

Package ‘transcriptogramer’

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Type Package

Title Transcriptional analysis based on transcriptograms

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Description R package for transcriptional analysis based on transcriptograms, a method to analyze transcriptomes that projects expression values on a set of ordered proteins, arranged such that the probability that gene products participate in the same metabolic pathway exponentially decreases with the increase of the distance between two proteins of the ordering. Transcriptograms are, hence, genome wide gene expression profiles that provide a global view for the cellular metabolism, while indicating gene sets whose expressions are altered.

Depends R (>= 3.4), methods

License GPL (>= 2)

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Imports biomaRt, data.table, doSNOW, foreach, ggplot2, graphics, grDevices, igraph, limma, parallel, progress, RedeR, snow, stats, tidyr, topGO

RoxygenNote 6.1.1

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, RUnit, BiocGenerics

SystemRequirements Java Runtime Environment (>= 6)

URL <https://github.com/arthurvinx/transcriptogramer>

BugReports <https://github.com/arthurvinx/transcriptogramer/issues>

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transcriptogramer-package

Transcriptional analysis based on transcriptograms

Description

R package for transcriptional analysis based on transcriptograms, a method to analyze transcriptomes that projects expression values on a set of ordered proteins, arranged such that the probability that gene products participate in the same metabolic pathway exponentially decreases with the increase of the distance between two proteins of the ordering. Transcriptograms are, hence, genome wide gene expression profiles that provide a global view for the cellular metabolism, while indicating gene sets whose expression are altered.

Author(s)

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References

da Silva, S. R. M., Perrone, G. C., Dinis, J. M., and de Almeida, R. M. C. (2014). Reproducibility enhancement and differential expression of non predefined functional gene sets in human genome. *BMC Genomics*.

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Morais, D. A. A., Almeida, R. M. C. and Dalmolin, R. J. S. (2019). Transcriptogramer: an R/Bioconductor package for transcriptional analysis based on protein–protein interaction. *Bioinformatics*.

Rybarczyk-Filho, J. L., Castro, M. A. A., Dalmolin, R. J. S., Moreira, J. C. F., Brunnet, L. G., and de Almeida, R. M. C. (2011). Towards a genome-wide transcriptogram: the *Saccharomyces cerevisiae* case. *Nucleic Acids Research*, 39(8), 3005-3016.

Xavier, L. A. da C., Bezerra, J. F., de Rezende, A. A., Oliveira, R. A. de C., Dalmolin, R. J. S., do Amaral, V. S. (2017). Analysis of genome instability biomarkers in children with non-syndromic orofacial clefts. *Mutagenesis*, 32(2), 313–321.

See Also

Bioconductor: [release](#), [devel](#)

Github: [source code](#), [bug reports](#)

References: (da Silva et al., 2014; de Almeida et al., 2016; Ferrareze et al., 2017; Morais et al., 2019; Rybarczyk-Filho et al., 2011; Xavier et al., 2017)

association

Association

Description

A subset of the Homo sapiens protein network data from STRINGdb, release 11. This subset contains only associations of proteins of combined score greater than or equal to 900.

Usage

association

Format

Each row of the data.frame contains two variables:

V1 The ENSEMBL Peptide ID of the first protein

V2 The ENSEMBL Peptide ID of the second protein

Author(s)

Diego Morais

See Also

[Hs900](#)

Examples

association

clusterEnrichment	<i>Term enrichment</i>
-------------------	------------------------

Description

If `species` is a character, this method uses the **biomaRt** package to build a Protein2GO list, if `species` is a `data.frame`, it will be used instead. The Protein2GO list will be used with the **topGO** package to detect the most significant terms of each cluster present in the DE slot of the object.

