

# Package ‘esetVis’

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**Type** Package

**Title** Visualizations of expressionSet Bioconductor object

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**Description** Utility functions for visualization of expressionSet (or SummarizedExperiment) Bioconductor object, including spectral map, tsne and linear discriminant analysis. Static plot via the ggplot2 package or interactive via the ggvis or rbokeh packages are available.

**Imports** mpm, hexbin, Rtsne, MLP, grid, Biobase, MASS, stats, utils, grDevices

**Suggests** ggplot2, ggvis, rbokeh, ggrepel, knitr, rmarkdown, ALL, hgu95av2.db, AnnotationDbi, pander, SummarizedExperiment

**biocViews** Visualization, DataRepresentation, DimensionReduction, PrincipalComponent, Pathways

**VignetteBuilder** knitr

**License** GPL-3

**RoxygenNote** 5.0.1

**NeedsCompilation** no

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esetLda

*plot a biplot of a linear discriminant analysis of an eSet object***Description**

esetLda reduces the dimension of the data contained in the [eSet](#) via a linear discriminant analysis on the specified grouping variable with the `lda` function and plot the subsequent biplot, possibly with sample annotation and gene annotation contained in the `eSet`.

**Usage**

```
esetLda(eset, ldaVar, psids = 1:nrow(eset), dim = c(1, 2),
  colorVar = NULL, color = if (is.null(colorVar)) "black" else NULL,
  shapeVar = NULL, shape = if (is.null(shapeVar)) 15 else NULL,
  sizeVar = NULL, size = if (is.null(sizeVar)) 2.5 else NULL,
  sizeRange = NULL, alphaVar = NULL, alpha = if (is.null(alphaVar)) 1 else
  NULL, alphaRange = NULL, title = "", symmetryAxes = c("combine",
  "separate", "none"), packageTextLabel = c("ggrepel", "ggplot2"),
  cloudGenes = TRUE, cloudGenesColor = "black",
  cloudGenesNBins = sqrt(length(psids)), cloudGenesIncludeLegend = FALSE,
  cloudGenesTitleLegend = "nGenes", topGenes = 10, topGenesCex = 2.5,
  topGenesVar = NULL, topGenesJust = c(0.5, 0.5), topGenesColor = "black",
  topSamples = 10, topSamplesCex = 2.5, topSamplesVar = NULL,
  topSamplesJust = c(0.5, 0.5), topSamplesColor = "black",
  geneSets = list(), geneSetsVar = NULL, geneSetsMaxNChar = NULL,
  topGeneSets = 10, topGeneSetsCex = 2.5, topGeneSetsJust = c(0.5, 0.5),
  topGeneSetsColor = "black", includeLegend = TRUE,
  includeLineOrigin = TRUE, typePlot = c("static", "interactive"),
  packageInteractivity = c("rbokeh", "ggvis"), figInteractiveSize = c(600,
  400), ggvisAdjustLegend = TRUE, interactiveTooltip = TRUE,
  interactiveTooltipExtraVars = NULL, returnAnalysis = FALSE)
```

**Arguments**

eset	expressionSet (or SummarizedExperiment) object with data
ldaVar	name of variable (in varLabels of the eset) used for grouping for lda, NULL by default
psids	featureNames of genes to include in the plot, all by default
dim	dimensions of the analysis to represent, first two dimensions by default
colorVar	name of variable (in varLabels of the eset) used for coloring, NULL by default
color	specified color(s) for the points, replicated if needed, used only if colorVar is NULL, a factor or character by default: 'black' if colorVar is not specified and default ggplot palette otherwise
shapeVar	name of variable (in varLabels of the eset) used for the shape, NULL by default
shape	specified shape(s) (pch) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '15' (filled square) if shapeVar is not specified and default ggplot shape(s) otherwise
sizeVar	name of variable (in varLabels of the eset) used for the size, NULL by default

size	specified size(s) (cex) for the points, replicated if needed, used only if sizeVar is NULL, a factor or character by default: '2.5' if sizeVar is not specified and default ggplot size(s) otherwise
sizeRange	size (cex) range used in the plot, possible only if the sizeVar is 'numeric' or 'integer'
alphaVar	name of variable (in varLabels of the eset) used for the transparency, NULL by default. This parameter is currently only available for static plot.
alpha	specified transparency(s) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static plot.
alphaRange	transparency (alpha) range used in the plot, possible only if the alphaVar is 'numeric' or 'integer' This parameter is currently only available for static plot.
title	plot title, "" by default
symmetryAxes	set symmetry for axes, either: <ul style="list-style-type: none"> <li>• 'combine' (by default): both axes are symmetric and with the same limits</li> <li>• 'separate': each axis is symmetric and has its own limits</li> <li>• 'none': axes by default (plot limits)</li> </ul>
packageTextLabel	package used to label the outlying genes/samples/gene sets, either ggrepel (by default, only used if package ggrepel is available), or ggplot2
cloudGenes	logical, if TRUE (by default), include the cloud of genes in the spectral map
cloudGenesColor	if cloudGenes is TRUE, color for the cloud of genes, black by default
cloudGenesNBins	number of bins to used for the clouds of genes, by default the square root of the number of genes
cloudGenesIncludeLegend	logical, if TRUE (FALSE by default) include the legend for the cloud of genes (in the top position if multiple legends)
cloudGenesTitleLegend	string with title for the legend for the cloud of genes 'nGenes' by default
topGenes	numeric indicating which percentile (if <1) or number (if >=1) of genes most distant to the origin of the plot to annotate, by default: 10 genes are selected If no genes should be annotated, set this parameter to 0 Currently only available for static plot.
topGenesCex	cex for gene annotation (used when topGenes > 0)
topGenesVar	variable of the featureData used to label the genes, by default: NULL, the featureNames are used for labelling (used when topGenes > 0)
topGenesJust	text justification for the genes (used when topGenes > 0 and if packageTextLabel is ggplot2), by default: c(0.5, 0.5) so centered
topGenesColor	text color for the genes (used when topGenes > 0), black by default
topSamples	numeric indicating which percentile (if <1) or number (if >=1) of samples most distant to the origin of the plot to annotate, by default: 10 samples are selected If no samples should be annotated, set this parameter to 0. Currently available for static plot.
topSamplesCex	cex for sample annotation (used when topSamples > 0)

