

# Package ‘damr’

March 16, 2019

**Title** Interface to Drosophila Activity Monitor System Result Files

**Date** 2018-05-17

**Version** 0.3.2

**Description** Loads behavioural data from the widely used Drosophila Activity Monitor System (DAMS, TriKinetics) 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** 6.0.1

**Roxygen** list(markdown = TRUE)

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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.
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### 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_dam_metadata	<i>Link DAM2 or DAM5 metadata to result files</i>
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### 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 <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 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

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load\_dam

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


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## Description

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

## Usage

```
load_dam(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\\_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)
```

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read_dam_file	<i>Reads data from a single DAM2 single beam or a DAM5 multibeam file</i>
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## 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 <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\\_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	<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_dam_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\\_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	<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_dam_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\\_dam\\_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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