Package ‘geva’

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Type Package
Title Gene Expression Variation Analysis (GEVA)
Description Statistic methods to evaluate variations of differential expression (DE) between multiple biological conditions. It takes into account the fold-changes and p-values from previous differential expression (DE) results that use large-scale data (*e.g.*, microarray and RNA-seq) and evaluates which genes would react in response to the distinct experiments. This evaluation involves an unique pipeline of statistical methods, including weighted summarization, quantile detection, cluster analysis, and ANOVA tests, in order to classify a subset of relevant genes whose DE is similar or dependent to certain biological factors.

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1
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'c_TYPEDList.R' 'c_SVAttribute.R' 'c_GEVAInput.R'
'c_GEVAsummary.R' 'c_GEVAgroupedSummary.R' 'c_GEVAQuantiles.R'
'c_GEVAQuantilesAdjusted.R' 'c_GEVAResults.R' 'summarization.R'
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'finalize.R' 'geva-package.R' 'hclustering.R' 'idealtesting.R'
'input.R'

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Description

Statistic methods to evaluate variations of differential expression (DE) between multiple biological conditions. It takes into account the fold-changes and p-values from previous differential expression (DE) results that use large-scale data (*e.g.*, microarray and RNA-seq) and evaluates which genes would react in response to the distinct experiments. This evaluation involves an unique pipeline of statistical methods, including weighted summarization, quantile detection, cluster analysis, and ANOVA tests, in order to classify a subset of relevant genes whose DE is similar or dependent to certain biological factors.

Statistic methods to evaluate variation between multiple biological conditions.

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See Also

Useful links:

- [https://github.com/sbcblab/geva](https://github.com/sbcblab/geva)

Description

Exhaustive list of generic methods exported from GEVA. Use `findMethods` to retrieve the specific usages.
Usage

inputvalues(object)
inputweights(object, normalized)
inputdata(object)
inputnames(object)
infolist(object, field, ...)
infolist(object) <- value
factors(object)
factors(object) <- value
classification.table(object)
classification.table(object) <- value
analysis.params(gobject)
featureTable(object)
featureTable(object) <- value
sv(object)
svattr(S, V)
elem.class(typedlist)
elem.class(typedlist) <- value
groupsets(object)
groupsets(object) <- value
groups(object)
scores(object, group)
centroids(object)
offsets(object)
sv.scores(object)
generics

qindexes(object)
qareasizes(object)
qcount(object)
quantiles(object)
quantiles.method(object)
group.rels(object)
cluster.method(object)
results.table(gres)
sv.data(object)
variation(object, ...)
get.summary.method(x)
get.variation.method(x)
get.distance.method(x)
as.SVTable(x, ...)

Arguments

object, x, gobject
object, x, gobject
normalized logical, whether to return values in the normalized scale
field When used with a information list, returns the information entry with the corresponding name
... Additional parameters. If used with an imported S3 method, passes the arguments to the default vector, matrix or data.frame implementation
value The value to be assigned
S Vector to construct the S slot
V Vector to construct the V slot
typedlist A TypedList object
group Character to filter the returned groups. Omit it to return all groups
gres A GEVAResults object

Value

See the specific usages for each method.
Examples

# Returing analysis parameters from an object
gsummary <- geva.summarize(geva.ideal.example(),
    summary.method="mean",
    variation.method="sd")
anpars <- analysis.params(gsummary)
print(anpars)
  # $summary.method
  # [1] "mean"
  # $variation.method
  # [1] "sd"

geva.cluster

GEVA Cluster Analysis

Description

Performs a cluster analysis from summarized data.

Usage

geva.cluster(
    sv,
    cluster.method = options.cluster.method,
    cl.score.method = options.cl.score.method,
    resolution = 0.3,
    distance.method = options.distance,
    ...,
    grouped.return = FALSE
)

options.cluster.method
  # c("hierarchical", "density", "quantiles")

options.cl.score.method
  # c("auto", "hclust.height", "density", "centroid")

options.distance
  # c("euclidean", "manhattan")

Arguments

sv                     a numeric SVTable object (usually GEVA Summary)
cluster.method          character, one of the main grouping methods (see 'Details')
cl.score.method         character, method used to calculate the cluster scores for each point. Ignored if cluster.method is quantiles
resolution numeric (0 to 1), used as a "zoom" parameter for cluster detection. A zero value returns the minimum number of clusters that can detected by the cluster.method, while 1 returns the maximum amount of clusters. Ignored if cluster.method is quantiles

distance.method character, two-point distance calculation method. Options are "euclidian" or "manhattan" distances

... further arguments passed to geva.dcluster(), geva.hcluster(), or geva.quantiles(). In addition, the following arguments are accepted:

• eps : numeric, defines the epsilon coefficient for density clustering (see 'Details')

• mink.p : numeric, parameter for the Minkowsky metric used in hierarchial clustering. Used as the p argument for fastcluster::hclust.vector()

• verbose : logical, whether to print the current progress (default is TRUE)

grouped.return logical, whether to concatenate the clustered and summarized data into a single object

Details

The cluster.method determines which grouping subroutine is used to classify the summarized data points based on distance and partitioning. Each option has their equivalent functions that can be called directly: "density" uses geva.dcluster(); "hierarchical" uses geva.hcluster(); and "quantiles" calls geva.quantiles(). However, this wrapper function can also be used to join GEVASummary and GEVAGroupSet objects into a single GEVAGroupedSummary object by setting grouped.return to TRUE.

The cl.score.method argument defines how scores are calculated for each SV point (row in sv) that was assigned to a cluster, (i.e., excluding non-clustered points). If specified as "auto", the parameter will be selected based on the cluster.method: "density" (rate of neighbor points) for the density method; and "hclust.height" (local hierarchy height) for the hierarchical method. The "centroid" method calculates the scores based on the proportional distance between each point to its cluster's centroid. Note that the cl.score.method argument is ignored if cluster.method is "quantiles", since quantile scores are always based on their local centroid distances.

The resolution value is a more accessible way to define the cluster separation threshold used in density and hierarchical clustering methods. Density clusters uses an epsilon value that represents the minimum distance of separation, whereas hierarchical clusters are defined by cutting the hierarchy tree wherever there is a minimum distance between two hierarchies. In this sense, resolution translates a value between 0 and 1 to proportional value for epsilon or hierarchical height (depending on the cluster.method) that would result in the least number of possible clusters for 0 and the highest number for 1. Nevertheless, if epsilon is specified as eps in the optional arguments, its value is used and resolution is ignored.

Value

This function produces a GEVAGroupSet-derived object, particularly a GEVACluster for the "hierarchical" and "density" cluster methods or a GEVAQuantiles for the "quantiles" method.

