# Package 'MetaPcor'

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**Type** Package

**Title** Meta-analysis of gene expression using partial correlation as effect size

**Version** 0.1.0

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**Description** This package performs meta-analysis of gene expression studies using partial correlation as effect size, to provide the means to construct a causal association gene network

**License** GPL-3

**Encoding** UTF-8

**NeedsCompilation** no

## R topics documented:

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DEG_meta                    *Differential expression analysis*

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### Description

Differential expression analysis, which keeps only the statistically significant genes from a given set of gene expression studies

### Usage

```
DEG_meta(folder_path, cases, controls)
```

## Arguments

| | |
|---|---|
| `folder_path` | A folder path where the gene expression studies are stored |
| `cases` | How the cases are named in the gene expression studies |
| `controls` | How the controls are named in the gene expression studies |

## Value

A list of data.tables containing gene expression columns of the statistically significant genes that occured from the differential epxression analysis

## Author(s)

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## Examples

```
DEG_ES <- DEG_meta(folder_path = 'studies/', cases = 'CASE',
controls = 'CONTROL')
```

---

enirchment_analysis       *Enrichment Analysis*

---

## Description

A function to conduct enrichment analysis with the statistically significant genes that occured from the meta-analysis

## Usage

```
enirchment_analysis(x)
```

## Arguments

| | |
|---|---|
| `x` | A dataframe object containing the results of the meta_pcor function |

## Value

A list with the results of the enrichment analysis with the gProfiler tool ([1]: A dataframe with the results of the enricment and [2] an interactive Manhattan plot with the statistically significant terms from the sources)

## Author(s)

Ioanna V. Sasilioglou, Georgios A. Manios, Polymnia V. Gkoumplia, Panagiota I. Kontou, Pantelis G. Bagos* (*correspondence to : pbagos@compgen.org)

### References

Uku Raudvere, Liis Kolberg, Ivan Kuzmin, Tambet Arak, Priit Adler,Hedi Peterson, Jaak Vilo, g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019 update), Nucleic Acids Research, Volume 47, Issue W1, 02 July 2019, Pages W191–W198, https://doi.org/10.1093/nar/gkz3

### See Also

https://biit.cs.ut.ee/gprofiler/gost

### Examples

```
ea_results <- enrichment_analysis(meta_pcor_results)
```

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meta_pcor                    *Partial Correlation Meta-Analysis Function*

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### Description

This function performs meta-analysis of partial correlation coefficients using neighborhood selection approach or shrinkage methods. The function accepts data from multiple studies as input and outputs a meta-analysis result that represents a summary of the partial correlation coefficients obtained from the individual studies.

### Usage

```
meta_pcor(file_names, option, method, meta_method= "random",
pvalue_thres = NULL, fdr_thres = NULL,
coef_thres = NULL,l1 = NULL ,l2 = NULL, norm_data = NULL, norm_method = NULL)
```

### Arguments

| | |
|---|---|
| file_names | a character vector containing the file names of the data to be analyzed. |
| option | The meta-analysis option to run (integer). 1: Pearson correlation and partial corrleation meta-analysis 2: Partial correlation meta-analysis with thresholds 3: Partial correlation meta-analysis without thresholds 4: Differential expression and partial correlation meta-analysis |
| method | a character string indicating the method to be used to estimate partial correlation coefficients. Available options are "sparse" and "shrinkage". |
| meta_method | a character string indicating the method to be used for the meta-analysis of the partial correlation coefficients. Available options are "random" and "fixed". Default is "random". |
| pvalue_thres | a numeric value specifying the threshold for p-values. |
| fdr_thres | a numeric value specifying the threshold for false discovery rate (FDR). |
| coef_thres | a numeric value specifying the threshold for correlation coefficient magnitude. |
| l1 | a numeric value specifying the parameter for neighborhood selection approach. |
| l2 | a numeric value specifying the parameter for neighborhood selection approach. |
| norm_data | a character string indicating whether data normalization should be performed. Available options are "YES" and "NO". Default is "NO". |
| norm_method | a character string indicating the method to be used for normalization. Available options are "RPKM" and "Z_SCOR_STAND","LOG2" and "QUANT_NORM". |

## Value

A data.table object is returned, containing the results of the meta-analysis.

