

# Package ‘omicsTools’

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**Title** Omics Data Process Toolbox

**Version** 1.0.5

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**Description** Processing and analyzing omics data from genomics, transcriptomics, proteomics, and metabolomics platforms. It provides functions for preprocessing, normalization, visualization, and statistical analysis, as well as machine learning algorithms for predictive modeling. 'omicsTools' is an essential tool for researchers working with high-throughput omics data in fields such as biology, bioinformatics, and medicine. The QC-RLSC (quality control-based robust LOESS signal correction) algorithm is used for normalization. Dunn et al. (2011) <[doi:10.1038/nprot.2011.335](https://doi.org/10.1038/nprot.2011.335)>.

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**Imports** bs4Dash, config (>= 0.3.1), dplyr, DT, golem (>= 0.3.5), magrittr, readr, shiny (>= 1.7.2), tibble

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**Suggests** spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**URL** <https://github.com/YaoxiangLi/omicsTools>

**BugReports** <https://github.com/YaoxiangLi/omicsTools/issues>

**NeedsCompilation** no

**Author** Yaoxiang Li [cre, aut] (ORCID: <<https://orcid.org/0000-0001-9200-1016>>),  
Zihao Zhang [aut],  
Meth Jayatilake [aut],  
Amrita Cheema [aut] (ORCID: <<https://orcid.org/0000-0003-4877-7583>>)

**Maintainer** Yaoxiang Li <[liyaoxiang@outlook.com](mailto:liyaoxiang@outlook.com)>

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impute	<i>Impute function</i>
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### Description

This function performs data cleaning and imputation on a given data matrix. It removes blank and NIST samples, features with NA values more than the specified threshold, and imputes remaining NA values with half of the smallest non-NA value.

### Usage

```
impute(data, percent = 0.2)
```

### Arguments

data	A data frame containing the sample data. The first column should contain the sample identifiers, and the rest of the columns contain the peaks.
percent	A numeric value between 0 and 1 representing the threshold of the percentage of NA values a feature should have for it to be removed from the dataset. Default value is 0.2.

### Value

A data frame with the first column as the sample identifiers and the rest of the columns containing the cleaned and imputed peak intensities.

### Author(s)

Yaoxiang Li <y1814@georgetown.edu>

Georgetown University, USA

License: GPL (>= 3)

### Examples

```
# Load the CSV data
data_file <- system.file("extdata", "example1.csv", package = "omicsTools")
data <- readr::read_csv(data_file)
# Apply the impute function
imputed_data <- omicsTools::impute(data, percent = 0.2)
```

```
# Write the imputed data to a new CSV file
readr::write_csv(imputed_data, paste0(tempdir(), "/imputed_data.csv"))
```

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normalize	<i>Normalize function</i>
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## Description

This function performs normalization on the input data matrix using the loess regression method. Normalization is done based on Quality Control (QC) samples in the data.

## Usage

```
normalize(data)
```

## Arguments

data	A data frame containing the sample data. The first column should contain the sample identifiers, and the rest of the columns contain the peaks to be normalized. QC samples should be indicated in the sample identifiers with 'QC'.
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## Value

A data frame with the first column as the sample identifiers and the rest of the columns containing the normalized peak intensities.

## Author(s)

Yaoxiang Li <yl1814@georgetown.edu>  
Georgetown University, USA  
License: GPL (>= 3)

## Examples

```
# Load the CSV data
data_file <- system.file("extdata", "example2.csv", package = "omicsTools")
data <- readr::read_csv(data_file)
# Apply the normalize function
normalized_data <- omicsTools::normalize(data)

# Write the normalized data to a new CSV file
readr::write_csv(normalized_data, paste0(tempdir(), "/normalized_data.csv"))
```

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`run_app`*Run the Shiny Application*

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**Description**

Run the Shiny Application

**Usage**

```
run_app(  
  onStart = NULL,  
  options = list(),  
  enableBookmarking = NULL,  
  uiPattern = "/",  
  ...  
)
```

**Arguments**

<code>onStart</code>	A function that will be called before the app is actually run. This is only needed for <code>shinyAppObj</code> , since in the <code>shinyAppDir</code> case, a global <code>.R</code> file can be used for this purpose.
<code>options</code>	Named options that should be passed to the <code>runApp</code> call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app.
<code>enableBookmarking</code>	Can be one of "url", "server", or "disable". The default value, <code>NULL</code> , will respect the setting from any previous calls to <code>enableBookmarking()</code> . See <code>enableBookmarking()</code> for more information on bookmarking your app.
<code>uiPattern</code>	A regular expression that will be applied to each GET request to determine whether the <code>ui</code> should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.
<code>...</code>	arguments to pass to <code>golem_opts</code> . See <code>'?golem::get_golem_options'</code> for more details.

**Value**

No return value, called for launch the application.

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