However, if grouped.return is TRUE and sv is a GEVASummary object, the produced GEVAGroupSet data will be concatenated to the input and returned as a GEVAGroupedSummary
See Also

Other geva.cluster: `geva.dcluster()`, `geva.hcluster()`, `geva.quantiles()`

Examples

```r
## Cluster analysis from a randomly generated input

# Preparing the data
ginput <- geva.ideal.example()  # Generates a random input example
gsummary <- geva.summarize(ginput)  # Summarizes with the default parameters

# Hierarchical clustering
gclust <- geva.cluster(gsummary, cluster.method="hierarchical")
plot(gclust)

# Density clustering
gclust <- geva.cluster(gsummary, cluster.method="density")
plot(gclust)

# Density clustering with slightly more resolution
гclust <- geva.cluster(gsummary,
  cluster.method="density",
  resolution=0.35)
plot(gclust)
```

geva.dcluster  

**GEVA Density Clustering**

Description

Performs a density cluster analysis from summarized data.

Usage

```r
geva.dcluster(
  sv,
  resolution = 0.3,
  dcluster.method = options.dcluster.method,
  cl.score.method = options.cl.score.method,
  minpts = 2,
  ...
  eps = NA_real_,
  include.raw.results = FALSE
)
```

options.dcluster.method
# c("dbscan", "optics")
Arguments

sv  a numeric SVTable object (usually GEVASummary)
resolution  numeric (0 to 1), used as a "zoom" parameter for cluster detection. A zero value returns the minimum number of clusters that can detected, while 1 returns the maximum amount of detectable clusters. Ignored if eps is specified

dcluster.method  character, density-based method for cluster separation
cl.score.method  character, method used to calculate the cluster scores for each point. If "auto", the "density" method is selected
minpts  integer, minimum number of points required to form a cluster
...  additional arguments. Accepts verbose (logical, default is TRUE) to enable or disable printing the current progress
eps  numeric, maximum neighborhood distance between points to be clustered
include.raw.results  logical, whether to attach intermediate results to the returned object

Details

This function performs a density cluster analysis with the aid of implemented methods from the dbscan::dbscan package. The available methods for the dcluster.method arguments are "dbscan" and "options", which internally call dbscan::dbscan() and dbscan::optics(), respectively.

The resolution value is an accessible way to define the cluster separation threshold used in density clustering. The DBSCAN algorithm uses an epsilon value that represents the minimum distance of separation, and resolution translates a value between 0 and 1 to a proproational value within the acceptable range of epsilon values. This allows defining the rate of clusters from 0 to 1, which results in the least number of possible clusters for 0 and the highest number for 1. Nevertheless, if epsilon is specified as eps in the optional arguments, its value is used and resolution is ignored.

The cl.score.method argument defines how scores are calculated for each SV point (row in sv) that was assigned to a cluster, (i.e., excluding non-clustered points). If specified as "auto", the parameter will be selected based on the rate of neighbor points ("density").

If include.raw.results is TRUE, some additional data will be attached to the info slot of the returned GEVACluster objects, including the kNN tree generated during the intermediate steps.

Value

A GEVACluster object

Note

In density clustering, only the most dense points are clustered. For the unclustered points, the grouping value is set to NA.

See Also

Other geva.cluster: geva.cluster(), geva.hcluster(), geva.quantiles()
Examples

```r
## Density clustering from a randomly generated input

# Preparing the data
ginput <- geva.ideal.example()  # Generates a random input example
gsummary <- geva.summarize(ginput)  # Summarizes with the default parameters

# Density clustering
gclust <- geva.dcluster(gsummary)
plot(gclust)

# Density clustering with slightly more resolution

gclust <- geva.dcluster(gsummary, resolution=0.35)
plot(gclust)
```

**Description**

Merges the obtained information (Summarization, Clustering, and Quantiles), then applies the final steps to produce the classification results for the SV points (genes).

**Usage**

```r
geva.finalize(
  gsummary,
  ...,
  p.value = 0.05,
  p.val.adjust = options.factoring.p.adjust,
  constraint.factors = TRUE
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gsummary</td>
<td>a GEVASummary object</td>
</tr>
<tr>
<td>...</td>
<td>Intermediate results produced from the gsummary object, such as clusters (GEVACluster), quantiles (GEVAQuantiles), or any other object inherited from GEVAGroupSet</td>
</tr>
<tr>
<td>p.value</td>
<td>numeric (0 to 1), p-value cutoff used in the ANOVA procedures (factor analysis only)</td>
</tr>
<tr>
<td>p.val.adjust</td>
<td>character, p-value correction method (factor analysis only). Possible values are: &quot;partial.quantiles&quot;, &quot;holm&quot;, &quot;hochberg&quot;, &quot;hommel&quot;, &quot;bonferroni&quot;, &quot;BH&quot;, &quot;BY&quot;, &quot;fdr&quot;, &quot;none&quot;</td>
</tr>
</tbody>
</table>
constraint.factors

logical. If TRUE, the S values are restricted to the range within the quantile centroids (factor analysis only)

Details

In this procedure, the SV points (i.e., each row in the GEVASummary object) are classified according to the detected quantiles (see geva.quantiles), whose results can be adjusted using other grouping analysis results such as clusters (see geva.cluster). To achieve the best statistical accuracy, both GEVAQuantiles and GEVACLuster objects must be given in the ... as optional arguments. If a GEVAQuantiles argument is not present, it is automatically calculated using the default parameters.

If multiple factors are present in the GEVASummary object (retrieved by factors(gsummary)), a factor analysis is also performed, giving two additional possible classifications (factor-dependent and factor-specific) besides the default ones (similar, basal, and sparse).

In factor analysis, an ANOVA is applied for each gene using Fisher’s and Levene’s tests to distinguish genes whose logFC (differential expression) variation is dependent or specific to the analyzed factors based on the p-value cutoff. The \( p.val.adjust \) argument defines how these p-values will be adjusted: by quantile separation between each factor ("partial.quantiles" method); or by one of the default methods listed in stats::p.adjust.methods.

The constraint.factors argument determines if the S values (summarized logFC) will be limited to the range between the quantile centroids during factor analysis. For example, if the quantile centroids were -0.90, 0.00, and 0.90 in the S axis, values such as -1.53 and 2.96 would be converted to -0.90 and 0.90, respectively. This constraint is particularly applied to avoid significative observations from ANOVA based on multiple degrees of differential expression.

In another example to illustrate the constraint of factors, given two sets of values: \( A = (-1.00, -1,10, 0.00, 0.20, 1.00, 1.15) \), and \( B = (0.00, 0.12, 1.11, 1.00, 1.95, 2.00) \), with the centroids located in \( C = (-0.90, 0.00, 0.90) \), and the factors \( F = (\text{Cond1, Cond1, Cond2, Cond2, Cond3, Cond3}) \). If constraint.factors is FALSE, both \( A \) and \( B \) are considered as significantly separated factors, whereas if TRUE, only \( A \) will present a significant separation, since in \( B \) the values 1.11, 1.00, 1.95, and 2.00 are converted to 0.90. In qualitative terms, if constraint.factors is TRUE, all values above 0.90 are considered the same over-expressed values, ensuring that they will fit in the same degree of differential expression. Hence, in this example using the constrained values, \( B \) would not represent a significant separation between the factors \( \text{Cond1, Cond2, and Cond3} \).

Value

A GEVAResults object, containing the entire set of results. The relevant genes can be retrieved using top.genes()

Note

To perform factor analysis, the following observations must be considered:

- The factors must be defined in the provided data. They can be retrieved using the factors accessor. If factors are not present or are entirely composed by NA, they can be assigned through factors<- by providing a factor or character vector of the same length of the input columns;
- Each factor must include two or more values, since the factor analysis is based on ANOVA and at least two values are needed to variance calculation;
• Columns whose factor value is NA are not considered.

See Also
p.adjust.methods

Examples

