Package: PANACEA (via r-universe)

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Title Personalized Network-Based Anti-Cancer Therapy Evaluation

Version 1.0.1.9000

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Description Identification of the most appropriate pharmacotherapy for each patient based on genomic alterations is a major challenge in personalized oncology. 'PANACEA' is a collection of personalized anti-cancer drug prioritization approaches utilizing network methods. The methods utilize personalized ``driverness'' scores from 'driveR' to rank drugs, mapping these onto a protein-protein interaction network. The ``distance-based'' method scores each drug based on these scores and distances between drugs and genes to rank given drugs. The ``RWR'' method propagates these scores via a random-walk with restart framework to rank the drugs. The methods are described in detail in Ulgen E, Ozisik O, Sezerman OU. 2023. PANACEA: network-based methods for pharmacotherapy prioritization in personalized oncology. Bioinformatics <doi:10.1093/bioinformatics/btad022>.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

URL https://github.com/egeulgen/PANACEA, https://egeulgen.github.io/PANACEA/

BugReports https://github.com/egeulgen/PANACEA/issues

Imports org.Hs.eg.db, DBI, igraph, reshape2

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Repository https://egeulgen.r-universe.dev

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Contents

`add_drugs_as_nodes` *Add Drugs as Nodes*

Description

Add Drugs as Nodes

Usage

```
add_drugs_as_nodes(W_mat, drug_target_interactions, edge_weight = 1000)
```

Arguments

`W_mat`	adjacency matrix for the chosen PIN
`drug_target_interactions`	data frame containing (processed) drugs and target genes
`edge_weight`	edge weight for drug-target gene interaction (default = 1000)

Value

adjacency matrix with the drugs added as nodes

`adj_list2mat` *Turn Adjacency List into Adjacency Matrix*

Description

Turn Adjacency List into Adjacency Matrix

Usage

```
adj_list2mat(adj_list)
```

Arguments

`adj_list`	Adjacency list

Value

Adjacency matrix

`convert2alias` *Convert Input Gene Symbols to Alias*

Description

Convert Input Gene Symbols to Alias

Usage

```
convert2alias(input_genes, target_genes)
```

Arguments

`input_genes`	vector of input genes
`target_genes`	vector of target genes

Value

vector of converted gene symbols (if any alias in target genes)

DGIdb_interactions_df *DGIdb Interactions Expert-curated Sources*

Description

Data frame containing drug-gene interactions from expert-curated sources (CancerCommons, CGI, ChemblInteractions, CIViC, ClearityFoundationBiomarkers, ClearityFoundationClinicalTrial, COSMIC, DoCM, MyCancerGenome, MyCancerGenomeClinicalTrial, TALC, TdgClinicalTrial, TEND) from DGIdb.

Usage

```
DGIdb_interactions_df
```

Format

a data frame containing 11323 rows and 2 variables:

drug_name Drug name

gene_name HGNC gene symbol for the interacting gene

example_driveR_res *Example driveR Result*

Description

Data frame containing 'driveR' results for a lung adenocarcinoma case.

Usage

```
example_driveR_res
```

Format

a data frame containing 106 rows and 3 variables:

gene_symbol HGNC gene symbol

driverness_prob 'driverness' probability

prediction driveR's prediction for whether the gene is a 'driver' or 'non-driver'

example_scores_dist *Example PANACEA "distance-based" Method Result*

Description

Vector containing 'PANACEA' "distance-based" results for a lung adenocarcinoma case. Names are drug names, values are scores

Usage

```
example_scores_dist
```

Format

named vector of 1423 values

example_scores_RWR *Example PANACEA "RWR" Method Result*

Description

Vector containing 'PANACEA' "RWR" results for a lung adenocarcinoma case. Names are drug names, values are scores

Usage

```
example_scores_RWR
```

Format

named vector of 1423 values

Laplacian.norm *Graph Laplacian Normalization*

Description

Graph Laplacian Normalization

Usage

```
Laplacian.norm(W)
```

Arguments

W	square symmetric adjacency matrix

Value

normalized adjacency matrix

`network_propagation` *Network Propagation (Random-walk with Restart)*

Description

Network Propagation (Random-walk with Restart)