topSamplesVar	variable of the phenoData used to label the samples, by default: NULL, the sampleNames are used for labelling (used when topSamples > 0)
topSamplesJust	text justification for the samples (used when topSamples > 0 and if packageTextLabel is ggplot2), by default: c(0.5, 0.5) so centered
topSamplesColor	text color for the samples (used when topSamples > 0), black by default
geneSets	list of gene sets/pathways, each containing identifiers of genes contained in the set. E.g. pathways from Gene Ontology databases output from the <a href="#">getGeneSetsForPlot</a> function or any custom list of pathways. The genes identifiers should correspond to the variable geneSetsVar contained in the phenoData, if not specified the featureNames are used. If several gene sets have the same name, they will be combine to extract the top gene sets.
geneSetsVar	variable of the featureData used to match the genes contained in geneSets, most probably ENTREZID, if not specified the featureNames of the eSet are used Only used when topGeneSets > 0 and the parameter geneSets is specified.
geneSetsMaxNChar	maximum number of characters for pathway names, by default keep entire names Only used when topGeneSets > 0 and the parameter geneSets is specified. If returnAnalysis is set to TRUE and geneSetsMaxNChar specified, the top pathways will be returned in the output object, named with the identifiers used in the plot (so with maximum geneSetsMaxNChar number of characters)
topGeneSets	numeric indicating which percentile (if <=1) or number (if >1) of gene sets most distant to the origin of the plot to annotate, by default: 10 gene sets are selected If no gene sets should be annotated, set this parameter to 0. Currently available for static plot. Only used when topGeneSets > 0 and the parameter geneSets is specified.
topGeneSetsCex	cex for gene sets annotation Only used when topGeneSets > 0 and the parameter geneSets is specified.
topGeneSetsJust	text justification for the gene sets by default: c(0.5, 0.5) so centered Only used when topGeneSets > 0, the parameter geneSets is specified and if packageTextLabel is ggplot2.
topGeneSetsColor	color for the gene sets (used when topGeneSets > 0 and geneSets is specified), black by default Only used when topGeneSets > 0 and the parameter geneSets is specified.
includeLegend	logical if TRUE (by default) include a legend, otherwise not
includeLineOrigin	if TRUE (by default) include vertical line at x = 0 and horizontal line at y = 0
typePlot	type of the plot returned, either 'static' (static) or 'interactive' (potentially interactive)
packageInteractivity	if typePlot is 'interactive', package used for interactive plot, either 'rbokeh' (by default) or 'ggvis'
figInteractiveSize	vector containing the size of the interactive plot, as [width, height] by default: c(600, 400). This is passed to the width and height parameters of: <ul style="list-style-type: none"> <li>• for rbokeh plots: the <code>rbokeh::figure</code> function</li> <li>• for ggvis plots: the <code>ggvis::set_options</code> function</li> </ul>

`ggvisAdjustLegend` logical, if TRUE (by default) adjust the legends in `ggvis` to avoid overlapping legends when multiple legends

`interactiveTooltip` logical, if TRUE, add hoover functionality showing sample annotation (variables used in the plot) in the plot

`interactiveTooltipExtraVars` name of extra variable(s) (in `varLabels` of the `eset`) to add in tooltip to label the samples, NULL by default

`returnAnalysis` logical, if TRUE (FALSE by default), return also the output of the analysis, and the outlying samples in the `topElements` element if any, otherwise only the plot object

### Value

if `returnAnalysis` is TRUE, return a list:

- `analysis`: output of the spectral map analysis, whose parameters can be given as input to the [esetPlotWrapper](#) function
  - `dataPlotSamples`: coordinates of the samples
  - `dataPlotGenes`: coordinates of the genes
  - `esetUsed`: expressionSet used in the plot
- `topElements`: list with top outlying elements if any, possibly genes, samples and gene sets
- `plot`: the plot output

otherwise return only the plot

### Author(s)

Laure Cougnaud

### References

Fisher, R. A. (1936). The Use of Multiple Measurements in Taxonomic Problems. *Annals of Eugenics*, 7 (2), 179–188

### See Also

the function used internally: [lda](#)

### Examples

```
# load data
library(ALL)
data(ALL)

# specify several variables in ldaVar (this might take a few minutes to run...)

# sample subsetting: currently cannot deal with missing values
samplesToRemove <- which(apply(pData(ALL)[, c("sex", "BT")], 1, anyNA))

# extract random features, because analysis is quite time consuming
retainedFeatures <- sample(featureNames(ALL), size = floor(nrow(ALL)/5))
```

```
# create the plot
esetLda(eset = ALL[retainedFeatures, -samplesToRemove],
  ldaVar = "BT", colorVar = "BT", shapeVar = "sex", sizeVar = "age",
  title = "Linear discriminant analysis on the ALL dataset")
```

---

esetPlotWrapper

*wrapper for biplot of features/samples contained in a eSet object*

---

## Description

Wrapper function used for all plots of the visualizations contained in the package.

