Package 'mslp'

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Type Package

Title Predict synthetic lethal partners of tumour mutations

Version 1.14.0

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 builtd-in support for data from cBioPortal.
The primary SLPs correlating with muations 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 identfy consensus SLPs leads to reduced cell viability when perturbed.

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Author Chunxuan Shao [aut, cre]

Maintainer Chunxuan Shao <chunxuan@outlook.com>

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` *Identify SLPs via compensation*

Description

Identify SLPs compensating for the loss of function of mutations. The up-regulated SLPs are selected via the rank prodcuts 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 `pp_tcga`.
`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 postive 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 *Identify consensus SLPs*

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 signficance 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 condsidered as "TRUE" SLPs via the rank product algorithm. Then for each repetion, 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 *Patients mutations to be use in the comp_slp*

Description

Mutations and related TCGA ids.

Usage

```
data(example_comp_mut)
```

Format

A data.table.

example_corrSLP *SLPs predicted by corr_slp*

Description

SLPs predicted by corr_slp

Usage

```
data(example_corrSLP)
```

Format

A data.table.

example_corr_mut *Patients mutations to be use in the corr_slp*

Description

Mutations and related TCGA ids.

Usage

```
data(example_corr_mut)
```

Format

A data.table.

example_expr *Expression data to be used in comp_slp*

Description

Expresion matrix, genes by samples.

Usage

```
data(example_expr)
```

Format

A matrix.

example_z *Expression data to be used in corr_slp*

Description

Z score matrix, genes by samples.

Usage

```
data(example_z)
```

Format

A matrix.

genie3 *Run GENIE3*

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

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

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 *Get sorted list of regulatory links in GENIE3 results*

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 *Merge SLPs*

Description

Merge predcted 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 datsets 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 muation 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 hpyermutations.

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, pl1 (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_tcga(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 *Identify SLPs in screen hits*

Description

Identify whether screen hits are SLPs of mutations deteced 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

cell	a cell line.
screen_data	a data.table of genomic screen results with three columns, "screen_entrez", "screen_symbol" and "cell_line".
cell_mut	cell line mutation data.
tumour_slp	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