```r
## Finalizing example using a random generated input
ginput <- geva.ideal.example()  # Generates a random input (for testing purposes only)
gsummary <- geva.summarize(ginput)  # Summarizes the input
gquant <- geva.quantiles(gsummary)  # Calculates the quantiles
gclust <- geva.cluster(gsummary)  # Calculates the clusters
gresults <- geva.finalize(gsummary, gquant, gclust)  # Finishes the results

head(top.genes(gresults))  # Prints the final results
plot(gresults)  # Plots the final SV-plot
```

Description

Performs a hierarchical cluster analysis from summarized data.

Usage

```r
geva.hcluster(
  sv,
  resolution = 0.3,
  hc.method = options.hc.method,
  hc.metric = options.hc.metric,
  cl.score.method = options.cl.score.method,
  ...
)
```

options.hc.metric
# c("euclidean", "maximum", "manhattan", "canberra",
# "binary", "minkowski")

options.hc.method
# c("centroid", "median", "ward", "single")
```
Arguments

sv a numeric SVTable object (usually GEVASummary)
resolution numeric (0 to 1), used as a "zoom" parameter for cluster detection. A zero value returns the minimum number of clusters that can detected, while 1 returns the maximum amount of detectable clusters
hc.method character, the agglomeration method to be used. Used as the method argument for fastcluster::hclust.vector()
hc.metric character, the distance measure to be used. Used as the metric argument for fastcluster::hclust.vector()
cl.score.method character, method used to calculate the cluster scores for each point. If "auto", the "hclust.height" method is selected

... additional arguments:
  - mink.p : numeric, parameter for the Minkowsky metric. Used as the p argument for fastcluster::hclust.vector()
  - verbose : logical, whether to print the current progress (default is TRUE)
include.raw.results logical, whether to attach intermediate results to the returned object

Details

This function performs a hierarchical cluster analysis with the aid of implemented methods from the fastcluster::fastcluster package, particularly the fastcluster::hclust.vector() function. The available methods for the hc.method and hc.metric are described in the function’s documentation page (see fastcluster::hclust.vector()).

The resolution value is an accessible way to define the cluster separation threshold used in hierarchical clustering. The algorithm produces a dendrogram-like hierarchy in which each level/node is separated by a distance (sometimes called "height") to the next level/node, and the resolution translates a value between 0 and 1 to a proportional value within the total hierarchy height. This allows defining the rate of clusters from 0 to 1, which results in the least number of possible clusters (usually two) for 0, and the highest number (approximately one cluster per point) for 1.

If include.raw.results is TRUE, some additional data will be attached to the info slot of the returned GEVACLuster objects, including the kNN tree generated during the intermediate steps.

Value

A GEVACLuster object

Note

In hierarchical clustering, all points are clustered. Therefore, setting resolution to 1 will result into one cluster per point, where the cluster analysis may become pointless (no pun intended).

See Also

Other geva.cluster: geva.cluster(), geva.dcluster(), geva.quantiles()
Examples

```r
## Hierarchical clustering from a randomly generated input

# Preparing the data
ginput <- geva.ideal.example() # Generates a random input example
gsummary <- geva.summarize(ginput) # Summarizes with the default parameters

# Hierarchical clustering
gclust <- geva.hcluster(gsummary)
plot(gclust)

# Hierarchical clustering with slightly more resolution
res <- 0.35

gclust <- geva.hcluster(gsummary, resolution=res)
plot(gclust)
```

geva.ideal.example

GEVA “Ideal” Example for Package Testing

Description

Generates a random example of GEVAInput object that simulates an ideal analysis dataset. Used for testing purposes only.

Usage

```r
geva.ideal.example(probecount = 10000, nfactors = 3, colsperfactor = 3)
```

Arguments

- **probecount**: integer, number of probes (i.e., table rows)
- **nfactors**: integer, number of factors (e.g., experimental groups)
- **colsperfactor**: integer, number of columns (e.g., experiments) per factor

Value

A GEVAInput object. The included tables are composed by `probecount` rows and `nfactors * colsperfactor` columns

See Also

geva.summarize
Examples

```r
## "Ideal" input example
ginput <- geva.ideal.example() # Generates a random example
gsummary <- geva.summarize(ginput) # Summarizes the generated data
plot(gsummary) # Plots the summarized data
```

Description

Helper functions used to edit the contents from a `GEVAInput`.

Usage

```r
geva.input.correct(ginput, na.rm = TRUE, inf.rm = TRUE, invalid.col.rm = TRUE)
```

```r
geva.input.filter优点
  
  geva.input.correct(ginput, na.rm = TRUE, inf.rm = TRUE, invalid.col.rm = TRUE)
  
  geva.input.filter优点
  
  geva.input.rename.rows优点
```

Arguments

- `ginput`: A `GEVAInput` object
- `na.rm`: logical; if TRUE, removes all rows containing NA
- `inf.rm`: logical; if TRUE, removes all rows containing infinite values (Inf or -Inf)
- `invalid.col.rm`: logical; if TRUE, searches for any column that is entirely composed by invalid values (according to the other arguments) and removes it before checking the rows
- `p.value.cutoff`: numeric (0 to 1), the p-value cutoff. Rows containing values above this threshold are removed
- `by.any`: logical, set to TRUE to delete the rows with at least one occurrence above the cutoff; or FALSE to delete only those rows in which all values are above the specified threshold
na.val numeric, the replacement for NA values

... optional arguments. Accepts verbose (logical, default is TRUE) to enable or disable printing the progress

attr.column character, target column with the values that will replace the current row names

dupl.rm.method character, method to remove duplicate names. The possible options are:

- "least.p.vals" : Keeps the duplicate that contains the least sum of p-values
- "order" : Keeps the first occurrence of the duplicate in the current row order

Details

geva.input.correct corrects the numeric input data (values and weights), removing rows that include invalid values such as NA or infinite.

geva.input.filter attempts to select the most relevant part of the input data, removing rows containing p.values (1 - weights) above a specific threshold.

geva.input.rename.rows replaces the row names with a column from the feature table (see GEVAInput). The column name specified for attr.column must be included in the names(featureTable(ginput)). Any duplicates are removed according to the dupl.rm.method, and the selected duplicates are stored as a new column named "renamed_id" inside the feature table from the returned object.

