Package 'mgsa'

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`mgsa-package` *Model-based gene set analysis*

Description

Model-based Gene Set Analysis (MGSA) is a Bayesian modeling approach for gene set enrichment. The package mgsa implements MGSA and tools to use MGSA together with the Gene Ontology.

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References

S. Bauer, J. Gagneur and P. N. Robinson. GOing Bayesian: model-based gene set analysis of genome-scale data. Nucleic acids research, 2010.

`alphaMcmcPost` *posterior estimates of the parameter alpha for each MCMC run*

Description

Posterior estimates of the parameter alpha for each MCMC run.

Usage

```
alphaMcmcPost(x)

## S4 method for signature 'MgsaMcmcResults'
alphaMcmcPost(x)
```

Arguments

x	a MgsaMcmcResults.

Value

`matrix`: Posterior estimates of the parameter alpha for each MCMC run.

`alphaPost` *Posterior for alpha*

Description

Realization values, posterior estimate and standard error for the parameter alpha.

Usage

```
alphaPost(x)

## S4 method for signature 'MgsaResults'
alphaPost(x)
```

Arguments

x	a MgsaResults.

Value

`data.frame`: realization values, posterior estimate and standard error for the parameter alpha.

betaMcmcPost *posterior estimates of the parameter beta for each MCMC run*

Description

Posterior estimates of the parameter beta for each MCMC run.

Usage

```
betaMcmcPost(x)

## S4 method for signature 'MgsaMcmcResults'
betaMcmcPost(x)
```

Arguments

x	a MgsaMcmcResults.

Value

matrix: Posterior estimates of the parameter beta for each MCMC run.

betaPost *Posterior for beta*

Description

Realization values, posterior estimate and standard error for the parameter beta.

Usage

```
betaPost(x)

## S4 method for signature 'MgsaResults'
betaPost(x)
```

Arguments

x	a MgsaResults.

Value

data.frame: realization values, posterior estimate and standard error for the parameter beta.

`createMgsaGoSets` *This functions takes a 1:1 mapping of go.ids to items and returns a full MgsaGOSets instance. The structure of GO is gathered from GO.db. It is sufficient to specify just the directly asserted mapping (or annotation), i.e., the most specific ones. The true path rule is taken account, that is, if an item is annotated to a term then it will be also annotated to more general terms (some people prefer to say that just the transitive closure is calculated).*

Description

This functions takes a 1:1 mapping of go.ids to items and returns a full MgsaGOSets instance. The structure of GO is gathered from GO.db. It is sufficient to specify just the directly asserted mapping (or annotation), i.e., the most specific ones. The true path rule is taken account, that is, if an item is annotated to a term then it will be also annotated to more general terms (some people prefer to say that just the transitive closure is calculated).

Usage

```
createMgsaGoSets(go.ids, items)
```

Arguments

`go.ids`	a character vector of GO ids (GO:00001234)
`items`	a vector of identifiers that are annotated to the term in the corresponding position of the go.ids vector.

`example-go` *Example GO sets for mgsa*

Description

This data is an example GO set for mgsa.

`example-o` *Example objects for mgsa*

Description

This data is an example objects for mgsa.

itemAnnotations *Item annotations of a MgsaSets*

Description

Item annotations of a MgsaSets.

Usage

```
itemAnnotations(sets, items)

## S4 method for signature 'MgsaSets,missing'
itemAnnotations(sets, items)

## S4 method for signature 'MgsaSets,character'
itemAnnotations(sets, items)
```

Arguments

sets	an instance of class MgsaSets.
items	character an optional vector specifying the items of interest.

Value

a data.frame: the item annotations.

itemIndices *Item indices of a MgsaSets*

Description

Returns the indices corresponding to the items

Usage

```
itemIndices(sets, items)

## S4 method for signature 'MgsaSets,character'
itemIndices(sets, items)

## S4 method for signature 'MgsaSets,numeric'
itemIndices(sets, items)
```

Arguments

`sets`	an instance of class `MgsaSets`.
`items`	`character` or `numeric` the items of interest.

Value

a `integer`: the item indices.

`length,MgsaSets-method` *Length of a MgsaSets.*

Description

Length (number of sets) of `MgsaSets`.

Usage

```
## S4 method for signature 'MgsaSets'
length(x)
```

Arguments

`x`	an instance of class `MgsaSets`.

Value

`integer` vector.

`mgsa` *Performs an MGSA analysis*

Description

Estimate marginal posterior of the MGSA problem with an MCMC sampling algorithm.

