

# Package ‘NeighborNet’

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**Title** Neighbor\_net analysis

**Version** 1.12.0

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**Description** Identify the putative mechanism explaining the active interactions between genes in the investigated phenotype.

**biocViews** Software, GeneExpression, StatisticalMethod, GraphAndNetwork

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.0

**Depends** methods

**Imports** graph, stats

**git\_url** <https://git.bioconductor.org/packages/NeighborNet>

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neighborNet	<i>Neighbor Net: An approach to infer putative disease-specific mechanisms using neighboring gene networks.</i>
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### Description

Neighbor Net: An approach to infer putative disease-specific mechanisms using neighboring gene networks.

### Usage

```
neighborNet(de, ref, listofgenes, threshold = 0.1, minsize = 2)
```

### Arguments

de	a vector including the differentially expressed genes; de must use the same id's as ref and the genes in the listofgenes
ref	the reference vector for all genes in the analysis
listofgenes	a list representing the neighbor networks associated to each gene; the name of the list must be the same as genes in the de
threshold	a threshold of choosing significant neighbor networks (default is 0.1)
minsize	minimum size of the neighbor networks that should be considered in the analysis (default is 2)

### Details

See details in the cited articles.

### Value

An object of class `graphNEL`.

### Author(s)

Sahar Ansari and Sorin Draghici

### References

Sahar Ansari, Michele Donato, Nafiseh Saberian, Sorin Draghici; An approach to infer putative disease-specific mechanisms using neighboring gene networks, *Bioinformatics*, Volume 33, Issue 13, 1 July 2017, Pages 1987–1994

**Examples**

```
# load multiple colorectal cancer study (public data available in GEO
# ID: GSE4183, GSE9348, GSE21510, GSE32323, GSE18671)
# These files contains the tables, produced by the limma package with
# added gene information.
# The table contains the expression fold change and significance of each
# probe set comparing colorectal cancer disease and normal.
load(system.file("extdata/dataColorectal4183.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal9348.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal21510.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal32323.RData", package = "NeighborNet"))
load(system.file("extdata/dataColorectal8671.RData", package = "NeighborNet"))
head(dataColorectal4183)

load(system.file("extdata/listofgenes.RData", package = "NeighborNet"))
head(listofgenes)

# select differentially expressed genes for each data set at p-value below 1%
# and absolute value for more than 1.5 and save their entrez ID in a vector de1 to de5
pvThreshold <- 0.01
foldThreshold <- 1.5
de1 <- dataColorectal4183$EntrezID [
  dataColorectal4183$adj.P.Val < pvThreshold &
  abs(dataColorectal4183$logFC) > foldThreshold]
de2 <- dataColorectal9348$EntrezID [
  dataColorectal9348$adj.P.Val < pvThreshold &
  abs(dataColorectal9348$logFC) > foldThreshold]
de3 <- dataColorectal21510$EntrezID [
  dataColorectal21510$adj.P.Val < pvThreshold &
  abs(dataColorectal21510$logFC) > foldThreshold]
de4 <- dataColorectal32323$EntrezID [
  dataColorectal32323$adj.P.Val < pvThreshold &
  abs(dataColorectal32323$logFC) > foldThreshold]
de5 <- dataColorectal8671$EntrezID [
  dataColorectal8671$adj.P.Val < pvThreshold &
  abs(dataColorectal8671$logFC) > foldThreshold]
all <- unique( c(dataColorectal4183$EntrezID, dataColorectal9348$EntrezID,
  dataColorectal21510$EntrezID, dataColorectal32323$EntrezID,
  dataColorectal8671$EntrezID))
de <- unique( c(de1,de2,de3,de4,de5))

sig_net <- neighborNet (de, all, listofgenes)
```

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