

# Package ‘cifti’

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**Type** Package

**Title** Toolbox for Connectivity Informatics Technology Initiative  
(‘CIFTI’) Files

**Version** 0.4.5

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**Description** Functions for the input/output and visualization of  
medical imaging data in the form of ‘CIFTI’ files  
<<https://www.nitrc.org/projects/cifti/>>.

**License** GPL-2

**Imports** xml2, oro.nifti, gifti, utils, R.utils

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1.9000

**Suggests** covr, knitr, rmarkdown, rgl, matrixStats

**VignetteBuilder** knitr

**NeedsCompilation** no

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cifti\_brain\_structs     *Extract Brain Structures from CIFTI Brain Models*

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### Description

Extracts the BrainStructure attribute from a BrainModel in a cifti object

### Usage

```
cifti_brain_structs(file)
```

### Arguments

file                    cifti object

### Value

A vector of brain structure names

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cifti\_coords\_gifti     *Map CIFTI values to Coordinates using GIFTI*

---

### Description

Maps the data portion of CIFTI data set from a Brain Model to the xyz coordinate triangles

### Usage

```
cifti_coords_gifti(file, gii_file, structure, add_one = TRUE)
```

### Arguments

file                    filename of CIFTI file or cifti object  
gii\_file                filename of corresponding GIFTI file or gifti object  
structure               Structure to map, must be one of the brain models in the CIFTI  
add\_one                 should 1 be added to indices (1-based vs. 0-based)

**Value**

List of coordinates and values

---

cifti_data	<i>Extract CIFTI data from file</i>
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**Description**

Extracts the data after the CIFTI XML information

**Usage**

```
cifti_data(fname, nim = NULL)
```

**Arguments**

fname	Filename of CIFTI
nim	NIfTI-2 header, if already parsed. If NULL, <a href="#">nifti_2_hdr</a> will be run on the CIFTI.

**Value**

Array of values

---

cifti_read_char	<i>Read characters with embedded nulls</i>
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**Description**

Simple wrapper for reading in character values with embedded nulls in a binary file

**Usage**

```
cifti_read_char(fid, n, to = "UTF-8")
```

**Arguments**

fid	identifier of the open file connection
n	number of elements to read
to	A character string describing the target encoding.

**Value**

Character vector

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cifti_xml_txt	<i>Extract CIFTI XML</i>
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**Description**

Extracts CIFTI XML from the CIFTI file

**Usage**

```
cifti_xml_txt(fname, nim = NULL)
```

```
cifti_xml(...)
```

**Arguments**

fname	filename of CIFTI
nim	NIfTI-2 header, if already parsed. If NULL, <a href="#">nifti_2_hdr</a> will be run on the CIFTI.
...	arguments to pass to <code>cifti_xml</code>

**Value**

Character string of XML information

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download_cifti_data	<i>Download CIFTI Test Data</i>
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**Description**

Downloads CIFTI test data from [https://www.nitrc.org/frs/download.php/8541/cifti-2\\_test\\_data-1.2.zip](https://www.nitrc.org/frs/download.php/8541/cifti-2_test_data-1.2.zip)

**Usage**

```
download_cifti_data(outdir = system.file(package = "cifti"),
  overwrite = FALSE, ...)
```

**Arguments**

outdir	Output directory for test file directory
overwrite	Should files be overwritten if already exist?
...	additional arguments to <a href="#">download.file</a>

**Value**

Vector of file names

---

get_cifti_type	<i>Get Generic CIFTI Type</i>
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---

**Description**

Wrapper for multiple types of CIFTI XML types.

**Usage**

```
get_cifti_type(fname, type = c("Volume", "Surface", "Parcel", "NamedMap",  
"BrainModel"))
```

```
cifti_as_list(fname, type = c("Volume", "Surface", "Parcel", "NamedMap",  
"BrainModel"))
```

**Arguments**

fname	File name of CIFTI file
type	type of data to extract from CIFTI XML

**Value**

List of output from each type

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have_cifti_test_data	<i>Check Presence of CIFTI Test Data</i>
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**Description**

Checks if CIFTI test data is downloaded

**Usage**

```
have_cifti_test_data(outdir = system.file(package = "cifti"))
```

**Arguments**

outdir	Output directory for test file directory
--------	--

**Value**

Logical indicator

---

`is.cifti`*Test if CIFTI*

---

**Description**

Simple wrapper to determine if class is CIFTI

**Usage**

```
is.cifti(x)
```

**Arguments**

x                    object to test

**Value**

Logical if x is CIFTI

---

`is_cifti_numeric`*Test of numeric CIFTI field*

---

**Description**

Wrapper of CIFTI fields for easy logical test

**Usage**

```
is_cifti_numeric(x)
```

**Arguments**

x                    character vector of names

**Value**

Logical of length same as x

---

matrix\_ind\_map\_nodes    *Extract MatrixIndicesMap nodes from CIFTI*

---

**Description**

Extracts the nodes from a CIFTI-2 file corresponding to the MatrixIndicesMap branch

