Package: skiftiTools (via r-universe)

October 11, 2026

Title Tools and Operations for Reading, Writing, Viewing, and Manipulating SKIFTI Files

Version 0.1.0

Description SKIFTI files contain brain imaging data in coordinates across Tract Based Spatial Statistics (TBSS) skeleton, which represent the brain white matter intensity values. 'skiftiTools' provides a unified environment for reading, writing, visualizing and manipulating SKIFTI-format data. It supports the ``subsetting", ``concatenating", and using data as data.frame for R statistical functions. The SKIFTI data is structured for convenient access to the data and metadata, and includes support for visualizations. For more information see Merisaari et al. (2024) <doi:10.57736/87d2-0608>.

Depends R (>= 4.2.0)

License GPL-3

Encoding UTF-8

Imports RNifti, stringr, R.utils, rmarchingcubes, Rvcg, png, rgl, oce, abind, methods, s2dv

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

URL https://github.com/haanme/skiftiTools

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

Config/pak/sysreqs cmake libfreetype6-dev libglu1-mesa-dev make texlive libicu-dev libpng-dev libuv1-dev libnetcdf-dev libgl1-mesa-dev zlib1g-dev

Repository https://haanme.r-universe.dev

Date/Publication 2025-10-10 08:39:08 UTC

RemoteUrl https://github.com/haanme/skiftitools

RemoteRef HEAD

RemoteSha 8d178f7888e8bf3f06d4c8b45c01aa2360b50382

Contents

concat 2
Nifti2Skifti 3
readSkifti 5
save_skeleton 6
Skifti2CSV 7
Skifti2Nifti 8
subset 9
writeSkifti 9

Index **12**

`concat` *Concatenate Skifti data*

Description

Concatenate Skifti data

Usage

```
concat(Skifti_data1, Skifti_data2)
```

Arguments

`Skifti_data1`	Skifti data object1
`Skifti_data2`	Skifti data object2

Value

concatenated Skifti data object

Examples

```
library(RNifti)
data<-array(0,dim=list(10,10,10,10))
for(t in 1:10) {
  for(x in 1:10) {
    for(y in 1:10) {
      for(z in 1:10) {
        data[x,y,z,t]<-t+x
      }
    }
  }
}
data_Nifti<-RNifti::retrieveNifti(data)
RNifti::writeNifti(data_Nifti, "data_Nifti.nii.gz", template = NULL, datatype = "auto")

data_skeleton<-array(0,dim=list(10,10,10))
```

```
data_skeleton[5,5,5]<-1
data_skeleton[6,6,6]<-1
data_skeleton[7,7,7]<-1
data_skeleton_Nifti<-RNifti::retrieveNifti(data_skeleton)
RNifti::writeNifti(data_skeleton_Nifti, "data_skeleton_Nifti.nii.gz", datatype = "auto")

data_Skifti<-Nifti2Skifti(Nifti_data="data_Nifti.nii.gz",
                          Nifti_skeleton="data_skeleton_Nifti.nii.gz",
                          selected_volumes=1:10,
                          Nifti_labels=NULL,
                          write_coordinates=TRUE,
                          verbose=FALSE)

data_Skifti_subset<-subset(data_Skifti, c(1,5,10))
m<-matrix(c(6,10,15,7,11,16,8,12,17), nrow=3, ncol=3)
rownames(m)<-c("vol1", "vol5", "vol10")

data_Skifti_subset1<-subset(data_Skifti, c(1,5))
data_Skifti_subset2<-subset(data_Skifti, c(10))
data_Skifti_concat<-concat(data_Skifti_subset1, data_Skifti_subset2)
m<-matrix(c(6,10,15,7,11,16,8,12,17), nrow=3, ncol=3)
rownames(m)<-c("vol1", "vol5", "")
```

`Nifti2Skifti` *Create a SKIFTI file from fsl TBSS skeleton data*

Description

Skeleton mask and corresponding image intensity data must be in Nifti format. The skeleton mask is used to determine the coordinates of intensity data. If optional label file is given, that is used to label the voxels.

