

Package ‘MetaPcor’

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Type Package

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

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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

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DE_analysis	<i>Differential Expression Analysis and Meta-analysis of Partial Correlation Coefficients</i>
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Description

This function performs differential expression analysis on gene expression data and performs a meta-analysis of correlation coefficients using sparse correlation and meta-correlation methods.

Usage

```
DE_analysis(folder_path, case, control, fold_threshold, p_value_threshold, l1)
```

Arguments

<code>folder_path</code>	Path to the folder containing gene expression data files.
<code>case</code>	String specifying the column name for the case samples in the gene expression data.
<code>control</code>	String specifying the column name for the control samples in the gene expression data.
<code>fold_threshold</code>	Numeric value specifying the fold-change threshold for considering genes as differentially expressed.
<code>p_value_threshold</code>	Numeric value specifying the p-value threshold for considering genes as statistically significant.
<code>l1</code>	Numeric value specifying the neighborhood size for sparse correlation calculation.

Details

The function reads gene expression data files from the specified folder path and performs the following steps:

1. Reads each data file.
2. Splits the data into case and control samples.
3. Applies log2 scale to the expression values.
4. Calculates the mean expression of each group.
5. Computes fold-change values between the case and control groups.
6. Performs a t-test to obtain p-values for each gene.
7. Applies fold-change and p-value thresholds to filter differentially expressed genes.
8. Performs sparse correlation analysis using the filtered gene expression data.
9. Performs meta-analysis of correlation coefficients using the sparse correlations.

Value

Returns the meta-analysis results as a `data.table`.

Examples

```
# Example usage of DE_analysis function
folder_path <- "/path/to/gene/expression/files"
case <- "CASE"
control <- "CONTROL"
fold_threshold <- 0
p_value_threshold <- 0.05
l1 <- 0.8

result <- DE_analysis(folder_path, case, control, fold_threshold, p_value_threshold, l1)
```

enrichment_analysis	<i>Enrichment Analysis</i>
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Description

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

Usage

```
enrichment_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 enrichment and [2] an interactive Manhattan plot with the statistically significant terms from the sources)

Author(s)

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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)
```

meta_pcor

*Partial Correlation Meta-Analysis Function***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 correlation 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.

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References

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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	<i>Meta-analysis function</i>
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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

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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 network 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

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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 correlation 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)

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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)
```

volc_plot

Volcano Plot

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

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Examples

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

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