

# Package ‘behavr’

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**Title** Canonical Data Structure for Behavioural Data

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**Description**

Implements an S3 class based on data.table to store and process efficiently ethomics (high-throughput behavioural) data.

**Depends** R (>= 3.00),  
data.table

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methods

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covr,  
knitr

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**URL** <https://github.com/rethomics/behavr>

**BugReports** <https://github.com/rethomics/behavr/issues>

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## R topics documented:

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|        |   |
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| behavr | <i>An S3 class, based on <a href="#">data.table</a>, to store ethomics data</i> |
|--------|---|

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## Description

In modern behavioural biology, it is common to record long time series of several *variables* (such as position, angle, fluorescence and many others) on multiple individuals. In addition to large multivariate time series, each individual is associated with a set of *metavariabes* (i.e. sex, genotype, treatment and lifespan ), which, together, form the *metadata*. Metavariabes are crucial in so far as they generally "contain" the biological question. During analysis, it is therefore important to be able to access, alter and compute interactions between both variables and metavariabes. `behavr` is a class that facilitates manipulation and storage of metadata and data in the same object. It is designed to be both memory-efficient and user-friendly. For instance, it abstracts joins between data and metavariabes.

## Usage

```
behavr(x, metadata)
```

```
setbehavr(x, metadata)
```

```
is.behavr(x)
```

## Arguments

|                       |  |
|-----------------------|--|
| <code>x</code>        | <a href="#">data.table</a> containing all measurements |
| <code>metadata</code> | <a href="#">data.table</a> containing the metadata     |

## Details

A `behavr` table is a [data.table](#). Therefore, it can be used by any function that would work on a [data.frame](#) or a [data.table](#). Most of the operation such as variable creation, subsetting and joins are inherited from the [data.table](#) `[]` operator, following the convention `DT[i, j, by]` (see [data.table](#) package for detail). These operations are applied on the data. Metadata can be accessed using `meta=TRUE: DT[i, j, by, meta=TRUE]`, which allows extraction of subsets, creation of metavariabes, etc.

Both `x` and `metadata` should have a **column set as key** with **the same name** (typically named `id`). `behavr()` copies `x`, whilst `setbehavr()` uses reference. `metadata` is always copied.

## References

- The relevant [rethomic tutorial section](#) – about metavariabes and variables in this context

**See Also**

- [data.table](#) – on which behavr is based
- [xmv](#) – to join metavariables
- [rejoin](#) – to join all metadata
- [bind\\_behavr\\_list](#) – to merge several behavr tables

**Examples**

```
# We generate some metadata and data
set.seed(1)
met <- data.table::data.table(id = 1:5,
                              condition = letters[1:5],
                              sex = c("M", "M", "M", "F", "F"),
                              key = "id")

data <- met[ ,
             list(t = 1L:100L,
                  x = rnorm(100),
                  y = rnorm(100),
                  eating = runif(100) > .5 ),
             by = "id"]

# we store them together in a behavr object d
# d is a copy of the data
d <- behavr(data, met)
print(d)
summary(d)

#' # we can also convert data to a behavr table without copy:
setbehavr(data, met)
print(data)
summary(data)

### Operations are just like in data.table
# row subsetting:
d[t < 10]
# column subsetting:
d[, .(id, t, x)]
# making new columns inline:
d[, x2 := 1 - x]
### Using `meta = TRUE` applies the operation on the metadata
# making new metavariables:
d[, treatment := interaction(condition,sex), meta = TRUE]
d[meta = TRUE]
```

## Description

This function is typically used to summarise (i.e. computing an aggregate of) a variable (y) for bins of a another variable x (typically time).

