

# Package: geva (via r-universe)

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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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**URL** <https://github.com/sbcblab/geva>

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**License** LGPL-3

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 'c\_GEVAGroupSet.R' 'c\_GEVACluster.R' 'funhelpers.R' 'linq.R'  
 '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'  
 'clusteringbase.R' 'matrixhelpers.R' 'statmath.R'  
 'dclustering.R' 'quantiles.R' 'factoring.R' 'scoremerge.R'  
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**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)
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

<code>object, x, gobject</code>	Primary object. See the documentation from each class for specific usages
<code>normalized</code>	logical, whether to return values in the normalized scale
<code>field</code>	When used with a information list, returns the information entry with the corresponding name
<code>...</code>	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 <a href="#">TypedList</a> object
group	Character to filter the returned groups. Omit it to return all groups
gres	A <a href="#">GEVResults</a> objec

**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 <a href="#">SVTable</a> object (usually <a href="#">GEVASummary</a> )
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 <code>cluster.method</code> is <code>quantiles</code>
resolution	numeric (0 to 1), used as a "zoom" parameter for cluster detection. A zero value returns the minimum number of clusters that can be detected by the <code>cluster.method</code> , while 1 returns the maximum amount of clusters. Ignored if <code>cluster.method</code> is <code>quantiles</code>
distance.method	character, two-point distance calculation method. Options are "euclidean" or "manhattan" distances
...	further arguments passed to <a href="#">geva.dcluster()</a> , <a href="#">geva.hcluster()</a> , or <a href="#">geva.quantiles()</a> . In addition, the following arguments are accepted: <ul style="list-style-type: none"> <li>• <code>eps</code> : numeric, defines the <i>epsilon</i> coefficient for density clustering (see ‘Details’)</li> <li>• <code>mink.p</code> : numeric, parameter for the Minkowsky metric used in hierarchical clustering. Used as the <code>p</code> argument for <a href="#">fastcluster::hclust.vector()</a></li> <li>• <code>verbose</code> : logical, whether to print the current progress (default is TRUE)</li> </ul>
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

```
## 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
gclust <- 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**

```
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**

<code>sv</code>	a numeric <a href="#">SVTable</a> object (usually <a href="#">GEVASummary</a> )
<code>resolution</code>	numeric (0 to 1), used as a "zoom" parameter for cluster detection. A zero value returns the minimum number of clusters that can be detected, while 1 returns the maximum amount of detectable clusters. Ignored if <code>eps</code> is specified
<code>dcluster.method</code>	character, density-based method for cluster separation
<code>cl.score.method</code>	character, method used to calculate the cluster scores for each point. If "auto", the "density" method is selected
<code>minpts</code>	integer, minimum number of points required to form a cluster
<code>...</code>	additional arguments. Accepts <code>verbose</code> (logical, default is TRUE) to enable or disable printing the current progress
<code>eps</code>	numeric, maximum neighborhood distance between points to be clustered
<code>include.raw.results</code>	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 proportional 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

```
## 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)
```

---

`geva.finalize`

*Concatenating GEVA calculations into the final results*

---

### 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

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

```
)

options.factoring.p.adjust
# c("partial.quantiles", "holm", "hochberg", "hommel",
#   "bonferroni", "BH", "BY", "fdr", "none")
```

## Arguments

<code>gsummary</code>	a <a href="#">GEVASummary</a> object
<code>...</code>	Intermediate results produced from the <code>gsummary</code> object, such as clusters ( <a href="#">GEVACluster</a> ), quantiles ( <a href="#">GEVAQuantiles</a> ), or any other object inherited from <a href="#">GEVAGroupSet</a>
<code>p.value</code>	numeric (0 to 1), p-value cutoff used in the ANOVA procedures (factor analysis only)
<code>p.val.adjust</code>	character, p-value correction method (factor analysis only). Possible values are: "partial.quantiles", "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
<code>constraint.factors</code>	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 significant 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 = (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 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

```
## 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**

```

geva.hcluster(
  sv,
  resolution = 0.3,
  hc.method = options.hc.method,
  hc.metric = options.hc.metric,
  cl.score.method = options.cl.score.method,
  ...,
  include.raw.results = FALSE
)

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

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

```

**Arguments**

sv	a numeric <a href="#">SVTable</a> object (usually <a href="#">GEVASummary</a> )
resolution	numeric (0 to 1), used as a "zoom" parameter for cluster detection. A zero value returns the minimum number of clusters that can be 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 <a href="#">fastcluster::hclust.vector()</a>
hc.metric	character, the distance measure to be used. Used as the metric argument for <a href="#">fastcluster::hclust.vector()</a>
cl.score.method	character, method used to calculate the cluster scores for each point. If "auto", the "hclust.height" method is selected
...	additional arguments: <ul style="list-style-type: none"> <li>• <code>mink.p</code> : numeric, parameter for the Minkowsky metric. Used as the p argument for <a href="#">fastcluster::hclust.vector()</a></li> <li>• <code>verbose</code> : logical, whether to print the current progress (default is TRUE)</li> </ul>
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