Value

A modified GEVAInput object

Examples

```r
## geva.input.correct example
goexample1 <- runif(1000, -1, 1) # Random column 1
goexample2 <- runif(1000, -1, 1) # Random column 2
goexample3 <- runif(1000, -1, 1) # Random column 3
goexample3[runif(1000, -1, 1) < 0] = NA # Random NA's
ginput = geva.merge.input(col1=goexample1, col2=goexample2, col3=goexample3)

# Before the correction:
print(nrow(ginput)) # Returns 1000
# Applies the correction (removes rows with NA's)
ginput <- geva.input.correct(ginput)
# After the correction:
print(nrow(ginput)) # Returns less than 1000
```

## ---

```r
## geva.input.filter example
goinput <- geva.ideal.example(1000) # Generates a random input
# Before the filter:
print(nrow(goinput)) # Returns 1000
# Applies the filter
```
```r
# geva.merge.input example
geva.merge.input(input1, input2)
```

### Description

Functions to read, load, and concatenate the experimental comparisons from the data input. This is the initial step to proceed with any GEVA analysis.

### Usage

```r
geva.merge.input(
  ...,
  col.values = "logFC",
  col.pvals = "adj.P.Val",
  col.other = NULL
)
```

```r
geva.read.tables(
  filenames = NULL,
  dirname = ".",
  col.values = "logFC",
  col.pvals = "adj.P.Val",
  col.other = NULL,
  ...,
  files.pattern = "\*.txt$",
  p.value.cutoff = 0.05,
  read.args = list()
)
```

### Arguments

... multiple matrix or data.frame objects. At least two arguments are required for `geva.merge.input`, but it's optional for `geva.read.tables`. The optional arguments in `geva.read.tables` are also passed to its internal call to `geva.merge.input` and `geva.input.filter`.

In addition, the following optional arguments are accepted:
• na.val: (numeric) value between 0 and 1 used as replacement when a p-value column is not present (default is NA)
• use.regex: (logical) whether to match the column names using regular expressions (default is FALSE)
• verbose: (logical) whether to print the current loading and merge progress (default is TRUE)

col.values character vector, possible name(s) to match the logFC column(s) from each table
col.pvals character vector, possible name(s) to match the p-value column(s) from each table
col.other character vector, name(s) to match additional columns (e.g., gene symbols). Ignored if NULL
filenames character vector with two or more file paths
dirname single character, base directory containing the input files. Ignored if filenames is specified
files.pattern single character, pattern used to filter the files inside dirname. Ignored if filenames is specified
p.value.cutoff numeric (0 to 1), initial p-value threshold. Rows entirely composed by p-values above this cutoff (i.e., no significant logFC) are removed after the final merge. Ignored if NA or NULL
read.args list of additional arguments passed to utils::read.table

Details

The geva.merge.input function takes multiple tables as arguments (e.g., matrix or data.frame objects), extracts the logFC columns from each table and merges them into a single GEVAInput dataset.

The column names are specified in the col.values and col.pvals arguments (character) and must correctly match the column names for logFC and p-value columns, respectively, in the inputs to be extracted. Multiple values for column names can also be specified as valid name possibilities if they differ among the tables.

The function geva.merge.input reads multiple tab-delimited text files containing, extracts the logFC columns from each table and merges into a single GEVAInput dataset.

Value

A GEVAInput object

Note

The inclusion of p-value columns is not technically required, but strongly recommended as they improve the statistical accuracy in the summarization steps. If the p-value (or adjusted p-value) columns are present, their values are converted to weights by applying 1 - pvalue for each pvalue element, otherwise an optional na.val optional argument can specified as replacement to the absent values (default is NA). Weights are used to accomodate the central logFC values towards the most significant observations and penalize potential statistical inaccuracies.
Examples

### EXAMPLE 1
geva.merge.input example with three randomly generated tables
(For demonstration purposes only)

# Number of rows
n <- 10000

# Random row (probe) names
probnms <- sprintf("PROBE_%s", 1:n)

# Random gene names (optional)
genenms <- paste0(sprintf("GENE_%s", 1:n), LETTERS[1:n %% (length(LETTERS)+1)]

# Random table 1
dt1 <- data.frame(row.names=probnms,
                  logfc=(rnorm(n, 0, sd=2) * rnorm(n, 0, sd=0.5)),
                  pvalues = runif(n, max=0.08),
                  genesymbol = genenms)

# Random table 2
dt2 <- data.frame(row.names=probnms,
                  logfc=(rnorm(n, 0, sd=2) * rnorm(n, 0, sd=0.5)),
                  pvalues = runif(n, max=0.08),
                  genesymbol = genenms)

# Random table 3
dt3 <- data.frame(row.names=probnms,
                  logfc=(rnorm(n, 0, sd=2) * rnorm(n, 0, sd=0.5)),
                  pvalues = runif(n, max=0.08),
                  genesymbol = genenms)

# Merges the three tables
ginput <- geva.merge.input(exp1=dt1, exp2=dt2, exp3=dt3,
                           col.values="logfc",
                           col.pvals="pvalues",
                           col.other="genesymbol")

# Prints the first rows from the merged table
print(head(ginput))  # values
print(head(inputweights(ginput)))  # weights

# ---
## Not run:

### EXAMPLE 2
geva.read.tables example with three tab-delimited files

# Table file examples. Each one has 3 columns: "logfe", "pvalues", and "genesymbol"
# Replace it with your tab-delimited files (e.g. exported from limma's topTable)
fnames <- c("dt1.txt", "dt2.txt", "dt3.txt")

ginput <- geva.read.tables(fnames,
                           col.values="logfc",
                           col.pvals="pvalues",
                           col.other="genesymbol")
geva.quantiles

**Description**

Calculates the quantiles of a SVTable.
Usage

geva.quantiles(
  sv,
  quantile.method = options.quantiles,
  initial.thresholds = c(S = NA_real_, V = NA_real_),
  nq.s = 3L,
  nq.v = 2L,
  comb.score.fn = prod,
  ...
)

options.quantiles
# c("range.slice", "proportional", "density", "k.max.sd",
# "custom")

Arguments

sv          a SVTable object (usually GEVASummary)
quantile.method character, method to detect the initial quantile thresholds. Ignored if initial.thresholds is specified with no NA elements
initial.thresholds  named numeric vector with the threshold that delimits the initial quantile
nq.s          integer, number of quantiles in S-axis (experimental, see ‘Note’)
nq.v          integer, number of quantiles in V-axis (experimental, see ‘Note’)
comb.score.fn  function applied to merge S and V score columns into a single column. The function must require only one argument of numeric vector type and return a single numeric value. Examples include prod or mean
...         additional arguments include:
  • qslice : numeric (0 to 1), the axis fraction used by "range.slice" and "density" methods (see 'Details'). Default is 0.25
  • k : integer, neighbor points used by "density" and "k.max.sd" methods (see 'Details'). Default is 16
  • verbose : logical, whether to print the current progress. Default is TRUE

Details

The quantile.method defines how the initial quantile (usually the one at the bottom center) is calculated. Each method has a specific way to estimate the first spatial delimiter, as described below:

"range.slice" (default) Separation is set at the nearest point to a fraction of the spatial range. This fraction can be specified by the qslice optional argument (numeric, default is 0.25, or 25%).

