

Package ‘LPS’

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Type Package

Title Linear Predictor Score, for Binary Inference from Multiple Continuous Variables

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URL <https://bioinformatics.ovsa.fr/LPS>

BugReports <https://github.com/maressyl/R.LPS/issues>

Description An implementation of the Linear Predictor Score approach, as initiated by Radmacher et al. (J Comput Biol 2001) and enhanced by Wright et al. (PNAS 2003) for gene expression signatures. Several tools for unsupervised clustering of gene expression data are also provided.

Depends graphics, grDevices, R (>= 2.10)

Imports stats, utils, methods

Suggests limma

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NeedsCompilation no

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clusterize	<i>Hierarchical clustering heat maps</i>
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Description

This function draws a heat map ordered according to hierarchical clusterings, similarly to [heatmap](#). It offers more control on layout and allows multiple row annotations.

`hclust.ward` is derivated from 'stats' package [hclust](#), with an alternative default (as arguments can not be passed to it).

`dist.COR` mimics 'stats' package [dist](#), computing distances as 1 - Pearson's correlation coefficient.

Usage

```
clusterize(expr, side = NULL, cex.col = NA, cex.row = NA, mai.left = NA,
  mai.bottom = NA, mai.right = 0.1, mai.top = 0.1, side.height = 1, side.col = NULL,
  side.srt = 0, side.cex = 1, col.heatmap = heat(), zlim = "0 centered",
  zlim.trim = 0.02, norm = c("rows", "columns", "none"), norm.clust = TRUE,
  norm.robust = FALSE, customLayout = FALSE, getLayout = FALSE, plot = TRUE,
  widths = c(1, 4), heights = c(1, 4), order.genes = NULL, order.samples = NULL,
  fun.dist = dist.COR, fun.hclust = hclust.ward, clust.genes = NULL,
  clust.samples = NULL)
  dist.COR(input)
  hclust.ward(input)
```

Arguments

<code>expr</code>	A numeric matrix, holding features (genes) in columns and observations (samples) in rows. Rows and columns will be ordered according to hierarchical clustering results.
<code>side</code>	To be passed to heat.map .
<code>cex.col</code>	To be passed to heat.map .
<code>cex.row</code>	To be passed to heat.map .
<code>mai.left</code>	To be passed to heat.map .
<code>mai.bottom</code>	To be passed to heat.map .
<code>mai.right</code>	To be passed to heat.map .
<code>mai.top</code>	To be passed to heat.map .
<code>side.height</code>	To be passed to heat.map .

side.col	To be passed to heat.map .
side.srt	To be passed to heat.map .
side.cex	To be passed to heat.map .
col.heatmap	To be passed to heat.map .
zlim	To be passed to heat.map .
zlim.trim	To be passed to heat.map .
norm	To be passed to heat.map .
norm.clust	Single logical value, whether to apply normalization before clustering or after. Normalization applied depends on norm.
norm.robust	To be passed to heat.map .
customLayout	Single logical value, as layout does not allow nested calls, set this to TRUE to make your own call to layout and embed this plot in a wider one.
getLayout	Single logical value, whether to only return the layout arguments that would be used with the set of arguments provided or not. It can prove useful to build custom layouts, e.g. merging this plot to an other. See also customLayout.
plot	To be passed to heat.map .
widths	To be passed to layout .
heights	To be passed to layout .
order.genes	A function taking the gene dendrogram and expr as arguments, and returning the same dendrogram ordered in a custom way.
order.samples	A function taking the sample dendrogram and expr as arguments, and returning the same dendrogram ordered in a custom way.
fun.dist	A function to be used for distance computation in clustering. Default value uses 1 - Pearson's correlation as distance. See dist for further details.
fun.hclust	A function to be used for agglomeration in clustering. See hclust for further details.
clust.genes	If not NULL, an object coercible to the dendrogram class (typically the output from hclust()) to use instead of a fresh hierarchical clustering of genes. The FALSE value can also be used to disable computation and/or plotting of the dendrogram.
clust.samples	If not NULL, an object coercible to the dendrogram class (typically the output from hclust()) to use instead of a fresh hierarchical clustering of samples. The FALSE value can also be used to disable computation and/or plotting of the dendrogram.
input	See hclust and dist respectively for further details.

Value

clusterize invisibly returns the same list as [heat.map](#), plus :

genes	The gene dendrogram.
samples	The sample dendrogram.

See [hclust](#) and [dist](#) respectively for the other functions.