Usage

```
Nifti2Skifti(
  Nifti_data = NULL,
  Nifti_skeleton = NULL,
  selected_volumes = NULL,
  Nifti_labels = NULL,
  write_coordinates = FALSE,
  verbose = FALSE
)
```

Arguments

`Nifti_data`	Intensity data in Nifti format (required)
`Nifti_skeleton`	Skeleton at same imaging space as the data, in Nifti format (required)
`selected_volumes`	Selected volume indexes starting from 1 (default==NULL, selecting all)

`Nifti_labels` Labeling data to be used inside mask, writing extra line to the output about labels (default==NULL, no extra labeling)

`write_coordinates` TRUE/FALSE(default) write coordinates of voxels in x,y,z ASCII format, in the same order as they appear in the skifti

`verbose` TRUE/FALSE(default) for verbose messages

Value

skifti object with default rownames as vol1, vol2 .... volN as indexes from the nifti data

Examples

```
#source('../../R/Skifti2Nifti.R')
#source('../../R/Nifti2Skifti.R')
library(RNifti)
data<-array(0,dim=list(10,10,10,10))
for(t in 1:10) {
  for(x in 1:10) {
    for(y in 1:10) {
      for(z in 1:10) {
        data[x,y,z,t]<-t+x
      }
    }
  }
}
data_Nifti<-RNifti::retrieveNifti(data)
RNifti::writeNifti(data_Nifti, "data_Nifti.nii.gz", template = NULL, datatype = "auto")

data_skeleton<-array(0,dim=list(10,10,10))
data_skeleton[5,5,5]<-1
data_skeleton[6,6,6]<-1
data_skeleton[7,7,7]<-1
data_skeleton_Nifti<-RNifti::retrieveNifti(data_skeleton)
RNifti::writeNifti(data_skeleton_Nifti, "data_skeleton_Nifti.nii.gz", datatype = "auto")

data_Skifti<-Nifti2Skifti(Nifti_data="data_Nifti.nii.gz",
                          Nifti_skeleton="data_skeleton_Nifti.nii.gz",
                          selected_volumes=c(1),
                          Nifti_labels=NULL,
                          write_coordinates=TRUE,
                          verbose=FALSE)

# Create Skifti
data_Nifti2<-Skifti2Nifti(data_Skifti)
RNifti::writeNifti(data_Nifti2[[1]], "data_Nifti.nii.gz", datatype = "auto")
data_Nifti2<-RNifti::readNifti("data_Nifti.nii.gz", internal = TRUE, volumes = NULL)
```

readSkifti *Read Skifti data*

Description

Read Skifti data

Usage

```
readSkifti(filename, verbose = FALSE)
```

Arguments

filename	file to read
verbose	TRUE/FALSE(default), for verbosity

Value

Skifti data object

Examples

```
#source('../../R/Skifti2Nifti.R')
#source('../../R/Nifti2Skifti.R')
library(RNifti)
data<-array(0,dim=list(10,10,10,10))
for(t in 1:10) {
  for(x in 1:10) {
    for(y in 1:10) {
      for(z in 1:10) {
        data[x,y,z,t]<-t+x
      }
    }
  }
}
data_Nifti<-RNifti::retrieveNifti(data)
RNifti::writeNifti(data_Nifti, "data_Nifti.nii.gz", template = NULL, datatype = "auto")

data_skeleton<-array(0,dim=list(10,10,10))
data_skeleton[5,5,5]<-1
data_skeleton[6,6,6]<-1
data_skeleton[7,7,7]<-1
data_skeleton_Nifti<-RNifti::retrieveNifti(data_skeleton)
RNifti::writeNifti(data_skeleton_Nifti, "data_skeleton_Nifti.nii.gz", datatype = "auto")

data_Skifti<-Nifti2Skifti(Nifti_data="data_Nifti.nii.gz",
                          Nifti_skeleton="data_skeleton_Nifti.nii.gz",
                          selected_volumes=c(1),
                          Nifti_labels=NULL,
```

```
                          write_coordinates=TRUE,
                          verbose=FALSE)

# Create Skifti
data_Nifti2<-Skifti2Nifti(data_Skifti)
RNifti::writeNifti(data_Nifti2[[1]], "data_Nifti.nii.gz", datatype = "auto")
data_Nifti2<-RNifti::readNifti("data_Nifti.nii.gz", internal = TRUE, volumes = NULL)
```

