $V$  grayordinates and  $T$  measurements, newdata should be a  $V \times Q$  matrix. If  $Q$  is not equal to  $T$ , then any column names or label tables will be removed. (A "dlabel" will be converted to a "dscalar".)

**Value**

The new "xifti"

**See Also**

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [apply\\_xifti\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [select\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

parc\_borders

*Parcellation borders*

---

**Description**

Identify vertices which lie on the border of different parcels.

**Usage**

```
parc_borders(parc, surf = NULL, hemisphere = c("left", "right"))
```

**Arguments**

|            |  |
|------------|--|
| parc       | Integer vector the same length as the number of vertices. Each entry indicates the parcel that vertex belongs to.  |
| surf       | The surface which the vertices belong to, or just the "faces" component ( $F \times 3$ matrix where each row indicates the vertices which comprise a face). If not provided, the (resampled) default hemisphere surface included with ciftiTools will be used. |
| hemisphere | Only used to choose which default surface to use if <code>is.null(surf)</code> . Should be "left" (default) or "right".  |



**Value**

Logical vector the same length as parc indicating if the vertex lies on a border.

---

|           |                                |
|-----------|--------------------------------|
| plot.surf | <i>S3 method: plot surface</i> |
|-----------|--------------------------------|

---

**Description**

Visualize a single surface

**Usage**

```
## S3 method for class 'surf'
plot(x, ...)
```

**Arguments**

|     |   |
|-----|---|
| x   | A "surf" object   |
| ... | Additional arguments to <a href="#">view_xifti_surface</a> . But, the hemisphere argument behaves differently: it can be either left or right to indicate which hemisphere x represents. It is only used if the "hemisphere" metadata entry in x is NULL. If both the argument and the metadata entry are NULL, the surface will be treated as the left hemisphere. |

---

|            |   |
|------------|---|
| plot.xifti | <i>S3 method: use view_xifti to plot a "xifti" object</i> |
|------------|---|

---

**Description**

S3 method: use view\_xifti to plot a "xifti" object

**Usage**

```
## S3 method for class 'xifti'
plot(x, ...)
```

**Arguments**

|     |  |
|-----|--|
| x   | A "xifti" object.  |
| ... | Additional arguments to <a href="#">view_xifti</a> , except what, which will be set to NULL. |

---

|            |                          |
|------------|--------------------------|
| read_cifti | <i>Read a CIFTI file</i> |
|------------|--------------------------|

---

**Description**

Read in a CIFTI file as a "xifti" object.

**Usage**

```
read_cifti(  
  cifti_fname = NULL,  
  surfL_fname = NULL,  
  surfR_fname = NULL,  
  brainstructures = c("left", "right"),  
  idx = NULL,  
  resamp_res = NULL,  
  resamp_method = c("barycentric", "adaptive"),  
  areaL_original_fname = NULL,  
  areaR_original_fname = NULL,  
  flat = FALSE,  
  mwall_values = c(NA, NaN),  
  verbose = FALSE,  
  ...  
)
```

```
readCifTI(  
  cifti_fname = NULL,  
  surfL_fname = NULL,  
  surfR_fname = NULL,  
  brainstructures = c("left", "right"),  
  idx = NULL,  
  resamp_res = NULL,  
  resamp_method = c("barycentric", "adaptive"),  
  areaL_original_fname = NULL,  
  areaR_original_fname = NULL,  
  flat = FALSE,  
  mwall_values = c(NA, NaN),  
  verbose = FALSE,  
  ...  
)
```

```
readcii(  
  cifti_fname = NULL,  
  surfL_fname = NULL,  
  surfR_fname = NULL,  
  brainstructures = c("left", "right"),  
  idx = NULL,
```

```

    resamp_res = NULL,
    resamp_method = c("barycentric", "adaptive"),
    areaL_original_fname = NULL,
    areaR_original_fname = NULL,
    flat = FALSE,
    mwall_values = c(NA, NaN),
    verbose = FALSE,
    ...
)

read_xifti(
  cifti_fname = NULL,
  surfL_fname = NULL,
  surfR_fname = NULL,
  brainstructures = c("left", "right"),
  idx = NULL,
  resamp_res = NULL,
  resamp_method = c("barycentric", "adaptive"),
  areaL_original_fname = NULL,
  areaR_original_fname = NULL,
  flat = FALSE,
  mwall_values = c(NA, NaN),
  verbose = FALSE,
  ...
)

```

### Arguments

|                              |   |
|------------------------------|---|
| <code>cifti_fname</code>     | File path to a CIFTI file (ending in ".d*.nii").  |
| <code>surfL_fname</code>     | (Optional) File path to a GIFTI surface geometry file representing the left cortex.   |
| <code>surfR_fname</code>     | (Optional) File path to a GIFTI surface geometry file representing the right cortex.  |
| <code>brainstructures</code> | Character vector indicating which brain structure(s) to obtain: "left" (left cortex), "right" (right cortex) and/or "subcortical" (subcortex and cerebellum). Can also be "all" (obtain all three brain structures). Default: c("left", "right") (cortex only).<br>If a brain structure is indicated but does not exist in the CIFTI file, a warning will occur and that brain structure will be skipped. |
| <code>idx</code>             | Numeric vector indicating the data indices (columns) to read. If NULL (default), read in all the data. Must be a subset of the indices present in the file, or an error will occur.<br>For high-resolution CIFTI files, reading in only a subset of the data saves memory, but will be slower than reading in the entire file due to the required intermediate steps.                                     |
| <code>resamp_res</code>      | Resolution to resample the cortical data and surface to. Default: NULL (do not resample). If not NULL, the data will have to be read in with <code>-cifti-separate</code> , which is slower than <code>-cifti-convert -to-gifti-ext</code> .  |

|  |  |
|--|--|
| resamp_method                              | <p>"barycentric" (default) or "adaptive" resampling for the metric or label data. These options correspond to the Workbench command options "BARYCENTRIC" and "ADAP_BARY_AREA", respectively.</p> <p>While adaptive resampling is recommended for metric or label data, it requires that <code>area[L/R]_original_fname</code> be provided.</p> <p>Note that surfaces will be resampled using barycentric resampling regardless of <code>resamp_method</code>, because barycentric resampling rather than adaptive resampling is recommended for surface data.</p>   |
| areaL_original_fname, areaR_original_fname | <p>File paths to the surfaces to use for vertex area correction during adaptive resampling. (Only used if resampling with the adaptive method.) <code>area[L/R]_fname</code> should match the current resolution of the data.</p> <p>The Workbench command for adaptive resampling requires the target surfaces for area correction too, but to make the workflow easier <code>ciftiTools</code> will resample <code>area[L/R]_fname</code> with the barycentric method and use that for the target surface.</p>   |
| flat                                       | <p>Should the result be flattened into a single matrix?</p> <p>If FALSE (default), the result will be a "xiffti" object.</p> <p>If TRUE, the result will be a <math>T \times G</math> matrix (<math>T</math> measurements, <math>G</math> grayordinates not including the medial wall if it's excluded from the ROI). All below arguments will be ignored because the brain structures cannot be identified. Surfaces will not be appended. Resampling is also not possible. <code>flat==TRUE</code> is the fastest way to read in just the CIFTI data.</p> <p>If TRUE, the grayordinates will be ordered by left cortex, right cortex, and then subcortex. Subcortical voxels will be ordered by alphabetical label. However, where each brainstructure (and subcortical structure) begins and ends cannot be determined. The medial wall locations and subcortical brain mask are also not included. The data matrix will be identical to that created by <code>-cifti-convert -to-gifti-ext</code>.</p> |
| mwall_values                               | <p>If the medial wall locations are not indicated in the CIFTI, use these values to infer the medial wall mask. Default: <code>c(NA, NaN)</code>. If NULL, do not attempt to infer the medial wall.</p>  |
| verbose                                    | <p>Should occasional updates be printed? Default: FALSE.</p>   |
| ...  | <p>Additional arguments to <code>read_cifti_convert</code> or <code>read_cifti_separate</code>.</p>  |

## Details

First, metadata is obtained with `info_cifti`. Then, if no resampling is requested, the `-cifti-convert -to-gifti-ext` Workbench Command is used to "flatten" the data and save it as a metric or label GIFTI file, which is read in and separated by brainstructure according to the metadata (`read_cifti_convert`). Otherwise, if sampling is requested, then the CIFTI is separated into its GIFTI and NIFTI components, resampled, and then re-assembled (`read_cifti_separate`). The former is much faster for large CIFTI files, so the latter is only used when necessary for resampling.

If `cifti_fname` is not provided, then only the surfaces are read in.

**Value**

If !flat, a "xifti" object. Otherwise, a  $T \times G$  matrix ( $T$  measurements,  $G$  grayordinates).

**Connectome Workbench**

This function interfaces with the "-cifti-convert" Workbench command if resampling is not needed, and the "-cifti-separate" Workbench command if resampling is needed.

**Label Levels**

xifti\$meta\$subcort\$labels is a factor with the following levels:

1. Cortex-L
2. Cortex-R
3. Accumbens-L
4. Accumbens-R
5. Amygdala-L
6. Amygdala-R
7. Brain Stem
8. Caudate-L
9. Caudate-R
10. Cerebellum-L
11. Cerebellum-R
12. Diencephalon-L
13. Diencephalon-R
14. Hippocampus-L
15. Hippocampus-R
16. Pallidum-L
17. Pallidum-R
18. Putamen-L
19. Putamen-R
20. Thalamus-L
21. Thalamus-R

These correspond to the same structures as given by ft\_read\_cifti in the cifti-matlab MATLAB toolbox. Note that the first two levels (left and right cortex) are not used.

**See Also**

Other commonly-used functions: [is.cifti\(\)](#), [resample\\_cifti\(\)](#), [smooth\\_cifti\(\)](#), [view\\_xifti\\_surface\(\)](#), [view\\_xifti\\_volume\(\)](#), [write\\_cifti\(\)](#)

Other functions for reading in CIFTI or GIFTI data: [as.xifti\(\)](#), [info\\_cifti\(\)](#), [load\\_parcs\(\)](#), [load\\_surf\(\)](#), [read\\_surf\(\)](#), [read\\_xifti2\(\)](#)

---

|           |                            |
|-----------|----------------------------|
| read_surf | <i>Get a "surf" object</i> |
|-----------|----------------------------|

---

### Description

Coerce a file path to a surface GIFTI, a "gifti" object, a list with entries "pointset" and "triangle", or a "surf" to a "surf".

### Usage

```
read_surf(surf, expected_hemisphere = NULL, resamp_res = NULL)
```

```
make_surf(surf, expected_hemisphere = NULL, resamp_res = NULL)
```

### Arguments

**surf** Either a file path to a surface GIFTI; a "gifti" read by [readgii](#); a list with entries "pointset" and "triangle"; or, a "surf" object.

**expected\_hemisphere** The expected hemisphere ("left" or "right") of surf. If the hemisphere indicated in the GIFTI metadata is the opposite, an error is raised. If NULL (default), use the GIFTI hemisphere.

**resamp\_res** The resolution to resample the surfaces to. If NULL (default), do not resample.

### Value

The "surf": a list with components "vertices" (3D spatial locations), "faces" (defined by three vertices), and "hemisphere" ("left", "right", or NULL if unknown).

### See Also

Other functions for reading in CIFTI or GIFTI data: [as.xifti\(\)](#), [info\\_cifti\(\)](#), [load\\_parcs\(\)](#), [load\\_surf\(\)](#), [read\\_cifti\(\)](#), [read\\_xifti2\(\)](#)

Other functions for working with GIFTI surface geometry data: [is\\_surf\(\)](#), [resample\\_surf\(\)](#), [rotate\\_surf\(\)](#), [view\\_surf\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

|             |  |
|-------------|--|
| read_xifti2 | <i>Read in GIFTI files as a "xifti" object</i> |
|-------------|--|

---

### Description

Read in GIFTI metric or label files as a "xifti" object. May also include surface geometry GIFTI files and perform resampling.

**Usage**

```

read_xifti2(
  cortexL = NULL,
  cortexL_mwall = NULL,
  cortexR = NULL,
  cortexR_mwall = NULL,
  mwall_values = c(NA, NaN),
  surfL = NULL,
  surfR = NULL,
  resamp_res = NULL,
  col_names = NULL,
  HCP_32k_auto_mwall = TRUE,
  read_dir = NULL,
  validate = TRUE
)

```

**Arguments**

`cortexL`, `cortexL_mwall`

Left cortex data and ROI. Each must be a path to a metric or label GIFTI file.

If `cortexL_mwall` is not provided, `cortexL` should have data for all vertices on the left cortical surface ( $V_L x T$  data matrix). There will not be a mask for the medial wall. Not providing the medial wall mask is appropriate for ".dlabels.nii" files where the medial wall may have its own label and therefore should not be treated as missing data.

