

# Package ‘NetworkComparisonTest’

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**Type** Package

**Title** Statistical Comparison of Two Networks Based on Several Invariance Measures

**Version** 2.2.2

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**Imports** stats, graphics, utils, Matrix, methods, reshape2, qgraph, networktools, IsingFit

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**Description** This permutation based hypothesis test, suited for several types of data supported by the estimateNetwork function of the bootnet package (Epskamp & Fried, 2018), assesses the difference between two networks based on several invariance measures (network structure invariance, global strength invariance, edge invariance, several centrality measures, etc.). Network structures are estimated with l1-regularization. The Network Comparison Test is suited for comparison of independent (e.g., two different groups) and dependent samples (e.g., one group that is measured twice). See van Borkulo et al. (2021), available from <[doi:10.1037/met0000476](https://doi.org/10.1037/met0000476)>.

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NetworkComparisonTest-package  
*Statistical Comparison of Two Networks Based on Several Invariance Measures*

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## Description

This permutation based hypothesis test, suited for several types of data supported by the estimateNetwork function of the bootnet package (Epskamp & Fried, 2018), assesses the difference between two networks based on several invariance measures (network structure invariance, global strength invariance, edge invariance, several centrality measures, etc.). Network structures are estimated with l1-regularization. The Network Comparison Test is suited for comparison of independent (e.g., two different groups) and dependent samples (e.g., one group that is measured twice).

## Details

Package: NetworkComparisonTest  
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## Author(s)

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## References

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van Borkulo, C. D., Boschloo, L., Borsboom, D., Penninx, B. W. J. H., Waldorp, L. J., & Schoevers, R.A. (2015). Association of symptom network structure with the course of depression. *JAMA Psychiatry*. 2015;72(12). doi:10.1001/jamapsychiatry.2015.2079

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 NCT

*NetworkComparisonTest: Statistical Comparison of Two Networks Based on Several Invariance Measures*

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## Description

This permutation based hypothesis test, suited for several types of data supported by the estimateNetwork function of the bootnet package (Epskamp & Fried, 2018), assesses the difference between two networks based on several invariance measures (network structure invariance, global strength invariance, edge invariance, several centrality measures, etc.). Network structures are estimated with l1-regularization. The Network Comparison Test is suited for comparison of independent (e.g., two different groups) and dependent samples (e.g., one group that is measured twice).

## Usage

```
NCT(
  data1,
  data2,
  gamma,
  it = 100,
  binary.data = FALSE,
  paired = FALSE,
  weighted = TRUE,
  AND = TRUE,
  abs = TRUE,
  test.edges = FALSE,
  edges = "all",
  progressbar = TRUE,
  make.positive.definite = TRUE,
  p.adjust.methods = c("none", "holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
    "fdr"),
  test.centralities = FALSE,
  centralities = c("strength", "expectedInfluence"),
  nodes = "all",
  communities = NULL,
  useCommunities = "all",
  estimator,
  estimatorArgs = list(),
  verbose = TRUE
)
```