"density" Separation is set at the point with the most proportional density by k neighbor points to its current spatial fraction. This method uses the optional arguments qslice (numeric,
default is 0.25, or 25%) for the desired spatial fraction, and k (numeric, default is 16) for the number of neighbor points;

"k.max.sd" Separation is set at the point with the greatest standard deviation of distance to its \( k \) neighbor points. The number of neighbor points can be specified by the \( k \) optional argument (numeric, default is 16);

"proportional" Separation is set at the exact axis division so that all quantiles have the size;

"custom" Uses the values specified in the initial.thresholds argument.

A custom initial separation point can be specified in the initial.thresholds as a numeric vector of two elements, where the first element refers to S axis and the second, to V axis. If one of the elements is NA, the initial quantile is calculated for that axis only. If both values are not NA, the quantile separation method is ignored and automatically set to "custom".

The \( nq.s \) and \( nq.v \) arguments determine the number of quantiles for the S and V axes, respectively. These parameters can be used to increase the number of possible partitions in the SV space, but their applicability is currently being tested (see 'Note').

The \( \text{comb.score.fn} \) is a function applied to the partial scores for each SV point to combine them into a single value. The result value is defined as the "quantile score" for a SV point. The function is applied iteratively to two-element numeric vectors.

Note

Customizing the number of quantiles by \( nq.s \) and \( nq.v \) is a experimental feature and the remaining analysis steps are mostly based on the default parameters for these arguments. Tests are being conducted to determine this feature’s applicability for the next releases.

See Also

geva.cluster

Other geva.cluster: geva.cluster(), geva.dcluster(), geva.hcluster()

Examples

```r
## Quantile detection from a randomly generated input

# Preparing the data
ginput <- geva.ideal.example()  # Generates a random input example
gsummary <- geva.summarize(ginput)  # Summarizes with the default parameters

# Default usage
gquants <- geva.quantiles(gsummary)  # Detects the quantiles
plot(gquants)  # Plots the quantiles

# Custom initial delimiters
gquants <- geva.quantiles(gsummary, initial.thresholds = c(S=1.00, V=0.5))
plot(gquants)  # Plots the quantiles

# Quantile detection using densities
gquants <- geva.quantiles(gsummary, quantile.method = 'density')
```
**geva.quick**

geva.quick(gobject, ...) # Plots the quantiles

---

**Description**

Given a `GEVAInput` object, applies the `geva.summarize()`, `geva.quantiles`, `geva.cluster`, and `geva.finalize` in a single call. Optional arguments are passed to the internal calls of these functions.

**Usage**

```r
geva.quick(gobject, ...)
```

**Arguments**

- `gobject` A `GEVAInput`, or any object that returns a `GEVAInput` upon calling `inputdata(gobject)` (e.g., `GEVASummary` or `GEVAResults`).
- `...` Optional arguments passed to `geva.summarize()`, `geva.quantiles()`, `geva.cluster()`, and `geva.finalize()`.

**Details**

This function performs the summarization, quantile detection, and clustering of an input data, then merges the results together and, if applicable, performs a factor analysis. If the `gobject` is not a `GEVAInput`, it must provide a valid `GEVAInput` object when called by `inputdata(gobject)`. Moreover, all parameters used in previous analysis will be taken into account. For instance, if `gobject` is a `GEVASummary` obtained by using `variation.method='mad'`, the internal call to `geva.summarize` in this function will use `variation.method='mad'` as well, unless if another parameter for `variation.method` is specified in the `...` arguments.

Therefore, this function can be useful not only as a shortcut to analyze `GEVAInput` but also for parameter testing when applied to a `GEVAResults` object, since the previous parameters are reused, while the specified parameters are overridden.

**Value**

A `GEVAResults` object

**Examples**

```r
## Basic usage using a random generated input
ginput <- geva.ideal.example() # Generates a random input example
gresults <- geva.quick(ginput) # Performs the entire analysis (default parameters)

print(head(top.genes(gresults))) # Prints the results
plot(gresults) # Plots the final SV-plot
```
## Example with non-default parameters

ginput <- geva.ideal.example()  # Generates a random input example
gresults <- geva.quick(ginput,
  summary.method="median",
  variation.method="mad",
  quantiles.method="density",
  cluster.method="density",
  resolution=0.32)

print(head(top.genes(gresults)))  # Prints the results
plot(gresults)  # Plots the final SV-plot

---

table of geva.summarize

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>geva.summarize</td>
<td>Summarizes the GEVAInput</td>
</tr>
</tbody>
</table>

### Description

Performs the summarization step by calculating the central points and variation estimates of logFC values from the input data.

### Usage

```r
geva.summarize(
  ginput,
  summary.method = options.summary,
  variation.method = options.variation,
  ...
)
```

- **options.summary**: `c("mean", "median")`
- **options.variation**: `c("sd", "var", "mad")`

### Arguments

- **ginput**: a GEVAInput object
- **summary.method**: single character, method used to calculate the central (summarized) logFC values
- **variation.method**: single character, method used to calculate the distribution degree (variation) of the logFC values
- **...**: additional arguments. Accepts verbose (logical, default is TRUE) to enable or disable printing the current progress
Details

The options.summary refer to the available operations to calculate central logFC values (mean or median), whereas options.variation presents three functions to calculate logFC variation (sd: Standard Deviation; var: Variance; and mad: Median Absolute Deviation). Moreover, all those operations include a weighted counterpart applied using the weights table from the GEVA Input object.

Value

A GEVASummary object

See Also

base::mean(), stats::median()
stats::var(), stats::sd(), stats::mad()

Examples

```r
## Summarization of a randomly generated input
ginput <- geva.ideal.example() # Generates a random input example
gsummary <- geva.summarize(ginput) # Summarizes with the default parameters
plot(gsummary) # Plots the summarized data
```

GEVACluster-class

GEVA Clustering Results

Description

The GEVACluster class represents the classification results from a cluster analysis. For each probe/gene, there is a assigned cluster among the g defined clusters.

This class inherits from GEVAGroupSet.

Value

A GEVACLuster object

Slots

grouping factor (m elements, g levels), cluster assignment for each gene/probe
(Inherited from GEVAGroupSet)

scores numeric vector (m elements) comprising a score value for each cluster assignment
(Inherited from GEVAGroupSet)

ftable data.frame (m lines) with additional cluster assignment features
(Inherited from GEVAGroupSet)
centroids numeric SVTable (g lines) with the S and V centroid coordinates for each cluster
(Inherited from GEVAGroupSet)
offsets numeric SVTable (m lines) with the S and V coordinate offsets each gene/probe from its
cluster centroid
(Inherited from GEVAGroupSet)
info list of supplementary information
(Inherited from GEVAGroupSet)
cluster.method character, method used in the cluster analysis (see geva.cluster)

Methods

(See also the inherited methods from GEVAGroupSet)

Plotting

lines(x, ...) Draws convex hulls around the clustered points
plot(x, y, ...) Draws a SV-plot that highlights the clustered points. Convex hulls are included
for visual purposes only and do not avoid enclosing points from other clusters on concave
parts.
Can be combined with another SVTable or GEVAGroupSet given as the y argument to include
additional graphical elements

Description

The GEVAGroupedSummary class inherits the GEVASummary class and includes group analysis data
(e.g., clustering and quantile detection).