## Author(s)

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Uku Raudvere, Liis Kolberg, Ivan Kuzmin, Tambet Arak, Priit Adler,Hedi Peterson, Jaak Vilo, g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019 update), Nucleic Acids Research, Volume 47, Issue W1, 02 July 2019, Pages W191–W198, https://doi.org/10.1093/nar/gkz3

## See Also

https://biit.cs.ut.ee/gprofiler/gost

## Examples

```
metapcor_result <- meta_pcor(GEO_names=c("GSE76427"),
target_namespace = c('ILLUMINA_HUMANHT_12_V4'), option = 2,
method = "sparse", meta_method = "random",
pvalue_thres = 0.01, l1 = 0.8, l2 = 0)


metapcor_result <- meta_pcor(folder_path = "/path/to/data/folder",
option = 1, method = "sparse",meta_method = "random",l1 = 0.8, l2 = 0)
```

---

my_meta                         *Meta-analysis function*

---

## Description

A function that performs meta-analysis of partial correlation coefficients

## Usage

```
my_meta(correlations, method)
```

## Arguments

| | |
|---|---|
| correlations | A partial correlation data.table object, which occurs from the results of the partial_neighborhood or the partial_shrinkage functions |
| method | Meta-analysis method to calculate the effect sizes ('random' or 'fixed') |

## Value

A data.table containing the results of the meta-analysis

**Author(s)**

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**Examples**

```
my_meta_results <- my_meta(correlations = sparse_partial_corr, method = 'random')
```

---

network_plot

---

**Description**

A function which plots an interactive causal association gene netowrk with the GraphViz package

**Usage**

```
network_plot(x)
```

**Arguments**

x                  A data.table object which contains the results of the meta_pcor function

**Value**

An interactive network plot of the causal association gene network

**Author(s)**

Ioanna V. Sasilioglou, Georgios A. Manios, Polymnia V. Gkoumplia, Panagiota I. Kontou, Pantelis G. Bagos* (*correspondence to : pbagos@compgen.org)

**Examples**

```
# Network plot
network_plot(meta_pcor_results)
```

---

pcor_neighborhood          *Spartial correlation estimation function*

---

**Description**

A function to calculate sparse partial correlation estimation with neighborhood selection approach method for each study

**Usage**

```
pcor_neighborhood(list_of_files, l1, l2=0, significant, pvalue_thres=NULL,
fdr_thres= NULL, coef_thres = NULL)
```

## Arguments

| | |
|---|---|
| `list_of_files` | A list of files that contain the transposed gene expression studies as data.table objects |
| `l1` | l1 Norm penalty. l1 = 0.8 is suggested (float) |
| `l2` | l2 value for sparse partial correaltion calculation. l2 = 0.0 is suggested (float) |
| `significant` | A boolean option ("TRUE" or "FALSE") to choose only the statistically significant pairs of partial correlations, either with a p-value or a FDR or a coefficient threshold |
| `pvalue_thres` | p-value threshold for the meta-analysis (float) |
| `fdr_thres` | FDR value threshold for the meta-analysis (float) |
| `coef_thres` | Coefficient threshold for the meta-analysis (float) |

## Value

A data.table object is returned with the partial correlations pairs

## Author(s)

Ioanna V. Sasilioglou, Georgios A. Manios, Polymnia V. Gkoumplia, Panagiota I. Kontou, Pantelis G. Bagos* (*correspondence to : pbagos@compgen.org)

## See Also

https://github.com/cran/space

## Examples

```
# Calculate sparse partial correlation estimation with neighborhood selection approach method for each study

sparse_partial_corr <- pcor_neighborhood(list_of_files = list_of_studies,
l1 = 0.8, l2 = 0.0, significant = TRUE, pvalue_thres = 0.05)
```

---

pcor_shrinkage

---

## Description

A function to calculate sparse partial correlation estimation with the shrinkage method for each study.

## Usage

```
pcor_shrinkage(x)
```

## Arguments

| | |
|---|---|
| `list_of_files` | A list of files that contain the transposed gene expression studies as data.table objects |
| `significant` | A boolean option ("TRUE" or "FALSE") to choose only the statistically significant pairs of partial correlations, either with a p-value or a FDR or a coefficient threshold |
| `pvalue_thres` | p-value threshold for the meta-analysis (float) |
| `fdr_thres` | FDR value threshold for the meta-analysis (float) |
| `coef_thres` | Coefficient threshold for the meta-analysis (float) |

## Value

A data.table object is returned with the partial correlations pairs

## Author(s)

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## Examples

```
shrinkage_partial_corr <- pcor_shrinkage(list_of_files, significant = TRUE, pvalue_thres = 0.05)
```

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| volc_plot | *Volcano Plot* |
|---|---|

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## Description

A function which produces an interactive volcano plot with the Plotly package

## Usage

```
volc_plot_plotly(x, pval_thres, coeff_thres)
```

## Arguments

| | |
|---|---|
| `x` | A data.table object which contains the results of the meta_pcor function |
| `pval_thres` | A p-value threshold for the volcano (float) |
| `coeff_thres` | A coefficient threshold for the volcano plot (float) |

## Value

An interactive volcano plot

## Author(s)

Ioanna V. Sasilioglou, Georgios A. Manios, Polymnia V. Gkoumplia, Panagiota I. Kontou, Pantelis G. Bagos* (*correspondence to : pbagos@compgen.org)

## Examples

```
# Volcano Plot
volc_plot<- volc_plot_plotly(meta_pcor_results, pval_thres = 0.05,
coeff_thres = 0.2)
```

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