Package ‘PPInfer’

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Type Package

Title Inferring functionally related proteins using protein interaction networks

Description Interactions between proteins occur in many, if not most, biological processes. Most proteins perform their functions in networks associated with other proteins and other biomolecules. This fact has motivated the development of a variety of experimental methods for the identification of protein interactions. This variety has in turn ushered in the development of numerous different computational approaches for modeling and predicting protein interactions. Sometimes an experiment is aimed at identifying proteins closely related to some interesting proteins. A network based statistical learning method is used to infer the putative functions of proteins from the known functions of its neighboring proteins on a PPI network. This package identifies such proteins often involved in the same or similar biological functions.

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PPIfer-package Inferring functionally related proteins using protein interaction networks

Description

Interactions between proteins occur in many, if not most, biological processes. Most proteins perform their functions in networks associated with other proteins and other biomolecules. This fact has motivated the development of a variety of experimental methods for the identification of protein interactions. This variety has in turn ushered in the development of numerous different computational approaches for modeling and predicting protein interactions. Sometimes an experiment is aimed at identifying proteins closely related to some interesting proteins. A network based statistical learning method is used to infer the putative functions of proteins from the known functions of its neighboring proteins on a PPI network. This package identifies such proteins often involved in the same or similar biological functions.

Details

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Author(s)

Dongmin Jung, Xijin Ge

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enrich.net  

Visualize network for the functional enrichment analysis

Description

The connection between nodes depends on the proportion of overlapping genes between two categories.

Usage

enrich.net(x, gene.set, node.id, node.name = node.id, pvalue,  
    n = 50, numChar = NULL, pvalue.cutoff = 0.05,  
    edge.cutoff = 0.05, degree.cutoff = 0,  
    edge.width = function(x) {10*x^2},  
    node.size = function(x) {2.5*log10(x)},  
    group = FALSE, group.color = c('red', 'green'),  
    group.shape = c('circle', 'square'),  
    legend.parameter = list('topright'),  
    show.legend = TRUE, ...)  

Arguments

x  
    a result with category and p-value of gene sets
gene.set  
    gene sets which is already used for functional enrichment
node.id  
    name of gene sets
node.name  
    label of nodes in the network (default: node.id)
pvalue  
    pvalues for categories
n  
    number of top categories (default: 50)
numChar  
    the maximal number of characters of the label of gene sets
pvalue.cutoff  
    nodes with p-values which are greater than pvalue.cutoff are removed (default: 0.05)
edge.cutoff  
    edges with the proportion which is less than edge.cutoff are removed (default: 0.05)
degree.cutoff  
    nodes with the degrees which are less than degree.cutoff are removed (default: 0)
edge.width  
    width of edges
node.size  
    size of nodes
group  
    variable for group
group.color  
    color for group (default: red and green for 2 groups)
group.shape  
    shape for group (default: circle and square for 2 groups)
legend.parameter  
    list of parameters for the legend
show.legend  
    show the legend (default: TRUE)
...  
    additional parameters for the igraph
Value

plot for the network. The size of nodes is proportional to the size of gene sets. The more significant categories are, the less transparent their nodes are.

Author(s)

Dongmin Jung, Xijin Ge

References


See Also

igraph

Examples

```r
data(examplePathways)
data(exampleRanks)
set.seed(1)
result.GSEA <- fgsea(examplePathways, exampleRanks, nperm = 1000)
enrich.net(result.GSEA, examplePathways, node.id = 'pathway', pvalue = 'pval', edge.cutoff = 0.6, degree.cutoff = 1, n = 50, vertex.label.cex = 0.75, show.legend = FALSE, edge.width = function(x) {5*sqrt(x)}, layout = igraph::layout.kamada.kawai)
```

GSEA.barplot

Visualize the gene set enrichment analysis

Description

For the functional enrichment analysis, we can visualize the result from the gene set enrichment analysis.

Usage

```r
GSEA.barplot(object, category, score, pvalue, top = 10, sort = NULL, decreasing = FALSE, numChar = NULL, title = NULL, transparency = 0.5, plot = TRUE)
```
Arguments

- **object**: a table with category, enrichment score and p-value of gene sets
- **category**: name of gene sets
- **score**: enrichment score
- **pvalue**: p-value of gene sets
- **top**: the number of top categories (default: 10)
- **sort**: a variable used for sorting data
- **decreasing**: logical indicating whether ascending or descending order (default: FALSE)
- **numChar**: the maximal number of characters of the name of gene sets
- **title**: title for the plot
- **transparency**: transparency (default: 0.5)
- **plot**: return plot when plot is true, otherwise return table (default: TRUE)

Value

GSEA barplot

Author(s)

Dongmin Jung, Xijin Ge

References


See Also

ggplot2

Examples

data(examplePathways)
data(exampleRanks)
set.seed(1)
result.GSEA <- fgsea(examplePathways, exampleRanks, nperm = 1000)
GSEA.barplot(result.GSEA, category = 'pathway', score = 'NES', pvalue = 'pval', sort = 'NES', decreasing = TRUE)
Description

Proteins can be classified by using networks to identify functionally closely related proteins.