Value

A GEVAGroupedSummary object

Slots

sv numeric matrix composed by two columns: S (summary) and V (variation)
(Inherited from SVTable)
inputdata GEVAInput-class with the data input
(Inherited from GEVASummary)
sv.method Names of the statistical methods used to summarize data
(Inherited from GEVASummary)
info list with additional information
(Inherited from GEVASummary)
groupsetlist TypedList of GEVAGroupSet objects
GEVAGroupSet-class

Methods

(See also the inherited methods from GEVASummary)

Conversion and coercion

as.expression(x, ginput, ...) Converts this object to expression
as.matrix(x, ...) Converts this object to matrix

Plotting

lines(x, ...) Draws delimiters within quantiles and convex hulls around the clustered points
plot(x, y, ...) Draws a SV-plot. The horizontal axis is for summary (S) and the vertical axis is for variation (V).
   In addition, highlights the included group sets
points(x, ...) Generic points implementation for GEVAGroupedSummary

Properties

analysis.params(gobject) Returns a list of analysis parameters passed to geva.cluster to obtain this object

Sub-slot accessors

cluster.method(object) Gets a character vector listing the cluster.method from each group set
quantiles(object) Gets the GEVAQuantiles, or NULL if not present

GEVAGroupSet-class  GEVA Grouping Results

Description

The GEVAGroupSet class represents the classification of summarized values from a SVTable, where each gene/probe has one assigned group among g defined groups. This is an abstract class. Inherits the GEVACluster and GEVAQuantiles classes.

Value

A GEVAGroupSet object
Slots

grouping factor \((m\text{ elements}, g\text{ levels})\) used to group the genes/probes
scores numeric vector \((m\text{ elements})\) with the assigned grouping scores for each gene/probe
ftable data.frame \((m\text{ lines})\) with additional grouping features
centroids numeric SVTable \((g\text{ lines})\) with the S and V centroid coordinates for each group
offsets numeric SVTable \((m\text{ lines})\) with the S and V coordinate offsets each gene/probe from its
group centroid
info list of additional information

Methods

Alternative accessors

levels(x) Returns the unique group names included in the group set.
   Equivalent to levels(groups(x))

Conversion and coercion

as.data.frame(x, row.names = names(x), ...) Returns a data.frame with the groups and
   scores slots as columns
as.expression(x, sv, ...) Gets the expression that reproduces this GEVAGroupSet object, in-
   cluding function parameters used by geva.cluster. The sv argument is optional but can be
   specified to replace the source SVTable
as.SVTable(x, which = c("sv", "offsets", "centroids"), ...) Retrieves a SVTable based
   on the contents indicated by which. The accepted arguments are: sv for the source data;
   offsets for the offsets slots; and centroids for the centroids slot

Dimension accessors

length(x) Returns the number of rows in the sv slot
names(x) Gets the assigned names by the classification and scores

Plotting

color.values(x, point.col = NULL, ...) Gets the colors associated to the grouped data points.
   If not present, generates random group colors.
   If point.col is a single character or an vector of the same length of data points, adjusts the
   color values to web RGBA
plot(x, y, ...) Draws a SV-plot that highlights the grouped information.
   Can be combined with another SVTable or GEVAGroupSet given as the y argument to include
   additional graphical elements
points(x, ...) Draws the grouped points
Properties

analysis.params(object) Returns a list of analysis parameters passed to geva.cluster to obtain this object

cluster.method(object) Returns the option used as the cluster.method argument when calling geva.cluster

Sub-slot accessors

classification.table(object) <- value Stores the classification data.frame on this object
classification.table(object) Returns a data.frame of predicted classifications, if supported by this object
sv.data(object) Returns a SVTable with the source SV coordinates
sv(object) Returns the numeric matrix in the SVTable from sv.data(object)

GEVAInput-class GEVA Input Data

Description

The GEVAInput class contains the initial data for GEVA usage. It stores numeric matrices of logFC values from differential expression comparison results. Options for calculations and summarizing are also included.

Value

A GEVAInput object

Slots

values numeric matrix (m*n) of log-ratio values, usually logFC
weights numeric matrix (m*n) of weighted values. If not defined, all weight values are equal to 1
factors factor (n elements) representing the grouping of the n columns. If not defined, all factors are equal to NA
ftable data.frame with m rows containing attribute columns associated to the features (e.g., probes or genes)
info list of supplementary information related to the input
Methods

**Alternative accessors**

levels(x) Returns the unique values from the assigned factors; or NA if there are no assigned factors in x

**Conversion and coercion**

as.array(x, ...) Converts this object to array

**Dimension accessors**

dim(x) Gets the dimensions defined for both matrices in values and weights slots
dimnames(x) <- value Sets the list with the row and column names.
        Individual dimension names can also be set using rownames<- and colnames<-
dimnames(x) Gets a list with the row and column names.
        Individual dimension names can also be accessed through rownames and colnames
inputnames(object) Gets the input column names (same as colnames(object))
length(x) Returns the number of rows in the values slot
names(x) Same as inputnames. For internal use

**Plotting**

plot(x, y, ...) Summarizes the input using the default parameters, then calls the plot on the returned GEVASummary object.
        Not intended to regular use and will give a warning if called

**Properties**

analysis.params(gobject) Returns a list of analysis parameters passed to geva.merge.input or geva.read.tables to obtain this object

**Subsetting**

head(x, n = 6L, ...) Returns the first parts of the values table
tail(x, n = 6L, ...) Returns the last parts of the values table
GEVAGroupSet

GEVAQuantiles-class GEVA Quantiles Grouping Results

Description

The GEVAQuantiles class represents the results of a quantile detection analysis. For each probe/gene, there is a assigned quantile among the g defined quantiles.

This class inherits from GEVAGroupSet and is inherited by GEVAQuantilesAdjusted.

Value

A GEVAQuantiles object

Slots

grouping factor (m elements, g levels), quantile assignment for each gene/probe
(Inherited from GEVAGroupSet)
scores numeric vector (m elements) with the assigned quantile scores for each gene/probe
(Inherited from GEVAGroupSet)
ftable data.frame (m lines) with additional quantile assignment features
(Inherited from GEVAGroupSet)
centroids numeric SVTable (g lines) with the S and V centroid coordinates for each quantile
(Inherited from GEVAGroupSet)
offsets numeric SVTable (m lines) with the S and V coordinate offsets each gene/probe from its quantile centroid
(Inherited from GEVAGroupSet)
info list of additional information
(Inherited from GEVAGroupSet)
svscores numeric SVTable (m lines) with individual partial scores for the assigned quantiles
qareasizes numeric SVTable (g lines) with the S and V sizes for each quantile
qindexes integer SVTable (g lines) representing the position index to each quantile, in terms of summary and variation
qcount integer attributes (SVIntAttribute) with the defined number of quantiles for the S and V axes
qcutoff numeric attributes (SVNumAttribute) with the initial quantile cutoff in S and V, starting from the point zero
qmethod character, method used to calculate the initial quantiles (see geva.quantiles())

