

Package: geisha (via r-universe)

August 23, 2024

Type Package

Title GEISHA Expression Data

Version 0.1.0

Description GEISHA expression data. These data are obtained from
GEISHA <<http://geisha.arizona.edu/geisha/downloads.jsp/>>.

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 2.10)

Imports rvest, httr, tibble, here, purrr, magrittr, dtplyr, dplyr,
data.table, glue, lubridate, stringr, rlang

Repository <https://ramiromagno.r-universe.dev>

RemoteUrl <https://github.com/ramiromagno/geisha>

RemoteRef HEAD

RemoteSha 10bada460e090c135970057827fc35fc13789dc3

Contents

| | |
|------------------------------------|---|
| expression_txt | 2 |
| expression_xml | 2 |
| get_dates_of_last_update | 3 |
| get_files | 4 |
| hh_stages | 4 |
| last_updates | 5 |
| read_expression_txt | 5 |
| read_expression_xml | 6 |

| | |
|--------------|----------|
| Index | 7 |
|--------------|----------|

| | |
|----------------|--|
| expression_txt | <i>GEISHA Expression Data (expression.txt)</i> |
|----------------|--|

Description

This dataset contains NCBI Gene ID, NCBI Gene Name, GEISHA ID, Ensembl ID, GO terms, embryo stages and tissue locations.

Usage

expression_txt

Format

A `tibble` of 7 variables (columns):

ncbi_gene_id NCBI gene identifier.

ensembl_gene_id Ensembl gene identifier.

gene_name NCBI gene name.

stages Hamilton-Hamburger stages.

locations Anatomical location.

geisha_id GEISHA identifier.

gene_ontology_id Gene ontology identifier.

Data set generation workflow can be found at the source of this package in `data-raw/data.R`.

Source

Original dataset from: <http://geisha.arizona.edu/geisha/expression.txt>.

| | |
|----------------|--|
| expression_xml | <i>GEISHA Expression Data (expression.xml)</i> |
|----------------|--|

Description

This dataset contains NCBI Gene ID, NCBI Gene Name, GEISHA ID, embryo stages and tissue locations.

Usage

expression_xml

Format

A `tibble` of 5 variables (columns):

`ncbi_gene_id` NCBI gene identifier.

`gene_name` NCBI gene name.

`geisha_id` GEISHA identifier.

`stage` Hamilton-Hamburger stages.

`location` Anatomical location.

Data set generation workflow can be found at the source of this package in `data-raw/data.R`.

Source

Original dataset from: <http://geisha.arizona.edu/geisha/expression.xml>.

`get_dates_of_last_update`

Get dates of last update of download files

Description

This function will scrape on-the-fly GEISHA's downloads page and retrieve the date of last update of the to-be-downloaded files.

Usage

```
get_dates_of_last_update(files = download_files())
```

Arguments

`files` file names to whose update date is to be checked in the downloads page.

Value

Returns a `tibble` with one file per row.

| | |
|-----------|--|
| get_files | <i>Get the files available to download from GEISHA</i> |
|-----------|--|

Description

This function retrieves those files available for download from the downloads' page of the GEISHA website. These files are saved to data-raw/ are meant to be used only by the package developer.

Usage

```
get_files(files = download_files())
```

Arguments

| | |
|-------|---|
| files | The name of the files to be downloaded. This parameter is set by default to download all available files. |
|-------|---|

| | |
|-----------|-----------------------------------|
| hh_stages | <i>Hamilton-Hamburguer stages</i> |
|-----------|-----------------------------------|

Description

This function returns a character vector of Hamilton-Hamburguer (HH) stages.

Usage

```
hh_stages(hh_prefix = FALSE)
```

Arguments

| | |
|-----------|---|
| hh_prefix | A logical indicating whether to include the prefix 'HH' in the after-laying egg stages, i.e., those stages numbered with arabic numerals. |
|-----------|---|

Value

A character vector of Hamilton-Hamburguer (HH) stages.

| | |
|--------------|--|
| last_updates | <i>Date of last update of download files</i> |
|--------------|--|

Description

Date of last update of download files

Usage

```
last_updates
```

Format

A [tibble](#) of 2 variables:

file File name.

date Date of last update by GEISHA.

| | |
|---------------------|--|
| read_expression_txt | <i>Imports data-raw/expression.txt as a tibble</i> |
|---------------------|--|

Description

This function reads data-raw/expression.txt as a tibble. This function is meant to be used only by the developer of this package.

Usage

```
read_expression_txt()
```

Value

Returns a tibble with the data present in expression.txt.

read_expression_xml *Imports data-raw/expression.xml as a tibble*

Description

This function reads data-raw/expression.xml as a tibble. This function is meant to be used only by the developer of this package.

Usage

```
read_expression_xml()
```

Value

Returns a tibble with (part of) the data present in expression.xml.

Index

* datasets

expression_txt, [2](#)

expression_xml, [2](#)

last_updates, [5](#)

expression_txt, [2](#)

expression_xml, [2](#)

get_dates_of_last_update, [3](#)

get_files, [4](#)

hh_stages, [4](#)

last_updates, [5](#)

read_expression_txt, [5](#)

read_expression_xml, [6](#)

tibble, [2](#), [3](#), [5](#)