Usage

```
clusterEnrichment(object, universe = NULL, species,
  ontology = "biological process", algorithm = "classic",
  statistic = "fisher", pValue = 0.05, adjustMethod = "BH",
  nCores = 1L, onlyGenesInDE = FALSE)

## S4 method for signature 'Transcriptogram'
clusterEnrichment(object, universe = NULL,
  species, ontology = "biological process", algorithm = "classic",
  statistic = "fisher", pValue = 0.05, adjustMethod = "BH",
  nCores = 1L, onlyGenesInDE = FALSE)
```

Arguments

<code>object</code>	An object of class <code>Transcriptogram</code> .
<code>universe</code>	A character vector containing ENSEMBL Peptide IDs, or <code>NULL</code> , if the universe is composed by all the proteins present in the ordering slot of object.
<code>species</code>	A character string specifying the species; or a <code>data.frame</code> containing two columns, the first one with ENSEMBL Peptide IDs (character), which may, or not, to contain the taxonomy ID of the species as prefix, and the second containing its respective Gene Ontology term (character).
<code>ontology</code>	A character string specifying the Gene Ontology domain, ignoring case sensitivity, the possible values are 'biological process', 'cellular component' and 'molecular function'. The default value of this argument is 'biological process'.
<code>algorithm</code>	Character string specifying which algorithm to use, the possible values are 'classic', 'elim', 'weight', 'weight01', 'lea' and 'parentchild'. The default value of this argument is 'classic'.
<code>statistic</code>	Character string specifying which test to use, the possible values are 'fisher', 'ks', 't', 'sum' and 'globaltest'. The default value of this argument is 'fisher'.
<code>pValue</code>	A numeric value between 0 and 1 giving the required family-wise error rate or false discovery rate. The default value of this argument is 0.05.
<code>adjustMethod</code>	Character string specifying p-value adjustment method, the possible values are 'none', 'BH', 'fdr' (equivalent to 'BH'), 'BY', 'hochberg', 'hommel', 'bonferroni', and 'holm'. The default value of this argument is 'BH'.

nCores	An integer number, referring to the number of processing cores to be used; or a logical value, TRUE indicating that all processing cores should be used, and FALSE indicating the use of just one processing core. The default value of this argument is 1.
onlyGenesInDE	Logical value, set as TRUE to use only the genes in the DE slot. Set as FALSE to use all the genes referring to the positions in the clusters slot. The default value of this argument is FALSE.

Value

This method creates a data.frame, containing the most significant terms of each cluster, to feed the Terms slot of an object of class Transcriptogram.

Author(s)

Diego Morais

See Also

[differentiallyExpressed](#), [transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [HsBPterms](#), [association](#), [transcriptogramStep1](#), [transcriptogramStep2](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)
levels <- c(rep(FALSE, 3), rep(TRUE, 3))
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01)
transcriptogram <- clusterEnrichment(transcriptogram, species = "Homo sapiens",
pValue = 0.005)

## this call also works
transcriptogram <- clusterEnrichment(transcriptogram, species = HsBPterms,
pValue = 0.005)

## End(Not run)
```

clusterVisualization *Displays graphs of the differentially expressed clusters*

Description

This method uses the **RedeR** package to display graphs of the differentially expressed clusters.

Usage

```
clusterVisualization(object, maincomp = FALSE, connected = FALSE,  
  host = "127.0.0.1", port = 9091, clusters = NULL,  
  onlyGenesInDE = FALSE, colors = NULL)  
  
