Package ‘esetVis’

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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
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characterORexpressionOrCall-class

S4 Class Union with character/expression/call

Description

This is used for the definition of the title/axes labels for the ggplot2 version
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 = 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:
  • '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

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 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 '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 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

# 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")

---

**esetPlot-class**

An S4 class to represent **esetPlot** object expressionSet with visualization data from dimension-reduction methods

Description

Constructor of the **esetPlot** class

Usage

```r
## S4 method for signature 'esetPlot'
initialize(.Object, ...)
```

Arguments

- `.Object` **esetPlot** object
- `...` additional class arguments

Value

S4 object of class **esetPlot**

Slots

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 sampleNames of **esetUsed**
dataPlotGenes data.frame with two columns 'X' and 'Y' with coordinates for the genes
**eset** expressionSet (or SummarizedExperiment) object with data
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 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.

alpha 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.

alphaRange transparency (alpha) range used in the plot, possible only if the alphaVar is 'numeric' or 'integer'

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 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 feature-Names 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 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.

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

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esetPlotInteractive-class

a S4 class to represent interactive plots

---

Description

a S4 class to represent interactive plots
esetPlotWrapper

Value

S4 object of class esetPlotInteractive

Slots

  includeTooltip logical, if TRUE, add hoover functionality showing sample annotation (variables used in the plot) in the plot
  tooltipVars name of extra phenotypic variable(s) to add in plotlyEsetPlot to label the samples
  sizePlot vector containing the size of the interactive plot, as [width, height], by default: c(600, 400).
  title string plot title, ” by default
  xlab string label for the x axis
  ylab string label for the y axis

Author(s)

  Laure Cougnaud

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
esetPlotWrapper

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'
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 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 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 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.

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 esetPlot 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.
esetSpectralMap

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**

```r
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(),
)
Arguments

eset expressionSet (or SummarizedExperiment) object with data
psids featureNames of genes to include in the plot, all by default
dim dimensions of the analysis to represent, first two dimensions by default
colorVar name of variable (in varLabels of the eset) used for coloring, 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

mpm.args: list with input parameters for the mpm function. The default value is: list(closure = 'none', center = 'double', normal = 'global', 'row.weight' = 'mean', col.weight = 'constant', logtrans = FALSE). This assumes that the data are already in a log scale.

plot.mpm.args: list with input parameters for the plot.mpm function. The default value is: list(scale = "uvc").

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

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 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 'plotly' (by default) (by default) or 'ggvis'.
esetSpectralMap

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

deprecated functions: 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 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()
  }
)
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, 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

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 Rtsne 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: 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) 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


See Also

the function used internally: `Rtsne` or `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,
sizeVar = "age", sizeRange = c(2, 6),
symmetryAxes = "separate",
topSamples = 15, topSamplesVar = "cod", topSamplesColor = "black",
topSamplesJust = c(1, 0), topSamplesCex = 3)
```

---

**formatManualScale**

```
extend manual scale values if required
```

**Description**

extend manual scale values if required

**Usage**

```r
formatManualScale(x, valVar, nameVar)
```

**Arguments**

- `x` : data.frame with `nameVar`
- `valVar` : fixed value of variable of aesthetic
- `nameVar` : name of variable for aesthetic

**Value**

vector of manual scales

**Author(s)**

Laure Cougnaud
formatOutput

format output of plotEset function

Description
format output of plotEset function

Usage
formatOutput(res, object, type, returnEsetPlot)

Arguments
res result of specific plotEset function
object esetPlot object or extended class
type string type of plot
returnEsetPlot logical, should the object be returned in the output function?

Value
result

Author(s)
Laure Cougnaud

getAddressLimits
generic for get axes limits

Description
generic for get axes limits

Usage
getAddressLimits(object)

## S4 method for signature 'esetPlot'
getAddressLimits(object)

Arguments
object plotEset object
Value

matrix with limits for axes: columns x and y

Author(s)

Laure Cougnaud

getCoordGeneSets

extract coordinates gene sets

Description

extract coordinates gene sets

Usage

getCoordGeneSets(dataPlotGenes, geneSets, esetUsed, geneSetsVar = list())

Arguments

dataPlotGenes  data.frame with two columns 'X' and 'Y' with coordinates for the genes
geneSets  geneSets list of gene sets, e.g. gene pathways, output from the 'getGeneSets' function in MLP the genes IDs must correspond to the sampleNames in the eset
esetUsed  expressionSet (or SummarizedExperiment) object with data
geneSetsVar  variable of the featureData used to match the genes contained in geneSets, most probably ENTREZID, if NULL the featureNames of the eSet are used
...

Value

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

Author(s)

Laure Cougnaud
**getDataPlotSamplesWithAnnotation**

get sample data for plot

---

**Description**

get sample data for plot

**Usage**

```r
getDataPlotSamplesWithAnnotation(object)
```

```r
  ## S4 method for signature 'esetPlot'
  getDataPlotSamplesWithAnnotation(object)
```

```r
  ## S4 method for signature 'ggvisEsetPlot'
  getDataPlotSamplesWithAnnotation(object)
```

```r
  ## S4 method for signature 'plotlyEsetPlot'
  getDataPlotSamplesWithAnnotation(object)
```

**Arguments**

- `object` : `plotEset` object

**Value**

data.frame with 'dataPlotSamples' binded with variables displayed in the plot

**Author(s)**

Laure Cougnaud

---

**getGeneSetsForPlot**

get gene sets for plot of `eSet` object.