Methods

(See also the inherited methods from GEVAGroupSet)

Conversion and coercion
as.expression(x, sv, ...) Converts this object to expression

as.SVTable(x, which = c("sv", "offsets", "centroids", "qindexes"), ..., row.names = names(x))
Converts this object to SVTable

**Plotting**

lines(x, ...) Draws the quantile delimiter lines

plot(x, y, ...) Draws a SV-plot that highlights the points from each quantile. Dashed lines are included as the quantile delimiters.
Can be combined with another SVTable or GEVAGroupSet given as the y argument to include additional graphical elements

**Properties**

cluster.method(object) Returns the option used as the cluster.method argument when calling geva.cluster.
Instances of this object always return 'quantiles'

**Sub-slot accessors**

classification.table(object) <- value Sets the data.frame with the qualitative contrasts of classification relevance

classification.table(object) Gets a data.frame with the qualitative contrasts of classification relevance

quantiles(object) Gets the unique quantile names

---

**GEVAQuantilesAdjusted-class**

*GEVA Adjusted Quantiles Results*

**Description**

The GEVAQuantilesAdjusted class represents the results of a quantile detection analysis with adjusted assignments based on relationships with other GEVAGroupSet objects. For each probe/gene, there is a assigned quantile among the g defined quantiles.

This class inherits from GEVAQuantiles.

**Value**

A GEVAQuantilesAdjusted object
GEVAResults-class

Slots

- grouping factor (m elements, g levels), quantile assignment for each gene/probe
  (Inherited from GEVAGroupSet)
- scores numeric vector (m elements) with the assigned quantile scores for each gene/probe
  (Inherited from GEVAGroupSet)
- ftable data.frame (m lines) with additional quantile assignment data
  (Inherited from GEVAGroupSet)
- centroids numeric SVTable (g lines) with the S and V centroid coordinates for each quantile
  (Inherited from GEVAGroupSet)
- offsets numeric SVTable (m lines) with the S and V coordinate offsets each gene/probe from its
  quantile centroid
  (Inherited from GEVAGroupSet)
- info list of additional information
  (Inherited from GEVAGroupSet)
- svscores numeric SVTable (m lines) with individual partial scores for the assigned quantiles
  (Inherited from GEVAQuantiles)
- qareasizes numeric SVTable (g lines) with the S and V sizes for each quantile
  (Inherited from GEVAQuantiles)
- qindexes integer SVTable (g lines) representing the position index to each quantile, in terms of
  summary and variation
  (Inherited from GEVAQuantiles)
- qcount integer attributes (SVIntAttribute) with the defined number of quantiles for the S and V
  axes
  (Inherited from GEVAQuantiles)
- qcutoff numeric attributes (SVNumAttribute) with the initial quantile cutoff in S and V, starting
  from the point zero
  (Inherited from GEVAQuantiles)
- grouprels TypedList of named factor elements representing external group relationships to the
  current quantiles

Methods

(See also the inherited methods from GEVAQuantiles and GEVAGroupSet)

Description

The GEVAResults class contains the final results from GEVA analyses. It represents the results
of multiple statistical approaches from summary/variation data, clustering, quantile detection, and
factor analysis (if applicable).
Value

A GEVAResults object

Slots

resultstable data.frame \((m \text{ lines})\) with classification results for the genes/probes
svdata GEVASummary used as input
quantdata GEVAQuantiles or GEVAQuantilesAdjusted with the final quantile assignments for
the summarized data
factoring data.frame \((m \text{ lines})\) with detailed results for the factor analyses, such as p-values for
each factor. If there was no factor analysis, this slot is NULL or empty
classiftable data.frame used as reference for the final classification
info list of supplementary information

Methods

Conversion and coercion

as.expression(x, gsummary, gquants, ...) Gets the expression that reproduces this GEVAResults
object, including function parameters used by geva.finalize. The gsummary and gquants
arguments are optional but can be specified to replace the internal GEVASummary and GEVAQuantiles,
respectively

Dimension accessors

dim(x) Returns the dimensions from the resultstable slot
dimnames(x) Returns a list with the row and column names from the results.table slot. Individual
dimension names can also be accessed through rownames and colnames
length(x) Returns the number of rows in the resultstable slot
names(x) Returns the column names from the resultstable slot

Plotting

plot(x, y, ...) Draws a SV-plot that highlights the relevant points from adjusted quantiles
points(x, which, ..., classif) Draws the results points.
If which (character vector) is given, plots only the matching genes/probes.
If classif (character vector) is given, plots only points with the matching classification

Properties

x$name <- value Extracts a column from the resultstable slot
x[i, j, ..., drop=TRUE] Extracts the contents from the resultstable slot
analysis.params(gobject) Returns a list of analysis parameters passed to geva.finalize or
geva.quick to obtain this object
**Sub-slot accessors**

- `featureTable(object)` Returns the features data.frame from the internal `GEVAInput`
- `head(x, ...)` Returns the first lines of `results.table(x)`
- `inputdata(object)` Returns the internal `GEVAInput`
- `inputvalues(object)` Returns the values matrix from the internal `GEVAInput`
- `inputweights(object, normalized)` Returns the weights matrix from the internal `GEVAInput`
- `levels(x)` Returns the factors used in factor analysis, if present

---

**Description**

The `GEVASummary` class represents the calculation results for summary and variation from a `GEVAInput`. This class inherits from `SVTable`.

**Value**

A `GEVASummary` object

**Slots**

- `sv` numeric matrix composed by two columns: `S` (summary) and `V` (variation)  
  (Inherited from `SVTable`)
- `inputdata` `GEVAInput-class` with the data input
- `sv.method` Names of the statistical methods used to summarize data
- `info` list with additional information

**Methods**

(See also the inherited methods from `SVTable`)

**Conversion and coercion**

- `as.expression(x, ginput, ...)` Gets the expression that reproduces this `GEVASummary` object, including function parameters used by `geva.summary`. The `ginput` argument is optional but can be specified to replace the internal `GEVAInput`
- `as.matrix(x, ...)` Equivalent to `sv(x)`

**Grouping**
groupsets(object) <- value Converts this instance to GEVAGroupedSummary and sets the list of GEVAGroupSet objects. Can be used with $<name>$ to specify the object name in the list. If value is a GEVAGroupSet, inserts the element and sets the name based on the value call.
groupsets(object) Gets the list of GEVAGroupSet objects attached to this instance. Only applicable for GEVAGroupedSummary objects.

Plotting

plot(x, y, ...) Draws a SV-plot. The horizontal axis is for summary (S) and the vertical axis is for variation (V).

Properties

analysis.params(gobject) Returns a list of analysis parameters passed to geva.summarize to obtain this object.
get.summary.method(x) Gets a character for the summarization method name.
get.variation.method(x) Gets a character for the variation calculation method name.

Sub-slot accessors

factors(object) <- value Sets the value to the factor slot in the internal GEVAInput.
factors(object) Gets the factor defined in the factors slot in the internal GEVAInput.
featureTable(object) Gets the data.frame from the ftable slot in the internal GEVAInput.
infolist(object, field = NULL, ...) Gets the list from the info slot.
    If recursive is TRUE, appends the contents from the info slot in the internal GEVAInput.
inputvalues(object) Gets the matrix from the values slot in the internal GEVAInput.
inputweights(object, normalized) Gets the matrix from the weights slot in the internal GEVAInput.