Usage

```
network_propagation(prior_vec, W_prime, alpha, max.iter = 1000, eps = 1e-04)
```

Arguments

prior_vec	vector of prior knowledge on selected genes (names are gene symbols)
W_prime	(Laplacian-normalized, symmetric) adjacency matrix
alpha	restart parameter, controlling trade-off between prior information and network smoothing
max.iter	maximum allowed number of iterations (default = 1000)
eps	epsilon value to assess the L2 norm of the difference between iterations (default = 1e-4)

Details

Implementing RWR following the following publications: Cowen L, Ideker T, Raphael BJ, Sharan R. Network propagation: a universal amplifier of genetic associations. Nat Rev Genet. 2017 Sep;18(9):551–62. Shnaps O, Perry E, Silverbush D, Sharan R. Inference of personalized drug targets via network propagation. Pac Symp Biocomput. 2016;21:156–67.

Value

vector of propagation values

PANACEA *PANACEA: Personalized Network-based Anti-Cancer Therapy Evaluation*

Description

Identification of the most appropriate pharmacotherapy for each patient based on genomic alterations is a major challenge in personalized oncology. PANACEA is a collection of personalized anticancer drug prioritization approaches utilizing network methods. The methods utilize personalized "driverness" scores from 'driveR' to rank drugs, mapping these onto a protein-protein interaction network (PIN). The "distance-based" method scores each drug based on these scores and distances between drugs and genes to rank given drugs. The "RWR" method propagates these scores via a random-walk with restart framework to rank the drugs.

Author(s)

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See Also

score_drugs for the wrapper function for scoring of drugs via network-based methods

process_drug_target_interactions *Process Drug-Target Interactions*

Description

Process Drug-Target Interactions

Usage

```
process_drug_target_interactions(
  drug_target_interactions,
  PIN_genes,
  drug_name_col = "drug_name",
  target_col = "gene_name"
)
```

Arguments

drug_target_interactions	data frame containing drugs and target genes
PIN_genes	gene symbols for the chosen PIN
drug_name_col	name of the column containing drug names (default = "drug_name")
target_col	name of the column containing drug targets (default = "converted_target_gene")

Value

processed drug-target interactions. Processing involves converting symbols missing in the PIN, merging drugs that have the same target gene(s)

`score_drugs` *Scoring of Drugs via Network-based Methods*

Description

Scoring of Drugs via Network-based Methods

Usage

```
score_drugs(driveR_res, drug_interactions_df, W_mat, method, ...)
```

Arguments

`driveR_res`	data frame of driveR results
`drug_interactions_df`	data frame of drug-gene interactions
`W_mat`	adjacency matrix for the PIN
`method`	scoring method (one of 'distance-based' or 'RWR')
`...`	additional arguments for `score_drugs_distance_based` or `score_drugs_RWR_based`

Details

This is the wrapper function for the two proposed methods for personalized scoring of drugs for individual cancer samples via network-based methods. The available methods are 'distance-based' and 'RWR'. For the 'distance-based' method, the score between a gene (g) and drug (d) is formulated as:

$$score(g, d) = driver(g)/(d(g, d) + 1)^2$$

where driver(g) is the driverness probability of gene g, as predicted by 'driveR' and d(g, d) is the distance withing the PIN between gene g and drug d. The final score of the drug d is then the average of the scores between each altered gene and d:

$$score(d) = \Sigma score(g, d)/|genes|$$

For the 'RWR' method, a random-walk with restart framework is used to propagate the driverness probabilities.

By default `DGIdb_interactions_df` is used as the `drug_interactions_df`.

If the `W_mat` argument is not supplied, the built-in STRNG data `STRING_adj_df` is used to generate `W_mat`.

Value

vector of scores per drug.