## Usage

```
bin_apply(data, y, x = "t", x_bin_length = mins(30), wrap_x_by = NULL,
  FUN = mean, ...)
```

```
bin_apply_all(data, ...)
```

## Arguments

|              |   |
|--------------|---|
| data         | <a href="#">data.table</a> or <a href="#">behavr</a> table (see details)  |
| y            | variable or expression to be aggregated   |
| x            | variable or expression to be binned   |
| x_bin_length | length of the bins (same unit as x)   |
| wrap_x_by    | numeric value defining wrapping period. NULL, the default, means no wrapping.                                   |
| FUN          | function used to aggregate (e.g. <a href="#">mean</a> , <a href="#">median</a> , <a href="#">sum</a> and so on) |
| ...          | additional arguments to be passed to FUN  |

## Details

bin\_apply expects data from a single individual, whilst bin\_apply\_all works on multiple individuals identified by a unique key. wrapping is typically used to compute averages across several periods. For instance, wrap\_x\_by = days(1), means bins will aggregate values across several days. In this case, the resulting 'x' can be interpreted as "time relative to the onset of the day" (i.e. Zeitgeber Time).

## See Also

- [behavr](#) – the documentation of the behavr object

## Examples

```
metadata <- data.frame(id = paste0("toy_experiment|",1:5))
dt <- toy_activity_data(metadata, duration = days(4))

# average by 30min time bins, default
dt_binned <- bin_apply_all(dt, moving)
# equivalent to
dt_binned <- dt[, bin_apply(.SD, moving), by = "id"]

# if w ewant the opposite of moving:
dt_binned <- bin_apply_all(dt, !moving)

# More advanced usage
dt <- toy_dam_data(metadata, duration = days(4))
```

```
# nsum activity per 60 minutes
dt_binned <- bin_apply_all(dt,
  activity,
  x = t,
  x_bin_length = mins(60),
  FUN = sum)

# average activity. time in ZT
dt_binned <- bin_apply_all(dt,
  activity,
  x = t,
  wrap_x_by = days(1)
)
```

---

|                  |   |
|------------------|---|
| bind_behavr_list | <i>Put together a list of <a href="#">behavr</a> tables</i> |
|------------------|---|

---

## Description

Bind all rows of both data and metadata from a list of [behavr](#) tables into a single one. It checks keys, number and names of columns are the same across all data. In addition, it forbids to bind metadata if it would result in duplicates (same id in two different metadata).

## Usage

```
bind_behavr_list(l)
```

## Arguments

1                    list of [behavr](#)

## Value

a single [behavr](#) object

## See Also

- [behavr](#) – the documentation of the behavr object

## Examples

```
met <- data.table::data.table(id = 1:5,
  condition = letters[1:5],
  sex = c("M", "M", "M", "F", "F"),
  key = "id")
data <- met[,list(t = 1L:100L,
  x = rnorm(100),
  y = rnorm(100),
```

```

      eating = runif(100) > .5),
      by = "id"]
d1 <- behavr(data, met)

met[,id := id+5]
data[,id := id+5]
data.table::setkeyv(met, "id")
data.table::setkeyv(data, "id")

d2 <- behavr(data, met)
d_all <- bind_behavr_list(list(d1, d2))
print(d_all)

```

---

meta

*Retrieve and set metadata*


---

## Description

This function returns the metadata from a [behavr](#) table.

## Usage

```
meta(x)
```

```
setmeta(x, new)
```

## Arguments

|     |                               |
|-----|-------------------------------|
| x   | <a href="#">behavr</a> object |
| new | a new metadata table          |

## Value

a [data.table](#) representing the metadata in x

## See Also

- [behavr](#) – the documentation of the behavr object
- [xmv](#) – to join metavariables

## Examples

```

set.seed(1)
met <- data.table::data.table(id = 1:5,
                             condition = letters[1:5],
                             sex = c("M", "M", "M", "F", "F"),
                             key = "id")

data <- met[,
            list(t = 1L:100L,

```

```

      x = rnorm(100),
      y = rnorm(100),
      eating = runif(100) > .5 ),
      by = "id"]

d <- behavr(data, met)
## show metadata
meta(d)
# same as:
d[meta = TRUE]
## set metadata
m <- d[meta = TRUE]
# only id > 2 is kept
setmeta(d, m[id < 3])
meta(d)

```

---

|              |   |
|--------------|---|
| print.behavr | <i>Print and summarise a <a href="#">behavr</a> table</i> |
|--------------|---|

---

## Description

Print and summarise a [behavr](#) table

## Usage

```

## S3 method for class 'behavr'
print(x, ...)

## S3 method for class 'behavr'
summary(object, detailed = F, ...)

