

Package ‘DriverNet’

September 17, 2025

Type Package

Title Drivernet: uncovering somatic driver mutations modulating transcriptional networks in cancer

Version 1.48.0

Date 2012-03-21

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Description DriverNet is a package to predict functional important driver genes in cancer by integrating genome data (mutation and copy number variation data) and transcriptome data (gene expression data). The different kinds of data are combined by an influence graph, which is a gene-gene interaction network deduced from pathway data. A greedy algorithm is used to find the possible driver genes, which may mutated in a larger number of patients and these mutations will push the gene expression values of the connected genes to some extreme values.

License GPL-3

LazyLoad yes

Depends R (>= 2.10), methods

biocViews Network

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

git_branch RELEASE_3_21

git_last_commit b361a0d

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-09-17

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DriverNet-package	<i>Drivernet: uncovering somatic driver mutations modulating transcriptional networks in cancer</i>
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Description

Description: DriverNet is a package to predict functional important driver genes in cancer by integrating genome data (mutation and copy number variation data) and transcriptome data (gene expression data). The different kinds of data are combined by an influence graph, which is a gene-gene interaction network deduced from pathway data. A greedy algorithm is used to find the possible driver genes, which may mutated in a larger number of patients and these mutations will push the gene expression values of the connected genes to some extreme values.

Details

Package:	DriverNet
Type:	Package
Version:	1.0.0
Date:	2012-03-21
License:	GPL-3
LazyLoad:	yes
Depends:	methods

Users would call preprocess_matrices on the three matrices to remove unnecessary data. The matrices returned are then be passed to other functions.

Author(s)

Ali Bashashati, Reza Haffari, Jiarui Ding, Gavin Ha, Kenneth Liu, Jamie Rosner and Sohrab Shah

Maintainer: Jiarui Ding <jiaruid@cs.ubc.ca>

References

Drivernet: uncovering somatic driver mutations modulating transcriptional networks in cancer, submitted.

Examples

```
data(samplePatientMutationMatrix)
data(samplePatientOutlierMatrix)
data(sampleInfluenceGraph)
data(sampleGeneNames)

driversList = computeDrivers(samplePatientMutationMatrix, samplePatientOutlierMatrix,
sampleInfluenceGraph, outputFolder=NULL, printToConsole=FALSE)

drivers(driversList)[1:10]

randomDriversResult = computeRandomizedResult(patMutMatrix=samplePatientMutationMatrix,
patOutMatrix=samplePatientOutlierMatrix, influenceGraph=sampleInfluenceGraph,
geneNameList= sampleGeneNames, outputFolder=NULL, printToConsole=FALSE,
numberOfRandomTests=20, weight=FALSE, perturbGraph=FALSE, perturbData=TRUE)

res = resultSummary(driversList, randomDriversResult, samplePatientMutationMatrix,
sampleInfluenceGraph, outputFolder=NULL, printToConsole=FALSE)
```

actualEvents

Actual events covered by driver mutations

Description

It gives a detailed list of events covered by the driver mutations selected by DriverNet.

Usage

```
actualEvents(x)
```

Arguments

x

See Also

computeDrivers DriverNetResult-class

Examples

```
data(sampleDriversList)
actualEvents(sampleDriversList)
```

computeDrivers	<i>Compute a list of driver mutations</i>
----------------	---

Description

Use a greedy algorithm to rank a list of driver mutations.

Usage

```
computeDrivers(patMutMatrix, patOutMatrix, influenceGraph, outputFolder = NULL,
printToConsole = FALSE, weighted = FALSE)
```

Arguments

patMutMatrix	Patient Mutation Matrix
patOutMatrix	Patient Outlier Matrix
influenceGraph	Influence Graph Matrix
outputFolder	The folder to store the log. If set to NULL, no log files will be written. If set to "", the log will be written to the current folder.
printToConsole	If set to TRUE, progress and result of the function will be printed to the console.
weighted	Must be set to FALSE in this version.

Value

An object of DriverNetResult class that can be passed to the resultSummary method.

Author(s)

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Examples

```
data(samplePatientMutationMatrix)
data(samplePatientOutlierMatrix)
data(sampleInfluenceGraph)
driversList = computeDrivers(samplePatientMutationMatrix, samplePatientOutlierMatrix,
sampleInfluenceGraph, outputFolder=NULL, printToConsole=FALSE)

drivers(driversList)[1:10]
```

`computeRandomizedResult`*Randomly compute lists of driver mutations*

Description

It renames the mutations in `patMutMatrix` with a randomized list of gene names and computes a list of driver mutations. It will repeat this process by `numberOfRandomTests` times. The result could be passed to the `resultSummary` method to calculate p-value for the driver mutations.

