

# Package ‘ieegio’

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**Title** File IO for Intracranial Electroencephalography

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**Description** Integrated toolbox supporting common file formats used for intracranial Electroencephalography (iEEG) and deep-brain stimulation (DBS) study.

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**VignetteBuilder** knitr

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ieegio_sample_data	<i>Download sample files</i>
--------------------	------------------------------

---

## Description

Download sample files

## Usage

```
ieegio_sample_data(file, test = FALSE, cache_ok = TRUE)
```

## Arguments

file	file to download; set to NULL to view all possible files
test	test whether the sample file exists instead of downloading them; default is FALSE
cache_ok	whether to use cache

## Value

When test is false, returns downloaded file path (character); when test is true, returns whether the expected sample exists (logical).

## Examples

```
# list available files
ieegio_sample_data()

# check if file edfPlusD.edf exists
ieegio_sample_data("edfPlusD.edf", test = TRUE)

## Not run:

ieegio_sample_data("edfPlusD.edf")
```

```
## End(Not run)
```

---

imaging-surface      *Read and write surface files*

---

## Description

Supports surface geometry, annotation, measurement, and time-series data. Please use the high-level function `read_surface`, which calls other low-level functions internally.

## Usage

```
read_surface(file, format = "auto", type = NULL, ...)  
  
write_surface(  
  x,  
  con,  
  format = c("gifti", "freesurfer"),  
  type = c("geometry", "annotations", "measurements", "color", "time_series"),  
  ...  
)  
  
io_read_fs(  
  file,  
  type = c("geometry", "annotations", "measurements"),  
  format = "auto",  
  name = basename(file),  
  ...  
)  
  
io_read_gii(file)  
  
io_write_gii(x, con, ...)
```

## Arguments

<code>file, con</code>	path the file
<code>format</code>	format of the file, see 'Arguments' section in <a href="#">read.fs.surface</a> (when file type is 'geometry') and <a href="#">read.fs.curv</a> (when file type is 'measurements')
<code>type</code>	type of the data; ignored if the file format is 'GIFTI'. For 'FreeSurfer' files, supported types are 'geometry' contains positions of mesh vertex nodes and face indices;

'annotations' annotation file (usually with file extension 'annot') containing a color look-up table and an array of color keys. These files are used to display discrete values on the surface such as brain atlas;

'measurements' measurement file such as 'sulc' and 'curv' files, containing numerical values (often with continuous domain) for each vertex node

... for read\_surface, the arguments will be passed to io\_read\_fs if the file is a 'FreeSurfer' file.

x surface (geometry, annotation, measurement) data

name name of the data; default is the file name

### Value

A surface object container

### Examples

```
library(ieegio)

# geometry
geom_file <- "gifti/GzipBase64/sujet01_Lwhite.surf.gii"

# measurements
shape_file <- "gifti/GzipBase64/sujet01_Lwhite.shape.gii"

# time series
ts_file <- "gifti/GzipBase64/fmri_sujet01_Lwhite_projection.time.gii"

if(ieegio_sample_data(geom_file, test = TRUE)) {

  geometry <- read_surface(ieegio_sample_data(geom_file))
  print(geometry)

  measurement <- read_surface(ieegio_sample_data(shape_file))
  print(measurement)

  time_series <- read_surface(ieegio_sample_data(ts_file))
  print(time_series)

  # merge measurement & time_series into geometry
  merged <- merge(geometry, measurement, time_series)
  print(merged)

  # make sure you install `rgl` package
  plot(merged, name = c("measurements", "Shape001"))

  plot(merged, name = "time_series",
       slice_index = c(1, 11, 21, 31))

}
```

---

imaging-volume	<i>Read and write volume data</i>
----------------	-----------------------------------

---

**Description**

Read and write volume data ('MRI', 'CT', etc.) in 'NIFTI' or 'MGH' formats. Please use `read_volume` and `write_volume` for high-level function. These functions will call other low-level functions internally.

**Usage**

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

write_volume(x, con, format = c("auto", "nifti", "mgh"), ...)

io_read_mgz(file, header_only = FALSE)

io_write_mgz(x, con, ...)

## S3 method for class 'ieegio_volume'
io_write_mgz(x, con, ...)

## S3 method for class 'ieegio_mgh'
io_write_mgz(x, con, ...)

## S3 method for class 'nifti'
io_write_mgz(x, con, ...)

## S3 method for class 'niftiImage'
io_write_mgz(x, con, ...)

## S3 method for class 'ants.core.ants_image.ANTsImage'
io_write_mgz(x, con, ...)

## S3 method for class 'array'
io_write_mgz(x, con, vox2ras = NULL, ...)

io_read_nii(
  file,
  method = c("oro", "rnifti", "ants"),
  header_only = FALSE,
  ...
)

