Package ‘mgi.report.reader’

July 7, 2024

Title  Read Mouse Genome Informatics Reports

Version  0.1.3

Description  Provides readers for easy and consistent importing of
Mouse Genome Informatics (MGI) report files:
<https://www.informatics.jax.org/downloads/reports/index.html>. These data
are provided by Baldarelli RM, Smith CL, Ringwald M, Richardson JE, Bult CJ,
Mouse Genome Informatics Group (2024) <doi:10.1093/genetics/iyae031>.

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Encoding  UTF-8

RoxygenNote  7.3.1

Depends  R (>= 2.10)

LazyData  true

Imports  data.table, dplyr, httr2, memoise, rlang, stringr, tibble,
vroom

URL  https://www.pattern.institute/mgi.report.reader/,
https://github.com/patterninstitute/mgi.report.reader/

BugReports  https://github.com/patterninstitute/mgi.report.reader/issues

Config/Needs/website  rmarkdown, patterninstitute/chic

Suggests  testthat (>= 3.0.0), tidyr

Config/testthat/edition  3

NeedsCompilation  no

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Description

`chromosomes()` returns mouse chromosome names.

Usage

`chromosomes(autosomal = TRUE, sexual = TRUE, mitochondrial = TRUE)`

Arguments

- `autosomal` Whether to include the autosomal chromosomes (1 thru 19).
- `sexual` Whether to include the sexual chromosomes (X and Y).
- `mitochondrial` Whether to include the mitochondrial chromosome (MT).

Value

A character vector of mouse chromosome names, or a subset thereof, or an empty character vector.
**feature_types**

**Examples**

```r
# All chromosomes.
chromosomes()

# Autosomal chromosomes.
chromosomes(autosomal = TRUE, sexual = FALSE, mitochondrial = FALSE)
```

---

**feature_types**  
*Genome Feature types*

---

**Description**

`feature_types()` returns different types of gene and genome features. For feature type definitions, see `?feature_type_definitions`.

**Usage**

`feature_types()`

**Value**

A character vector of feature types’ names.

**Examples**

`feature_types()`

---

**feature_type_definitions**  
*Genome Feature Type Definitions*

---

**Description**

A dataset containing different types of gene and genome features along with their Sequence Ontology (SO) identifiers and definitions.

**Usage**

`feature_type_definitions`
Format

A tibble with 71 rows and 3 variables:

- **feature_type** Character. The type of gene or genome feature.
- **so_id** Character. The Sequence Ontology identifier associated with the feature type.
- **definition** Character. The definition of the feature type.

Source

The table in [https://www.informatics.jax.org/userhelp/GENE_feature_types_help.shtml](https://www.informatics.jax.org/userhelp/GENE_feature_types_help.shtml) and a few other terms found in MGI reports.

Examples

```r
print(feature_type_definitions, n = Inf)
```

<table>
<thead>
<tr>
<th>marker_types</th>
<th>Genetic marker types</th>
</tr>
</thead>
</table>

Description

*marker_types()* returns MGI marker types. See *marker_type_definitions* for the meaning of each type.

Usage

`marker_types()`

Value

A character vector.

Examples

`marker_types()`
Genetic Marker Type Definitions

Description
A dataset of marker types definitions. Use instead `marker_types()` for the marker type names as a single character vector.

Usage
`marker_type_definitions`

Format
A `tibble` with 10 rows and 2 variables:
- `marker_type` Character. The type of genetic marker.
- `definition` Character. The definition of the marker type.

Source
The cross-references in the entry definition for marker at MGI glossary: https://www.informatics.jax.org/glossary(marker/).

Examples
`print(marker_type_definitions, n = Inf)`

---

Browse MGI markers identifiers online

Description
`open_marker_id_in_mgi()` launches the web browser and opens a tab for each MGI accession identifier on the Mouse Genome Informatics web interface: https://www.informatics.jax.org.

Usage
`open_marker_id_in_mgi(marker_id)`

Arguments
- `marker_id` A character vector. MGI accession identifiers.
Value

Returns TRUE if successful, or FALSE otherwise. But note that this function is run for its side effect of launching the browser.

Examples

# Read about Acta1 (actin alpha 1, skeletal muscle) online.
open_marker_symbol_in_mgi("Acta1")

# `open_marker_symbol_in_mgi()` is vectorized, so you can open multiple pages.
# NB: think twice if you really need to open many tabs at once.
open_marker_symbol_in_mgi(c("Acta1", "Hes1"))
read_report

**Read an MGI report**

**Description**

`read_report()` imports data from an MGI report into R as a tidy data set.

