

Package ‘mslp’

May 16, 2024

Type Package

Title Predict synthetic lethal partners of tumour mutations

Version 1.6.0

Description An integrated pipeline to predict the potential synthetic lethality partners (SLPs) of tumour mutations, based on gene expression, mutation profiling and cell line genetic screens data. It has built-in support for data from cBioPortal. The primary SLPs correlating with mutations in WT and compensating for the loss of function of mutations are predicted by random forest based methods (GENIE3) and Rank Products, respectively. Genetic screens are employed to identify consensus SLPs leads to reduced cell viability when perturbed.

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Encoding UTF-8

LazyData false

RoxygenNote 7.2.3

Depends R (>= 4.2.0)

Imports data.table (>= 1.13.0), doRNG, fmsb, foreach, magrittr, org.Hs.eg.db, pROC, randomForest, RankProd, stats, utils

Suggests BiocStyle, doFuture, future, knitr, rmarkdown, roxygen2, tinytest

VignetteBuilder knitr

biocViews Pharmacogenetics, Pharmacogenomics

git_url <https://git.bioconductor.org/packages/mslp>

git_branch RELEASE_3_19

git_last_commit 23e640d

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-15

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Contents

| | |
|----------------------------|----|
| comp_slp | 2 |
| cons_slp | 3 |
| corr_slp | 4 |
| est_im | 5 |
| example_compSLP | 6 |
| example_comp_mut | 7 |
| example_corrSLP | 7 |
| example_corr_mut | 7 |
| example_expr | 8 |
| example_z | 8 |
| genie3 | 8 |
| getlink | 10 |
| merge_slp | 10 |
| pp_tcga | 11 |
| scr_slp | 13 |

| | |
|--------------|-----------|
| Index | 15 |
|--------------|-----------|

| | |
|----------|---------------------------------------|
| comp_slp | <i>Identify SLPs via compensation</i> |
|----------|---------------------------------------|

Description

Identify SLPs compensating for the loss of function of mutations. The up-regulated SLPs are selected via the rank products algorithm, with option `calculateProduct = FALSE` for a robust results and capacity on large datasets.

Usage

```
comp_slp(
  zscore_data,
  mut_data,
  mutgene = NULL,
  positive_perc = 0.5,
  p_thresh = 0.01,
  ...
)
```

Arguments

| | |
|-------------|---|
| zscore_data | a matrix (genes by patients) reflecting gene expression related to wide type samples. For example, generated from <code>pp_tcga</code> . |
| mut_data | a data.table with columns "patientid" and "mut_entrez". |
| mutgene | identify SLPs for sepecific muatation (gene symbols). If NULL (by default), the intersection genes between zscore_data and mut_data are used. |

positive_perc keep genes with positive zscore in at least positive_perc * number of mutation patients.
p_thresh pvalue threshold to filter out results.
 ... additional parameters to [RankProducts](#).

Value

A data.table with predicted SLPs.

mut_entrez Entrez ids of mutations.

mut_symbol Gene symbols of mutations.

slp_entrez Entrez ids of SLPs.

slp_symbol Gene symbols of SLPs.

pvalue p_value from [RankProducts](#).

fdr "BH" adjusted pvalue via [p.adjust](#).

Examples

```

#- Toy examples, see vignette for more.
#- Add the parallel backend.
require(future)
require(doFuture)
plan(multisession, workers = 2)
data("example_z")
data("example_comp_mut")
res <- comp_slp(example_z, example_comp_mut)
plan(sequential)

```

| | |
|----------|--------------------------------|
| cons_slp | <i>Identify consensus SLPs</i> |
|----------|--------------------------------|

Description

Identify consensus SLPs based on Cohen's Kappa or hypergeometric test.

Usage

```
cons_slp(screen_slp, tumour_slp)
```

Arguments

screen_slp screen hits data annotated with SLPs information, generated by [scr_slp](#).

tumour_slp the merged SLPs data predicted by [corr_slp](#) and [comp_slp](#).

Details

Consensus SLPs are enriched screen hits that are SLPs of same mutations in different cell lines. For each common mutation, the SLPs predicted from human tumour data are used as the total sets. We used either Cohen's Kappa coefficient on a confusion matrix, or Hypergeometric test, to test the significance of overlapping of screen hits.

Value

A data.table.

mut_entrez Entrez ids of mutations.

mut_symbol Gene symbols of mutations.

cons_slp_entrez Entrez ids of consensus SLPs.

cons_slp_symbol Gene symbols of Consensus SLPs.

cell_1, cell_2 From which pair of cell lines the consensus SLPs predicted.

judgement Judgement based on Cohen's Kappa.

kappa_value Cohen's Kappa coefficient

pvalue pvalue for Cohen's Kappa coefficient.

fdr "BH" adjusted pvalue via [p.adjust](#).