io_write_nii(x, con, ...)
```

```
## S3 method for class 'array'
io_write_nii(x, con, vox2ras = NULL, ...)
```

### Arguments

file	file path to read volume data
header_only	whether to read header data only; default is FALSE
format	format of the file to be written; choices are 'auto', 'nifti' or 'mgh'; default is to 'auto' detect the format based on file names, which will save as a 'MGH' file when file extension is 'mgz' or 'mgh', otherwise 'NIFTI' format. We recommend explicitly setting this argument
...	passed to other methods
x	volume data (such as 'NIFTI' image, array, or 'MGH') to be saved
con	file path to store image
vox2ras	a 4x4 transform matrix from voxel indexing (column, row, slice) to scanner (often 'T1-weighted' image) 'RAS' (right-anterior-superior) coordinate
method	method to read the file; choices are 'oro' (using <a href="#">readNIFTI</a> ), 'rnifti' (using <a href="#">readNifti</a> ), and 'ants' (using <a href="#">as_ANTsImage</a> ).

### Format

format of the file; default is auto-detection, other choices are 'nifti' and 'mgh';

### Value

imaging readers return `ieegio_volume` objects.

### Examples

```
library(ieegio)

nifti_file <- "brain.demosubject.nii.gz"

# Use `ieegio_sample_data(nifti_file)`
# to download sample data

if( ieegio_sample_data(nifti_file, test = TRUE) ) {

# ---- NIFTI examples -----

file <- ieegio_sample_data(nifti_file)

# basic read
vol <- read_volume(file)

# voxel to scanner RAS
```

```

vol$transforms$vox2ras

# to freesurfer surface
vol$transforms$vox2ras_tkr

# to FSL
vol$transforms$vox2fsl

image(vol$data[, , 128], asp = 1, axes = FALSE)

# ---- using other methods -----
# default
vol <- read_volume(file, method = "oro", format = "nifti")
vol$header

# lazy-load nifti
vol2 <- read_volume(file, method = "rnifti", format = "nifti")
vol2$header

# Using ANTsPyx
vol3 <- read_volume(file, method = "ants", format = "nifti")
vol3$header

# ---- write -----

# write as NIfTI
f <- tempfile(fileext = ".nii.gz")

write_volume(vol, f, format = "nifti")

# alternative method
write_volume(vol$header, f, format = "nifti")

# write to mgz/mgh
f2 <- tempfile(fileext = ".mgz")

write_volume(vol, f, format = "mgh")

# clean up
unlink(f)
unlink(f2)

}

```

---

io\_h5\_valid

*Check whether a 'HDF5' file can be opened for read/write*


---

### Description

Check whether a 'HDF5' file can be opened for read/write

**Usage**

```
io_h5_valid(file, mode = c("r", "w"), close_all = FALSE)

io_h5_names(file)
```

**Arguments**

file	path to file
mode	'r' for read access and 'w' for write access
close_all	whether to close all connections or just close current connection; default is false. Set this to TRUE if you want to close all other connections to the file

**Value**

io\_h5\_valid returns a logical value indicating whether the file can be opened. io\_h5\_names returns a character vector of dataset names.

**Examples**

```
x <- array(1:27, c(3,3,3))
f <- tempfile()

# No data written to the file, hence invalid
io_h5_valid(f, 'r')

io_write_h5(x, f, 'dset')
io_h5_valid(f, 'w')

# Open the file and hold a connection
ptr <- hdf5r::H5File$new(filename = f, mode = 'w')

# Can read, but cannot write
io_h5_valid(f, 'r') # TRUE
io_h5_valid(f, 'w') # FALSE

# However, this can be reset via `close_all=TRUE`
io_h5_valid(f, 'r', close_all = TRUE)
io_h5_valid(f, 'w') # TRUE

# Now the connection is no longer valid
ptr

# clean up
unlink(f)
```



---

`io_read_h5`*Lazy Load 'HDF5' File via [hdf5r-package](#)*

---

**Description**

Wrapper for class [LazyH5](#), which load data with "lazy" mode - only read part of dataset when needed.

**Usage**

```
io_read_h5(file, name, read_only = TRUE, ram = FALSE, quiet = FALSE)
```

**Arguments**

<code>file</code>	'HDF5' file
<code>name</code>	group/data_name path to dataset (H5D data)
<code>read_only</code>	only used if ram=FALSE, whether the returned <a href="#">LazyH5</a> instance should be read only
<code>ram</code>	load data to memory immediately, default is false
<code>quiet</code>	whether to suppress messages

**Value**

If ram is true, then return data as arrays, otherwise return a [LazyH5](#) instance.

**See Also**

[io\\_write\\_h5](#)

**Examples**

```
file <- tempfile()
x <- array(1:120, dim = c(4,5,6))

# save x to file with name /group/dataset/1
io_write_h5(x, file, '/group/dataset/1', quiet = TRUE)

# read data
y <- io_read_h5(file, '/group/dataset/1', ram = TRUE)
class(y) # array

z <- io_read_h5(file, '/group/dataset/1', ram = FALSE)
class(z) # LazyH5

dim(z)

# clean up
unlink(file)
```

---

 io\_write\_h5

*Save objects to 'HDF5' file without trivial checks*


---

### Description

Save objects to 'HDF5' file without trivial checks

### Usage

