

Package ‘pathwayTMB’

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Type Package

Title Pathway Based Tumor Mutational Burden

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Description A systematic bioinformatics tool to develop a new pathway-based gene panel for tumor mutational burden (TMB) assessment (pathway-based tumor mutational burden, PTMB), using somatic mutations files in an efficient manner from either The Cancer Genome Atlas sources or any in-house studies as long as the data is in mutation annotation file (MAF) format. Besides, we develop a multiple machine learning method using the sample's PTMB profiles to identify cancer-specific dysfunction pathways, which can be a biomarker of prognostic and predictive for cancer immunotherapy.

License GPL (>= 2)

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final_character	<i>final_character, the example's final signature</i>
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Description

final_character, a potential marker for cancer prognostic and immunotherapy, generated by 'get_final_signature'

Usage

final_character

Format

An object of class character of length 2.

GenePathwayOncoplots	<i>draw an GenePathwayOncoplots</i>
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Description

takes output generated by read.maf and draws an GenePathwayOncoplots.

Usage

```
GenePathwayOncoplots(
  maffile,
  gene_path,
  freq_matrix,
  risk_score,
  cut_off,
  final_character,
  isTCGA = FALSE,
  top = 20,
  clinicalFeatures = "sample_group",
  annotationColor = c("red", "green"),
  sortByAnnotation = TRUE,
  removeNonMutated = FALSE,
  drawRowBar = TRUE,
  drawColBar = TRUE,
  leftBarData = NULL,
  leftBarLims = NULL,
  rightBarData = NULL,
  rightBarLims = NULL,
  topBarData = NULL,
  logColBar = FALSE,
  draw_titv = FALSE,
  showTumorSampleBarcodes = FALSE,
  fill = TRUE,
  showTitle = TRUE,
  titleText = NULL
)
```

Arguments

<code>maffile</code>	an MAF object generated by <code>read.maf</code> .
<code>gene_path</code>	User input pathways geneset list.
<code>freq_matrix</code>	The mutations matrix, generated by <code>'get_mut_matrix'</code> .
<code>risk_score</code>	Samples' PTMB-related risk score, which could be a biomarker for survival analysis and immunotherapy prediction.
<code>cut_off</code>	A threshold value (the median risk score as the default value). Using this value to divide the sample into high and low risk groups with different overall survival.
<code>final_character</code>	The pathway signature, use to map gene in the GenePathwayOncoplots.
<code>isTCGA</code>	Is input MAF file from TCGA source. If TRUE uses only first 12 characters from Tumor_Sample_Barcode.
<code>top</code>	how many top genes to be drawn, genes are arranged from high to low depending on the frequency of mutations. defaults to 20.
<code>clinicalFeatures</code>	columns names from 'clinical.data' slot of MAF to be drawn in the plot. Default "sample_group".

annotationColor	Custom colors to use for sample annotation-"sample_group". Must be a named list containing a named vector of colors. Default "red" and "green".
sortByAnnotation	logical sort oncomatrix (samples) by provided 'clinicalFeatures'. Sorts based on first 'clinicalFeatures'. Defaults to TRUE. column-sort.
removeNonMutated	Logical. If TRUE removes samples with no mutations in the GenePathwayOncoplots for better visualization. Default FALSE.
drawRowBar	logical. Plots right barplot for each gene. Default TRUE.
drawColBar	logical plots top barplot for each sample. Default TRUE.
leftBarData	Data for leftside barplot. Must be a data.frame with two columns containing gene names and values. Default 'NULL'.
leftBarLims	limits for 'leftBarData'. Default 'NULL'.
rightBarData	Data for rightside barplot. Must be a data.frame with two columns containing to gene names and values. Default 'NULL' which draws distribution by variant classification. This option is applicable when only 'drawRowBar' is TRUE.
rightBarLims	limits for 'rightBarData'. Default 'NULL'.
topBarData	Default 'NULL' which draws absolute number of mutation load for each sample. Can be overridden by choosing one clinical indicator(Numeric) or by providing a two column data.frame containing sample names and values for each sample. This option is applicable when only 'drawColBar' is TRUE.
logColBar	Plot top bar plot on log10 scale. Default FALSE.
draw_titv	logical Includes TiTv plot. Default FALSE
showTumorSampleBarcodes	logical to include sample names.
fill	Logical. If TRUE draws genes and samples as blank grids even when they are not altered.
showTitle	Default TRUE.
titleText	Custom title. Default 'NULL'.