```
## 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
gclust <- geva.hcluster(gsummary,
                       resolution=0.35)
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

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

**Arguments**

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

**Value**

A [GEVAInput](#) object. The included tables are composed by probecount rows and nfactors \* colspfactor columns

**See Also**

[geva.summarize](#)

**Examples**

```
## "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
```

---

geva.input.correct      *GEVA Input Post-processing*

---

**Description**

Helper functions used to edit the contents from a [GEVAInput](#).

**Usage**

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

geva.input.filter(
  ginput,
  p.value.cutoff = 0.05,
  by.any = FALSE,
  na.val = 0,
  ...
)

geva.input.rename.rows(
  ginput,
  attr.column,
  dupl.rm.method = c("least.p.vals", "order")
)
```

**Arguments**

<code>ginput</code>	A <a href="#">GEVAInput</a> object
<code>na.rm</code>	logical; if TRUE, removes all rows containing NA
<code>inf.rm</code>	logical; if TRUE, removes all rows containing infinite values (Inf or -Inf)
<code>invalid.col.rm</code>	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
<code>p.value.cutoff</code>	numeric (0 to 1), the p-value cutoff. Rows containing values above this threshold are removed
<code>by.any</code>	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
<code>na.val</code>	numeric, the replacement for NA values
<code>...</code>	optional arguments. Accepts <code>verbose</code> (logical, default is TRUE) to enable or disable printing the progress
<code>attr.column</code>	character, target column with the values that will replace the current row names
<code>dupl.rm.method</code>	character, method to remove duplicate names. The possible options are: <ul style="list-style-type: none"> <li>• <code>"least.p.vals"</code> : Keeps the duplicate that contains the least sum of p-values</li> <li>• <code>"order"</code> : Keeps the first occurrence of the duplicate in the current row order</li> </ul>

**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**

```
## geva.input.correct example
colexample1 <- runif(1000, -1, 1)      # Random column 1
colexample2 <- runif(1000, -1, 1)      # Random column 2
colexample3 <- runif(1000, -1, 1)      # Random column 3
colexample3[runif(1000, -1, 1) < 0] = NA # Random NA's
```

```

ginput = geva.merge.input(col1=colexample1,
                          col2=colexample2,
                          col3=colexample3)

# 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

## ---
## geva.input.filter example
ginput <- geva.ideal.example(1000) # Generates a random input
# Before the filter:
print(nrow(ginput)) # Returns 1000
# Applies the filter
ginput <- geva.input.filter(ginput)
# After the filter:
print(nrow(ginput)) # Returns less than 1000

## ---
## geva.input.rename.rows example
ginput <- geva.ideal.example() # Generates a random input
# Renames to 'Symbol'
ginput <- geva.input.rename.rows(ginput,
                                attr.column = "Symbol")
print(head(ginput)) # The row names are set now as the gene symbols

```

---

geva.merge.input

*GEVA Input Processing and Merge*


---

## 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

```

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

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 <code>geva.merge.input</code> , but it's optional for <code>geva.read.tables</code> . The optional arguments in <code>geva.read.tables</code> are also passed to its internal call to <code>geva.merge.input</code> and <a href="#">geva.input.filter</a> . In addition, the following optional arguments are accepted: <ul style="list-style-type: none"> <li><code>na.val</code>: (numeric) value between 0 and 1 used as replacement when a p-value column is not present (default is NA)</li> <li><code>use.regex</code>: (logical) whether to match the column names using <a href="#">regular expressions</a> (default is FALSE)</li> <li><code>verbose</code>: (logical) whether to print the current loading and merge progress (default is TRUE)</li> </ul>
<code>col.values</code>	character vector, possible name(s) to match the <i>logFC</i> column(s) from each table
<code>col.pvals</code>	character vector, possible name(s) to match the p-value column(s) from each table
<code>col.other</code>	character vector, name(s) to match additional columns ( <i>e.g.</i> , gene symbols). Ignored if NULL
<code>filenames</code>	character vector with two or more file paths
<code>dirname</code>	single character, base directory containing the input files. Ignored if <code>filenames</code> is specified
<code>files.pattern</code>	single character, pattern used to filter the files inside <code>dirname</code> . Ignored if <code>filenames</code> is specified
<code>p.value.cutoff</code>	numeric (0 to 1), initial p-value threshold. Rows entirely composed by p-values above this cutoff ( <i>i.e.</i> , no significant <i>logFC</i> ) are removed after the final merge. Ignored if NA or NULL
<code>read.args</code>	list of additional arguments passed to <a href="#">utils::read.table</a>