References

Landis JR, Koch GG (1977) The measurement of observer agreement for categorical data. *Biometrics*, 33: 159-174.

Examples

```
#- See the examples in the vignette.
if (FALSE) k_res <- cons_slp(scr_res, merged_res)
```

corr_slp

Identify SLPs via correlation

Description

Identify SLPs of mutations based on co-expression. GENIE3 is employed to find genes highly correlated with mutations in wide type patients.

Usage

```
corr_slp(
  expr_data,
  mut_data,
  mutgene = NULL,
  im_thresh = 0.001,
  topgene = 2000,
  ...
)
```

Arguments

| | |
|-----------|---|
| expr_data | an expression matrix, genes by patients. |
| mut_data | a data.table with columns "patientid" and "mut_entrez". |
| mutgene | identify SLPs for sepecific muatation (gene symbols). If NULL (by default), the intersection genes between expr_data and mut_data are used. |
| im_thresh | minimum importance threshold. |
| topgene | top N genes above the im_thresh. |
| ... | further parameters to genie3 . |

Value

A data.table with predicted SLPs.

mut_entrez Entrez ids of mutations.

mut_symbol Gene symbols of mutations.

slp_entrez Entrez ids of SLPs.

slp_symbol Gene symbols of SLPs.

fdr "BH" adjusted pvalue via [p.adjust](#).

im The importance value returned by [genie3](#).

Examples

```
#- Toy examples, see vignette for more.
require(future)
require(doFuture)
plan(multisession, workers = 2)
data("example_expr")
data("example_corr_mut")
res <- corr_slp(example_expr, example_corr_mut)
plan(sequential)
```

 est_im

Estimate the importance threshold for GENIE3

Description

Estimate the importance threshold based on repetition GENIE3 results via ROC.

Usage

```
est_im(permu_data, fdr_thresh = 0.001)
```

Arguments

| | |
|------------|---|
| permu_data | permuated corr_slp results. |
| fdr_thresh | fdr threshold to selected "TRUE" SLPs. |

Details

We first generate a SLPs by repetition matrix from repetition GENIE3 results. SLPs with high im value in repetitions are selected and considered as "TRUE" SLPs via the rank product algorithm. Then for each repetition, we perform receiver operating characteristic curve analysis and select an optimal threshold by "youden" approach. The optimal thresholds are averaged to get the final threshold.

Value

A data.table with mut_entrez (mutation entrez_id) and roc_thresh (estimated im threshold).

Examples

```
#- Toy examples.
require(future)
require(doFuture)
plan(multisession, workers = 2)
data(example_expr)
data(example_corr_mut)
mutgene <- sample(intersect(example_corr_mut$mut_entrez, rownames(example_expr)), 2)
nperm <- 5
res <- lapply(seq_len(nperm), function(x) corr_slp(example_expr,
                                                    example_corr_mut, mutgene = mutgene))
roc_thresh <- est_im(res)
plan(sequential)
```

example_compSLP

SLPs predicted by comp_slp

Description

SLPs predicted by comp_slp

Usage

```
data(example_compSLP)
```

Format

A data.table.

| | |
|------------------|---|
| example_comp_mut | <i>Patients mutations to be use in the comp_slp</i> |
|------------------|---|

Description

Mutations and related TCGA ids.

Usage

```
data(example_comp_mut)
```

Format

A data.table.

| | |
|-----------------|-----------------------------------|
| example_corrSLP | <i>SLPs predicted by corr_slp</i> |
|-----------------|-----------------------------------|

Description

SLPs predicted by corr_slp

Usage

```
data(example_corrSLP)
```

Format

A data.table.

| | |
|------------------|---|
| example_corr_mut | <i>Patients mutations to be use in the corr_slp</i> |
|------------------|---|

Description

Mutations and related TCGA ids.

Usage

```
data(example_corr_mut)
```

Format

A data.table.

| | |
|--------------|---|
| example_expr | <i>Expression data to be used in comp_slp</i> |
|--------------|---|

Description

Expresion matrix, genes by samples.

Usage

```
data(example_expr)
```

Format

A matrix.

| | |
|-----------|---|
| example_z | <i>Expression data to be used in corr_slp</i> |
|-----------|---|

Description

Z score matrix, genes by samples.

Usage

```
data(example_z)
```

Format

A matrix.

| | |
|--------|-------------------|
| genie3 | <i>Run GENIE3</i> |
|--------|-------------------|

Description

Calculate the weight matrix between genes via randomForest, modified from original codes by Huynh-Thu, V.A.