Examples

```
toy_data <- data.frame(
  gene_symbol = c("TP53", "EGFR", "KDR", "ATM"),
  driverness_prob = c(0.94, 0.92, 0.84, 0.72)
)
toy_interactions <- DGIdb_interactions_df[1:25, ]
res <- score_drugs(
  driveR_res = toy_data,
  drug_interactions_df = toy_interactions, # leave blank for default
  W_mat = toy_W_mat, # leave blank for default
  method = "distance-based",
  verbose = FALSE
)
```

---

score_drugs_distance_based

Distance-based Scoring of Drugs

Description

Distance-based Scoring of Drugs

Usage

```
score_drugs_distance_based(
  driveR_res,
  drug_interactions_df,
  W_mat,
  driver_prob_cutoff = 0.05,
  drug_name_col = "drug_name",
  target_col = "gene_name",
  verbose = TRUE
)
```

Arguments

driveR_res	data frame of driveR results
drug_interactions_df	data frame of drug-gene interactions
W_mat	adjacency matrix for the PIN
driver_prob_cutoff	cut-off value for 'driverness_prob' (default = 0.05)
drug_name_col	for 'drug_interactions_df', the column name containing drug names/identifiers
target_col	for 'drug_interactions_df', the column name containing target gene symbols
verbose	boolean to control verbosity (default = TRUE)

Value

vector of scores per drug. Drugs with the same target gene(s) are merged (via process_drug_target_interactions)

Examples

```
toy_data <- data.frame(
  gene_symbol = c("TP53", "EGFR", "KDR", "ATM"),
  driverness_prob = c(0.94, 0.92, 0.84, 0.72)
)
toy_interactions <- DGIdb_interactions_df[1:100, ]
res <- score_drugs_distance_based(
  driveR_res = toy_data,
  drug_interactions_df = toy_interactions,
  W_mat = toy_W_mat, verbose = FALSE
)
```

---

score_drugs_RWR_based *RWR-based Scoring of Drugs*

Description

RWR-based Scoring of Drugs

Usage

```
score_drugs_RWR_based(
  driveR_res,
  drug_interactions_df,
  W_mat,
  alpha = 0.05,
  max.iter = 1000,
  eps = 1e-04,
  drug_name_col = "drug_name",
  target_col = "gene_name",
  verbose = TRUE
)
```

Arguments

driveR_res	data frame of driveR results
drug_interactions_df	data frame of drug-gene interactions
W_mat	adjacency matrix for the PIN
alpha	restart parameter, controlling trade-off between prior information and network smoothing
max.iter	maximum allowed number of iterations (default = 1000)

eps	epsilon value to assess the L2 norm of the difference between iterations (default = 1e-4)
drug_name_col	for 'drug_interactions_df', the column name containing drug names/identifiers
target_col	for 'drug_interactions_df', the column name containing target gene symbols
verbose	boolean to control verbosity (default = TRUE)

Value

vector of scores per drug. Drugs with the same target gene(s) are merged (via process_drug_target_interactions)

Examples

```
toy_data <- data.frame(
  gene_symbol = c("TP53", "EGFR", "KDR", "ATM"),
  driverness_prob = c(0.94, 0.92, 0.84, 0.72)
)
toy_interactions <- DGIdb_interactions_df[1:100, ]
res <- score_drugs_RWR_based(
  driveR_res = toy_data,
  drug_interactions_df = toy_interactions,
  W_mat = toy_W_mat, verbose = FALSE
)
```

STRING_adj_df *Adjacency List for STRING v11.5 - High Confidence Interactions*

Description

Data frame of adjacency list for STRING v11.5 interactions with combined score > 700 (high confidence)

Usage

```
STRING_adj_df
```

Format

a data frame with 887797 rows and 3 variables:

protein1 Interactor 1

protein2 Interactor 2

value edge weight(combined score)

`toy_W_mat` *Toy Adjacency Matrix (for examples)*

Description

Symmetric matrix containing example adjacency data

Usage

```
toy_W_mat
```

Format

matrix of 84 rows and 84 columns

Index