## S4 method for signature 'Transcriptogram'  
clusterVisualization(object,  
  maincomp = FALSE, connected = FALSE, host = "127.0.0.1",  
  port = 9091, clusters = NULL, onlyGenesInDE = FALSE,  
  colors = NULL)
```

Arguments

object	An object of class Transcriptogram.
maincomp	Logical value, set as TRUE if you want to display only the main component of each cluster. The default value of this argument is FALSE.
connected	Logical value, set as TRUE if you want to display only connected nodes. The default value of this argument is FALSE.
host	The domain name of the machine that is running the RedeR XML-RPC server.
port	An integer specifying the port on which the XML-RPC server should listen.
clusters	An integer vector specifying the clusters to be displayed. If NULL, all clusters will be displayed.
onlyGenesInDE	Logical value, set as TRUE to use only the genes in the DE slot. Set as FALSE to use all the genes referring to the positions in the clusters slot. The default value of this argument is FALSE.
colors	Color vector used to distinguish the clusters. If NULL, the rainbow palette will be used to generate the colors. The color vector must contain a color for each cluster.

Details

RedeR package requirements: Java Runtime Environment (≥ 6).

Value

This method returns an object of the RedPort Class.

Author(s)

Diego Morais

See Also

[differentiallyExpressed](#), [transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [association](#), [transcriptogramStep1](#), [transcriptogramStep2](#), [RedPort](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)
levels <- c(rep(FALSE, 3), rep(TRUE, 3))
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01,
DEsymbols)
rdp <- clusterVisualization(transcriptogram)

## End(Not run)
```

connectivityProperties

Calculates average graph properties as function of node connectivity

Description

Calculates network properties as function of node connectivity/degree (k), such as: probability of a protein of the graph has degree k, average assortativity of the nodes of degree k, and the average clustering coefficient of the nodes of degree k.

Usage

```
connectivityProperties(object)

## S4 method for signature 'Transcriptogram'
connectivityProperties(object)
```

Arguments

object An object of class Transcriptogram.

Details

The assortativity of a node can be measured by the average degree of its neighbors.

Value

This method returns a data.frame containing: unique degrees (k) of the nodes of the graph, probability (pk) of a node of the graph has degree k, average assortativity (ak) of the nodes of degree k, and the average clustering coefficient (ck) of the nodes of degree k.

Author(s)

Diego Morais

See Also

[transcriptogramPreprocess](#), [Hs900](#), [association](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900)
## Not run:
cProperties <- connectivityProperties(transcriptogram)

## End(Not run)
```

DE

Get DE

Description

Gets the content of the DE slot of an object of class Transcriptogram.

Usage

```
DE(object)

## S4 method for signature 'Transcriptogram'
DE(object)
```

Arguments

object An object of class Transcriptogram.

Value

This method returns the content of the DE slot of an object of class Transcriptogram.

Author(s)

Diego Morais

See Also

[Hs900](#), [association](#), [transcriptogramPreprocess](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)
levels <- c(rep(FALSE, 3), rep(TRUE, 3))
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01)
DE(transcriptogram)

## End(Not run)
```

DEsymbols

Dictionary Protein2Symbol

Description

A mapping between ENSEMBL Peptide ID and Symbol (Gene Name). This dataset was created to map the Homo sapiens proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

DEsymbols

Format

Each row of the data.frame contains two variables:

ensembl_peptide_id The ENSEMBL Peptide ID

external_gene_name The Gene Name

Author(s)

Diego Morais

Examples

DEsymbols

differentiallyExpressed

Identify which genes are differentially expressed

Description

This method uses the **limma** package to identify which genes are differentially expressed, meeting the pValue requirement, for the contrast "case-control". The levels length must be equal to the number of samples present in the transcriptogramS2 slot of the object, and its contents is related to the order that the samples appear. FALSE must be used to indicate case samples, and TRUE to indicate control samples. If species is NULL, no translation will be done, if species is a character, the **biomaRt** package will be used to translate the ENSEMBL Peptide ID to Symbol (Gene Name), and if species is a data.frame, it will be used instead. If the translation fail for some protein, its ENSEMBL Peptide ID will be present into the Symbol column. This method also groups the differentially expressed proteins detected in clusters, and plots a graphical representation of this clustering.

