Package 'PANACEA'

August 19, 2023

Title Personalized Network-Based Anti-Cancer Therapy Evaluation

Version 1.0.1

Maintainer Ege Ulgen <egeulgen@gmail.com>

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>.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.2.3

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

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

biocViews

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

Suggests rmarkdown, knitr, testthat (>= 3.0.0), covr

Config/testthat/edition 3

Depends R (>= 4.0)

LazyData true

LazyDataCompression xz

VignetteBuilder knitr

NeedsCompilation yes

R topics documented:

---

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, COS-MIC, 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 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 (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)

Maintainer: Ege Ulgen <egeulgen@gmail.com> (ORCID) [copyright holder]

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