

# Package ‘signet’

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**Type** Package

**Title** signet: Selection Inference in Gene NETworks

**Version** 1.4.0

**Date** 2018-11-22

**Description** An R package to detect selection in biological pathways.  
Using gene selection scores and biological pathways data,  
one can search for high-scoring subnetworks of genes within pathways  
and test their significance.

**Depends** R (>= 3.4.0)

**Imports** graph, igraph, RBGL, graphics, utils, stats, methods

**Suggests** graphite, BiocStyle, knitr, rmarkdown

**biocViews** Software, Pathways, DifferentialExpression, GeneExpression,  
NetworkEnrichment, GraphAndNetwork, KEGG

**License** GPL-2

**LazyData** true

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

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kegg_human	<i>Pathway examples. See <code>browseVignettes("signet")</code> to see how to prepare the pathways for running simulated annealing.</i>
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### Description

Pathway examples. See `browseVignettes("signet")` to see how to prepare the pathways for running simulated annealing.

### Usage

```
kegg_human
```

### Format

An object of class `list` of length 3.

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nullDist	<i>Null distribution</i>
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### Description

Generate the high-scores null distribution to compute empirical p-values for each biological pathway.

### Usage

```
nullDist(pathways, scores, n = 1000, background)
```

### Arguments

pathways	A list of graphNEL objects.
scores	A data frame in which the first column corresponds to the gene ID and the second column contains the gene scores.
n	Number of null high-scores to compute (default = 1000).
background	Optional. Background distribution computed using the <code>backgroundDist</code> function.

### Value

A vector of subnetworks scores obtained under the null hypothesis. Must be used as input of the `testSubnet` function.

## Examples

```
# Get KEGG pathways from the package graphite:
# library(graphite)
# kegg <- pathways("hsapiens", "kegg")
# kegg_human <- lapply(kegg, pathwayGraph)

data(daub13) # load the gene scores

# generate the null distribution (here, only 5 values, but
# at least 1000 are advised)
null <- nullDist(kegg_human, scores, n = 5)
```

---

scores

*Example of gene selection scores.*

---

## Description

A dataset of gene selection scores.

## Usage

```
scores
```

## Format

A data frame with 17918 rows and 2 variables:

**gene** Gene identifier (Entrez gene ID)

**score** Gene selection score ...

## Details

These gene scores are the one used in Daub et al. (2013). For a set of SNPs, a z-score has been computed to represent an overall genetic differentiation among several human populations. A gene score corresponds to the maximal value among SNPs located within a given gene.

The table has been generated using the pipeline described here ("Human populations project"): <https://github.com/CMPPG/polysel>

## Source

Daub, J. T., Hofer, T., Cutivet, E., Dupanloup, I., Quintana-Murci, L., Robinson-Rechavi, M., & Excoffier, L. (2013). Evidence for polygenic adaptation to pathogens in the human genome. *Molecular biology and evolution*, 30(7), 1544-1558.

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searchSubnet	<i>Search for a high scoring subnetwork</i>
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### Description

A simulated annealing algorithm to find the highest scoring subnetwork within a graph.

### Usage

```
searchSubnet(pathway, scores, iterations = 1000, background)
```

### Arguments

pathway	A gene network, or a list of gene networks, in the graphNEL format.
scores	A data frame with two columns: gene identifiers list (IDs have to be the same as for the pathways, e.g. Entrez) and associated scores.
iterations	Number of iterations.
background	For development purposes.

### Value

A signet object or a list of signet objects. Each signet object consists in a table with gene IDs, their state, their score; the subnetwork score and size and the p-value.

### Examples

```
# Get KEGG pathways from the package graphite:
# library(graphite)
# kegg <- pathways("hsapiens", "kegg")
# kegg_human <- lapply(kegg, pathwayGraph)

data(daub13) # load the example gene scores

#run the search in all the pathways with 2500 iterations (default)
example <- searchSubnet(kegg_human, scores)
summary(example)
```

---

signet	<i>Selection Inference in Gene NETWORKS</i>
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### Description

Implements a simulated annealing approach to search for high scoring subnetworks of genes within biological pathways and to test for their significance.

### Examples

```
## A complete workflow is described in signet vignette:
browseVignettes("signet")
```

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Signet-class	<i>An S4 class to represent a pathway and the results of the associated simulated annealing run.</i>
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### Description

An S4 class to represent a pathway and the results of the associated simulated annealing run.

