Package ‘DriverNet’

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Type Package

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

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

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

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

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biocViews Network

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DriverNet-package

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.

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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


Examples

data(samplePatientMutationMatrix)
data(samplePatientOutlierMatrix)
actualEvents 3

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  Compute a list of driver mutations

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

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

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)

Ali Bashashati, Reza Haffari, Jiarui Ding, Gavin Ha, Kenneth Liu, Jamie Rosner and Sohrab Shah
Maintainer: Jiarui Ding <jiaruid@cs.ubc.ca>

Examples

data(samplePatientMutationMatrix)
data(samplePatientOutlierMatrix)
data(sampleInfluenceGraph)
driversList = computeDrivers(samplePatientMutationMatrix, samplePatientOutlierMatrix, sampleInfluenceGraph, outputFolder=NULL, printToConsole=FALSE)
drivers(driversList)[1:10]

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

- **patMutMatrix**: Patient Mutation Matrix
- **patOutMatrix**: Patient Expression(Outlier) Matrix
- **influenceGraph**: Influence Graph Matrix
- **geneNameList**: A list of gene names that the new mutation names will be randomly chosen from.
- **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.
- **numberOfRandomTests**: Number of lists of randomized driver mutations to be generated.
- **weighted**: Must be set to FALSE in this version.
- **purturbGraph**: Must be set to FALSE in this version.
- **purturbData**: Must be set to TRUE 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)

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

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

Examples

```r
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, purturbGraph=FALSE, purturbData=TRUE)
```

DriverNetResult-class

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

See Also

- `computeDrivers`

Examples

```r
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

```r
data(sampleDriversList)
drivers(sampleDriversList)
drivers(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**
```r
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)**
Ali Bashashati, Reza Haffari, Jiarui Ding, Gavin Ha, Kenneth Liu, Jamie Rosner and Sohrab Shah

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

**See Also**
- `computeDrivers`

**Examples**
```r
data(samplePatientExpressionMatrix)
samplePatientOutlierMatrix = getPatientOutlierMatrix(samplePatientExpressionMatrix)
```

---

preprocessMatrices

*Remove unnecessary entries from matrices*

**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**
```r
preprocessMatrices(patMutMatrix, patOutMatrix, influenceGraph)
```
resultSummary

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)

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

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

Examples

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

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

resultSummary

Summarize result for drivers ranking.

Description

Ranks the drivers.

Usage

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

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

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

Examples

data(sampleDriversList)
data(sampleRandomDriversResult)
data(samplePatientMutationMatrix)
data(sampleInfluenceGraph)

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

---

**sampleDriversList**  
*Sample DriverNet result*

Description

An object of DriverNetResult class that obtained from running the computeDrivers 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
**sampleGeneNames**

*Sample gene names*

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

**Usage**

```r
data(sampleGeneNames)
```

**Format**

A factor of gene names

**Examples**

```r
data(sampleGeneNames)
```

---

**sampleInfluenceGraph**

*Sample influence graph*

A binary matrix representing influence graph between genes.

**Usage**

```r
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, `sampleInfluenceGraph[i, j] = 1`.

**Examples**

```r
data(sampleInfluenceGraph)
```
samplePatientExpressionMatrix

*Sample patient expression matrix*

**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 `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**

```r
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**

```r
data(samplePatientOutlierMatrix)
```

---

**sampleRandomDriversResult**  
*Sample Result from computeRandomizedResult*

**Description**

A sample result from running `computeRandomizedResult` with `numberOfRandomTests = 20`.

**Usage**

```r
data(sampleRandomDriversResult)
```

**Format**

A list of predicted drivers from different runs.

**See Also**

`computeRandomizedResult`

**Examples**

```r
data(sampleRandomDriversResult)
```
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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