Usage

```
differentiallyExpressed(object, levels, pValue = 0.05,
  species = object@Protein2Symbol, adjustMethod = "BH",
  trend = FALSE, title = "Differential expression",
  boundaryConditions = TRUE, colors = NULL)

## S4 method for signature 'Transcriptogram'
differentiallyExpressed(object, levels,
  pValue = 0.05, species = object@Protein2Symbol,
  adjustMethod = "BH", trend = FALSE,
  title = "Differential expression", boundaryConditions = TRUE,
  colors = NULL)
```

Arguments

object	An object of class Transcriptogram.
levels	A logical vector that classify the columns, referring to samples, of the transcriptogramS2 slot of the object. FALSE must be used to indicate case samples, and TRUE to indicate control samples.
pValue	A numeric value between 0 and 1 giving the required family-wise error rate or false discovery rate. The default value of this argument is 0.05.
species	A character string that will be used, ignoring case sensitivity, to translate the ENSEMBL Peptide ID to Symbol (Gene Name); or a data.frame containing two columns, the first one with ENSEMBL Peptide IDs (character), which may, or not, to contain the taxonomy ID of the species as prefix, and the second containing its respective Symbol (character). The default value of this argument is the content of the object Protein2Symbol slot.

<code>adjustMethod</code>	Character string specifying p-value adjustment method, the possible values are 'none', 'BH', 'fdr' (equivalent to 'BH'), 'BY' and 'holm'. The default value for this argument is 'BH'.
<code>trend</code>	Logical value, set as TRUE to use the limma-trend approach for RNA-Seq. The default value of this argument is FALSE.
<code>title</code>	An overall title for the plot. The default value of this argument is "Differential expression"
<code>boundaryConditions</code>	Logical value, defines whether the clusters limits will be extended using the current value of the radius slot. If TRUE, nearby clusters will be merged if its limits overlap. The default value of this argument is TRUE.
<code>colors</code>	Color vector used to distinguish the clusters. If NULL, the rainbow palette will be used to generate the colors. The color vector must contain a color for each cluster.

Value

This method creates a data.frame to feed the DE slot of an object of class Transcriptogram. This data.frame of differentially expressed proteins contains log2-fold-change, raw p-values, adjusted p-values, and an integer number that indicates if the protein is downregulated (-1) or upregulated (1).

Author(s)

Diego Morais

See Also

[transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [association](#), [DEsymbols](#), [transcriptogram-Step1](#), [transcriptogramStep2](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)
levels <- c(rep(FALSE, 3), rep(TRUE, 3))
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01)

## translating ENSEMBL Peptide IDs to Symbols
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01,
"Homo sapiens")

## these calls also works
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01,
"H sapiens")

transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01,
DEsymbols)
```

```
## End(Not run)
```

enrichmentPlot *Projects Gene Ontology terms on the ordering*

Description

Plots the ratio (number of genes related to a term inside the window/total number of genes in the window) from a set of Gene Ontology terms.

Usage

```
enrichmentPlot(object, nCores = 1L, nTerms = 1L, GOIDs = NULL,  
                title = "Enrichment", alpha = 0.15, colors = NULL)  
  
## S4 method for signature 'Transcriptogram'  
enrichmentPlot(object, nCores = 1L,  
                nTerms = 1L, GOIDs = NULL, title = "Enrichment", alpha = 0.15,  
                colors = NULL)
```

Arguments

object	An object of class Transcriptogram.
nCores	An integer number, referring to the number of processing cores to be used; or a logical value, TRUE indicating that all processing cores should be used, and FALSE indicating the use of just one processing core. The default value of this argument is 1.
nTerms	An integer number referring to the number of top terms from each cluster. The default value of this argument is 1.
GOIDs	A character vector containing the Gene Ontology accessions to be plotted. If NULL, the top nTerms of each cluster will be used.
title	An overall title for the plot. The default value of this argument is "Enrichment"
alpha	The alpha value indicates the color transparency of the clusters regions. This value goes from 0 to 1, where 0 is completely transparent, and 1 is opaque.
colors	Color vector used to distinguish the clusters. If NULL, the rainbow palette will be used to generate the colors. The color vector must contain a color for each cluster.

Value

This method returns an ggplot2 object.

Author(s)

Diego Morais

See Also

[differentiallyExpressed](#), [transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [HsBPTerms](#), [association](#), [transcriptogramStep1](#), [transcriptogramStep2](#), [clusterEnrichment](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)
levels <- c(rep(FALSE, 3), rep(TRUE, 3))
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01)
transcriptogram <- clusterEnrichment(transcriptogram, species = "Homo sapiens",
pValue = 0.005)
enrichmentPlot(transcriptogram)

## End(Not run)
```

