

# Package: esetVis (via r-universe)

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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, methods

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

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

**VignetteBuilder** knitr

**License** GPL-3

**NeedsCompilation** no

**RoxygenNote** 7.2.3

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**Repository** <https://bioc.r-universe.dev>

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|         |                                                                                          |
|---------|------------------------------------------------------------------------------------------|
| eSetLda | <i>plot a biplot of a linear discriminant analysis of an <a href="#">eSet</a> object</i> |
|---------|------------------------------------------------------------------------------------------|

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## 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 = character(),
  color = if (length(colorVar) == 0) "black" else character(),
  shapeVar = character(),
  shape = if (length(shapeVar) == 0) 15 else numeric(),
  sizeVar = character(),
  size = if (length(sizeVar) == 0) {
    ifelse(typePlot[1] == "interactive" &&
      packageInteractivity[1] == "plotly", 20, 2.5)
  } else {
    numeric()
  },
  sizeRange = numeric(),
  alphaVar = character(),
  alpha = if (length(alphaVar) == 0) 1 else numeric(),
  alphaRange = numeric(),
  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 = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
  "plotly", 10, 2.5),
topGenesVar = character(),
topGenesJust = c(0.5, 0.5),
topGenesColor = "black",
topSamples = 10,
topSamplesCex = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
  "plotly", 10, 2.5),
topSamplesVar = character(),
topSamplesJust = c(0.5, 0.5),
topSamplesColor = "black",
geneSets = list(),
geneSetsVar = character(),
geneSetsMaxNChar = numeric(),
topGeneSets = 10,
topGeneSetsCex = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
  "plotly", 10, 2.5),
topGeneSetsJust = c(0.5, 0.5),
topGeneSetsColor = "black",
includeLegend = TRUE,
includeLineOrigin = TRUE,
typePlot = c("static", "interactive"),
packageInteractivity = c("plotly", "ggvis"),
figInteractiveSize = c(600, 400),
ggvisAdjustLegend = TRUE,
interactiveTooltip = TRUE,
interactiveTooltipExtraVars = character(),
returnAnalysis = FALSE,
returnEsetPlot = FALSE
)

```

## Arguments

|          |                                                                                                                                                                                                                 |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| eset     | expressionSet (or SummarizedExperiment) object with data                                                                                                                                                        |
| ldaVar   | name of variable (in varLabels of the eset) used for grouping for lda                                                                                                                                           |
| 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, empty by default                                                                                                                                 |
| color    | character or factor with specified color(s) for the points, replicated if needed. This is used only if colorVar is empty. 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, empty by default                                                                                                                                |
| shape    | character or factor with specified shape(s) (pch) for the points, replicated if needed. This is used only if shapeVar is empty. 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, empty by default                                                                                                                                                                                                   |
| size                    | character or factor with specified size(s) (cex) for the points, replicated if needed. This is used only if sizeVar is empty. By default: '2.5' if sizeVar is not specified (20 for a plotly plot) 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, empty by default. This parameter is currently only available for static plot and ggvis (only numeric in this case).                                                                                        |
| alpha                   | character or factor with specified transparency(s) for the points, replicated if needed. This is used only if shapeVar is empty. By default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static and ggvis. |
| 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 and ggvis 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 plot                                                                                                                                                                                                             |
| 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: empty, 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: empty, 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 'plotly' (by default) (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:

- for plotly plots: the `ggplotly` 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 plotlyEsetPlot to label the samples, empty 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

returnEsetPlot logical, if TRUE return also the `esetPlot` 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 = data.frame(),
  esetUsed,
  xlab = "",
  ylab = "",
  colorVar = character(0),
  color = if (length(colorVar) == 0) "black" else character(0),
  shapeVar = character(0),
  shape = if (length(shapeVar) == 0) 15 else numeric(0),
  sizeVar = character(0),
  size = if (length(sizeVar) == 0) {
    ifelse(typePlot[1] == "interactive" &&
      packageInteractivity[1] == "plotly", 20, 2.5)
  } else {
    numeric()
  },
  },
```

```

sizeRange = numeric(0),
alphaVar = character(0),
alpha = if (length(alphaVar) == 0) 1 else numeric(0),
alphaRange = numeric(0),
title = "",
symmetryAxes = c("combine", "separate", "none"),
cloudGenes = TRUE,
cloudGenesColor = "black",
cloudGenesNBins = if (nrow(dataPlotGenes) > 0) sqrt(nrow(dataPlotGenes)) else numeric(),
cloudGenesIncludeLegend = FALSE,
cloudGenesTitleLegend = "nGenes",
packageTextLabel = c("ggrepel", "ggplot2"),
topGenes = 10,
topGenesCex = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
  "plotly", 10, 2.5),
topGenesVar = character(0),
topGenesJust = c(0.5, 0.5),
topGenesColor = "black",
topSamples = 10,
topSamplesCex = 2.5,
topSamplesVar = character(0),
topSamplesJust = c(0.5, 0.5),
topSamplesColor = "black",
geneSets = list(),
geneSetsVar = character(0),
geneSetsMaxNChar = numeric(0),
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 = character(0),
packageInteractivity = c("plotly", "ggvis"),
returnTopElements = FALSE,
returnEsetPlot = 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, empty by default                                                                                                                                                                                                   |
| color                   | character or factor with specified color(s) for the points, replicated if needed. This is used only if colorVar is empty. 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, empty by default                                                                                                                                                                                                  |
| shape                   | character or factor with specified shape(s) (pch) for the points, replicated if needed. This is used only if shapeVar is empty. 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, empty by default                                                                                                                                                                                                   |
| size                    | character or factor with specified size(s) (cex) for the points, replicated if needed. This is used only if sizeVar is empty. By default: '2.5' if sizeVar is not specified (20 for a plotly plot) 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, empty by default. This parameter is currently only available for static plot and ggvis (only numeric in this case).                                                                                        |
| alpha                   | character or factor with specified transparency(s) for the points, replicated if needed. This is used only if shapeVar is empty. By default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static and ggvis. |
| 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 and ggvis 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 plot                                                                                                                                                                                                             |
| 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: empty, 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: empty, 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: <ul style="list-style-type: none"> <li>• for plotly plots: the <a href="#">ggplotly</a> 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 plotlyEsetPlot to label the samples, empty by default                                                                                                                                                                                                                       |
| packageInteractivity        | if typePlot is 'interactive', package used for interactive plot, either 'plotly' (by default) (by default) or 'ggvis'.                                                                                                                                                                                                                     |
| returnTopElements           | logical, if TRUE return also the top elements                                                                                                                                                                                                                                                                                              |
| returnEsetPlot              | logical, if TRUE return also the <a href="#">esetPlot</a> object                                                                                                                                                                                                                                                                           |

## 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 plotly 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 = character(),
  color = if (length(colorVar) == 0) "black" else character(),
  shapeVar = character(),
  shape = if (length(shapeVar) == 0) 15 else numeric(),
  sizeVar = character(),
  size = if (length(sizeVar) == 0) {
    ifelse(typePlot[1] == "interactive" &&
      packageInteractivity[1] == "plotly", 20, 2.5)
  } else {
    numeric()
  },
  sizeRange = numeric(),
  alphaVar = character(),
  alpha = if (length(alphaVar) == 0) 1 else numeric(),
  alphaRange = numeric(),
  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 = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
    "plotly", 10, 2.5),
  topGenesVar = character(),
  topGenesJust = c(0.5, 0.5),
  topGenesColor = "black",
  topSamples = 10,
  topSamplesCex = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
    "plotly", 10, 2.5),
  topSamplesVar = character(),
  topSamplesJust = c(0.5, 0.5),
  topSamplesColor = "black",
  geneSets = list(),
  geneSetsVar = character(),
```

```

geneSetsMaxNChar = numeric(),
topGeneSets = 10,
topGeneSetsCex = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
  "plotly", 10, 2.5),
topGeneSetsJust = c(0.5, 0.5),
topGeneSetsColor = "black",
includeLegend = TRUE,
includeLineOrigin = TRUE,
typePlot = c("static", "interactive"),
packageInteractivity = c("plotly", "ggvis"),
figInteractiveSize = c(600, 400),
ggvisAdjustLegend = TRUE,
interactiveTooltip = TRUE,
interactiveTooltipExtraVars = character(),
returnAnalysis = FALSE,
returnEsetPlot = FALSE
)

