

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.

URL <http://dipterix.org/ieegio/>

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

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Author Zhengjia Wang [aut, cre] (ORCID:
<<https://orcid.org/0000-0001-5629-1116>>)

Maintainer Zhengjia Wang <dipterix.wang@gmail.com>

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as_ieegio_surface	<i>Convert other surface formats to ieegio surface</i>
-------------------	--

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

<code>x</code>	R object or file path
<code>...</code>	passed to default method
<code>vertices</code>	n by 3 matrix, each row is a vertex node position
<code>faces</code>	(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
<code>face_start</code>	(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
<code>transform</code>	(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.
<code>vertex_colors</code>	(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"))

```

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
)

}
```

convert-fst	<i>Convert 'FST' files to other formats</i>
-------------	---

Description

'HDF5', 'CSV' are common file formats that can be read into 'Matlab' or 'Python'

Usage

```
convert_fst_to_hdf5(fst_path, hdf5_path, exclude_names = NULL)
```

```
convert_fst_to_csv(fst_path, csv_path, exclude_names = NULL)
```

Arguments

fst_path	path to 'FST' file
hdf5_path	path to 'HDF5' file; if file exists before the conversion, the file will be erased first. Please make sure the files are backed up.
exclude_names	table names to exclude
csv_path	path to 'CSV' file; if file exists before the conversion, the file will be erased first. Please make sure the files are backed up.

Value

convert_fst_to_hdf5 will return a list of data saved to 'HDF5'; convert_fst_to_csv returns the normalized 'CSV' path.

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-streamlines *Read and write streamlines*

Description

High-level functions to read and write streamlines, supporting 'TCK', 'TRK', 'TT' (read-only), 'VTK' poly-data (including legacy '.vtk', 'XML'-based '.vtp', 'HDF5'-based '.vtpb')

Usage

```
read_streamlines(file, ...)

write_streamlines(
  x,
  con,
  format = c("auto", "tck", "trk", "vtk", "vtp", "vtpb"),
  ...
)

as_ieegio_streamlines(x, ...)

## Default S3 method:
as_ieegio_streamlines(x, vox2ras = NULL, ..., class = NULL)
```

Arguments

file, con	path to the streamline data
...	passed to low-level functions accordingly
x	R object that can be converted into an ieegio streamlines instance
format	format to write to file, the file extensions must match with the format
vox2ras	volume index to 'RAS' coordinate transform matrix; default is identity matrix and used by 'TRK' format
class	additional class to be added to the instance

Value

read_streamlines and as_ieegio_streamlines returns a streamlines instance.

Examples

```
# toy example
curve <- function(t) {
  x <- sin(4 * t + sample(300, 1) / 100) + t + sample(seq_along(t)) / length(t) / 10
  y <- cos(sin(t) + 5 * t) + sample(seq_along(t)) / length(t) / 10
  z <- t * 3
  cbind(x, y, z)
}

# 10 lines, each line is represented by nx3 matrix
tracts <- lapply(seq(100, 109), function(n) {
  curve(seq_len(n) / 100)
}))

# convert to streamline
x <- as_ieegio_streamlines(tracts)

# Display
print(x)
plot(x, col = 1:10)

if(system.file(package = "r3js") != '') {
  plot(x, method = "r3js")
}

# Subset the first line (transformed)
coords <- x[[1]]$coords
head(coords)

# Save different formats
tdir <- tempfile()
dir.create(tdir, showWarnings = FALSE, recursive = TRUE)

write_streamlines(x, file.path(tdir, "sample.tck"))
write_streamlines(x, file.path(tdir, "sample.trk"))
```

```

write_streamlines(x, file.path(tdir, "sample.trk.gz"))

## Not run:

# Require Python
write_streamlines(x, file.path(tdir, "sample.vtk"))
write_streamlines(x, file.path(tdir, "sample.vtp"))
write_streamlines(x, file.path(tdir, "sample.vtpb"))

## End(Not run)

# Read formats
y <- read_streamlines(file.path(tdir, "sample.trk"))

# Compare x and y
diffs <- mapply(
  x = as.vector(x),
  y = as.vector(y),
  function(x, y) {
    range(x$coords - y$coords)
  }
)
# Should be floating errors
max(abs(diffs))

unlink(tdir, recursive = TRUE)

```

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"),
  ...,
  name = 1

```

```

)

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, for write_surface, this is either 'gifti' or 'freesurfer'; for read_surface, 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; for io_read_fs, this argument must be a character, and default is the file name; for write_surface, this argument can be an integer or a character, representing the index or name of the corresponding measurement or annotation column.