GPL570

Dictionary Protein2Probe

Description

A mapping between ENSEMBL Peptide ID and probe identifier, for the Homo sapiens and the platform GPL570, [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array.

Usage

GPL570

Format

Each row of the data.frame contains two variables:

Protein The ENSEMBL Peptide ID

Probe The probe identifier

Details

This dataset was created to map the Homo sapiens proteins, from STRINGdb release 11, of combined score greater than or equal to 700.

Author(s)

Diego Morais

See Also[GSE9988](#)**Examples**

GPL570

GSE9988*Dataset containing expression values*

Description

Expression values, obtained by microarray, of 3 cases and 3 controls referring to the Gene Expression Omnibus accession number GSE9988. The data.frame has 6 columns, each one contains expression values of a sample, the first 3 columns are case samples, and the last 3 are control samples. Each row contains expression values obtained by the probe mentioned in its respective row-name. The expression values were normalized using the **affy** package and, to reduce the required storage space, this data.frame contains only 6 samples (GSM252443, GSM252444, GSM252445, GSM252465, GSM252466, GSM252467). The rows of each sample are composed only by probes mapped, by the GPL570 dictionary, to proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

GSE9988

Format

An object of class data.frame with 27828 rows and 6 columns.

Author(s)

Diego Morais

Source[GSE9988](#)**See Also**[GPL570](#)**Examples**

GSE9988

Hs700	<i>Ordered Homo sapiens proteins of combined score greater than or equal to 700</i>
-------	---

Description

A character vector containing the Homo sapiens proteins, from STRINGdb release 11, of combined score greater than or equal to 700.

Usage

Hs700

Format

An object of class character of length 17185.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 1451645000.

Author(s)

Diego Morais

Examples

Hs700

Hs800	<i>Ordered Homo sapiens proteins of combined score greater than or equal to 800</i>
-------	---

Description

A character vector containing the Homo sapiens proteins, from STRINGdb release 11, of combined score greater than or equal to 800.

Usage

Hs800

Format

An object of class character of length 14711.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 808731532.

Author(s)

Diego Morais

Examples

Hs800

Hs900

Ordered Homo sapiens proteins of combined score greater than or equal to 900

Description

A character vector containing the Homo sapiens proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

Hs900

Format

An object of class character of length 12396.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 489730786.

Author(s)

Diego Morais

Examples

Hs900

HsBPTerms

Dictionary Protein2GO

Description

A mapping between ENSEMBL Peptide ID and Gene Ontology, biological processes, terms. This dataset was created to map the Homo sapiens proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

HsBPTerms

Format

Each row of the data.frame contains two variables:

ensembl_peptide_id The ENSEMBL Peptide ID

go_id The Gene Ontology ID

Author(s)

Diego Morais

Examples

HsBPTerms

Mm700

Ordered Mus musculus proteins of combined score greater than or equal to 700

Description

A character vector containing the Mus musculus proteins, from STRINGdb release 11, of combined score greater than or equal to 700.

Usage

Mm700

Format

An object of class character of length 16690.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 964301098.

Author(s)

Diego Morais

Examples

Mm700

Mm800	<i>Ordered Mus musculus proteins of combined score greater than or equal to 800</i>
-------	---

Description

A character vector containing the Mus musculus proteins, from STRINGdb release 11, of combined score greater than or equal to 800.

Usage

Mm800

Format

An object of class character of length 13655.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 497514808.