If `cortexL_mwall` is provided, `cortexL` should either have data for all vertices on the left cortical surface ( $V_L x T$  data matrix, with filler values e.g. 0 or NaN for medial wall vertices), or have data only for non-medial wall vertices ( $(V_L - mwall_L) x T$  data matrix). The medial wall mask will be the 0 values in `cortexL_mwall`. The medial wall mask should be provided whenever the medial wall should be treated as missing data.

Since the unmasked cortices must have the same number of vertices, `V_L` should match `V_R`, or `resamp_res` must be set.

`cortexR`, `cortexR_mwall`

Right cortex data and ROI. Each must be a path to a metric or label GIFTI file.

If `cortexR_mwall` is not provided, `cortexR` should have data for all vertices on the right cortical surface ( $V_R x T$  data matrix). There will not be a mask for the medial wall. Not providing the medial wall mask is appropriate for ".dlabels.nii" files where the medial wall may have its own label and therefore should not be treated as missing data.

If `cortexR_mwall` is provided, `cortexR` should either have data for all vertices on the right cortical surface ( $V_R x T$  data matrix, with filler values e.g. 0 or NaN for medial wall vertices), or have data only for non-medial wall vertices ( $(V_R - mwall_R) x T$  data matrix). The medial wall mask will be the 0 values in `cortexR_mwall`. The medial wall mask should be provided whenever the medial wall should be treated as missing data.

Since the unmasked cortices must have the same number of vertices, `V_L` should match `V_R`, or `resamp_res` must be set.

|                    |  |
|--------------------|--|
| mwall_values       | If cortex[L/R]_mwall was not provided, or if it was invalid (i.e. bad length or all TRUE), the medial wall mask will be inferred from rows in cortex[L/R] that are constantly one of these values. Default: c(NA, NaN). If NULL, do not attempt to infer the medial wall from the data values. NULL should be used if NA or NaN are legitimate values that non-medial wall vertices might take on. |
| surfL, surfR       | (Optional) File path(s) to surface GIFTI(s) for the left or right cortex.  |
| resamp_res         | Resolution to resample the cortical data and surface to. Default: NULL (do not resample). If provided, the original resolutions of the cortex data and surfaces may differ.  |
| col_names          | Names of each measurement/column in the data. Overrides names indicated in the data components.  |
| HCP_32k_auto_mwall | If left and/or right cortex data is provided, and the number of vertices matches that of the HCP 32k mesh (29696 on left, and 29716 on right), should the medial wall masks be added to the "xifti" if not provided? Default: TRUE.  |
| read_dir           | (Optional) Append a directory to all file names in the arguments. If NULL (default), do not modify file names.   |
| validate           | Validate that the result is a "xifti" object? Default: TRUE. If FALSE, the result may not be properly formatted if the inputs were invalid.  |

**Value**

The "xifti" object containing all the data in the input giftis.

**See Also**

Other functions for reading in CIFTI or GIFTI data: [as.xifti\(\)](#), [info\\_cifti\(\)](#), [load\\_parcs\(\)](#), [load\\_surf\(\)](#), [read\\_cifti\(\)](#), [read\\_surf\(\)](#)

---

|              |  |
|--------------|--|
| remove_xifti | <i>Remove a component from a "xifti"</i> |
|--------------|--|

---

**Description**

Remove a brain structure, surface, or subcortical structure from a "xifti".

**Usage**

```
remove_xifti(xifti, remove = NULL, remove_sub = NULL)
```

**Arguments**

|            |   |
|------------|---|
| xifti      | A "xifti" object.   |
| remove     | A character vector containing one or more of the following: "cortex_left", "cortex_right", "subcortical", "surf_left", and "surf_right". Each of these components will be removed from xifti. |
| remove_sub | A vector containing subcortical structures to be removed from xifti. Can be specified with names, or with numeric factor values: see <a href="#">substructure_table</a> .                     |



**Value**

The new "xifti" with the requested component(s) removed

**See Also**

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [apply\\_xifti\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [newdata\\_xifti\(\)](#), [select\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

|                |                            |
|----------------|----------------------------|
| resample_cifti | <i>Resample CIFTI data</i> |
|----------------|----------------------------|

---

**Description**

Performs spatial resampling of CIFTI data on the cortical surface by separating it into GIFTI and NIFTI files, resampling the GIFTIs, and then putting them together. (The subcortex is not resampled.)

**Usage**

```
resample_cifti(
  x = NULL,
  cifti_target_fname = NULL,
  surfL_original_fname = NULL,
  surfR_original_fname = NULL,
  surfL_target_fname = NULL,
  surfR_target_fname = NULL,
  resamp_res,
  resamp_method = c("barycentric", "adaptive"),
  areaL_original_fname = NULL,
  areaR_original_fname = NULL,
  write_dir = NULL,
  mwall_values = c(NA, NaN),
  verbose = TRUE
)
```

```
resampleCIFTI(
  x = NULL,
  cifti_target_fname = NULL,
  surfL_original_fname = NULL,
  surfR_original_fname = NULL,
  surfL_target_fname = NULL,
  surfR_target_fname = NULL,
  resamp_res,
  resamp_method = c("barycentric", "adaptive"),
  areaL_original_fname = NULL,
  areaR_original_fname = NULL,
  write_dir = NULL,
```

```

    mwall_values = c(NA, NaN),
    verbose = TRUE
)

resamplecii(
  x = NULL,
  cifti_target_fname = NULL,
  surfL_original_fname = NULL,
  surfR_original_fname = NULL,
  surfL_target_fname = NULL,
  surfR_target_fname = NULL,
  resamp_res,
  resamp_method = c("barycentric", "adaptive"),
  areal_original_fname = NULL,
  areaR_original_fname = NULL,
  write_dir = NULL,
  mwall_values = c(NA, NaN),
  verbose = TRUE
)

resample_xifti(
  x = NULL,
  cifti_target_fname = NULL,
  surfL_original_fname = NULL,
  surfR_original_fname = NULL,
  surfL_target_fname = NULL,
  surfR_target_fname = NULL,
  resamp_res,
  resamp_method = c("barycentric", "adaptive"),
  areal_original_fname = NULL,
  areaR_original_fname = NULL,
  write_dir = NULL,
  mwall_values = c(NA, NaN),
  verbose = TRUE
)

```

### Arguments

- x                    The CIFTI file name or "xifti" object to resample. If NULL, the result will be a "xifti" with resampled surfaces given by surfL\_original\_fname and surfR\_original\_fname.
- cifti\_target\_fname    File name for the resampled CIFTI. Will be placed in write\_dir. If NULL, will be written to "resampled.d\*.nii". write\_dir will be appended to the beginning of the path.
- surfL\_original\_fname, surfR\_original\_fname    (Optional) Path to a GIFTI surface geometry file representing the left/right cortex. One or both can be provided. These will be resampled too, and are convenient for visualizing the resampled data.

If `x` is a "xifti" object with surfaces, these arguments will override the surfaces in the "xifti".

|   |   |
|---|---|
| <code>surfL_target_fname, surfR_target_fname</code>     | (Optional) File names for the resampled GIFTI surface geometry files. Will be placed in <code>write_dir</code> . If NULL (default), will use default names created by <code>resample_cifti_default_fname</code> .   |
| <code>resamp_res</code>                                 | Target resolution for resampling (number of cortical surface vertices per hemisphere).  |
| <code>resamp_method</code>                              | "barycentric" (default) or "adaptive" resampling for the metric or label data. These options correspond to the Workbench command options "BARYCENTRIC" and "ADAP_BARY_AREA", respectively.<br>While adaptive resampling is recommended for metric or label data, it requires that <code>area[L/R]_original_fname</code> be provided.<br>Note that surfaces will resampled using barycentric resampling regardless of <code>resamp_method</code> , because barycentric resampling rather than adaptive resampling is recommended for surface data. |
| <code>areaL_original_fname, areaR_original_fname</code> | File paths to the surfaces to use for vertex area correction during adaptive resampling. (Only used if resampling with the adaptive method.) <code>area[L/R]_original_fname</code> should match the current resolution of the data.<br>The Workbench command for adaptive resampling requires the target surfaces for area correction too, but to make the workflow easier <code>ciftiTools</code> will resample <code>area[L/R]_original_fname</code> with the barycentric method and use that for the target surface.                           |
| <code>write_dir</code>                                  | Where to write the resampled CIFTI (and surfaces if present.) If NULL (default), will use the current working directory if <code>x</code> was a CIFTI file, and a temporary directory if <code>x</code> was a "xifti" object.   |
| <code>mwall_values</code>                               | If the medial wall locations are not indicated in the CIFTI, use these values to infer the medial wall mask. Default: <code>c(NA, NaN)</code> . If NULL, do not attempt to infer the medial wall.<br>Correctly indicating the medial wall locations is important for resampling, because the medial wall mask is taken into account during resampling calculations.   |
| <code>verbose</code>                                    | Should occasional updates be printed? Default: TRUE.  |

### Details

Can accept a "xifti" object as well as a path to a CIFTI-file.

If surface data is included, it will be resampled with the barycentric method even if `resamp_method=="adaptive"` because the barycentric method is recommended for surface geometry data.

### Value

A named character vector of written files: "cifti" and potentially "surfL" (if `surfL_original_fname` was provided) and/or "surfR" (if `surfR_original_fname` was provided).

**Connectome Workbench**

This function interfaces with the "-metric-resample", "-label-resample", and/or "-surface-resample" Workbench commands, depending on the input.

**See Also**

Other commonly-used functions: [is\\_cifti\(\)](#), [read\\_cifti\(\)](#), [smooth\\_cifti\(\)](#), [view\\_xifti\\_surface\(\)](#), [view\\_xifti\\_volume\(\)](#), [write\\_cifti\(\)](#)

---

resample\_cifti\_from\_template

*Resample a CIFTI from a template*

---

**Description**

Resample a CIFTI from a template, ensuring the new CIFTI's resolution matches that of the template.

**Usage**

```
resample_cifti_from_template(original_fname, template_fname, target_fname)
```

**Arguments**

`original_fname` A CIFTI file to resample.

`template_fname` A CIFTI file to use as the template.

`target_fname` The file name to save the resampled CIFTI.

**Value**

The `target_fname`, invisibly

**Connectome Workbench**

This function interfaces with the "-cifti-resample" Workbench command.

---

|                |   |
|----------------|---|
| resample_gifti | <i>Resample a GIFTI file (with its ROI)</i> |
|----------------|---|

---

**Description**

Perform spatial resampling of GIFTI data on the cortical surface (metric and label), or of GIFTI surface geometry data itself.

**Usage**

```
resample_gifti(  
  original_fname,  
  target_fname,  
  hemisphere = c("left", "right"),  
  file_type = NULL,  
  original_res = NULL,  
  resamp_res = NULL,  
  resamp_method = c("barycentric", "adaptive"),  
  area_original_fname = NULL,  
  area_target_fname = NULL,  
  ROIcortex_original_fname = NULL,  
  ROIcortex_target_fname = NULL,  
  sphere_original_fname = NULL,  
  sphere_target_fname = NULL,  
  read_dir = NULL,  
  write_dir = NULL  
)
```

```
resampleGIFTI(  
  original_fname,  
  target_fname,  
  hemisphere,  
  file_type = NULL,  
  original_res = NULL,  
  resamp_res,  
  ROIcortex_original_fname = NULL,  
  ROIcortex_target_fname = NULL,  
  read_dir = NULL,  
  write_dir = NULL  
)
```

```
resamplegii(  
  original_fname,  
  target_fname,  
  hemisphere,  
  file_type = NULL,  
  original_res = NULL,
```

```

    resamp_res,
    ROIcortex_original_fname = NULL,
    ROIcortex_target_fname = NULL,
    read_dir = NULL,
    write_dir = NULL
)

```

## Arguments

**original\_fname** The GIFTI file to resample.

**target\_fname** Where to save the resampled file.

**hemisphere** "left" (default) or "right". An error will occur if the hemisphere indicated in the GIFTI metadata does not match.

**file\_type** "metric", "label", "surf", or NULL (default) to infer from original\_fname.

**original\_res** The resolution of the original file. If NULL (default), infer from the file. Alternatively, provide sphere\_original\_fname which will override original\_res. In general, original\_res should be used when the original file is in registration with the spheres created by the Workbench command `-surface-create-sphere`, and sphere\_original\_fname should be used when it is not compatible.

**resamp\_res** Target resolution for resampling (number of cortical surface vertices per hemisphere). Alternatively, provide sphere\_target\_fname which will override resamp\_res. In general, resamp\_res should be used when the target file will be in registration with the spheres created by the Workbench command `-surface-create-sphere`, and sphere\_target\_fname should be used when it is not compatible.

**resamp\_method** "barycentric" (default) or "adaptive" resampling. These options correspond to the Workbench command options "BARYCENTRIC" and "ADAP\_BARY\_AREA", respectively. While adaptive resampling is recommended for metric or label data, it requires that area\_original\_fname be provided.