Usage

```
mgsa(o, sets, population = NULL, p = seq(min(0.1, 1/length(sets)), min(0.3,
  20/length(sets)), length.out = 10), ...)

## S4 method for signature 'integer,list'
mgsa(o, sets, population = NULL, p = seq(1, min(20,
  floor(length(sets)/3)), length.out = 10)/length(sets), ...)

## S4 method for signature 'numeric,list'
mgsa(o, sets, population = NULL, p = seq(1, min(20,
  floor(length(sets)/3)), length.out = 10)/length(sets), ...)

## S4 method for signature 'character,list'
mgsa(o, sets, population = NULL, p = seq(1,
  min(20, floor(length(sets)/3)), length.out = 10)/length(sets), ...)

## S4 method for signature 'logical,list'
mgsa(o, sets, population = NULL, p = seq(min(0.1,
  1/length(sets)), min(0.3, 20/length(sets)), length.out = 10), ...)

## S4 method for signature 'character,MgsaSets'
mgsa(o, sets, population = NULL,
  p = seq(min(0.1, 1/length(sets)), min(0.3, 20/length(sets)), length.out =
  10), ...)
```

Arguments

o	The observations. It can be a numeric, integer, character or logical. See details.
sets	The sets. It can be an MgsaSets or a list. In this case, each list entry is a vector of type numeric, integer, character. See details.
population	The total population. Optional. A numeric, integer or character vector. Default to NULL. See details.
p	Grid of values for the parameter p. Values represent probabilities of term activity and therefore must be in [0,1].
...	Optional arguments that are passed to the methods. Supported parameters are alpha Grid of values for the parameter alpha. Values represent probabilities of false-positive events and hence must be in [0,1]. numeric. beta Grid of values for the parameter beta. Values represent probabilities of false-negative events and hence must be in [0,1]. numeric. steps The number of steps of each run of the MCMC sampler. integer of length 1. A recommended value is 1e6 or greater. burnin The number of burn-in MCMC steps, until sample collecting begins. integer of length 1. A recommended value is half of total MCMC steps. thin The sample collecting period. An integer of length 1. A recommended value is 100 to reduce autocorrelation of subsequently collected samples.

`flip.freq` The frequency of MCMC Gibbs step that randomly flips the state of a random set from active to inactive or vice versa. `numeric` from (0,1].

`restarts` The number of different runs of the MCMC sampler. `integer` of length 1. Must be greater or equal to 1. A recommended value is 5 or greater.

`threads` The number of threads that should be used for concurrent restarts. A value of 0 means to use all available cores. Default to 0.

Details

The function can handle items (such as genes) encoded as `character` or `integer`. For convenience `numeric` items can also be provided but these values should essentially be integers. The type of items in the observations `o`, the `sets` and in the optional `population` should be consistent. In the case of `character` items, `o` and `population` should be of type `character` and `sets` can either be an `MgsaSets` or a `list` of `character` vectors. In the case of `integer` items, `o` should be of type `integer`, `numeric` (but essentially with integer values), or `logical` and entries in `sets` as well as the `population` should be `integer`. When `o` is `logical`, it is first coerced to integer with a call on `which`. Observations outside the `population` are not taken into account. If `population` is `NULL`, it is defined as the union of all sets.

The default grid value for p is such that between 1 and 20 sets are active in expectation. The lower limit is constrained to be lower than 0\.1 and the upper limit lower than 0\.3 independently of the total number of sets to make sure that complex solutions are penalized. Marginal posteriors of activity of each set are estimated using an MCMC sampler as described in Bauer et al., 2010. Because convergence of an MCM sampler is difficult to assess, it is recommended to run it several times (using `restarts`). If variations between runs are too large (see `MgsaResults`), the number of steps (`steps`) of each MCMC run should be increased.

Value

An `MgsaMcmcResults` object.

References

Bauer S., Gagneur J. and Robinson P. GOing Bayesian: model-based gene set analysis of genome-scale data. Nucleic Acids Research (2010) http://nar.oxfordjournals.org/content/38/11/3523.full

See Also

`MgsaResults`, `MgsaMcmcResults`

Examples

```
## observing items A and B, with sets {A,B,C} and {B,C,D}
mgsa(c("A", "B"), list(set1 = LETTERS[1:3], set2 = LETTERS[2:4]))

## same case with integer representation of the items and logical observation
mgsa(c(TRUE,TRUE,FALSE,FALSE), list(set1 = 1:3, set2 = 2:4))

## a small example with gene ontology sets and plot
```

```
data(example)
fit = mgsa(example_o, example_go)
## Not run:
plot(fit)
## End(Not run)
```

MgsaGoSets-class *Gene Ontology annotations*

Description

This class represents gene ontology annotations.

Details

For now, it is identical to the parental class MgsaSets.