Usage

```
computeRandomizedResult(patMutMatrix, patOutMatrix, influenceGraph,  
geneNameList, outputFolder = NULL, printToConsole = FALSE,  
numberOfRandomTests = 500, weighted = FALSE, perturbGraph = FALSE,  
perturbData = TRUE)
```

Arguments

<code>patMutMatrix</code>	Patient Mutation Matrix
<code>patOutMatrix</code>	Patient Expression(Outlier) Matrix
<code>influenceGraph</code>	Influence Graph Matrix
<code>geneNameList</code>	A list of gene names that the new mutation names will be randomly chosen from.
<code>outputFolder</code>	The folder to store the log. If set to <code>NULL</code> , no log files will be written. If set to <code>""</code> , the log will be written to the current folder.
<code>printToConsole</code>	If set to <code>TRUE</code> , progress and result of the function will be printed to the console.
<code>numberOfRandomTests</code>	Number of lists of randomized driver mutations to be generated.
<code>weighted</code>	Must be set to <code>FALSE</code> in this version.
<code>perturbGraph</code>	Must be set to <code>FALSE</code> in this version.
<code>perturbData</code>	Must be set to <code>TRUE</code> in this version.

Value

A list of numeric vectors where each vector stores the number of events covered by the randomly identified drivers. The list can be passed to the `resultSummary` method to compute p-values.

Author(s)

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Examples

```
data(samplePatientMutationMatrix)
data(samplePatientOutlierMatrix)
data(sampleInfluenceGraph)
data(sampleGeneNames)

randomDriversResult = computeRandomizedResult(patMutMatrix=samplePatientMutationMatrix,
patOutMatrix=samplePatientOutlierMatrix, influenceGraph=sampleInfluenceGraph,
geneNameList=sampleGeneNames, outputFolder=NULL, printToConsole=FALSE,
numberOfRandomTests=20, weight=FALSE, perturbGraph=FALSE, perturbData=TRUE)
```

DriverNetResult-class *Class "DriverNetResult"*

Description

A class storing the result from running the `computeDrivers` function. It contains the list of driver mutations found, the detailed events covered by these drivers and the total number of events in the test data.

Objects from the Class

Objects can be created by calls of the form `new("DriverNetResult", drivers=..., actualEvents=..., totalEvents=...)`.

Slots

drivers: Object of class "character" ~~
actualEvents: Object of class "list" ~~
totalEvents: Object of class "numeric" ~~

Methods

actualEvents signature(x = "DriverNetResult"): ...
drivers signature(x = "DriverNetResult"): ...
totalEvents signature(x = "DriverNetResult"): ...

Author(s)

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See Also

[computeDrivers](#)

Examples

```
data(sampleDriversList)
drivers(sampleDriversList)[1:10]
```

drivers

List of driver mutations identified by DriverNet

Description

It gives the list of driver mutations identified by DriverNet ranked by the number of events that they cover.

Usage

```
drivers(x)
```

Arguments

x

See Also

computeDrivers DriverNetResult-class

Examples

```
data(sampleDriversList)
actualEvents(sampleDriversList)
```

getPatientOutlierMatrix

Compute the patient outlier matrix

Description

Given a real-value patient expression matrix, compute the patient outlier matrix and remove the genes which are not expressed.

Usage

```
getPatientOutlierMatrix(patExpMatrix, th=2)
```

Arguments

patExpMatrix	Patient Expression Matrix
th	The threshold, the default value is 2 (the gene expression values outside the 2 standard deviation range are considered as outliers).

Value

The output patOutMatrix is an input to the computeDrivers method

Author(s)

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See Also

computeDrivers

Examples

```
data(samplePatientExpressionMatrix)
samplePatientOutlierMatrix = getPatientOutlierMatrix(samplePatientExpressionMatrix)
```

preprocessMatrices	<i>Remove unnecessary entries from matrices</i>
--------------------	---

Description

Remove patients (rows) which are not in both matrices from patMutMatrix and patOutMatrix. Remove mutations (columns) from patMutMatrix if they are not a row of influenceGraph. Remove expressions (columns) from patOutMatrix if they are not a column of influenceGraph.

Usage

```
preprocessMatrices(patMutMatrix, patOutMatrix, influenceGraph)
```

Arguments

patMutMatrix	Patient Mutation Matrix
patOutMatrix	Patient Outlier Matrix
influenceGraph	Influence Graph Matrix

Value

1	Reduced version of Patient Mutation Matrix
2	Reduced version of Patient Expression(Outlier) Matrix
3	Influence Graph Matrix

Note

The dimension of influenceGraph is not changed.

