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

License GPL-3

Encoding UTF-8

NeedsCompilation no

R topics documented:

DEG_meta

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

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)

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Examples

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

---

meta_pcor

Description

The main function of the package. All options can be run with this funciton.

Usage

```
meta_pcor(folder_path = NULL, GEO_names = NULL, target_namespace = NULL,
option, method, meta_method = "random",
pvalue_thres = NULL, fdr_thres = NULL,
coef_thres = NULL,l1  = NULL,l2 = NULL)
```

Arguments

`folder_path`	The folder path where local gene expression studies are stored (character)
`GEO_names`	Enter the GSE ID of the study (character)
`target_namespace`	
	Enter the target namespace of gConvert for probe to gene name conversion (character).
`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`	The partial correlation option to run (character). Available options : "sparse" or "shrinkage".
`meta_method`	Choose the model of the meta-analysis (character). Available options : "random" or "fixed".
`pvalue_thres`	p-value threshold for the meta-analysis to use when option = 2 (float).
`fdr_thres`	FDR value threshold for the meta-analysis to use when option = 2 (float).
`coef_thres`	Coefficient threshold for the meta-analysis to use when option = 2 (float).
`l1`	l1 value for sparse partial correaltion calculation. l1 = 0.8 is suggested. (float).
`l2`	l2 value for sparse partial correaltion calculation. l2 = 0 is suggested. (float).

Value

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

Author(s)

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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)
```

---

my_meta

Description

A function that performs meta-analysis of partial correlations

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)

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Examples

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

```
pcor_neighborhood
```

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 value for sparse partial correaltion calculation. 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)

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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

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)

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Examples

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

Index