

Package ‘SPIA’

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Title Signaling Pathway Impact Analysis (SPIA) using combined evidence of pathway over-representation and unusual signaling perturbations

Author Adi Laurentiu Tarca <atarca@med.wayne.edu>, Purvesh Kathri <purvesh@cs.wayne.edu> and Sorin Draghici <sorin@wayne.edu>

Depends R (>= 2.10), graphics

Suggests graph, Rgraphviz, KEGGgraph, hgu133plus2.db

Maintainer Adi Laurentiu Tarca <atarca@med.wayne.edu>

Description This package implements the Signaling Pathway Impact Analysis (SPIA) which uses the information from a list of differentially expressed genes and their log fold changes together with signaling pathways topology, in order to identify the pathways most relevant to the condition under the study.

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URL <http://bioinformatics.oxfordjournals.org/cgi/reprint/btn577v1>

biocViews Microarray, GraphsAndNetworks

Collate spia.R plotP.R combfunc.R getP2.R

Imports graphics

LazyLoad yes

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colorectalcancer	<i>Results from a microarray experiment comparing colorectal cancer samples and normal tissue samples.</i>
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Description

The colorectal dataset consists: i) an named vector `DE_Colorectal`, which represents the \log_2 fold changes of the genes chosen as differentially expressed between colorectal cancer and normal samples based on data from Hong et al, 2007, using a $FDR=0.1$ and the universe of all Entrez gene IDs available on the array, `ALL_Colorectal`. These two vectors were obtained starting from the top dataframe which is the output from the `topTable` function of the `limma` package using the RMA processed gene expression data downloaded from GEE (GSE4107). The microarray platform used was Affymetrix HGU-133PLUS2.0.

Usage

```
data(colorectalcancer)
```

Source

Yi Hong and Kok Sun Ho and Kong Weng Eu and Peh Yean Cheah, A susceptibility gene set for early onset colorectal cancer that integrates diverse signaling pathways: implication for tumorigenesis, *Clin Cancer Res*, 2007, 13(4),1107-14.

combfunc	<i>Combining two p-values using Fisher's product or normal inversion method</i>
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Description

Combining two p-values using Fisher's product or normal inversion methods.

Usage

```
combfunc(p1=NULL,p2=NULL,combine="fisher")
```

Arguments

<code>p1</code>	A vector of probabilities.
<code>p2</code>	A vector of probabilities.
<code>combine</code>	A string with the name of the method to be used. Options include "fisher", "norminv"

Details

Two vectors of p-values are combined into a vector of global p-values.

Value

A vector of p-values.

Author(s)

Adi Laurentiu Tarca <atarca@med.wayne.edu>, Purvesh Khatri, Sorin Draghici

References

Adi L. Tarca, Sorin Draghici, Purvesh Khatri, et. al, A Signaling Pathway Impact Analysis for Microarray Experiments, 2008, *Bioinformatics*, 2009, 25(1):75-82.

See Also

[spia](#)

Examples

```
# Examples use colorectal cancer dataset
p1=c(0.2,0.4,0.1)
p2=c(0.01,0.7,0.01)
pG=combfunc(p1,p2,combine="fisher")
pG=combfunc(p1,p2,combine="norminv")
```

plotP

SPIA two-way evidence plot

Description

Plots each pathway as a point, using the over-representation p-value, pNDE, and perturbations accumulation p-value, pPERT, as coordinates. In addition the regions where FDR and FWER adjusted pG values are less than the specified threshold are plotted. The function determines automatically which method (fisher or norminv) was used to combine the two p-values into pG, and plots the regions described above accordingly.

Usage

```
plotP(x, threshold=0.05)
```

Arguments

x	A data frame produced by spia function.
threshold	A numerical value between 0 and 1 to be used as significance threshold in inferring pathway significance.

Details

In this plot each pathway is a point and the coordinates are the log of pNDE (using a hypergeometric model) and the p-value from perturbations, pPERT. The oblique lines in the plot show the significance regions based on the combined evidence.

Value

This function does not return any value. It only generates a plot.

Author(s)

Adi Laurentiu Tarca <atarca@med.wayne.edu>, Purvesh Khatri, Sorin Draghici

References

Adi L. Tarca, Sorin Draghici, Purvesh Khatri, et. al, A Signaling Pathway Impact Analysis for Microarray Experiments, 2008, *Bioinformatics*, 2009, 25(1):75-82.

