Package: sigora (via r-universe)

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Type Package

Title Signature Over-Representation Analysis

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URL https://github.com/wolski/sigora

BugReports https://github.com/wolski/sigora/issues

Imports stats, slam

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Description Pathway analysis is a method of statistically linking observations on the molecular level to biological processes or pathways on the systems (i.e., organism, organ, tissue, cell) level. Traditionally, pathway analysis methods regard pathways as collections of single genes and treat all genes in a pathway as equally informative. However, this can lead to identifying spurious pathways as statistically significant since components are often shared amongst pathways. SIGORA seeks to avoid this pitfall by focusing on genes or gene pairs that are (as a combination) specific to a single pathway. In relying on such pathway gene-pair signatures (pathway GPS), SIGORA inherently uses the status of other genes in the experimental context to identify the most relevant pathways. The current version allows for pathway analysis of human and mouse datasets. In addition, it contains pre-computed pathway-GPS data for pathways in the KEGG and Reactome pathway repositories and mechanisms for extracting GPS from user-supplied repositories.

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License GPL-3

NeedsCompilation no

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`genesFromRandomPathways`

Function to randomly select genes associated with random pathways.

Description

This function first randomly selects a number (np) of pathways, then randomly selects a number (ng) of genes that are associated with at least one of the selected pathways. The function can be used to compare Sigora's performance to traditional over-representation tests.

Usage

```
genesFromRandomPathways(GPSrepo, np, ng)
```

Arguments

`GPSrepo`	A signature repository (created by `makeGPS()`) or one of the precompiled options.
`np`	How many pathways to select
`ng`	Number of genes to select

Value

`selectedPathways`
: A vector containing the "np" originally selected pathways.

`genes`
: A vector containing the "ng" selected genes from selectedPathways.

References

Foroushani AB, Brinkman FS, and Lynn DJ (2013).“Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures.”*PeerJ*, **1**

See Also

sigora-package

Examples

```
data(kegH)

## Select 50 genes from 3 human KEGG pathways
set.seed(12345)
a1 <- genesFromRandomPathways(kegH, 3, 50)

## Originally selected pathways
a1[["selectedPathways"]]

## What are the genes?
a1[["genes"]]

## Sigora's results
sigoraRes <- sigora(
  queryList = a1[["genes"]],
  GPSrepo = kegH,
  level = 4
)
head(sigoraRes$summary_results)

## Compare to traditional methods results
oraRes <- ora(
  geneList = a1[["genes"]],
  GPSrepo = kegH
)
head(oraRes)
```

`getGenes` *List genes involved in present GPS for a specific pathway in the summary_results*

Description

This function lists the genes involved in the present GPS for a pathway of interest, ordered by their contribution to the significance of the pathway.

Usage

```
getGenes(yy, i, idmap = load_data("idmap"))
```

Arguments

yy	A sigora analysis result object (created by `sigora`).
i	The rank position of the pathway of interest in summary_results.
idmap	A data frame for converting between different gene identifier types (e.g. ENSEMBL, ENTREZ and HGNC symbols). Most users do not need to set this argument, as there is a built-in conversion table.

Value

A table (data frame) with ids of the relevant genes, ranked by their contribution to the statistical significance of the pathway.

See Also

`sigora`

Examples

```
data(kegH)
set.seed(12345)

a1 <- genesFromRandomPathways(kegH, 3, 50)

## Originally selected pathways
a1[["selectedPathways"]]

## What are the genes?
a1[["genes"]]

## Sigora's results with this input:
sigoraRes <- sigora(
  GPSrepo = kegH,
  queryList = a1[["genes"]],
  level = 2
)

## Genes related to the first significant result
head(getGenes(sigoraRes, 1))
```

getURL *Highlight the relevant genes for a specific pathway in its diagram*

Description

This function highlights the genes involved in the present GPS for a pathway of interest in its diagram. Please note that this functionality is only implemented for results of Reactome- or KEGG-based analyses.

Usage

```
getURL(yy, i)
```

Arguments

yy	A sigora analysis result object (created by `sigora`).
i	The rank position of the pathway of interest in summary_results.

Value

The URL of the pathway diagram, where the relevant genes from your original query list are highlighted.

