

# Package ‘CNA2Subpathway’

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**Type** Package

**Title** Identification of Dysregulated Subpathway Driven by Copy Number Aberration

**Version** 0.1.0

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**Description** Identification of dysregulated subpathway driven by Copy Number Aberrations(CNA).We first integrated CNA and gene expression data to calculate CNADEscore for each gene in cancer.Secondly,we construct a subpathway network based on the biological function relationship between subpathways,and the weight of this network regulated by the CNADEscore.Finally,we use an eigenvector centrality measure to determine the significance of a subpathway,and the statistical significance of these subpathways is assessed using a bootstrap-based randomization method.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 2.10)

**RoxygenNote** 7.0.2

**Imports** igraph,  
discover,  
graphics

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

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CNA2Subpathway-package	CNA2Subpathway
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**Description**

Identification of dysregulated subpathway driven by Copy Number Aberration.

**Details**

Identification of dysregulated subpathway driven by Copy Number Aberration.

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envData	<i>The variables in the environment include an copy number variation data, amplified genes,deleted genes, an example expression profile, A matrix of subpathway infomation, Biological functions data, Jac-card coefficient of the network point, Overlapping genes of the network point, A list of subpathway map infomation, A binary matrix of CNA profile, A matric of CNADEscore, Optimized subpathway, and the sta-tistical significance p value and FDR for these optimal subpathways</i>
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**Description**

Identification of dysregulated subpathways driven by Copy Number aberrations(CNA). We firstly calculate the CNADEscore by copy number aberration and gene expression. Secondly, we constructing subpathways network that implicitly links subpathways through their common function and weight of the network based on the CNADEscore. Finally, we calculate an eigenvector centrality and the statistical significance of these subpathways is assessed using a bootstrap-based ran-domization method.

**Format**

An environment variable

**Details**

The environment variable includes the variable ampGene, delGene,CNAlabelresult,GEP,CNAP,GoInfo,SubPathwayInfo

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getCNADEscore	<i>getCNADEscore</i>
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### Description

The function `getCNADEscore` used calculate the CNADEscore. The CNADEscore is defined as differentially expressed genes driven by CNA. We used the Student's t-test to calculate the t scores with the CNA label, and standardized them to a normal distribution with a mean of 0 and an SD of 1.

### Usage

```
getCNADEscore(inexpData, CNALabel)
```

### Arguments

<code>inexpData</code>	Gene Expression profile(GEP)
<code>CNALabel</code>	The CNA label (the result of function <code>getCNALabel</code> )

### Value

A matrix of the Student's t-test result and CNADEscore

### Examples

```
# obtain GEP data
GEP<-GetExampleData("GEP")
# obtain the result of getCNALabel function
CNALabelresult<-GetExampleData("CNALabelresult")
# Calculate the CNA-DEscore
CNADEscore<-getCNADEscore(GEP,CNALabelresult)
# view first the ten gene CNA-DEscore
head(CNADEscore[1:10,])
```

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getCNALabel	<i>getCNALabel</i>
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### Description

The function `getCNALabel` used to discretize the CNA profile to a binary matrix.

### Usage

```
getCNALabel(CNAprofile, ampGene, delGene)
```

### Arguments

<code>CNAprofile</code>	Copy Number Alteration profile
<code>ampGene</code>	A vector of strings, the gene symbol of amplified genes
<code>delGene</code>	A vector of strings, the gene symbol of deleted genes

Value

A binary matrix

Examples

```
# obtain Copy number variation profile data
CNAP<-GetExampleData("CNAP")
head(CNAP[1:10,1:10])
# obtion amplified genes
ampGene<-GetExampleData("ampGene")
# obtion deleted genes
delGene<-GetExampleData("delGene")
# Obtin the CNA label.
CNAlabelresult<-getCNAlabel(CNAP,ampGene,delGene)
# get the result of the getCNAlabel function
CNAlabelresult<-GetExampleData("CNAlabelresult")
# view first ten genes and ten sample of the label
head(CNAlabelresult[1:10,1:10])
```

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GetExampleData	<i>GetExampleData</i>
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Description

Get the example data of test package for litte trials

Usage

```
GetExampleData(exampleData)
```

Arguments

exampleData      Acharacter,shouldbeoneof"ampGene","delGene","GEP","CNAP", "SubPathway-Info","GoInfo","GoSubPconGene","Jaccardscore","SubPathwaymapdata","CNAlabelresult","CNAlabelresult","CNA2Subpathwayresult".

Value

data

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IDSubPath	<i>IDSubPath</i>
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Description

The function IDSubPath used to find significant dysregulate subpathways by the IDSCNA method. According our method, in this function, the user need input 6 variable. Four of six variable can obtain from our example data, those data from KEGG and GO, and the user can change at will also. The "CNADEscore" variable is result of function getCNADEscore. And the last variable is nperm, that representative number of disturbances, usually nperm = 1000 or bigger as statistically significant.