**area\_original\_fname, area\_target\_fname** File paths to the surfaces to use for vertex area correction during adaptive resampling. (Ignored if resampling with the barycentric method.) area\_original\_fname should match the current resolution of the data, and area\_target\_fname should match resamp\_res. If area\_target\_fname is not provided, area\_original\_fname will be resampled with the barycentric method, and the result will be used as area\_target\_fname.

**ROIcortex\_original\_fname** The name of the ROI file corresponding to original\_fname. Leave as NULL (default) if this doesn't exist or shouldn't be resampled.

**ROIcortex\_target\_fname** The name of the resampled ROI file. Only applicable if ROIcortex\_original\_fname is provided.

**sphere\_original\_fname, sphere\_target\_fname** File paths to the sphere surfaces in the original and target resolutions. If possible, the simpler arguments original\_res and resamp\_res can be used instead. But those depend on the surface being compatible with that created by

|           |  |
|-----------|--|
|           | -surface-create-sphere, which isn't always true. Therefore sphere_original_fname and sphere_target_fname can be used if needed.                                |
| read_dir  | Directory to append to the path of every file name in original_fname and ROIcortex_original_fname. If NULL (default), do not append any directory to the path. |
| write_dir | Directory to append to the path of every file name in target_fname and ROIcortex_target_fname. If NULL (default), do not append any directory to the path.     |

**Value**

The resampled GIFTI file name, invisibly

**Connectome Workbench**

This function interfaces with the "-metric-resample", "-label-resample", and/or "-surface-resample" Workbench commands, depending on the input.

---

|               |                                 |
|---------------|---------------------------------|
| resample_surf | <i>Resample a "surf" object</i> |
|---------------|---------------------------------|

---

**Description**

Resample a "surf" object by writing it to a GIFTI, using the Connectome Workbench to resample it, and then reading the new file. The barycentric resampling method, which is recommended for anatomical surfaces, will be used.

**Usage**

```
resample_surf(surf, resamp_res, hemisphere = c("left", "right"))
```

**Arguments**

|            |   |
|------------|---|
| surf       | A "surf" object   |
| resamp_res | The desired resolution  |
| hemisphere | "left" or "right". Only used if not indicated by surf\$hemisphere. An error will be raised if it does not match the hemisphere indicated in the intermediate written GIFTI. |

**Value**

The new "surf"

**Connectome Workbench**

This function interfaces with the "-surface-resample" Workbench command.

**See Also**

Other functions for working with GIFTI surface geometry data: [is\\_surf\(\)](#), [read\\_surf\(\)](#), [rotate\\_surf\(\)](#), [view\\_surf\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

|             |                               |
|-------------|-------------------------------|
| rotate_surf | <i>Rotate a "surf" object</i> |
|-------------|-------------------------------|

---

**Description**

Rotate a "surf". Can be used to adjust the mesh orientation prior to [view\\_xifti\\_surface](#).

**Usage**

```
rotate_surf(surf, r1 = 0, r2 = 0, r3 = 0, units = c("radians", "degrees"))
```

**Arguments**

|            |   |
|------------|---|
| surf       | The "surf" object: see <a href="#">is_surf</a> .  |
| r1, r2, r3 | Angle to rotate along the first, second, and third column's axis, in units (e.g. changing r1 will change the vertex positions in the second and third dimensions/columns, since the mesh is being rotated with respect to the first column's axis). Default: 0.<br><br>With <a href="#">view_xifti_surface</a> and other mesh rendering functions that use <code>rgl</code> , these rotations seem to correspond to yaw, pitch, and roll, respectively. |
| units      | "radians" (default) or "degrees".   |

**Value**

The rotated "surf"

**See Also**

Other functions for working with GIFTI surface geometry data: [is\\_surf\(\)](#), [read\\_surf\(\)](#), [resample\\_surf\(\)](#), [view\\_surf\(\)](#), [write\\_surf\\_gifti\(\)](#)



---

|            |                                   |
|------------|-----------------------------------|
| ROY_BIG_BL | <i>"ROY_BIG_BL" color palette</i> |
|------------|-----------------------------------|

---

### Description

"ROY\_BIG\_BL", the default palette from the Connectome Workbench.

### Usage

```
ROY_BIG_BL(min = 0, max = 1, mid = NULL, half = NULL, pos_half = FALSE)
```

### Arguments

|          |  |
|----------|--|
| min      | The minimum value for the color mapping. As in the original palette, the last color (aqua) is actually placed at the bottom .5\ the minimum and maximum. Default: 0  |
| max      | The maximum value for the color mapping. If this value is lower than the minimum, the color mapping will be reversed. If this is equal to the minimum, a palette with only the color black will be returned. Default: 1. |
| mid      | (Optional) The midpoint value for the color mapping. If NULL (default), the true midpoint is used.   |
| half     | "positive" or "negative" to use the positive half (black -> red -> yellow) or negative half (black -> blue -> purple -> green -> aqua) only. NULL (default) or FALSE to use entire palette.                              |
| pos_half | Deprecated. Use half.  |

### Details

Yields the landmark color hex codes and values for the "ROY\_BIG\_BL" palette. This is the same color palette as the default Connectome Workbench palette. Source: <https://github.com/Washington-University/workbench/blob/master/src/Files/PaletteFile.cxx>

### Value

A data.frame with two columns: "color" (character: color hex codes) and "value" (numeric)

---

run\_wb\_cmd

*Wrapper for Connectome Workbench Commands*


---

**Description**

Runs a Connectome Workbench command that has already been formatted.

**Usage**

```
run_wb_cmd(cmd, intern = TRUE, ignore.stdout = NULL, ignore.stderr = NULL)
```

**Arguments**

|                              |   |
|------------------------------|---|
| cmd                          | The full command, beginning after the workbench path.   |
| intern                       | Return printed output? If FALSE, return logical indicating success instead. Default: TRUE.  |
| ignore.stdout, ignore.stderr | The "ignore.stdout" and "ignore.stderr" arguments to <a href="#">system</a> . Should be logical or NULL. If NULL (default), messages will be controlled by <code>ciftiTools.getOption("suppress_msgs")</code> and errors will not be ignored. |

**Value**

If `intern==TRUE`, the printed output of the command. If `intern==FALSE`, a logical indicating if the command finished successfully.

---

S3\_Math

*"xifti" S3 Math methods*


---

**Description**

Math methods for "xifti" objects.

**Usage**

```
## S3 method for class 'xifti'
Math(x, ...)
```

**Arguments**

|     |                                      |
|-----|--------------------------------------|
| x   | The "xifti"                          |
| ... | Additional arguments to the function |

**Details**

Uses [transform\\_xifti](#).

---

S3\_Ops

*"xiffti" S3 Ops methods*

---

### Description

Ops methods for "xiffti" objects.

### Usage

```
## S3 method for class 'xiffti'  
Ops(e1, e2 = NULL)
```

### Arguments

e1, e2            The arguments to the operation. "xiffti" objects will be converted to matrices temporarily

### Details

Uses [transform\\_xiffti](#).

---

S3\_Summary

*"xiffti" S3 Summary methods*

---

### Description

Summary methods for "xiffti" objects.

### Usage

```
## S3 method for class 'xiffti'  
Summary(..., na.rm = FALSE)
```

### Arguments

...            The "xiffti" and additional numeric arguments will be converted to matrices  
na.rm         Remove NA values? Default: FALSE.

---

|             |                    |
|-------------|--------------------|
| scale_xifti | <i>Scale CIFTI</i> |
|-------------|--------------------|

---

**Description**

Scale CIFTI data. Similar to [scale](#).

**Usage**

```
scale_xifti(xifti, center = TRUE, scale = TRUE)
```

**Arguments**

|               |                                      |
|---------------|--------------------------------------|
| xifti         | A "xifti" object.                    |
| center, scale | Arguments to <a href="#">scale</a> . |

**Value**

The input "xifti" with scaled columns.

---

|              |                                    |
|--------------|------------------------------------|
| select_xifti | <i>Select columns of a "xifti"</i> |
|--------------|------------------------------------|

---

**Description**

Select column indices to keep in a "xifti". Can also be used to reorder the columns.

**Usage**

```
select_xifti(xifti, idx, add_meta = "select")
```

**Arguments**

|          |  |
|----------|--|
| xifti    | A "xifti" object.  |
| idx      | The column indices to keep, in order.  |
| add_meta | Add idx to xifti\$meta\$cifti\$misc[[add_meta]] for reference. Default: "select". If NULL or an empty string, do not add a metadata entry. |

**Value**

The "xifti" with only the selected columns.

**See Also**

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [apply\\_xifti\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [newdata\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [transform\\_xifti\(\)](#)

---

|                |                              |
|----------------|------------------------------|
| separate_cifti | <i>Separate a CIFTI file</i> |
|----------------|------------------------------|

---

**Description**

Separate a CIFTI file into GIFTI files for the cortical data and NIFTI files for the subcortical data and labels. ROIs can also be written to indicate the medial wall mask (cortex) and volume mask (subcortex). This uses the Connectome Workbench command `-cifti-separate`.

**Usage**

```
separate_cifti(  
  cifti_fname,  
  brainstructures = c("left", "right"),  
  cortexL_fname = NULL,  
  cortexR_fname = NULL,  
  subcortVol_fname = NULL,  
  subcortLabs_fname = NULL,  
  ROI_brainstructures = "all",  
  ROIcortexL_fname = NULL,  
  ROIcortexR_fname = NULL,  
  ROIsubcortVol_fname = NULL,  
  write_dir = NULL  
)
```

```
separateCIFTI(  
  cifti_fname,  
  brainstructures = c("left", "right"),  
  cortexL_fname = NULL,  
  cortexR_fname = NULL,  
  subcortVol_fname = NULL,  
  subcortLabs_fname = NULL,  
  ROI_brainstructures = "all",  
  ROIcortexL_fname = NULL,  
  ROIcortexR_fname = NULL,  
  ROIsubcortVol_fname = NULL,  
  write_dir = NULL  
)
```

```
separatecii(  
  cifti_fname,  
  brainstructures = c("left", "right"),  
  cortexL_fname = NULL,  
  cortexR_fname = NULL,  
  subcortVol_fname = NULL,  
  subcortLabs_fname = NULL,  
  ROI_brainstructures = "all",
```

```

ROIcortexL_fname = NULL,
ROIcortexR_fname = NULL,
ROIsubcortVol_fname = NULL,
write_dir = NULL
)

```

## Arguments

**cifti\_fname** File path to a CIFTI file (ending in ".d\*.nii").

**brainstructures** Character vector indicating which brain structure(s) to obtain: "left" (left cortex), "right" (right cortex) and/or "subcortical" (subcortex and cerebellum). Can also be "all" (obtain all three brain structures). Default: c("left", "right") (cortex only).  
If a brain structure is indicated but does not exist in the CIFTI file, a warning will occur and that brain structure will be skipped.

**cortexL\_fname, cortexR\_fname** (Optional) GIFTI file names (\*.func/label.gii) to save the [left/right] cortex data to. If not provided, defaults to "\*[L/R].\[func/label\].gii", where \* is the file name component of cifti\_fname. Will be written in write\_dir. dtseries and dscalar files should use "func", whereas dlabel files should use "label".

**subcortVol\_fname, subcortLabs\_fname** (Optional) NIFTI file names to save the subcortical [volume/labels] to. If not provided, defaults to "\*[/.labels].nii", where \* is the file name component of cifti\_fname. Will be written in write\_dir.

**ROI\_brainstructures** Which ROIs should be obtained? "all" (default) to obtain ROIs for each of the brainstructures. NULL to not obtain any ROIs. This should be a subset of brainstructures.

**ROIcortexL\_fname, ROIcortexR\_fname** (Optional) GIFTI file names (\*.func/label.gii) to save the [left/right] cortex ROI to. If not provided, defaults to "\*ROI\_[L/R].\[func/label\].gii", where \* is the file name component of cifti\_fname. The cortical ROIs typically represent the medial wall mask, with values of 1 for in-ROI (non-medial wall) vertices and 0 for out-of-ROI (medial wall) vertices. Will be written in write\_dir. dtseries and dscalar files should use "func", whereas dlabel files should use "label".

**ROIsubcortVol\_fname** (Optional) NIFTI file names to save the subcortical ROI to. If not provided, defaults to "\*ROI.nii", where \* is the file name component of cifti\_fname. The subcortical ROI typically represents the volumetric mask for the entire subcortical structure, with values of 1 for in-ROI (in subcortex) voxels and 0 for out-of-ROI (not in subcortex) voxels. Will be written in write\_dir.

**write\_dir** Where should the separated files be placed? NULL (default) will write them to the current working directory.  
write\_dir must already exist, or an error will occur.

**Details**

Time unit, start, and step (dtseries files) will not be written to the GIFTI/NIFTIs. Column names (dscalar files) will not be written to the GIFTIs, as well as label names and colors (dlabel files). (Haven't checked the NIFTIs yet.)

