Package ‘iModMixData’

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Title Data for iModMix Package

Version 1.1.0

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.

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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

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`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)
```

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