Package: ieegio (via r-universe)

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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.

URL http://dipterix.org/ieegio/

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

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Contents

`as_ieegio_surface` *Convert other surface formats to* `ieegio` *surface*

Description

Convert other surface formats to `ieegio` surface

Usage

```
as_ieegio_surface(x, ...)

## Default S3 method:
as_ieegio_surface(
  x,
  vertices = x,
  faces = NULL,
  face_start = NA,
  transform = NULL,
  vertex_colors = NULL,
  annotation_labels = NULL,
  annotation_values = NULL,
```

```
  measurements = NULL,
  time_series_slice_duration = NULL,
  time_series_value = NULL,
  name = NULL,
  ...
)

## S3 method for class 'character'
as_ieegio_surface(x, ...)

## S3 method for class 'ieegio_surface'
as_ieegio_surface(x, ...)

## S3 method for class 'mesh3d'
as_ieegio_surface(x, ...)

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

Arguments

x	R object or file path
...	passed to default method
vertices	n by 3 matrix, each row is a vertex node position
faces	(optional) face index, either zero or one-indexed (Matlab and R start counting from 1 while C and Python start indices from 0); one-index face order is recommended
face_start	(optional) either 0 or 1, indicating whether faces is zero or one-indexed; default is NA, which will check whether the minimum value of faces is 0. If so, then faces will be bumped by 1 internally
transform	(optional) a 4 by 4 matrix indicating the vertex position to scanner RAS transform. Default is missing (identity matrix), i.e. the vertex positions are already in the scanner RAS coordinate system.
vertex_colors	(optional) integer or color (hex) vector indicating the vertex colors
annotation_labels	(optional) a data frame containing at the following columns. Though optional, annotation_labels must be provided when annotation_values is provided "Key" unique integers to appear in annotation_values, indicating the key of the annotation label "Label" a character vector (strings) of human-readable labels of the corresponding key "Color" hex string indicating the color of the key/label
annotation_values	(optional) an integer table where each column is a vector of annotation key (for example, 'FreeSurfer' segmentation key) and each row corresponds to a vertex node

`measurements` (optional) a numeric table where each column represents a variable (for example, curvature) and each row corresponds to a vertex node. Unlike annotations, which is for discrete node values, `measurements` is for continuous values

`time_series_slice_duration` (optional) a numeric vector indicating the duration of each slice; default is `NA`

`time_series_value` (optional) a numeric matrix (`n` by `m`) where `n` is the number of vertices and `m` is the number of time points, hence each column is a time slice and each row is a vertex node.

`name` (optional) name of the geometry

Value

An `ieeg_surface` object; see `read_surface` or 'Examples'.

Examples

```
# ---- Simple usage
# vertices only
dodecahedron_vert <- matrix(
  ncol = 3, byrow = TRUE,
  c(-0.62, -0.62, -0.62, 0.62, -0.62, -0.62, -0.62, 0.62, -0.62,
    0.62, 0.62, -0.62, -0.62, -0.62, 0.62, 0.62, -0.62, 0.62,
    -0.62, 0.62, 0.62, 0.62, 0.62, 0.62, 0.00, -0.38, 1.00,
    0.00, 0.38, 1.00, 0.00, -0.38, -1.00, 0.00, 0.38, -1.00,
    -0.38, 1.00, 0.00, 0.38, 1.00, 0.00, -0.38, -1.00, 0.00,
    0.38, -1.00, 0.00, 1.00, 0.00, -0.38, 1.00, 0.00, 0.38,
    -1.00, 0.00, -0.38, -1.00, 0.00, 0.38)
)

point_cloud <- as_ieegio_surface(dodecahedron_vert)
plot(point_cloud, col = "red")

# with face index
dodecahedron_face <- matrix(
  ncol = 3L, byrow = TRUE,
  c(1, 11, 2, 1, 2, 16, 1, 16, 15, 1, 15, 5, 1, 5, 20, 1, 20, 19,
    1, 19, 3, 1, 3, 12, 1, 12, 11, 2, 11, 12, 2, 12, 4, 2, 4, 17,
    2, 17, 18, 2, 18, 6, 2, 6, 16, 3, 13, 14, 3, 14, 4, 3, 4, 12,
    3, 19, 20, 3, 20, 7, 3, 7, 13, 4, 14, 8, 4, 8, 18, 4, 18, 17,
    5, 9, 10, 5, 10, 7, 5, 7, 20, 5, 15, 16, 5, 16, 6, 5, 6, 9,
    6, 18, 8, 6, 8, 10, 6, 10, 9, 7, 10, 8, 7, 8, 14, 7, 14, 13)
)
mesh <- as_ieegio_surface(dodecahedron_vert,
                          faces = dodecahedron_face)
plot(mesh)