## Usage

```
esetPlotWrapper(dataPlotSamples, dataPlotGenes = NULL, esetUsed, xlab = "",
  ylab = "", colorVar = NULL, color = if (is.null(colorVar)) "black" else
  NULL, shapeVar = NULL, shape = if (is.null(shapeVar)) 15 else NULL,
  sizeVar = NULL, size = if (is.null(sizeVar)) 2.5 else NULL,
  sizeRange = NULL, alphaVar = NULL, alpha = if (is.null(alphaVar)) 1 else
  NULL, alphaRange = NULL, title = "", symmetryAxes = c("combine",
  "separate", "none"), cloudGenes = TRUE, cloudGenesColor = "black",
  cloudGenesNBins = if (!is.null(dataPlotGenes)) sqrt(nrow(dataPlotGenes))
  else NULL, cloudGenesIncludeLegend = FALSE,
  cloudGenesTitleLegend = "nGenes", packageTextLabel = c("ggrepel",
  "ggplot2"), topGenes = 10, topGenesCex = 2.5, topGenesVar = NULL,
  topGenesJust = c(0.5, 0.5), topGenesColor = "black", topSamples = 10,
  topSamplesCex = 2.5, topSamplesVar = NULL, topSamplesJust = c(0.5, 0.5),
  topSamplesColor = "black", geneSets = list(), geneSetsVar = NULL,
  geneSetsMaxNChar = NULL, topGeneSets = 10, topGeneSetsCex = 2.5,
  topGeneSetsJust = c(0.5, 0.5), topGeneSetsColor = "black",
  includeLegend = TRUE, includeLineOrigin = TRUE, typePlot = c("static",
  "interactive"), figInteractiveSize = c(600, 400),
  ggvisAdjustLegend = TRUE, interactiveTooltip = TRUE,
  interactiveTooltipExtraVars = NULL, packageInteractivity = c("rbokeh",
  "ggvis"), returnTopElements = FALSE)
```

## Arguments

dataPlotSamples	data.frame with columns 'X', 'Y' with coordinates for the samples and with rownames which should correspond and be in the same order as the sample-Names of esetUsed
dataPlotGenes	data.frame with two columns 'X' and 'Y' with coordinates for the genes
esetUsed	expressionSet (or SummarizedExperiment) object with data
xlab	label for the x axis
ylab	label for the y axis
colorVar	name of variable (in varLabels of the eset) used for coloring, NULL by default
color	specified color(s) for the points, replicated if needed, used only if colorVar is NULL, a factor or character by default: 'black' if colorVar is not specified and default ggplot palette otherwise

shapeVar	name of variable (in varLabels of the eset) used for the shape, NULL by default
shape	specified shape(s) (pch) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '15' (filled square) if shapeVar is not specified and default ggplot shape(s) otherwise
sizeVar	name of variable (in varLabels of the eset) used for the size, NULL by default
size	specified size(s) (cex) for the points, replicated if needed, used only if sizeVar is NULL, a factor or character by default: '2.5' if sizeVar is not specified and default ggplot size(s) otherwise
sizeRange,	size (cex) range used in the plot, possible only if the sizeVar is 'numeric' or 'integer'
alphaVar	name of variable (in varLabels of the eset) used for the transparency, NULL by default. This parameter is currently only available for static plot.
alpha	specified transparency(s) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static plot.
alphaRange	transparency (alpha) range used in the plot, possible only if the alphaVar is 'numeric' or 'integer' This parameter is currently only available for static plot.
title	plot title, " by default
symmetryAxes	set symmetry for axes, either: <ul style="list-style-type: none"> <li>• 'combine' (by default): both axes are symmetric and with the same limits</li> <li>• 'separate': each axis is symmetric and has its own limits</li> <li>• 'none': axes by default (plot limits)</li> </ul>
cloudGenes	logical, if TRUE (by default), include the cloud of genes in the spectral map
cloudGenesColor	if cloudGenes is TRUE, color for the cloud of genes, black by default
cloudGenesNBins	number of bins to used for the clouds of genes, by default the square root of the number of genes
cloudGenesIncludeLegend	logical, if TRUE (FALSE by default) include the legend for the cloud of genes (in the top position if multiple legends)
cloudGenesTitleLegend	string with title for the legend for the cloud of genes 'nGenes' by default
packageTextLabel	package used to label the outlying genes/samples/gene sets, either ggrepel (by default, only used if package ggrepel is available), or ggplot2
topGenes	numeric indicating which percentile (if <1) or number (if >=1) of genes most distant to the origin of the plot to annotate, by default: 10 genes are selected If no genes should be annotated, set this parameter to 0 Currently only available for static plot.
topGenesCex	cex for gene annotation (used when topGenes > 0)
topGenesVar	variable of the featureData used to label the genes, by default: NULL, the featureNames are used for labelling (used when topGenes > 0)
topGenesJust	text justification for the genes (used when topGenes > 0 and if packageTextLabel is ggplot2), by default: c(0.5, 0.5) so centered

topGenesColor	text color for the genes (used when topGenes > 0), black by default
topSamples	numeric indicating which percentile (if <1) or number (if >=1) of samples most distant to the origin of the plot to annotate, by default: 10 samples are selected If no samples should be annotated, set this parameter to 0. Currently available for static plot.
topSamplesCex	cex for sample annotation (used when topSamples > 0)
topSamplesVar	variable of the phenoData used to label the samples, by default: NULL, the sampleNames are used for labelling (used when topSamples > 0)
topSamplesJust	text justification for the samples (used when topSamples > 0 and if packageTextLabel is ggplot2), by default: c(0.5, 0.5) so centered
topSamplesColor	text color for the samples (used when topSamples > 0), black by default
geneSets	list of gene sets/pathways, each containing identifiers of genes contained in the set. E.g. pathways from Gene Ontology databases output from the <a href="#">getGeneSetsForPlot</a> function or any custom list of pathways. The genes identifiers should correspond to the variable geneSetsVar contained in the phenoData, if not specified the featureNames are used. If several gene sets have the same name, they will be combine to extract the top gene sets.
geneSetsVar	variable of the featureData used to match the genes contained in geneSets, most probably ENTREZID, if not specified the featureNames of the eSet are used Only used when topGeneSets > 0 and the parameter geneSets is specified.
geneSetsMaxNChar	maximum number of characters for pathway names, by default keep entire names Only used when topGeneSets > 0 and the parameter geneSets is specified. If returnAnalysis is set to TRUE and geneSetsMaxNChar specified, the top pathways will be returned in the output object, named with the identifiers used in the plot (so with maximum geneSetsMaxNChar number of characters)
topGeneSets	numeric indicating which percentile (if <=1) or number (if >1) of gene sets most distant to the origin of the plot to annotate, by default: 10 gene sets are selected If no gene sets should be annotated, set this parameter to 0. Currently available for static plot. Only used when topGeneSets > 0 and the parameter geneSets is specified.
topGeneSetsCex	cex for gene sets annotation Only used when topGeneSets > 0 and the parameter geneSets is specified.
topGeneSetsJust	text justification for the gene sets by default: c(0.5, 0.5) so centered Only used when topGeneSets > 0, the parameter geneSets is specified and if packageTextLabel is ggplot2.
topGeneSetsColor	color for the gene sets (used when topGeneSets > 0 and geneSets is specified), black by default Only used when topGeneSets > 0 and the parameter geneSets is specified.
includeLegend	logical if TRUE (by default) include a legend, otherwise not
includeLineOrigin	if TRUE (by default) include vertical line at x = 0 and horizontal line at y = 0
typePlot	type of the plot returned, either 'static' (static) or interactive' (potentially interactive)