```
io_write_h5(
  x,
  file,
  name,
  chunk = "auto",
  level = 4,
  replace = TRUE,
  new_file = FALSE,
  ctype = NULL,
  quiet = FALSE,
  ...
)
```

### Arguments

x	an array, a matrix, or a vector
file	path to 'HDF5' file
name	path/name of the data; for example, "group/data_name"
chunk	chunk size
level	compress level from 0 - no compression to 10 - max compression
replace	should data be replaced if exists
new_file	should removing the file if old one exists
ctype	data type such as "character", "integer", or "numeric". If set to NULL then automatically detect types. Note for complex data please store separately the real and imaginary parts.
quiet	whether to suppress messages, default is false
...	passed to other LazyH5\$save

### Value

Absolute path of the file saved

### See Also

[io\\_read\\_h5](#)

**Examples**

```
file <- tempfile()
x <- array(1:120, dim = 2:5)

# save x to file with name /group/dataset/1
io_write_h5(x, file, '/group/dataset/1', chunk = dim(x))

# load data
y <- io_read_h5(file, '/group/dataset/1')

# read data to memory
y[]

# clean up
unlink(file)
```

---

LazyH5

*Lazy 'HDF5' file loader*

---

**Description**

provides hybrid data structure for 'HDF5' file

**Public fields**

quiet whether to suppress messages

**Methods****Public methods:**

- [LazyH5\\$finalize\(\)](#)
- [LazyH5\\$print\(\)](#)
- [LazyH5\\$new\(\)](#)
- [LazyH5\\$save\(\)](#)
- [LazyH5\\$open\(\)](#)
- [LazyH5\\$close\(\)](#)
- [LazyH5\\$subset\(\)](#)
- [LazyH5\\$get\\_dims\(\)](#)
- [LazyH5\\$get\\_type\(\)](#)

**Method** `finalize()`: garbage collection method

*Usage:*

`LazyH5$finalize()`

*Returns:* none

**Method print():** overrides print method

*Usage:*

```
LazyH5#print()
```

*Returns:* self instance

**Method new():** constructor

*Usage:*

```
LazyH5$new(file_path, data_name, read_only = FALSE, quiet = FALSE)
```

*Arguments:*

`file_path` where data is stored in 'HDF5' format

`data_name` the data stored in the file

`read_only` whether to open the file in read-only mode. It's highly recommended to set this to be true, otherwise the file connection is exclusive.

`quiet` whether to suppress messages, default is false

*Returns:* self instance

**Method save():** save data to a 'HDF5' file

*Usage:*

```
LazyH5$save(
  x,
  chunk = "auto",
  level = 7,
  replace = TRUE,
  new_file = FALSE,
  force = TRUE,
  ctype = NULL,
  size = NULL,
  ...
)
```

*Arguments:*

`x` vector, matrix, or array

`chunk` chunk size, length should matches with data dimension

`level` compress level, from 1 to 9

`replace` if the data exists in the file, replace the file or not

`new_file` remove the whole file if exists before writing?

`force` if you open the file in read-only mode, then saving objects to the file will raise error. Use `force=TRUE` to force write data

`ctype` data type, see [mode](#), usually the data type of `x`. Try `mode(x)` or `storage.mode(x)` as hints.

`size` deprecated, for compatibility issues

`...` passed to self `open()` method

**Method open():** open connection

*Usage:*

```
LazyH5$open(new_dataset = FALSE, robj, ...)
```

*Arguments:*

`new_dataset` only used when the internal pointer is closed, or to write the data

`robj` data array to save

`...` passed to `createDataSet` in `hdf5r` package

**Method** `close()`: close connection

*Usage:*

```
LazyH5$close(all = TRUE)
```

*Arguments:*

`all` whether to close all connections associated to the data file. If true, then all connections, including access from other programs, will be closed

**Method** `subset()`: subset data

*Usage:*

```
LazyH5$subset(..., drop = FALSE, stream = FALSE, envir = parent.frame())
```

*Arguments:*

`drop` whether to apply `drop` the subset

`stream` whether to read partial data at a time

`envir` if `i, j, ...` are expressions, where should the expression be evaluated

`i, j, ...` index along each dimension

*Returns:* subset of data

**Method** `get_dims()`: get data dimension

*Usage:*

```
LazyH5$get_dims(stay_open = TRUE)
```

*Arguments:*

`stay_open` whether to leave the connection opened

*Returns:* dimension of the array

**Method** `get_type()`: get data type

*Usage:*

```
LazyH5$get_type(stay_open = TRUE)
```

*Arguments:*

`stay_open` whether to leave the connection opened

*Returns:* data type, currently only character, integer, raw, double, and complex are available, all other types will yield "unknown"

---

low-level-read-write *Low-level file read and write*

---

## Description

Interfaces to read from or write to files with common formats.

## Usage

```
io_read_fst(  
    con,  
    method = c("proxy", "data_table", "data_frame", "header_only"),  
    ...,  
    old_format = FALSE  
)
```

