Package: CLAMPData (via r-universe)

November 25, 2026

Type Package

Title Experiment data for CLAMP package

Version 1.0.0

Description Curated CLAMP resources (latent variables, loadings, priors, and example matrices) for use with the CLAMP package, distributed via ExperimentHub.

License MIT + file LICENSE

Encoding UTF-8

LazyData false

Depends R (>= 4.5.0)

Imports ExperimentHub, utils

Suggests ExperimentHubData, knitr, rmarkdown, BiocStyle, rhdf5, testthat (>= 3.0.0)

VignetteBuilder knitr

biocViews ExperimentHub, ExperimentData, RNASeqData, ExpressionData

BugReports https://github.com/pivlab/CLAMPData/issues

URL https://github.com/pivlab/CLAMPData

Config/roxygen2/version 8.0.0

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:33:13 UTC

RemoteUrl https://github.com/bioc/CLAMPData

RemoteRef RELEASE_3_24

RemoteSha b42f89a2569c6f75c33e3fb3f4bcd1151843c03b

Contents

clamp_h5_schema 2
GSE164416_DP_htseq_counts_txt_gz 2
human_gene_v2_5_alz_h5 3
islets_metadata_csv 3
list_clamp_data 4
read_clamp_alz_expression 4
read_islet_counts 5
read_islet_metadata 5
validate_clamp_h5 6

Index **7**

`clamp_h5_schema` *Expected HDF5 schema for CLAMP expression files*

Description

Returns a data frame of the paths, types, and purpose of each dataset required in a CLAMP HDF5 expression file.

Usage

```
clamp_h5_schema()
```

Value

A data frame with columns `path`, `type`, and `description`.

Examples

```
clamp_h5_schema()
```

`GSE164416_DP_htseq_counts_txt_gz`
GSE164416_DP_htseq_counts_txt_gz

Description

Retrieves the raw count matrix (path to gzipped file) for the GSE164416 dataset from ExperimentHub.

Usage

```
GSE164416_DP_htseq_counts_txt_gz()
```

Value

A character string representing the local file path to the downloaded resource.

Examples

```
if (interactive()) {
    counts_path <- GSE164416_DP_htseq_counts_txt_gz()
    print(counts_path)
}
```

`human_gene_v2_5_alz_h5` *human_gene_v2_5_alz_h5*

Description

Retrieves the H5 file (path) containing gene sets and pathway priors from ExperimentHub.

Usage

```
human_gene_v2_5_alz_h5()
```

Value

A character string representing the local file path to the downloaded resource.

Examples

```
if (interactive()) {
    h5_path <- human_gene_v2_5_alz_h5()
    print(h5_path)
}
```

`islets_metadata_csv` *islets_metadata_csv*

Description

Retrieves the metadata CSV file (path) for the islets example from ExperimentHub.

Usage

```
islets_metadata_csv()
```

Value

A character string representing the local file path to the downloaded resource.

Examples

```
if (interactive()) {
    metadata_path <- islets_metadata_csv()
    print(metadata_path)
}
```

`list_clamp_data` *List available CLAMPData datasets*

Description

Returns a data frame of all datasets in the package, one row per resource. The `accessor` column names the function that returns the local file path for each resource.

Usage

```
list_clamp_data()
```

Value

A `data.frame` with columns `name`, `accessor`, `description`, `type`, `species`, `eh_id`, and `version`.

Examples

```
datasets <- list_clamp_data()
datasets[, c("name", "type", "eh_id")]
```

`read_clamp_alz_expression`
Load the Alzheimer expression matrix

Description

Downloads the Alzheimer HDF5 file via ExperimentHub, validates it against `clamp_h5_schema`, and returns the expression matrix oriented as genes x samples with gene symbols and sample identifiers as row and column names

Usage

```
read_clamp_alz_expression()
```

Value

A numeric matrix with gene symbols as row names and sample identifiers as column names.

Examples

```
if (interactive()) {
    expr <- read_clamp_alz_expression()
    dim(expr)
}
```

`read_islet_counts` *Load islet count table*

Description

Downloads the GSE164416 HTSeq count file via ExperimentHub and reads it as a data frame

Usage

```
read_islet_counts()
```

Value

A data frame with an `ensembl` gene-ID column and one count column per sample.

Examples

```
if (interactive()) {
    counts <- read_islet_counts()
    dim(counts)
}
```

`read_islet_metadata` *Load islet sample metadata*

Description

Downloads the islet sample metadata CSV via ExperimentHub and reads it as a data frame

Usage

```
read_islet_metadata()
```

Value

A data frame with one row per sample.

Examples

```
if (interactive()) {
    meta <- read_islet_metadata()
    head(meta)
}
```

`validate_clamp_h5` *Validate a CLAMP HDF5 file*

Description

Checks that an HDF5 file contains the datasets CLAMP expects (see `clamp_h5_schema`).

Usage

```
validate_clamp_h5(path)
```

Arguments

`path`	Path to an HDF5 file.

Value

`TRUE` invisibly if the file is valid; otherwise stops with a message listing the missing datasets.

Examples

```
if (interactive()) {
    validate_clamp_h5(human_gene_v2_5_alz_h5())
}
```

Index

clamp_h5_schema, 2, *4*, *6*

GSE164416_DP_htseq_counts_txt_gz, 2

human_gene_v2_5_alz_h5, 3

islets_metadata_csv, 3

list_clamp_data, 4

read_clamp_alz_expression, 4
read_islet_counts, 5
read_islet_metadata, 5

validate_clamp_h5, 6