Package 'iModMixData'

March 3, 2026

Title Data for iModMix Package

Version 1.0.0

Description Provides example datasets for the iModMix package, including gene, protein, and metabolite partial correlation matrices derived from ccRCC4 and FloresData_K_TK studies. The data are preprocessed and ready to use for testing, demonstrating iModMix workflows, and exploring correlation networks.

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

biocViews ExperimentData, ExpressionData, MassSpectrometryData, ExperimentHub

URL https://github.com/biodatalab/iModMixData

BugReports https://github.com/biodatalab/iModMixData/issues

Imports ExperimentHub

Suggests knitr, testthat

Config/testthat/edition 3

VignetteBuilder knitr

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

git_branch RELEASE_3_22

git_last_commit 4b6ab7c

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-03-03

Author Isis Narvaez-Bandera [aut, cre] (ORCID: <https://orcid.org/0000-0001-7320-618X>)

Maintainer Isis Narvaez-Bandera <isis.narvaez@upr.edu>

Contents

loadPartialCorGenes *Load PartialCorGenes data*

Description

Loads the PartialCorGenes dataset from ExperimentHub.

Usage

```
loadPartialCorGenes()
```

Details

The dataset contains partial correlation values between genes derived from the ccRCC4 study. The original expression data were preprocessed using `load_data()` which includes:

- Filtering features with >10% missing values

- Removing features with low variance

- Scaling and KNN imputation of missing values

Partial correlations were then calculated using `partial_cors()`: rho = 0.25.

Rows correspond to genes, columns correspond to samples. Each entry represents the partial correlation of the gene with other genes, adjusted for covariates.

Value

A `data.frame` with genes as rows and samples as columns.

Source

ccRCC4 study. Original data processed for iModMix.

Examples

```
genes <- loadPartialCorGenes()
head(genes)
dim(genes)
```

```
loadPartialCorMetabolites
```
Load PartialCorMetabolites data

Description

Loads the PartialCorMetabolites dataset from ExperimentHub.

Usage

```
loadPartialCorMetabolites()
```

Details

The dataset contains partial correlation values between metabolites derived from the FloresData_K_TK study. Data were preprocessed similarly to genes:

- Filtering features with >10% missing values
- Removing features with low variance
- Scaling and KNN imputation of missing values

Partial correlations were calculated using `partial_cors()` with rho = 0.25.

Rows correspond to metabolites, columns correspond to samples. Each entry represents the partial correlation of the metabolite with other metabolites, adjusted for covariates.

Value

A `data.frame` with metabolites as rows and samples as columns.

Source

FloresData_K_TK study. Original data processed for iModMix.

Examples

```
metabolites <- loadPartialCorMetabolites()
head(metabolites)
dim(metabolites)
```

```
loadPartialCorProt
```
Load PartialCorProt data

Description

Loads the PartialCorProt dataset from ExperimentHub.

Usage

```
loadPartialCorProt()
```

Details

The dataset contains partial correlation values between proteins derived from the FloresData_K_TK study. Data were preprocessed similarly to genes and metabolites:

- Filtering features with >10% missing values
- Removing features with low variance
- Scaling and KNN imputation of missing values

Partial correlations were calculated using `partial_cors()` with rho = 0.25.

Rows correspond to proteins, columns correspond to samples. Each entry represents the partial correlation of the protein with other proteins, adjusted for covariates.

Value

A `data.frame` with proteins as rows and samples as columns.

Source

FloresData_K_TK study. Original data processed for iModMix.

Examples

```
proteins <- loadPartialCorProt()
head(proteins)
dim(proteins)
```

Index