See Also

sigora

Examples

```
data(kegH)
set.seed(12345)

a1 <- genesFromRandomPathways(kegH, 3, 50)

## Originally selected pathways
a1[["selectedPathways"]]

## What are the genes?
a1[["genes"]]

## Sigora's results with this input
sigoraRes <- sigora(
  GPSrepo = kegH,
  queryList = a1[["genes"]],
  level = 2
)

## Diagram for the most significant result;
## genes from our list are highlighted in red
```

```
getURL(sigoraRes, 1)
```

---

idmap *Identifier mappings for protein coding genes.*

Description

A mapping table for ENSEMBL, ENTREZ and gene names (HGNC/MGI symbols) of human and mouse protein coding gene.

Source

www.ensembl.org/biomart/martview

Examples

```
data(idmap)
head(idmap)
```

---

kegH *Pathway GPS data, extracted from KEGG repository (human).*

Description

KEGG human pathway GPS data, extracted by `makeGPS`, default settings. This data can be used by `sigora` to preform signature over-representation.

Source

<http://www.genome.jp/kegg/pathway.html>

References

Kanehisa, M., Goto, S., Sato, Y., Furumichi, M., & Tanabe, M. 2012. "KEGG for integration and interpretation of large-scale molecular data sets." *Nucleic Acids Research* **40**(D1).

See Also

`makeGPS`, `sigora` , `reaH`

Examples

```
data(kegH)
str(kegH)
```

kegM — *Pathway GPS data, extracted from KEGG repository (mouse).*

Description

KEGG mouse pathway GPS data, extracted by `makeGPS`, default settings. This data can be used by `sigora` to preform signature over-representation.

Source

<http://www.genome.jp/kegg/pathway.html>

References

Kanehisa, M., Goto, S., Sato, Y., Furumichi, M., & Tanabe, M. 2012. "KEGG for integration and interpretation of large-scale molecular data sets." *Nucleic Acids Research* **40**(D1).

Examples

```
data(kegM)
str(kegM)
```

load_data — *Load and return data when lazyLoad false insted of using data(datastr)*

Description

Load and return data when lazyLoad false insted of using data(datastr)

Usage

```
load_data(datastr, package = "sigora")
```

Arguments

`datastr`	name of datasets
`package`	default sigora

Value

Returns the data object

Examples

```
idmap <- load_data("idmap")
```

makeGPS *Create your own Signature Object.*

Description

Given a repository of gene-pathway associations either in a tab delimited file with three columns (pathwayID, pathway Description, Gene) or a corresponding data frame, this function identifies all Gene Pair Signatures (pairs of genes that are as a combination unique to a single pathway) and Pathway Unique Genes (genes that are uniquely associated with a single pathway) and stores them in a format that is usable by `sigora`. Please also see the "Details" and "Note" sections below.

Usage

```
makeGPS(
  pathwayTable = NULL,
  fn = NULL,
  maxLevels = 5,
  saveFile = NULL,
  repoName = "userrepo",
  maxFunperGene = 100,
  maxGenesperPathway = 500,
  minGenesperPathway = 10
)
```

Arguments

`pathwayTable`	A data frame describing gene-pathway associations in following format: pathwayID, pathwayName, Gene. Either pathwayTable or fn should be provided.
`fn`	Where to find the repository. Either pathwayTable or fn should be provided.
`maxLevels`	For hierarchical repositories, the number of levels to consider (default: 5).
`saveFile`	Where to save the object as an rda file.
`repoName`	Repository name.
`maxFunperGene`	A cutoff threshold; genes with more than this number of associated pathways are excluded to speed up the GPS identification process (default: 100).
`maxGenesperPathway`	A cutoff threshold; pathways with more than this number of associated genes are excluded to speed up the GPS identification process (default: 500).
`minGenesperPathway`	A cutoff threshold, pathways with less than this number of associated genes are excluded to speed up the GPS identification process (default: 10).

Details

The primary purpose of makeGPS is to convert a user-supplied gene-pathway association table to a repository of weighted Gene Pair Signatures (GPS) that are unique features of pathways. Such GPS can than be used for signature (gene-pair) based analyses using sigora. Additionally, the resulting object also retains the original single gene-pathway associations for the purpose of followup analyses, such as comparison of Sigora's results to traditional methods. ora is an implementation of the traditional (individual gene) Overrepresentation Analysis.

