

Package ‘damr’

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Title Interface to Drosophila Activity Monitor System Result Files

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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>

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Roxygen list(markdown = TRUE)

R topics documented:

| | |
|--------------------------------|---|
| damr_example | 2 |
| link_dam_metadata | 2 |
| load_dam | 3 |
| read_dam_file | 5 |
| single_file_metadata | 6 |
| two_files_metadata | 6 |

| | |
|--------------|----------|
| Index | 7 |
|--------------|----------|

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|--------------|---------------------------------|
| damr_example | <i>Get path to damr example</i> |
|--------------|---------------------------------|

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 with all the files
damr_example_dir()
```

| | |
|-------------------|---|
| link_dam_metadata | <i>Link DAM2 or DAM5 metadata to result files</i> |
|-------------------|---|

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 containing 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, with 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 | <i>Reads data from a single DAM2 single beam or a DAM5 multibeam file</i> |
|---------------|---|

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)
```

| | |
|----------------------|---|
| single_file_metadata | <i>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.</i> |
|----------------------|---|

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

| | |
|--------------------|---|
| two_files_metadata | <i>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.</i> |
|--------------------|---|

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

*Topic **datasets**

single_file_metadata, [6](#)

two_files_metadata, [6](#)

behavr, [5](#)

behavr::behavr, [4](#)

damr_example, [2](#)

damr_example_dir (damr_example), [2](#)

data.frame, [2](#), [3](#)

data.table, [3](#)

data.table::data.table, [3](#), [4](#)

link_dam2_metadata (link_dam_metadata),
[2](#)

link_dam_metadata, [2](#), [4](#), [6](#)

load_dam, [2](#), [3](#), [3](#), [5](#)

load_dam2 (load_dam), [3](#)

OlsonNames, [5](#)

read_dam2_file (read_dam_file), [5](#)

read_dam_file, [4](#), [5](#)

single_file_metadata, [6](#)

two_files_metadata, [6](#)