```

## Arguments

|                        |                                                                                                                                                                                                                                                                                                             |
|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>eset</code>      | expressionSet (or SummarizedExperiment) object with data                                                                                                                                                                                                                                                    |
| <code>psids</code>     | featureNames of genes to include in the plot, all by default                                                                                                                                                                                                                                                |
| <code>dim</code>       | dimensions of the analysis to represent, first two dimensions by default                                                                                                                                                                                                                                    |
| <code>colorVar</code>  | name of variable (in <code>varLabels</code> of the <code>eset</code> ) used for coloring, empty by default                                                                                                                                                                                                  |
| <code>color</code>     | character or factor with specified color(s) for the points, replicated if needed. This is used only if <code>colorVar</code> is empty. By default: 'black' if <code>colorVar</code> is not specified and default ggplot palette otherwise                                                                   |
| <code>shapeVar</code>  | name of variable (in <code>varLabels</code> of the <code>eset</code> ) used for the shape, empty by default                                                                                                                                                                                                 |
| <code>shape</code>     | character or factor with specified shape(s) ( <code>pch</code> ) for the points, replicated if needed. This is used only if <code>shapeVar</code> is empty. By default: '15' (filled square) if <code>shapeVar</code> is not specified and default ggplot shape(s) otherwise                                |
| <code>sizeVar</code>   | name of variable (in <code>varLabels</code> of the <code>eset</code> ) used for the size, empty by default                                                                                                                                                                                                  |
| <code>size</code>      | character or factor with specified size(s) ( <code>cex</code> ) for the points, replicated if needed. This is used only if <code>sizeVar</code> is empty. By default: '2.5' if <code>sizeVar</code> is not specified (20 for a plotly plot) and default ggplot size(s) otherwise                            |
| <code>sizeRange</code> | size ( <code>cex</code> ) range used in the plot, possible only if the <code>sizeVar</code> is 'numeric' or 'integer'                                                                                                                                                                                       |
| <code>alphaVar</code>  | name of variable (in <code>varLabels</code> of the <code>eset</code> ) used for the transparency, empty by default. This parameter is currently only available for static plot and ggvis (only numeric in this case).                                                                                       |
| <code>alpha</code>     | character or factor with specified transparency(s) for the points, replicated if needed. This is used only if <code>shapeVar</code> is empty. By default: '1' if <code>alphaVar</code> is not specified and default ggplot alpha otherwise This parameter is currently only available for static and ggvis. |