**figInteractiveSize**  
vector containing the size of the interactive plot, as [width, height] by default: c(600, 400). This is passed to the width and height parameters of:

- for rbokeh plots: the `bokeh::figure` function
- for ggvis plots: the `ggvis::set_options` function

**ggvisAdjustLegend**  
logical, if TRUE (by default) adjust the legends in ggvis to avoid overlapping legends when multiple legends

**interactiveTooltip**  
logical, if TRUE, add hover functionality showing sample annotation (variables used in the plot) in the plot

**interactiveTooltipExtraVars**  
name of extra variable(s) (in `varLabels` of the eset) to add in tooltip to label the samples, NULL by default

**packageInteractivity**  
if `typePlot` is 'interactive', package used for interactive plot, either 'rbokeh' (by default) or 'ggvis'

**returnTopElements**  
logical, if TRUE (FALSE by default) return the outlying elements labelled in the plot (if any)

**Value**

if `typePlot` is:

- **static:**
  - if `returnTopElements` is TRUE, and top elements can be displayed, a list with:
    - \* `'topElements'`: the top elements labelled in the plot
    - \* `'plot'`: the ggplot object
  - otherwise, the ggplot object only
- **interactive:** a ggvis or rbokeh object, depending on the `packageInteractivity` parameter

**Author(s)**

Laure Cougnaud

**Examples**

```
library(ALL)
data(ALL)

## run one spectral map analysis

# create custom color palette
colorPalette <- c("dodgerblue", colorRampPalette(c("white", "dodgerblue2", "darkblue"))(5)[-1],
"red", colorRampPalette(c("white", "red3", "darkred"))(5)[-1])

# run the analysis
# with 'returnAnalysis' set to TRUE to have all objects required for the esetPlotWrapper
outputEsetSPM <- esetSpectralMap(eset = ALL,
title = "Acute lymphoblastic leukemia dataset \n Spectral map complete",
```

```

colorVar = "BT", color = colorPalette,
shapeVar = "sex", shape = 15:16,
sizeVar = "age", sizeRange = c(2, 6),
symmetryAxes = "separate",
topGenes = 10, topGenesJust = c(1, 0), topGenesCex = 2, topGenesColor = "darkgrey",
topSamples = 15, topSamplesVar = "cod", topSamplesColor = "black",
topSamplesJust = c(1, 0), topSamplesCex = 3, returnAnalysis = TRUE)

# plot the biplot
print(outputEsetSPM$plot)

## re-call the plot function, to change some visualizations parameters
esetPlotWrapper(
  dataPlotSamples = outputEsetSPM$analysis$dataPlotSamples,
  dataPlotGenes = outputEsetSPM$analysis$dataPlotGenes,
  esetUsed = outputEsetSPM$analysis$esetUsed,
  title = paste("Acute lymphoblastic leukemia dataset \n Spectral map"),
  colorVar = "BT", color = colorPalette,
  shapeVar = "relapse",
  sizeVar = "age", sizeRange = c(2, 6),
  topSamplesVar = "cod", topGenesVar = "SYMBOL"
)

```

---

esetSpectralMap

*plot a spectral map biplot of an eSet.*


---

## Description

esetSpectralMap reduces the dimension of the data contained in the [eSet](#) with the [mpm](#) function and plot the subsequent biplot of the specified dimensions, possibly with gene and sample annotation contained in the [eSet](#). A spectral map with the default parameters is equivalent to a principal component analysis on the log-transformed, double centered and global normalized data (from documentation of the [mpm](#) function).

## Usage

```

esetSpectralMap(eset, psids = 1:nrow(eset), dim = c(1, 2),
  colorVar = NULL, color = if (is.null(colorVar)) "black" else NULL,
  shapeVar = NULL, shape = if (is.null(shapeVar)) 15 else NULL,
  sizeVar = NULL, size = if (is.null(sizeVar)) 2.5 else NULL,
  sizeRange = NULL, alphaVar = NULL, alpha = if (is.null(alphaVar)) 1 else
  NULL, alphaRange = NULL, title = "", mpm.args = list(closure = "none",
  center = "double", normal = "global", row.weight = "mean", col.weight =
  "constant", logtrans = FALSE), plot.mpm.args = list(scale = "uvc"),
  symmetryAxes = c("combine", "separate", "none"),
  packageTextLabel = c("ggrepel", "ggplot2"), cloudGenes = TRUE,
  cloudGenesColor = "black", cloudGenesNBins = sqrt(length(psids)),
  cloudGenesIncludeLegend = FALSE, cloudGenesTitleLegend = "nGenes",
  topGenes = 10, topGenesCex = 2.5, topGenesVar = NULL,
  topGenesJust = c(0.5, 0.5), topGenesColor = "black", topSamples = 10,
  topSamplesCex = 2.5, topSamplesVar = NULL, topSamplesJust = c(0.5, 0.5),
  topSamplesColor = "black", geneSets = list(), geneSetsVar = NULL,