---

**Description**

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

Usage

geneSetsForPlot(
  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 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

getMethodsInputObjectEsetVis

getMethodsInputObjectEsetVis

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

Description

This returns an error is 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
getTopElements

create geom_text object with top genes/sample/pathways

Description

create geom_text object with top genes/sample/pathways

Usage

getTopElements(
  top,
  type = c("gene", "sample", "geneSets"),
  var = character(),
  dataPlotGenes = data.frame(),
  dataPlotSamples = data.frame(),
  esetUsed,
  geneSets = list(),
  geneSetsVar = character(),
  geneSetsMaxNChar = numeric()
)

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'

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

Value

Data.frame with coordinates and labels of the top elements
Author(s)
Laure Cougnaud

Description
visualize and esetPlot with the 'ggplot2' package

Usage
ggPlotEset(object)

Arguments
object object of class esetPlot

Value
ggplot object

Author(s)
Laure Cougnaud

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
Description

a S4 class for ggvis plot

Value

S4 object of class ggvisEsetPlot

Slots

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

alphaRange transparency (alpha) range used in the plot, c(0.1, 1) by default.

Author(s)

Laure Cougnaud

Description

visualize and esetPlot with the the `ggvis` package

Usage

ggvisPlotEset(object)

Arguments

object object of class esetPlot

Value

ggvis plot object

Author(s)

Laure Cougnaud
plotEset

plot an plotEset object

Description
plot an plotEset object

Usage
plotEset(object, returnEsetPlot = FALSE)
## S4 method for signature 'ggplotEsetPlot'
plotEset(object, returnEsetPlot = FALSE)
## S4 method for signature 'ggvisEsetPlot'
plotEset(object, returnEsetPlot = FALSE)
## S4 method for signature 'plotlyEsetPlot'
plotEset(object, returnEsetPlot = FALSE)

Arguments
- object: object of class esetPlot
- returnEsetPlot: logical, if TRUE return also the esetPlot object, such as can be re-use for future call to plotEset

Value
the plot object if returnEsetPlot is FALSE, otherwise a list with 'plot': the plot object and 'esetPlot': the esetPlot object

Author(s)
Laure Cougnaud

plotlyEsetPlot-class
a S4 class to represent plotly plots

Description
a S4 class to represent plotly plots

Value
S4 object of class plotlyEsetPlot
plotTopElements

Slots

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

size specified size(s) (cex) for the points, replicated if needed, used only if sizeVar is empty, a factor or character by default: '20' if sizeVar is not specified

Author(s)

Laure Cougnaud

plotlyPlotEset visualize and esetPlot with the the 'plotly' package

Description

visualize and esetPlot with the the 'plotly' package

Usage

plotlyPlotEset(object)

Arguments

object object of class esetPlot

Value

plotly plot

Author(s)

Laure Cougnaud

plotTopElements plot top elements for a static plot

Description

This create geom_text object with top genes/sample/pathways
Usage

plotTopElements(
    packageTextLabel = c("ggrepel", "ggplot2"),
    cex = 1,
    just = c(0.5, 0.5),
    color = "black",
    returnTopElements = FALSE,
    ...
)

Arguments

packageTextLabel
  package used to label the outlying genes/samples/gene sets, either 'ggrepel' (by
default, only used if package ggrepel is available), or 'ggplot2'
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
returnTopElements
  logical if TRUE (FALSE by default) return the outlying elements

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

setFixElement

check if the aesthetic is fixed (e.g. color, shape, size 'palette')

Description

check if the aesthetic is fixed (e.g. color, shape, size 'palette')

Usage

setFixElement(typeVar, valVar)
Arguments

typeVar  name of variable for aesthetic
valVar  fixed value of variable of aesthetic

Value

logical, if TRUE the element is fixed

Author(s)

Laure Cougnaud

Description

This is the case only if typeVar and valVar are specified, and if the variable is not numeric or integer (doesn’t work with ggplot2)

Usage

setManualScale(x, typeVar, valVar)

Arguments

x  data.frame with typeVar
typeVar  name of variable for aesthetic
valVar  fixed value of variable of aesthetic

Value

logical, if TRUE the manual scale should be set

Author(s)

Laure Cougnaud
**simpleCap**  
*capitalize the first letter of a word*

**Description**  
capitalize the first letter of a word

**Usage**  
simpleCap(x)

**Arguments**  

| x        | string |

**Value**  
string with first letter capitalized

**varToFm**  
Get formula for a specific variable, to be used in aesthetic specification in *plot_ly*.

**Description**  
Get formula for a specific variable, to be used in aesthetic specification in *plot_ly*.

**Usage**  
varToFm(var)

**Arguments**  

| var | Character vector with variable to combine. Otherwise with the ‘+’ operator. |

**Value**  
*as.formula*

**Author(s)**  
Laure Cougnaud
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