Author(s)

Sylvain Mareschal

See Also[heat.map](#), [heatmap](#), [hclust](#), [dist](#)**Examples**

```

# Data with features in columns
data(rosenwald)
group <- rosenwald.cli$group
expr <- t(rosenwald.expr)[,1:100]

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)

# Simple heat map
clusterize(expr)

# With annotation (row named data.frame)
side <- data.frame(group, row.names=rownames(expr))
clusterize(expr, side=side)

```

heat

*Heatmap palette generation***Description**

This function generates a ramp of colors for [heat.map](#) derived functions.

Usage

```

heat(colors = c("#8888FF", "#000000", "#FF4444"), n = 256, shapeFun = heat.exp, ...)
heat.exp(n, part, base = 1.015)
heat.lin(n, part)

```

Arguments

colors	Character vector of length 3, determining starting, middle and final colors.
n	Single integer value, amount of colors / values to generate.
shapeFun	Function taking at least 2 arguments : n and part. heat.exp and heat.lin are provided as examples.
...	Further arguments to heat will be passed to shapeFun.
part	Single integer, defined as 1 while generating colors between the first two boundaries, and 2 otherwise.
base	Single numeric value, base for exponential slope.

Value

heat returns a character vector of colors in hexadecimal representation.

heat.lin and heat.expr return n numeric values, defining a curve whose slope will be mimicked during color interpolation.

Author(s)

Sylvain Mareschal

See Also

[colorRampPalette](#)

[heat.map](#), [clusterize](#), [predict.LPS](#)

Examples

```
# Classical heatmap colors
palette <- heat(c("green", "black", "red"))
heat.scale(zlim=c(-2,2), col.heatmap=palette)

# Two distinct shapes provided
heat.scale(zlim=c(-2,2), col.heatmap=heat(shapeFun=heat.lin))
heat.scale(zlim=c(-2,2), col.heatmap=heat(shapeFun=heat.exp))
```

heat.map

Enhanced heat map plotting

Description

This function draws a heatmap from a matrix, similarly to [image](#). It also offers normalization and annotation features, with more control than [heatmap](#).

side can provide multiple sample annotations, and are handled differently depending on their class :

numeric are attributed grey shades from the minimum to the maximum, which are provided in the legend

factor have their levels attributed colors using a default or custom palette. Hexadecimal color codes starting with # and color names known by R are used "as is".

character are printed as is in a blank cell. Hexadecimal color codes starting with # and color names known by R are used as background colors instead of text.

logical are plotted in dark (TRUE) or light (FALSE) gray, leaving NAs in white.

Usage

```
heat.map(expr, side = NULL, cex.col = NA, cex.row = NA, mai.left = NA,
  mai.bottom = NA, mai.right = 0.1, mai.top = 0.1, side.height = 1, side.col = NULL,
  side.srt = 0, side.cex = 1, col.heatmap = heat(), zlim = "0 centered",
  zlim.trim = 0.02, norm = c("rows", "columns", "none"), norm.robust = FALSE,
  customLayout = FALSE, getLayout = FALSE, font = c(1, 3), xaxt = "s", yaxt = "s")
```

Arguments

<code>expr</code>	A numeric matrix, holding features (genes) in columns and observations (samples) in rows. Column and row order will not be altered.
<code>side</code>	An annotation data.frame for <code>expr</code> , or NULL. Must contain at least a row for each <code>expr</code> row, and one or many annotation column. Merging is performed on row names, so rows must be named following the same conventions as <code>expr</code> . Hexadecimal color definitions will be used "as is", other values will be attributed colors according to <code>side.col</code> .
<code>cex.col</code>	Single numeric value, character expansion factor for column names. NA will compute a value from <code>expr</code> size, similarly to heatmap .
<code>cex.row</code>	Single numeric value, character expansion factor for row names. NA will compute a value from <code>expr</code> size, similarly to heatmap .
<code>mai.left</code>	Single numeric value, left margin in inches (for row names). Use NA for an automatic value computed from row name lengths. See par .
<code>mai.bottom</code>	Single numeric value, bottom margin in inches (for column names). Use NA for an automatic value computed from column name lengths. See par .
<code>mai.right</code>	Single numeric value, right margin in inches (for higher level functions). See par .
<code>mai.top</code>	Single numeric value, top margin in inches. See par .
<code>side.height</code>	Single numeric value, scaling factor for annotation track.
<code>side.col</code>	A function returning as many colors as requested by its sole argument, defining the colors to be used for side legend. Default uses a custom palette for few values, and a derivative of rainbow if more than 8 colors are needed.
<code>side.srt</code>	Single numeric value, determining the string rotation angle when writing character side columns (default is 0, horizontal, 90 is suggested for vertical text on busy heat maps).
<code>side.cex</code>	Single numeric value, the character expansion factor to use for character side columns.
<code>col.heatmap</code>	Character vector of colors, to be used for the cells of the heat map.
<code>zlim</code>	Numeric vector of length two, defining minimal and maximal <code>expr</code> values that will be mapped to colors in <code>col.heatmap</code> . Values outside of this range will be rounded to the nearest boundary. Two special values are also allowed: "0 centered" to get a symmetrical range around 0 (with the default palette, it enforces 0 as the center color), and "range" to get <code>expr</code> range after normalization.
<code>zlim.trim</code>	Single numeric value between 0 and 1, defining the proportion of extreme values (equally split on both sides) to remove before computing "0 centered" or "range" <code>zlim</code> .