`save_skeleton` *Create png from mask and data in Nifti format*

Description

Skeleton mask and corresponding image intensity data must be in Nifti format. The skeleton mask is used to determine the coordinates of intensity data.

Usage

```
save_skeleton(
  mask,
  data,
  img_hdr,
  output,
  legend_title,
  scale,
  keep_temp = FALSE,
  palette = "lajolla",
  verbose = FALSE
)
```

Arguments

`mask`	Intensity data in Nifti object format
`data`	Skeleton at same imaging space as the data, in Nifti format
`img_hdr`	Nifti header object
`output`	Output PNG filename
`legend_title`	Title to be shown
`scale`	scaling for intensity values, tune for better color depth
`keep_temp`	TRUE/FALSE(default) to keep temporary png images
`palette`	color palette
`verbose`	TRUE/FALSE(default), for verbosity

Value

No output, as resuts are saved to a png file

Skifti2CSV *Create a Nifti file from Skifti data*

Description

Skeleton mask and corresponding image intensity data in Nifti format. The skeleton mask is used to determine the coordinates of intensity data. If optional label file is given, that is used to label the voxels.

Usage

```
Skifti2CSV(Skifti_data, filename, overwrite = FALSE, sep = ";")
```

Arguments

Skifti_data	Intensity data in Nifti format
filename	file to read'
overwrite	TRUE/FALSE(default) to overwrite existing data
sep	file separator to be written default ';'

Value

CSV filename

Examples

```
library(RNifti)
data<-array(0,dim=list(10,10,10,10))
for(t in 1:10) {
  for(x in 1:10) {
    for(y in 1:10) {
      for(z in 1:10) {
        data[x,y,z,t]<-t+x
      }
    }
  }
}
data_Nifti<-RNifti::retrieveNifti(data)
RNifti::writeNifti(data_Nifti, "data_Nifti.nii.gz", template = NULL, datatype = "auto")

data_skeleton<-array(0,dim=list(10,10,10))
data_skeleton[5,5,5]<-1
data_skeleton[6,6,6]<-1
data_skeleton[7,7,7]<-1
data_skeleton_Nifti<-RNifti::retrieveNifti(data_skeleton)
RNifti::writeNifti(data_skeleton_Nifti, "data_skeleton_Nifti.nii.gz", datatype = "auto")

data_Skifti<-Nifti2Skifti(Nifti_data="data_Nifti.nii.gz",
```

```
                          Nifti_skeleton="data_skeleton_Nifti.nii.gz",
                          selected_volumes=1:10,
                          Nifti_labels=NULL,
                          write_coordinates=TRUE,
                          verbose=FALSE)

Skifti2CSV(data_Skifti, "data_Skifti.csv", overwrite=TRUE, sep=';')
data_csv<-read.csv2("data_Skifti.csv", ';', header = FALSE, row.names = NULL)
```

`Skifti2Nifti` *Create a Nifti file from Skifti data*

Description

Skeleton mask and corresponding image intensity data in Nifti format. The skeleton mask is used to determine the coordinates of intensity data. If optional label file is given, that is used to label the voxels.