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,
xyz_t_units = c("NIFTI_UNITS_MM", "NIFTI_UNITS_SEC"),
intent_code = "NIFTI_INTENT_NONE",
...,
gzipped = NA
)

```

Arguments

<code>file</code>	file path to read volume data
<code>header_only</code>	whether to read header data only; default is FALSE
<code>format</code>	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
<code>...</code>	passed to other methods
<code>x</code>	volume data (such as 'Nifti' image, array, or 'MGH') to be saved
<code>con</code>	file path to store image
<code>vox2ras</code>	a 4x4 transform matrix from voxel indexing (column, row, slice) to scanner (often 'T1-weighted' image) 'RAS' (right-anterior-superior) coordinate
<code>method</code>	method to read the file; choices are 'oro' (using readNIFTI), 'rnifti' (using readNifti), and 'ants' (using as_ANTsImage).
<code>gzipped</code>	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.
<code>datatype_code, xyz_t_units, intent_code</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-trk

Read or write 'TCK' streamlines

Description

Low-level functions; for high-level functions, please use [read_streamlines](#) or [as_ieegio_streamlines](#) instead.

Low-level functions, supports compressed files; for high-level functions, please use [read_streamlines](#) or [as_ieegio_streamlines](#) instead.

Usage

```

io_read_tck(file)

io_write_tck(
  x,
  con,
  datatype = c("Float32LE", "Float32BE", "Float64LE", "Float64BE")
)

io_read_trk(file, half_voxel_offset = TRUE)

io_write_trk(x, con, half_voxel_offset = NA)

```

Arguments

file, con	file path to the streamline file
x	imaging-streamlines instance
datatype	data storage type to write, default is 'Float32LE', 4-byte little 'endian' float; other choices are 'Float32BE', 'Float64LE', and 'Float64BE'
half_voxel_offset	whether to add 0.5 millimeter shift on each side, default is TRUE. See 'Details' for explanation.

Details

'TRK' gains popularity due to its ability to store streamline attributes. However, this file format suffer from ambiguous definition in the initial 'TrackVis' implementation. Typically in a medical image file, there might exists a 4-by-4 matrix that maps the volume indices to the corresponding anatomical right-anterior-superior 'RAS' locations. However, the original definition of 'TRK' does not have this. Since version 2, 'TRK' introduced such matrix, but it was interpreted differently. Instead of the volume index space, the source space is conformed 1 millimeter space, with the origin at the first 'voxel' corner instead of the center. Therefore there is a 0.5 mm shift at each direction, and `half_voxel_offset` is designed to offset this shift.

What has made this issue complicated was that some software, such as 'DSI-studio', seemed to ignore that offset when converting from their own format to the 'TRK' format. If the file is generated in such way, please set `half_voxel_offset=FALSE` to turn off the offset correction. We always recommend that user store data in 'TCK' format.

Value

`io_read_tck` returns a `ieegio` streamline object, `io_write_tck` returns the connection or file path. `io_read_trk` returns an [imaging-streamlines](#) instance.

Examples

```
# run `ieegio_sample_data("streamlines/CNVII_R.tck")` to
# download sample data

if( ieegio_sample_data("streamlines/CNVII_R.tck", test = TRUE) ) {

  path <- ieegio_sample_data("streamlines/CNVII_R.tck")

  # Read
  streamlines <- io_read_tck(path)

  plot(streamlines)

  # write
  tfile <- tempfile(fileext = ".tck")
  io_write_tck(streamlines, tfile, datatype = streamlines$header$datatype)

  # verify two files are identical
  digest::digest(file = tfile) == digest::digest(file = path)

  unlink(tfile)
}
```

```

# This example uses sample data, run
# `ieegio_sample_data("streamlines/CNVII_R.trk")` to download

if( ieegio_sample_data("streamlines/CNVII_R.trk", test = TRUE) ) {

  path <- ieegio_sample_data("streamlines/CNVII_R.trk")
  tfile <- tempfile(fileext = ".trk")

  # read
  x <- io_read_trk(path)

  # write
  io_write_trk(x, tfile)

  # compare two files
  file.size(path) == file.size(tfile)

  src_raw <- readBin(path, "raw", n = file.size(path))
  dst_raw <- readBin(tfile, "raw", n = file.size(tfile))

  equal_raw <- src_raw == dst_raw

  # Some reserved information are removed
  all(equal_raw[-c(945:947)])

  unlink(tfile)
}

```

io-tt

Read 'TT' streamline file

Description

Writer is not implemented yet. Please save as a 'TCK' file.

Usage

```
io_read_tt(file)
```

Arguments

file path to the streamline file

Value

An [imaging-streamlines](#) instance.

Examples