ROI/medial wall behavior: If there are 32k vertices in the left cortex with 3k representing the medial wall, then both cortexL\_fname and ROIcortexL\_fname will have 32k entries, 3k of which having a value of 0 indicating the medial wall. The non-medial wall entries will have the data values in cortexL\_fname and a value of 1 in ROIcortexL\_fname. Thus, exporting ROIcortexL\_fname is vital if the data values include 0, because 0-valued non-medial wall vertices and medial wall vertices cannot be distinguished from one another within cortexL\_fname alone.

**Value**

A named character vector with the file paths to the written NIFTI and GIFTI files

**Connectome Workbench**

This function interfaces with the "-cifti-separate" Workbench command.

**See Also**

Other functions for writing CIFTI or GIFTI data: [write\\_cifti\(\)](#), [write\\_metric\\_gifti\(\)](#), [write\\_subcort\\_nifti\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

|                 |                                 |
|-----------------|---------------------------------|
| set_names_xifti | <i>Set "xifti" column names</i> |
|-----------------|---------------------------------|

---

**Description**

Change the column names of a "dscalar" or "dlabel" "xifti" object.

**Usage**

```
set_names_xifti(xifti, names)
```

**Arguments**

|       |   |
|-------|---|
| xifti | A "dscalar" or "dlabel" "xifti" object.   |
| names | The new column names, as a character vector with length equal to the same number of columns in xifti. |

**Value**

xifti with the new column names.

---

`smooth_cifti`*Smooth CIFTI data*

---

**Description**

Spatially smooth the metric data of a CIFTI file or "xifti" object.

**Usage**

```
smooth_cifti(  
  x,  
  cifti_target_fname = NULL,  
  surf_FWHM = 5,  
  vol_FWHM = 3,  
  surfL_fname = NULL,  
  surfR_fname = NULL,  
  cerebellum_fname = NULL,  
  subcortical_zeroes_as_NA = FALSE,  
  cortical_zeroes_as_NA = FALSE,  
  subcortical_merged = FALSE  
)
```

```
smoothCifTI(  
  x,  
  cifti_target_fname = NULL,  
  surf_FWHM = 5,  
  vol_FWHM = 5,  
  surfL_fname = NULL,  
  surfR_fname = NULL,  
  cerebellum_fname = NULL,  
  subcortical_zeroes_as_NA = FALSE,  
  cortical_zeroes_as_NA = FALSE,  
  subcortical_merged = FALSE  
)
```

```
smoothcii(  
  x,  
  cifti_target_fname = NULL,  
  surf_FWHM = 5,  
  vol_FWHM = 5,  
  surfL_fname = NULL,  
  surfR_fname = NULL,  
  cerebellum_fname = NULL,  
  subcortical_zeroes_as_NA = FALSE,  
  cortical_zeroes_as_NA = FALSE,  
  subcortical_merged = FALSE  
)
```



```

smooth_xifti(
  x,
  cifti_target_fname = NULL,
  surf_FWHM = 5,
  vol_FWHM = 5,
  surfL_fname = NULL,
  surfR_fname = NULL,
  cerebellum_fname = NULL,
  subcortical_zeroes_as_NA = FALSE,
  cortical_zeroes_as_NA = FALSE,
  subcortical_merged = FALSE
)

```

### Arguments

**x** The CIFTI file name or "xifti" object to smooth.

**cifti\_target\_fname** File name for the smoothed CIFTI. If NULL, will be written to "smoothed.d\*.nii" in the current working directory if x was a CIFTI file, and in a temporary directory if x was a "xifti" object.

**surf\_FWHM, vol\_FWHM** The full width at half maximum (FWHM) parameter for the gaussian surface or volume smoothing kernel, in mm. Default: 5 for cortex (surface) and 3 for subcortex (volume).

**surfL\_fname, surfR\_fname** (Required if the corresponding cortex is present) Surface GIFTI files for the left and right cortical surfaces. If not provided, the surfaces in x are used, but if those are also not present, the default surfaces will be used.

**cerebellum\_fname** (Optional) Surface GIFTI file for the cerebellar surface

**subcortical\_zeroes\_as\_NA, cortical\_zeroes\_as\_NA** Should zero-values in the subcortical volume or cortex be treated as NA? Default: FALSE.

**subcortical\_merged** Smooth across subcortical structure boundaries? Default: FALSE.

### Details

If the CIFTI is a ".dlabel" file (intent 3007), then it will be converted to a ".dscalar" file because the values will no longer be integer indices. Unless the label values were ordinal, this is probably not desired so a warning will be printed.

Can accept a "xifti" object as well as a path to a CIFTI-file.

Surfaces are required for each hemisphere in the CIFTI. If they are not provided, the default inflated surfaces will be used.

Conversion for sigma:  $\sigma * 2 * \sqrt{2 * \log(2)} = FWHM$

**Value**

The `cifti_target_fname`, invisibly, if `x` was a CIFTI file name. A "xifti" object if `x` was a "xifti" object.

**Connectome Workbench**

This function interfaces with the `"-cifti-smoothing"` Workbench command.

**See Also**

Other commonly-used functions: [is.cifti\(\)](#), [read\\_cifti\(\)](#), [resample\\_cifti\(\)](#), [view\\_xifti\\_surface\(\)](#), [view\\_xifti\\_volume\(\)](#), [write\\_cifti\(\)](#)

---

|                           |                                   |
|---------------------------|-----------------------------------|
| <code>smooth_gifti</code> | <i>Smooth a metric GIFTI file</i> |
|---------------------------|-----------------------------------|

---

**Description**

Smooths metric GIFTI data along the cortical surface. The results are written to a new GIFTI file.

**Usage**

```
smooth_gifti(
  original_fname,
  target_fname,
  surf_fname = NULL,
  surf_FWHM = 5,
  hemisphere = c("left", "right"),
  ROI_fname = NULL,
  zeroes_as_NA = FALSE
)
```

```
smoothGIFTI(
  original_fname,
  target_fname,
  surf_fname,
  surf_FWHM = 5,
  zeroes_as_NA = FALSE
)
```

```
smoothgii(
  original_fname,
  target_fname,
  surf_fname,
  surf_FWHM = 5,
  zeroes_as_NA = FALSE
)
```

**Arguments**

|                |   |
|----------------|---|
| original_fname | The GIFTI file to smooth.   |
| target_fname   | Where to save the smoothed file.  |
| surf_fname     | Surface GIFTI files cortical surface along which to smooth. If not provided, the default inflated surfaces will be used.  |
| surf_FWHM      | The full width at half maximum (FWHM) parameter for the gaussian surface smoothing kernel, in mm. Default: 5  |
| hemisphere     | The cortex hemisphere: "left" or "right". Only used if surf_fname is NULL.  |
| ROI_fname      | The ROI to limit smoothing to, as a metric file. This is used to exclude the medial wall from smoothing. If not provided (default) all the data is smoothed across the surface. |
| zeroes_as_NA   | Should zero-values be treated as NA? Default: FALSE.  |

**Value**

The smoothed GIFTI file name, invisibly

**Connectome Workbench**

This function interfaces with the "-metric-smoothing" Workbench command.

---

|                    |                           |
|--------------------|---------------------------|
| substructure_table | <i>Substructure table</i> |
|--------------------|---------------------------|

---

**Description**

Table of labels for cortex hemispheres (left and right) and subcortical substructures. The names used by the CIFTI format and the names used by `ciftiTools` are given.

**Usage**

```
substructure_table()
```

**Details**

The names used by `ciftiTools` are based on those in `FT_READ_CIFTI` from the FieldTrip MATLAB toolbox.

**Value**

A data.frame with each substructure along the rows. The first column gives the CIFTI format name and the second column gives the `ciftiTools` name.

---

|              |                                  |
|--------------|----------------------------------|
| summary.surf | <i>Summarize a "surf" object</i> |
|--------------|----------------------------------|

---

### Description

Summary method for class "surf"

### Usage

```
## S3 method for class 'surf'  
summary(object, ...)  
  
## S3 method for class 'summary.surf'  
print(x, ...)  
  
## S3 method for class 'surf'  
print(x, ...)
```

### Arguments

|        |   |
|--------|---|
| object | Object of class "surf". See <a href="#">is.surf</a> and <a href="#">make_surf</a> . |
| ...    | further arguments passed to or from other methods.                                  |
| x      | bject of class "surf".  |

---

|               |                                   |
|---------------|-----------------------------------|
| summary.xifti | <i>Summarize a "xifti" object</i> |
|---------------|-----------------------------------|

---

### Description

Summary method for class "xifti"

### Usage

```
## S3 method for class 'xifti'  
summary(object, ...)  
  
## S3 method for class 'summary.xifti'  
print(x, ...)  
  
## S3 method for class 'xifti'  
print(x, ...)
```

**Arguments**

object      Object of class "xifti".  
 ...        further arguments passed to or from other methods.  
 x          A "xifti" object.

---

supported\_intents      *The NIFTI intents supported by ciftiTools*

---

**Description**

Table of CIFTI file types (NIFTI intents) supported by ciftiTools.

**Usage**

```
supported_intents()
```

**Details**

See [https://www.nitrc.org/forum/attachment.php?attachid=334&group\\_id=454&forum\\_id=1955](https://www.nitrc.org/forum/attachment.php?attachid=334&group_id=454&forum_id=1955) for information about the different NIFTI intents.

**Value**

A data.frame with each supported file type along the rows, and column names "extension", "intent\_code", "value", and "intent\_name"

---

transform\_xifti      *Apply a univariate transformation to a "xifti" or pair of "xifti"s.*

---

**Description**

Apply a univariate transformation to each value in a "xifti" or pair of "xifti"s. If a pair, they must share the same dimensions (brainstructures) and number of measurements.

**Usage**

```
transform_xifti(xifti, FUN, xifti2 = NULL, idx = NULL, ...)
```

**Arguments**

|        |  |
|--------|--|
| xifti  | A "xifti" object.  |
| FUN    | The function. If xifti2 is not provided, it should be a univariate function like log or sqrt. If xifti2 is provided, it should take in two arguments, like '+' or pmax.  |
| xifti2 | The second xifti, if applicable. Otherwise, NULL (default)   |
| idx    | The column indices for which to apply the transformation. If NULL (default), apply to all columns. If two "xifti" objects, were provided, the values in the first (xifti) will be retained for columns that are not transformed. |
| ...    | Additional arguments to FUN  |

**Details**

If the "xifti" had the dlabel intent, and the transformation creates any value that is not a label value (e.g. a non-integer), then it is converted to a dscalar.

Technically, the function does not have to be univariate: it only has to return the same number of values as the input. The function will be applied to the matrix for each brain structure separately. For example, the function  $\text{function}(q)\{(q - \text{mean}(q)) / \text{sd}(q)\}$  will scale each brainstructure, while scale will scale each column of each brainstructure.

**Value**

A "xifti" storing the result of applying FUN to the input(s). The data dimensions will be the same. The metadata of xifti will be retained, and the metadata of xifti2 will be discarded (if provided).

**See Also**

Other functions for manipulating 'xifti' objects: [add\\_surf\(\)](#), [apply\\_xifti\(\)](#), [combine\\_xifti\(\)](#), [convert\\_to\\_dlabel\(\)](#), [merge\\_xifti\(\)](#), [newdata\\_xifti\(\)](#), [remove\\_xifti\(\)](#), [select\\_xifti\(\)](#)

---

unmask\_subcortex      *Undo a volumetric mask*

---

**Description**

Un-applies a mask to vectorized data to yield its volumetric representation. The mask and data should have compatible dimensions: the number of rows in dat should equal the number of locations within the mask. This is used for the subcortical CIFTI data.

**Usage**

```
unmask_subcortex(dat, mask, fill = NA)
```

**Arguments**

|      |  |
|------|--|
| dat  | Data matrix with locations along the rows and measurements along the columns. If only one set of measurements were made, this may be a vector. |
| mask | Volumetric binary mask. TRUE indicates voxels inside the mask.   |
| fill | The value for locations outside the mask. Default: NA.   |

**Value**

The 3D or 4D unflattened volume array

---

|               |                            |
|---------------|----------------------------|
| use_color_pal | <i>Use a color palette</i> |
|---------------|----------------------------|

---

**Description**

Applies a palette to a data vector to yield a vector of colors.

**Usage**

```
use_color_pal(data_values, pal, color_NA = "white", indices = FALSE)
```

**Arguments**

|             |   |
|-------------|---|
| data_values | The values to map to colors   |
| pal         | The palette to use to map values to colors  |
| color_NA    | The color to use for NA values. Default: "white".   |
| indices     | Return the numeric indices of colors in pal\$value rather than the colors themselves. A value of 0 will be used for missing data. Default: FALSE. |

**Value**

A character vector of color names (or integers if indices).

---

|                |                 |
|----------------|-----------------|
| vertices_Param | <i>vertices</i> |
|----------------|-----------------|

---

**Description**

vertices

**Arguments**

|          |  |
|----------|--|
| vertices | A $V \times 3$ matrix, where each row contains the Euclidean coordinates at which a given vertex in the mesh is located. $V$ is the number of vertices in the mesh |
|----------|--|

view\_comp

*View composite of images***Description**

Create a single image which displays multiple image files. Tailored to support composite layouts of plots from `view_xiffti`.