# with vertex colors
mesh <- as_ieegio_surface(dodecahedron_vert,
```

```
                          faces = dodecahedron_face,
                          vertex_colors = sample(20))
plot(mesh, name = "color")

# with annotations
mesh <- as_ieegio_surface(
  dodecahedron_vert,
  faces = dodecahedron_face,
  annotation_labels = data.frame(
    Key = 1:3,
    Label = c("A", "B", "C"),
    Color = c("red", "green", "blue")
  ),
  annotation_values = data.frame(
    MyVariable = c(rep(1, 7), rep(2, 7), rep(3, 6))
  )
)
plot(mesh, name = "annotations")

# with measurements
mesh <- as_ieegio_surface(
  dodecahedron_vert,
  faces = dodecahedron_face,
  measurements = data.frame(
    MyVariable = dodecahedron_vert[, 1]
  )
)
plot(mesh, name = "measurements",
     col = c("blue", "gray", "red"))
```

`as_ieegio_volume` *Convert objects to 'ieegio' image volumes*

Description

Convert array, path, or 'NIfTI' images in other formats to `'ieegio'` image volume instance

Usage

```
as_ieegio_volume(x, ...)

## S3 method for class 'character'
as_ieegio_volume(x, ...)

## S3 method for class 'ieegio_volume'
as_ieegio_volume(x, ...)
```

```
## S3 method for class 'array'
as_ieegio_volume(x, vox2ras = NULL, as_color = is.character(x), ...)

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

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

## S3 method for class 'ants.core.ants_image.ANTsImage'
as_ieegio_volume(x, ...)
```

Arguments

x	R object such as array, image path, or objects such as 'RNifti' or 'oro.nifti' image instances
...	passed to other methods
vox2ras	a 4x4 'affine' matrix representing the transform from 'voxel' index (column-row-slice) to 'RAS' (right-anterior-superior) coordinate. This transform is often called 'xform', 'sform', 'qform' in 'NIfTI' terms, or 'Norig' in 'FreeSurfer'
as_color	for converting arrays to volume, whether to treat x as array of colors; default is true when x is a raster matrix (matrix of color strings) and false when x is not a character array.

Value

An ieegio volume object; see imaging-volume

Examples

```
shape <- c(50, 50, 50)
vox2ras <- matrix(
  c(-1, 0, 0, 25,
    0, 0, 1, -25,
    0, -1, 0, 25,
    0, 0, 0, 1),
  nrow = 4, byrow = TRUE
)

# continuous
x <- array(rnorm(125000), shape)

volume <- as_ieegio_volume(x, vox2ras = vox2ras)
plot(volume, zoom = 3, pixel_width = 0.5)

# color rgb(a)
x <- array(
  sample(c("red","blue", "green", "cyan", "yellow"),
         12500, replace = TRUE),
```

```
  shape
)
rgb <- as_ieegio_volume(x, vox2ras = vox2ras)
plot(rgb, zoom = 3, pixel_width = 0.5)
```

---

burn_volume *Burn image at given positions*

Description

Burn image at given positions with given color and radius.

Usage

```
burn_volume(
  image,
  ras_position,
  col = "red",
  radius = 1,
  reshape = FALSE,
  alpha = FALSE,
  blank_underlay = FALSE,
  ...,
  preview = NULL
)
```

Arguments

image	volume
ras_position	image-defined right-anterior-posterior positions, an nx3 matrix, each row is an 'RAS' coordinate
col	vector of integer or characters, color of each contact
radius	vector of positive number indicating the burning radius
reshape	whether to reshape the image at a different resolution; default is false; can be TRUE (image resolution will be doubled), a single number (size of isotropic volume along one side), or a length of three defining the new shape.
alpha	whether to include alpha (transparent) channel. Default is false for compatibility concerns (legacy software might not support reading alpha channel). In this case, the background will be black. If alpha=TRUE is set, then the background will be fully transparent.
blank_underlay	whether to use blank image or the input image as underlay; default is FALSE (using image as underlay); alternative is TRUE, and use black or transparent background
...	passed to as_ieegio_volume, useful if image is an array
preview	indices (integer) of the position to visualize; default is NULL (no preview)

Value

Color image that is burnt; see imaging-volume.

Examples

