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

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pathifier-package   *Quantify deregulation of pathways in cancer*

Description

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Details

Package:	pathifier
Type:	Package
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Date:	2013-03-15
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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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References

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Examples

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  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