**Usage**

```
view_comp(
  img,
  ncol = NULL,
  nrow = NULL,
  legend = NULL,
  title = NULL,
  legend_height = 0.3,
  title_height = 0.1,
  title_fsize = 5,
  newpage = is.null(fname),
  fname = NULL,
  ...
)
```

**Arguments**

|  |  |
|--|--|
| <code>img</code>                         | Character vector of paths to images to include. They will be arranged by row.  |
| <code>ncol, nrow</code>                  | Control the layout of the composite image. <code>NULL</code> (default) will use approximately same numbers of rows and columns.  |
| <code>legend</code>                      | File path to a legend image to add, or <code>NULL</code> (default) to not add a legend.  |
| <code>title</code>                       | A length-one character vector to use as the title, or <code>NULL</code> (default) to not add a title.  |
| <code>legend_height, title_height</code> | Heights of the legend and title, if applicable. Specified relative to all the plots, so <code>.1</code> would mean the height is a tenth of the height of all the plots. Default: <code>.1</code> for the title and <code>.3</code> for the legend.  |
| <code>title_fsize</code>                 | Multiplier for font size. Default: 5   |
| <code>newpage</code>                     | Call <code>grid::grid.newpage</code> before rendering? Default: <code>is.null(fname)</code> .  |
| <code>fname</code>                       | If <code>NULL</code> (default), print the result. Otherwise, save to a PNG file at this location. Will override <code>newpage</code> to <code>FALSE</code> .   |
| <code>...</code>                         | Additional arguments to <code>gridExtra::arrangeGrob</code> . The arguments <code>grobs</code> and <code>layout_matrix</code> should be avoided because they are determined based on <code>img</code> . adjusting widths may be useful, e.g. to make the subcortex subplot be less wide than the cortex subplot. |



**Details**

Requires the following packages: png, grid, gridExtra

How it works: the non-legend images (plots) are composited in a call to `grid::arrangeGrob`. If a title or legend exists, it's added to the top and bottom, respectively, of the plots after with another call to `grid::arrangeGrob`.

**Value**

The composite plot

---

|           |                              |
|-----------|------------------------------|
| view_surf | <i>View "surf" object(s)</i> |
|-----------|------------------------------|

---

**Description**

Visualize one or two "surf" objects(s), or the "surf" component(s) in a "xifti" using an interactive Open GL window made with rgl. The rgl package is required.

**Usage**

```
view_surf(
  ...,
  view = c("both", "lateral", "medial"),
  widget = NULL,
  title = NULL,
  fname = FALSE,
  cex.title = NULL,
  text_color = "black",
  bg = NULL,
  alpha = 1,
  edge_color = NULL,
  vertex_color = NULL,
  vertex_size = 0,
  material = NULL,
  width = NULL,
  height = NULL,
  zoom = NULL
)
```

**Arguments**

|      |  |
|------|--|
| ...  | One of: A "surf" object; two "surf" objects; or, a "xifti" object. If a "surf" object has an empty "hemisphere" metadata entry, it will be set to the opposite side of the other's if known; otherwise, it will be set to the left side. If both are unknown, the first will be taken as the left and the second as the right. |
| view | Which view to display: "lateral", "medial", or "both". If NULL (default), both views will be shown. Each view will be plotted in a separate panel row.   |

|               |   |
|---------------|---|
| widget        | Display the plot in an htmlwidget? Should be logical or NULL (default), in which case a widget will be used only if needed ( <code>length(idx)&gt;1</code> & <code>isFALSE(fname)</code> ), <code>fname</code> is a file path to an .html file, or if <code>rgl.useNULL()</code> .  |
| title         | Optional title(s) for the plot(s). It will be printed at the top in a separate subplot with 1/4 the height of the brain cortex subplots.<br>Default: NULL will not use any title if <code>length(idx)==1</code> . Otherwise, it will use the time index (".dtseries") or name (.dscalar or .dlabel) of each data column.<br>To use a custom title(s), use a length 1 character vector (same title for each plot) or length <code>length(idx)</code> character vector (different title for each plot). Set to NULL or an empty character to omit the title.<br>If the title is non-empty but does not appear, try lowering <code>cex.title</code> .  |
| fname         | Save the plot(s) (and color legend if applicable)?<br>If <code>isFALSE(fname)</code> (default), no files will be written.<br>If <code>fname</code> is a length-1 character vector ending in ".html", an html with an interactive widget will be written.<br>If neither of the cases above apply, a png image will be written for each <code>idx</code> . If <code>isTRUE(fname)</code> the files will be named by the data column names (underscores will replace spaces). Or, set <code>fname</code> to a length 1 character vector to name files by this suffix followed by the <code>fname_suffix</code> . Or, set <code>fname</code> to a character vector with the same length as <code>idx</code> to name the files exactly.  |
| cex.title     | Font size multiplier for the title. NULL (default) will use 2 for titles less than 20 characters long, and smaller sizes for increasingly longer titles.  |
| text_color    | Color for text in title and colorbar legend. Default: "black".  |
| bg            | Background color. NULL will use "white". Does not affect the color legend or color bar if printed separately: those will always have white backgrounds.   |
| alpha         | Transparency value for mesh coloring, between 0 and 1. Default: 1.0 (no transparency).  |
| edge_color    | Outline each edge in this color. Default: NULL (do not outline the edges).  |
| vertex_color  | Draw each vertex in this color. Default: "black". Vertices are only drawn if <code>vertex_size &gt; 0</code>  |
| vertex_size   | Draw each vertex with this size. Default: 0 (do not draw the vertices).   |
| material      | A list of materials from <a href="#">material3d</a> to use. For example, <code>list(lit=FALSE, smooth=FALSE)</code> will use exact colors from the color scale, rather than adding geometric shading and interpolating vertex colors. If NULL, use defaults.  |
| width, height | The dimensions of the RGL window, in pixels. If both are NULL (default), these dimensions depend on type of output (Open GL window or widget) and subplots ( <code>hemisphere</code> , <code>view</code> , <code>title</code> , and <code>slider_title</code> ) and are chosen to be the largest plot within a 1500 x 700 area (Open GL window) or 600 x 700 area (widget) that maintains a brain hemisphere subplot dimensions ratio of 10 x 7. Specifying only one will set the other to maintain this aspect ratio. Both can be specified to set the dimensions exactly, but note that the dimensions cannot be larger than the screen resolution. (These arguments do not affect the size of the legend, which cannot be controlled.)<br>The plot will be taller than height to accommodate a title or color bar. |

|                   |  |
|-------------------|--|
|                   | If multiple <code>idx</code> are being composited together, these arguments refer to a single <code>idx</code> within the composited plot, and not the composited plot itself. |
| <code>zoom</code> | Adjust the sizes of the brain meshes. Default: NULL (will be set to 0.6 or 160\ widget.)   |

### Details

This function works as a wrapper to `view_xifti_surface`, but some arguments are not applicable (e.g. color scheme and legend). Also, instead of using the hemisphere argument, name the surface arguments `surfL` or `surfR` (see description for parameter `...`). Finally, the default value for `param` is "surf", not "xifti".

### Navigating and Embedding the Interactive Plots

To navigate the interactive Open GL window and html widget, left click and drag the cursor to rotate the meshes. Use the scroll wheel or right click and drag to zoom. Press the scroll wheel and drag to change the field-of-view. For Open GL windows, execute `snapshot` to save the current window as a .png file, `close3d` to close the window, and `view3d` to programmatically control the perspective.

To embed an interactive plot in an R Markdown document, first execute `rgl::setupKnitr()` to prepare the document for embedding the widget. Then execute the plot command as you normally would to create a widget (i.e. without specifying `fname`, and by requesting more than one `idx` or by setting `widget` to TRUE). When the R Markdown document is knitted, the interactive widget should be displayed below the chunk in which the plot command was executed. See the vignette for an example.

### Embedding the Static Plots

To embed a static plot in an R Markdown document, first execute `rgl::setupKnitr()` to prepare the document for embedding the snapshot of the Open GL window. Then execute the plot command as you normally would to create an Open GL window (i.e. without specifying `fname`, and by requesting only one `idx`). In the options for the chunk in which the plot command is executed, set `rgl=TRUE`, `format="png"`. You can also control the image dimensions here e.g. `fig.height=3.8`, `fig.width=5`. When the R Markdown document is knitted, the static plots should be displayed below the chunk in which the plot command was executed. See the vignette for an example.

### See Also

Other functions for working with GIFTI surface geometry data: `is_surf()`, `read_surf()`, `resample_surf()`, `rotate_surf()`, `write_surf_gifti()`

---

view\_xifti

*View a "xifti" object*

---

**Description**

Displays the data in a "xifti" object using `view_xifti_surface` and/or `view_xifti_volume`. Compared to calling these two functions separately on the same data, this function may be more convenient since the automatic choice of color mode and limits is determined across the entire data and shared between the two plots. Also, if writing files the subcortical plots will not overwrite the cortical plots.

**Usage**

```
view_xifti(xifti, what = NULL, ...)
```

```
view_cifti(xifti, ...)
```

```
viewCIfTI(xifti, ...)
```

```
viewcii(xifti, ...)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>xifti</code> | A "xifti" object.  |
| <code>what</code>  | "surface", "volume", or "both". NULL will infer based on the contents of the "xifti": if there is data, plot the surface cortex data if present, and the volumetric subcortical data otherwise. If there is no data, plot the surface geometry if present, and do nothing otherwise. |
| <code>...</code>   | Additional arguments to pass to either view function.  |

**Value**

The return value of `view_xifti_surface` or `view_xifti_volume`.

---

|                                 |  |
|---------------------------------|--|
| <code>view_xifti_surface</code> | <i>View cortical surface data in a "xifti"</i> |
|---------------------------------|--|

---

**Description**

Visualize "xifti" cortical data using an interactive Open GL window or htmlwidget made with `rgl`. The `rmarkdown` package is required for the htmlwidget functionality.

**Usage**

```
view_xifti_surface(  
  xifti = NULL,  
  surfL = NULL,  
  surfR = NULL,  
  color_mode = "auto",  
  zlim = NULL,  
)
```

```
    colors = NULL,  
    idx = NULL,  
    hemisphere = NULL,  
    together = NULL,  
    together_ncol = NULL,  
    together_title = NULL,  
    view = c("both", "lateral", "medial"),  
    widget = NULL,  
    title = NULL,  
    slider_title = "Index",  
    fname = FALSE,  
    fname_suffix = c("names", "idx"),  
    legend_fname = "[fname]_legend",  
    legend_ncol = NULL,  
    legend_alllevels = FALSE,  
    legend_embed = NULL,  
    digits = NULL,  
    scientific = NA,  
    cex.title = NULL,  
    text_color = "black",  
    bg = NULL,  
    NA_color = "white",  
    borders = FALSE,  
    alpha = 1,  
    edge_color = NULL,  
    vertex_color = NULL,  
    vertex_size = 0,  
    material = NULL,  
    shadows = 1,  
    width = NULL,  
    height = NULL,  
    zoom = NULL  
)
```

```
view_cifti_surface(  
  xifti = NULL,  
  surfL = NULL,  
  surfR = NULL,  
  color_mode = "auto",  
  zlim = NULL,  
  colors = NULL,  
  idx = NULL,  
  hemisphere = NULL,  
  together = NULL,  
  together_ncol = NULL,  
  together_title = NULL,  
  view = c("both", "lateral", "medial"),  
  widget = NULL,  
)
```

```
title = NULL,  
slider_title = "Index",  
fname = FALSE,  
fname_suffix = c("names", "idx"),  
legend_fname = "[fname]_legend",  
legend_ncol = NULL,  
legend_alllevels = FALSE,  
legend_embed = NULL,  
digits = NULL,  
scientific = NA,  
cex.title = NULL,  
text_color = "black",  
bg = NULL,  
NA_color = "white",  
borders = FALSE,  
alpha = 1,  
edge_color = NULL,  
vertex_color = NULL,  
vertex_size = 0,  
material = NULL,  
shadows = 1,  
width = NULL,  
height = NULL,  
zoom = NULL  
)  
  
viewCifTI_surface(  
  xifti = NULL,  
  surfL = NULL,  
  surfR = NULL,  
  color_mode = "auto",  
  zlim = NULL,  
  colors = NULL,  
  idx = NULL,  
  hemisphere = NULL,  
  together = NULL,  
  together_ncol = NULL,  
  together_title = NULL,  
  view = c("both", "lateral", "medial"),  
  widget = NULL,  
  title = NULL,  
  slider_title = "Index",  
  fname = FALSE,  
  fname_suffix = c("names", "idx"),  
  legend_fname = "[fname]_legend",  
  legend_ncol = NULL,  
  legend_alllevels = FALSE,  
  legend_embed = NULL,
```