Usage

```r
net.infer(target, kernel, top = NULL, cross = 0,
  C = 1, nu = 0.2, epsilon = 0.1, cache1 = 40,
  tol1 = 0.001, shrinking1 = TRUE, cache2 = 40,
  tol2 = 0.001, shrinking2 = TRUE)
```

Arguments

- `target`: set of interesting proteins or target class
- `kernel`: the regularized Laplacian matrix for a graph
- `top`: number of top proteins most closely related to target class (default: all proteins except for target and pseudo-absence class)
- `cross`: if a integer value k>0 is specified, a k-fold cross validation on the training data is performed to assess the quality of the model
- `C`: cost of constraints violation for SVM (default: 1)
- `nu`: The nu parameter for OCSVM (default: 0.2)
- `epsilon`: epsilon in the insensitive-loss function for OCSVM (default: 0.1)
- `cache1`: cache memory in MB for OCSVM (default: 40)
- `tol1`: tolerance of termination criterion for OCSVM (default: 0.001)
- `shrinking1`: option whether to use the shrinking-heuristics for OCSVM (default: TRUE)
- `cache2`: cache memory in MB for SVM (default: 40)
- `tol2`: tolerance of termination criterion for SVM (default: 0.001)
- `shrinking2`: option whether to use the shrinking-heuristics for SVM (default: TRUE)

Value

- `list`: list of a target class used in the model
- `error`: training error
- `CVerror`: cross validation error, (when cross > 0)
- `top`: top proteins
- `score`: decision values for top proteins

Author(s)

Dongmin Jung, Xijin Ge
References

See Also
ksvm

Examples

# example 1
## Not run:
string.db.9606 <- STRINGdb$new(version = '11', species = 9606,
                              score_threshold = 999)
string.db.9606.graph <- string.db.9606$get_graph()
K.9606 <- net.kernel(string.db.9606.graph)
rownames(K.9606) <- substring(rownames(K.9606), 6)
colnames(K.9606) <- substring(colnames(K.9606), 6)
target <- colnames(K.9606)[1:100]
infer <- net.infer(target, K.9606, 10)

## End(Not run)

# example 2
data(litG)
litG <- igraph.from.graphNEL(litG)
sg <- decompose(litG, min.vertices = 50)
sg <- sg[[1]]
K <- net.kernel(sg)
litG.infer <- net.infer(names(V(sg))[1:10], K, top=20)

net.infer.ST
Inferring functionally related proteins with self training

Description
This function is the self-training version of net.infer. The function net.infer is the special case of net.infer.ST where a single iteration is conducted.

Usage

net.infer.ST(target, kernel, top = NULL, C = 1, nu = 0.2,
             epsilon = 0.1, cache1 = 40, tol1 = 0.001, shrinking1 = TRUE,
             cache2 = 40, tol2 = 0.001, shrinking2 = TRUE, thrConf = 0.9,
             maxIts = 10, percFull = 1, verbose = FALSE)
Arguments

- **target**: set of interesting proteins or target class
- **kernel**: the regularized Laplacian matrix for a graph
- **top**: number of top proteins most closely related to target class (default: all proteins except for target and pseudo-absence class)
- **C**: cost of constraints violation for SVM (default: 1)
- **nu**: The nu parameter for OCSVM (default: 0.2)
- **epsilon**: epsilon in the insensitive-loss function for OCSVM (default: 0.1)
- **cache1**: cache memory in MB for OCSVM (default: 40)
- **tol1**: tolerance of termination criterion for OCSVM (default: 0.001)
- **shrinking1**: option whether to use the shrinking-heuristics for OCSVM (default: TRUE)
- **cache2**: cache memory in MB for SVM (default: 40)
- **tol2**: tolerance of termination criterion for SVM (default: 0.001)
- **shrinking2**: option whether to use the shrinking-heuristics for SVM (default: TRUE)
- **thrConf**: A number between 0 and 1, indicating the required classification confidence for an unlabelled case to be added to the labelled data set with the label predicted by the classification algorithm (default: 0.9)
- **maxIts**: The maximum number of iterations of the self-training process (default: 10)
- **percFull**: A number between 0 and 1. If the percentage of labelled cases reaches this value the self-training process is stoped (default: 1)
- **verbose**: A boolean indicating the verbosity level of the function. (default: FALSE)

Value

- **list**: list of a target class used in the model
- **error**: training error
- **top**: top proteins
- **score**: decision values for top proteins

Author(s)

Dongmin Jung, Xijin Ge

See Also

self.train

Examples

data(litG)
litG <- igraph.from.graphNEL(litG)
sg <- decompose(litG, min.vertices = 50)
sg <- sg[[1]]
K <- net.kernel(sg)
litG.infer.ST <- net.infer.ST(names(V(sg))[1:10], K, top=20)
net.kernel

Kernel matrix for a graph

Description

This function gives the regularized Laplacian matrix for a graph.