norm	Single character value, normalization to be performed (use "none" to perform no normalization). "rows" will center and scale genes, while "columns" will center and scale samples. The functions used depend on norm.robust.
norm.robust	Single logical value, if TRUE median and mad will be used for centering and scaling, else mean and sd .
customLayout	Single logical value, as layout does not allow nested calls, set this to TRUE to make your own call to layout and embed this plot in a wider one. See also getLayout .
getLayout	Single logical value, whether to only return the layout arguments that would be used with the set of arguments provided or not. It can prove useful to build custom layouts, e.g. merging this plot to an other. See also customLayout .
font	Integer vector of length two, the font used to draw X and Y axis labels respectively (see par). Default is to print X labels (usually samples) in normal font and Y labels (usually genes) in italic font.
xaxt	Single letter, whether to print column labels ("s") or not ("n").
yaxt	Single letter, whether to print row labels ("s") or not ("n").

Value

Invisibly returns a named list :

zlim	Final value of the <code>zlim</code> argument.
col.heatmap	Final value of the <code>col.heatmap</code> argument.
legend	If <code>side</code> is used, a named character vector of colors used for annotation.
cex.col	Final value of the <code>cex.col</code> argument.
cex.row	Final value of the <code>cex.row</code> argument.
mai.left	Final value of the <code>mai.left</code> argument.
mai.bottom	Final value of the <code>mai.bottom</code> argument.

Author(s)

Sylvain Mareschal

See Also

[clusterize](#), [heatmap](#)

Examples

```
# Data with features in columns
data(rosenwald)
group <- rosenwald.cli$group
expr <- t(rosenwald.expr)[,1:100]

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)
```

```
# Simple heat map
heat.map(expr)

# With annotation (row named data.frame)
side <- data.frame(group, row.names=rownames(expr))
heat.map(expr, side=side)
```

heat.scale	<i>Plots a heat map color scale, for legend</i>
------------	---

Description

This function plots a color scale using a custom color palette, to legend [heat.map](#) derivated functions.

Usage

```
heat.scale(zlim, col.heatmap, at = -10:10, labels = NULL, horiz = TRUE,
           robust = FALSE, customMar = FALSE, title=NA)
```

Arguments

zlim	Numeric vector of length 2, minimum and maximum of values in the palette. Should correspond to zlim in heat.map , consider to use heat.map invisible return to get special values.
col.heatmap	Character vector of colors used in the heat map. Should correspond to col.heatmap in heat.map , consider to use heat.map invisible return to get special values.
at	Numeric vector, values shown in the axis.
labels	Character vector as long as at, defining the values to show at at.
horiz	Single logical value, whether to plot an horizontal or a vertical scale.
robust	Single logical value, whether to legend median and mad or mean and sd. Should correspond to heat.map norm.robust value.
customMar	Single logical value, whether to skip the call to par to set mar or not.
title	Single character value, the axis title to use (NA for automatic generation).

Author(s)

Sylvain Mareschal

See Also

[heat.map](#), [clusterize](#), [predict.LPS](#)

Description

This function trains a Linear Predictor Score model, given pre-computed coefficients. It uses data with known classes to fit the model.

It has numerous way to be called, and all the arguments are not mandatory. See the 'Examples' section.