```
digits = NULL,
scientific = NA,
cex.title = NULL,
text_color = "black",
bg = NULL,
NA_color = "white",
borders = FALSE,
alpha = 1,
edge_color = NULL,
vertex_color = NULL,
vertex_size = 0,
material = NULL,
shadows = 1,
width = NULL,
height = NULL,
zoom = NULL
)

viewcii_surface(
  xifti = NULL,
  surfL = NULL,
  surfR = NULL,
  color_mode = "auto",
  zlim = NULL,
  colors = NULL,
  idx = NULL,
  hemisphere = NULL,
  together = NULL,
  together_ncol = NULL,
  together_title = NULL,
  view = c("both", "lateral", "medial"),
  widget = NULL,
  title = NULL,
  slider_title = "Index",
  fname = FALSE,
  fname_suffix = c("names", "idx"),
  legend_fname = "[fname]_legend",
  legend_ncol = NULL,
  legend_alllevels = FALSE,
  legend_embed = NULL,
  digits = NULL,
  scientific = NA,
  cex.title = NULL,
  text_color = "black",
  bg = NULL,
  NA_color = "white",
  borders = FALSE,
  alpha = 1,
```

```

edge_color = NULL,
vertex_color = NULL,
vertex_size = 0,
material = NULL,
shadows = 1,
width = NULL,
height = NULL,
zoom = NULL
)

```

## Arguments

|              |   |
|--------------|---|
| xifti        | A "xifti" object.   |
| surfL, surfR | (Optional) The brain surface model to use. Each can be a "surf" object, any valid argument to <a href="#">read_surf</a> , or one of "very inflated", "inflated", or "midthickness". If provided, it will override xifti\$surf\$cortex_left or xifti\$surf\$cortex_right if it exists. Leave as NULL (default) to use xifti\$surf\$cortex_left or xifti\$surf\$cortex_right if it exists, or the default inflated surfaces if it does not exist.   |
| color_mode   | (Optional) "sequential", "qualitative", "diverging", or "auto" (default). Auto mode will use the qualitative color mode if the "xifti" object represents a .dlabel CIFTI (intent 3007). Otherwise, it will use the diverging mode if the data contains both positive and negative values, and the sequential mode if the data contains >90\ <a href="#">make_color_pal</a> for more details.  |
| zlim         | (Optional) Controls the mapping of values to each color in colors. If the length is longer than one, using -Inf will set the value to the data minimum, and Inf will set the value to the data maximum. See <a href="#">make_color_pal</a> description for more details.  |
| colors       | (Optional) "ROY_BIG_BL", vector of colors to use, the name of a ColorBrewer palette (see <a href="#">RColorBrewer::brewer.pal.info</a> and <a href="#">colorbrewer2.org</a> ), the name of a viridisLite palette, or a data.frame with columns "color" and "value" (will override zlim). If NULL (default), will use the positive half of "ROY_BIG_BL" (sequential), "Set2" (qualitative), or the full "ROY_BIG_BL" (diverging). An exception to these defaults is if the "xifti" object represents a .dlabel CIFTI (intent 3007), in which case the colors in the label table will be used. See <a href="#">make_color_pal</a> for more details. |
| idx          | The time/column index of the data to display. NULL (default) will display the first column.<br><br>If its length is greater than one, and isFALSE(fname), a widget must be used since a single OpenGL window cannot show multiple indexes. A slider will be added to the widget to control what time/column is being displayed.   |
| hemisphere   | Which brain cortex to display: "both" (default), "left", or "right". Each will be plotted in a separate panel column.<br><br>If a brain cortex is requested but no surface is available, a default inflated surface will be used.   |



This argument can also be NULL (default). In this case, the default inflated surface included with `ciftiTools` will be used for each cortex with data (i.e. if `xifti$data$cortex_left` and/or `xifti$data$cortex_right` exist). Surfaces without data will be colored white.

|                |  |
|----------------|--|
| together       | <p>Only applies if saving image files (<code>!isFALSE(fname)</code>). Use this argument to create and save a composite image which combines multiple plots. NULL (default) will not combine any plots. Otherwise, this argument should be a character vector with one or more of the following entries:</p> <p>"leg" to combine the color legend with each "xifti" data plot. Overrides/ignores <code>legend_embed</code>.</p> <p>"idx" to place all the plots for the different "idx" in a grid. If the data is not qualitative, a shared color bar will be added to the bottom of the composite. If the data is qualitative, a shared color legend will be added to the bottom only if "leg" is in together. For greater control see <code>view_comp</code> or <code>grid::arrangeGrob</code>.</p> |
| together_ncol  | <p>If "idx" %in% together, this determines the number of columns to use in the array of subplots for different indices. By default, the number of columns and rows will be determined such that they are about equal.</p>  |
| together_title | <p>If a composite image is made based on together, use this argument to add a grand title to the composite image. Should be a length-one character vector or NULL (default) to not add a grand title.</p>  |
| view           | <p>Which view to display: "lateral", "medial", or "both". If NULL (default), both views will be shown. Each view will be plotted in a separate panel row.</p>  |
| widget         | <p>Display the plot in an <code>htmlwidget</code>? Should be logical or NULL (default), in which case a widget will be used only if needed (<code>length(idx)&gt;1 &amp; isFALSE(fname)</code>, <code>fname</code> is a file path to an <code>.html</code> file, or if <code>rgl.useNULL()</code>).</p>  |
| title          | <p>Optional title(s) for the plot(s). It will be printed at the top in a separate subplot with 1/4 the height of the brain cortex subplots.</p> <p>Default: NULL will not use any title if <code>length(idx)==1</code>. Otherwise, it will use the time index (<code>".dtseries"</code>) or name (<code>".dscalar</code> or <code>".dlabel</code>) of each data column.</p> <p>To use a custom title(s), use a length 1 character vector (same title for each plot) or length <code>length(idx)</code> character vector (different title for each plot). Set to NULL or an empty character to omit the title.</p> <p>If the title is non-empty but does not appear, try lowering <code>cex.title</code>.</p>   |
| slider_title   | <p>Text at bottom of plot that will be added if a slider is used, to provide a title for it. Default: "Index". If NULL or an empty character, no title will be added.</p>  |
| fname          | <p>Save the plot(s) (and color legend if applicable)?</p> <p>If <code>isFALSE(fname)</code> (default), no files will be written.</p> <p>If <code>fname</code> is a length-1 character vector ending in <code>".html"</code>, an <code>html</code> with an interactive widget will be written.</p> <p>If neither of the cases above apply, a <code>png</code> image will be written for each <code>idx</code>. If <code>isTRUE(fname)</code> the files will be named by the data column names (underscores will replace spaces). Or, set <code>fname</code> to a length 1 character vector to name files by this suffix followed by the <code>fname_suffix</code>. Or, set <code>fname</code> to a character vector with the same length as <code>idx</code> to name the files exactly.</p>           |

|                  |   |
|------------------|---|
| fname_suffix     | Either the data column names ("names") or the index value ("idx").  |
| legend_fname     | Save the color legend? Since the legend is the same for each idx only one legend is written even if <code>length(idx)&gt;1</code> . This argument can be NULL to not save the legend, an exact file path, or a length-one character vector with "[fname]" in it, which will name the legend based on <code>fname[1]</code> . For example, if <code>fname[1]</code> is "plots/my_cifti.png" and <code>legend_fname</code> is " <code>\"[fname]_legend</code> " (default), then the legend plot will be saved to "plots/my_cifti_legend.png". |
| legend_ncol      | Number of columns in color legend. If NULL (default), use 10 entries per row. Only applies if the color legend is used (qualitative data).  |
| legend_alllevels | Show all label levels in the color legend? If FALSE (default), just show the levels present in the data being viewed. Only applies if the color legend is used (qualitative data).  |
| legend_embed     | Should the colorbar be embedded in the plot? It will be positioned in the bottom-left corner, in a separate subplot with 1/4 the height of the brain cortex subplots. Default: TRUE. If FALSE, print/save it separately instead.<br>Only applies if the color bar is used (sequential or diverging data) or if "leg" %in% together. Otherwise the color legend (qualitative data) cannot be embedded at the moment.   |
| digits           | The number of digits for the colorbar legend ticks. If NULL (default), let <code>format</code> decide.  |
| scientific       | Use scientific notation? If NA (default), let <code>format</code> decide.   |
| cex.title        | Font size multiplier for the title. NULL (default) will use 2 for titles less than 20 characters long, and smaller sizes for increasingly longer titles.  |
| text_color       | Color for text in title and colorbar legend. Default: "black".  |
| bg               | Background color. NULL will use "white". Does not affect the color legend or color bar if printed separately: those will always have white backgrounds.   |
| NA_color         | The color for the medial wall and NA values. Default: "white". Also used to color the entire surface for <code>view_surf</code> .   |
| borders          | Only applicable if <code>color_mode</code> is "qualitative". Border vertices will be identified (those that share a face with at least one vertex of a different value) and colored over. If this argument is TRUE borders will be colored in black; provide the name of a different color to use that instead. If FALSE or NULL (default), do not draw borders.  |
| alpha            | Transparency value for mesh coloring, between 0 and 1. Default: 1.0 (no transparency).  |
| edge_color       | Outline each edge in this color. Default: NULL (do not outline the edges).  |
| vertex_color     | Draw each vertex in this color. Default: "black". Vertices are only drawn if <code>vertex_size &gt; 0</code>  |
| vertex_size      | Draw each vertex with this size. Default: 0 (do not draw the vertices).   |
| material         | A list of materials from <code>material3d</code> to use. For example, <code>list(lit=FALSE, smooth=FALSE)</code> will use exact colors from the color scale, rather than adding geometric shading and interpolating vertex colors. If NULL, use defaults.   |

|               |   |
|---------------|---|
| shadows       | Number from 0 (maximum added lighting) to 1 (no added lighting) to control the darkness and extent of shadowing on the 3D surface. Default: 1. Shadows help render the shape of the surface, but can be distracting if interpretation of the data depends on small differences in brightness along the color scale.   |
| width, height | The dimensions of the RGL window, in pixels. If both are NULL (default), these dimensions depend on type of output (Open GL window or widget) and subplots (hemisphere, view, title, and slider_title) and are chosen to be the largest plot within a 1500 x 700 area (Open GL window) or 600 x 700 area (widget) that maintains a brain hemisphere subplot dimensions ratio of 10 x 7. Specifying only one will set the other to maintain this aspect ratio. Both can be specified to set the dimensions exactly, but note that the dimensions cannot be larger than the screen resolution. (These arguments do not affect the size of the legend, which cannot be controlled.)<br><br>The plot will be taller than height to accommodate a title or color bar.<br><br>If multiple idx are being composited with together, these arguments refer to a single idx within the composited plot, and not the composited plot itself. |
| zoom          | Adjust the sizes of the brain meshes. Default: NULL (will be set to 0.6 or 160\ widget.)  |

### Value

If a png or html file(s) were written, the names of the files for each index (and color legend if applicable) will be returned. Otherwise, the widget itself is returned if a widget was used, and the rgl object IDs are returned if an Open GL window was used. The rgl object IDs are useful for further programmatic manipulation of the Open GL window.

### Navigating and Embedding the Interactive Plots

To navigate the interactive Open GL window and html widget, left click and drag the cursor to rotate the meshes. Use the scroll wheel or right click and drag to zoom. Press the scroll wheel and drag to change the field-of-view. For Open GL windows, execute `snapshot` to save the current window as a .png file, `close3d` to close the window, and `view3d` to programmatically control the perspective.

To embed an interactive plot in an R Markdown document, first execute `rgl::setupKnitr()` to prepare the document for embedding the widget. Then execute the plot command as you normally would to create a widget (i.e. without specifying `fname`, and by requesting more than one `idx` or by setting `widget` to TRUE). When the R Markdown document is knitted, the interactive widget should be displayed below the chunk in which the plot command was executed. See the vignette for an example.

### Embedding the Static Plots

To embed a static plot in an R Markdown document, first execute `rgl::setupKnitr()` to prepare the document for embedding the snapshot of the Open GL window. Then execute the plot command as you normally would to create an Open GL window (i.e. without specifying `fname`, and by requesting only one `idx`). In the options for the chunk in which the plot command is executed, set `rgl=TRUE`, `format="png"`. You can also control the image dimensions here e.g. `fig.height=3.8`, `fig.width=5`. When the R Markdown document is knitted, the static plots should be displayed below the chunk in which the plot command was executed. See the vignette for an example.

**See Also**

Other commonly-used functions: [is\\_cifti\(\)](#), [read\\_cifti\(\)](#), [resample\\_cifti\(\)](#), [smooth\\_cifti\(\)](#), [view\\_xifti\\_volume\(\)](#), [write\\_cifti\(\)](#)

---

|                   |   |
|-------------------|---|
| view_xifti_volume | <i>View subcortical data in a "xifti"</i> |
|-------------------|---|

---

**Description**

Visualize the subcortical data in a "xifti" using a series of 2D slices (based on [overlay](#)) or an interactive widget (based on `papayar::papaya`). Note: `papayar` has been removed from CRAN so the widget is not available. If `papayar` returns to CRAN the widget will be made available again.

**Usage**