Value

No return value

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mu_fre = 0.01,is.TCGA=FALSE,sur=sur)
#perform the function 'get_PTMB'
PTMB_matrix<-get_PTMB(freq_matrix=mut_matrix,genesmbol=genesmbol,gene_path=gene_path)
set.seed(1)
```

```
final_character<-get_final_signature(PTMB=PTMB_matrix,sur=sur)
#calculate the riskscore
riskscore<-plotKMcurves(t(PTMB_matrix[final_character,]),sur=sur,plots=FALSE)$risk_score
cut<-median(riskscore)
GenePathwayOncoplots(maf, gene_path, mut_matrix, riskscore, cut, final_character)
```

genesmbol	<i>genesmbol, the coding genes' length</i>
-----------	--

Description

genesmbol, a list of coding genes' length, generated by 'get_gene_length'.

Usage

```
genesmbol
```

Format

An object of class list of length 34931.

gene_path	<i>gene_path, the pathways geneset</i>
-----------	--

Description

gene_path, a list of KEGG Non-metabolic pathways geneset.

Usage

```
gene_path
```

Format

An object of class list of length 27.

get_final_signature *Filter cancer-specific dysfunction pathways.*

Description

The function 'get_final_signature', using to filter cancer-specific dysfunction pathways (a potential marker for cancer prognostic and immunotherapy), is the main function of our analysis.

Usage

```
get_final_signature(PTMB, sur, pval_cutoff = 0.01)
```

Arguments

PTMB	The pathway tumor mutation burden matrix, generated by 'get_PTMB'.
sur	A nx2 data frame of samples' survival data, the first line is samples' survival event and the second line is samples' overall survival.
pval_cutoff	A threshold value (0.01 as the default value) to identify the differential PTMB pathway.

Value

Return the final PTMB signature, could be a potential marker for prognostic and immunotherapy prediction.

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mut_fre = 0.01,is.TCGA=FALSE,sur=sur)
#perform the function 'get_PTMB'
PTMB_matrix<-get_PTMB(freq_matrix=mut_matrix,genesmbol=genesmbol,gene_path=gene_path)
set.seed(1)
final_character<-get_final_signature(PTMB=PTMB_matrix,sur=sur)
```

get_mut_matrix	<i>Converts MAF into mutation matrix.</i>
----------------	---

Description

The function 'get_mut_matrix' converts mutation annotation file (MAF) format data into a mutations matrix. Then use the fisher exact test to select the geneset with higher mutation frequency in alive sample group. Finally return the higher mutation frequency matrix.

Usage

```
get_mut_matrix(
  maffile,
  is.TCGA = TRUE,
  mut_fre = 0,
  nonsynonymous = TRUE,
  cut_Cox.pval = 1,
  cut_HR = 1,
  sur
)
```

Arguments

maffile	Input mutation annotation file (MAF) format data. It must be an absolute path or the name related to the current working directory.
is.TCGA	Is input MAF file from TCGA source. If TRUE uses only first 15 characters from Tumor_Sample_Barcode.
mut_fre	A threshold value(zero as the default value). The genes with a given mutation frequency equal or greater than the threshold value are retained for the following analysis.
nonsynonymous	Logical, tell if extract the non-synonymous somatic mutations (nonsense mutation, missense mutation, frame-shift indels, splice site, nonstop mutation, translation start site, inframe indels).
cut_Cox.pval	The significant cut_off pvalue for the univariate Cox regression.
cut_HR	The cut_off HR for the univariate Cox regression, uses to select the genes with survival benefit mutations.
sur	A nx2 data frame of samples' survival data, the first line is samples' survival event and the second line is samples' overall survival.

Value

The survival-related mutations matrix.