```
io_write_fst(x, con, compress = 50, ...)
```

```
io_read_ini(con, ...)
```

```
io_read_json(con, ...)
```

```
io_write_json(  
    x,  
    con = stdout(),  
    ...,  
    digits = ceiling(-log10(.Machine$double.eps)),  
    pretty = TRUE,  
    serialize = TRUE  
)
```

```
io_read_mat(  
    con,  
    method = c("auto", "R.matlab", "pymatreader", "mat73"),  
    verbose = TRUE,  
    on_convert_error = c("warning", "error", "ignore"),  
    ...  
)
```

```
io_write_mat(x, con, method = c("R.matlab", "scipy"), ...)
```

```
io_read_yaml(con, ...)
```

```
io_write_yaml(x, con, ..., sorted = FALSE)
```

## Arguments

con                    connection or file

```

method          method to read table. For 'fst', the choices are
                 'proxy' do not read data to memory, query the table when needed;
                 'data_table' read as data.table;
                 'data_frame' read as data.frame;
                 'header_only' read 'fst' table header.
                 For 'mat', the choices are
                 'auto' automatically try the native option, and then 'pymatreader' if fails;
                 'R.matlab' use the native method (provided by readMat); only support 'MAT
                    5.0' format;
                 'pymatreader' use 'Python' library 'pymatreader';
                 'mat73' use 'Python' library 'mat73'.
...             passed to internal function calls
old_format      see fst
x               data to write to disk
compress        compress level from 0 to 100; default is 50
digits, pretty  for writing numeric values to 'json' format
serialize       set to TRUE to serialize the data to 'json' format (with the data types, default); or
                 FALSE to save the values without types
verbose         whether to print out the process
on_convert_error
                 for reading 'mat' files with 'Python' modules, the results will be converted
                 to R objects in the end. Not all objects can be converted. This input defines
                 the behavior when the conversion fails; choices are "error", "warning", or
                 "ignore"
sorted          whether to sort the list; default is FALSE

```

## Value

The reader functions returns the data extracted from files, mostly as R objects, with few exceptions on some 'Matlab' files. When reading a 'Matlab' file requires using 'Python' modules, `io_read_mat` will try its best effort to convert 'Python' objects to R. However, such conversion might fail. In this case, the result might partially contain 'Python' objects with warnings.

## Examples

```

# ---- fst -----

f <- tempfile(fileext = ".fst")
x <- data.frame(
  a = 1:10,
  b = rnorm(10),
  c = letters[1:10]
)

```

```
io_write_fst(x, con = f)

# default reads in proxy
io_read_fst(f)

# load as data.table
io_read_fst(f, "data_table")

# load as data.frame
io_read_fst(f, "data_frame")

# get header
io_read_fst(f, "header_only")

# clean up
unlink(f)

# ---- json -----
f <- tempfile(fileext = ".json")

x <- list(a = 1L, b = 2.3, c = "a", d = 1+1i)

# default is serialize
io_write_json(x, f)

io_read_json(f)

cat(readLines(f), sep = "\n")

# just values
io_write_json(x, f, serialize = FALSE, pretty = FALSE)

io_read_json(f)

cat(readLines(f), sep = "\n")

# clean up
unlink(f)

# ---- Matlab .mat -----

## Not run:

f <- tempfile(fileext = ".mat")

x <- list(a = 1L, b = 2.3, c = "a", d = 1+1i)

# save as MAT 5.0
io_write_mat(x, f)
```



```
io_read_mat(f)

# require setting up Python environment

io_read_mat(f, method = "pymatreader")

# MAT 7.3 example
sample_data <- ieegio_sample_data("mat_v73.mat")
io_read_mat(sample_data)

# clean up
unlink(f)

## End(Not run)

# ---- yaml -----
f <- tempfile(fileext = ".yaml")

x <- list(a = 1L, b = 2.3, c = "a")
io_write_yaml(x, f)

io_read_yaml(f)

# clean up
unlink(f)
```

---

NWBHDF5IO

*Creates a NWBHDF5IO file container*

---

## Description

Class definition for 'PyNWB' container; use [read\\_nwb](#) for construction function.

## Active bindings

opened Whether the container is opened.

## Methods

### Public methods:

- [NWBHDF5IO\\$new\(\)](#)
- [NWBHDF5IO\\$get\\_handler\(\)](#)
- [NWBHDF5IO\\$open\(\)](#)

- `NWBHDF5IO$close()`
- `NWBHDF5IO$close_linked_files()`
- `NWBHDF5IO$read()`
- `NWBHDF5IO$with()`
- `NWBHDF5IO$clone()`

**Method** `new()`: Initialize the class

*Usage:*

```
NWBHDF5IO$new(path = NULL, mode = c("r", "w", "r+", "a", "w-", "x"), ...)
```

*Arguments:*

`path` Path to a '.nwb' file

`mode` Mode for opening the file

... Other parameters passed to `nwb$NWBHDF5IO`

**Method** `get_handler()`: Get internal file handler. Please make sure you close the handler correctly.

*Usage:*

```
NWBHDF5IO$get_handler()
```

*Returns:* File handler, i.e. 'PyNWB' NWBHDF5IO instance.

**Method** `open()`: Open the connections, must be used together with `$close` method. For high-level method, see `$with`

*Usage:*