```
view_xifti_volume(
  xifti,
  structural_img = "MNI",
  color_mode = "auto",
  zlim = NULL,
  colors = NULL,
  structural_img_colors = gray(0:255/280),
  title = NULL,
  idx = NULL,
  plane = c("axial", "sagittal", "coronal"),
  convention = c("neurological", "radiological"),
  n_slices = 9,
  slices = NULL,
  together = NULL,
  together_ncol = NULL,
  together_title = NULL,
  widget = FALSE,
  fname = FALSE,
  fname_suffix = c("names", "idx"),
  fname_sub = FALSE,
  legend_fname = "[fname]_legend",
  legend_ncol = NULL,
  legend_alllevels = FALSE,
  legend_embed = NULL,
  digits = NULL,
  scientific = NA,
  cex.title = NULL,
  ypos.title = 0,
  xpos.title = 0,
  orientation_labels = TRUE,
  crop = TRUE,
  text_color = "white",
```

```
    bg = NULL,
    width = NULL,
    height = NULL,
    ...
)

view_cifti_volume(
  xifti,
  structural_img = "MNI",
  color_mode = "auto",
  zlim = NULL,
  colors = NULL,
  structural_img_colors = gray(0:255/280),
  title = NULL,
  idx = NULL,
  plane = c("axial", "sagittal", "coronal"),
  convention = c("neurological", "radiological"),
  n_slices = 9,
  slices = NULL,
  together = NULL,
  together_ncol = NULL,
  together_title = NULL,
  widget = FALSE,
  fname = FALSE,
  fname_suffix = c("names", "idx"),
  fname_sub = FALSE,
  legend_fname = "[fname]_legend",
  legend_ncol = NULL,
  legend_alllevels = FALSE,
  legend_embed = NULL,
  digits = NULL,
  scientific = NA,
  cex.title = NULL,
  ypos.title = 0,
  xpos.title = 0,
  orientation_labels = TRUE,
  crop = TRUE,
  text_color = "white",
  bg = NULL,
  width = NULL,
  height = NULL,
  ...
)

viewCifTI_volume(
  xifti,
  structural_img = "MNI",
  color_mode = "auto",
```

```
zlim = NULL,
colors = NULL,
structural_img_colors = gray(0:255/280),
title = NULL,
idx = NULL,
plane = c("axial", "sagittal", "coronal"),
convention = c("neurological", "radiological"),
n_slices = 9,
slices = NULL,
together = NULL,
together_ncol = NULL,
together_title = NULL,
widget = FALSE,
fname = FALSE,
fname_suffix = c("names", "idx"),
fname_sub = FALSE,
legend_fname = "[fname]_legend",
legend_ncol = NULL,
legend_alllevels = FALSE,
legend_embed = NULL,
digits = NULL,
scientific = NA,
cex.title = NULL,
ypos.title = 0,
xpos.title = 0,
orientation_labels = TRUE,
crop = TRUE,
text_color = "white",
bg = NULL,
width = NULL,
height = NULL,
...
)

viewcii_volume(
  xifti,
  structural_img = "MNI",
  color_mode = "auto",
  zlim = NULL,
  colors = NULL,
  structural_img_colors = gray(0:255/280),
  title = NULL,
  idx = NULL,
  plane = c("axial", "sagittal", "coronal"),
  convention = c("neurological", "radiological"),
  n_slices = 9,
  slices = NULL,
  together = NULL,
```

```

together_ncol = NULL,
together_title = NULL,
widget = FALSE,
fname = FALSE,
fname_suffix = c("names", "idx"),
fname_sub = FALSE,
legend_fname = "[fname]_legend",
legend_ncol = NULL,
legend_alllevels = FALSE,
legend_embed = NULL,
digits = NULL,
scientific = NA,
cex.title = NULL,
ypos.title = 0,
xpos.title = 0,
orientation_labels = TRUE,
crop = TRUE,
text_color = "white",
bg = NULL,
width = NULL,
height = NULL,
...
)

```

### Arguments

|                |   |
|----------------|---|
| xifti          | A "xifti" object.   |
| structural_img | The structural MRI image on which to overlay the subcortical plot. Can be a file name, "MNI" (default) to use the MNI T1-weighted template included in ciftiTools, or NULL to use a blank image.  |
| color_mode     | (Optional) "sequential", "qualitative", "diverging", or "auto" (default). Auto mode will use the qualitative color mode if the "xifti" object represents a .dlabel CIFTI (intent 3007). Otherwise, it will use the diverging mode if the data contains both positive and negative values, and the sequential mode if the data contains >90% <a href="#">make_color_pal</a> for more details.  |
| zlim           | (Optional) Controls the mapping of values to each color in colors. If the length is longer than one, using -Inf will set the value to the data minimum, and Inf will set the value to the data maximum. See <a href="#">make_color_pal</a> description for more details.  |
| colors         | (Optional) "ROY_BIG_BL", vector of colors to use, the name of a ColorBrewer palette (see <a href="#">RColorBrewer::brewer.pal.info</a> and <a href="#">colorbrewer2.org</a> ), the name of a viridisLite palette, or a data.frame with columns "color" and "value" (will override zlim). If NULL (default), will use the positive half of "ROY_BIG_BL" (sequential), "Set2" (qualitative), or the full "ROY_BIG_BL" (diverging). An exception to these defaults is if the "xifti" object represents a .dlabel CIFTI (intent 3007), in which case the colors in the label table will be used. See <a href="#">make_color_pal</a> for more details. |

|                       |   |
|-----------------------|---|
| structural_img_colors | Colors to use for the background image. These will be assigned in order from lowest to highest value with equal spacing between the colors. (color_mode, zlim and colors have no bearing on the background image colors.) This argument is used as the col.x argument to oro.nifti::overlay directly. Default: gray(0:255/280). To use the oro.nifti::overlay default instead set this argument to gray(0:64/64).   |
| title                 | Optional title(s) for the plot(s). It will be printed at the top.<br>Default: NULL will not use any title if length(idx)==1. Otherwise, it will use the time index (".dtseries") or name (.dscalar or .dlabel) of each data column.<br>To use a custom title(s), use a length 1 character vector (same title for each plot) or length length(idx) character vector (different title for each plot). Set to NULL or an empty character to omit the title.<br>If the title is non-empty but does not appear, try lowering cex.title.  |
| idx                   | The time/column index of the data to display. NULL (default) will display the first column.<br>If widget, only one index at a time may be displayed.<br>If !widget and the length of idx is greater than one, a new plot will be created for each idx. These can be toggled between using the arrows at the top of the display window if working interactively in RStudio; or, these will be written to separate files if !isFALSE(fname).  |
| plane                 | The plane to display for the slices: "axial" (default), "sagittal" or "coronal". Ignored if widget.   |
| convention            | "neurological" (default) or "radiological". Neurological convention will display the left side of the brain on the left side of axial and coronal images, and in the first few slices of a series of sagittal images. Radiological convention will display the right side of the brain on the left side of axial and coronal images, and in the first few slices of a series of sagittal images.  |
| n_slices              | The number of slices to display. Default: 9. The slices will be selected in a way that visualizes as much of the subcortex as possible. Ignored if widget.  |
| slices                | Which slices to display. If provided, this argument will override n_slices. Should be a numeric vector with integer values between one and the number of slices in plane. Ignored if widget.  |
| together              | Only applies if saving image files (!isFALSE(fname)). Use this argument to create and save a composite image which combines multiple plots. NULL (default) will not combine any plots. Otherwise, this argument should be a character vector with one or more of the following entries:<br>"leg" to combine the color legend with each "xifti" data plot. Overrides/ignores legend_embed.<br>"idx" to place all the plots for the different "idx" in a grid. If the data is not qualitative, a shared color bar will be added to the bottom of the composite. If the data is qualitative, a shared color legend will be added to the bottom only if "leg" is in together. For greater control see view_comp or grid::arrangeGrob. |



|                     |  |
|---------------------|--|
| together_ncol       | If "idx" %in% together, this determines the number of columns to use in the array of subplots for different indices. By default, the number of columns and rows will be determined such that they are about equal.   |
| together_title      | If a composite image is made based on together, use this argument to add a grand title to the composite image. Should be a length-one character vector or NULL (default) to not add a grand title.   |
| widget              | Create an interactive widget using papayar? Otherwise display static 2D slices. Default: FALSE.<br>Note that the widget can only display one idx at a time.<br>Note: papayar has been removed from CRAN so the widget is not available. If papayar returns to CRAN the widget will be made available again.  |
| fname, fname_suffix | Save the plot(s) (and color legend if applicable)?<br>If isFALSE(fname) (default), no files will be written.<br>If widget, these arguments are ignored.<br>If neither of the cases above apply, a png image will be written for each idx. If isTRUE(fname) the files will be named by the data column names (underscores will replace spaces). Or, set fname to a length 1 character vector to name files by this suffix followed by the fname_suffix: either the data column names ("names") or the index value ("idx"). Or, set fname to a character vector with the same length as idx to name the files exactly. |
| fname_sub           | Add "_sub" to the end of the names of the files being saved? Default: FALSE. This is useful if cortical plots of the same data are being saved too.  |
| legend_fname        | Save the color legend? Since the legend is the same for each idx only one legend is written even if length(idx)>1. This argument can be NULL to not save the legend, an exact file path, or a length-one character vector with "[fname]" in it, which will name the legend based on fname\[1\]. For example, if fname\[1\] is "plots/my_ciffti.png" and legend_fname is "\[fname\]_legend" (default), then the legend plot will be saved to "plots/my_ciffti_legend.png".  |
| legend_ncol         | Number of columns in color legend. If NULL (default), use 10 entries per row. Only applies if the color legend is used (qualitative data).   |
| legend_alllevels    | Show all label levels in the color legend? If FALSE (default), just show the levels present in the data being viewed. Only applies if the color legend is used (qualitative data).   |
| legend_embed        | Should the colorbar be embedded in the plot? It will be positioned at the bottom. Default: TRUE. If FALSE, print/save it separately instead.<br>Only applies if the color bar is used (sequential or diverging data). The color legend (qualitative data) cannot be embedded at the moment.  |
| digits              | The number of digits for the colorbar legend ticks. If NULL (default), let <code>format</code> decide.   |
| scientific          | Use scientific notation? If NA (default), let <code>format</code> decide.  |
| cex.title           | Font size multiplier for the title. NULL (default) will use 1.2 for titles less than 20 characters long, and smaller sizes for increasingly longer titles. If saving a PNG and PDF file, the default will also scale with width relative to the default value of width.  |

|                        |   |
|------------------------|---|
| ypos.title, xpos.title | The positioning of the title can be finicky, especially when using an R Markdown document interactively in which case it appears too high in the plot. Use these arguments to nudge the title up or down (ypos.title) or left or right (xpos.title).  |
| orientation_labels     | Show orientation labels at the top left and top right of the plot? These will indicate the directions along the left-right axis for each slice image. Default: TRUE. Ignored if widget. The vertical positioning is controlled by ypos.title, and the font size is controlled by cex.title.   |
| crop                   | Crop the slice subplots to the subcortical structures, instead of showing the full anatomical image? Default: TRUE. Ignored if widget.  |
| text_color             | Color for text in title and colorbar legend. Default: "white". If "white", will use black instead for the color   |
| bg                     | Background color. NULL will use "black". Does not affect the color legend or color bar if printed separately: those will always have white backgrounds.   |
| width, height          | The dimensions of the plot, in pixels. Only affects saved images (if !isFALSE(fname)). If NULL, file dimensions will be 400 x 600 pixels for PNGs and 4 x 6 in. for PDFs.<br><br>Currently, there is no way to control the dimensions of the plot if working interactively in RStudio or creating a knitted R Markdown document. The default appears to be a wide aspect ratio. |
| ...                    | Additional arguments to pass to papayar::papaya or oro.nifti::overlay. Note that for oro.nifti::overlay the following additional arguments should not be provided since they are pre-determined inside this function or by the arguments listed above: x, y, plane, col.y, col.x, zlim.y, oma, plot.type, bg.   |

## Details

Note that color\_mode, zlim, and colors only affect the color scale of the data values whereas structural\_img\_colors only affects the color scale of the background image.

Currently, the color-related arguments only affect the 2D slice view. The color limits and palette must be edited using the widget controls once it's rendered.

Arguments concerning anatomical orientation assume that the subcortical data is stored in the following way: first dimension is normal to the sagittal plane, going left to right; second dimension is normal to the coronal plane, going from the front of the head (anterior) to the back (posterior); third dimension is normal to the axial plane, going from the top of the head (superior) to the neck (inferior).

For non-interactive plots, if n\_slices > 1 and convention="neurological", axial slices are ordered from the neck (inferior) to the top of the head (superior), sagittal slices are ordered left to right, and coronal slices are ordered back (posterior) to front (anterior). If convention="radiological", sagittal slices are instead ordered right to left.

**Value**

If a png or pdf file(s) were written, the names of the files for each index (and color legend if applicable) will be returned. Otherwise, NULL is invisibly returned.

**See Also**

Other commonly-used functions: [is.cifti\(\)](#), [read\\_cifti\(\)](#), [resample\\_cifti\(\)](#), [smooth\\_cifti\(\)](#), [view\\_xifti\\_surface\(\)](#), [write\\_cifti\(\)](#)

---

|             |   |
|-------------|---|
| write_cifti | <i>Write a CIFTI file from a "xifti" object</i> |
|-------------|---|

---

**Description**

Write out a "xifti" object as a CIFTI file and (optionally) GIFTI surface files.

**Usage**

