

# Package: CausCor (via r-universe)

September 6, 2024

**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>

**License** MIT + file LICENSE

**Language** en-US

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.2

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

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Repository** <https://sugym.r-universe.dev>

**RemoteUrl** <https://github.com/sugym/causcor>

**RemoteRef** HEAD

**RemoteSha** 2c99f3481eeb43638fc13b9fce022bed62e354b5

## Contents

filter_40 . . . . .	2
filter_cc . . . . .	2
filter_n . . . . .	3
plot_16 . . . . .	4
save_text . . . . .	4

<b>Index</b>	<b>5</b>
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 filter\_40

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


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### 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.

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 filter\_cc

*Make list of A-B pair causal correlations*


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### 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.

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filter_n	<i>Make list of A-B pair causal correlations - Normal Filtering version</i>
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**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.

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plot\_16                      *Save scatter plots*

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### **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.

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save\_text                      *Save list as a text file*

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### **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".

# Index

filter\_40, 2

filter\_cc, 2

filter\_n, 3

plot\_16, 4

save\_text, 4