|                         |                                                                                                                                                                                                                                                                                          |
|-------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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 and ggvis 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 = 'double', normal = 'global', 'row.weight' = 'mean', col.weight = 'constant', logtrans = FALSE)</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 plot                                                                                                                                                                                                                    |
| 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: empty, 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: <code>c(0.5, 0.5)</code> 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: empty, 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 'plotly' (by default) (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:

- for plotly plots: the [ggplotly](#) 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 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 `plotlyEsetPlot` to label the samples, empty 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

**returnEsetPlot** logical, if TRUE return also the [esetPlot](#) 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 = character(),
  color = if (length(colorVar) == 0) "black" else character(),
  shapeVar = character(),
  shape = if (length(shapeVar) == 0) 15 else numeric(),
  sizeVar = character(),
  size = if (length(sizeVar) == 0) {
    ifelse(typePlot[1] == "interactive" &&
      packageInteractivity[1] == "plotly", 20, 2.5)
  } else {
    numeric()
  }
```

```

},
  sizeRange = numeric(),
  alphaVar = character(),
  alpha = if (length(alphaVar) == 0) 1 else numeric(),
  alphaRange = numeric(),
  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 = ifelse(typePlot[1] == "interactive" && packageInteractivity[1] ==
    "plotly", 10, 2.5),
  topSamplesVar = character(),
  topSamplesJust = c(0.5, 0.5),
  topSamplesColor = "black",
  includeLegend = TRUE,
  includeLineOrigin = TRUE,
  typePlot = c("static", "interactive"),
  packageInteractivity = c("plotly", "ggvis"),
  figInteractiveSize = c(600, 400),
  ggvisAdjustLegend = TRUE,
  interactiveTooltip = TRUE,
  interactiveTooltipExtraVars = character(),
  returnAnalysis = FALSE,
  returnEsetPlot = FALSE
)

```

## Arguments

|                       |                                                                                                                                                                                                                                         |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>eset</code>     | expressionSet (or SummarizedExperiment) object with data                                                                                                                                                                                |
| <code>psids</code>    | featureNames of genes to include in the plot, all by default                                                                                                                                                                            |
| <code>trace</code>    | logical, if TRUE (by default), print some messages during tsne is running                                                                                                                                                               |
| <code>colorVar</code> | name of variable (in varLabels of the eset) used for coloring, empty by default                                                                                                                                                         |
| <code>color</code>    | character or factor with specified color(s) for the points, replicated if needed. This is used only if colorVar is empty. By default: 'black' if colorVar is not specified and default ggplot palette otherwise                         |
| <code>shapeVar</code> | name of variable (in varLabels of the eset) used for the shape, empty by default                                                                                                                                                        |
| <code>shape</code>    | character or factor with specified shape(s) (pch) for the points, replicated if needed. This is used only if shapeVar is empty. By default: '15' (filled square) if shapeVar is not specified and default ggplot shape(s) otherwise     |
| <code>sizeVar</code>  | name of variable (in varLabels of the eset) used for the size, empty by default                                                                                                                                                         |
| <code>size</code>     | character or factor with specified size(s) (cex) for the points, replicated if needed. This is used only if sizeVar is empty. By default: '2.5' if sizeVar is not specified (20 for a plotly plot) 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, empty by default. This parameter is currently only available for static plot and ggvis (only numeric in this case).                                                                                        |
| alpha                        | character or factor with specified transparency(s) for the points, replicated if needed. This is used only if shapeVar is empty. By default: '1' if alphaVar is not specified and default ggplot alpha otherwise This parameter is currently only available for static and ggvis. |
| 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 and ggvis 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 <a href="#">Rtsne</a> function. This should be a function which takes a matrix as input and return a matrix, e.g. the dist 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 ggrepel (by default, only used if package ggrepel is available), or ggplot2                                                                                                                                    |
| 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: empty, 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                                                                                                                                                                                                           |
| 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 'plotly' (by default) (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:

- for plotly plots: the [ggplotly](#) 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 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 plotlyEsetPlot to label the samples, empty 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

**returnEsetPlot** logical, if TRUE return also the [esetPlot](#) 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)
)
```

---

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 esetPlotW
```

---

ggplotEsetPlot-class    *a S4 class to represent ggplot plots*

---

**Description**

a S4 class to represent ggplot plots

**Value**

S4 object of class ggplotEsetPlot

**Slots**

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

title string or expression with plot title, " by default

xlab string or expression with label for the x axis

ylab string or expression with label for the y axis

**Author(s)**

Laure Cougnaud

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