Package: OmicsPrepR (via r-universe)

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Title Unified Preprocessing Toolkit for Proteomics and Metabolomics

Version 0.1.0

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Description An integrated R package providing unified workflows for quality control, normalization, and visualization of proteomic and metabolomic data. The package simplifies preprocessing through automated imputation, scaling, and 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

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

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

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

Repository https://ikemillar.r-universe.dev

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RemoteUrl https://github.com/ikemillar/omicsprepr

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Contents

`export_clean` *Export Cleaned Omics Data*

Description

Exports processed omics data to a CSV file for downstream analysis.

Usage

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

Arguments

`data`	A data frame containing the cleaned omics data.
`file_path`	A character string specifying the output file path.

Value

A message confirming export success.

Examples

```
## Not run:
export_clean(my_cleaned_data, "output/cleaned_data.csv")

## End(Not run)
```

`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.

`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

```
## Not run:
data <- load_omics("data.csv", type = "proteomics")

## End(Not run)
```

`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.

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