# Package 'scopr'

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**Title** Read Ethoscope Data

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**Version** 0.3.6

**Description** Handling of behavioural data from the Ethoscope platform
(Geissmann, Garcia Rodriguez, Beckwith, French, Jamasb and Gilestro (2017) <DOI:10.1371/journal.pbio.2003026>).
Ethoscopes (<https://ethoscope.net>) are an open source/open hardware framework made of interconnected raspberry pis (<https://www.raspberrypi.org>) designed to quantify the behaviour of multiple small animals in a distributed and real-time fashion. The default tracking algorithm records primary variables such as xy coordinates, dimensions and speed.
This package is part of the rethomics framework <https://rethomics.github.io/>.

**Depends** R (>= 3.00), behavr

**Imports** data.table, readr, stringr, RSQLite, memoise

**Suggests** testthat, covr, knitr, ggetho, zeitgebr

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**URL** https://github.com/rethomics/scopr

**BugReports** https://github.com/rethomics/scopr/issues

**Config/roxygen2/version** 8.1.1

**NeedsCompilation** no

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`experiment_info` *Retrieve information about an experiment*

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## Description

This function is used to obtain experimental information – such as *time and date* of the experiment, *acquisition device*, and *version of the software* – embedded in a result file (`.db`) generated by the ethoscope platform.

## Usage

```
experiment_info(FILE)
```

## Arguments

| | |
|---|---|
| `FILE` | the name of the input file |

## Value

a list containing fields for metadata entries

## See Also

- load_ethoscope – to load the actual data
- list_result_files – to list available files

`link_ethoscope_metadata_remote` *Link ethoscope metadata to the matching result files*

## Description

These functions augment metadata so it can be subsequently loaded (with load_ethoscope).

## Usage

```
link_ethoscope_metadata_remote(
  x,
  remote_dir,
  result_dir,
  index_file = "index.txt",
  overwrite_local = FALSE,
  verbose = TRUE
)

link_ethoscope_metadata(x, result_dir = NULL, index_file = NULL)
```

## Arguments

| | |
|---|---|
| `x` | object such as a data.frame, or the name of a file (see detail) |
| `remote_dir` | the url of the result directory on the data server |
| `result_dir` | the directory where all data are saved |
| `index_file` | the name of an index_file, in `result_dir` (useful for loading remote data). |
| `overwrite_local` | whether to download all files. The default, `FALSE`, is to only fetch files if they are newer on the remote. |
| `verbose` | whether to print progress (a logical) |

## Details

These function will augment metadata from two different types of inputs (`x`):

1. A data.frame (recomended) In this case, the function will try to match requested data with data available on `result_dir`. The provided data.table::data.table has typically one row per requested individual and the columns (not necessarily in this order):
   - `machine_name` – the name of the machine in which the individual was (e.g. `"ETHOSCOPE_001"`)
   - `date` – the start date of the experiment formatted as `"YYYY-MM-DD"`
   - `region_id` – the ROI in which the animal was. When *not provided, all regions are queried*.
   - `time` – the start time of the experiment formatted as "HH:MM:SS". When *not provided*, and multiple experiment for the same machine exist, *only the last one is loaded*.

- ??? – 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.
3. A vector of `.db` files to be read.

## Value

a data.table::data.table with the same rows as x, and extra columns for further data loading

## References

- metadata tutorial – how to work with metadata

## See Also

- load_ethoscope – to load the actual data
- list_result_files – to list available file

## Examples

```
# Metadata with no region_id -> all regions will be loaded with the same metadata
dir <- paste0(scopr_example_dir(), "/ethoscope_results/")
data(no_region_id_metadata)
metadata <- link_ethoscope_metadata(no_region_id_metadata, dir)
print(metadata)

# Metadata with region_id ->  only stated regions will be loaded with specific metadata
data(region_id_metadata)
metadata <- link_ethoscope_metadata(region_id_metadata, dir)
print(metadata)

## Not run:
# If your files are stored on a remote server,
# this will download to a local directory only the needed files
REMOTE <- "ftp://a/remote/server/"
LOCAL_DIR <- "/where/I/store/the/data/"
metadata <- link_ethoscope_metadata_remote(region_id_metadata,
                                           REMOTE,
                                           LOCAL_DIR)


## End(Not run)
```

## list_result_files *List all available result files*

### Description

This function discovers all ethoscope result files and put them in a data.table::data.table. This is useful to figure out when and which experiments were performed.