See Also

readGAF

MgsaMcmcResults-class *Instances of this class are used to hold the additional information that was provided by running (possibly multiple times) an MCMC algorithm.*

Description

Instances of this class are used to hold the additional information that was provided by running (possibly multiple times) an MCMC algorithm.

Slots

nsamples how many samples collected per MCMC run

steps how many steps per MCMC run

restarts how many MCMC runs

alphaMcmcPost posterior estimates for each MCMC run of the parameter alpha

betaMcmcPost posterior estimates for each MCMC run of the parameter beta

pMcmcPost posterior estimates for each MCMC run of the parameter p

setsMcmcPost posterior estimates for each MCMC run of the sets marginal posterior probabilities

The columns of the matrices alphaMcmcPost, betaMcmcPost, pMcmcPost and setsMcmcPost stores the posterior estimates for each individual MCMC run. The row order matches the one of the slot alphaPost, betaPost, pPots, and setsResults respectively.

Accessor methods exist for each slot.

See Also

mgsa

MgsaResults-class *Results of an MGSA analysis*

Description

The results of an MGSA analysis.

Slots

`populationSize` The number of items in the population.

`studySetSizeInPopulation` The number of items both in the study set and in the population.

`alphaPost` with columns `value`, `estimate` and `std.error`.

`betaPost` with columns `value`, `estimate` and `std.error`.

`pPost` with columns `value`, `estimate` and `std.error`.

`setsResults` with columns `inPopulation`, `inStudySet`, `estimate` and `std.error`.

The columns of the slots `alphaPost`, `betaPost`, and `pPost` contains a realization value, its posterior estimate and standard error for the parameters alpha, beta and p respectively.

The columns of the slot `setsResults` contains the number of items of the set in the population, the number of items of the set in the study set, the estimate of its marginal posterior probability and its standard error. The `rownames` are the names of the sets if available.

Because an `MgsaResults` is the outcome of an MGSA analysis (see `mgsa`), accessors but no replacement methods exist for each slot.

See Also

mgsa

MgsaSets-class *Sets of items and their annotations*

Description

This class describes sets, items and their annotations.

Details

Internally, the method `mgsa` indexes all elements of the sets before fitting the model. In case `mgsa` must be run on several observations with the same gene sets, computations can be speeded up by performing this indexing once for all. This can be achieved by building a `MgsaSets`. In order to ensure consistency of the indexing, no replace method for any slot is provided. Accessors are available.

The data frames `setAnnotations` and `itemAnnotations` allow to store annotations. No constraint is imposed on the number and names of their columns.

Slots

`sets` A list whose elements are vector of item indices.

`itemName2ItemIndex` The mapping of item names to index.

`numberOfItems` How many items?

`setAnnotations` Annotations of the sets. The `rownames` are set names.

`itemAnnotations` Annotations of the items. The `rownames` are item names.

See Also

`MgsaGoSets`, `readGAF`, `mgsa`

Examples

```
new("MgsaSets", sets=list(set1=c("a", "b"), set2=c("b", "c")))
```

`nsamples` *How many samples per MCMC run collected*

Description

how many samples collected per MCMC run.

Usage

```
nsamples(x)

## S4 method for signature 'MgsaMcmcResults'
nsamples(x)
```

Arguments

`x`	a `MgsaMcmcResults`.

Value

`integer`: how many samples per MCMC run collected.

plot,MgsaResults-method *Plot method for MgsaResults objects*

Description

Plot method for MgsaResults objects

Usage

```
## S4 method for signature 'MgsaResults'
plot(x, y, ...)
```

Arguments

x	a MgsaResults
y	unused
...	unused

pMcmcPost *posterior estimates of the parameter p for each MCMC run*

Description

Posterior estimates of the parameter p for each MCMC run.

Usage

```
pMcmcPost(x)

## S4 method for signature 'MgsaMcmcResults'
pMcmcPost(x)
```

Arguments

x	a MgsaMcmcResults.

Value

matrix: Posterior estimates of the parameter p for each MCMC run.

populationSize *Size of the population of a MgsaResults*

Description

The size of the population on which the analysis was run.

Usage

```
populationSize(x)

## S4 method for signature 'MgsaResults'
populationSize(x)
```

Arguments

x	a MgsaResults.

Value

integer: the size of the population.

pPost *Posterior for beta*

Description

Realization values, posterior estimate and standard error for the parameter p.

Usage

```
pPost(x)

## S4 method for signature 'MgsaResults'
pPost(x)
```

Arguments

x	a MgsaResults.