Usage

```
LPS(data, coeff, response, k, threshold, formula, method = "fdr", ...)
```

Arguments

data	Continuous data used to retrieve classes, as a <code>data.frame</code> or <code>matrix</code> , with samples in rows and features (genes) in columns. Rows and columns should be named. Some precautions must be taken concerning data normalization, see the corresponding section below.
coeff	Pre-computed coefficients for the model, as returned by <code>LPS.coeff</code> (see there for format details).
response	Already known classes for the samples provided in <code>data</code> , preferably as a two-level factor. Can be missing if a formula with a response element is provided, but this argument precedes.
k	Single integer value, amount of features to include in the model, in decreasing order of coefficient. Can be missing if <code>threshold</code> or <code>formula</code> are provided, but this argument precedes other both of them.
threshold	Single numeric value, p-value threshold to apply for feature selection. Can be missing if <code>k</code> or <code>formula</code> are provided, but <code>k</code> precedes on it and it precedes on <code>formula</code> .
formula	A formula object, describing the model to fit (several templates are handled, see 'Examples'). The formula response element (before the "~" sign) can replace the response argument if it is not provided. The variables (after the "~" sign) can be a single integer (standing for the <code>k</code> argument), a single numeric (standing for the <code>threshold</code> argument) or a sum of feature names to use directly. "." is also handled in the usual way (all data columns), and "1" is a more efficient way to refer to all numeric columns of data.
method	Single character value, to be passed to <code>p.adjust</code> when <code>threshold</code> is provided.
...	Further arguments are passed to <code>model.frame</code> if response is missing (thus defined via <code>formula</code>). <code>subset</code> and <code>na.action</code> may be particularly useful for cross-validation schemes, see <code>model.frame.default</code> for details. <code>subset</code> is always handled but masked in "..." for compatibility reasons.

Value

An object of (S3) class "LPS" :

coeff	Named numeric vector, the coefficients used in the model.
classes	Character vector, the labels of the two groups to be predicted.
scores	List of two numeric vectors, training dataset scores sorted by group.
means	Numeric vector, score means of each group in the training dataset.
sds	Numeric vector, score <i>sd</i> of each group in the training dataset.
ovl	Numeric value, overlapping coefficient as returned by OVL .
k	Integer value, amount of features selected in the model (if relevant).
p.threshold	Numeric value, threshold used for feature selection (if relevant).
p.method	Character value, p-value correction used for feature selection (if relevant).

Normalization

As expression values are directly used in the score, gene centering and scaling are strongly recommended. For Affymetrix raw expression values (strictly positive, linear and absolute), Wright et al. suggests a multiplicative centering on a median of 1000 followed by a log₂ transformation. For log-ratio, gene centering and scaling should not be necessary, as they are naturally 0-centered.

Time efficiency

Using a numeric matrix as data and a factor as response is the fastest way to compute coefficients, if time consumption matters (as in cross-validation schemes). `formula` is there only for consistency with R modeling functions, and to provide response, `k` or `threshold` in a single way.

Author(s)

Sylvain Mareschal

References

Radmacher MD, McShane LM, Simon R. *A paradigm for class prediction using gene expression profiles*. J Comput Biol. 2002;9(3):505-11.

Wright G, Tan B, Rosenwald A, Hurt EH, Wiestner A, Staudt LM. *A gene expression-based method to diagnose clinically distinct subgroups of diffuse large B cell lymphoma*. Proc Natl Acad Sci U S A. 2003 Aug 19;100(17):9991-6.

Bohers E, Mareschal S, Bouzefen A, Marchand V, Ruminy P, Maingonnat C, Menard AL, Etancelin P, Bertrand P, Dubois S, Alcantara M, Bastard C, Tilly H, Jardin F. *Targetable activating mutations are very frequent in GCB and ABC diffuse large B-cell lymphoma*. Genes Chromosomes Cancer. 2014 Feb;53(2):144-53.

See Also

[LPS.coeff](#)

Examples

```

# Data with features in columns
data(rosenwald)
group <- rosenwald.cli$group
expr <- t(rosenwald.expr)

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)

# Coefficients
coeff <- LPS.coeff(data=expr, response=group)

# 10 best features (straightforward)
m <- LPS(data=expr, coeff=coeff, response=group, k=10)

# 10 best features (formula)
### 'k' MUST be an integer, or will be understood as a 'threshold'
### Numbers are "numeric", enforce integer with "L" or "as.integer"
m <- LPS(data=as.data.frame(expr), coeff=coeff, formula=group~10L)
k <- as.integer(10)
m <- LPS(data=as.data.frame(expr), coeff=coeff, formula=group~k)

# FDR threshold
thr <- 0.01
m <- LPS(data=expr, coeff=coeff, response=group, threshold=thr)
m <- LPS(data=as.data.frame(expr), coeff=coeff, formula=group~0.01)
m <- LPS(data=as.data.frame(expr), coeff=coeff, formula=group~thr)

# Custom model
m <- LPS(data=expr, coeff=coeff[ c("27481", "17013") ], response=group, k=2)
m <- LPS(data=as.data.frame(expr), coeff=coeff, formula=group~`27481`+`17013`)
### Notice backticks in formula for syntactically invalid names

# Complete model
m <- LPS(data=expr, coeff=coeff, response=group, k=ncol(expr))
m <- LPS(data=expr, coeff=coeff, response=group, threshold=1)
### m <- LPS(data=as.data.frame(expr), coeff=coeff, formula=group~.)
### The last is correct but (really) slow on large datasets