Value

A GPS repository, to be used by sigora and ora.

Note

This function relies on package slam, which should be installed from CRAN. It is fairly memory intensive, and it is recommended to be run on a machine with at least 6GB of RAM. Also, make sure to save and reuse the resulting GPS repository in future analyses!

References

Foroushani AB, Brinkman FS and Lynn DJ (2013).“Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures.”*PeerJ*, **1**

See Also

sigora, sigora-package

Examples

```
data(nciTable, idmap)

## What the input looks like
head(nciTable)

## Create a SigObject. Use the "saveFile" parameter for reuse.

  nciH <- makeGPS(pathwayTable = nciTable)
  ils <- grep("^IL", idmap[, "Symbol"], value = TRUE)
  ilnci <- sigora(queryList = ils, GPSrepo = nciH, level = 3)
```

nciTable *NCI human gene-pathway associations.*

Description

PID-NCI human pathway repository, as a data frame with three columns corresponding to : pathwayId , pathwayName, gene. This is an example of the expected format for the input data to `makeGPS`.

Details

This dataset is provided to illustrate how to create your own GPS repositories.`nciTable` is a dataframe with three columns corresponding to pathwayId, pathwayName and gene. Each row describes the association between an individual gene and a PID-NCI pathway. As you see in the `examples`, section, one can convert this dataframe to a `GPS repository` using `makeGPS`, and save the results for future reuse. Using this created `GPS repository` one can preform Signature Over-representation Analysis on lists of genes of interest.

Source

<https://github.com/NCIP/pathway-interaction-database/tree/master/download>

Examples

```
data(nciTable, idmap)
nciH <- makeGPS(pathwayTable = nciTable)
ils <- grep("^IL", idmap[, "Symbol"], value = TRUE)
ilnci <- sigora(
  queryList = ils, GPSrepo = nciH, level = 3
)
```

ora *Traditional Over-Representation Analysis.*

Description

Traditional over-representation analysis by hypergeometric test: pathways are treated as collections of individual genes, and all genes are treated as equally informative. This function is provided for comparison of the results of traditional methods to Sigora.

Usage

```
ora(geneList, GPSrepo, idmap = load_data("idmap"))
```

Arguments

geneList	A vector containing the list of genes of interest (e.g. differentially expressed genes). The following identifier types are supported: Gene Symbols, ENTREZ IDs or ENSEMBL IDs.
GPSrepo	A GPS-repository (either one of the provided precomputed GPS repositories) or one created by makeGPS.
idmap	A dataframe for converting between different gene-identifier types (e.g. ENSEMBL, ENTREZ and HGNC Symbols). Most users do not need to set this argument, as there is a built-in conversion table.

Details

The primary purpose of makeGPS is to create a GPS repository. It does, however, retain the original single gene-pathway associations for the purpose of followup analyses, such as comparison of Sigora's results to traditional methods. ora is an implementation of the traditional (individual gene) over-representation analysis.

Value

A data frame with individual gene ORA results, with Bonferroni p-value < 0.05.

See Also

sigora-package

Examples

```
## Select 50 genes from 3 mouse pathways
data(kegM)
set.seed(12345)
a1 <- genesFromRandomPathways(kegM, 3, 50)

## Originally selected pathways
a1[["selectedPathways"]]

## Compare to traditional methods results
oraRes <- ora(a1[["genes"]], kegM)
dim(oraRes)
head(oraRes)
```

---

reaH *Pathway GPS data, extracted from the Reactome repository (human).*

Description

Reactome human pathway GPS data, extracted by makeGPS, default settings. This data can be used by sigora to preform signature over-representation.

Source

<http://www.reactome.org/>

References

Matthews, L., Gopinath, G., Gillespie, M., Caudy, M., Croft, D., et al. 2009. "Reactome knowledgebase of human biological pathways and processes." *Nucleic acids research* **37**(Database issue).

Examples

```
data(reaH)
str(reaH)
```

---

reaM *Pathway GPS data, extracted from Reactome repository (mouse).*

Description

Reactome mouse pathway GPS data, extracted by `makeGPS`, default settings. This data can be used by `sigora` to preform signature over-representation.