You may call this function in two alternative ways:

- Using `report_key`: this is the easiest approach. A report key maps to a report currently hosted at MGI, e.g. `read_report("marker_list2")` reads MRK_List2.rpt directly from MGI server into R. See Supported Reports below for options.

- Using `report_file` and `report_type`: this approach is more flexible as you can read directly from a file or URL.

**Supported Reports:**
The set of currently supported reports:

```
reports
#> # A tibble: 13 x 4
#> report_key report_file          report_type report_name                  
#> <chr>       <chr>               <chr>           <chr>                      
#> 1 marker_list1 MRK_List1.rpt    MRK_List1       Mouse Gene~               
#> 2 marker_list2 MRK_List2.rpt    MRK_List2       Mouse Gene~               
#> 3 marker_coordinates MGI_MRK_Coord.rpt MGI_MRK_Coord MGI Marker~ 
#> 4 gene_model_coordinates MGI_Gene_Model_Coord.rpt MGI_Gene_Model_Coord MGI Marker~ 
#> 5 sequence_coordinates MGI_GTGUP.gff MGI_GTGUP MGI Sequence~ 
#> 6 genbank_refseq_ensembl_ids MRK_Sequence.rpt MRK_Sequence MGI Marker~ 
#> 7 swiss_trembl_ids MRK_SwissProt_TrEMBL.rpt MRK_SwissProt MGI Marker~ 
#> 8 swiss_prot_ids MRK_SwissProt.rpt MRK_SwissProt MGI Marker~ 
#> 9 gene_trap_ids MRK_GeneTrap.rpt MRK_GeneTrap MGI Marker~ 
#> 10 ensembl_ids MRK_ENSEMBL.rpt MRK_ENSEMBL MGI Marker~ 
#> 11 biotype_conflicts MGI_BioTypeConflict.rpt MGI_BioTypeConflict MGI Marker~ 
#> 12 primers PRB_PrimerSeq.rpt PRB_PrimerSeq MGI Marker~ 
#> 13 interpro_domains MGI_InterProDomains.rpt MGI_InterProDomains MGI Marker~ 
```

**Usage**

```r
read_report(
    report_key = NULL,
    report_file = NULL,
    report_type = NULL,
    n_max = Inf
)
```
Arguments

- `report_key` A character vector. A key used to uniquely refer to an MGI report.
- `report_file` A character vector. The file path or URL to an MGI report file.
- `report_type` A character vector. The type of an MGI report.
- `n_max` Maximum number of lines to read.

Value

A tibble with report data in tidy format. The set of variables is dependent on the specific report requested:

- For "marker_list1", see `vignette("marker_list1")`.
- For "marker_list2", see `vignette("marker_list2")`.
- For "marker_coordinates", see `vignette("marker_coordinates")`.
- For "gene_model_coordinates", see `vignette("gene_model_coordinates")`.
- For "sequence_coordinates", see `vignette("sequence_coordinates")`.
- For "genbank_reseq_ensembl_ids", see `vignette("genbank_reseq_ensembl_ids")`.
- For "swiss_trembl_ids", see `vignette("swiss_trembl_ids")`.
- For "swiss_prot_ids", see `vignette("swiss_prot_ids")`.
- For "gene_trap_ids", see `vignette("gene_trap_ids")`.
- For "ensembl_ids", see `vignette("ensembl_ids")`.
- For "biotype_conflicts", see `vignette("biotype_conflicts")`.
- For "primers", see `vignette("primers")`.
- For "interpro_domains", see `vignette("interpro_domains")`.

---

**report-attributes**

*Get MGI report specs by report key*

Description

Set of functions to retrieve metadata details of a MGI report.

Usage

- `report_file(report_key)`
- `report_name(report_key)`
- `report_type(report_key)`
- `report_url(report_key)`
Arguments

report_key
A character vector. A key used to uniquely refer to an MGI report.

Value

A character vector:

- report_name(): report title.
- report_type(): report type.
- report_url(): report remote location.

Examples

```r
report_file("marker_list1")
report_name("marker_list1")
report_type("marker_list1")
report_url("marker_list1")
```

Description

reports is a data set of supported MGI reports, meaning reports that {mgi.report.reader} can currently read into R. To browse all reports made available by MGI visit https://www.informatics.jax.org/downloads/reports/.