```

LPS.coeff

Linear Predictor Score coefficient computation

Description

As Linear Predictor Score coefficients are genuinely t statistics, this function provides a faster implementation for large datasets than using `t.test`.

Usage

```
LPS.coeff(data, response, formula = ~1, type = c("t", "limma"),
          p.value = TRUE, log = FALSE, weighted = FALSE, ...)
```

Arguments

data	Continuous data used to retrieve classes, as a <code>data.frame</code> or <code>matrix</code> , with samples in rows and features (genes) in columns. Rows and columns should be named. NA values are silently ignored. Some precautions must be taken concerning data normalization, see the corresponding section in LPS manual page.
response	Already known classes for the samples provided in data, preferably as a two-level factor. Can be missing if a formula with a response element is provided, but this argument precedes.
formula	A formula object, describing the features to consider in data. The formula response element (before the "~" sign) can replace the response argument if it is not provided. The features can be enumerated in the variable section of the formula (after the "~" sign). "." is also handled in the usual way (all data columns), and "1" is a more efficient way to refer to all numeric columns of data.
type	Single character value, "t" to compute genuine t statistics (unequal variances and unpaired samples) or "limma" to use the <code>lmFit()</code> and <code>eBayes()</code> t statistics from this microarray oriented Bioconductor package.
p.value	Single logical value, whether to compute (two-sided) p-values or not.
log	Single logical value, whether to log-transform t or not (sign will be preserved). Original description of the LPS does not include log-transformation, but it may be useful to not over-weight discriminant genes in large series. Values between -1 and 1 are transformed to 0 to avoid sign shifting, as it generally comes with non significant p-values.
weighted	Single logical value, whether to divide t (or log-transformed t) by gene mean or not. We recommend to normalize data only by samples and use <code>weighted = TRUE</code> to include gene centering in the model, rather than centering and scaling genes by normalizing independantly each series as Wright et al. did.
...	Further arguments are passed to <code>model.frame</code> if response is missing (thus defined via formula). <code>subset</code> and <code>na.action</code> may be particularly useful for cross-validation schemes, see <code>model.frame.default</code> for details. <code>subset</code> is always handled but masked in "..." for compatibility reasons.

Value

Always returns a row named numeric matrix, with a "t" column holding statistics computed. If `p.value` is `TRUE`, a second "p.value" column is added.

Note

Using a numeric matrix as data and a factor as response is the fastest way to compute coefficients, if time consumption matters (as in cross-validation schemes). `formula` was added only for consis-

tency with other R modeling functions, and eventually to subset features to compute coefficients for.

Author(s)

Sylvain Mareschal

References

<http://www.bioconductor.org/packages/release/bioc/html/limma.html>

See Also

[LPS](#)

Examples

```
# Data with features in columns
data(rosenwald)
group <- rosenwald.cli$group
expr <- t(rosenwald.expr)

# All features, all samples
k <- LPS.coeff(data=expr, response=group)
k <- LPS.coeff(formula=group~1, data=as.data.frame(expr))
### LPS.coeff(formula=group~., data=as.data.frame(expr), na.action=na.pass)
### The last is correct but (really) slow on large datasets

# Feature subset, all samples
k <- LPS.coeff(data=expr[, c("27481","17013") ], response=group)
k <- LPS.coeff(formula=group~`27481`+`17013`, data=as.data.frame(expr))
### Notice backticks in formula for syntactically invalid names

# All features, sample subset
training <- rosenwald.cli$set == "Training"
### training <- sample.int(nrow(expr), 10)
### training <- which(rosenwald.cli$set == "Training")
### training <- rownames(subset(rosenwald.cli, set == "Training"))
k <- LPS.coeff(data=expr, response=group, subset=training)
k <- LPS.coeff(formula=group~1, data=as.data.frame(expr), subset=training)

# NA handling by model.frame()
k <- LPS.coeff(formula=group~1, data=as.data.frame(expr), na.action=na.omit)
```

OVL*Overlap quantification for LPS object*

Description

Quantify the overlap between gaussian distributions of the two group scores, to assess model efficiency (best models should not overlap, to prevent from false discovery).

