

# Package: geisha (via r-universe)

August 22, 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://patterninstitute.r-universe.dev>

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

**RemoteRef** HEAD

**RemoteSha** 10bada460e090c135970057827fc35fc13789dc3

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

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

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`get_dates_of_last_update`

*Get dates of last update of download files*

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### **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.

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get_files	<i>Get the files available to download from GEISHA</i>
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**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.
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hh_stages	<i>Hamilton-Hamburguer stages</i>
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**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.
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**Value**

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

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last_updates	<i>Date of last update of download files</i>
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**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.

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

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read\_expression\_xml *Imports data-raw/expression.xml as a tibble*

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**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.

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