Package 'OmicNetR'

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Type Package

Title Network-Based Integration of Multi-Omics Data Using Sparse CCA

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Description Provides an end-to-end workflow for integrative analysis of two omics layers using sparse canonical correlation analysis (sCCA), including sample alignment, feature selection, network edge construction, and visualization of gene-metabolite relationships. The underlying methods are based on penalized matrix decomposition and sparse CCA (Witten, Tibshirani and Hastie (2009) <doi:10.1093/biostatistics/kxp008>), with design principles inspired by multivariate integrative frameworks such as mixOmics (Rohart et al. (2017) <doi:10.1371/journal.pcbi.1005752>).

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Encoding UTF-8

LazyData true

Imports stats, graphics, grDevices, ggplot2, igraph

Suggests knitr, rmarkdown, testthat (>= 3.0.0), mixOmics

VignetteBuilder knitr

RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

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Contents

`align_omics` *Align Multi-Omic Datasets*

Description

Ensures that X and Y matrices have matching samples in the exact same order.

Usage

```
align_omics(X, Y)
```

Arguments

`X`	Matrix or data frame (Samples x Features).
`Y`	Matrix or data frame (Samples x Features).

Value

A list containing the aligned X and Y matrices.

`generate_dummy_omics` *Generate Dummy Multi-Omics Data*

Description

Generates synthetic, linked RNA-seq and Metabolomics datasets.

Usage

```
generate_dummy_omics(
  n_samples = 50,
  n_genes = 1000,
  n_metabolites = 200,
  n_linked = 10
)
```

Arguments

`n_samples`	Number of samples (rows).
`n_genes`	Number of genes (columns in X).
`n_metabolites`	Number of metabolites (columns in Y).
`n_linked`	Number of features linked by a hidden variable.

Value

A list containing X (RNA-seq matrix), Y (Metabolomics matrix), and metadata.

`omics_example` *Example Multi-Omics Dataset*

Description

A simulated multi-omics dataset included in the OmicNetR package. This dataset is intended for demonstrating data alignment, sparse CCA analysis, and network visualization functions.

Usage

```
omics_example
```

Format

A list with the following components:

X A numeric matrix of gene expression values (samples in rows, genes in columns).

Y A numeric matrix of metabolite abundances (samples in rows, metabolites in columns).

Details

The dataset is small by design and should not be used for biological inference. It is provided solely for examples, vignettes, and unit testing.

Source

Simulated data generated within the OmicNetR package.

`omic_scca` *Perform Sparse Canonical Correlation Analysis (sCCA)*

Description

Fits a sparse PLS model in canonical mode to identify shared variation.

Usage

```
omic_scca(X, Y, n_components = 2, penalty_X = 0.9, penalty_Y = 0.9)
```

Arguments

X	Normalized RNA-seq matrix (Samples x Features).
Y	Normalized Metabolomics matrix (Samples x Features).
n_components	Number of components.
penalty_X	Sparsity for X (0 to 1, where 1 is most sparse).
penalty_Y	Sparsity for Y (0 to 1, where 1 is most sparse).

Value

An object of class "OmicNetR_sCCA" (a named list) with:

- canonical_correlations: numeric vector of per-component correlations/variance explained from the fitted model.
- loadings: list with matrices X and Y (feature weights) for each component.
- variates: list with matrices X and Y (sample scores) for each component.
- penalties: list with penalty_X and penalty_Y used to set sparsity.

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plot_bipartite_network

Plot Bi-partite sCCA Weight Network

Description

Optimized version using Base-R igraph engine to prevent memory exhaustion.

Usage

```
plot_bipartite_network(
  net_data,
  gene_color = "#1F77B4",
  metabolite_color = "#FF7F0E",
  layout_type = "fr"
)
```

Arguments

net_data	The edge list data frame from scca_to_network().
gene_color	Color for gene nodes.
metabolite_color	Color for metabolite nodes.
layout_type	igraph layout to use (default "fr").

Value

A graph object (invisibly).

plot_correlation_heatmap *Global Gene-Metabolite Correlation Heatmap*

Description

Visualizes the correlation matrix with a gradient color scale.

Usage

```
plot_correlation_heatmap(scca_model, X, Y, top_n = 20)
```

Arguments

scca_model	The result object from omic_scca().
X	Aligned RNA-seq matrix.
Y	Aligned Metabolomics matrix.
top_n	Number of top features from each omic to include.

Value

(Invisible) A numeric matrix of correlations between the selected features in X and Y.

plot_pathway_circle *Canonical Loading Pathway Circle Plot*

Description

Visualizes top feature importance in a radial layout.

Usage

```
plot_pathway_circle(scca_model, top_features = 40, pathway_db = "KEGG")
```

Arguments

scca_model	The result object from omic_scca().
top_features	Number of most weighted features to map.
pathway_db	Conceptual database name for labeling.

Value

A ggplot2 object.

`scca_to_network` *Convert sCCA Loadings to Network Edges*

Description

Generates an edge list for network plotting from sCCA loadings.

Usage

```
scca_to_network(scca_model, comp_select = 1, weight_threshold = 0.05)
```

Arguments

`scca_model`	The result object from omic_scca().
`comp_select`	Which canonical component to use.
`weight_threshold`	Minimum absolute product of weights to include an edge.

Value

A `data.frame` of edges with one row per gene-metabolite pair passing the threshold, containing:

- `Gene`: character, feature name from X.
- `Metabolite`: character, feature name from Y.
- `Weight_Product`: numeric, product of the selected loadings (edge weight).
- `Interaction_Type`: character, `"Positive"` or `"Negative"` based on the sign of `Weight_Product`.

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