

Package ‘bayestraitr’

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Type Package
Title Functions for improving workflow between BayesTraits and R
Version 0.1.0
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Description This package holds functions for creating files to use as inputs into BayesTraits
and read files to bring BayesTraits output into R for further exploration of analyses.
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Encoding UTF-8
LazyData true
Depends
Suggests ape, testthat
Imports dplyr, stringr, tidyr, tidyverse, purrr
RoxygenNote 6.0.1

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bt_read.log	<i>Read BayesTraits Log files</i>
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Description

Given a the path of a BayesTraits log file, this function will find the start of the logged output and import the data as a data.frame into R.

Usage

```
bt_read.log(filename)
```

Arguments

filename the path to the BayesTraits log file

Value

A data.frame of the logs found in the BayesTraits log file & a list of settings taken from the header of the file

bt_read.schedule	<i>Read BayesTraits Schedule files</i>
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Description

Given a the path of a BayesTraits Schedule file, this function will find the start of the logged output and import the data as a data.frame into R.

Usage

```
bt_read.schedule(filename)
```

Arguments

filename the path to the BayesTraits Schedule file

Value

A data.frame of the schedule found in the BayesTraits schedule file & a list of settings taken from the header of the file

bt_read.stones	<i>Read BayesTraits Stones files</i>
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Description

Given a the path of a BayesTraits Stones file, this function will find the start of the stones output and import the data. It will also find the marginal likelihood and return both items in a list.

Usage

```
bt_read.stones(filename)
```

Arguments

filename the path to the BayesTraits Schedule file

Value

A data.frame of the schedule found in the BayesTraits schedule file & a list of settings taken from the header of the file

bt_write	<i>Write / Create BayesTraits tree and data files</i>
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Description

Given a tree & data.frame or vector, this function will create input files for BayesTraits with the suffix *.bttrees and *btdata. This function will also format the data file for BayesTrait (e.g. remove or replace NA values with "-")

Usage

```
bt_write(tree, data, variables, dir = "./", na.omit = FALSE, filename)
```

Arguments

tree	an object of class phylo or list of phylo objects
data	a data.frame
variables	a character string or character vector of the names of columns to subset to, alternatively you can use the numeric values to indicate the column
dir	the directory to save the output files to. Defaults to current directory
na.omit	a TRUE/FALSE argument to specify whether NA values should be removed from your final data file
optional:	used to name the output file. Will use variable names by default.

Value

two files will be saved to the specified directory *.bttrees holding the pruned tree files and *.btdata holding the subset and formatted data.

hello	<i>Hello, World!</i>
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Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

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