```
NWBHDF5IO$open()
```

*Returns:* container itself

*Examples:*

```
\dontrun{
```

```
# low-level method to open NWB file, for safer methods, see
```

```
# `container$with()` below
```

```
container$open()
```

```
data <- container$read()
```

```
# process data...
```

```
# Make sure the container is closed!
```

```
container$close()
```

```
}
```

**Method** `close()`: Close the connections (low-level method, see 'with' method below)

*Usage:*

```
NWBHDF5IO$close(close_links = TRUE)
```

*Arguments:*

`close_links` Whether to close all files linked to from this file; default is true

*Returns:* Nothing

**Method** `close_linked_files()`: Close all opened, linked-to files. 'MacOS' and 'Linux' automatically release the linked-to file after the linking file is closed, but 'Windows' does not, which prevents the linked-to file from being deleted or truncated. Use this method to close all opened, linked-to files.

*Usage:*

```
NWBHDF5IO$close_linked_files()
```

*Returns:* Nothing

**Method** `read()`: Read the 'NWB' file from the 'IO' source. Please use along with '\$with' method

*Usage:*

```
NWBHDF5IO$read()
```

*Returns:* 'NWBFile' container

**Method** `with()`: Safe wrapper for reading and handling 'NWB' file. See class examples.

*Usage:*

```
NWBHDF5IO$with(expr, quoted = FALSE, envir = parent.frame())
```

*Arguments:*

`expr` R expression to evaluate

`quoted` Whether `expr` is quoted; default is false

`envir` environment for `expr` to evaluate; default is the parent frame (see `parent.frame()`)

*Returns:* Whatever results generated by `expr`

*Examples:*

```
\dontrun{

container$with({
  data <- container$read()
  # process data
})

}
```

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
NWBHDF5IO$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

**Examples**

```

## Not run:

# Running this example requires a .nwb file

library(rnwb)
container <- NWBHDF5IO$new(path = file)
container$with({

  data <- container$read()
  electrode_table <- data$electrodes[convert = TRUE]

})

print(electrode_table)

## End(Not run)

## -----
## Method `NWBHDF5IO$open`
## -----

## Not run:

# low-level method to open NWB file, for safer methods, see
# `container$with()` below

container$open()

data <- container$read()

# process data...

# Make sure the container is closed!
container$close()

## End(Not run)

## -----
## Method `NWBHDF5IO$with`
## -----

## Not run:

container$with({
  data <- container$read()
  # process data
})

```

```
## End(Not run)
```

---

```
plot.ieegio_surface Plot '3D' surface objects
```

---

## Description

Plot '3D' surface objects

## Usage

```
## S3 method for class 'ieegio_surface'
plot(
  x,
  method = c("basic", "full"),
  transform = 1L,
  name = "auto",
  vlim = NULL,
  col = c("black", "white"),
  slice_index = NULL,
  ...
)
```

## Arguments

x	'ieegio_surface' object, see <a href="#">read_surface</a>
method	plot method; 'basic' for just rendering the surfaces; 'full' for rendering with axes and title
transform	which transform to use, can be a 4-by-4 matrix; if the surface contains transform matrix, then this argument can be an integer index of the transform embedded, or the target (transformed) space name; print names(x\$transforms) for choices
name	attribute and name used for colors, options can be 'color' if the surface has color matrix; c('annotations', varname) for rendering colors from annotations with variable varname; c('measurements', varname) for rendering colors from measurements with variable varname; 'time_series' for plotting time series slices; or "flat" for flat color; default is 'auto', which will plot the first available data. More details see 'Examples'.
vlim	when plotting with continuous data (name is measurements or time-series), the value limit used to generate color palette; default is NULL: the range of the values. This argument can be length of 1 (creating symmetric value range) or 2. If set, then values exceeding the range will be trimmed to the limit
col	color or colors to form the color palette when value data is continuous; when name="flat", the last color will be used
slice_index	when plotting the name="time_series" data, the slice indices to plot; default is to select a maximum of 4 slices
...	ignored

**Examples**

```

library(ieegio)

# geometry
geom_file <- "gifti/GzipBase64/sujet01_Lwhite.surf.gii"

# measurements
shape_file <- "gifti/GzipBase64/sujet01_Lwhite.shape.gii"

# time series
ts_file <- "gifti/GzipBase64/fmri_sujet01_Lwhite_projection.time.gii"

if(ieegio_sample_data(geom_file, test = TRUE)) {

  geometry <- read_surface(ieegio_sample_data(geom_file))
  measurement <- read_surface(ieegio_sample_data(shape_file))
  time_series <- read_surface(ieegio_sample_data(ts_file))
  ts_demean <- apply(
    time_series$time_series$value,
    MARGIN = 1L,
    FUN = function(x) {
      x - mean(x)
    }
  )
  time_series$time_series$value <- t(ts_demean)

  # merge measurement & time_series into geometry (optional)
  merged <- merge(geometry, measurement, time_series)
  print(merged)

