Package 'damr'

October 15, 2017

Title Read Drosophila Activity Monitor Data

Date 2017-07-26

Version 0.0.0.9000

Description
Retreive behavioural data from the widely used Drosophila Activity Monitor System (DAMS).

Depends R (>= 3.00),
behavr,
data.table

Imports dplyr,
readr,
hms,
tidyr,
magrittr

Suggests testthat,
covr,
knitr

License GPL-3

Encoding UTF-8

LazyData true

URL https://github.com/rethomics/damr

BugReports https://github.com/rethomics/damr/issues

RoxygenNote 6.0.1

Roxygen list(markdown = TRUE)

R topics documented:

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damr_example   *Get path to damr example*

Description

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

Usage

```
damr_example(path = NULL)

damr_example_dir()
```

Arguments

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

Author(s)

Hadley Wickham (modified from readr)

Examples

```
# list all files
damr_example()
# get path to one file
damr_example("M014.txt")
# get the directory wih all the files
damr_example_dir()
```

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link_dam2_metadata   *Link DAM2 metadata to result files*

Description

This function checks and add columns to DAM2 metadata. This way, if can be subsequenctly loaded
(via [load_dam2](#)).

Usage

```
link_dam2_metadata(x, result_dir)
```

Arguments

x	object such as a data.frame, or the name of a file (see detail)
result_dir	the root directory where all daily data are saved

Details

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

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 individial 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 formated 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 formated as "HH:MM:SS". When *not provided*, and multiple expriment 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.

Each row of the metadata describes one individual with one set of conditions (when region_id is specified), or in each monitor (when it is not). It must have the following columns:

- file – the location of a data file (e.g. "Monitor3.txt").
- start_datetime – the first day **and time** of the requested experiment (e.g. "2014-12-28 18:00:00").
- stop_datetime – the last day and time of the requested experiment (e.g. "2014-12-30 19:00:00" or simply "2014-12-30").
- region_id – the channel (between 1 and 32) in which the animal was in (e.g. 20). region_id is optional. If not provided, all 32 channels are loaded *with the same conditions*.
- ??? *any number of arbitrary columns* to associate conditions/treatments/genotypes/... to the previous columns.

The time in data is expressed relatively to start_date. In other words, if you do circadian analysis, and your D->L`` transitions are at 09:00:00, you want to setstart_datetime = "YYY-MM-DD 09:00:00". The root directory is the folder where your files live. For instance,result_dir = "C:/where/I/Store/my/txt/files/"`

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_dam2 – to subsequently load the actual data

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load_dam2 *Load DAM2 data from one or several continuous files*

Description

Uses "linked metadata" to load data from DAM2 arrays.

Usage

```
load_dam2(metadata, FUN = NULL, ...)
```

Arguments

metadata	[data.table::data.table](#) used to load data (see detail)
FUN	function (optional) to transform the data from each animal immediately after is has been loaded.
...	extra arguments to be passed to FUN

Details

the linked metadata should be generated using [link_dam2_metadata](#).

Value

A [behavr::behavr](#) table. In addition to the metadata, it contains the data, whith the columns:

- id – autogenerated unique identifier, one per animal
- t – time
- activity – number of beam crosses

References

- [behavr tutorial](#) – how to work with the obtained [behavr](#) table

See Also

- [behavr::behavr](#) – the class of the resulting object
- [read_dam2_file](#) – to load data from a single file (without metadata)

Examples

```
# This is where our data lives
root_dir <- damr_example_dir()

# Metadata already made for us.
# It defines condition and genotype of each animal
data(single_file_metadata)
```

```
print(single_file_metadata)

metadata <- link_dam2_metadata(single_file_metadata, root_dir)

# we find and load the matching data
dt <- load_dam2(metadata)
print(dt)

# genotype and condition to our metadata:
print(dt[meta=TRUE])

# Just the first few reads, we run `head()` on each animal
dt <- load_dam2(metadata, FUN=head)
print(dt)
```

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read_dam2_file	*Reads data from a single DAM2 file*

Description

This function retreives activity data in a DAM2 file. It allows selection of a date range and channels (i.e. regions).

Usage

```
read_dam2_file(path, region_id = 1:32, start_datetime = -Inf,
  stop_datetime = +Inf, tz = "UTC")
```

Arguments

path	location of the file to read (character)
region_id	vector of unique regions to read
start_datetime, stop_datetime	
	the start and the end of an the experiment (see details)
tz	the timezone (see OlsonNames for a list)

Details

start_datetime and stop_datetime are formated as "YYYY-MM-DD HH:MM:SS". start_datetime is used as the reference time (ZT0). Therefore, if you are interested in circadian analysis and D->L transitions are at 10:00:00, you probably want to set start_datetime = "YYYY-MM-DD 10:00:00".

Value

A behavr table. The metadata contains an autogenerated id per animal. The data has the columns:

- id – autogenerated unique identifier, one per animal
- t – time
- activity – number of beam crosses

See Also

load_dam2 == to load data from many files and biological conditions using metadata

Examples

```
path <- damr_example("M064.txt")
dt <- read_dam2_file(path, region_id = c(1:3), start_datetime = "2017-06-30 15:00:00")
print(dt)
```

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single_file_metadata   *A simple toy metadata defining the experimental conditions of 32 an-*
                         imals monitored at the same time in a single DAM2 monitor. Each
                         animal has its own channel (region_id), as well as a condition and
                         genotype. It serves as an example for link_dam2_metadata.

Description

A simple toy metadata defining the experimental conditions of 32 animals monitored at the same
time in a single DAM2 monitor. Each animal has its own channel (region_id), as well as a condition
and genotype. It serves as an example for link_dam2_metadata.

Usage

```
single_file_metadata
```

Format

An object of class data.frame with 32 rows and 6 columns.

Author(s)

Quentin Geissmann

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two_files_metadata   *A toy metadata defining the experimental conditions of 64 animals*
                         monitored at the same time in two separate DAM2 monitors. Each
                         animal has its own channel (region_id), as well as a condition and
                         genotype. It serves as an example for link_dam2_metadata.

Description

A toy metadata defining the experimental conditions of 64 animals monitored at the same time in
two separate DAM2 monitors. Each animal has its own channel (region_id), as well as a condition
and genotype. It serves as an example for link_dam2_metadata.

Usage

```
two_files_metadata
```

Format

An object of class data.frame with 64 rows and 6 columns.

Author(s)

Quentin Geissmann

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