Source

<http://www.reactome.org/>

References

Matthews, L., Gopinath, G., Gillespie, M., Caudy, M., Croft, D., et al. 2009. "Reactome knowledgebase of human biological pathways and processes." *Nucleic acids research* **37**(Database issue).

See Also

`makeGPS`, `sigora` , `kegM`

Examples

```
data(reaM)
str(reaM)
```

sigora *Sigora's main function.*

Description

This function determines which Signatures (GPS) from a collection of GPS data (GPSrepo argument) for the specified pathway repository are present in the specified list of genes of interest (queryList argument)). It then uses the distribution function of hypergeometric probabilities to identify the pathways whose GPS are over-represented among the present GPS and saves the results to the file specified in the saveFile argument.

Usage

```
sigora(
  GPSrepo,
  level,
  markers = FALSE,
  queryList = NULL,
  saveFile = NULL,
  weighting.method = "invhm",
  idmap = load_data("idmap")
)
```

Arguments

GPSrepo	An object created by makeGPS or one of the precompiled GPS data collections that are provided with this package (currently for KEGG and Reactome). e.g. reaH for human Reactome GPS, kegH for human KEGG GPS, and reaM and kegM for corresponding mouse GPS. See the examples section for creating and using your own GPS.
level	In hierarchical repositories (e.g. Reactome) number of levels to consider. Recommended value for KEGG: 2, for Reactome: 4.
markers	Whether to take single genes that are uniquely associated with only one pathway into account (i.e. should pathway unique genes/PUGs be considered GPS?). Recommended value: TRUE (1).
queryList	A user specified list of genes of interest ("query list"), as a vector of ENSEMBL/ ENTREZ IDs or gene symbols (HGNC/MGI).
saveFile	If provided, the results are saved here as a tab delimited file, including, for each pathway, a list of genes ordered by their contribution to the statistical significance of the pathway.
weighting.method	The weighting method or GPS. The default weighting scheme for the GPS is the reciproc of the harmonic mean of the degrees of the two component genes of a GPS. A wide range of alternative weighting schemes are pre-implemented (see below). Additional user defined weighting schemes are also supported. Currently, the following alternatives are pre-implemented:

'noweights','cosine','topov','reciprod','jac','justPUGs'and'invhm'.
Additional user defined weighting schemes are also supported (see section examples).
'noweights': assigns a constant of 1 to all GPS.
'cosine': all GPS are weighted by the cosine of the degrees of their consituent genes.
'topov': all GPS are weighted by topological overlap of their consituent genes.
'reciprod': all GPS are weighted by reciproc of product of the number of pathway annotations of their consituent genes.
'jac':all GPS are weighted by the jaccard similarity of the pathway annotations consituent genes.
'justPUGs': Analysis is performed using PUGs only.
'invhm': all GPS are weighted by the reciproc of the harmonic mean of the degrees of their consituent genes (default).

`idmap` A dataframe for converting between different gene-identifier types (e.g. ENSEMBL, ENTREZ and HGNC-Symbols of genes). Most users do not need to set this argument, as there is a built-in conversion table.

Value

`summary_results`
A dataframe listing the analysis results.

`detailed_results`
A dataframe describing the detailed evidence (present Gene-Pair Signatures) for each pathway.

References

Foroushani AB, Brinkman FS and Lynn DJ (2013)."Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures."*PeerJ*, **1**

See Also

sigora-package , makeGPS

Examples

```
## Query list
ils <- grep(
  "^IL", load_data("idmap")[["Symbol"]], value = TRUE
)

## Using precompiled GPS repositories
sigRes.ilreact <- sigora(
  queryList = ils, GPSrepo = load_data("reaH"), level = 4
)


  sigRes.ilkeg <- sigora(
```

```
  queryList = ils, GPSrepo = load_data("kegH"), level = 2
)

## User created GPS repository
nciH <- makeGPS(pathwayTable = load_data("nciTable"))
sigRes.ilnci <- sigora(
  queryList = ils, GPSrepo = nciH, level = 2
)

## User defined weighting schemes
myfunc <- function(a, b) {
  1 / log(a + b)
}

sigora(
  queryList = ils,
  GPSrepo = nciH,
  level = 2,
  weighting.method = myfunc
)
```

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