Usage

```
genie3(
  expr.matrix,
  ngene = NULL,
  K = "sqrt",
  nb.trees = 1000,
  input.idx = NULL,
  importance.measure = "IncNodePurity",
  trace = FALSE,
  ...
)
```

Arguments

| | |
|---------------------------------|---|
| <code>expr.matrix</code> | expression matrix (genes by samples). |
| <code>ngene</code> | an integer, only up to the first <code>ngene</code> (included) targets (responsible variables). |
| <code>K</code> | choice of number of input genes randomly, must be one of "sqrt", "all", an integer. |
| <code>nb.trees</code> | number of trees in ensemble for each target gene (default 1000). |
| <code>input.idx</code> | subset of genes used as input genes (default all genes). A vector of indices or gene names is accepted. |
| <code>importance.measure</code> | type of variable importance measure, "IncNodePurity" or "%IncMSE". |
| <code>trace</code> | index of currently computed gene is reported (default FALSE). |
| <code>...</code> | parameter to <code>randomForest</code> . |

Value

A weighted adjacency matrix of inferred network, element w_{ij} (row i , column j) gives the importance of the link from regulatory gene i to target gene j .

References

Huynh-Thu, V.A., Irrthum, A., Wehenkel, L., and Geurts, P. (2010). Inferring Regulatory Networks from Expression Data Using Tree-Based Methods. *PLoS ONE* 5, e12776.

Examples

```
#- Toy examples.
mtx <- matrix(sample(1000, 100), nrow = 5)
mtx <- rbind(mtx[1, ] * 2 + rnorm(20), mtx)
colnames(mtx) <- paste0("s_", seq_len(ncol(mtx)))
rownames(mtx) <- paste0("g_", seq_len(nrow(mtx)))
res <- genie3(mtx, nb.trees = 100)
```

| | |
|---------|--|
| getlink | <i>Get sorted list of regulatory links in GENIE3 results</i> |
|---------|--|

Description

Take genie3 output and sort the links.

Usage

```
getlink(weight.matrix, report.max = NULL)
```

Arguments

`weight.matrix` a weighted adjacency matrix as returned by `genie3`.
`report.max` maximum number of links to report (default all links).

Value

A data.table of links with columns "from.gene", "to.gene", "im".

Examples

```
mtx <- matrix(sample(1000, 100), nrow = 5)
mtx <- rbind(mtx[1, ] * 2 + rnorm(20), mtx)
colnames(mtx) <- paste0("s_", seq_len(ncol(mtx)))
rownames(mtx) <- paste0("g_", seq_len(nrow(mtx)))
res <- genie3(mtx, nb.trees = 10)
res_link <- getlink(res)
```

| | |
|-----------|-------------------|
| merge_slp | <i>Merge SLPs</i> |
|-----------|-------------------|

Description

Merge predicted SLPs from `comp_slp` and `corr_slp`.

Usage

```
merge_slp(comp_data, corr_data)
```

Arguments

`comp_data` predicted SLPs from [comp_slp](#).
`corr_data` predicted SLPs from [corr_slp](#).

Value

A data.table.

mut_entrez Entrez ids of mutations.

mut_symbol Gene symbols of mutations.

slp_entrez Entrez ids of SLPs.

slp_symbol Gene symbols of SLPs.

pvalue p_value from [RankProducts](#).

fdr "BH" adjusted pvalue via [p.adjust](#).

im The importance value returned by [genie3](#).

dualhit Whether the slp is identified by [corr_slp](#) and [comp_slp](#).

Examples

```
data("example_z")
data("example_comp_mut")
comp_res <- comp_slp(example_z, example_comp_mut)

data("example_expr")
data("example_corr_mut")
corr_res <- corr_slp(example_expr, example_corr_mut)

res <- merge_slp(comp_res, corr_res)
```

pp_tcga

Process tumour genomic data

Description

Preprocess mutation, cna, expression and zscore datasets in TCGA PanCancer Atlas by cBioPortal.

Usage

```
pp_tcga(  
  p_mut,  
  p_cna,  
  p_exprs,  
  p_score,  
  freq_thresh = 0.02,  
  expr_thresh = 10,  
  hypermut_thresh = 300  
)
```

Arguments

| | |
|-----------------|--|
| p_mut | path of mutation data, like "data_mutations_uniprot.txt" provided by cBioPortal. |
| p_cna | path of copy number variation data, like "data_CNA.txt". |
| p_exprs | path of normalized RNAseq expression data, like "data_RNA_Seq_v2_expression_median.txt". |
| p_score | path of zscore data, like "data_RNA_Seq_v2_mRNA_median_Zscores.txt". |
| freq_thresh | threshold to select recurrent mutations. |
| expr_thresh | threshold to remove low expression genes. |
| hypermut_thresh | threshold for hypermutations. |

Details

It is designed to process the TCGA data provided by cBioPortal. In mutation data, "Missense_Mutation", "Nonsense_Mutation", "Frame_Shift_Del", "Frame_Shift_Ins", "In_Frame_Del", "In_Frame_Ins", "Nonstop_Mutation" are selected for the downstream analysis. In CNA data, genes with GISTIC value equal to -2 are used. Patients with hypermutations are removed. Low expression genes, or genes that are not detected in any patient are filtered out.