Usage

```
Skifti2Nifti(Skifti_data)
```

Arguments

`Skifti_data`	Intensity data in Nifti format

Value

Nifti skeleton file for Skifti data

Examples

```
#source('../../R/Skifti2Nifti.R')
#source('../../R/Nifti2Skifti.R')
library(RNifti)
data<-array(0,dim=list(10,10,10,10))
for(t in 1:10) {
  for(x in 1:10) {
    for(y in 1:10) {
      for(z in 1:10) {
        data[x,y,z,t]<-t+x
      }
    }
  }
}
data_Nifti<-RNifti::retrieveNifti(data)
RNifti::writeNifti(data_Nifti, "data_Nifti.nii.gz", template = NULL, datatype = "auto")

data_skeleton<-array(0,dim=list(10,10,10))
data_skeleton[5,5,5]<-1
```

```
data_skeleton[6,6,6]<-1
data_skeleton[7,7,7]<-1
data_skeleton_Nifti<-RNifti::retrieveNifti(data_skeleton)
RNifti::writeNifti(data_skeleton_Nifti, "data_skeleton_Nifti.nii.gz", datatype = "auto")

data_Skifti<-Nifti2Skifti(Nifti_data="data_Nifti.nii.gz",
                          Nifti_skeleton="data_skeleton_Nifti.nii.gz",
                          selected_volumes=c(1),
                          Nifti_labels=NULL,
                          write_coordinates=TRUE,
                          verbose=FALSE)

# Create Skifti
data_Nifti2<-Skifti2Nifti(data_Skifti)
RNifti::writeNifti(data_Nifti2[[1]], "data_Nifti.nii.gz", datatype = "auto")
data_Nifti2<-RNifti::readNifti("data_Nifti.nii.gz", internal = TRUE, volumes = NULL)
```

`subset` *Get subset of Skifti data*

Description

Get subset of Skifti data

Usage

```
subset(Skifti_data, volumes)
```

Arguments

`Skifti_data`	Skifti data object
`volumes`	selection

Value

Skifti data object of subset

`writeSkifti` *Write Skifti data*

Description

Write Skifti data

Usage

```
writeSkifti(
  Skifti_data,
  basename,
  overwrite = FALSE,
  compress = "none",
  verbose = FALSE
)
```

Arguments

Skifti_data	Skifti data object
basename	basename to write without suffix
overwrite	TRUE/FALSE(default) to overwrite existing data
compress	bz2/zip/none(default) to select compression method
verbose	TRUE/FALSE(default), for verbosity

Value

filename where Skifti data was written

Examples

```
#source('../../R/Skifti2Nifti.R')
#source('../../R/Nifti2Skifti.R')
library(RNifti)
data<-array(0,dim=list(10,10,10,10))
for(t in 1:10) {
  for(x in 1:10) {
    for(y in 1:10) {
      for(z in 1:10) {
        data[x,y,z,t]<-t+x
      }
    }
  }
}
data_Nifti<-RNifti::retrieveNifti(data)
RNifti::writeNifti(data_Nifti, "data_Nifti.nii.gz", template = NULL, datatype = "auto")

data_skeleton<-array(0,dim=list(10,10,10))
data_skeleton[5,5,5]<-1
data_skeleton[6,6,6]<-1
data_skeleton[7,7,7]<-1
data_skeleton_Nifti<-RNifti::retrieveNifti(data_skeleton)
RNifti::writeNifti(data_skeleton_Nifti, "data_skeleton_Nifti.nii.gz", datatype = "auto")

data_Skifti<-Nifti2Skifti(Nifti_data="data_Nifti.nii.gz",
                          Nifti_skeleton="data_skeleton_Nifti.nii.gz",
                          selected_volumes=c(1),
                          Nifti_labels=NULL,
```

```
                            write_coordinates=TRUE,
                            verbose=FALSE)

    # Create Skifti
    data_Nifti2<-Skifti2Nifti(data_Skifti)
    RNifti::writeNifti(data_Nifti2[[1]], "data_Nifti.nii.gz", datatype = "auto")
    data_Nifti2<-RNifti::readNifti("data_Nifti.nii.gz", internal = TRUE, volumes = NULL)
```

Index

concat, 2

Nifti2Skifti, 3

readSkifti, 5

save_skeleton, 6
Skifti2CSV, 7
Skifti2Nifti, 8
subset, 9

writeSkifti, 9