Author(s)

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Examples

```
data(samplePatientMutationMatrix)
data(samplePatientOutlierMatrix)
data(sampleInfluenceGraph)
tmp = preprocessMatrices(samplePatientMutationMatrix, samplePatientOutlierMatrix,
sampleInfluenceGraph)

smallerPatientMutationMatrix = tmp[[1]]
smallerPatientOutlierMatrix = tmp[[2]]
influenceGraph = tmp[[3]]
```

resultSummary	<i>Summarize result for drivers ranking.</i>
---------------	--

Description

Ranks the drivers.

Usage

```
resultSummary(mainResult, randResult, patMutMatrix, influenceGraph,
outputFolder = NULL, printToConsole = FALSE)
```

Arguments

mainResult	An object of DriverNetResult class created by the computeDrivers method.
randResult	A list of vectors representing driver coverage generated by computeRandomizedResult.
patMutMatrix	Patient Mutation Matrix
influenceGraph	Influence Graph Matrix
outputFolder	The folder to store the summary file. If set to NULL, no files will be written. If set to "", the files will be written to the current folder.
printToConsole	If set to TRUE, progress and result of the function will be printed to the console.

Value

A matrix storing the summary result.

Author(s)

Ali Bashashati, Reza Haffari, Jiarui Ding, Gavin Ha, Kenneth Liu, Jamie Rosner and Sohrab Shah
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Examples

```
data(sampleDriversList)
data(sampleRandomDriversResult)
data(samplePatientMutationMatrix)
data(sampleInfluenceGraph)
res = resultSummary(sampleDriversList, sampleRandomDriversResult,
samplePatientMutationMatrix, sampleInfluenceGraph, outputFolder=NULL,
printToConsole=FALSE)
```

sampleDriversList	<i>Sample DriverNet result</i>
-------------------	--------------------------------

Description

An object of DriverNetResult class that obtained from running the codecomputeDrivers function.

Usage

```
data(sampleDriversList)
```

Format

Formal class ‘DriverNetResult’ with 3 slots (1) @ drivers: a character vector of the driver gene name; (2) @ actualEvents: the covered events in each mutated patient; (3) @totalEvents: the total number of outliers

See Also

```
computeDrivers
```

Examples

```
data(sampleDriversList)

drivers(sampleDriversList)[1:10]
```

sampleGeneNames	<i>Sample gene names</i>
-----------------	--------------------------

Description

A list of gene names used to generate permutation of names in computeRandomizedResult method.

Usage

```
data(sampleGeneNames)
```

Format

A factor of gene names

Examples

```
data(sampleGeneNames)
```

sampleInfluenceGraph	<i>Sample influence graph</i>
----------------------	-------------------------------

Description

A binary matrix representing influence graph between genes.

Usage

```
data(sampleInfluenceGraph)
```

Format

A two-dimensional binary matrix. The row and column names are gene names. If two genes i and j are in the same pathway, $\text{sampleInfluenceGraph}[i, j] = 1$.

Examples

```
data(sampleInfluenceGraph)
```

samplePatientExpressionMatrix	<i>Sample patient expression matrix</i>
-------------------------------	---

Description

A real-value matrix representing gene expressions in patients.

Usage

```
data(samplePatientExpressionMatrix)
```

Format

A two-dimensional real value matrix. The row names are patients, and column names are genes. The entry $\text{samplePatientExpressionMatrix}[i, j]$ is the gene expression values of gene j in patient i .

Examples

```
data(samplePatientExpressionMatrix)
```

```
samplePatientMutationMatrix
```

Sample patient mutation matrix

Description

A binary matrix representing gene mutations in patients.

Usage

```
data(samplePatientMutationMatrix)
```

Format

A two-dimensional binary matrix. The row names are patients, and column names are genes. If gene j is mutated in patient i , `samplePatientMutationMatrix[i, j]=1`.

Examples

```
data(samplePatientMutationMatrix)
```

```
samplePatientOutlierMatrix
```

Sample patient outlier matrix

Description

A binary matrix representing gene expressions in patients.

Usage

```
data(samplePatientOutlierMatrix)
```

Format

A two-dimensional binary matrix. The row names are patients, and column names are genes. If genes j is an outlier in patient i , `samplePatientOutlierMatrix[i, j] = 1`.

Examples

```
data(samplePatientOutlierMatrix)
```

sampleRandomDriversResult	
	<i>Sample Result from computeRandomizedResult</i>

Description

A sample result from running computeRandomizedResult with numberOfRandomTests = 20.

Usage

data(sampleRandomDriversResult)

Format

A list of predicted drivers from different runs.

See Also

computeRandomizedResult

Examples

data(sampleRandomDriversResult)

totalEvents	<i>Total number of events in the data</i>
-------------	---

Description

Total number of events in the data

Usage

totalEvents(x)

Arguments

x

See Also

computeDrivers DriverNetResult-class

Examples

data(sampleDriversList)
totalEvents(sampleDriversList)

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