

Package ‘riot’

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Title R Inputs/Outputs for Tractography

Version 1.1.0

Description An input-output interface for reading in and writing out common VTK formats that store tractography data. This data comes in the form of 3D polygons with possibly attributes at each point. These are obtained via tracking algorithms from diffusion MRI and are a non-invasive way of studying brain structural connectivity.

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Encoding UTF-8

RoxygenNote 7.2.3

LinkingTo Rcpp

Imports Rcpp, readr, fs, cli, rlang, tibble, purrr, dplyr

URL <https://github.com/astamm/riot>

BugReports <https://github.com/astamm/riot/issues>

Suggests covr, testthat (>= 3.0.0), withr

SystemRequirements cmake (>= 3.15.0) used only but systematically on macOS and Linux platforms to build VTK from source.

Config/testthat/edition 3

NeedsCompilation yes

Author Aymeric Stamm [aut, cre] (<<https://orcid.org/0000-0002-8725-3654>>),
Jeroen Ooms [ctb],
Lee Thomason [ctb] (Author of the TinyXML2 C++ XML parser),
Tim Schäfer [ctb] (Author of the freesurferformats R package)

Maintainer Aymeric Stamm <aymeric.stamm@cnrs.fr>

Repository CRAN

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R topics documented:

| | |
|---------------------------|---|
| read_fascicles | 2 |
| write_fascicles | 2 |

Index **4**

read_fascicles *Import fascicles into R*

Description

Import fascicles into R

Usage

```
read_fascicles(file)
```

Arguments

file Path to the file containing the tractography data. Currently supported files are .vtk, .vtp, **medInria** .fds, .tck/.tsf **MRtrix**, .trk **TrackVis** file formats.

Value

A [tibble](#) storing the set of fascicles.

Examples

```
uf_left_vtk <- read_fascicles(system.file("extdata", "UF_left.vtk", package = "riot"))
```

write_fascicles *Export fascicles from R*

Description

Export fascicles from R

Usage

```
write_fascicles(x, file)
```

Arguments

x An object of class maf_df storing tractography data.

file Path to a file into which the tractography data should be saved. Currently supported files are .vtk, .vtp and **medInria** .fds file formats.

Value

The input tractography data (invisibly) so that the function can be used in pipes.

Examples

```
uf_left <- read_fascicles(system.file("extdata", "UF_left.vtp", package = "riot"))
## Not run:
out <- fs::file_temp(ext = ".vtp")
write_fascicles(uf_left, file = out)

## End(Not run)
```

Index

`read_fascicles`, [2](#)

`tibble`, [2](#)

`write_fascicles`, [2](#)