

# Package ‘damr’

August 31, 2017

**Title** Read Drosophila Activity Monitor Data

**Date** 2017-07-26

**Version** 0.0.0.9000

**Description** Retrieve behavioural data from the widely used Drosophila Activity Monitors.

**Depends** R (>= 2.10)

**Imports** behavr,  
data.table,  
dplyr,  
readr,  
hms,  
tidyr,  
magrittr

**Suggests** testthat

**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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|            |   |
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| query_dam2 | <i>Retrieves DAM2 data from one or several continuous files</i> |
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### Description

Uses a query mechanism to get data from a DAM2 array. This is useful when using the default behaviour of TriKinetics software where data is simply appended to a single long file per monitor.

### Usage

```
query_dam2(result_dir, query, FUN = NULL, ...)
```

## Arguments

|            |  |
|------------|--|
| result_dir | the root directory where all daily data are saved  |
| query      | <a href="#">data.frame</a> representing a formatted query used to request data (see detail)      |
| FUN        | function (optional) to transform the data from each animal immediately after it has been loaded. |
| ...        | extra arguments to be passed to FUN  |

## Details

query must be a [data.frame](#) (or [data.table](#)) object. Conceptually, each row of the query describes one animal with one set of conditions (when region\_id is specified), or in each monitor (when it is not). It must have the following columns:

- file – the location of a data file (e.g. "Monitor3.txt").
- 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.

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 10:00:00, you want to set start\_datetime = "YYY-MM-DD 10:00:00".

The root directory is the folder where your files live. For instance, result\_dir = "C:/where/I/Store/my/txt/files/"

## Value

A [behav](#) table. The metadata contains all the query columns and 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

[read\\_dam2\\_file](#) to load data from a single file (without a query).

## Examples

```
# This is where our data lives
root_dir <- damr_example_dir()

# A query already made for us.
# It defines condition and genotype of each animal
data(single_file_query)
print(single_file_query)
```

```
# we find and load the matching data
dt <- query_dam2(root_dir,single_file_query)
print(dt)

# genotype and condition to our metadata:
print(dt[meta=TRUE])

# Just the first few reads, we run `head()` on each animal
dt <- query_dam2(root_dir, single_file_query, FUN=head)
print(dt)
```

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read\_dam2\_file

*Reads data from a single DAM2 file*


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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 [behave](#) 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**

[query\\_dam2](#) to load data from many files and biological conditions using a query system

**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_query | <i>A simple toy query 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="#">query_dam2</a>.</i> |
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**Description**

A simple toy query 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 [query\\_dam2](#).

**Usage**

```
single_file_query
```

**Format**

An object of class `data.frame` with 32 rows and 6 columns.

**Author(s)**

Quentin Geissmann

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|                 |   |
|-----------------|---|
| two_files_query | <i>A toy query 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="#">query_dam2</a>.</i> |
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**Description**

A toy query 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 [query\\_dam2](#).

**Usage**

`two_files_query`

**Format**

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

**Author(s)**

Quentin Geissmann

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