## 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 be specified as replacement to the absent values (default is NA). Weights are used to accommodate 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: "logfc", "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")

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

# ---

### EXAMPLE 3
## geva.read.tables example with tab-delimited files in a directory

# Directory name (replace it with a directory containing the table files)
dirnm <- "C:/User/robertplant123/Documents/R/gevaexamples"

# In this example, table files contain 3 columns: "logfc", "pvalues", and "genesymbol"
# Reads all txt files in the directory
ginput <- geva.read.tables(dirname=dirnm,
                          col.values="logfc",
                          col.pvals="pvalues",
                          col.other="genesymbol")

# (Optional step)
# Let's assume that all table file names start with "dt" and ends with the ".txt" extension,
# such as dt1.txt, dt2.txt and so on...
fname_pattern <- c("^dt.+?\\.txt$") # Defines a RegEx pattern to find the files
# Loads only files that match the file name pattern
ginput <- geva.read.tables(dirname=dirnm,
                          files.pattern=fname_pattern,
                          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

## End(Not run)
```

---

geva.quantiles

*GEVA Quantiles Detection*


---

## 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 <a href="#">SVTable</a> object (usually <a href="#">GEVASummary</a> )
quantile.method	character, method to detect the initial quantile thresholds. Ignored if <code>initial.thresholds</code> 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 <code>prod</code> or <code>mean</code>
...	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 `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

```
## 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')
plot(gquants) # Plots the quantiles
```

---

geva.quick

*All-In-One Function for GEVA Intermediate Procedures*


---

## 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

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

## Arguments

gobject	A <a href="#">GEVAInput</a> , or any object that returns a <a href="#">GEVAInput</a> upon calling <code>inputdata(gobject)</code> (e.g., <a href="#">GEVASummary</a> or <a href="#">GEVAResults</a> ).
...	Optional arguments passed to <a href="#">geva.summarize()</a> , <a href="#">geva.quantiles()</a> , <a href="#">geva.cluster()</a> , and <a href="#">geva.finalize()</a>

## 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

```
## 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
```

---

geva.summarize

*Summarizes the GEVAInput*

---

## Description

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

## Usage

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

```
options.summary
# c("mean", "median")

options.variation
# c("sd", "var", "mad")
```

## Arguments

<code>ginput</code>	a <a href="#">GEVAInput</a> object
<code>summary.method</code>	single character, method used to calculate the central (summarized) <i>logFC</i> values
<code>variation.method</code>	single character, method used to calculate the distribution degree (variation) of the <i>logFC</i> values
<code>...</code>	additional arguments. Accepts <code>verbose</code> (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 [GEVAInput](#) object.

## Value

A [GEVASummary](#) object

## See Also

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

## Examples

```
## 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](#))

f`table` 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

---

 GEVAGroupedSummary-class

*GEVA Grouped Summary-Variation Table*


---

### 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

### 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 ( $m$  elements,  $g$  levels) used to group the genes/probes

`scores` numeric vector ( $m$  elements) with the assigned grouping scores for each gene/probe

`fhtable` `data.frame` ( $m$  lines) with additional grouping features

`centroids` numeric `SVTable` ( $g$  lines) with the S and V centroid coordinates for each group

`offsets` numeric `SVTable` ( $m$  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, including 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(gobject)` 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	<i>GEVA Input Data</i>
-----------------	------------------------

---

**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

---

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](#))

fable 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

### 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](#))

fhtable 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](#))

---

GEVAResults-class      *GEVA Results Table*

---

**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` ( $m$  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` ( $m$  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

---

GEVASummary-class

*GEVA Summary-Variation Table*

---

**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

**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	<i>Summary-Variation Table</i>
---------------	--------------------------------

---

### Description

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

This class is inherited by [GEVSummary](#).

### 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

```
## 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))
```

---

top.genes

*Top Results from GEVA*


---

## Description

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

## Usage

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

## Arguments

gevarresults	a <a href="#">GEVAResults</a> 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 <code>featureTable(gevarresults)</code> ). 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 `gevarresults` 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

```
## 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)

# Gets a table that includes all the top genes
dtgenes <- top.genes(gresults) # Gets the top genes table
head(dtgenes)                 # Prints the first results
```

```

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

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

# Gets only the factor-specific genes
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

```

---

TypedList-class	<i>Type-strict List (TypedList-class)</i>
-----------------	---

---

## 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

### Examples

```
## Creates a TypedList 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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