Package ‘CLAMPData’

June 23, 2026

Type Package

Title Experiment data for CLAMP package

Version 0.99.5

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

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Encoding UTF-8

LazyData false

Depends R (>= 4.6.0)

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

git_url https://git.bioconductor.org/packages/CLAMPData

git_branch devel

git_last_commit 869b631

git_last_commit_date 2026-06-08

Repository Bioconductor 3.24

Date/Publication 2026-06-23

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Contents

`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())
}
```

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