Package 'OmicsPrepR'

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Title Unified Preprocessing Toolkit for Proteomics and Metabolomics

Version 0.1.1

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Description Provides unified workflows for quality control, normalization, and visualization of proteomic and metabolomic data. The package simplifies preprocessing through automated imputation, scaling, and principal component analysis (PCA)-based exploratory analysis, enabling researchers to prepare omics datasets efficiently for downstream statistical and machine learning analyses.

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Encoding UTF-8

Imports ggplot2, stats, utils

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

RoxygenNote 7.3.3

URL https://github.com/ikemillar/OmicsPrepR

BugReports https://github.com/ikemillar/OmicsPrepR/issues

NeedsCompilation no

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Repository CRAN

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Contents

`export_clean` *Export Cleaned Omics Data*

Description

Saves a cleaned omics dataset to a CSV file.

Usage

```
export_clean(data, file_path)
```

Arguments

`data`	A cleaned omics data frame or matrix.
`file_path`	Path to the file where the data will be saved.

Value

None. A file is written to disk.

Examples

```
# Create sample data
data <- matrix(rnorm(100), nrow = 10)
cleaned_data <- as.data.frame(data)

# Save to a temporary location (CRAN policy compliant)
temp_file <- tempfile(fileext = ".csv")
export_clean(cleaned_data, temp_file)
```

`impute_missing` *Impute Missing Values in Omics Data*

Description

Impute Missing Values in Omics Data

Usage

```
impute_missing(data, method = c("mean", "median"))
```

Arguments

data	Omics data frame with missing values.
method	Imputation method ("mean", "median").

Value

Data frame with imputed values.

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integrate_omics *Integrate Proteomic and Metabolomic Data*

Description

Integrate Proteomic and Metabolomic Data

Usage

```
integrate_omics(prot, met)
```

Arguments

prot	Proteomics data frame.
met	Metabolomics data frame.

Value

A merged data frame with common samples.

---

load_omics *Load Proteomics or Metabolomics Data*

Description

Load Proteomics or Metabolomics Data

Usage

```
load_omics(file, type = c("proteomics", "metabolomics"))
```

Arguments

file	Path to data file (.csv or .tsv)
type	Type of omics data ("proteomics" or "metabolomics")

Value

A data frame containing the omics dataset

Examples

```
# Create a temporary CSV file with example omics data
tmp <- tempfile(fileext = ".csv")
write.csv(matrix(rnorm(20), nrow = 5), tmp, row.names = FALSE)

# Load the omics data
data <- load_omics(tmp, type = "proteomics")
head(data)
```

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normalize_omics *Normalize Omics Data*

Description

Normalize Omics Data

Usage

```
normalize_omics(data, method = c("zscore", "log2"))
```

Arguments

data	A numeric data frame of omics values.
method	Normalization method ("zscore", "log2", "quantile").

Value

Normalized data frame.

---

plot_omics *Plot Omics Data (PCA, Heatmap, or Density)*

Description

Visualizes omics datasets using PCA, heatmap, or density plot options.

Arguments

data	A numeric matrix or data frame containing omics measurements.
type	A character string specifying the visualization type. One of "pca", "heatmap", or "density".

Value

A plot object (for PCA and density) or a heatmap visualization.

Examples

```
data <- matrix(rnorm(100), nrow = 10)
plot_omics(data, type = "pca")
```

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