Package 'pathifier'

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Type Package

Title Quantify deregulation of pathways in cancer

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Description Pathifier is an algorithm that infers pathway deregulation scores for each tumor sample on the basis of expression data. This score is determined, in a context-specific manner, for every particular dataset and type of cancer that is being investigated. The algorithm transforms gene-level information into pathway-level information, generating a compact and biologically relevant representation of each sample.

License Artistic-1.0

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Contents

pathifier-package *Quantify deregulation of pathways in cancer*

Description

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Details

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Author(s)

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References

Drier Y, Sheffer M, Domany E. Pathway-based personalized analysis of cancer. *Proceedings of the National Academy of Sciences*, 2013, vol. 110(16) pp:6388-6393. (www.pnas.org/cgi/doi/10.1073/pnas.1219651110)

See more information on : http://www.weizmann.ac.il/pathifier/

Examples

```
data(KEGG) # Two pathways of the KEGG database
data(Sheffer) # The colorectal data of Sheffer et al.
PDS<-quantify_pathways_deregulation(sheffer$data, sheffer$allgenes,
  kegg$gs, kegg$pathwaynames, sheffer$normals, attempts = 100,
  logfile="sheffer.kegg.log", min_exp=sheffer$minexp, min_std=sheffer$minstd)
```

KEGG *Two pathways of the KEGG database*

Description

Two pathways (MISMATCH REPAIR and REGULATION OF AUTOPHAGY) of the KEGG database

Usage

```
data(KEGG)
```

Format

`pathwaynames` The names of the pathways

`gs` The list of genes (by official gene symbol) in each pathway

Source

Kanehisa M, Goto S, Sato Y, Furumichi M and Tanabe M. KEGG for integration and interpretation of large-scale molecular datasets. *Nucleic Acids Res*, 2012, Vol 40(Database issue):D109-D114.

Examples

```
data(KEGG)
```

`quantify_pathways_deregulation` *Quantify deregulation of pathways in cancer*

Description

Pathifier is an algorithm that infers pathway deregulation scores for each tumor sample on the basis of expression data. This score is determined, in a context-specific manner, for every particular dataset and type of cancer that is being investigated. The algorithm transforms gene-level information into pathway-level information, generating a compact and biologically relevant representation of each sample.

Usage

```
quantify_pathways_deregulation(data, allgenes, syms, pathwaynames, normals = NULL,
ranks = NULL, attempts = 100, maximize_stability = TRUE, logfile = "", samplings = NULL,
min_exp = 4, min_std = 0.4)
```

Arguments

data	The n x m mRNA expression matrix, where n is the number of genes and m the number of samples.
allgenes	A list of n identifiers of genes.
syms	A list of p pathways, each pathway is a list of the genes it contains (as appear in "allgenes").
pathwaynames	The names of the p pathways.
normals	A list of m logicals, true if a normal sample, false if tumor.
ranks	External knowledge on the ranking of the m samples, if exists (to use initial guess)
attempts	Number of runs to determine stability.
maximize_stability	If true, throw away components leading to low stability of sampling noise.
logfile	Name of the file the log should be written to (use stdout if empty).
samplings	A matrix specifying the samples that should be chosen in each sampling attempt, chooses a random matrix if samplings is NULL.
min_exp	The minimal expression considered as a real signal. Any values below are thresholded to be min_exp.
min_std	The minimal allowed standard deviation of each gene. Genes with lower standard deviation are divided by min_std instead of their actual standard deviation. (Recommended: set min_std to be the technical noise).

Value

scores	The deregulation scores, the main output of pathifier
genesinpathway	The genes of each pathway used to devise its dregulation score
newmeanstd	Average standart devaition after omitting noisy components
origmeanstd	Originial average standart devaition, before omitting noisy components
pathwaysize	The number of components used to devise the pathway score
curves	The prinicipal curve learned for every pathway
curves_order	The order of the points of the prinicipal curve learned for every pathway
z	Z-scores of the expression matrix used to learn prinicpal curve
compin	The components not omitted due to noise
xm	The average expression over all normal samples
xs	The standart devation of expression over all normal samples
center	The centering used by the PCA
rot	The matrix of variable loadings of the PCA
pctaken	The number of principal components used
samplings	A matrix specifying the samples that should be chosen in each sampling attempt
sucess	Pathways for which a deregulation score was sucessfully computed
logfile	Name of the file the log was written to

Author(s)

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Examples

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  kegg$gs, kegg$pathwaynames, sheffer$normals, attempts = 100,
  logfile="sheffer.kegg.log", min_exp=sheffer$minexp, min_std=sheffer$minstd)
```

`Sheffer` *Sheffer et al. colorectal dataset*

Description

Partial data from Sheffer et al. paper

Usage

```
data(Sheffer)
```

Format

`data` the expression data

`samples` sample names

`normals` which of the samples is a normal sample

`minstd` minimal standart deviation allowed

`minexp` minimal value of experssion allowed

`allgenes` the list of genes (by official gene symbol)

Source

Sheffer et.\ al. Association of survival and disease progression with chromosomal instability: A genomic exploration of colorectal cancer. *PNAS*, 2009, Vol 106(17) pp: 7131-7136.

Examples

```
data(Sheffer)
```

Index