Usage

net.kernel(g, decay = 0.5)

Arguments

- **g**: graph
- **decay**: decaying constant (default: 0.5)

Value

the regularized Laplacian matrix

Author(s)

Dongmin Jung, Xijin Ge

See Also

laplacian_matrix

Examples

# example 1
## Not run:
string.db.9606 <- STRINGdb$new(version = '1.11', species = 9606,
    score_threshold = 999)
string.db.9606.graph <- string.db.9606$get_graph()
K.9606 <- net.kernel(string.db.9606.graph)

## End(Not run)

# example 2
data(litG)
litG <- igraph.from.graphNEL(litG)
sg <- decompose(litG, min.vertices=50)
sg <- sg[[1]]
K <- net.kernel(sg)
Over-representation Analysis

Description
the result from the over-representation analysis

Usage
ORA(pathways, gene.id, minSize = 1, maxSize = Inf,  
p.adjust.methods = NULL)

Arguments
- **pathways**: list of gene sets
- **gene.id**: set of genes
- **minSize**: Minimal size of a gene set
- **maxSize**: Maximal size of a gene set
- **p.adjust.methods**: a correction method

Value
ORA result

Author(s)
Dongmin Jung, Xijin Ge

See Also
fisher.test

Examples
```
data(examplePathways)  
data(exampleRanks)  
geneNames <- names(exampleRanks)  
set.seed(1)  
gene.id <- sample(geneNames, 100)  
ORA(examplePathways, gene.id)
```
ORA.barplot

**Visualize the over-representation analysis**

**Description**

For the functional enrichment analysis, we can visualize the result from the over-representation analysis.

**Usage**

```r
ORA.barplot(object, category, size, count, pvalue, top = 10,
            sort = NULL, decreasing = FALSE, p.adjust.methods = NULL,
            numChar = NULL, title = NULL, transparency = 0.5,
            plot = TRUE)
```

**Arguments**

- `object`: a table with category, size, count and p-value of gene sets
- `category`: name of gene sets
- `size`: size of gene sets
- `count`: count of gene sets
- `pvalue`: p-value of gene sets
- `top`: the number of top categories (default: 10)
- `sort`: a variable used for sorting data
- `decreasing`: logical indicating whether ascending or descending order (default: FALSE)
- `p.adjust.methods`: a correction method
- `numChar`: the maximal number of characters of the name of gene sets
- `title`: title for the plot
- `transparency`: transparency (default: 0.5)
- `plot`: return plot when plot is true, otherwise return table (default: TRUE)

**Value**

ORA barplot

**Author(s)**

Dongmin Jung, Xijin Ge

**References**

ppi.infer.human

Inferring functionally related proteins using protein networks for human

Description

This function is designed for human protein-protein interaction from STRING database. Default format is 'hgnc'. The number of proteins is 10 in default. Note that the number of proteins used as a target may be different from the number of proteins in the input since mapping between formats is not always one-to-one in getBM.

Usage

ppi.infer.human(target, kernel, top = 10, classifier = net.infer, input = "hgnc_symbol", output = "hgnc_symbol", ...)

Arguments

target set of interesting proteins or target class
kernel the regularized Laplacian matrix for a graph
top number of top proteins most closely related to target class (default: 10)
classifier net.infer or net.infer.ST (default: net.infer)
input input format
output output format
... additional parameters for the chosen classifier

Value

list list of a target class used in the model
error training error
CError cross validation error, (when cross > 0 in net.infer)
top top proteins
score decision values for top proteins

See Also

p.adjust, ggplot2

Examples

data(examplePathways)
data(exampleRanks)
geneNames <- names(exampleRanks)
set.seed(1)
gene.id <- sample(geneNames, 100)
result.ORA <- ORA(examplePathways, gene.id)
ORA.barplot(result.ORA, category = "Category", size = "Size",
            count = "Count", pvalue = "pvalue", sort = "pvalue")
Author(s)