```
if(interactive()) {

dim <- c(6, 6, 6)
image <- as_ieegio_volume(
  array(rnorm(prod(dim)), dim),
  vox2ras = rbind(cbind(diag(1, 3), -dim / 2),
                  c(0, 0, 0, 1))
)

ras_positions <- rbind(c(1, -1, 1.5), c(-2.25, -1, -0.75))


burned <- burn_volume(
  image,
  ras_positions,
  col = c("red", "green"),
  radius = 0.5,
  reshape = c(24, 24, 24)
)

plot(
  burned,
  position = ras_positions[1, ],
  zoom = 15,
  pixel_width = 0.25
)

}
```

---

ieegio_sample_data *Download sample files*

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

file, con	path the file
format	format of the file, see 'Arguments' section in read.fs.surface (when file type is 'geometry') and read.fs.curv (when file type is 'measurements')
type	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 for read_surface, and the file path for write_surface

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 *Read and write volume data*

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("rnifti", "oro", "ants"),
  header_only = FALSE,
  ...
)

io_write_nii(x, con, ...)

## S3 method for class 'ieegio_nifti'
io_write_nii(x, con, ...)

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

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

## S3 method for class 'nifti'
io_write_nii(x, con, gzipped = NA, ...)

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

## S3 method for class 'array'
io_write_nii(
  x,
  con,
  vox2ras = NULL,
  datatype_code = NULL,
  xyzt_units = c("NIFTI_UNITS_MM", "NIFTI_UNITS_SEC"),
  intent_code = "NIFTI_INTENT_NONE",
  ...,
  gzipped = NA
)
```

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 rec-

	ommend 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 `readNIfTI`), `'rnifti'` (using `readNifti`), and `'ants'` (using `as_ANTsImage`).
`gzipped`	for writing `'nii'` data: whether the file needs to be compressed; default is inferred from the file name. When the file ends with `'nii'`, then no compression is used; otherwise the file will be compressed. If the file name does not end with `'nii'` nor `'nii.gz'`, then the file extension will be added automatically.
`datatype_code`, `xyzt_units`, `intent_code`	additional flags for 'NIfTI' headers, for advanced users

Format

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

Value

Imaging readers return `ieegio_volume` objects. The writers return the file path to where the file is saved to.

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

plot(vol, position = c(10, 0, 30))

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

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

## Not run:
# requires additional python environment

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


## End(Not run)

# ---- 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

file	'HDF5' file
name	group/data_name path to dataset (H5D data)
read_only	only used if ram=FALSE, whether the returned LazyH5 instance should be read only
ram	load data to memory immediately, default is false
quiet	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. The class is not intended for direct-use. Please see `io_read_h5` and `io_write_h5`.

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("auto", "r3js", "rgl_basic", "rgl_full"),
  transform = 1L,
  name = "auto",
  vlim = NULL,
  col = c("black", "white"),
  slice_index = NULL,
  ...
)
```

Arguments

`x`	`'ieegio_surface'` object, see `read_surface`
`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)

  # ---- 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),
       slice_index = 1L)

  plot(
    merged,
    name = "time_series",
    vlim = c(-25, 25),
    slice_index = 64,
    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),
  col = c("black", "white"),
  alpha = NA,
  crosshair_gap = 4,
  crosshair_lty = 2,
  crosshair_col = "#00FF00A0",
  label_col = crosshair_col,
  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 read_volume
position	position in 'RAS' (right-anterior-superior) coordinate system on which cross-hair should focus
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$transforms; this needs to be the transform matrix from voxel index to 'RAS' (right-anterior-superior coordinate system), often called 'xform', 'sform', 'qform' in 'NIfTI' terms, or 'Norig' in 'FreeSurfer'
zoom	zoom-in level
pixel_width	pixel size, ranging from 0.05 to 50; default is the half of zoom or 1, whichever is greater; the unit of pixel_width divided by zoom is milliliter
col	color palette for continuous x values
alpha	opacity value if the image is to be displayed with transparency
crosshair_gap	the cross-hair gap in milliliter
crosshair_lty	the cross-hair line type
crosshair_col	the cross-hair color; set to NA to hide
label_col	the color of anatomical axis labels (i.e. "R" for right, "A" for anterior, and "S" for superior); default is the same as crosshair_col
continuous	reserved
vlim	the range limit of the data; default is computed from range of x$data; data values exceeding the range will be trimmed
add	whether to add the plot to existing underlay; default is FALSE
main, ...	passed to image
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 <- "nifti/rnifti_example.nii.gz"
nifti_rgbfile <- "nifti/rnifti_example_rgb.nii.gz"

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


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

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

underlay_path <- ieegio_sample_data(nifti_file)
overlay_path <- ieegio_sample_data(nifti_rgbfile)

# basic read
underlay <- read_volume(underlay_path)
overlay <- read_volume(overlay_path)

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 = underlay, position = ras_position, crosshair_gap = 10,
       crosshair_lty = 2, zoom = 3, which = which,
       main = sprintf("%s T1RAS=[%s]", which, ras_str))
  plot(x = overlay, position = ras_position,
       crosshair_gap = 10, label_col = NA,
       add = TRUE, alpha = 0.9, zoom = 5, which = which)
}


}
```