```
# This example uses sample data, run
# `ieegio_sample_data("streamlines/CNVII_R.trk")` to download

if( ieegio_sample_data("streamlines/CNVII_R.tt.gz", test = TRUE) ) {

  path <- ieegio_sample_data("streamlines/CNVII_R.tt.gz")

  # read
  x <- io_read_tt(path)

  plot(x)

}
```

io-vtk-streamlines	<i>Read or write streamline data in 'VTK' format</i>
--------------------	--

Description

This reader uses 'Python' 'vtk' package, supports '.vtk', '.vtp', '.pvtp', '.vtpb' formats.

Usage

```
io_read_vtk_streamlines(file)

io_write_vtk_streamlines(x, con, binary = TRUE)
```

Arguments

file, con	file path to the 'VTK' file, the format will be inferred from the file extension (with default '.vtk')
x	An imaging-streamlines object
binary	for legacy '.vtk' file only, whether to store the data as binary file or 'ASCII' plain text; default is true (binary).

Value

`io_read_vtk_streamlines` returns an [imaging-streamlines](#) object, while `io_write_vtk_streamlines` writes the data to file

Examples

```
# This example shows how to convert tck to vtk

# run `ieegio_sample_data("streamlines/CNVII_R.tck")` to
# download sample data

if( ieegio_sample_data("streamlines/CNVII_R.tck", test = TRUE) ) {

  path <- ieegio_sample_data("streamlines/CNVII_R.tck")

  streamlines <- as_ieegio_streamlines(path)

  # write to vtk
  tfile <- tempfile(fileext = ".vtk")
  io_write_vtk_streamlines(streamlines, con = tfile)

  # read
  vtk_streamlines <- io_read_vtk_streamlines(tfile)

  # compare
  plot(streamlines)
  plot(vtk_streamlines)

  # 0 0
  range(streamlines[[1]]$coords - vtk_streamlines[[1]]$coords)

}
```

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_fstarray_or_h5

Function try to load 'FST' arrays, if not found, read 'HDF5' arrays

Description

Experimental function; use with caution.

Usage

```
io_read_fstarray_or_h5(
  fst_path,
  h5_path,
  h5_name,
  fst_need_transpose = FALSE,
  fst_need_drop = FALSE,
```

```

    ram = FALSE
  )

```

Arguments

fst_path	'FST' file cache path
h5_path	alternative 'HDF5' file path
h5_name	'HDF5' data name
fst_need_transpose	does 'FST' data need transpose?
fst_need_drop	drop dimensions
ram	whether to load to memory directly or perform lazy loading

Details

RAVE stores data with redundancy. One electrode data is usually saved with two copies in different formats: 'HDF5' and 'FST', where 'HDF5' is cross-platform and supported by multiple languages such as Matlab, Python, etc, while 'FST' format is supported by R only, with super high read/write speed. `load_fst_or_h5` checks whether the presence of 'FST' file, if failed, then it reads data from persistent 'HDF5' file.

Value

If 'FST' cache file exists, returns [LazyFST](#) object, otherwise returns [LazyH5](#) instance

io_read_h5	<i>Lazy Load 'HDF5' File via hdf5r-package</i>
------------	--

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

<code>x</code>	an array, a matrix, or a vector
<code>file</code>	path to 'HDF5' file
<code>name</code>	path/name of the data; for example, "group/data_name"
<code>chunk</code>	chunk size
<code>level</code>	compress level from 0 - no compression to 10 - max compression
<code>replace</code>	should data be replaced if exists
<code>new_file</code>	should removing the file if old one exists
<code>ctype</code>	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.
<code>quiet</code>	whether to suppress messages, default is false
<code>...</code>	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)
```

 LazyFST

 R6 Class to Load 'FST' Files

Description

provides low-level hybrid array loading for 'FST' file; used internally

Value

none

none

none

vector, dimensions

subset of data

Methods**Public methods:**

- [LazyFST\\$open\(\)](#)
- [LazyFST\\$close\(\)](#)
- [LazyFST\\$save\(\)](#)
- [LazyFST\\$new\(\)](#)
- [LazyFST\\$get_dims\(\)](#)
- [LazyFST\\$subset\(\)](#)

Method `open()`: to be compatible with [LazyH5](#)

Usage:

`LazyFST$open(...)`

Arguments:

... ignored

Method `close()`: close the connection

Usage:

`LazyFST$close(..., .remove_file = FALSE)`

Arguments:

... ignored

`.remove_file` whether to remove the file when garbage collected

Method `save()`: to be compatible with [LazyH5](#)

Usage:

`LazyFST$save(...)`

Arguments:

... ignored

Method `new()`: constructor

Usage:

```
LazyFST$new(file_path, transpose = FALSE, dims = NULL, ...)
```

Arguments:

`file_path` where the data is stored

`transpose` whether to load data transposed

`dims` data dimension, only support 1 or 2 dimensions

... ignored

Method `get_dims()`: get data dimension

Usage:

```
LazyFST$get_dims(...)
```

Arguments:

... ignored

Method `subset()`: subset data

Usage:

```
LazyFST$subset(i = NULL, j = NULL, ..., drop = TRUE)
```

Arguments:

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

`drop` whether to apply [drop](#) the subset

Author(s)

Zhengjia Wang

Examples

```
library(ieegio)

# Data to save, 8 MB
x <- matrix(rnorm(1000000), ncol = 100)

# Save to local disk
f <- tempfile()
io_write_fst(as.data.frame(x), con = f)

# Load via LazyFST
dat <- LazyFST$new(file_path = f, dims = c(10000, 100))

# dat < 1 MB

# Check whether the data is identical
range(dat[] - x)
```

```
system.time(dat[,1])

system.time(dat[1:100,])
```

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\\$do_finalize\(\)](#)
- [LazyH5\\$print\(\)](#)
- [LazyH5\\$new\(\)](#)
- [LazyH5\\$save\(\)](#)
- [LazyH5\\$open\(\)](#)
- [LazyH5\\$close\(\)](#)
- [LazyH5\\$subset\(\)](#)
- [LazyH5\\$get_dims\(\)](#)
- [LazyH5\\$get_type\(\)](#)

Method `do_finalize()`: garbage collection method

Usage:

`LazyH5$do_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"

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)

```

merge.ieegio_surface *Merge two 'ieegio' surfaces*

Description

Either merge surface objects by attributes or merge geometries

Usage

```

## S3 method for class 'ieegio_surface'
merge(
  x,
  y,
  ...,
  merge_type = c("attribute", "geometry"),
  merge_space = c("model", "world"),
  transform_index = 1,
  verbose = TRUE
)

```

Arguments

x, y, ...	'ieegio' surface objects, see as_ieegio_surface or read_surface . Object x must contain geometry information.
merge_type	type of merge:

	"attribute" merge $y, \dots$ into x by attributes such as color, measurements, annotations, or time-series data, assuming $x, y, \dots$ all refer to the same geometry, hence the underlying number of vertices should be the same. "geometry" merge $y, \dots$ into x by geometry; this requires the surfaces to merge have geometries and cannot be only surface attributes. Two mesh objects will be merged into one, and face index will be re-calculated. The merge happens in transformed space, Notice the attributes will be ignored and eventually discarded during merge.
merge_space	space to merge the geometries; only used when merge_type is "geometry". Default is to directly merge the surfaces in "model" space, i.e. assuming the surfaces share the same transform; alternatively, if the model to world transforms are different, users can choose to merge in "world" space, then all the surfaces will be transformed into world space and mapped back to the model space in x
transform_index	which local-to-world transform to use when merging geometries in the world space; default is the first transform for each surface object. The transform list can be obtained from <code>surface\$geometry\$transforms</code> and <code>transform_index</code> indicates the index of the transform matrices. The length of <code>transform_index</code> can be either 1 (same for all surfaces) or the length of all the surfaces, (i.e. length of <code>list(x,y,\dots)</code>), when the index needs to be set for each surface respectively. If any index is set to NA, then it means no transform is to be applied and that surface will be merged assuming its model space is the world space.
verbose	whether to verbose the messages

Value

A merged surface object

Examples

```
# Construct example geometry
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)
)

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)
)

x0 <- as_ieegio_surface(dodecahedron_vert, faces = dodecahedron_face)

plot(x0)

# ---- merge by attributes -----

# point-cloud but with vertex measurements
y1 <- as_ieegio_surface(
  dodecahedron_vert,
  measurements = data.frame(MyVariable = dodecahedron_vert[, 1]),
  transform = diag(c(2,1,0.5,1))
)

plot(y1)

# the geometry of `y1` will be discarded and only attributes
# (in this case, measurements:MyVariable) will be merged to `x`

z1 <- merge(x0, y1, merge_type = "attribute")

plot(z1)

# ---- merge by geometry -----

y2 <- as_ieegio_surface(
  dodecahedron_vert + 4, faces = dodecahedron_face,
  transform = diag(c(2, 1, 0.5, 1))
)

plot(y2)

# merge directly in model space: transform matrix of `y2` will be ignored
z2 <- merge(x0, y2, merge_type = "geometry", merge_space = "model")

plot(z2)