Usage

reports

Format

A tibble of 4 variables:

- report_key  A string key used to uniquely refer to an MGI report, which is only meaningful within the context of the {mgi.report.reader}.
- report_type  MGI report type. The type is used internally to find the appropriate reader for parsing, and is only meaningful within the context of {mgi.report.reader}.
Examples

    reports

---

report_example  Report example

Description

    report_example() returns the local path of an example report file. These files are typically very small and are useful for demonstrations. These are mostly used in the Examples section of functions and in unit tests.

Usage

    report_example(report_file)

Arguments

    report_file  File basename.

Examples

    report_example("MRK_List1-EX01.rpt")
    report_example("MRK_List1-EX02.rpt")
    report_example("MRK_List1-EX03.rpt")

---

report_last_modified  Report last modification date

Description

    report_last_modified() returns the last modified date and time of the report source: local file or remote file. If a local file, the modification date will be that indicated by the file system; if a remote file, the date of last update is that provided by HTTP header "last-modified".

    MGI updates its reports weekly, every Thursday. However, not all reports are updated each week. The return value of this function is the closest you will get to a versioning of MGI report files.

Usage

    report_last_modified(tbl)
**Arguments**

- `tbl`  
  Report data as a tibble.

**Value**

A last modified date-time as a POSIXct object.

**Examples**

```r
if (FALSE) {
    markers <- read_report("marker_list1", n_max = 10L)

    # When was the report file last updated?
    report_last_modified(markers)
}
```

---

**report_source**  

*Report source*

**Description**

`report_source()` returns the source used to obtain the report data: a file path or an URL.

**Usage**

`report_source(tbl)`

**Arguments**

- `tbl`  
  Report data as a tibble.

**Value**

A single string with an absolute path to a file on disk or an URL.

**Examples**

```r
if (FALSE) {
    markers <- read_report("marker_list1", n_max = 10L)

    # Where did the data come from?
    report_source(markers)
}
```
symbol_to_identifier  
Convert marker symbols to updated marker identifiers

Description

symbol_to_identifier() remaps old marker symbols to, in-use, most up to date markers.

Usage

symbol_to_identifier(x, report_file = NULL, n_max = Inf)

Arguments

x  
A character vector of marker symbols to be remapped.

report_file  
The path to a MRK_List1.rpt file. Leave this as NULL and the function will automatically download the report from https://www.informatics.jax.org/downloads/reports/MRK_List1.rpt.

n_max  
Maximum number of lines to read from the report_file.

Examples

rpt_ex01 <- report_example("MRK_List1-EX01.rpt")
read_report(report_file = rpt_ex01, report_type = "MRK_List1") |> 
dplyr::select("marker_status", "marker_symbol", "marker_id_now")

# NB:
# - "1700024N20Rik" has two conflicting mappings, so maps to `NA`.
# - "Hes1" is not present in MRK_List1-EX01.rpt, so maps to `NA`.
# - "P1pbp" (official) and "Prosc" (withdrawn) both map to "MGI:1891207"

marker_symbols <- c("2200002F22Rik", "P1pbp", "Prosc", "1700024N20Rik", "Hes1")
symbol_to_identifier(x = marker_symbols, report_file = rpt_ex01)

symbol_to_symbol  
Update marker symbols

Description

symbol_to_symbol() remaps old marker symbols to, in-use, most up to date symbols.

Usage

symbol_to_symbol(x, report_file = NULL, n_max = Inf)
symbol_to_symbol

Arguments

x  A character vector of marker symbols to be remapped.
report_file The path to a MRK_List1.rpt file. Leave this as NULL and the function will automatically download the report from https://www.informatics.jax.org/downloads/reports/MRK_List1.rpt.
n_max Maximum number of lines to read from the report_file.

Value

A character vector of most up to date symbols.

Examples

rpt_ex01 <- report_example("MRK_List1-EX01.rpt")
read_report(report_file = rpt_ex01, report_type = "MRK_List1") |> 
dplyr::select("marker_status", "marker_symbol", "marker_symbol_now")

# NB:
# - "1700024N20Rik" has two conflicting mappings, so maps to `NA`.
# - "Hes1" is not present in MRK_List1-EX01.rpt, so maps to `NA`.
# - "Plpbp" (official) and "Prosc" (withdrawn) both map to "Plpbp"

marker_symbols <- c("2200002F22Rik", "Plpbp", "Prosc", "1700024N20Rik", "Hes1")
symbol_to_symbol(x = marker_symbols, report_file = rpt_ex01)
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