  # ---- plot method/style -----
  plot(merged, "basic")
  plot(merged, "full")

  # ---- plot data -----

  ## Measurements or annotations

  # the first column of `measurements`
  plot(merged, name = "measurements")

  # equivalent to
  plot(merged, name = list("measurements", 1L))

  # equivalent to
  measurement_names <- names(merged$measurements$data_table)
  plot(merged, name = list("measurements", measurement_names[[1]]))

  ## Time-series

```

```

# automatically select 4 slices, trim the color palette
# from -25 to 25
plot(merged, name = "time_series", vlim = c(-25, 25))

plot(
  merged,
  name = "time_series",
  vlim = c(-25, 25),
  slice_index = c(1, 17, 33, 49, 64, 80, 96, 112, 128),
  col = c("#053061", "#2166ac", "#4393c3",
          "#92c5de", "#d1e5f0", "#ffffff",
          "#fddbc7", "#f4a582", "#d6604d",
          "#b2182b", "#67001f")
)
}

```

---

plot.ieegio\_volume      *Plot '3D' volume in anatomical slices*

---

### Description

Plot '3D' volume in anatomical slices

### Usage

```

## S3 method for class 'ieegio_volume'
plot(
  x,
  position = c(0, 0, 0),
  center_position = FALSE,
  which = c("coronal", "axial", "sagittal"),
  slice_index = 1L,
  transform = "vox2ras",
  zoom = 1,
  pixel_width = max(zoom/2, 1),
  crosshair_gap = 4,
  crosshair_lty = 2,
  col = c("black", "white"),
  crosshair_col = "#00FF00A0",
  continuous = TRUE,
  vlim = NULL,
  add = FALSE,
  main = "",

```

```

axes = FALSE,
background = col[[1]],
foreground = col[[length(col)]],
...,
.xdata = x$data
)

```

### Arguments

x	'ieegio_volume' object; see <a href="#">read_volume</a>
position	cross-hair focused position
center_position	whether to center canvas at position, default is FALSE
which	which slice to plot; choices are "coronal", "axial", and "sagittal"
slice_index	length of 1: if x has fourth dimension (e.g. 'fMRI'), then which slice index to draw
transform	which transform to apply, can be a 4-by-4 matrix, an integer or name indicating the matrix in x\$transforms; this needs to be the transform matrix from voxel index to 'RAS' (right-anterior-superior coordinate system), often called 'xform', 'sform', 'qform' in 'NIfTI' terms, or 'Norig' in 'FreeSurfer'
zoom	zoom-in level
pixel_width	pixel size, ranging from 0.05 to 50; default is the half of zoom or 1, whichever is greater; the unit of pixel_width divided by zoom is milliliter
crosshair_gap	the cross-hair gap in milliliter
crosshair_lty	the cross-hair line type
col	color palette for continuous x values
crosshair_col	the cross-hair color; set to NA to hide
continuous	reserved
vlim	the range limit of the data; default is computed from range of x\$data; data values exceeding the range will be trimmed
add	whether to add the plot to existing underlay; default is FALSE
main, ...	passed to <a href="#">image</a>
axes	whether to draw axes; default is FALSE
background, foreground	background and foreground colors; default is the first and last elements of col
.xdata	default is x\$data, used to speed up the calculation when multiple different angles are to be plotted

### Examples

```

library(ieegio)

nifti_file <- "brain.demosubject.nii.gz"

```



```

# Use `ieegio_sample_data(nifti_file)`
#   to download sample data

if( ieegio_sample_data(nifti_file, test = TRUE) ) {

# ---- NIfTI examples -----

file <- ieegio_sample_data(nifti_file)

# basic read
vol <- read_volume(file)

par(mfrow = c(1, 3), mar = c(0, 0, 3.1, 0))

ras_position <- c(-50, -10, 15)

ras_str <- paste(sprintf("%.0f", ras_position), collapse = ",")

for(which in c("coronal", "axial", "sagittal")) {
  plot(x = vol, position = ras_position, crosshair_gap = 10,
       crosshair_lty = 2, zoom = 3, which = which,
       main = sprintf("%s T1RAS=[%s]", which, ras_str))
}

}

```

---

pynwb\_module

*Install 'NWB' via 'pynwb'*


---

### Description

Install 'NWB' via 'pynwb'

### Usage

```
install_pynwb(python_ver = "auto", verbose = TRUE)
```

```
pynwb_module(force = FALSE, error_if_missing = TRUE)
```

### Arguments

python_ver	'Python' version, see <a href="#">configure_conda</a> ; default is "auto", which is suggested
verbose	whether to print the installation messages
force	whether to force-reload the module
error_if_missing	whether to raise errors when the module fails to load; default is true

**Value**

A 'Python' module pynwb.

---

read_bci2000	<i>Read 'BCI2000' data file</i>
--------------	---------------------------------

---

**Description**

Read 'BCI2000' data file

**Usage**