Author(s)

Diego Morais

Examples

Mm800

Mm900 *Ordered Mus musculus proteins of combined score greater than or equal to 900*

Description

A character vector containing the Mus musculus proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

Mm900

Format

An object of class character of length 11141.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 282900384.

Author(s)

Diego Morais

Examples

Mm900

orderingProperties *Calculates graph properties projected on the ordered proteins*

Description

Calculates protein (node) properties, such as: degree/connectivity, number of triangles and clustering coefficient; and properties of the window, region of n ($\text{radius} * 2 + 1$) proteins centered at a protein, such as: connectivity, clustering coefficient and modularity.

Usage

```
orderingProperties(object, nCores = 1L)
```

```
## S4 method for signature 'Transcriptogram'  
orderingProperties(object, nCores = 1L)
```

Arguments

object	An object of class Transcriptogram.
nCores	An integer number, referring to the number of processing cores to be used; or a logical value, TRUE indicating that all processing cores should be used, and FALSE indicating the use of just one processing core. The default value of this argument is 1.

Details

Connectivity/degree of a node is the number of edges it presents. A triangle of a node represents a pair of connected neighbors, the number of triangles on the adjacency list of a node is required to calculate its clustering coefficient. The clustering coefficient of a node measures, in the interval [0, 1], the likelihood that any two of its neighbors are themselves connected, this is calculated by the ratio between the number of triangles that the node has, and the maximum possible number of edges on its cluster ($\text{nodeTriangles} / (\text{nodeDegree} * (\text{nodeDegree} - 1) / 2)$). The window connectivity is the average connectivity calculated over the window. The window clustering coefficient, a value in the interval [0, 1], is the average clustering coefficient calculated over the window. The window modularity, a value in the interval [0, 1], is defined as the ratio between the total number of edges between any two nodes of the window, and the sum of the degrees of the nodes presents in the window. The window considers periodic boundary conditions to deal with proteins near the ends of the ordering.

Value

This method returns a data.frame containing: ENSEMBL Peptide ID, its position on the ordering, node degree, number of triangles and clustering coefficient, and window connectivity, clustering coefficient and modularity.

Author(s)

Diego Morais

References

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See Also

[transcriptogramPreprocess](#), [Hs900](#), [association](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 2)
## Not run:
oProperties <- orderingProperties(transcriptogram)

## End(Not run)
```

radius<-

Radius

Description

Retrieve or set the content of the radius slot of an object of class `Transcriptogram`.

Usage

```
radius(object) <- value

radius(object)

## S4 replacement method for signature 'Transcriptogram'
radius(object) <- value

## S4 method for signature 'Transcriptogram'
radius(object)
```

Arguments

<code>object</code>	An object of class <code>Transcriptogram</code> .
<code>value</code>	An non-negative integer referring to the window radius required for some methods.

Value

This method returns the content of the radius slot of an object of class `Transcriptogram`.

Author(s)

Diego Morais

See Also

[Hs900](#), [association](#), [transcriptogramPreprocess](#), [transcriptogramStep2](#), [orderingProperties](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
radius(transcriptogram) <- 80
radius(transcriptogram)
```

Rn700

Ordered Rattus norvegicus proteins of combined score greater than or equal to 700

Description

A character vector containing the Rattus norvegicus proteins, from STRINGdb release 11, of combined score greater than or equal to 700.

Usage

Rn700

Format

An object of class character of length 17021.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 920071574.

Author(s)

Diego Morais

Examples

Rn700

Rn800 *Ordered Rattus norvegicus proteins of combined score greater than or equal to 800*

Description

A character vector containing the Rattus norvegicus proteins, from STRINGdb release 11, of combined score greater than or equal to 800.

Usage

Rn800

Format

An object of class character of length 13887.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 453159596.

Author(s)

Diego Morais

Examples

Rn800

Rn900 *Ordered Rattus norvegicus proteins of combined score greater than or equal to 900*

Description

A character vector containing the Rattus norvegicus proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

Rn900

Format

An object of class character of length 10788.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 222438518.

