

Package ‘scopr’

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Title Read Ethoscope Data

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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>

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R topics documented:

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

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
```

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

Description

This function builds an index which lists the available experimental file. It is useful to build indices when outting 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))

| | |
|--------------------|---|
| 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

| | |
|-------------|---|
| parse_query | <i>Build a query for loading ethoscope data</i> |
|-------------|---|

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 data.frame , 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](#) (recommended) 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 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.
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)
```

| | |
|------------------|--|
| query_ethoscopes | <i>Read data from ethoscope result files</i> |
|------------------|--|

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 | <code>data.table::data.table</code> obtained by <code>parse_query</code> |
| 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 is 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
```

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

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

| | |
|-----------------|--|
| 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> |
|-----------------|--|

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

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

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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