Value

data.frame: realization values, posterior estimate and standard error for the parameter p.

readGAF *Read a Gene Ontology annotation file*

Description

Creates a MgsaGoSets using gene ontology annotations provided by a file in GAF 1.0 or 2.0 format.

Usage

```
readGAF(filename, evidence=NULL, aspect=c("P", "F", "C"))
```

Arguments

filename	The name of the Gene Ontology annotation file. It must be in the GAF 1.0 or 2.0 format. It may be gzip-compressed.
evidence	character or NULL. Only annotations with evidence code in evidence are returned. If NULL (default), annotations of all evidence codes are returned.
aspect	character with values in P, C or F. Only annotations of the listed GO namespaces P (biological process), F (molecular function) or C (cellular component) are returned. By default, annotations of the three namespaces are returned.

Details

The function extracts from the annotation file all direct gene annotations and infers from the Gene Ontology all the indirect annotations (due to term relationships). This is done using the package Go.db which provides the ontology as a database and RSQLite for querying the database.

Value

An MgsaGoSets object.

References

The Gene Ontology Consortium. Gene Ontology: tool for the unification of biology. Nature Genetics, 2000. The GAF file format: http://www.geneontology.org/GO.format.annotation.shtml GO evidence codes: http://www.geneontology.org/GO.evidence.shtml

See Also

MgsaGoSets, mgsa

Examples

```
## parsing provided example file (yeast)
gofile = system.file("example_files/gene_association_head.sgd", package="mgsa")
readGAF(gofile)
## only annoations infered from experiment or a direct assay
readGAF(gofile, evidence=c("EXP", "IDA"))
```

restarts *How many MCMC runs*

Description

how many MCMC runs.

Usage

```
restarts(x)

## S4 method for signature 'MgsaMcmcResults'
restarts(x)
```

Arguments

x	a MgsaMcmcResults.

Value

integer: how many MCMC runs.

setAnnotations *Set annotations of a MgsaSets*

Description

Set annotations of a MgsaSets.

Usage

```
setAnnotations(sets, names)

## S4 method for signature 'MgsaSets,missing'
setAnnotations(sets, names)

## S4 method for signature 'MgsaSets,character'
setAnnotations(sets, names)
```

Arguments

sets	an instance of class MgsaSets.
names	character an optional vector specifying the names of interest.

Value

a data.frame: the set annotations.

setsMcmcPost — *posterior estimates of the the set marginal probabilities for each MCMC run*

Description

Posterior estimates of the set marginal probabilities for each MCMC run.

Usage

```
setsMcmcPost(x)

## S4 method for signature 'MgsaMcmcResults'
setsMcmcPost(x)
```

Arguments

x	a MgsaMcmcResults.

Value

matrix: Posterior estimates of the set marginal probabilities for each MCMC run.

setsResults — *Posterior for each set*

Description

Number of items of the set in the population, the number of items of the set in the study set, the estimate of its marginal posterior probability and its standard error.

Usage

```
setsResults(x)

## S4 method for signature 'MgsaResults'
setsResults(x)
```

Arguments

x	a MgsaResults.

Value

data.frame: For each set, number of items of the set in the population, number of items of the set in the study set, estimate of its marginal posterior probability and standard error.

---

show,MgsaResults-method *Show an MgsaResults*

Description

Show an MgsaResults.

Usage

```
## S4 method for signature 'MgsaResults'
show(object)
```

Arguments

object	an instance of class MgsaResults.

Value

an invisible NULL

---

show,MgsaSets-method *Show an MgsaSets*

Description

Show an MgsaSets.

Usage

```
## S4 method for signature 'MgsaSets'
show(object)
```

Arguments

object	an instance of class MgsaSets.

Value

an invisible NULL

steps *How many steps per MCMC run*

Description

how many steps per MCMC run.

Usage

```
steps(x)

## S4 method for signature 'MgsaMcmcResults'
steps(x)
```

Arguments

x	a MgsaMcmcResults.

Value

integer: how many steps per MCMC run.

studySetSizeInPopulation *Size of the study set of a MgsaResults*

Description

The size of the study set on which the analysis was run.

Usage

```
studySetSizeInPopulation(x)

## S4 method for signature 'MgsaResults'
studySetSizeInPopulation(x)
```

Arguments

x	a MgsaResults.

Value

integer: the size of the study set.

subMgsaSets *Subset of an MgsaSets*

Description

Returns a subset of an MgsaSets that contains only the specified items. Empty sets are removed.

Usage

```
subMgsaSets(sets, items)

## S4 method for signature 'MgsaSets,character'
subMgsaSets(sets, items)
```

Arguments

sets	an MgsaSets.
items	character. The items to restrict on.

Value

an MgsaSets.

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