**Usage**

```
matrix_ind_map_nodes(fname)
```

**Arguments**

fname            File of CIFTI data

**Value**

Nodes of class xml\_nodeset

---

nifti\_2\_hdr            *Read Nifti-2 Header*

---

**Description**

Reads a Nifti-2 header from a filename

**Usage**

```
nifti_2_hdr(fname, verbose = FALSE, warn = -1)
```

**Arguments**

fname            Filename  
 verbose        Print diagnostic messages  
 warn            Should warnings be printed? Passed to [options](#)

**Value**

Object of class nifti

**Note**

The unused\_str part of the header is not returned, but is an empty string of 15 characters. This code was adapted by the oro.nifti package

---

parse\_brain\_model      *Parse BrainModel from CIFTI*

---

**Description**

Extracts information about BrainModels from CIFTI file

**Usage**

```
parse_brain_model(nodeset)
```

```
get_brain_model(fname)
```

**Arguments**

nodeset      Set of XML nodes corresponding to BrainModel

fname      filename of CIFTI file

**Value**

List of values

**Examples**

```
## Not run:  
doc = cifti_xml(fname)  
nodes = xml_find_all(doc, "/CIFTI/Matrix/MatrixIndicesMap")  
nodeset = xml_find_all(nodes, "./BrainModel")  
  
## End(Not run)
```

---

parse\_named\_map      *Parse Named Map from CIFTI*

---

**Description**

Extracts information about Named Maps from CIFTI file

**Usage**

```
parse_named_map(nodeset)
```

```
get_named_map(fname)
```



**Arguments**

nodeset           Set of XML nodes corresponding to NamedMap  
fname             filename of CIFTI file

**Value**

List of values

**Examples**

```
## Not run:  
doc = cifti_xml(fname)  
nodes = xml_find_all(doc, "/CIFTI/Matrix/MatrixIndicesMap")  
nodeset = xml_find_all(nodes, "./NamedMap")  
parse_named_map(nodeset)  
  
## End(Not run)
```

---

parse\_parcel

*Parse Parcel from CIFTI*

---

**Description**

Extracts information about Parcels from CIFTI file

**Usage**

```
parse_parcel(nodeset)  
  
get_parcel(fname)
```

**Arguments**

nodeset           Set of XML nodes corresponding to Parcel  
fname             filename of CIFTI file

**Value**

List of values

---

parse_surface	<i>Parse Surface from CIFTI</i>
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---

**Description**

Extracts information about Surfaces from CIFTI file

**Usage**

```
parse_surface(nodeset)
```

```
get_surface(fname)
```

**Arguments**

nodeset	Set of XML nodes corresponding to Surface
---------	---

fname	filename of CIFTI file
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**Value**

List of values

**Examples**

```
## Not run:  
doc = cifti_xml(fname)  
nodes = xml_find_all(doc, "/CIFTI/Matrix/MatrixIndicesMap")  
nodeset = xml_find_all(nodes, "./Surface")  
parse_volume(nodeset)  
  
## End(Not run)
```

---

parse_volume	<i>Parse Volume from CIFTI</i>
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**Description**

Extracts information about Volumes from CIFTI file

**Usage**

```
parse_volume(nodeset)
```

```
get_volume(fname)
```

**Arguments**

nodeset            Set of XML nodes corresponding to Volume  
 fname             filename of CIFTI file

**Value**

List of values

**Examples**

```
## Not run:
doc = cifti_xml(fname)
nodes = xml_find_all(doc, "/CIFTI/Matrix/MatrixIndicesMap")
nodeset = xml_find_all(nodes, "./Volume")
parse_volume(nodeset)

## End(Not run)
```

---

 read\_cifti

*Read CIFTI File*


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**Description**

Reads CIFTI Files

**Usage**

```
read_cifti(fname, drop_data = TRUE, trans_data = TRUE)
readCIFTI(fname, drop_data = TRUE, trans_data = TRUE)
readcii(fname, drop_data = TRUE, trans_data = TRUE)
```

**Arguments**

fname             file name of CIFTI file  
 drop\_data        Should the empty data dimensions be dropped?  
 trans\_data       Should the data be transposed

**Value**

List of information from the CIFTI file

**Examples**

```
outdir = tempdir()
if (have_cifti_test_data(outdir = outdir)) {
  files = download_cifti_data(outdir = outdir)
  fname = grep("MyelinAndCorrThickness.32k_fs_LR.dscalar",
  files, value = TRUE)
  res = read_cifti(fname)
}
```

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