```

```

geneSetsMaxNChar = NULL, topGeneSets = 10, topGeneSetsCex = 2.5,
topGeneSetsJust = c(0.5, 0.5), topGeneSetsColor = "black",
includeLegend = TRUE, includeLineOrigin = TRUE, typePlot = c("static",
"interactive"), packageInteractivity = c("rbokeh", "ggvis"),
figInteractiveSize = c(600, 400), ggvisAdjustLegend = TRUE,
interactiveTooltip = TRUE, interactiveTooltipExtraVars = NULL,
returnAnalysis = FALSE)

```

## Arguments

eset	expressionSet (or SummarizedExperiment) object with data
psids	featureNames of genes to include in the plot, all by default
dim	dimensions of the analysis to represent, first two dimensions by default
colorVar	name of variable (in varLabels of the eset) used for coloring, NULL by default
color	specified color(s) for the points, replicated if needed, used only if colorVar is NULL, a factor or character by default: 'black' if colorVar is not specified and default ggplot palette otherwise
shapeVar	name of variable (in varLabels of the eset) used for the shape, NULL by default
shape	specified shape(s) (pch) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '15' (filled square) if shapeVar is not specified and default ggplot shape(s) otherwise
sizeVar	name of variable (in varLabels of the eset) used for the size, NULL by default
size	specified size(s) (cex) for the points, replicated if needed, used only if sizeVar is NULL, a factor or character by default: '2.5' if sizeVar is not specified and default ggplot size(s) otherwise
sizeRange	size (cex) range used in the plot, possible only if the sizeVar is 'numeric' or 'integer'
alphaVar	name of variable (in varLabels of the eset) used for the transparency, NULL by default. This parameter is currently only available for static plot.
alpha	specified transparency(s) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static plot.
alphaRange	transparency (alpha) range used in the plot, possible only if the alphaVar is 'numeric' or 'integer' This parameter is currently only available for static plot.
title	plot title, "" by default
mpm.args	list with input parameters for the <code>mpm</code> function. The default value is: <code>list(closure = 'none', center = 'none')</code> . This assumes that the data are already in a log scale.
plot.mpm.args	list with input parameters for the <code>plot.mpm</code> function. The default value is: <code>list(scale = "uv")</code> .
symmetryAxes	set symmetry for axes, either: <ul style="list-style-type: none"> <li>'combine' (by default): both axes are symmetric and with the same limits</li> <li>'separate': each axis is symmetric and has its own limits</li> <li>'none': axes by default (plot limits)</li> </ul>
packageTextLabel	package used to label the outlying genes/samples/gene sets, either <code>ggrepel</code> (by default, only used if package <code>ggrepel</code> is available), or <code>ggplot2</code>

cloudGenes	logical, if TRUE (by default), include the cloud of genes in the spectral map
cloudGenesColor	if cloudGenes is TRUE, color for the cloud of genes, black by default
cloudGenesNBins	number of bins to used for the clouds of genes, by default the square root of the number of genes
cloudGenesIncludeLegend	logical, if TRUE (FALSE by default) include the legend for the cloud of genes (in the top position if multiple legends)
cloudGenesTitleLegend	string with title for the legend for the cloud of genes 'nGenes' by default
topGenes	numeric indicating which percentile (if <1) or number (if >=1) of genes most distant to the origin of the plot to annotate, by default: 10 genes are selected If no genes should be annotated, set this parameter to 0 Currently only available for static plot.
topGenesCex	cex for gene annotation (used when topGenes > 0)
topGenesVar	variable of the featureData used to label the genes, by default: NULL, the featureNames are used for labelling (used when topGenes > 0)
topGenesJust	text justification for the genes (used when topGenes > 0 and if packageTextLabel is ggplot2), by default: c(0.5, 0.5) so centered
topGenesColor	text color for the genes (used when topGenes > 0), black by default
topSamples	numeric indicating which percentile (if <1) or number (if >=1) of samples most distant to the origin of the plot to annotate, by default: 10 samples are selected If no samples should be annotated, set this parameter to 0. Currently available for static plot.
topSamplesCex	cex for sample annotation (used when topSamples > 0)
topSamplesVar	variable of the phenoData used to label the samples, by default: NULL, the sampleNames are used for labelling (used when topSamples > 0)
topSamplesJust	text justification for the samples (used when topSamples > 0 and if packageTextLabel is ggplot2), by default: c(0.5, 0.5) so centered
topSamplesColor	text color for the samples (used when topSamples > 0), black by default
geneSets	list of gene sets/pathways, each containing identifiers of genes contained in the set. E.g. pathways from Gene Ontology databases output from the <a href="#">getGeneSetsForPlot</a> function or any custom list of pathways. The genes identifiers should correspond to the variable geneSetsVar contained in the phenoData, if not specified the featureNames are used. If several gene sets have the same name, they will be combine to extract the top gene sets.
geneSetsVar	variable of the featureData used to match the genes contained in geneSets, most probably ENTREZID, if not specified the featureNames of the eSet are used Only used when topGeneSets > 0 and the parameter geneSets is specified.
geneSetsMaxNChar	maximum number of characters for pathway names, by default keep entire names Only used when topGeneSets > 0 and the parameter geneSets is specified. If returnAnalysis is set to TRUE and geneSetsMaxNChar specified, the top pathways will be returned in the output object, named with the identifiers used in the plot (so with maximum geneSetsMaxNChar number of characters)

