

# Package ‘iModMixData’

November 4, 2025

**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>

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

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

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| loadPartialCorGenes | <i>Load PartialCorGenes data</i> |
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**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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