See Also

[spia](#)

Examples

```
# Examples use colorectal cancer dataset
data(colorectalcancer)

# pathway analysis based on combined evidence of ORA and perturbations
# use nB=2000 or larger for more accurate results
res<-spia(de=DE_Colorectal, all=ALL_Colorectal, organism="hsa", nB=200, plots=FALSE, verbose=TRUE, beta=NULL, co

#Generate the evidence plot
plotP(res, threshold=0.1)

res<-spia(de=DE_Colorectal, all=ALL_Colorectal, organism="hsa", nB=200, plots=FALSE, verbose=TRUE, beta=NULL, co

#Generate the evidence plot
plotP(res, threshold=0.1)
```

spia

Signaling Pathway Impact Analysis (SPIA) based on over-representation and signaling perturbations accumulation

Description

This function implements the SPIA algorithm to analyze KEGG signaling pathways.

Usage

```
spia(de=NULL, all=NULL, organism="hsa", pathids=NULL, nB=2000, plots=FALSE, verbose=TRUE, beta=NULL, com
```


Purvesh Khatri, Sorin Draghici, Adi L. Tarca, Sonia S. Hassan, Roberto Romero. A system biology approach for the steady-state analysis of gene signaling networks. Progress in Pattern Recognition, Image Analysis and Applications, Lecture Notes in Computer Science. 4756:32-41, November 2007.

Draghici, S., Khatri, P., Tarca, A.L., Amin, K., Done, A., Voichita, C., Georgescu, C., Romero, R.: A systems biology approach for pathway level analysis. Genome Research, 17, 2007.

See Also

[plotP](#)

Examples

```
# Example using a colorectal cancer dataset obtained using Affymetrix geneChip technology (GEE GSE4107).
# Suppose that proper preprocessing was performed and a two group moderated t-test was applied. The topTab
# result from limma package for this data set is called "top".
#The following lines will annotate each probeset to an entrez ID identifier, will keep the most significant
#gene ID and retain those with FDR<0.05 as differentially expressed.
#You can run these lines if hgu133plus2.db package is available

#data(colorectalcancer)
#x <- hgu133plus2ENTREZID
#top$ENTREZ<-unlist(as.list(x[top$ID]))
#top<-top[!is.na(top$ENTREZ),]
#top<-top[!duplicated(top$ENTREZ),]
#tg1<-top[top$adj.P.Val<0.1,]
#DE_Colorectal=tg1$logFC
#names(DE_Colorectal)<-as.vector(tg1$ENTREZ)
#ALL_Colorectal=top$ENTREZ

data(colorectalcancer)

# pathway analysis using SPIA; # use nB=2000 or higher for more accurate results
res<-spia(de=DE_Colorectal, all=ALL_Colorectal, organism="hsa",beta=NULL,nB=2000,plots=FALSE, verbose=TRUE)
res
# Create the evidence plot
plotP(res)

#now combine pNDE and pPERT using the normal inversion method without running spia function again
res$pG=combfunc(res$pNDE,res$pPERT,combine="norminv")
res$pGFdr=p.adjust(res$pG,"fdr")
res$pGFWER=p.adjust(res$pG,"bonferroni")
plotP(res,threshold=0.05)
#highlight the colorectal cancer pathway in green
points(I(-log(pPERT))~I(-log(pNDE)),data=res[res$ID=="05210",],col="green",pch=19,cex=1.5)
```

Description

The Vessels dataset consists an named vector `DE_Vessels` , which represents the log2 fold changes of the genes chosen as differentially expressed between umbilical veins and arteries tissue (Kim et al, 2008), and the universe of all Entrez gene IDs available on the array, `ALL_Vessels`. The microarray platform used was Illumina's Human-6 v2 expression BeadChip.

Usage

```
data(Vessels)
```

Source

These data was produced at the Perinatology Research Branch, of Wayne State University (Detroit), and accompanies the publication:

Kim JS, Romero R, Tarca A, Lajeunesse C, Han YM, Kim MJ, Suh YL, Draghici S, Mittal P, Gotsch F, Kusanovic JP, Hassan S, Kim CJ, Gene expression profiling demonstrates a novel role for fetal fibrocytes and the umbilical vessels in human fetoplacental development, *J Cell Mol Med*, 2008, PMID: 18298660.

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