### Usage

```
## S4 method for signature 'Signet'  
show(object)  
  
## S4 method for signature 'Signet'  
summary(object)  
  
## S4 method for signature 'Signet,missing'  
plot(x, y, ...)  
  
## S4 method for signature 'Signet'  
initialize(.Object, pathway, scores, iterations)
```

### Arguments

object	A signet object.
x	A signet object.
y	Omitted when plotting a Signet object.
...	Other graphical parameters.
.Object	Object to initialize.
pathway	Biological pathway (graphNEL object).
scores	Gene scores list.
iterations	Number of simulated annealing iterations.

### Value

A plot of the simulated annealing run.

A signet object.

### Methods (by generic)

- show: Print the summary a Signet object.
- summary: Print the summary of a Signet object
- plot: Plot a Signet object
- initialize: Initialize a Signet object

**Slots**

connected\_comp A graphNEL object (biological pathway)  
network A data frame (gene IDs and scores)  
SA A data frame (information on the simulated annealing run)  
subnet\_score A numeric value (subnetwork score)  
aggregate\_score A numeric value (aggregate subnetwork score)  
mean\_score A numeric value (average gene score in the pathway)  
subnet\_size An integer value (subnetwork size)  
subnet\_genes A factor (subnetwork genes)  
p.value A numeric value (empirical p-value)

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SignetList-class      *An S4 class to represent a list of "Signet" objects.*

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**Description**

An S4 class to represent a list of "Signet" objects.

**Usage**

```
## S4 method for signature 'SignetList'
initialize(.Object, list)

## S4 method for signature 'SignetList'
x[[i]]

## S4 method for signature 'SignetList,ANY,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'SignetList'
summary(object, ...)
```

**Arguments**

.Object	A SignetList object.
list	A list of Signet objects.
x	A SignetList object.
i	Index specifying elements to extract or replace.
j	Unused for SignetList objects.
...	Unused for SignetList objects.
drop	Unused for SignetList objects.
object	A SignetList object.

**Value**

Results of the simulated annealing run for a list of pathways.

A SignetList object.

A data frame containing summary statistics for each element (network and subnetwork sizes, subnetwork score, p-value, significant genes list)

**Methods (by generic)**

- initialize: Initialize a SignetList
- [[: Access the ith element (signet object) of the SignetList
- [: Access the ith element (signet object) of the SignetList
- summary: Summarize the SignetList.

**Slots**

results A list of Signet objects.

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testSubnet	<i>Test the significance of high-scoring subnetworks found using simulated annealing.</i>
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**Description**

Test the significance of high-scoring subnetworks found using simulated annealing.

**Usage**

```
testSubnet(sigObj, null)
```

**Arguments**

sigObj	A list of signet objects obtained using the searchSubnet function.
null	Vector of null subnetwork scores generated using the nullDist function.

**Value**

For each signet object, a p-value is computed given the provided empirical null distribution.

**Examples**

```
# Get KEGG pathways from the package graphite:
# library(graphite)
# kegg <- pathways("hsapiens", "kegg")
# kegg_human <- lapply(kegg, pathwayGraph)

data(daub13) # load the gene scores from Daub et al. (2013)

#run the search in all the pathways with 2500 iterations (default)
example <- searchSubnet(kegg_human, scores)
```

```
# generate the null distribution (here, only 5 values, but
# at least 1000 are advised)
null <- nullDist(kegg_human, scores, n = 5)
example <- testSubnet(example, null) #now, 'example' includes p-values
summary(example)
```

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writeXGMML

*Write Cytoscape input file*


---

## Description

This function allows to write an XGMML file to represent the results in Cytoscape.

## Usage

```
writeXGMML(sigObj, filename = "signet_output.xgmml", threshold = 0.01)
```

## Arguments

sigObj	A signet or signetList object.
filename	The desired file name. Default is "signet_output.xgmml".
threshold	Significance threshold (default: 0.01). If a signetList is provided, all subnetworks with a p-value below this threshold will be merged and represented.

## Value

Writes an XGMML file in the working directory. If a single pathway (signet object) is provided, the whole pathway is represented and nodes belonging to the highest-scoring subnetwork (HSS) are highlighted in red. If a list of pathways (signetList) is provided, all subnetworks with a p-value below a given threshold (default: 0.01) are merged and represented. Note that in this case, only the nodes belonging to HSS are kept for representation.

## Examples

```
# Get KEGG pathways from the package graphite:
# library(graphite)
# kegg <- pathways("hsapiens", "kegg")
# kegg_human <- lapply(kegg, pathwayGraph)

data(daub13) # load the gene scores from Daub et al. (2013)

#run the search in all the pathways with 2500 iterations (default)
example <- searchSubnet(kegg_human, scores)

#write Cytoscape input file for the first pathway:
writeXGMML(example[[1]], filename=tempfile())
```



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