topGeneSets	numeric indicating which percentile (if $\leq 1$ ) or number (if $> 1$ ) of gene sets most distant to the origin of the plot to annotate, by default: 10 gene sets are selected. If no gene sets should be annotated, set this parameter to 0. Currently available for static plot. Only used when <code>topGeneSets &gt; 0</code> and the parameter <code>geneSets</code> is specified.
topGeneSetsCex	cex for gene sets annotation. Only used when <code>topGeneSets &gt; 0</code> and the parameter <code>geneSets</code> is specified.
topGeneSetsJust	text justification for the gene sets by default: <code>c(0.5, 0.5)</code> so centered. Only used when <code>topGeneSets &gt; 0</code> , the parameter <code>geneSets</code> is specified and if <code>packageName</code> is <code>ggplot2</code> .
topGeneSetsColor	color for the gene sets (used when <code>topGeneSets &gt; 0</code> and <code>geneSets</code> is specified), black by default. Only used when <code>topGeneSets &gt; 0</code> and the parameter <code>geneSets</code> is specified.
includeLegend	logical if TRUE (by default) include a legend, otherwise not
includeLineOrigin	if TRUE (by default) include vertical line at $x = 0$ and horizontal line at $y = 0$
typePlot	type of the plot returned, either 'static' (static) or 'interactive' (potentially interactive)
packageInteractivity	if <code>typePlot</code> is 'interactive', package used for interactive plot, either 'rbokeh' (by default) or 'ggvis'
figInteractiveSize	vector containing the size of the interactive plot, as [width, height] by default: <code>c(600, 400)</code> . This is passed to the width and height parameters of: <ul style="list-style-type: none"> <li>• for rbokeh plots: the <code>bokeh::figure</code> function</li> <li>• for ggvis plots: the <code>ggvis::set_options</code> function</li> </ul>
ggvisAdjustLegend	logical, if TRUE (by default) adjust the legends in ggvis to avoid overlapping legends when multiple legends
interactiveTooltip	logical, if TRUE, add hover functionality showing sample annotation (variables used in the plot) in the plot
interactiveTooltipExtraVars	name of extra variable(s) (in <code>varLabels</code> of the <code>eset</code> ) to add in tooltip to label the samples, NULL by default
returnAnalysis	logical, if TRUE (FALSE by default), return also the output of the analysis, and the outlying samples in the <code>topElements</code> element if any, otherwise only the plot object

## Value

if `returnAnalysis` is TRUE, return a list:

- `analysis`: output of the spectral map analysis, can be given as input to the `esetPlotWrapper` function
  - `dataPlotSamples`: coordinates of the samples
  - `dataPlotGenes`: coordinates of the genes

- esetUsed: expressionSet used in the plot
- axisLabels: axes labels indicating percentage of variance explained by the selected axes
- axesContributionsPercentages: percentages of variance explained by each axis (not only the ones specified in dim)
- topElements: list with top outlying elements if any, possibly genes, samples and gene sets
- plot: the plot output

otherwise return only the plot

### Author(s)

Laure Cougnaud

### References

Lewi, P.J. (1976). Spectral mapping, a technique for classifying biological activity profiles of chemical compounds. *Arzneimittel Forschung (Drug Research)*, 26, 1295–1300

### See Also

the function used internally: [mpm](#) and [spectralMap](#) for spectral map in base R graphics

### Examples

```
library(ALL)
data(ALL)

## complete example (most of the parameters are optional)
# create custom color palette
colorPalette <- c("dodgerblue", colorRampPalette(c("white", "dodgerblue2", "darkblue"))(5)[-1],
"red", colorRampPalette(c("white", "red3", "darkred"))(5)[-1])
# plot the spectral map
print(esetSpectralMap(eset = ALL,
title = "Acute lymphoblastic leukemia dataset \n Spectral map complete",
colorVar = "BT", color = colorPalette,
shapeVar = "sex", shape = 15:16,
sizeVar = "age", sizeRange = c(2, 6),
symmetryAxes = "separate",
topGenes = 10, topGenesJust = c(1, 0), topGenesCex = 2, topGenesColor = "darkgrey",
topSamples = 15, topSamplesVar = "cod", topSamplesColor = "black",
topSamplesJust = c(1, 0), topSamplesCex = 3)
)

# see vignette for other examples, especially one with gene sets specification
```

---

esetTsne

*plot a t-SNE of an eSet object*

---

### Description

esetTsne reduces the dimension of the data contained in the [eSet](#) via t-Distributed Stochastic Neighbor Embedding with the [Rtsne](#) function and plot the subsequent biplot, possibly with sample annotation contained in the eSet.

## Usage

```
esetTsne(eset, psids = 1:nrow(eset), trace = TRUE, colorVar = NULL,
  color = if (is.null(colorVar)) "black" else NULL, shapeVar = NULL,
  shape = if (is.null(shapeVar)) 15 else NULL, sizeVar = NULL, size = if
  (is.null(sizeVar)) 2.5 else NULL, sizeRange = NULL, alphaVar = NULL,
  alpha = if (is.null(alphaVar)) 1 else NULL, alphaRange = NULL,
  title = "", Rtsne.args = list(perplexity = floor((ncol(eset) - 1)/3),
  theta = 0.5, dims = 2, initial_dims = 50),
  fctTransformDataForInputTsne = NULL, symmetryAxes = c("combine",
  "separate", "none"), packageTextLabel = c("ggrepel", "ggplot2"),
  topSamples = 10, topSamplesCex = 2.5, topSamplesVar = NULL,
  topSamplesJust = c(0.5, 0.5), topSamplesColor = "black",
  includeLegend = TRUE, includeLineOrigin = TRUE, typePlot = c("static",
  "interactive"), packageInteractivity = c("rbokeh", "ggvis"),
  figInteractiveSize = c(600, 400), ggvisAdjustLegend = TRUE,
  interactiveTooltip = TRUE, interactiveTooltipExtraVars = NULL,
  returnAnalysis = FALSE)
```

