Package 'scopr'

September 19, 2019

Title Read Ethoscope Data

Date 2018-05-26

Version 0.3.2

Description Handling of behavioural data from the Ethoscope platform
(Geissmann, Garcia Rodriguez, Beckwith, French, Jamasb and Gile-
stro (2017) <DOI:10.1371/journal.pbio.2003026>).
Ethoscopes (<http://gilestrolab.github.io/ethoscope/>) are an open source/open hardware frame-
work made of
interconnected raspberry pis (<https://www.raspberrypi.org>) designed to quantify the be-
haviour of multiple
small animals in a distributed and real-
time fashion. The default tracking algorithm records primary variables
such as xy coordinates, dimensions and speed.
This package is part of the rethomics framework <http://rethomics.github.io/>.

Depends R (>= 3.00),
behavr

Imports data.table,
readr,
stringr,
RSQLite,
memoise

Suggests testthat,
covr,
knitr,
ggetho,
zeitgebr

License GPL-3

Encoding UTF-8

LazyData true

URL <https://github.com/rethomics/scopr>

BugReports <https://github.com/rethomics/scopr/issues>

RoxygenNote 6.0.1

Roxygen list(markdown = TRUE)

1

R **topics documented:**

Index   **9**

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experiment_info   *Retrieve information about an experiment*

Description

This function is used to obtain experimental information – such as *time and date* of the experiment, *acquisition device*, and *version of the software* – embedded in a result file (`.db`) generated by the ethoscope platform.

Usage

```
experiment_info(FILE)
```

Arguments

FILE   the name of the input file

Value

a list containing fields for metadata entries

See Also

- [load_ethoscope](#) – to load the actual data

- [list_result_files](#) – to list available files

```
link_ethoscope_metadata_remote
```
                            Link ethoscope metadata to the matching result files

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Description

These functions augment metadata so it can be subsequently loaded (with [load_ethoscope](#)).

Usage

```
link_ethoscope_metadata_remote(x, remote_dir, result_dir,
  index_file = "index.txt", overwrite_local = FALSE, verbose = TRUE)

link_ethoscope_metadata(x, result_dir = NULL, index_file = NULL)
```

Arguments

x	object such as a [data.frame,](#) or the name of a file (see detail)
remote_dir	the url of the result directory on the data server
result_dir	the directory where all data are saved
index_file	the name of an index_file, in `result_dir` (useful for loading remote data).
overwrite_local	
	whether to download all files. The default, FALSE, is to only fetch files if they are newer on the remote.
verbose	whether to print progress (a logical)

Details

These function will augment metadata from two different types of inputs (x):

1. A [data.frame](#) (recomended) In this case, the function will try to match requested data with data available on `result_dir`. The provided [data.table](#) has typically one row per requested individual and the columns (not necessarily in this order):

    - machine_name – the name of the machine in which the individual was (e.g. "ETHOSCOPE_001")
    - date – the start date of the experiment formatted as "YYYY-MM-DD"
    - region_id – the ROI in which the animal was. When *not provided, all regions are queried*.
    - time – the start time of the experiment formatted as "HH:MM:SS". When *not provided*, and multiple experiment for the same machine exist, *only the last one is loaded*.
    - ??? – any number of arbitrary columns* to associate conditions/treatments/genotypes/... to the previous columns.

2. The name of a CSV file that contains a table as described in 1.

3. A vector of .db files to be read.

Value

a [data.table::data.table](#) with the same rows as x, and extra columns for further data loading

References

- [metadata tutorial](#) – how to work with metadata

See Also

- [load_ethoscope](#) – to load the actual data
- [list_result_files](#) – to list available file

Examples

```
# Metadata with no region_id -> all regions will be loaded with the same metadata
dir <- paste0(scopr_example_dir(), "/ethoscope_results/")
data(no_region_id_metadata)
metadata <- link_ethoscope_metadata(no_region_id_metadata, dir)
print(metadata)

# Metadata with region_id ->  only stated regions will be loaded with specific metadata
data(region_id_metadata)
metadata <- link_ethoscope_metadata(region_id_metadata, dir)
print(metadata)

## Not run:
# If your files are stored on a remote server,
# this will download to a local directory only the needed files
REMOTE <- "ftp://a/remote/server/"
LOCAL_DIR <- "/where/I/store/the/data/"
metadata <- link_ethoscope_metadata_remote(region_id_metadata,
                                            REMOTE,
                                            LOCAL_DIR)


## End(Not run)
```

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list_result_files   *List all available result files*

Description

This function discovers all ethoscope result files and put them in a [data.table::data.table](#). This is useful to figure out when and which experiments were performed.

