

# Package ‘damr’

November 28, 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** readr

**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 | <i>Get path to damr example</i> |
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### 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()
```

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|                    |   |
|--------------------|---|
| link_dam2_metadata | <i>Link DAM2 metadata to result files</i> |
|--------------------|---|

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### 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 <a href="#">data.frame</a> , 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 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

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load\_dam2

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*Load DAM2 data from one or several continuous files*


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## Description

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

## Usage

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

## Arguments

|          |  |
|----------|--|
| metadata | <a href="#">data.table::data.table</a> 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, with 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 | <i>Reads data from a single DAM2 file</i> |
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## 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 <a href="#">OlsonNames</a> 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\\_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 | <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 <a href="#">link_dam2_metadata</a>.</i> |
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### 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 | <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 <a href="#">link_dam2_metadata</a>.</i> |
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### 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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