Package 'scopr'

October 19, 2020

```
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 (<a href="http://gilestrolab.github.io/ethoscope/">http://gilestrolab.github.io/ethoscope/</a>) are an open source/open hardware frame-
      work made of
      interconnected raspberry pis (<a href="https://www.raspberrypi.org">https://www.raspberrypi.org</a>) 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 <a href="http://rethomics.github.io/">http://rethomics.github.io/</a>>.
Depends R (>= 3.00),
      behavr
Imports data.table,
      readr,
      stringr,
      RSQLite,
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Suggests testthat,
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```

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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

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):

- 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.

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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/")</pre>
data(no_region_id_metadata)
metadata <- link_ethoscope_metadata(no_region_id_metadata, dir)</pre>
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)</pre>
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,</pre>
                                             REMOTE,
                                             LOCAL_DIR)
## End(Not run)
```

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)
```

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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

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

data.table::data.table used to load data (see detail) metadata 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) optional vector of columns to be selected from the db file. Time (t) is always columns 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. number of cores to use for optional parallel processing (experimental). ncores FUN function (optional) to transform the data from each individual immediately after is has been loaded. extra arguments to be passed to FUN

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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</pre>
```

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()
```

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