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mut_fre = 0.01,is.TCGA=FALSE,sur=sur)
```

get_PTMB

Calculate the Pathway-based Tumor Mutational Burden.

Description

The function 'get_PTMB' uses to calculate the Pathway-based Tumor Mutational Burden (PTMB). PTMB is defined as pathway-based tumor mutational burden corrected by genes' length and number.

Usage

```
get_PTMB(freq_matrix, genesmbol, path_mut_cutoff = 0, gene_path)
```

Arguments

freq_matrix	The mutations matrix,generated by 'get_mut_matrix'.
genesmbol	The genes' length matrix,generated by 'get_gene_length'.
path_mut_cutoff	A threshold value(zero percent as the default value).Pathways with a given mutation frequency equal or greater than the threshold value are retained for the following analysis.
gene_path	User input pathways geneset list.

Value

Return the Pathway-based Tumor Mutational Burden matrix.

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mut_fre = 0.01,is.TCGA=FALSE,sur=sur)
#perform the function 'get_PTMB'
PTMB_matrix<-get_PTMB(freq_matrix=mut_matrix,genesmbol=genesmbol,gene_path=gene_path)
```

mut_matrix	<i>mut_matrix, mutations matrix</i>
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Description

mut_matrix, the mutations matrix, generated by 'get_mut_matrix'

Usage

```
mut_matrix
```

Format

An object of class matrix (inherits from array) with 673 rows and 35 columns.

plotKMcurves	<i>Drawing Kaplan Meier Survival Curves Using the final survival-related PTMB.</i>
--------------	--

Description

The function 'plotKMcurves' uses to draw Kaplan-Meier Survival Curves based on PTMB-related riskscore. The riskscore is generated by the signature's PTMB and the coefficient of "Univariate" or "Multivariate" cox regression.

Usage

```
plotKMcurves(
  sig_PTMB,
  sur,
  method = "Multivariate",
  returnAll = TRUE,
  pval = TRUE,
  color = NULL,
  plots = TRUE,
  palette = NULL,
  linetype = 1,
  conf.int = FALSE,
  pval.method = FALSE,
  test.for.trend = FALSE,
  surv.median.line = "none",
  risk.table = FALSE,
  cumevents = FALSE,
  cumcensor = FALSE,
  tables.height = 0.25,
  add.all = FALSE,
  ggtheme = theme_survminer()
)
```

Arguments

<code>sig_PTMB</code>	The signature's PTMB matrix, which rows are samples and columns are pathways.
<code>sur</code>	A nx2 data frame of samples' survival data, the first line is samples' survival event and the second line is samples' overall survival.
<code>method</code>	Method must be one of "Univariate" and "Multivariate".
<code>returnAll</code>	Logical value. Default is TRUE. If TRUE, return the riskscore and the coefficient of cox regression.
<code>pval</code>	Logical value, a numeric or a string. If logical and TRUE, the p-value is added on the plot. If numeric, then the computed p-value is substituted with the one passed with this parameter. If character, then the customized string appears on the plot.
<code>color</code>	Color to be used for the survival curves. If the number of strata/group (<code>n.strata</code>) = 1, the expected value is the color name. For example <code>color = "blue"</code> . If <code>n.strata > 1</code> , the expected value is the grouping variable name. By default, survival curves are colored by strata using the argument <code>color = "strata"</code> , but you can also color survival curves by any other grouping variables used to fit the survival curves. In this case, it's possible to specify a custom color palette by using the argument <code>palette</code> .
<code>plots</code>	logical value. Default is TRUE. If TRUE, plot the Kaplan Meier Survival Curves.
<code>palette</code>	the color palette to be used. Allowed values include "hue" for the default hue color scale; "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmarty". See details section for more information. Can be also a numeric vector of length(groups); in this case a basic color palette is created using the function <code>palette</code> .
<code>linetype</code>	line types. Allowed values includes i) "strata" for changing linetypes by strata (i.e. groups); ii) a numeric vector (e.g., <code>c(1, 2)</code>) or a character vector <code>c("solid", "dashed")</code> .
<code>conf.int</code>	logical value. If TRUE, plots confidence interval.
<code>pval.method</code>	whether to add a text with the test name used for calculating the pvalue, that corresponds to survival curves' comparison - used only when <code>pval=TRUE</code>
<code>test.for.trend</code>	logical value. Default is FALSE. If TRUE, returns the test for trend p-values. Tests for trend are designed to detect ordered differences in survival curves. That is, for at least one group. The test for trend can be only performed when the number of groups is > 2.
<code>surv.median.line</code>	character vector for drawing a horizontal/vertical line at median survival. Allowed values include one of <code>c("none", "hv", "h", "v")</code> . v: vertical, h:horizontal.
<code>risk.table</code>	Allowed values include: (1) TRUE or FALSE specifying whether to show or not the risk table. Default is FALSE. (2) "absolute" or "percentage". Shows the absolute number and the percentage of subjects at risk by time, respectively. (3) "abs_pct" to show both absolute number and percentage. (4) "nrisk_cumcensor" and "nrisk_cumevents".