Usage

```
OVL(means, sds, cutoff=1e-4, n=1e4)
```

Arguments

means	Numeric vector of two values, the means of the gaussian distributions.
sds	Numeric vector of two values, the standard deviations of the gaussian distributions.
cutoff	Single numeric value, minimal quantile for integration range definition (distributions will be considered between their cutoff and $1 - \text{cutoff}$ quantiles only). The lesser it is, the more precise the returned value will be.
n	Single integer value, the amount of equi-distant points to use for the computation. The greater it is, the more precise the returned value will be.

Value

Returns the proportion of the overlap between the two gaussian distributions N1 and N2, i.e. $\min(N1, N2) / (N1 + N2)$.

Author(s)

Sylvain Mareschal

See Also

[LPS-class](#), [LPS](#), [link{dnorm}](#)

Examples

```
# Full overlap between identical distributions
OVL(c(0,0), c(1,1))

# Increasing shift
OVL(c(0,1), c(1,1))
OVL(c(0,2), c(1,1))
OVL(c(0,3), c(1,1))
OVL(c(0,10), c(1,1))
```

`plot.LPS`*Plot method for LPS objects*

Description

This function plots the distributions of the LPS scores in each group for a fitted [LPS](#) object.

Usage

```
## S3 method for class 'LPS'  
plot(x, y, method=c("Wright", "Radmacher", "exact"), threshold = 0.9,  
      values = FALSE, col.classes = c("#FFCC00", "#1144CC"), xlim, yaxt = "s",  
      xlab = "LPS", ylab, las = 0, lwd = 2,...)
```

Arguments

<code>x</code>	An object of class "LPS", as returned by LPS .
<code>y</code>	Single character value defining y axis : "density" or (bayesian) "probability".
<code>method</code>	Single character value, the method to use for predictions. See predict.LPS .
<code>threshold</code>	Single numeric value, the confidence threshold to use for the "gray zone" (scores for which none of the two groups can be assigned with a probability greater than this threshold). See predict.LPS .
<code>values</code>	Single logical value, whether to plot individual scores from the training series or not.
<code>col.classes</code>	Character vector of two values giving to each class a distinct color.
<code>xlim</code>	To be passed to plot , see plot.default .
<code>yaxt</code>	To be passed to plot , see par .
<code>xlab</code>	To be passed to plot , see plot.default .
<code>ylab</code>	To be passed to plot , see plot.default .
<code>las</code>	To be passed to plot , see par .
<code>lwd</code>	To be passed to plot , see par .
<code>...</code>	Further arguments to be passed to plot or par .

Author(s)

Sylvain Mareschal

See Also

[LPS](#)

Examples

```

# Data with features in columns
data(rosenwald)
group <- rosenwald.cli$group
expr <- t(rosenwald.expr)

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)

# Coefficients
coeff <- LPS.coeff(data=expr, response=group)

# 10 best features model
m <- LPS(data=expr, coeff=coeff, response=group, k=10)

# Distributions of scores in each group
plot(m, "density")

# Probability for each group along the score axis
plot(m, "probability", yaxt="s")

```

predict.LPS

Predict method for LPS objects

Description

This function allow predictions to be made from a fitted [LPS](#) model and a new dataset. It can also plot a gene expression heatmap to visualize results of the prediction.

Usage

```

## S3 method for class 'LPS'
predict(object, newdata, type=c("class", "probability", "score"),
  method = c("Wright", "Radmacher", "exact"), threshold = 0.9, na.rm = TRUE,
  subset = NULL, col.lines = "#FFFFFF", col.classes = c("#FFCC00", "#1144CC"),
  plot = FALSE, side = NULL, cex.col = NA, cex.row = NA, mai.left = NA,
  mai.bottom = NA, mai.right = 1, mai.top = 0.1, side.height = 1, side.col = NULL,
  col.heatmap = heat(), zlim = "0 centered", norm = c("rows", "columns", "none"),
  norm.robust = FALSE, customLayout = FALSE, getLayout = FALSE, ...)

```

Arguments

object	An object of class "LPS", as returned by LPS .
newdata	Continuous data used to retrieve classes, as a <code>data.frame</code> or <code>matrix</code> , with samples in rows and features (genes) in columns. Rows and columns should be named. It can also be a named numeric vector of already computed scores.

