Package 'behavr'

August 10, 2017

Title Cannonical Data Structure for Behavioural Data

Date 2017-07-25

Version 0.3.0.9003

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

Imports data.table,
hms,
methods

Suggests testthat

License GPL-3

Encoding UTF-8

LazyData true

URL https://github.com/rethomics/behavr

BugReports https://github.com/rethomics/behavr/issues

RoxygenNote 6.0.1

Roxygen list(markdown = TRUE)

R topics documented:

behavr *An S3 class, based on data.table, to store ethomics data*

Description

In modern behavioural biology, it is common to record long time series of several *variables* (such as position, angle, fluorescence and so on) on multiple individuals. In addition to large multivariate time series, each individual is associated with a set of *metavariables* (i.e. sex, genotype, treatment and lifespan), which, together, form the *metadata*. Metavariables 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 metavariables. `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 metavariables.

Usage

```
behavr(x, metadata)

is.behavr(x)
```

Arguments

`x`	data.table containing all measurments
`metadata`	data.table containing the metadata

Details

Both `x` and `metadata` should have a **column set as key** with **the same name** (typically named `id`).

See Also

- the `behavr` webpage
- 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

```
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)
print(d)
summary(d)
```

`bind_behavr_list` *Put together a list of behavr tables*

Description

Bind all rows of both data and metadata from a list of behavr tables into a single behavr table. 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

`l`	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)
```

`bin_apply` *Bin a variable (typically time) and compute an aggregate for each bin*

Description

This function is typically used to summarise (i.e. computing an aggreate 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, string_xy = FALSE, ...)

bin_apply_all(data, ...)
```

Arguments

`data`	data.table or behavr table (see details)
`y`	variable to be aggregated
`x`	variable to be binned
`x_bin_length`	length of the bins (same unit as 'x")
`wrap_x_by`	numeric value defining wrapping period. `NULL`, the defsult, means no wrapping.
`FUN`	function used to aggregate (e.g. mean, median, sum and so on)
`string_xy`	logical whether the names of the variables are quoted
`...`	additional arguments to be passed to `FUN`

Details

`bin_apply` expects data from a single individal. `bin_apply_all` works on multiple individuals identified by a unique key. `wrapping` is typically used to compute averages accross several periods. For instance,`wrap_x_by = days(1)`, means bins will aggreate values accross several days. In this case, the resulting x can be interpreted as "time relative to the onset of the day" (i.e. ZT).

Examples

```
query <- data.frame(experiment_id = "toy_experiment",
                    region_id = 1:5)
dt <- toy_activity_data(query, 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"]

# More advanced usage
dt <- toy_dam_data(query, 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)
                           )
```

`meta` *Retreive and set metadata*

Description

This function returns the meta data from a behavr object

Usage

```
meta(x)

setmeta(x, new)
```

Arguments

`x`	a behavr object
`new`	a new metadata table

Value

a data.table representing the metadata in `x`

See Also

behavr to generate a behavr object, xmv to map metavariables to data

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 *Print and summarise a behavr table*

Description

Print and summarise a behavr table

Usage

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

## S3 method for class 'behavr'
summary(object, ...)
```

Arguments

x, object	behavr table
...	arguments passed on to further method

See Also

- behavr – to generate x
- print.default
- summary.default

`rejoin` *Join data and metadata*

Description

This function joins the data of a behavr object to its 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 large memory usage.

Usage

```
rejoin(x)
```

Arguments

x	a behavr object

Value

a data.table

See Also

behavr to generate 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)
```

time_conversion *Time conversion utilities*

Description

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

Usage

```
days(x)

hours(x)

mins(x)
```

Arguments

x	a numerical vector to be converted in second

Details

Most fucntions in the rethomics framewhor 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 *Generate toy activity and sleep data mimiking Drosophila behaviour in tubes*

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

toy_ethoscope_data(...)

toy_dam_data(...)
```

Arguments

query	query (i.e. a dataframe where every row defines an animal). Typically queries have, at least, the columns experiment_id and region_id. The default value (NULL), will generate data for a single animal.
seed	random seed used (see set.seed)
rate_range	a parameter defining the boundaries of rate at which animals wake up. It will be uniformely distributed between animals, but fixed for 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 simulate_animal_activity

Value

A behavr table with the query 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)

Examples

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

# advanced, using a query
query<- data.frame(experiment_id = "toy_experiment",
                   region_id = 1:10,
                   condition = c("A", "B"))


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

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

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

xmv *Extract 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 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)
```

Index