Author(s)

Diego Morais

Examples

Rn900

Sc700

Ordered Saccharomyces cerevisiae proteins of combined score greater than or equal to 700

Description

A character vector containing the Saccharomyces cerevisiae proteins, from STRINGdb release 11, of combined score greater than or equal to 700.

Usage

Sc700

Format

An object of class character of length 6157.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 163374428.

Author(s)

Diego Morais

Examples

Sc700

Sc800 *Ordered Saccharomyces cerevisiae proteins of combined score greater than or equal to 800*

Description

A character vector containing the Saccharomyces cerevisiae proteins, from STRINGdb release 11, of combined score greater than or equal to 800.

Usage

Sc800

Format

An object of class character of length 5847.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 85930192.

Author(s)

Diego Morais

Examples

Sc800

Sc900 *Ordered Saccharomyces cerevisiae proteins of combined score greater than or equal to 900*

Description

A character vector containing the Saccharomyces cerevisiae proteins, from STRINGdb release 11, of combined score greater than or equal to 900.

Usage

Sc900

Format

An object of class character of length 5213.

Details

Generated by The Transcriptogramer V.1.0 for Windows. Input arguments: isothermal steps - 100; Monte Carlo steps - 20000; cooling factor - 0.5; alpha value - 1.0; percentual energy for initial temperature - 0.0001. Final energy: 38447790.

Author(s)

Diego Morais

Examples

Sc900

Terms

Get terms

Description

Gets the content of the Terms slot of an object of class Transcriptogram.

Usage

```
Terms(object)
```

```
## S4 method for signature 'Transcriptogram'  
Terms(object)
```

Arguments

object An object of class Transcriptogram.

Value

This method returns the content of the Terms slot of an object of class Transcriptogram.

Author(s)

Diego Morais

See Also

[differentiallyExpressed](#), [transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [HsBPterms](#), [association](#), [transcriptogramStep1](#), [transcriptogramStep2](#), [clusterEnrichment](#)

Examples

```

transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)
levels <- c(rep(FALSE, 3), rep(TRUE, 3))
transcriptogram <- differentiallyExpressed(transcriptogram, levels, 0.01)
transcriptogram <- clusterEnrichment(transcriptogram, species = "Homo sapiens",
pValue = 0.005)
Terms(transcriptogram)

## End(Not run)

```

Transcriptogram-class *Class Transcriptogram*

Description

This S4 class includes methods to use expression values with ordered proteins.

Slots

association A data.frame containing two columns, with rows containing ENSEMBL Peptide IDs that are connected.

ordering A data.frame containing two columns, the first one with ENSEMBL Peptide IDs, and the second containing its respective position.

transcriptogramS1 A data.frame produced as the result of averaging over all identifiers related to the same protein.

transcriptogramS2 A data.frame produced as the result of averaging over the window.

radius An non-negative integer referring to the window radius.

status An integer used internally to check the status of the object.

DE A data.frame of differentially expressed proteins.

clusters A list indicating the first and the last position belonging to each cluster.

pbcc Logical value used internally to indicate the overlapping of the first and the last cluster.

Protein2Symbol A data.frame containing two columns, the first one with ENSEMBL Peptide IDs, and the second containing its respective Symbol.

Protein2GO A data.frame containing two columns, the first one with ENSEMBL Peptide IDs, and the second containing its respective Gene Ontology accession.

Terms A data.frame containing the enriched Gene Ontology terms.

genesInTerm A list of GO terms and its respective ENSEMBL Peptide IDs, feeded by the clusterEnrichment() method.

Author(s)

Diego Morais

See Also

[transcriptogramPreprocess](#), [DE](#), [radius](#), [orderingProperties](#), [connectivityProperties](#), [transcriptogramStep1](#), [transcriptogramStep2](#), [differentiallyExpressed](#), [clusterVisualization](#), [clusterEnrichment](#), [enrichmentPlot](#)

transcriptogramPreprocess

Creates an object of class Transcriptogram

Description

Constructor for the Transcriptogram object.