---

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 configure_conda; 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 *Read 'BCI2000' data file*

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 *Read 'BrainVision' data*

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 *Read 'NWB' format*

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 `NWBHDF5IO` 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)
```

`resample_volume` *Down-sample or super-sample volume*

Description

Using nearest-neighbor.

Usage

```
resample_volume(x, new_dim, na_fill = NA)
```

Arguments

`x`	image volume
`new_dim`	new dimension
`na_fill`	value to fill if missing

Value

A new volume with desired shape

Examples

```
# ---- Toy example ----------------------------

dm <- c(6, 6, 6)
arr <- array(seq_len(prod(dm)) + 0.5, dm)
orig <- as_ieegio_volume(
  arr, vox2ras = cbind(diag(1, nrow = 4, ncol = 3), c(-dm / 2, 1)))

# resample
downsampled <- resample_volume(orig, new_dim = c(3, 3, 3))
dim(downsampled)

# up-sample on coronal
upsampled <- resample_volume(orig, new_dim = c(20, 20, 24))
dim(upsampled)
```

```
par(mfrow = c(2, 2), mar = c(0, 0, 2.1, 0.1))
plot(orig, pixel_width = 0.5, zoom = 20, main = "Original")
plot(downsampled, pixel_width = 0.5, zoom = 20, main = "Down-sampled")
plot(upsampled, pixel_width = 0.5, zoom = 20, main = "Super-sampled")
plot(
  orig,
  main = "Overlay super-sample (diff)",
  col = c("black", "white"),
  pixel_width = 0.5, zoom = 20
)
plot(
  upsampled,
  add = TRUE,
  col = c("white", "black"),
  pixel_width = 0.5, zoom = 20,
  alpha = 0.5
)

# ---- Real example ---------------------------
nifti_file <- "brain.demosubject.nii.gz"

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

  orig <- read_volume(ieegio_sample_data(nifti_file))
  dim(orig)

  # resample
  downsampled <- resample_volume(orig, new_dim = c(30, 30, 30))
  dim(downsampled)

  # up-sample on coronal
  upsampled <- resample_volume(orig, new_dim = c(300, 300, 64))
  dim(upsampled)

  par(mfrow = c(2, 2), mar = c(0, 0, 2.1, 0.1))
  plot(orig, main = "Original")
  plot(downsampled, main = "Down-sampled")
  plot(upsampled, main = "Super-sampled")
  plot(
    orig,
    main = "Overlay super-sample",
    col = c("black", "white"),
    zoom = 2,
    vlim = c(0, 255)
  )
  plot(
    upsampled,
    add = TRUE,
    col = c("white", "black"),
    zoom = 2,
    alpha = 0.5,
    vlim = c(0, 255)
  )
```

```
}
```

`SignalDataCache` *Class definition for signal cache*

Description

This class is an internal abstract class

Methods

Public methods:

- `SignalDataCache$get_header()`
- `SignalDataCache$get_annotations()`
- `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_annotations()`**:** Get annotation information, often a large table

Usage:

```
SignalDataCache$get_annotations(...)
```

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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