Some precautions must be taken concerning data normalization, see the corresponding section in LPS manual page.

type	Single character value, return type of the predictions to be made ("class", "probability" or "score"). See 'Value' section.
method	Single character value, the method to use to make predictions ("Wright", "Radmacher" or "exact"). See 'Details' section.
threshold	Threshold to use for class prediction. "Wright" method was designed with 0.9, "Radmacher" method makes no use of the threshold.
na.rm	Single logical value, if TRUE samples with one or many NA features will be scored too (concerned feature is removed for the concerned sample, which might be discutable).
subset	A subsetting vector to apply on newdata rows. See [for handled values.
col.lines	If graph is TRUE, a single character value to be used for line drawing on the heatmap.
col.classes	If graph is TRUE, a character vector of two values giving to each class a distinct color.
plot	To be passed to heat.map .
side	To be passed to heat.map .
cex.col	To be passed to heat.map .
cex.row	To be passed to heat.map .
mai.left	To be passed to heat.map .
mai.bottom	To be passed to heat.map .
mai.right	To be passed to heat.map (used to plot score coefficients).
mai.top	To be passed to heat.map .
side.height	To be passed to heat.map .
side.col	To be passed to heat.map .
col.heatmap	To be passed to heat.map .
zlim	To be passed to heat.map .
norm	To be passed to heat.map .
norm.robust	To be passed to heat.map .
customLayout	To be passed to heat.map .
getLayout	To be passed to heat.map .
...	Ignored, just there to match the predict generic function.

Details

The "Compound covariate predictor" from Radmacher et al. (`method = "Radmacher"`) simply assign each sample to the closest group (comparing the sample score to the mean scores of each group in the training dataset).

The "Linear Predictor Score" from Wright et al. (`method = "Wright"`) modelizes scores in each training sub-group with a distinct gaussian distribution, and computes the probability for a sample to be in one of them or the other using a bayesian rule.

The "exact" mode is still under development and should not be used.

Value

For a "class" type, returns a character vector with group assignment for each new sample (possibly NA), named according to data row names.

For a "probability" type, returns a numeric matrix with two columns (probabilities to be in each group) and a row for each new sample, row named according to data row names and column named according to the group labels.

For a "score" type, returns a numeric vector with LPS score for each new sample, named according to data row names. Notice the score is the same for all methods.

If plot is TRUE, returns the list returned by `heat.map`, with data described above in the first un-named element.

Author(s)

Sylvain Mareschal

References

Radmacher MD, McShane LM, Simon R. *A paradigm for class prediction using gene expression profiles*. J Comput Biol. 2002;9(3):505-11.

Wright G, Tan B, Rosenwald A, Hurt EH, Wiestner A, Staudt LM. *A gene expression-based method to diagnose clinically distinct subgroups of diffuse large B cell lymphoma*. Proc Natl Acad Sci U S A. 2003 Aug 19;100(17):9991-6.

See Also

[LPS](#)

Examples

```
# Data with features in columns
data(rosenwald)
group <- rosenwald.cli$group
expr <- t(rosenwald.expr)

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)

# Coefficients
coeff <- LPS.coeff(data=expr, response=group)

# 10 best features model
m <- LPS(data=expr, coeff=coeff, response=group, k=10)

# Class prediction plot
predict(m, expr, plot=TRUE)

# Wright et al. class prediction
```

```
table(
  group,
  prediction = predict(m, expr),
  exclude = NULL
)

# More stringent threshold
table(
  group,
  prediction = predict(m, expr, threshold=0.99),
  exclude = NULL
)

# Radmacher et al. class prediction
table(
  group,
  prediction = predict(m, expr, method="Radmacher"),
  exclude = NULL
)

# Probabilities
predict(m, expr, type="probability", method="Wright")
predict(m, expr, type="probability", method="Radmacher")
predict(m, expr, type="probability", method="exact")

# Probability plot
predict(m, expr, type="probability", plot=TRUE)

# Annotated probability plot
side <- data.frame(group, row.names=row.names(expr))
predict(m, expr, side=side, type="probability", plot=TRUE)

# Score plot
predict(m, expr, type="score", plot=TRUE)
```

Rosenwald dataset

Rosenwald et al. Lymphochip data

Description

This dataset contains 60 Diffuse Large B-Cell Lymphomas analysed on Lymphochip microarrays, as published by Rosenwald et al. The "Germinal Center B-cell like" and "Activated B-Cell like" subtypes, as determined by hierarchical clustering, were predicted by a LPS approach in Wright et al.

To minimize package size, values were rounded at 3 decimals and only 60 DLBCL from the 240 series were randomly selected (40 from the "Training" set, 20 from the "Validation" set), excluding "Type III" sub-types.