```
read_bci2000(
  file,
  extract_path = getOption("ieegio.extract_path", NULL),
  header_only = FALSE,
  cache_ok = TRUE,
  verbose = TRUE
)
```

**Arguments**

file	file path to the data file
extract_path	location to where the extracted information is to be stored
header_only	whether to only load header data
cache_ok	whether existing cache should be reused; default is TRUE. This input can speed up reading large data files; set to FALSE to delete cache before importing.
verbose	whether to print processing messages; default is TRUE

**Value**

A cached object that is readily to be loaded to memory; see [SignalDataCache](#) for class definition.

**Examples**

```
if( ieegio_sample_data("bci2k.dat", test = TRUE) ) {
  file <- ieegio_sample_data("bci2k.dat")

  x <- read_bci2000(file)
  print(x)

  channel <- x$get_channel(1)

  plot(
    channel$time,
    channel$value,
```

```

    type = "l",
    main = channel$info$Label,
    xlab = "Time",
    ylab = channel$info$Unit
  )
}

```

---

read_brainvis	<i>Read 'BrainVision' data</i>
---------------	--------------------------------

---

## Description

Read 'BrainVision' data

## Usage

```

read_brainvis(
  file,
  extract_path = getOption("ieegio.extract_path", NULL),
  header_only = FALSE,
  cache_ok = TRUE,
  verbose = TRUE
)

```

## Arguments

file	file path to the data file
extract_path	location to where the extracted information is to be stored
header_only	whether to only load header data
cache_ok	whether existing cache should be reused; default is TRUE. This input can speed up reading large data files; set to FALSE to delete cache before importing.
verbose	whether to print processing messages; default is TRUE

## Value

A cached object that is readily to be loaded to memory; see [SignalDataCache](#) for class definition.

## Examples

```

if( ieegio_sample_data("brainvis.dat", test = TRUE) ) {
  # ensure the header and marker files are downloaded as well
  ieegio_sample_data("brainvis.vhdr")
  ieegio_sample_data("brainvis.dat")
  file <- ieegio_sample_data("brainvis.vmrk")

  x <- read_brainvis(file)
}

```

```
print(x)

x$get_header()

x$get_channel_table()

x$get_annotations()

channel <- x$get_channel(10)

plot(
  channel$time,
  channel$value,
  type = "l",
  main = channel$info$Label,
  xlab = "Time",
  ylab = channel$info$Unit
)
}
```

---

read\_edf

*Read 'EDF' or 'BDF' data file*

---

## Description

Read 'EDF' or 'BDF' data file

## Usage

```
read_edf(
  con,
  extract_path = getOption("ieegio.extract_path", NULL),
  header_only = FALSE,
  cache_ok = TRUE,
  begin = 0,
  end = Inf,
  convert = TRUE,
  verbose = TRUE
)
```

## Arguments

con	file or connection to the data file
extract_path	location to where the extracted information is to be stored
header_only	whether to only load header data
cache_ok	whether existing cache should be reused; default is TRUE. This input can speed up reading large data files; set to FALSE to delete cache before importing.

begin, end	begin and end of the data to read
convert	whether to convert digital numbers to analog signals; default is TRUE
verbose	whether to print processing messages; default is TRUE

**Value**

A cached object that is readily to be loaded to memory; see [SignalDataCache](#) for class definition.

**Examples**

```
# ---- EDF/BDF(+) -----
# Run `ieegio_sample_data("edfPlusD.edf")` to download sample data
# Tun example if the sample data exists
if(ieegio_sample_data("edfPlusD.edf", test = TRUE)) {
  edf_path <- ieegio_sample_data("edfPlusD.edf")
  data <- read_edf(edf_path)
  data$get_header()
  data$get_annotations()
  data$get_channel_table()
  channel <- data$get_channel(1)
  plot(
    channel$time,
    channel$value,
    type = "l",
    main = channel$info$Label,
    xlab = "Time",
    ylab = channel$info$Unit
  )
}
```

---

read\_nsx

*Read ('BlackRock') 'NEV' 'NSx' data*


---

**Description**

Read ('BlackRock') 'NEV' 'NSx' data

**Usage**

```

read_nsx(
    file,
    extract_path = getOption("ieegio.extract_path", NULL),
    header_only = FALSE,
    cache_ok = TRUE,
    include_waveform = FALSE,
    verbose = TRUE
)

```

**Arguments**

file	file path to the data file
extract_path	location to where the extracted information is to be stored
header_only	whether to only load header data
cache_ok	whether existing cache should be reused; default is TRUE. This input can speed up reading large data files; set to FALSE to delete cache before importing.
include_waveform	whether to include 'waveform' data (usually for online spike sorting); default is FALSE
verbose	whether to print processing messages; default is TRUE

**Value**

A cached object that is readily to be loaded to memory; see [SignalDataCache](#) for class definition.

---

read_nwb	<i>Read 'NWB' format</i>
----------	--------------------------

---

**Description**

Life cycle: experimental. Read "Neurodata Without Borders" ('NWB' format) file. Unlike other readers read\_nwb returns low-level 'Python' class handler via pynwb module.

**Usage**