### Usage

```
list_result_files(result_dir, index_file = NULL)
```

### Arguments

| | |
|---|---|
| result_dir | the root directory where all data are saved, or the path to a remote directory. |
| index_file | the name of an index_file, in result_dir (needed for loading remote data). |

### Value

a data.table::data.table. Each row is a single experimental file, and columns describe details such as its path, start date and time, and the name and id of the ethoscope used.

### See Also

- load_ethoscope – to load the actual data
- experiment_info – to show the metadata of a specific experiment

## load_ethoscope *Load data from ethoscope result files*

### Description

This function is used to import behavioural data generated by the ethoscope platform. That is it loads multiple .db files into a single R behavr::behavr table.

### Usage

```
load_ethoscope(
  metadata,
  min_time = 0,
  max_time = Inf,
  reference_hour = NULL,
  verbose = TRUE,
  columns = NULL,
  cache = NULL,
```

```
  ncores = 1,
  FUN = NULL,
  map_arg = NULL,
  ...
)
```

## Arguments

| | |
|---|---|
| metadata | data.table::data.table used to load data (see detail) |
| min_time, max_time | load only data between min_time and max_time (in seconds). This time is *relative to the start of the experiment*. |
| reference_hour | hour, in the day, to use as ZT0 reference. When unspecified, time will be relative to the start of the experiment. |
| verbose | whether to print progress (a logical) |
| columns | optional vector of columns to be selected from the db file. Time (t) is always implicitly selected. When NULL and if FUN is set, columns can be retrieved automatically (from the attributes of FUN). |
| cache | the name of a local directory to cache results for faster subsequent data loading. |
| ncores | number of cores to use for optional parallel processing (experimental). |
| FUN | function (optional) to transform the data from each individual immediately after is has been loaded. |
| map_arg | a list to map FUN arguments to metavariables values. See details |
| ... | extra arguments to be passed to FUN |

## Details

the linked metadata should be generated using link_ethoscope_metadata. map_arg is a list of the form list(fun_arg = "metavariable"). When provided, FUN will set specific arguments (fun_arg) to the value of a (quoted) metavariable.

## 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 (s)
- Several variables recorded by ethoscopes (position, angle, width/height and others), or computed by FUN. Distance units (e.g. xy position, height/width) are expressed as a fraction of the width of the ROI they originate from.

## References

- behavr tutorial – how to work with the obtained behavr::behavr table

## See Also

- behavr::behavr – to understand the output format
- experiment_info – to show information about a file/experiment
- list_result_files – to list available files

## Examples

```
dir <- paste0(scopr_example_dir(), "/ethoscope_results/")
data(region_id_metadata)
metadata <- link_ethoscope_metadata(region_id_metadata, dir)
print(metadata)

# Default data loading
dt <- load_ethoscope(metadata)
dt

# We use reference hour to set zt0 to 09:00 GMT
dt <- load_ethoscope(metadata, reference_hour=9)
dt

# Only load x and y positions
dt <- load_ethoscope(metadata, columns=c("x", "y"), reference_hour=9)
dt
# apply function whilst loading the data
dt <- load_ethoscope(metadata, reference_hour=9, FUN=head)
dt
```

---

`no_region_id_metadata` *Simple toy metadata defining three experiments, with one condition (`test`) per experiment. Implicitly, 20 individuals are in each experiment It serves as a simple example.*

---

## Description

Simple toy metadata defining three experiments, with one condition (`test`) per experiment. Implicitly, 20 individuals are in each experiment It serves as a simple example.

## Usage

```
no_region_id_metadata
```

## Format

An object of class `data.frame` with 3 rows and 4 columns.

## Author(s)

Quentin Geissmann

region_id_metadata *Simple toy metadata experimental conditions for 15 individuals in three experiments. the condition (*test*) is linked to the experiments, and another condition (*treatment*) is per individual. It serves as a simple example. #'*

## Description

Simple toy metadata experimental conditions for 15 individuals in three experiments. the condition (test) is linked to the experiments, and another condition (treatment) is per individual. It serves as a simple example. #'

## Usage

```
region_id_metadata
```

## Format

An object of class data.frame with 15 rows and 6 columns.

## Author(s)

Quentin Geissmann

scopr_example *Get path to scopr example*

## Description

scopr comes with a sample DAM2 files in its inst/extdata directory. scopr_example allow make them easy to access.

## Usage

```
scopr_example(path = NULL)

scopr_example_dir()
```

## Arguments

| | |
|---|---|
| path | Name of file. If NULL, the example files will be listed. |

## Examples

```
# list all files
scopr_example()
```

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