Usage

```
data(rosenwald)
```

Format

`rosenwald.expr` is a numeric matrix of expression values, with probes in rows and samples in columns. Both dimensions are named, probes by there "UNIQID" and samples by there "LYM numbers". Many NA values are present.

`rosenwald.cli` is a data.frame with a row for each sample, and 4 factor columns described below. Rows are named by samples "LYM numbers", in the same order than `rosenwald.expr`.

set the "Training" or "Validation" set the sample comes from.

group the DLBCL sub-type that is to be predicted ("GCB" or "ABC").

follow.up follow-up of the patient, in years.

status status of the patient at the end of the follow-up ("Dead" or "Alive").

Source

<http://11mpp.nih.gov/DLBCL/>

References

Rosenwald A et al. *The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma*. N Engl J Med. 2002 Jun 20;346(25):1937-47.

Wright G et al. *A gene expression-based method to diagnose clinically distinct subgroups of diffuse large B cell lymphoma*. Proc Natl Acad Sci U S A. 2003 Aug 19;100(17):9991-6.

surv.colors

Produces visual representation of survival data

Description

This function generates color shades for each individual, according to their respective right-censored survival data (event occurred or not, after which follow-up time). This can prove useful to annotate heat maps with survival data.

Two color scales are used, one for right-censored individuals (lost of sight before the event occurs, yellow with default colors) and an other for individual with observed events (death, relapse ... black in default colors). Shades are generated according to their impact : fast events and long follow-ups without event have strong colors, while late events and short follow-up without event are light-colored.

Usage

```
surv.colors(time, event, eventColors = c("#000000", "#CCCCCC"),
            censColors = c("#FFFFFF", "#FFDD00"))
```

Arguments

time	Numeric vector, the follow-up times of each individual (see Surv in the survival package).
event	Logical vector, whether an event (death, relapse ...) occurred at the end of each individual follow-up or not (see Surv in the survival package).
eventColors	Character vector of length 2, the boundaries of the color scale to generate for individuals with events.
censColors	Character vector of length 2, the boundaries of the color scale to generate for right-censored individuals.

Value

Returns a character vector, named according to time names.

Author(s)

Sylvain Mareschal

See Also

[surv.scale](#), [heat.map](#)

Examples

```
# Rosenwald's dataset (hand-picked prognostic probes)
data(rosenwald)
probes <- c("30580", "16006", "32315", "16978", "26588")
expr <- t(rosenwald.expr[ probes ,])

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)

# Survival colors
surv <- with(rosenwald.cli, surv.colors(time=follow.up, event=status=="Dead"))

# Color scale legend
with(rosenwald.cli, surv.scale(time=follow.up, event=status=="Dead"))

# Annotated clustering
side <- data.frame(OS=surv, row.names=row.names(rosenwald.cli))
clusterize(expr, side=side)
```

surv.scale *Plots a survival color scale, for legend*

Description

This function plots a color scale using a custom color palette, to legend `surv.colors` annotations.

Usage

```
surv.scale(time, event, eventColors = c("#000000", "#CCCCCC"),
           censColors = c("#FFFFEE", "#FFDD00"))
```

Arguments

time	Numeric vector, the follow-up times of each individual (see <code>Surv</code> in the survival package).
event	Logical vector, whether an event (death, relapse ...) occurred at the end of each individual follow-up or not (see <code>Surv</code> in the survival package).
eventColors	Character vector of length 2, the boundaries of the color scale to generate for individuals with events.
censColors	Character vector of length 2, the boundaries of the color scale to generate for right-censored individuals.

Author(s)

Sylvain Mareschal

See Also

[surv.colors](#), `survival::Surv`

Examples

```
# Rosenwald's dataset (hand-picked prognostic probes)
data(rosenwald)
probes <- c("30580", "16006", "32315", "16978", "26588")
expr <- t(rosenwald.expr[ probes ,])

# NA imputation (feature's mean to minimize impact)
f <- function(x) { x[ is.na(x) ] <- round(mean(x, na.rm=TRUE), 3); x }
expr <- apply(expr, 2, f)

# Survival colors
surv <- with(rosenwald.cli, surv.colors(time=follow.up, event=status=="Dead"))

# Annotated clustering
side <- data.frame(OS=surv, row.names=row.names(rosenwald.cli))
clusterize(expr, side=side)
```

```
# Color scale legend  
with(rosenwald.cli, surv.scale(time=follow.up, event=status=="Dead"))
```

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