```

## Arguments

|           |                                       |
|-----------|---------------------------------------|
| x, object | <a href="#">behavr</a> table          |
| ...       | arguments passed on to further method |
| detailed  | whether summary should be consise     |

## See Also

- [behavr](#) – to generate x
- [print.default](#)
- [summary.default](#)

---

`rejoin`*Join data and metadata*

---

### Description

This function joins the data of a `behavr` table to its own metadata. When dealing with large data sets, it is preferable to keep metadata and data separate until a summary of data is computed. Indeed, joining many metavariables to very long time series may result in unnecessary – and prohibitively – large memory usage.

### Usage

```
rejoin(x)
```

### Arguments

`x` `behavr` object

### Value

a `data.table`

### See Also

- `behavr` – to formally create a `behavr` object

### Examples

```
set.seed(1)
met <- data.table::data.table(id = 1:5,
                              condition = letters[1:5],
                              sex = c("M", "M", "M", "F", "F"),
                              key = "id")

data <- met[,
            list(t = 1L:100L,
                 x = rnorm(100),
                 y = rnorm(100),
                 eating = runif(100) > .5 ),
            by = "id"]

d <- behavr(data, met)
summary_d <- d[, .(test = mean(x)), by = id]
rejoin(summary_d)
```



---

|           |   |
|-----------|---|
| stitch_on | <i>Stitch behavioural data by putting together the same individuals recorded over different experiments on the basis of a user defined identifier</i> |
|-----------|---|

---

## Description

This function can merge rows of data from the same individual that was recorded over multiple experiments. A usual scenario in which `stitch_on` can be used is when an experiment is interrupted and a new recording is started on the same biological subjects. Stitching assumes the users has defined a *unique id* in the metadata that refers to a specific individual. Then, if any data that comes from the same unique id, it is merged.

## Usage

```
stitch_on(x, on, time_ref = "datetime", use_time = F, time_variable = "t")
```

## Arguments

|               |  |
|---------------|--|
| x             | <a href="#">behavr</a> object  |
| on            | name of a metavariable serving as a unique id (per individual)         |
| time_ref      | name of a metavariable used to align time (e.g. "date", or "datetime") |
| use_time      | whether to use time as well as date                                    |
| time_variable | name of the variable describing time                                   |

## Details

When several rows of the metadata match a unique id (several experiments), the first (in time) experiment is used as the reference id. The data from the following one(s) will be added with a time lag equals to the difference between the values of `time_ref`. When data is not aligned to circadian time, it makes sense to set `use_time = TRUE`. Otherwise, the assumption is that the time is already aligned to a circadian reference, so only the date is used.

## Value

a [behavr](#) table

## See Also

- [behavr](#) – to formally create a `behavr` object

**Examples**

```

set.seed(1)
met1 <- data.table::data.table(uid = 1:5, id = 1:5,
                                condition = letters[1:5],
                                sex=c("M", "M", "M", "F", "F"),
                                key="id")
met2 <- data.table::data.table(uid = 1:4, id = 6:9,
                                condition = letters[1:4],
                                sex=c("M", "M", "M", "F"),
                                key="id")
met1[, datetime := as.POSIXct("2015-01-02")]
met2[, datetime := as.POSIXct("2015-01-03")]
met <- rbind(met1, met2)
data.table::setkeyv(met, "id")
t <- 1L:100L
data <- met[,list(t=t, x=rnorm(100), y=rnorm(100), eating=runif(100) > .5 ), by="id"]
d <- behavr(data, met)
summary(d)
d2 <- stitch_on(d, on ="uid")
summary(d2)

```

time\_conversion

*Time conversion utilities***Description**

Trivial functions to convert time to seconds – as behavr uses second as a conventional unit of time.

**Usage**

```
days(x)
```

```
hours(x)
```

```
mins(x)
```

**Arguments**

x                      numeric vector to be converted in second

**Details**

Most functions in the rethomics framework will use seconds as a unit of time. It is always preferable to call a function like `my_function(days(1.5))` rather than `my_function(60*60*24*1.5)`.

