Package 'transcriptogramer'

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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.

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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

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VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, RUnit, BiocGenerics

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

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Contents

transcriptogramer-package . . . 3
association . . . 4
clusterEnrichment . . . 5
clusterVisualization . . . 6
connectivityProperties . . . 8
DE . . . 9
DEsymbols . . . 10
differentiallyExpressed . . . 11
enrichmentPlot . . . 13
GPL570 . . . 14
GSE9988 . . . 15
Hs700 . . . 16
Hs800 . . . 16
Hs900 . . . 17
HsBPTerms . . . 18
Mm700 . . . 18
Mm800 . . . 19
Mm900 . . . 20
orderingProperties . . . 20
radius<- . . . 22
Rn700 . . . 23
Rn800 . . . 24
Rn900 . . . 24
Sc700 . . . 25
Sc800 . . . 26
Sc900 . . . 26
Terms . . . 27
Transcriptogram-class . . . 28
transcriptogramPreprocess . . . 29
transcriptogramStep1 . . . 30
transcriptogramStep2 . . . 31

Index **34**

`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

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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 *Term enrichment*

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

object	An object of class Transcriptogram.
universe	A character vector containing ENSEMBL Peptide IDs, or NULL, if the universe is composed by all the proteins present in the ordering slot of object.
species	A character string specifying the species; 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 Gene Ontology term (character).
ontology	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'.
algorithm	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'.
statistic	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'.
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.
adjustMethod	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 lenght 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.

adjustMethod	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'.
trend	Logical value, set as TRUE to use the limma-trend approach for RNA-Seq. The default value of this argument is FALSE.
title	An overall title for the plot. The default value of this argument is "Differential expression"
boundaryConditions	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.
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 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, 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)

## 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 rowname. 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 *Ordered Homo sapiens proteins of combined score greater than or equal to 700*

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 *Ordered Homo sapiens proteins of combined score greater than or equal to 800*

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 — *Ordered Mus musculus proteins of combined score greater than or equal to 800*

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 (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 (nodeTriangles / (nodeDegree * (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

`object`	An object of class Transcriptogram.
`value`	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.

`pbc` 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, Hs900)
```

`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 (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

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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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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)
```

Index

∗ **datasets**
association, 4
DEsymbols, 10
GPL570, 14
GSE9988, 15
Hs700, 16
Hs800, 16
Hs900, 17
HsBPTerms, 18
Mm700, 18
Mm800, 19
Mm900, 20
Rn700, 23
Rn800, 24
Rn900, 24
Sc700, 25
Sc800, 26
Sc900, 26

association, 4, *6, 7*, *9*, *12*, *14*, *22, 23*, *27*, *29*, *31*, *33*

clusterEnrichment, 5, *14*, *27*, *29*
clusterEnrichment,Transcriptogram-method *(*clusterEnrichment*)*, 5
clusterEnrichment-method *(*clusterEnrichment*)*, 5
clusterVisualization, 6, *29*
clusterVisualization,Transcriptogram-method *(*clusterVisualization*)*, 6
clusterVisualization-method *(*clusterVisualization*)*, 6
connectivityProperties, 8, *29*
connectivityProperties,Transcriptogram-method *(*connectivityProperties*)*, 8
connectivityProperties-method *(*connectivityProperties*)*, 8

DE, 9, *29*
DE,Transcriptogram-method *(*DE*)*, 9
DE-method *(*DE*)*, 9
DEsymbols, 10, *12*
differentiallyExpressed, *6, 7*, 11, *14*, *27*, *29*
differentiallyExpressed,Transcriptogram-method *(*differentiallyExpressed*)*, 11
differentiallyExpressed-method *(*differentiallyExpressed*)*, 11

enrichmentPlot, 13, *29*
enrichmentPlot,Transcriptogram-method *(*enrichmentPlot*)*, 13
enrichmentPlot-method *(*enrichmentPlot*)*, 13

GPL570, *6, 7*, *12*, *14*, 14, *15*, *27*, *31*, *33*
GSE9988, *6, 7*, *12*, *14, 15*, 15, *27*, *31*, *33*

Hs700, 16
Hs800, 16
Hs900, *4*, *6, 7*, *9*, *12*, *14*, 17, *22, 23*, *27*, *29*, *31*, *33*
HsBPTerms, *6*, *14*, 18, *27*

Mm700, 18
Mm800, 19
Mm900, 20

orderingProperties, 20, *23*, *29*
orderingProperties,Transcriptogram-method *(*orderingProperties*)*, 20
orderingProperties-method *(*orderingProperties*)*, 20

radius, *29*
radius *(*radius<-*)*, 22
radius,Transcriptogram-method *(*radius<-*)*, 22
radius-method *(*radius<-*)*, 22
radius<-, 22

radius<-,Transcriptogram-method
(radius<-), 22
RedPort, 7
Rn700, 23
Rn800, 24
Rn900, 24

Sc700, 25
Sc800, 26
Sc900, 26

Terms, 27
Terms,Transcriptogram-method (Terms), 27
Terms-method (Terms), 27
Transcriptogram-class, 28, 29
transcriptogramer
(transcriptogramer-package), 3
transcriptogramer-package, 3
transcriptogramPreprocess, 6, 7, 9, 12, 14, 22, 23, 27, 29, 29, 31, 33
transcriptogramStep1, 6, 7, 12, 14, 27, 29, 30, 33
transcriptogramStep1,Transcriptogram-method
(transcriptogramStep1), 30
transcriptogramStep1-method
(transcriptogramStep1), 30
transcriptogramStep2, 6, 7, 12, 14, 23, 27, 29, 31
transcriptogramStep2,Transcriptogram-method
(transcriptogramStep2), 31
transcriptogramStep2-method
(transcriptogramStep2), 31