Package 'damr'

April 2, 2020

Title Interface to Drosophila Activity Monitor System Result Files

Date 2019-07-12

Version 0.3.4

Description Loads behavioural data from the widely used Drosophila Activity Monitor System (DAMS, TriKinetics <https://trikinetics.com/>) into the rethomics framework.

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

Imports readr

Suggests testthat,
covr,
knitr,
ggetho,
zeitgebr

License GPL-3

Encoding UTF-8

LazyData true

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

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

RoxygenNote 6.1.1

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()
```

---

link_dam_metadata *Link DAM2 or DAM5 metadata to result files*

Description

This function checks and add columns to DAMS metadata. This way, it can subsequently be loaded (via [load_dam](#)).

Usage

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

   - file – the name of a data file (e.g. "Monitor3.txt"), it has to exists in result_dir.
   - 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.

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

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 set start_datetime = "YYY-MM-DD 09:00:00". The result_directory`` is the folder conraining all result (.txt) files (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 used for further data loading

References

- [the rethomics workflow](#) – on the concept of "linking"
- [metadata tutorial](#) – how to work with metadata

See Also

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

| load_dam | *Load DAMS data from one or several continuous text files* |

Description

Uses "linked metadata" to load data from either single beam (DAM2) or multibeam (DAM5) arrays.

Usage

```
load_dam(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_dam_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

- damr tutorial – how to use this function in practice

See Also

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

Examples

```
# This is where our toy 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)
# Linking:
metadata <- link_dam_metadata(single_file_metadata, root_dir)

# We find and load the matching data
dt <- load_dam(metadata)
print(dt)
# An example of the use of FUN,
# we load only the first few reads by run `head()` on each animal,
# on the fly (no pun intended)
dt <- load_dam(metadata, FUN = head)
print(dt)
```

---

read_dam_file *Reads data from a single DAM2 single beam or a DAM5 multibeam file*

Description

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

Usage

```
read_dam_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 formatted 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_dam](#) – to load data from many files and biological conditions using metadata (the recommended alternative)

Examples

```
path <- damr_example("M064.txt")
dt <- read_dam_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_dam_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_dam_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_dam_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_dam_metadata.

Usage

```
two_files_metadata
```

Format

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

Author(s)

Quentin Geissmann

Index