## Arguments

eset	expressionSet (or SummarizedExperiment) object with data
psids	featureNames of genes to include in the plot, all by default
trace	logical, if TRUE (by default), print some messages during tsne is running
colorVar	name of variable (in varLabels of the eset) used for coloring, NULL by default
color	specified color(s) for the points, replicated if needed, used only if colorVar is NULL, a factor or character by default: 'black' if colorVar is not specified and default ggplot palette otherwise
shapeVar	name of variable (in varLabels of the eset) used for the shape, NULL by default
shape	specified shape(s) (pch) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '15' (filled square) if shapeVar is not specified and default ggplot shape(s) otherwise
sizeVar	name of variable (in varLabels of the eset) used for the size, NULL by default
size	specified size(s) (cex) for the points, replicated if needed, used only if sizeVar is NULL, a factor or character by default: '2.5' if sizeVar is not specified and default ggplot size(s) otherwise
sizeRange	size (cex) range used in the plot, possible only if the sizeVar is 'numeric' or 'integer'
alphaVar	name of variable (in varLabels of the eset) used for the transparency, NULL by default. This parameter is currently only available for static plot.
alpha	specified transparency(s) for the points, replicated if needed, used only if shapeVar is NULL, a factor or character by default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static plot.
alphaRange	transparency (alpha) range used in the plot, possible only if the alphaVar is 'numeric' or 'integer' This parameter is currently only available for static plot.
title	plot title, "" by default
Rtsne.args	arguments for the Rtsne function, by default: perplexite parameter = optimal number of neighbours, theta = speed/accuracy trade-off (increase for less accuracy), set to 0.0 for exact TSNE

fctTransformDataForInputTsne	function which transform the data in the eSet object before calling the <code>Rtsne</code> function. This should be a function which takes a matrix as input and return a matrix, e.g. the <code>dist</code> function.
symmetryAxes	set symmetry for axes, either: <ul style="list-style-type: none"> <li>• 'combine' (by default): both axes are symmetric and with the same limits</li> <li>• 'separate': each axis is symmetric and has its own limits</li> <li>• 'none': axes by default (plot limits)</li> </ul>
packageTextLabel	package used to label the outlying genes/samples/gene sets, either <code>ggrepel</code> (by default, only used if package <code>ggrepel</code> is available), or <code>ggplot2</code>
topSamples	numeric indicating which percentile (if $<1$ ) or number (if $\geq 1$ ) of samples most distant to the origin of the plot to annotate, by default: 10 samples are selected. If no samples should be annotated, set this parameter to 0. Currently available for static plot.
topSamplesCex	cex for sample annotation (used when <code>topSamples &gt; 0</code> )
topSamplesVar	variable of the <code>phenoData</code> used to label the samples, by default: <code>NULL</code> , the <code>sampleNames</code> are used for labelling (used when <code>topSamples &gt; 0</code> )
topSamplesJust	text justification for the samples (used when <code>topSamples &gt; 0</code> and if <code>packageTextLabel</code> is <code>ggplot2</code> ), by default: <code>c(0.5, 0.5)</code> so centered
topSamplesColor	text color for the samples (used when <code>topSamples &gt; 0</code> ), black by default
includeLegend	logical if <code>TRUE</code> (by default) include a legend, otherwise not
includeLineOrigin	if <code>TRUE</code> (by default) include vertical line at $x = 0$ and horizontal line at $y = 0$
typePlot	type of the plot returned, either 'static' (static) or 'interactive' (potentially interactive)
packageInteractivity	if <code>typePlot</code> is 'interactive', package used for interactive plot, either 'rbokeh' (by default) or 'ggvis'
figInteractiveSize	vector containing the size of the interactive plot, as [width, height] by default: <code>c(600, 400)</code> . This is passed to the width and height parameters of: <ul style="list-style-type: none"> <li>• for <code>rbokeh</code> plots: the <code>bokeh::figure</code> function</li> <li>• for <code>ggvis</code> plots: the <code>ggvis::set_options</code> function</li> </ul>
ggvisAdjustLegend	logical, if <code>TRUE</code> (by default) adjust the legends in <code>ggvis</code> to avoid overlapping legends when multiple legends
interactiveTooltip	logical, if <code>TRUE</code> , add hover functionality showing sample annotation (variables used in the plot) in the plot
interactiveTooltipExtraVars	name of extra variable(s) (in <code>varLabels</code> of the <code>eSet</code> ) to add in tooltip to label the samples, <code>NULL</code> by default
returnAnalysis	logical, if <code>TRUE</code> ( <code>FALSE</code> by default), return also the output of the analysis, and the outlying samples in the <code>topElements</code> element if any, otherwise only the plot object



**Value**

if returnAnalysis is TRUE, return a list:

- analysis: output of the spectral map analysis, whose elements can be given to the [esetPlotWrapper](#) function
  - dataPlotSamples: coordinates of the samples
  - esetUsed: expressionSet used in the plot
- topElements: list with top outlying elements if any, possibly genes, samples and gene sets
- plot: the plot output

otherwise return only the plot

**Author(s)**

Laure Cougnaud

**References**

L.J.P. van der Maaten and G.E. Hinton (2008). Visualizing High-Dimensional Data Using t-SNE. *Journal of Machine Learning Research*, 2579–2605

**See Also**

the function used internally: [Rtsne](#) or <http://homepage.tudelft.nl/19j49/t-SNE.html> for further explanations about this technique.

**Examples**

```
library(ALL)
data(ALL)

## complete example (most of the parameters are optional)

# create custom color palette
colorPalette <- c("dodgerblue", colorRampPalette(c("white", "dodgerblue2", "darkblue"))(5)[-1],
"red", colorRampPalette(c("white", "red3", "darkred"))(5)[-1])

# create tsne
print(esetTsne(eset = ALL,
title = "Acute lymphoblastic leukemia dataset \n Tsne complete",
colorVar = "BT", color = colorPalette,
shapeVar = "sex", shape = 15:16,
sizeVar = "age", sizeRange = c(2, 6),
symmetryAxes = "separate",
topSamples = 15, topSamplesVar = "cod", topSamplesColor = "black",
topSamplesJust = c(1, 0), topSamplesCex = 3)
)
```

---

getCoordGeneSets      *extract coordinates gene sets*

---

### Description

extract coordinates gene sets

### Usage

```
getCoordGeneSets(dataPlotGenes, geneSets, esetUsed, geneSetsVar = NULL)
```

### Arguments

dataPlotGenes    data.frame with two columns 'X' and 'Y' with coordinates for the genes

geneSets        geneSets list of gene sets, e.g. gene pathways, output from the 'getGeneSets' function in MLP the genes IDs must correspond to the sampleNames in the eset

esetUsed        expressionSet (or SummarizedExperiment) object with data

geneSetsVar    variable of the featureData used to match the genes contained in geneSets, most probably ENTREZID, if NULL the featureNames of the eSet are used

### Value

data.frame with two columns 'X' and 'Y' with coordinates for the gene sets

### Author(s)

Laure Cougnaud

Laure Cougnaud

---

getGeneSetsForPlot      *get gene sets for plot of eSet object.*

---

### Description

get and format gene sets to be used as geneSets for the functions: [esetSpectralMap](#), [esetLda](#), or [esetPlotWrapper](#) Use the [getGeneSets](#) function to get the gene sets, combine all databases, and format the gene sets name if required.

