

# Package ‘DCN’

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**Type** Package

**Title** Identifying differential co-expression subnetwork

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**Description** Identification of differential subnetworks from a differential co-expression network.

**License** GPL(>=2)

**NeedsCompilation** no

**Depends** R (>= 3.5.0)

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DCN-package	<i>Identifying differential subnetworks</i>
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## Description

Identification of differential subnetworks from a differential co-expression network.

## Author(s)

Wei Liu

Maintainer: Wei Liu <freelw@qq.com>

## References

Liu et al., Identification of lncRNA associated differential subnetworks in esophageal squamous cell carcinoma by differential co-expression analysis, 2020.

**Examples**

```
library("igraph")
data(g)
res <- getDiffSubnetwork(graph = g, seed = "AL121899.1",
                        d = 2, r = 0.1, alpha=0.7 ,th = 0.01)
plot(res$subg)
```

g

*The differential co-expression network***Description**

The differential co-expression network. It is an igraph object with at least two vertex attributes ("name" and "DE") and one edge attribute ("DC").

**Usage**

```
data("g")
```

**Format**

An igraph R object.

**Details**

g is a differential co-expression network. There are 2074 nodes and 3917 edges in g. Each node in the graph represents a PCG/lncRNA. Each node has three attributes: "name", "DE", and "Type". "name" represents gene name of the node. "DE" represents the differential expression score of the node. "Type" represents the type (PCG/lncRNA) of the gene. Each edge has one attribute "DC" which represents the differential co-expression score of the edge.

**Examples**

```
data(g)
```

getDC

*Get differential co-expression score.***Description**

Get differential co-expression score of a graph.

**Usage**

```
getDC(g)
```

**Arguments**

g An igraph object with two vertex attributes ("name" and "DE") and one edge attribute ("DC").

**Value**

The differential co-expression score of g.

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getDE	<i>Get differential expression score.</i>
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**Description**

Get differential expression score of a graph.

**Usage**

```
getDE(g)
```

**Arguments**

g	An igraph object with two vertex attributes ("name" and "DE") and one edge attribute ("DC").
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**Value**

The differential expression score of g.

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getDiffSubnetwork	<i>Get differential co-expression subnetwork</i>
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**Description**

A differential subnetwork identification method for differential co-expression network.

**Usage**

```
getDiffSubnetwork(graph, seed, d = 2, r = 0.05, alpha = 0.7, th = 0.5^6)
```

**Arguments**

graph	An igraph object with at least two vertex attributes ("name" and "DE") and one edge attribute ("DC").
seed	The seed node. Should be the name of a vertex in graph.
d	A positive integer that controls the searching space.
r	A positive real number that controls the increasing rate of the subnetwork score.
alpha	A real number between 0 and 1 that controls the relative weight of differential expression score and differential co-expression score.
th	A threshold ( $> 0$ ) of differential co-expression score. Edges with differential co-expression score $< th$ will not be added into the differential subnetwork.

## Details

This function implements a differential subnetwork searching algorithm which considers both the differential expression score and the differential co-expression score. The search starts from a seed and iteratively adds neighboring nodes. At each iteration, the search considers addition of a node from the neighbors of nodes in the current subnetwork and the corresponding edges connect this node and the current subnetwork. The addition which yields maximum score is adopted. The search will stop if no node satisfies the following two conditions: (i) the number of edges in the shortest path between this node and the seed is less than or equal to  $d$ ; and (ii) the addition of this node increase the score of the subnetwork over an improvement rate  $r$ . The graph should have at least two vertex attributes ("name" and "DE") and one edge attribute ("DC"). "name" of a vertex represents the gene name of this vertex; "DE" of a vertex represents the  $t$  statistic in a paired, two-tailed  $t$ -test comparing the expression values of this vertex (gene) between tumor samples and normal samples; "DC" of an edge represents the weight of differential co-expression (differential co-expression score) between the corresponding two vertices.

## Value

subg	The identified differential co-expression subnetwork.
D	The subnetwork score of subg.
DE	The differential expression score of subg.
DC	The differential co-expression score of subg.

## Author(s)

Wei Liu <freelw@qq.com>

## References

Liu et al., Identification of lncRNA associated differential subnetworks in esophageal squamous cell carcinoma by differential co-expression analysis, 2020.

## Examples

```
library("igraph")
data(g)
res <- getDiffSubnetwork(graph = g, seed = "AL121899.1",
                        d = 2, r = 0.1, alpha=0.7 ,th = 0.01)
plot(res$subg)
```

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