Package ‘CausCor’

January 20, 2025

Title Calculate Correlations and Estimate Causality

Version 0.1.3

Description This tool performs pairwise correlation analysis and estimate causality.
Particularly, it is useful for detecting the metabolites that would be altered by the gut bacteria.

URL `https://github.com/sugym/CausCor`

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Language en-US

Encoding UTF-8

RoxygenNote 7.1.2

Imports cowplot, dplyr, ggplot2, grDevices, magrittr, stats, WriteXLS

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

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Contents

`filter_40` *Make list of A-B pair causal correlations - 40% Filtering version*

Description

Make list of A-B pair causal correlations - 40% Filtering version

Usage

```
filter_40(
  a_mat,
  b_mat,
  a_category,
  b_category,
  min_cor,
  min_r2,
  min_sample = ceiling((ncol(a_mat) - 1) * 0.4),
  max_sample = ncol(a_mat) - 1 - min_sample
)
```

Arguments

`a_mat`	Matrix of measurements of A for each sample.
`b_mat`	Matrix of measurements of B for each sample.
`a_category`	Category name of A.
`b_category`	Category name of B.
`min_cor`	Minimum spearman correlation coefficient.
`min_r2`	Minimum R2 score.
`min_sample`	Minimum number of samples. The default is 40% of the total samples.
`max_sample`	Maximum number of samples. The default is 60% of the total samples.

`filter_cc` *Make list of A-B pair causal correlations*

Description

Make list of A-B pair causal correlations

Usage

```
filter_cc(
  a_mat,
  b_mat,
  a_category,
  b_category,
  min_cor,
  min_r2,
  min_sample,
  max_sample = ncol(a_mat) - 1,
  direction = T
)
```

Arguments

`a_mat`	Matrix of measurements of A for each sample.
`b_mat`	Matrix of measurements of B for each sample.
`a_category`	Category name of A.
`b_category`	Category name of B.
`min_cor`	Minimum spearman correlation coefficient.
`min_r2`	Minimum R2 score.
`min_sample`	Minimum number of samples.
`max_sample`	Maximum number of samples. The default is the total number of samples.
`direction`	Extract only directional associations where a change in category A causes a change in category B. The default is True.

`filter_n` *Make list of A-B pair causal correlations - Normal Filtering version*

Description

Make list of A-B pair causal correlations - Normal Filtering version

Usage

```
filter_n(a_mat, b_mat, a_category, b_category, min_cor, min_r2, min_sample)
```

Arguments

`a_mat`	Matrix of measurements of A for each sample.
`b_mat`	Matrix of measurements of B for each sample.
`a_category`	Category name of A.
`b_category`	Category name of B.

`min_cor`	Minimum spearman correlation coefficient.
`min_r2`	Minimum R2 score.
`min_sample`	Minimum number of samples.

`plot_16` *Save scatter plots*

Description

Save scatter plots

Usage

```
plot_16(a_mat, b_mat, list, out_info, x_italic = F, y_italic = T)
```

Arguments

`a_mat`	Matrix of measurements of A for each sample.
`b_mat`	Matrix of measurements of B for each sample.
`list`	List of results.
`out_info`	Output directory.
`x_italic`	Italicize the x-axis label of the plot. The default is False.
`y_italic`	Italicize the y-axis label of the plot. The default is True.

`save_text` *Save list as a text file*

Description

Save list as a text file

Usage

```
save_text(list, out_info, file_type)
```

Arguments

`list`	List of results.
`out_info`	Output directory.
`file_type`	Choose from "excel", "csv", "tsv".

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