Dongmin Jung, Xijin Ge

See Also

net.infer, net.infer.ST, getBM

Examples

# example 1
string.db.9606 <- STRINGdb$new(version = '11', species = 9606, score_threshold = 999)
string.db.9606.graph <- string.db.9606$get_graph()
K.9606 <- net.kernel(string.db.9606.graph)
rownames(K.9606) <- substring(rownames(K.9606), 6)
colnames(K.9606) <- substring(colnames(K.9606), 6)
target <- colnames(K.9606)[1:100]
infer.human <- ppi.infer.human(target, K.9606, input = "ensembl_peptide_id")

## Not run:
# example 2
library(graph)
data(apopGraph)
target <- nodes(apopGraph)
apoptosis.infer <- ppi.infer.human(target, K.9606, 100)

# example 3
library(KEGGgraph)
library(KEGG.db)
pName <- "p53 signaling pathway"
pId <- mget(pName, KEGGPATHNAME2ID)[[1]]
getKGMLurl(pId, organism = "hsa")
p53 <- system.file("extdata/hsa04115.xml", package="KEGGgraph")
p53graph <- parseKGML2Graph(p53, expandGenes=TRUE)
entrez <- translateKEGGID2GeneID(nodes(p53graph))
http::set_config(http::config(ssl_verifypeer = FALSE))
human.ensembl <- useEnsembl(biomart = "ensembl", dataset = "hsapiens_gene_ensembl")
target <- getBM(attributes=c('entrezgene', 'hgnc_symbol'),
               filter = 'entrezgene', values = entrez,
               mart = human.ensembl)[,2]
p53.infer <- ppi.infer.human(target, K.9606, 100)

## End(Not run)
Description

This function is designed for mouse protein-protein interaction from STRING database. Default format is 'mgi'. The number of proteins is 10 in default. Note that the number of proteins used as a target may be different from the number of proteins in the input since mapping between formats is not always one-to-one in getBM.

Usage

```r
ppi.infer.mouse(target, kernel, top = 10, classifier = net.infer,
                 input = "mgi_symbol", output = "mgi_symbol", ...)
```

Arguments

- `target`: set of interesting proteins or target class
- `kernel`: the regularized Laplacian matrix for a graph
- `top`: number of top proteins most closely related to target class (default: 10)
- `classifier`: net.infer or net.infer.ST (default: net.infer)
- `input`: input format
- `output`: output format
- `...`: additional parameters for the chosen classifier

Value

- `list`: list of a target class used in the model
- `error`: training error
- `CVerror`: cross validation error, (when cross > 0 in net.infer)
- `top`: top proteins
- `score`: decision values for top proteins

Author(s)

Dongmin Jung, Xijin Ge

See Also

`net.infer`, `net.infer.ST`, `getBM`

Examples

```r
string.db.10090 <- STRINGdb$new(version = '11', species = 10090,
                              score_threshold = 999)
string.db.10090.graph <- string.db.10090$get_graph()
K.10090 <- net.kernel(string.db.10090.graph)
rownames(K.10090) <- substring(rownames(K.10090), 7)
colnames(K.10090) <- substring(colnames(K.10090), 7)
target <- colnames(K.10090)[1:100]
infer.mouse <- ppi.infer.mouse(target, K.10090, input="ensembl_peptide_id")
```
self.train.kernel

Self training for a kernel matrix

Description

This function can be used for classification of semi-supervised data by using the kernel support vector machine.

Usage

self.train.kernel(K, y, type = 'response', C = 1, cache = 40, tol = 0.001, shrinking = TRUE, thrConf = 0.9, maxIts = 10, percFull = 1, verbose = FALSE)

Arguments

* K  kernel matrix
* y   lable vector
* type one of response, probabilities ,votes, decision indicating the type of output (default: response)
* C   cost of constraints violation for SVM (default: 1)
* cache cache memory in MB for SVM (default: 40)
* tol tolerance of termination criterion for SVM (default: 0.001)
* shrinking option whether to use the shrinking-heuristics for OCSVM (default: TRUE)
* thrConf A number between 0 and 1, indicating the required classification confidence for an unlabelled case to be added to the labelled data set with the label predicted by the classification algorithm (default: 0.9)
* maxIts The maximum number of iterations of the self-training process (default: 10)
* percFull A number between 0 and 1. If the percentage of labelled cases reaches this value the self-training process is stopped (default: 1)
* verbose A boolean indicating the verbosity level of the function (default: FALSE)

Value

prediction from the SVM

Author(s)

Dongmin Jung, Xijin Ge

References

Examples

data(litG)
litG <- igraph.from.graphNEL(litG)
sg <- decompose(litG, min.vertices = 50)
sg <- sg[[1]]
K <- net.kernel(sg)
y <- rep(NA, length(V(sg)))
y[1:10] <- 1
y[11:20] <- 0
y <- factor(y)
self.train.kernel(K, y)
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