# merge x, y2 in the world space where transforms will be respected
z3 <- merge(x0, y2, merge_type = "geometry", merge_space = "world")

plot(z3)

```

Description

Merge volume data into base image. The images must be static 3-dimensional volume data. Currently time-series or 4-dimensional data is not supported.

Usage

```
## S3 method for class 'ieegio_volume'
merge(x, y, ..., thresholds = 0, reshape = dim(x), na_fill = NA)
```

Arguments

<code>x</code>	base image to be merged
<code>y, ...</code>	images to be merged into <code>x</code>
<code>thresholds</code>	numerical threshold for <code>y, ...</code> , can be length of one or more, if images to overlay is more than one. The image values lower than the threshold will be trimmed out
<code>reshape</code>	output shape, default is the dimension of <code>x</code> ; if changed, then the underlay will be sampled into the new shape
<code>na_fill</code>	how to handle missing values; default is NA; for compatibility, you might want to set to 0

Value

Merged volume with dimension reshape.

Examples

```
base_array <- array(0, c(15, 15, 15))
base_array[4:6, 4:6, 4:6] <- runif(27) * 255

# generate a 15x15x15 mask with 1mm spacing
vox2ras1 <- diag(1, 4)
vox2ras1[1:3, 4] <- -5
x <- as_ieegio_volume(base_array, vox2ras = vox2ras1)

# 15x15x15 mask with 0.5mmx1mmx1mm spacing but oblique to `x`
vox2ras2 <- matrix(
  nrow = 4, byrow = TRUE,
  c(
    2, 0.2, -0.1, -3,
    -0.2, 1, 0.4, -4,
    0.3, -0.1, 1, -1,
    0, 0, 0, 1
  )
)
# vox2ras2[1:3, 4] <- c(-3,-4, -1)
base_array[4:6, 4:6, 4:6] <- runif(27) * 255
y <- as_ieegio_volume(base_array, vox2ras = vox2ras2)
```

```

# merge y into x and up-sample mask to 64^3 volume
# set to higher number to get better interpolation quality
# Only voxels of y>0 will be merged to x
z <- merge(x, y, reshape = c(64, 64, 64), thresholds = 0)

# Visualize

oldpar <- par(mfrow = c(1, 3), mar = c(0, 0, 2, 0))

zoom <- 10
crosshair_ras <- c(0, 0, 0)
pixel_width <- 2

plot(x,
     zoom = zoom,
     position = crosshair_ras,
     pixel_width = pixel_width,
     main = "Original - underlay")
plot(y,
     zoom = zoom,
     position = crosshair_ras,
     pixel_width = pixel_width,
     main = "Original - overlay")
plot(
  z,
  zoom = zoom,
  position = crosshair_ras,
  pixel_width = pixel_width,
  main = "Merged & up-sampled")

# reset graphical state
par(oldpar)

```

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

<code>x</code>	'ieegio_volume' object; see read_volume
<code>position</code>	position in 'RAS' (right-anterior-superior) coordinate system on which cross-hair should focus
<code>center_position</code>	whether to center canvas at position, default is FALSE
<code>which</code>	which slice to plot; choices are "coronal", "axial", and "sagittal"
<code>slice_index</code>	length of 1: if x has fourth dimension (e.g. 'fMRI'), then which slice index to draw
<code>transform</code>	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'
<code>zoom</code>	zoom-in level
<code>pixel_width</code>	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
<code>col</code>	color palette for continuous x values
<code>alpha</code>	opacity value if the image is to be displayed with transparency
<code>crosshair_gap</code>	the cross-hair gap in milliliter
<code>crosshair_lty</code>	the cross-hair line type
<code>crosshair_col</code>	the cross-hair color; set to NA to hide
<code>label_col</code>	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
<code>continuous</code>	reserved
<code>vlim</code>	the range limit of the data; default is computed from range of x\$data; data values exceeding the range will be trimmed
<code>add</code>	whether to add the plot to existing underlay; default is FALSE
<code>main, ...</code>	passed to image
<code>axes</code>	whether to draw axes; default is FALSE
<code>background, foreground</code>	background and foreground colors; default is the first and last elements of col
<code>.xdata</code>	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)
}

}

```

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	<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	<i>Read 'EDF' or 'BDF' data file</i>
----------	--------------------------------------

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 NWBHDF5IO initialize function

Value

A [NWBHDF5IO](#) instance

Examples

```
if(i EEGIO_sample_data("nwb_sample.nwb", test = TRUE)) {
  file <- i EEGIO_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 `rpy2::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	<i>Down-sample or super-sample volume</i>
-----------------	---

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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