SVAttribute-class Summary-Variation Attribute Field

Description

This S4 class stores two character slots representing attribute fields for summary and variation. The SVAttribute class is abstract and must be instantiated as SVChrAttribute (for character), SVNumAttribute (for numeric), or SVIntAttribute (for integer).

Arguments

S the summary value
V the variation value
SVAttribute-class

Value

A SVAttribute object

Slots

S either character or numeric or integer of length one
V either character or numeric or integer of length one

Methods

Alternative accessors

summary(object, ...) Returns the contents from S slot
sv(object) Returns the contents as a named vector
variation(object, ...) Returns the contents from S slot

Constructors

sv.data(object) For internal use. Returns the equivalent object
svattr(S, V) Creates a new SVAttribute

Conversion and coercion

as.character(x, ...) Converts this object to character
as.vector(x, ...) Converts this object to vector

Dimension accessors

dim(x) For internal use, always returns NULL
names(x) Returns the slot names (always c('S', 'V'))

Properties

x$name <- value Queries the vector contents (equivalent to the indexer). Only accepts $S and $V
x[i, j, ..., drop=TRUE] Indexer to access the vector values. Only accepts 'S' or 'V' as i arguments

Note

The slots S and V must be of the same class (either character, numeric, or integer).
SVTable-class Summary-Variation Table

Description

The SVTable class stores a matrix composed by two columns: $S$ (for summary) and $V$ (for variation).

This class is inherited by GEVASummary.

Value

A SVTable object

Slots

$sv$ matrix composed by two columns: $S$ (summary) and $V$ (variation)

Methods

Alternative accessors

summary(object, ...) Returns the $S$ column
sv.data(object) Equivalent to returning this object itself
variation(object, ...) Returns the $V$ column

Constructor

svtable(S, V, row.names = NULL) Creates a SVTable from the vectors $S$ and $V$

Conversion and coercion

as.data.frame(x, ...) Converts this object to data.frame
as.matrix(x, ...) Converts this object to matrix
as.SVTable.data.frame(x, row.names = rownames(x), ...) Converts a data.frame to a SVTable
as.SVTable.matrix(x, row.names = rownames(x), ...) Converts a matrix to a SVTable
as.SVTable(x, ...) Returns the same object

Dimension accessors

dimnames(x) Gets a list with the row and column names from the $sv$ slot.
    Individual dimension names can also be accessed through rownames and colnames
dim(x) Gets the dimensions from the $sv$ slot
length(x) Returns the number of rows in the $sv$ slot
names(x)  Always returns c('S', 'V')

**Formatting and evaluation**

format(x, ...)  Generic format implementation for SVTable

with(data, expr, ...)  Generic with implementation for SVTable

**Plotting**

plot(x, y, ...)  Draws a SV-plot. The horizontal axis is for summary (S) and the vertical axis is for variation (V)

points(x, ...)  Draws the SV points in the plot

**Subsetting**

head(x, n = 6L, ...)  Returns the first parts of the matrix contents

tail(x, n = 6L, ...)  Returns the last parts of the matrix contents

**Validation**

is.na(x)  Generic is.na implementation for SVTable

**Note**

The matrix from sv slot can be numeric, character, or any other supported type by matrix. The same slot from GEVASummary, however, is always a numeric matrix.

**Examples**

```r
## Creates a SV-table where:
# - S has elements from 1 to 10; and
# - V has elements from 10 to 1
svtab <- svtable(seq.int(1, 10), seq.int(10, 1))
```

<table>
<thead>
<tr>
<th>top.genes</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Top Results from GEVA</strong></td>
<td></td>
</tr>
</tbody>
</table>

**Description**

Extracts the genes with a relevant classification according to the GEVA results.
Usage

top.genes(
  gevaresults,
  classif = c("similar", "factor-dependent", "factor-specific"),
  which.spec = levels(gevaresults),
  add.cols = NULL,
  ...
  names.only = FALSE
)

Arguments

gevaresults  a GEVAResults object
classif  character vector, filters the returned genes by their final classification. Possible options are "similar", "factor-dependent", "factor-specific", "sparse", and "basal". Multiple options can be combined
which.spec  factor, filters the specific factors to be returned
add.cols  character vector with column names from the feature table (accessed by featureTable(gevaresults)). The matching columns will be added to the returned table
...  optional arguments (not used in this version)
names.only  logical, set to TRUE to return only the table row names

Value

If names.only is FALSE (the default), returns a subset of the resultstable slot (data.frame) from the gevaresults that includes only the filtered genes according to the function parameters.

Otherwise, if names.only is TRUE, returns only the row names (character vector) of this table subset.

Examples

```r
## Basic usage with a random generated input
ginput <- geva.ideal.example() # Generates a random input example
gresults <- geva.quick(ginput) # Performs the entire analysis (default parameters)

dgenes <- top.genes(gresults) # Gets the top genes table
head(dgenes) # Prints the first results

# Appends the "Symbol" column to the results table
dgenes <- top.genes(gresults, add.cols="Symbol")
head(dgenes) # Prints the first results

# Appends all feature columns to the results table
dgenes <- top.genes(gresults, add.cols=names(featureTable(gresults)))
head(dgenes) # Prints the first results

# Gets only the factor-specific genes
```
**TypedList-class**

TypedList-class

*Type-strict List (TypedList-class)*

---

**Description**

List containing elements of the same class or inheritance.

**Value**

A **TypedList** object

**Slots**

- **Data** list of internal contents. Elements must match or inherit a common class  
  *(Inherited from list)*

  **elem.class** character representing the class related to the elements

**Methods**

**Constructors**

typed.list(..., elem.class = NA_character_) Creates a TypedList from the elements in ...  
  derived from the class elem.class

**Conversion and coercion**

as.list(x, ...) Converts this object to list  
as.typed.list.list(x, elem.class = NA_character_) Converts a list to a TypedList if its  
  elements inherit the same type  
as.typed.list(x, elem.class = NA_character_) Coerces a TypedList to support the inherited  
  class indicated by elem.class  
as.typed.list.vector(x, elem.class = NA_character_) Converts a vector to a TypedList

**Properties**

x[i, j, ...] <- value Sets a value to this list. The value argument must be compatible to the  
  current list type

```r
dtgenes <- top.genes(gresults, "factor-specific")
head(dtgenes)  # Prints the first results

# Gets only the factor-specific genes for "Cond_1" factor (if any)
dtgenes <- top.genes(gresults, "factor-specific", "Cond_1")
head(dtgenes)  # Prints the first results
```
Examples

```r
## Creates a TypeList that stores list-derived objects
tpls = typed.list(A=list(1L:5L),
    B=data.frame(v1=LETTERS[1L:10L]),
    elem.class = 'list')

# Note: The 'elem.class' above is optional, since the # class is automatically detected from the first argument
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