Package: GANPA (via r-universe)

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Type Package

Title Gene Association Network-Based Pathway Analysis (GANPA)

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Depends GANPAdata

Imports graphics, stats, grDevices, utils

Description A network-based gene weighting algorithm for pathway enrichment analysis, using either RNA-seq or microarray data. Zhaoyuan Fang, Weidong Tian and Hongbin Ji (2012) <doi:10.1038/cr.2011.149>.

License GPL-2

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RemoteUrl https://github.com/cran/GANPA

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Contents

`GANPA-package` *Gene Association Network-based Pathway Analysis*

Description

This package implements a network-based gene weighting algorithm for pathways, as well as a gene-weighted gene set analysis approach for microarray data pathway analysis.

Author(s)

Zhaoyuan Fang, Weidong Tian and Hongbin Ji

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References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted.*

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov. Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *PNAS* 2005 102(43): 15545-15550.

`GSE.Test.Main` *Gene-weighted pathway significance analysis*

Description

Test the significance of pathways in microarray experiments. This includes a network-based gene weighting algorithm for pathways. Classical and gene-weighted versions of gene set analysis approaches are both used. When required, this function also corrects for gene weighting biases caused by multiple-subunit protein.

Usage

```
GSE.Test.Main(gExprs.obj, gsets, gNET, check.exprs = TRUE, msp.groups,
     size.min = 15, size.max = 500, permN = 1000, randN = 30,
     permFDR.cutoff = 0.5, output.label = "", msp.correction = TRUE)
```

Arguments

`gExprs.obj`	Gene expression experiment data object.
`gsets`	A list of gene sets.
`gNET`	A gene association network stored in a list.

`check.exprs`	Logical (TRUE by default). Check and correct the missing values and scaling in the gExprs.obj. If the scale is natural, it will be converted to log2.
`msp.groups`	A list of multi-subunit proteins.
`size.min`	Minimum size of gene sets used for analysis. By default 15 genes.
`size.max`	Maximum size of gene sets used for analysis. By default 500 genes.
`permN`	Sample permutation times. By default 1000 times.
`randN`	Gene randomization times. Can be set smaller (say, 30) if you do not care randomization-based significance so as to be faster.
`permFDR.cutoff`	Sample permutation FDR cutoff. A number between 0 and 1. Set it larger if wish to see the significance of more gene sets.
`output.label`	A label to name output files, e.g. "P53.C2".
`msp.correction`	Logical (TRUE). Whether to do a correction for multi-subunit proteins in gene weighting.

Value

It will write analysis results to .csv files.

Author(s)

Zhaoyuan Fang, Weidong Tian and Hongbin Ji

References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted.*

Examples

```
# Not to run
# library(GANPAdata)
# data("gExprs.p53", "gsets.msigdb.pnas", "gNET", "msp.groups",
#      package="GANPAdata")
# GSE.Test.Main(gExprs.obj=gExprs.p53, gsets=gsets.msigdb.pnas,
#      gNET=gNET, check.exprs=TRUE, msp.groups=msp.groups,
#      size.min=15, size.max=500, permN=1000, randN=30,
#      permFDR.cutoff=0.5, output.label="P53\_C2", msp.correction=TRUE)
```

`weight.gsets.test` *Weight genes in pathways with a gene association network*

Description

Given a gene functional association network, the gene weights in a list of pathways are assigned, with genes not present in the network assigned basic weights.

Usage

```
weight.gsets.test(isets, gsets)
```

Arguments

`isets`	A gene association network stored in a list.
`gsets`	Pathways stored in the form of a list of gene sets.

Value

A list of named numeric vectors storing gene weights, with gene names in the vector names.

Author(s)

Zhaoyuan Fang, Weidong Tian and Hongbin Ji

References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted*.

See Also

`weight.gsets.with.msprot`

`weight.gsets.with.msprot` *Weight genes in pathways with a gene association network after correction for multi-subunit proteins*

Description

Given a gene functional association network and a list of multi-subunit proteins, the gene weights in a list of pathways are assigned with a procedure of correction for multi-subunit proteins.

Usage

```
weight.gsets.with.msprot(gsets, isets.multi, msp.groups)
```

Arguments

`gsets`	A gene association network stored in a list.
`isets.multi`	Pathways stored in the form of a list of gene sets.
`msp.groups`	A list of multi-subunit proteins.

Value

A list of named numeric vectors storing gene weights, with gene names in the vector names.

Author(s)

Zhaoyuan Fang, Weidong Tian and Hongbin Ji

References

Zhaoyuan Fang, Weidong Tian and Hongbin Ji. A Network-Based Gene Weighting Approach for Pathway Analysis. *Submitted*.

See Also

`weight.gsets.test`

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