**Usage**

```
IDSubPath(CNADEscore, nperm, Subpathway, Go, Jaccard, Go_SubPath_gene)
```

**Arguments**

CNADEscore	The CNA-DEscore of genes.
nperm	input Number of disturbance(>=1000).
Subpathway	Subpathway information from SuupathwayMiner.
Go	Biological functions data from Gene Ontology.
Jaccard	Jaccard score shared by a sub-pathway with biological function. Used to optimization.
Go_SubPath_gene	Genes symble shared by a sub-pathway with biological function. Used to optimization.

**Value**

Optimized subpathway, and the statistical significance p value and FDR for these optimal subpathways

**Examples**

```
# load depend package
require(igraph)
# obtain subpathway data
SubPathwayInfo<-GetExampleData("SubPathwayInfo")
# obtain biological functions data
GoInfo<-GetExampleData("GoInfo")
# obtain some genes shared by a sub-pathway with biological function
GoSubPconGene<-GetExampleData("GoSubPconGene")
# obtain Jaccardscore shared by a sub-pathway with biological function
Jaccardscore<-GetExampleData("Jaccardscore")
# obtain the result of getDEGscore function
CNADEscore<-GetExampleData("CNADEscore")
# run the IDSubPath function
#CNA2Subpathwayresult<-IDSubPath(CNADEscore,nperm=100,
#                               Subpathway=SubPathwayInfo,Go=GoInfo,
#                               Jaccard=Jaccardscore,Go_SubPath_gene=GoSubPconGene)
# get the result of the IDSCNA function #only show
CNA2Subpathwayresult<-GetExampleData("CNA2Subpathwayresult")
# View the result top 10 subpathways
head(CNA2Subpathwayresult[1:10,])
```

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plotDiscovermap

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plotDiscovermap

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**Description**

we use copy number variation data to polt discover.

**Usage**

```
plotDiscovermap(genes, CNAmatrix)
```

**Arguments**

genes	A vector of strings. The user interesting and happened CNA genes symbol.
CNAmatrix	The copy number variation matrix. It takes the from of a binary matrix. Only 0 and 1 are allowed as values.

**Value**

Groupwise test of the discover result

**Examples**

```
# load depend package
require(discover)
# input gene
genes <- c("AKT3", "AKT1", "CALML5", "PIK3CA", "PIK3R1", "CALM1", "CALM3", "CALML3")
# get the result of the getCNALabel function
CNALabelresult<-GetExampleData("CNALabelresult")
# plot discover
discover<-plotDiscovermap(genes,CNALabelresult)
plot(discover)
```

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plotSubPathway

*plotSubPathway*


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**Description**

The function plotsubpathway can visualization of a subpathway network map.

**Usage**

```
plotSubPathway(
  subpathwayID,
  subpathwaydata,
  layout = NULL,
  margin = 0,
  vertex.label.cex = 0.8,
  vertex.label.font = 0.8,
  vertex.label.dist = 1,
  vertex.size = 12,
  edge.arrow.width = 3,
  edge.label.cex = 0.6,
  vertex.label.color = "black",
  vertex.color = "#F08080",
  vertex.frame.color = "dimgray",
  edge.color = "grey70",
  edge.label.color = "dimgray",
  sub = NULL,
  main = NULL
)
```

**Arguments**

subpathwayID	subpathway id number
subpathwaydata	The subpathwaymap data
layout	A matrix of x-y coordinates with two dims. Determine the placement of the nodes for drawing a graph.
margin	A numeric. The value is usually between -0.5 and 0.5, which is able to zoom in or out a subpathway graph. The default is 0.
vertex.label.cex	A numeric vector of node label size.
vertex.label.font	A numeric vector of label font.
vertex.label.dist	A numeric vector of label dist.
vertex.size	A numeric vector of Node size. See plot.igraph.
edge.arrow.width	Edge arrow width. The default is 3.
edge.label.cex	Edge label size.
vertex.label.color	A vector of node label colors. The default is black.
vertex.color	A vector of node colors. The default is the KEGG node color.
vertex.frame.color	A vector of node frame color. The default is dimgray.
edge.color	A vector of edge color. The default is dimgray
edge.label.color	A vector of edge label color. The default is dimgray.
sub	A character string of subtitle.
main	A character string of main title.

**Value**

a subpathway map

**Examples**

```
# load depend package
require(igraph)
# obtain subpathwaymap data
SubPathwaymapdata<-GetExampleData("SubPathwaymapdata")
# plot network graph of the subpathway 04915_13
plotSubPathway("04915_13",SubPathwaymapdata)
```

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