Value

Return a list of mut_data, expr_data and zscore_data, while expr_data and zscore_data are matrix (entrez_id by patients), mut_data is a data.table with two columns of "patientid" and "mut_entrez".

References

Cerami et al. The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. *Cancer Discovery*. May 2012 2; 401. Gao et al. Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. *Sci. Signal*. 6, p11 (2013).

Examples

```
#- See vignette for more details.
if (FALSE) {
  P_mut <- "data_mutations_extended.txt"
  P_cna <- "data_CNA.txt"
  P_expr <- "data_RNA_Seq_v2_expression_median.txt"
  P_z <- "data_RNA_Seq_v2_mRNA_median_Zscores.txt"
  res <- pp_tcg(P_mut, P_cna, P_expr, P_z)
  saveRDS(res$mut_data, "mut_data.rds")
  saveRDS(res$expr_data, "expr_data.rds")
  saveRDS(res$zscore_data, "zscore_data.rds")
}
```

| | |
|---------|-------------------------------------|
| scr_slp | <i>Identify SLPs in screen hits</i> |
|---------|-------------------------------------|

Description

Identify whether screen hits are SLPs of mutations detected in both patients and cell lines, based on predicted SLPs in [corr_slp](#) and [comp_slp](#).

Usage

```
scr_slp(cell, screen_data, cell_mut, tumour_slp)
```

Arguments

| | |
|--------------------------|--|
| <code>cell</code> | a cell line. |
| <code>screen_data</code> | a data.table of genomic screen results with three columns, "screen_entrez", "screen_symbol" and "cell_line". |
| <code>cell_mut</code> | cell line mutation data. |
| <code>tumour_slp</code> | merged SLPs. |

Value

A data.table.

cell_line Name of cell lines.

screen_entrez Entrez ids of hits.

screen_symbol Gene symbols of hits.

mut_entrez Entrez ids of mutations.

mut_symbol Gene symbols of mutations.

is_slp Whether the targeted gene is a SLP.

pvalue p_value from [RankProducts](#).

fdr "BH" adjusted pvalue via [p.adjust](#).

im The importance value returned by [genie3](#).

dualhit Whether the slp is identified by [corr_slp](#) and [comp_slp](#).

Examples

```
require(future)
require(doFuture)
plan(multisession, workers = 2)
library(magrittr)
library(data.table)
data(example_compSLP)
data(example_corrSLP)
merged_res <- merge_slp(example_compSLP, example_corrSLP)
```

```
##- Toy hits data.
screen_1 <- merged_res[, .(slp_entrez, slp_symbol)] %>%
  unique %>%
  .[sample(nrow(.), round(.8 * nrow(.)))] %>%
  setnames(c(1, 2), c("screen_entrez", "screen_symbol")) %>%
  .[, cell_line := "cell_1"]

screen_2 <- merged_res[, .(slp_entrez, slp_symbol)] %>%
  unique %>%
  .[sample(nrow(.), round(.8 * nrow(.)))] %>%
  setnames(c(1, 2), c("screen_entrez", "screen_symbol")) %>%
  .[, cell_line := "cell_2"]

screen_hit <- rbind(screen_1, screen_2)

##- Toy mutations data.
mut_1 <- merged_res[, .(mut_entrez)] %>%
  unique %>%
  .[sample(nrow(.), round(.8 * nrow(.)))] %>%
  .[, cell_line := "cell_1"]

mut_2 <- merged_res[, .(mut_entrez)] %>%
  unique %>%
  .[sample(nrow(.), round(.8 * nrow(.)))] %>%
  .[, cell_line := "cell_2"]

mut_info <- rbind(mut_1, mut_2)

##- Hits that are identified as SLPs.
scr_res <- lapply(c("cell_1", "cell_2"), scr_slp, screen_hit, mut_info, merged_res)
scr_res[lengths(scr_res) == 0] <- NULL
scr_res <- rbindlist(scr_res)
plan(sequential)
```

Index

* datasets

- example_comp_mut, 7
- example_compSLP, 6
- example_corr_mut, 7
- example_corrSLP, 7
- example_expr, 8
- example_z, 8

comp_slp, 2, 3, 10, 11, 13
cons_slp, 3
corr_slp, 3, 4, 5, 10, 11, 13

est_im, 5
example_comp_mut, 7
example_compSLP, 6
example_corr_mut, 7
example_corrSLP, 7
example_expr, 8
example_z, 8

genie3, 5, 8, 11, 13
getlink, 10

merge_slp, 10

p.adjust, 3–5, 11, 13
pp_tcga, 2, 11

RankProducts, 3, 11, 13

scr_slp, 3, 13