```
write_cifti(
  xifti,
  cifti_fname,
  surfL_fname = NULL,
  surfR_fname = NULL,
  verbose = TRUE
)
```

```
writeCifti(
  xifti,
  cifti_fname,
  surfL_fname = NULL,
  surfR_fname = NULL,
  verbose = TRUE
)
```

```
writeci(
  xifti,
  cifti_fname,
  surfL_fname = NULL,
  surfR_fname = NULL,
  verbose = TRUE
)
```

```
write_xifti(
  xifti,
  cifti_fname,
  surfL_fname = NULL,
  surfR_fname = NULL,
```

```

    verbose = TRUE
  )

```

### Arguments

`xifti` A "xifti" object.

`cifti_fname` File path to a CIFTI file (ending in ".d\*.nii").

`surfL_fname, surfR_fname` If the [left/right] surface is present, it will be written to a GIFTI file at this file path. If NULL (default), do not write out the surface.

`verbose` Should occasional updates be printed? Default: TRUE.

### Value

Named character vector of the written files

### Connectome Workbench

This function interfaces with the "-cifti-create-dense-timeseries", "-cifti-create-dense-scalar", or "-cifti-create-label" Workbench Command, depending on the input.

### See Also

Other commonly-used functions: [is.cifti\(\)](#), [read\\_cifti\(\)](#), [resample\\_cifti\(\)](#), [smooth\\_cifti\(\)](#), [view\\_xifti\\_surface\(\)](#), [view\\_xifti\\_volume\(\)](#)

Other functions for writing CIFTI or GIFTI data: [separate\\_cifti\(\)](#), [write\\_metric\\_gifti\(\)](#), [write\\_subcort\\_nifti\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

`write_metric_gifti`      *Write a data matrix to a GIFTI metric file*

---

### Description

Write the data for the left or right cortex to a metric GIFTI file.

### Usage

```

write_metric_gifti(
  x,
  gifti_fname,
  hemisphere = c("left", "right"),
  intent = NULL,
  data_type = NULL,
  encoding = NULL,
  endian = c("LittleEndian", "BigEndian"),
  col_names = NULL,
  label_table = NULL
)

```

**Arguments**

|             |   |
|-------------|---|
| x           | A $V \times T$ data matrix (V vertices, T measurements). This can also be an object from <code>gifti::readgii</code> , or a length $T$ list of length $V$ vectors.  |
| gifti_fname | Where to write the GIFTI file.  |
| hemisphere  | "left" (default) or "right". Ignored if data is already a "gifti" object.   |
| intent      | "NIFTI_INTENT_*". NULL (default) will use metadata if data is a "gifti" object, or "NONE" if it cannot be inferred. If not NULL and data is a "gifti" object, it will overwrite the existing intent. See <a href="https://nifti.nimh.nih.gov/nifti-1/documentation/nifti1fields/nifti1fields_pages/group__NIFTI1__INTENT__CODES.html/document_v">https://nifti.nimh.nih.gov/nifti-1/documentation/nifti1fields/nifti1fields_pages/group__NIFTI1__INTENT__CODES.html/document_v</a> .  |
| data_type   | the type of data: "NIFTI_TYPE_*" where * is "INT32" or "FLOAT32". If NULL (default), the data type will be inferred. If not NULL and data is a "gifti" object, it will overwrite the existing data type.  |
| encoding    | One of "ASCII", "Base64Binary", or "GZipBase64Binary". If NULL (default), will use the metadata if data is a GIFTI object, or "ASCII" if the data_type is "NIFTI_TYPE_INT32" and "GZipBase64Binary" if the data_type is "NIFTI_TYPE_FLOAT32". If not NULL and data is a "gifti" object, it will overwrite the existing data type.   |
| endian      | "LittleEndian" (default) or "BigEndian". If data is a "gifti" object, it will overwrite the existing endian.  |
| col_names   | The names of each data column in <code>gii</code> (or entries in <code>gii\$data</code> ).  |
| label_table | A <code>data.frame</code> with labels along rows. The row names should be the label names. The column names should be among: "Key", "Red", "Green", "Blue", and "Alpha". The "Key" column is required whereas the others are optional (but very often included). Values in the "Key" column should be non-negative integers, typically beginning with 0. The other columns should be floating-point numbers between 0 and 1.<br><br>Although CIFTI files support a different label table for each data column, GIFTI files only support a single label table. So this label table should be applicable to each data column. |

**Value**

Whether the GIFTI was successfully written

**See Also**

Other functions for writing CIFTI or GIFTI data: [separate\\_cifti\(\)](#), [write\\_cifti\(\)](#), [write\\_subcort\\_nifti\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

write\_subcort\_nifti     *Write subcortical data to NIFTI files*

---

### Description

Write subcortical data to NIFTI files representing the data values, subcortical structure labels, and volumetric mask. The input formats of `subcortVol`, `subcortLabs`, and `subcortMask` correspond to the data structures of `xiffti$data$subcort`, `xiffti$meta$subcort$labels`, and `xiffti$meta$subcort$mask` respectively. `subcortVol` and `subcortLabs` should be vectorized, so if they are volumes consider using `RNifti::writeNIFTI`.

### Usage

```
write_subcort_nifti(
  subcortVol,
  subcortLabs,
  subcortMask,
  trans_mat = NULL,
  trans_units = NULL,
  col_names = NULL,
  label_table = NULL,
  subcortVol_fname,
  subcortLabs_fname,
  ROIsubcortVol_fname = NULL,
  fill = 0
)
```

### Arguments

|   |   |
|---|---|
| <code>subcortVol</code>   | A vectorized data matrix: V voxels by T measurements  |
| <code>subcortLabs</code>  | Numeric (0 and 3-21) or factor vector corresponding to subcortical structure labels. See <a href="#">substructure_table</a> .   |
| <code>subcortMask</code>  | Logical volumetric mask. Values of 0 represent out-of-mask voxels (not subcortical), and values of 1 represent in-mask voxels (subcortical),  |
| <code>trans_mat</code>  | The TransformationMatrixIJKtoXYZ, or equivalently the desired sform matrix ( <code>srow_x</code> , <code>srow_y</code> and <code>srow_z</code> ) to write. If NULL, do not write it (all zeroes). |
| <code>trans_units</code>  | The units of <code>trans_mat</code> . Currently not used.   |
| <code>col_names</code>  | (Optional) Column names.  |
| <code>label_table</code>  | (Optional) data.frame of labels and their colors.   |
| <code>subcortVol_fname</code> , <code>subcortLabs_fname</code> , <code>ROIsubcortVol_fname</code> | File path to a NIFTI to save the corresponding data. <code>ROIsubcortVol_fname</code> is optional but the rest is required.   |
| <code>fill</code>   | Values to use for out-of-mask voxels. Default: 0.   |

**Details**

All file path arguments are required except ROIsubcortVol\_fname. If not provided, the volumetric mask will not be written. (It's redundant with the 0 values in subcortLabs\_fname because valid labels have positive indexes.)

Note that for label data (i.e. if label\_table is provided) only one label table can be saved.

**Value**

Named character vector with the "subcortVol", "subcortLabs", and "ROIsubcortVol" file names (if written)

**Connectome Workbench**

This function interfaces with the "-volume-label-import" Workbench Command.

**See Also**

Other functions for writing CIFTI or GIFTI data: [separate\\_cifti\(\)](#), [write\\_cifti\(\)](#), [write\\_metric\\_gifti\(\)](#), [write\\_surf\\_gifti\(\)](#)

---

|                  |   |
|------------------|---|
| write_surf_gifti | <i>Write a "surf" to a GIFTI surface file</i> |
|------------------|---|

---

**Description**

Write the data for the left or right surface to a surface GIFTI file.

**Usage**

```
write_surf_gifti(
  x,
  gifti_fname,
  hemisphere = c("left", "right"),
  encoding = NULL,
  endian = c("LittleEndian", "BigEndian")
)

write_surf(
  x,
  gifti_fname,
  hemisphere = c("left", "right"),
  encoding = NULL,
  endian = c("LittleEndian", "BigEndian")
)
```

**Arguments**

|             |  |
|-------------|--|
| x           | A "surf" object, an object from <code>gifti::readgii</code> , or a list with elements "pointset" and "triangle".   |
| gifti_fname | Where to write the GIFTI file.   |
| hemisphere  | "left" (default) or "right". Ignored if data is already a "gifti" object, or if it is a "surf" object with the hemisphere metadata already specified.  |
| encoding    | A length-2 vector with elements chosen among "ASCII", "Base64Binary", and "GZipBase64Binary". If NULL (default), will use the metadata if data is a "gifti" object, or "GZipBase64Binary" for the "pointset" and "ASCII" for the "triangles" if data is not already a GIFTI. |
| endian      | "LittleEndian" (default) or "BigEndian".   |

**Value**

Whether the GIFTI was successfully written

**See Also**

Other functions for writing CIFTI or GIFTI data: [separate\\_cifti\(\)](#), [write\\_cifti\(\)](#), [write\\_metric\\_gifti\(\)](#), [write\\_subcort\\_nifti\(\)](#)

Other functions for working with GIFTI surface geometry data: [is\\_surf\(\)](#), [read\\_surf\(\)](#), [resample\\_surf\(\)](#), [rotate\\_surf\(\)](#), [view\\_surf\(\)](#)

---

write\_xifti2

*Write a "xifti" object to GIFTI and NIFTI files*

---

**Description**

Write metric or label GIFTIs for the cortical surface data and NIFTIs for the subcortical labels and mask in a "xifti" object. Each present brainstructure will be written; if a brainstructure is absent the corresponding file is not written.

**Usage**

```
write_xifti2(
  xifti,
  brainstructures = NULL,
  cortexL_fname = NULL,
  cortexR_fname = NULL,
  subcortVol_fname = NULL,
  subcortLabs_fname = NULL,
  ROI_brainstructures = "all",
  ROICortexL_fname = NULL,
  ROICortexR_fname = NULL,
  ROIsubcortVol_fname = NULL,
```



```

    write_dir = NULL,
    verbose = FALSE
)

```

## Arguments

**xifti** A "xifti" object.

**brainstructures** Character vector indicating which brain structure(s) to obtain: "left" (left cortex), "right" (right cortex) and/or "subcortical" (subcortex and cerebellum). Can also be "all" (obtain all three brain structures). Default: c("left", "right") (cortex only).  
If a brain structure is indicated but does not exist in the CIFTI file, a warning will occur and that brain structure will be skipped.

**cortexL\_fname, cortexR\_fname** (Optional) GIFTI file names (\*.func/label.gii) to save the [left/right] cortex data to. If not provided, defaults to "\*[L/R].\[func/label\].gii", where \* is the file name component of cifti\_fname. Will be written in write\_dir.  
dtseries and dscalar files should use "func", whereas dlabel files should use "label".

**subcortVol\_fname, subcortLabs\_fname** (Optional) NIFTI file names to save the subcortical [volume/labels] to. If not provided, defaults to "\*[/.labels].nii", where \* is the file name component of cifti\_fname. Will be written in write\_dir.

**ROI\_brainstructures** Which ROIs should be obtained? "all" (default) to obtain ROIs for each of the brainstructures. NULL to not obtain any ROIs. This should be a subset of brainstructures.

**ROIcortexL\_fname, ROIcortexR\_fname** (Optional) GIFTI file names (\*.func/label.gii) to save the [left/right] cortex ROI to. If not provided, defaults to "\*ROI\_[L/R].\[func/label\].gii", where \* is the file name component of cifti\_fname. The cortical ROIs typically represent the medial wall mask, with values of 1 for in-ROI (non-medial wall) vertices and 0 for out-of-ROI (medial wall) vertices. Will be written in write\_dir.  
dtseries and dscalar files should use "func", whereas dlabel files should use "label".

**ROIsubcortVol\_fname** (Optional) NIFTI file names to save the subcortical ROI to. If not provided, defaults to "\*ROI.nii", where \* is the file name component of cifti\_fname. The subcortical ROI typically represents the volumetric mask for the entire subcortical structure, with values of 1 for in-ROI (in subcortex) voxels and 0 for out-of-ROI (not in subcortex) voxels. Will be written in write\_dir.

**write\_dir** Where should the separated files be placed? NULL (default) will write them to the current working directory.  
write\_dir must already exist, or an error will occur.

**verbose** Should occasional updates be printed? Default: FALSE.

**Value**

List of written files

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