Usage

```
transcriptogramPreprocess(association, ordering, radius = 0L)
```

Arguments

association	A matrix, or data.frame, containing two columns of ENSEMBL Peptide IDs (character); or the path for a file containing two columns, no header, with rows composed by the ENSEMBL Peptide IDs of two proteins that are connected.
ordering	A character vector containing ordered ENSEMBL Peptide IDs; a data.frame containing two columns, the first one with ENSEMBL Peptide IDs (character), and the second containing its respective position (non-negative integer); or the path for a file containing two columns, a row for the headers, with rows composed respectively by a ENSEMBL Peptide ID and its respective position.
radius	An non-negative integer referring to the window radius required for some methods.

Value

A preprocessed object of class Transcriptogram.

Author(s)

Diego Morais

See Also

[Transcriptogram-class](#), [association](#), [Hs900](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs9000)
```

```
transcriptogramStep1 Calculates the average of the expression values related to the same protein
```

Description

For each transcriptome sample, this method assigns to each protein the average of the expression values of all the identifiers related to it. It is necessary a dictionary to map the identifiers to proteins.

Usage

```
transcriptogramStep1(object, expression, dictionary, nCores = 1L)

## S4 method for signature 'Transcriptogram'
transcriptogramStep1(object, expression,
  dictionary, nCores = 1L)
```

Arguments

object	An object of class Transcriptogram.
expression	A matrix, or data.frame, containing normalized expression values from samples of microarrays or RNA-Seq (log2-counts-per-million).
dictionary	A matrix, or data.frame, containing two columns, the first column must contains the ENSEMBL Peptide ID, and the second column must contains values that appear as rownames in expression, in order to recognize the ENSEMBL Peptide ID of the other column.
nCores	An integer number, referring to the number of processing cores to be used; or a logical value, TRUE indicating that all processing cores should be used, and FALSE indicating the use of just one processing core. The default value of this argument is 1.

Value

This method creates a data.frame to feed the transcriptogramS1 slot of an object of class Transcriptogram. Each row of the data.frame contains: an ENSEMBL Peptide ID, its respective position in the ordering and the mean of the expression values of the identifiers related to the same protein.

Author(s)

Diego Morais

References

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See Also

[transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [association](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)

## End(Not run)
```

`transcriptogramStep2` *Calculates the average of the expression values using a sliding window*

Description

To each position of the ordering, this method assigns a value equal to the average of the expression values inside a window, region of n ($\text{radius} * 2 + 1$) proteins centered at a protein. The window considers periodic boundary conditions to deal with proteins near the ends of the ordering.

Usage

```
transcriptogramStep2(object, nCores = 1L)

## S4 method for signature 'Transcriptogram'
transcriptogramStep2(object, nCores = 1L)
```

Arguments

object	An object of class Transcriptogram.
nCores	An integer number, referring to the number of processing cores to be used; or a logical value, TRUE indicating that all processing cores should be used, and FALSE indicating the use of just one processing core. The default value of this argument is 1.

Value

This method creates a data.frame to feed the transcriptogramS2 slot of an object of class Transcriptogram. Each row of the data.frame contains: the ENSEMBL Peptide ID used as center of the window, its position on the ordering, and the mean of the expression values of the window.

Author(s)

Diego Morais

References

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See Also

[transcriptogramPreprocess](#), [GSE9988](#), [GPL570](#), [Hs900](#), [association](#), [transcriptogramStep1](#)

Examples

```
transcriptogram <- transcriptogramPreprocess(association, Hs900, 50)
## Not run:
transcriptogram <- transcriptogramStep1(transcriptogram, GSE9988, GPL570)
transcriptogram <- transcriptogramStep2(transcriptogram)

## End(Not run)
```

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