

# Package ‘scopr’

September 4, 2017

**Title** Read Ethoscope Data

**Date** 2017-08-08

**Version** 0.0.0.9000

## Description

Retreive behavioural data from the Ethoscope platform (<http://gilestrolab.github.io/ethoscope/>).

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

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

**Suggests** testthat

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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

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

**RoxygenNote** 6.0.1

**Roxygen** list(markdown = TRUE)

## R topics documented:

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|                   |  |
|-------------------|--|
| list_result_files | <i>List all available result files</i> |
|-------------------|--|

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**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                                |
| index_file | the name of an index_file, in result_dir (useful 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**

- [query\\_ethoscopes](#) – to load the actual data
- [parse\\_query](#) – to generate a query
- [read\\_metadata](#) – to show the metadata of a specific experiment

**Examples**

```
todo
```

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|                 |  |
|-----------------|--|
| make_index_file | <i>Used by platform administrators to make an index file listing all experiments</i> |
|-----------------|--|

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### Description

This function builds an index which lists the available experimental file. It is useful to build indices when outing data on a remote server (e.g. FTP).

### Usage

```
make_index_file(result_dir, index_file = "index.txt")
```

### Arguments

|            |  |
|------------|--|
| result_dir | the root directory where all data are saved                                |
| index_file | the name of an index_file, in result_dir (useful for loading remote data). |

### Value

the path to the index file written (in result\_dir))

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|                    |   |
|--------------------|---|
| no_region_id_query | <i>A simple toy query defining three experiments to query, with one condition (test) per experiment. Implicitly, 20 animals are in each experiment It serves as a simple example.</i> |
|--------------------|---|

---

### Description

A simple toy query defining three experiments to query, with one condition (test) per experiment. Implicitly, 20 animals are in each experiment It serves as a simple example.

### Usage

```
no_region_id_query
```

### Format

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

### Author(s)

Quentin Geissmann

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 parse\_query

*Build a query for loading ethoscope data*


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## Description

These functions make a query table, which is essential for subsequent loading of ethoscope data (via [query\\_ethoscopes](#)).

## Usage

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

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

## Arguments

|                 |  |
|-----------------|--|
| x               | object such as a <a href="#">data.frame</a> , or the name of a file (see detail)                           |
| result_dir      | the root directory where all data are saved  |
| index_file      | the name of an index_file, in result_dir (useful for loading remote data).                                 |
| remote_dir      | the url of the result directory on the data server   |
| 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 generate a query from three different types of inputs:

1. A vector of names of .db files (only for local queries with parse\_query)
2. 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](#) 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 formated 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 formated as "HH:MM:SS". *When not provided, and multiple expriment 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.
3. The name of a CSV file that contains a table as described in 2.

**Value**

a `data.table::data.table`. It contains the columns:

- `path` – the file to retrieve the data from
- `experiment_id` – an autogenerated unique id for the experiment
- `region_id` – a unique identifier of each individual (region of interest) within an experiment
- Variables already present in `x` (if `x` was a `data.frame`).

**References**

- `TODO` – to understand the magical power of the query system!

**See Also**

- [query\\_ethoscopes](#) – to load the actual data
- [list\\_result\\_files](#) – to list available file

**Examples**

```
# a query with no region_id, all regions will be loaded with the same metadata
dir <- paste0(scopr_example_dir(), "/ethoscope_results/")
data(no_region_id_query)
query <- parse_query(no_region_id_query, dir)
print(query)
# a query with region_id, only stated regions will be loaded with specific metadata
data(region_id_query)
query <- parse_query(region_id_query, dir)
print(query)
```

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query\_ethoscopes

*Read data from ethoscope result files*


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**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**

```
query_ethoscopes(query, min_time = 0, max_time = Inf,
  reference_hour = NULL, verbose = TRUE, columns = NULL, cache = NULL,
  ncores = 1, FUN = NULL, ...)
```

## Arguments

|                |  |
|----------------|--|
| query          | <a href="#">data.table::data.table</a> obtained by <a href="#">parse_query</a>                                     |
| min_time       | Exclude data before min_time (in seconds). This time is <i>relative to the start of the experiment</i> .           |
| max_time       | Exclude data after max_time (in seconds). It is also 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        | optionnal vector of columns to be selected from the db file. Time (t) is always implicitly selected.               |
| cache          | the name of a local directory to cache results for faster subsequent data loading                                  |
| ncores         | number of cores to use for optionnal parallel processing   |
| FUN            | function (optional) to transform the data from each individual immediately after it has been loaded.               |
| ...            | extra arguments to be passed to FUN  |

## Details

todo

## Value

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

## References

- todo

## See Also

- [behavr::behavr](#) – to understand the output format
- [parse\\_query](#) – to generate a query
- [read\\_metadata](#) – to show the metadata of a specific experiment
- [list\\_result\\_files](#) – to list available files

**Examples**

```

dir <- paste0(scopr_example_dir(), "/ethoscope_results/")
data(region_id_query)
query <- parse_query(region_id_query, dir)
print(query)

# default data loading
dt <- query_ethoscopes(query)
dt

# we use reference hour to set zt0 to 09:00 GMT
dt <- query_ethoscopes(query, reference_hour=9)
dt

#' # only load x and y positions
dt <- query_ethoscopes(query, columns=c("x", "y"), reference_hour=9)
dt
# apply function whilst loading the data
# todo use sleep
dt <- query_ethoscopes(query, reference_hour=9, FUN=head)
dt

```

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|               |  |
|---------------|--|
| read_metadata | <i>Retrieve metadata from an ethoscope result file</i> |
|---------------|--|

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**Description**

This function is used to obtain metadata – 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**

```
read_metadata(FILE)
```

**Arguments**

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

**Value**

a list containing fields for metadata entries

**See Also**

- [query\\_ethoscopes](#) – to load the actual data
- [list\\_result\\_files](#) – to list available files

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|                 |  |
|-----------------|--|
| region_id_query | <i>A simple toy query experimental conditions for 15 animals in three experiments. the condition (test) is linked to the experiments, and another condition (treatment) is per animal. It serves as a simple example. #'</i> |
|-----------------|--|

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### Description

A simple toy query experimental conditions for 15 animals in three experiments. the condition (test) is linked to the experiments, and another condition (treatment) is per animal. It serves as a simple example. #'

### Usage

```
region_id_query
```

### Format

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

### Author(s)

Quentin Geissmann

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|               |                                  |
|---------------|----------------------------------|
| scopr_example | <i>Get path to scopr example</i> |
|---------------|----------------------------------|

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### 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.

### Author(s)

Hadley Wickham (modified from `readr`)



### **Examples**

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

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