```
read_nwb(file, mode = c("r", "w", "r+", "a", "w-", "x"), ...)
```

**Arguments**

file	path to 'NWB' file
mode	file open mode; default is 'r' (read-only)
...	passed to <a href="#">NWBHDF5IO</a> initialize function

**Value**

A `NWBHDF5IO` instance

**Examples**

```
if(ieegio_sample_data("nwb_sample.nwb", test = TRUE)) {
  file <- ieegio_sample_data("nwb_sample.nwb")

  # Create NWBIO container
  container <- read_nwb(file)

  # Open connection
  container$open()

  # read meta data
  data <- container$read()
  data

  # get `test_timeseries` data
  ts_data <- data$get_acquisition("test_timeseries")
  ts_data

  # read timeseries data into memory
  ts_arr <- ts_data$data[]
  ts_arr

  # Convert Python array to R
  # using `rpymat::py_to_r(ts_arr)` or
  as.numeric(ts_arr)

  # Make sure you close the connection
  container$close()
}

# Requires setting up Python environment
# run `ieegio::install_pynwb()` to set up environment first

## Not run:

# Replicating tutorial
# https://pynwb.readthedocs.io/en/stable/tutorials/general/plot\_file.html

library(rpymat)

# Load Python module
pynwb <- import("pynwb")
uuid <- import("uuid")
datetime <- import("datetime")
```

```

np <- import("numpy")
tz <- import("dateutil.tz")

# 2018L is 2018 as integer
session_start_time <- datetime.datetime(
    2018L, 4L, 25L, 2L, 30L, 3L,
    tzinfo=tz.gettz("US/Pacific"))

# ---- Create NWB file object -----
nwbfile <- pynwb.NWBFile(
    session_description="Mouse exploring a closed field",
    identifier=py_str(uuid.uuid4()),
    session_start_time=session_start_time,
    session_id="session_4321",
    experimenter=py_list(c("Baggins, Frodo")),
    lab="Bag End Laboratory",
    institution="University of Middle Earth at the Shire",
    experiment_description="Thank you Bilbo Baggins.",
    keywords=py_list(c("behavior", "exploration"))
)

# ---- Add subject -----
subject <- pynwb.file.Subject(
    subject_id="001",
    age="P90D",
    description="mouse 5",
    species="Mus musculus",
    sex="M"
)

nwbfile.subject <- subject

nwbfile

# ---- Add TimeSeries -----
data <- seq(100, 190, by = 10)
time_series_with_rate <- pynwb.TimeSeries(
    name="test_timeseries",
    description="an example time series",
    data=data,
    unit="m",
    starting_time=0.0,
    rate=1.0
)
time_series_with_rate

nwbfile.add_acquisition(time_series_with_rate)

# ---- New Spatial positions -----
position_data <- cbind(
    seq(0, 10, length.out = 50),

```



```

    seq(0, 9, length.out = 50)
  )
  position_timestamps = seq(0, 49) / 200

  spatial_series_obj = pynwb$behavior$SpatialSeries(
    name="SpatialSeries",
    description="(x,y) position in open field",
    data=position_data,
    timestamps=position_timestamps,
    reference_frame="(0,0) is bottom left corner",
  )
  spatial_series_obj

  position_obj = pynwb$behavior$Position(
    spatial_series=spatial_series_obj)
  position_obj

  # ---- Behavior Processing Module -----
  behavior_module <- nwbfile$create_processing_module(
    name="behavior", description="processed behavioral data"
  )
  behavior_module$add(position_obj)

  nwbfile$processing$behavior

  # omit some process

  # ---- Write -----
  f <- normalizePath(tempfile(fileext = ".nwb"),
                    winslash = "/",
                    mustWork = FALSE)
  io <- pynwb$NWBHDF5IO(f, mode = "w")
  io$write(nwbfile)
  io$close()

  ## End(Not run)

```

---

SignalDataCache

*Class definition for signal cache*


---

### Description

This class is an internal abstract class

**Methods****Public methods:**

- [SignalDataCache\\$get\\_header\(\)](#)
- [SignalDataCache\\$get\\_annotatations\(\)](#)
- [SignalDataCache\\$get\\_channel\\_table\(\)](#)
- [SignalDataCache\\$get\\_channel\(\)](#)
- [SignalDataCache\\$delete\(\)](#)

**Method** `get_header()`: Get header information, often small list object

*Usage:*

`SignalDataCache$get_header(...)`

*Arguments:*

... passed to child methods

**Method** `get_annotatations()`: Get annotation information, often a large table

*Usage:*

`SignalDataCache$get_annotatations(...)`

*Arguments:*

... passed to child methods

**Method** `get_channel_table()`: Get channel table

*Usage:*

`SignalDataCache$get_channel_table(...)`

*Arguments:*

... passed to child methods

**Method** `get_channel()`: Get channel data

*Usage:*

`SignalDataCache$get_channel(x, ...)`

*Arguments:*

x channel order or label

... passed to child methods

*Returns:* Channel signal with time-stamps inheriting class 'ieegio\_get\_channel'

**Method** `delete()`: Delete file cache

*Usage:*

`SignalDataCache$delete(...)`

*Arguments:*

... passed to child methods

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