	Show the number at risk and, the cumulative number of censoring and events, respectively.
cumevents	logical value specifying whether to show or not the table of the cumulative number of events. Default is FALSE.
cumcensor	logical value specifying whether to show or not the table of the cumulative number of censoring. Default is FALSE.
tables.height	numeric value (in [0 - 1]) specifying the general height of all tables under the main survival plot.
add.all	a logical value. If TRUE, add the survival curve of pooled patients (null model) onto the main plot.
ggtheme	function, ggplot2 theme name. Default value is theme_survminer. Allowed values include ggplot2 official themes: see theme.

Value

Return a list of riskscore and coefficient of cox regression.

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mut_fre = 0.01,is.TCGA=FALSE,sur=sur)
#perform the function 'get_PTMB'
PTMB_matrix<-get_PTMB(freq_matrix=mut_matrix,genesmbol=genesmbol,gene_path=gene_path)
set.seed(1)
final_character<-get_final_signature(PTMB=PTMB_matrix,sur=sur)
#plot the K-M survival curve
plotKMcurves(t(PTMB_matrix[final_character,]),sur=sur,risk.table = TRUE)
```

plotMutInteract	<i>Exact tests to detect mutually exclusive, co-occurring and altered gene-sets or pathways.</i>
-----------------	--

Description

Performs Pair-wise Fisher's Exact test to detect mutually exclusive or co-occurring events.

Usage

```
plotMutInteract(
  freq_matrix,
  genes,
  pvalue = c(0.05, 0.01),
```

```

returnAll = TRUE,
fontSize = 0.8,
showSigSymbols = TRUE,
showCounts = FALSE,
countStats = "all",
countType = "all",
countsFontSize = 0.8,
countsFontColor = "black",
colPal = "BrBG",
nShiftSymbols = 5,
sigSymbolsSize = 2,
sigSymbolsFontSize = 0.9,
pvSymbols = c(46, 42),
limitColorBreaks = TRUE
)

```

Arguments

freq_matrix	The mutations matrix, generated by 'get_mut_matrix'.
genes	List of genes or pathways among which interactions should be tested.
pvalue	Default c(0.05, 0.01) p-value threshold. You can provide two values for upper and lower threshold.
returnAll	If TRUE returns test statistics for all pair of tested genes. Default FALSE, returns for only genes below pvalue threshold.
fontSize	cex for gene names. Default 0.8.
showSigSymbols	Default TRUE. Highlight significant pairs.
showCounts	Default TRUE. Include number of events in the plot.
countStats	Default 'all'. Can be 'all' or 'sig'.
countType	Default 'cooccur'. Can be 'all', 'cooccur', 'mutexcl'.
countsFontSize	Default 0.8.
countsFontColor	Default 'black'.
colPal	colPalBrewer palettes. See RColorBrewer::display.brewer.all() for details.
nShiftSymbols	shift if positive shift SigSymbols by n to the left, default = 5.
sigSymbolsSize	size of symbols in the matrix and in legend.
sigSymbolsFontSize	size of font in legends.
pvSymbols	vector of pch numbers for symbols of p-value for upper and lower thresholds c(upper, lower).
limitColorBreaks	limit color to extreme values. Default TRUE.

Value

list of data.tables

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mut_fre = 0.01,is.TCGA=FALSE,sur=sur)
#perform the function `get_PTMB`
PTMB_matrix<-get_PTMB(freq_matrix=mut_matrix,genesmbol=genesmbol,gene_path=gene_path)
set.seed(1)
final_character<-get_final_signature(PTMB=PTMB_matrix,sur=sur)
plotMutInteract(freq_matrix=PTMB_matrix, genes=final_character,nShiftSymbols =0.3)
```

plotROC

plot the ROC curve

Description

This function uses to plot a ROC curve.