### Usage

```
getGeneSetsForPlot(entrezIdentifiers, species = "Human",
  geneSetSource = c("GOBP", "GOMF", "GOCC", "KEGG"), useDescription = TRUE,
  trace = TRUE)
```

**Arguments**

entrezIdentifiers	string with Entrez Gene identifiers of the genes of interest
species	species to use, given to the <a href="#">getGeneSets</a> function
geneSetSource	gene set source, either 'GOBP', 'GOMF', 'GOCC' or 'KEGG'. Multiple choices are available
useDescription	logical, if TRUE (by default) use the description to label the gene sets, otherwise use the original gene set identifiers Function 'substr' is used.
trace	logical, if TRUE (by default) a few extra information are printed during the process

**Value**

list with gene sets, each element is a gene set and contains the ENTREZ IDs of the genes contained in this set. If useDescription is:

- FALSE: pathways are labelled with identifiers (Gene Ontology IDs for GOBP, GOMF and GOCC, KEGG IDs for KEGG)
- TRUE: pathways are labelled with gene sets descriptions

**Author(s)**

Laure Cougnaud

**See Also**

the function used internally: [getGeneSets](#)

**Examples**

```
# example dataset
library(ALL)
data(ALL)

# get gene annotation from probe IDs
library("hgu95av2.db")
probeIDs <- featureNames(ALL)
geneInfo <- select(hgu95av2.db, probeIDs, "ENTREZID", "PROBEID")

# get pathway annotation for the genes contained in the ALL dataset (can take a few minutes)
geneSets <- getGeneSetsForPlot(entrezIdentifiers = geneInfo$ENTREZID, species = "Human",
geneSetSource = 'GOBP',
useDescription = FALSE, trace = TRUE)
head(geneSets) # returns a pathway list of genes

# gene sets labelled with gene sets description
geneSets <- getGeneSetsForPlot(entrezIdentifiers = geneInfo$ENTREZID, species = "Human",
geneSetSource = 'GOBP', useDescription = TRUE, trace = TRUE)
head(geneSets) # returns a pathway list of genes

# see also vignette for an example of the use of this function as input for the esetSpectralMap, esetLda or eset
```

---

getMethodsInputObjectEsetVis

*wrapper to extract useful functions, depending if the object is an ExpressionSet or a SummarizedExperiment.*

---

### Description

This returns an error if x is not of the correct class. The package SummarizedExperiment should be available if x is of class SummarizedExperiment.

### Usage

```
getMethodsInputObjectEsetVis(x)
```

### Arguments

x                    object

### Value

if the object is an ExpressionSet or a SummarizedExperiment, returns a list with the functions specific of the class of x, and equivalent of the ExpressionSet functions: 'sampleNames', 'featureNames', 'fData', 'pData', 'exprs'

- sampleNames: sample names
- featureNames: feature names
- fData: feature annotation
- pData: sample annotation
- exprs: data matrix
- varLabels: sample annotation variables
- fvarLabels: feature annotation variables

### Author(s)

Laure Cougnaud

---

plotTopElements

*create geom\_text object with top genes/sample/pathways*

---

### Description

create geom\_text object with top genes/sample/pathways

### Usage

```
plotTopElements(top, type = c("gene", "sample", "geneSets"), var = NULL,
  cex = 1, just = c(0.5, 0.5), color = "black", dataPlotGenes = NULL,
  dataPlotSamples = NULL, esetUsed, geneSets = NULL, geneSetsVar = NULL,
  geneSetsMaxNChar = NULL, returnTopElements = FALSE,
  packageTextLabel = c("ggrepel", "ggplot2"))
```

**Arguments**

top	numeric, number of top elements
type	type of elements to plot, either 'gene', 'sample', or 'geneSets'
var	variable used to annotate the elements, only used for 'gene' and 'sample'
cex	cex of text in the plot
just	justification of elements in the plot, only use if packageTextLabel is 'ggplot2'
color	color for the elements in the plot
dataPlotGenes	data.frame with two columns 'X' and 'Y' with coordinates for the genes
dataPlotSamples	data.frame with two columns 'X' and 'Y' with coordinates for the samples
esetUsed	expressionSet (or SummarizedExperiment) object with data
geneSets	list of gene sets, e.g. gene pathways, output from the 'getGeneSets' function in MLP the genes IDs must correspond to the sampleNames in the eset. If several gene sets have the same name, they will be combine to extract the top gene sets.
geneSetsVar	variable of the featureData used to match the genes contained in geneSets, most probably ENTREZID, if not specified the featureNames of the eSet are used
geneSetsMaxNChar	maximum number of characters for pathway names, by default keep entire names
returnTopElements	logical if TRUE (FALSE by default) return the outlying elements
packageTextLabel	package used to label the outlying genes/samples/gene sets, either 'ggrepel' (by default, only used if package ggrepel is available), or 'ggplot2'

**Value**

- if the elements are present in the data: if returnTopElements is:
  - TRUE: return a list with two arguments:
    - \* topElements: string with top elements labelled in the plot
    - \* geomText: output of geom\_text
  - FALSE: only return the output of geom\_text
- if not, return NULL

**Author(s)**

Laure Cougnaud

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