**Value**

number of seconds corresponding to x (1d = 86400s, 1h = 3600s and 1min = 60s)

---

|                   |   |
|-------------------|---|
| toy_activity_data | <i>Generate toy activity and sleep data mimicking Drosophila behaviour in tubes</i> |
|-------------------|---|

---

## Description

This function generates random data that emulates some of the features of fruit fly activity and sleep. This is designed **exclusively to provide material for examples and tests** as it generates "realistic" datasets of arbitrary length.

## Usage

```
toy_activity_data(metadata = NULL, seed = 1, rate_range = 1/c(60, 10),
  duration = days(5), sampling_period = 10, ...)

toy_ethoscope_data(...)

toy_dam_data(...)
```

## Arguments

|                 |  |
|-----------------|--|
| metadata        | <a href="#">data.frame</a> where every row defines an individual. Typically metadata has, at least, the column id. The default value (NULL), will generate data for a single animal. |
| seed            | random seed used (see <a href="#">set.seed</a> )   |
| rate_range      | parameter defining the boundaries of the rate at which animals wake up. It will be uniformly distributed between animals, but fixed within each animal.                              |
| duration        | length (in seconds) of the data to generate  |
| sampling_period | sampling period (in seconds) of the resulting data   |
| ...             | additional arguments to be passed to <code>simulate_animal_activity</code>   |

## Value

a [behavr](#) table with the metadata columns as metavariables. In addition to id and t columns different methods will output different variables:

- `toy_activity_data` will have asleep and moving (1/10s)
- `toy_dam_data` will have activity (1/60s)
- `toy_ethoscope_data` will have xy\_dist\_log10x1000, has\_interacted and x (2/1s)

## See Also

- [behavr](#) – to formally create a behavr object

## Examples

```
# just one animal, no metadata needed
dt <- toy_ethoscope_data(duration = days(3))

# advanced, using a metadata
metadata <- data.frame(id = paste0("toy_experiment|", 1:9),
  condition = c("A", "B", "C"))

metadata
# Data that could come from loadEthoscopeData:
dt <- toy_ethoscope_data(metadata, duration = days(1))
print(dt)

# Some DAM-like data
dt <- toy_dam_data(metadata, seed = 2, duration = days(3))
print(dt)

# data where behaviour is annotated e.g. by a classifier
dt <- toy_activity_data(metadata, 3)
print(dt)
```

---

xmv

---

*Expand a metavariable and map it against the data*


---

## Description

This function eXpands a MetaVariable from a parent `behavr` object. That is, it matches this variable (from metadata) to the data *by id*.

## Usage

```
xmv(var)
```

## Arguments

`var`                      the name of the variable to be extracted

## Details

This function *can only be called within between the [] of a parent `behavr` object*. It is intended to facilitate operations between data and metadata. For instance, when one wants to modify a column of the data according to a metavariable.

## Value

a vector of the same type as `var`, but of the same length as the number of row in the parent data. As each row of data is matched against metadata for this specific variable.

### See Also

- [behavr](#) – to formally create a behavr object
- [rejoin](#) – to join all metadata with data

### Examples

```
#### First, we create some data

library(data.table)
set.seed(1)
data <- data.table(
  id = rep(c("A", "B"), times = c(10,26)),
  t = c(1:10, 5:30),
  x = rnorm(36), key = "id"
)

metadata = data.table(id = c("A", "B"),
  treatment = c("w", "z"),
  lifespan = c(19, 32),
  ref_x = c(1, 0),
  key = "id")
dt <- behavr(data, metadata)
summary(dt)

#### Subsetting using metadata

dt[xmv(treatment) == "w"]
dt[xmv(treatment) == "w"]
dt[xmv(lifespan) < 30]

#### Allocating new columns using metavariable

# Just joining lifespan (not necessary)
dt[, lif := xmv(lifespan)]
print(dt)
# Anonymously (more useful)
dt[, x2 := x - xmv(ref_x)]
print(dt)
```

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