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, Rsne, 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

R topics documented:

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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
esetLda

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:

- 'combine' (by default): both axes are symmetric and with the same limits
- 'separate': each axis is symmetric and has its own limits
- 'none': axes by default (plot limits)

colored variables

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

**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**


**See Also**

the function used internally: lda

**Examples**

```r
# 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

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**Description**

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

**Usage**

```r
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", 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:
  • 'combine' (by default): both axes are symmetric and with the same limits
  • 'separate': each axis is symmetric and has its own limits
  • 'none': axes by default (plot limits)

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 ggrepel

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 ggrepel), 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 getGeneSetsForPlot 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 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

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 \nSpectral map complete",


esetSpectralMap

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,
```r

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**

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


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 getGeneSetsForPlot 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:
  • 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 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, can be given as input to the esetPlotWrapper function
  – dataPlotSamples: coordinates of the samples
  – dataPlotGenes: coordinates of the genes
esetSne

- 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 \nSpectral 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 RTnse function and plot the subsequent biplot, possibly with sample annotation contained in the eSet.
esetTsne

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 alphaVar 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 RTnse 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:

- ’combine’ (by default): both axes are symmetric and with the same limits
- ’separate’: each axis is symmetric and has its own limits
- ’none’: axes by default (plot limits)

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: 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
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:

- 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 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 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


See Also

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

Examples

```r
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,
si"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)

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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

geneSetSource = c("GOBP", "GOMF", "GOCC", "KEGG"), useDescription = TRUE, trace = TRUE)
getGeneSetsForPlot

Arguments

- **entrezIdentifiers**: string with Entrez Gene identifiers of the genes of interest
- **species**: species to use, given to the `getGeneSets` 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"))
plotTopElements

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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