Usage

```
list_result_files(result_dir, index_file = NULL)
```

Arguments

`result_dir`	the root directory where all data are saved, or the path to a remote directory.
`index_file`	the name of an index_file, in `result_dir` (needed for loading remote data).

Value

a [data.table::data.table](#). Each row is a single experimental file, and columns describe details such as its `path`, start `date` and `time`, and the name and id of the ethoscope used.

See Also

- [load_ethoscope](#) – to load the actual data
- [experiment_info](#) – to show the metadata of a specific experiment

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load_ethoscope	*Load data from ethoscope result files*

Description

This function is used to import behavioural data generated by the [ethoscope platform](#). That is it loads multiple `.db` files into a single R [behavr::behavr](#) table.

Usage

```
load_ethoscope(metadata, min_time = 0, max_time = Inf,
  reference_hour = NULL, verbose = TRUE, columns = NULL, cache = NULL,
  ncores = 1, FUN = NULL, ...)
```

Arguments

`metadata`	[data.table::data.table](#) used to load data (see detail)
`min_time, max_time`	
	load only data between `min_time` and `max_time` (in seconds). This time is *relative to the start of the experiment*.
`reference_hour`	hour, in the day, to use as ZT0 reference. When unspecified, time will be relative to the start of the experiment.
`verbose`	whether to print progress (a logical)
`columns`	optional vector of columns to be selected from the db file. Time (t) is always implicitly selected. When `NULL` and if `FUN` is set, columns can be retrieved automatically (from the attributes of `FUN`).
`cache`	the name of a local directory to cache results for faster subsequent data loading.
`ncores`	number of cores to use for optional parallel processing (experimental).
`FUN`	function (optional) to transform the data from each individual immediately after is has been loaded.
`...`	extra arguments to be passed to `FUN`

Details

the linked metadata should be generated using link_ethoscope_metadata.

Value

A behavr table. In addition to the metadata, it contains the data, with the columns:

- `id` – autogenerated unique identifier, one per animal

- `t` – time (s)

- Several variables recorded by ethoscopes (position, angle, width/height and others), or computed by FUN. Distance units (e.g. xy position, height/width) are expressed as a fraction of the width of the ROI they originate from.

References

- behavr tutorial – how to work with the obtained behavr table

See Also

- behavr::behavr – to understand the output format

- experiment_info – to show information about a file/experiment

- list_result_files – to list available files

Examples

```
dir <- paste0(scopr_example_dir(), "/ethoscope_results/")
data(region_id_metadata)
metadata <- link_ethoscope_metadata(region_id_metadata, dir)
print(metadata)

# Default data loading
dt <- load_ethoscope(metadata)
dt

# We use reference hour to set zt0 to 09:00 GMT
dt <- load_ethoscope(metadata, reference_hour=9)
dt

# Only load x and y positions
dt <- load_ethoscope(metadata, columns=c("x", "y"), reference_hour=9)
dt
# apply function whilst loading the data
dt <- load_ethoscope(metadata, reference_hour=9, FUN=head)
dt
```

| no_region_id_metadata | *Simple toy metadata defining three experiments, with one condition (test) per experiment. Implicitly, 20 individuals are in each experiment It serves as a simple example.* |

Description

Simple toy metadata defining three experiments, with one condition (test) per experiment. Implicitly, 20 individuals are in each experiment It serves as a simple example.

Usage

```
no_region_id_metadata
```

Format

An object of class data.frame with 3 rows and 4 columns.

Author(s)

Quentin Geissmann

| region_id_metadata | *Simple toy metadata experimental conditions for 15 individuals in three experiments. the condition (test) is linked to the experiments, and another condition (treatment) is per individual. It serves as a simple example. #'* |

Description

Simple toy metadata experimental conditions for 15 individuals in three experiments. the condition (test) is linked to the experiments, and another condition (treatment) is per individual. It serves as a simple example. #'

Usage

```
region_id_metadata
```

Format

An object of class data.frame with 15 rows and 6 columns.

Author(s)

Quentin Geissmann

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scopr_example *Get path to scopr example*

Description

scopr comes with a sample DAM2 files in its `inst/extdata` directory. `scopr_example` allow make them easy to access.

Usage

```
scopr_example(path = NULL)

scopr_example_dir()
```

Arguments

path   Name of file. If `NULL`, the example files will be listed.

Examples

```
# list all files
scopr_example()
```

Index