Usage

```
plotROC(
  riskscore,
  response,
  main,
  add = FALSE,
  col = par("col"),
  legacy.axes = TRUE,
  print.auc = FALSE,
  grid = FALSE,
  auc.polygon = FALSE,
  auc.polygon.col = "skyblue",
  max.auc.polygon = FALSE,
  max.auc.polygon.col = "#EEEEEE"
)
```

Arguments

riskscore	a numeric vector of the same length than response, containing the predicted value of each observation.
response	a factor, numeric or character vector of responses (true class), typically encoded with 0 (controls) and 1 (cases). Only two classes can be used in a ROC curve.
main	the title of the ROC curve
add	if TRUE, the ROC curve will be added to an existing plot. If FALSE (default), a new plot will be created.

<code>col</code>	the color of the ROC curve
<code>legacy.axes</code>	a logical indicating if the specificity axis (x axis) must be plotted as decreasing "specificity" (FALSE) or increasing "1 - specificity" (TRUE, the default) as in most legacy software. This affects only the axis, not the plot coordinates.
<code>print.auc</code>	boolean. Should the numeric value of AUC be printed on the plot?
<code>grid</code>	boolean or numeric vector of length 1 or 2. Should a background grid be added to the plot? Numeric: show a grid with the specified interval between each line; Logical: show the grid or not. Length 1: same values are taken for horizontal and vertical lines. Length 2: grid value for vertical (<code>grid[1]</code>) and horizontal (<code>grid[2]</code>). Note that these values are used to compute <code>grid.v</code> and <code>grid.h</code> . Therefore if you specify a <code>grid.h</code> and <code>grid.v</code> , it will be ignored.
<code>auc.polygon</code>	boolean. Whether or not to display the area as a polygon.
<code>auc.polygon.col</code>	color (<code>col</code>) for the AUC polygon.
<code>max.auc.polygon</code>	boolean. Whether or not to display the maximal possible area as a polygon.
<code>max.auc.polygon.col</code>	color (<code>col</code>) for the maximum AUC polygon.

Value

No return value

Examples

```
#get the path of the mutation annotation file and samples' survival data
maf<-system.file("extdata","data_mutations_extended.txt",package = "pathwayTMB")
sur_path<-system.file("extdata","sur.csv",package = "pathwayTMB")
sur<-read.csv(sur_path,header=TRUE,row.names = 1)
#perform the function 'get_mut_matrix'
mut_matrix<-get_mut_matrix(maffile=maf,mu_fre = 0.01,is.TCGA=FALSE,sur=sur)
#perform the function 'get_PTMB'
PTMB_matrix<-get_PTMB(freq_matrix=mut_matrix,genesmbol=genesmbol,gene_path=gene_path)
set.seed(1)
final_character<-get_final_signature(PTMB=PTMB_matrix,sur=sur)
#calculate the riskscore
riskscore<-plotKMcurves(t(PTMB_matrix[final_character,]),sur=sur,plots=FALSE)$risk_score
#get the path of samples' immunotherapy response data
res_path<-system.file("extdata","response.csv",package = "pathwayTMB")
response<-read.csv(res_path,header=TRUE,stringsAsFactors =FALSE,row.name=1)
plotROC(riskscore=riskscore,response=response,main="Objective Response",print.auc=TRUE)
```

PTMB_matrix	<i>PTMB_matrix, the Pathway-based Tumor Mutational Burden matrix</i>
-------------	--

Description

PTMB_matrix, the pathway tumor mutation burden matrix, generated by 'get_PTMB'

Usage

PTMB_matrix

Format

An object of class data.frame with 27 rows and 35 columns.

sur	<i>sur, the samples' survival data</i>
-----	--

Description

sur, a nx2 data frame, the samples' survival data

Usage

sur

Format

An object of class data.frame with 110 rows and 2 columns.

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