

Package ‘damr’

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Title Read Drosophila Activity Monitor Data

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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>

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R topics documented:

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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_dam2_metadata | <i>Link DAM2 metadata to result files</i> |
|--------------------|---|

Description

This function checks and add columns to DAM2 metadata. This way, it can subsequently be 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.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 setstart_datetime = "YYY-MM-DD 09:00:00". The result_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

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 [behr::behr](#) 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

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

See Also

- [behr::behr](#) – 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)

```

read_dam2_file

Reads data from a single DAM2 file

Description

This function retrieves 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 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 [behav](#) 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)
```

| | |
|----------------------|--|
| 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_dam2_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_dam2_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_dam2_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_dam2_metadata](#).

two_files_metadata

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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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