

# Package ‘damr’

September 9, 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)

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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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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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