**Arguments**

<code>data1</code>	One of two datasets. The dimension of the matrix is <code>nobs x nvars</code> ; each row is a vector of observations of the variables. Must be cross-sectional data. Can also be the result of <code>estimateNetwork</code> from the <code>bootnet</code> package.
<code>data2</code>	The other of two datasets. The dimension of the matrix is <code>nobs x nvars</code> ; each row is a vector of observations of the variables. Must be cross-sectional data. Can also be the result of <code>estimateNetwork</code> from the <code>bootnet</code> package.
<code>gamma</code>	A single value between 0 and 1. When not entered, <code>gamma</code> is set to 0.25 for binary data and 0.50 for gaussian data. Networks are estimated with this value for hyperparameter <code>gamma</code> in the extended BIC.
<code>it</code>	The number of iterations (permutations).
<code>binary.data</code>	Logical. Can be <code>TRUE</code> or <code>FALSE</code> to indicate whether the data is binary or not. If <code>binary.data</code> is <code>FALSE</code> , the data is regarded gaussian. This argument is ignored when using <code>estimateNetwork()</code> output as input for NCT.
<code>paired</code>	Logical. Can be <code>TRUE</code> or <code>FALSE</code> to indicate whether the samples are dependent or not. If <code>paired</code> is <code>TRUE</code> , relabeling is performed within each pair of observations. If <code>paired</code> is <code>FALSE</code> , relabeling is not restricted to pairs of observations. Note that, currently, dependent data is assumed to entail one group measured twice.
<code>weighted</code>	Logical. Can be <code>TRUE</code> or <code>FALSE</code> to indicate whether the networks to be compared should be weighted or not. If not, the estimated networks are dichotomized. Defaults to <code>TRUE</code> .
<code>AND</code>	Logical. Can be <code>TRUE</code> or <code>FALSE</code> to indicate whether the AND-rule or the OR-rule should be used to define the edges in the network. Defaults to <code>TRUE</code> . Only necessary for binary data.
<code>abs</code>	Logical. Should global strength consider the absolute value of edge weights, or the raw value (i.e., global expected influence)?
<code>test.edges</code>	Logical. Can be <code>TRUE</code> or <code>FALSE</code> to indicate whether or not differences in individual edges should be tested.
<code>edges</code>	Character or list. When <code>'all'</code> , differences between all individual edges are tested. When provided a list with one or more pairs of indices referring to variables, the provided edges are tested.
<code>progressbar</code>	Logical. Should the pbar be plotted in order to see the progress of the estimation procedure? Defaults to <code>TRUE</code> .
<code>make.positive.definite</code>	If <code>make.positive.definite = TRUE</code> , the covariance matrices used for the <code>glasso</code> are projected to the nearest positive definite matrices, if they are not yet positive definite. This is useful for small <code>n</code> , for which it is very likely that at least one of the bootstrap comparisons involves a covariance matrix that is not positive definite.
<code>p.adjust.methods</code>	Character. Can be one of <code>"holm"</code> , <code>"hochberg"</code> , <code>"hommel"</code> , <code>"bonferroni"</code> , <code>"BH"</code> , <code>"BY"</code> , <code>"fdr"</code> , or <code>"none"</code> . To control (or not) for testing of multiple edges. Defaults to <code>"none"</code> .

<code>test.centrality</code>	Logical. Should centrality metrics be compared across networks?
<code>centrality</code>	Type of centrality metrics to test. Can be any of c("all", "closeness", "betweenness", "strength", "expectedInfluence", "bridgeStrength", "bridgeCloseness", "bridgeBetweenness", "bridgeExpectedInfluence")
<code>nodes</code>	Specific nodes for centrality tests. Can be character names or index numbers. Only used if <code>test.centrality=TRUE</code>
<code>communities</code>	Passed to <code>bridge()</code> if computing bridge centrality
<code>useCommunities</code>	Passed to <code>bridge()</code> if computing bridge centrality
<code>estimator</code>	A function that takes data as input and returns a network structure. This can be used for custom estimation algorithms. Note, supplying this function will overwrite the arguments <code>binary.data</code> , <code>AND</code> , <code>gamma</code> and <code>make.positive.definite</code> .
<code>estimatorArgs</code>	Arguments to the estimator function.
<code>verbose</code>	Logical: Should some warnings and notes be printed?

## Value

NCT returns a 'NCT' object that contains the following items:

- `glstrinv.real` The difference in global strength between the networks of the observed data sets.
- `glstrinv.perm` The difference in global strength between the networks of the permuted data sets.
- `glstrinv.sep` The global strength values of the individual networks
- `glstrinv.pval` The p value resulting from the permutation test concerning difference in global strength.
- `nwinv.real` The value of the maximum difference in edge weights of the observed networks.
- `nwinv.perm` The values of the maximum difference in edge weights of the permuted networks.
- `nwinv.pval` The p value resulting from the permutation test concerning the maximum difference in edge weights.
- `einv.pvals` p-values (corrected for multiple testing or not according to 'p.adjust.methods') per edge from the permutation test concerning differences in edges weights. Only returned if `test.edges = TRUE`.
- `einv.real` The value of the difference in edge weight of the observed networks (multiple values if more edges are called to test). Only if `test.edges = TRUE`.
- `einv.perm` The values of the difference in edge weight of the permuted networks. Only if `test.edges = TRUE`.
- `diffcen.real` The values of the difference in centralities of the observed networks. Only if `test.centrality = TRUE`.
- `diffcen.perm` The values of the difference in centralities of the permuted networks. Only if `test.centrality = TRUE`.
- `diffcen.pval` p-values(corrected for multiple testing or not according to 'p.adjust.methods') per node from the permutation test concerning differences in centralities. Only if `test.centrality = TRUE`.

## Examples

```

library(IsingSampler)
library(IsingFit)
library(bootnet)

### Simulate binary datasets under null hypothesis:
### underlying network structures are similar
# Input:
N <- 6 # Number of nodes
nSample <- 500 # Number of samples

# Ising parameters:
set.seed(123)
Graph <- matrix(sample(0:1,N^2,TRUE,prob = c(0.8, 0.2)),N,N) * runif(N^2,0.5,2)
Graph <- pmax(Graph,t(Graph))
Graph[4,1] <- Graph[4,1]*-1
Graph[1,4] <- Graph[1,4]*-1
Graph[5,1] <- Graph[5,1]*-1
Graph[1,5] <- Graph[1,5]*-1
Graph[6,1] <- Graph[6,1]*-1
Graph[1,6] <- Graph[1,6]*-1
diag(Graph) <- 0
Thresh <- -rowSums(Graph) / 2

# Simulate:
data1 <- IsingSampler(nSample, Graph, Thresh)
data2 <- IsingSampler(nSample, Graph, Thresh)
colnames(data1) <- colnames(data2) <- c('V1', 'V2', 'V3', 'V4', 'V5', 'V6')

### Compare networks of data sets using NCT ###
## Networks can be compared by either (1) feeding the data directly into NCT (whereby
## you need to specify arguments such as "gamma" and "binary.data") or (2) by using
## estimateNetwork() (bootnet package) and feeding that output into NCT. For the latter
## option, we refer to the help file of estimateNetwork() for its usage. Below, both
## options are illustrated. We recommend using estimateNetwork(), since this function
## has implemented many network estimation methods.

## gamma = 0 (in estimateNetwork this hyperparameter is called "tuning"; to illustrate
## how to specify a different value than the default)
## iterations (it) set to 10 to save time
## Note: Low number of iterations can give unreliable results; should be 1000 at least

## Testing whether there are differences in the three aspects that are validated
## (network invariance, global strength, edge weight)
## 2 edges are tested here: between variable 1 and 2, and between 3 and 6 (can be
## "list(c(2,1),c(6,3))" as well)

## (1) Feeding data directly into NCT
set.seed(123)
NCT_a <- NCT(data1, data2, gamma=0, it=10, binary.data = TRUE,
             test.edges=TRUE, edges=list(c(1,2),c(3,6)))
summary(NCT_a)

```

```

## Plot results of global strength invariance test (not reliable with only 10
# permutations!)
plot(NCT_a, what="strength")

## (2) Feeding the estimateNetwork() output into NCT
est_1 <- estimateNetwork(data1, default = "IsingFit", tuning = 0)
est_2 <- estimateNetwork(data2, default = "IsingFit", tuning = 0)
## When using estimateNetwork() output, there is no need to specify gamma and binary.data
## This yields similar output as NCT_a
set.seed(123)
NCT_b <- NCT(est_1, est_2, it=10, test.edges=TRUE,
             edges=list(c(1,2),c(3,6)))
summary(NCT_b)

## Next, an example of testing whether there are differences in node strength
# when data is paired (e.g., a group which is measured pre- and post-treatment).
# Also, here you can see how to specify that you want to take the sign of node strength
# into account (by default, the absolute value is taken and, therefore, the sign is
# ignored).
# we don't run these two examples by default as they take too long for the R CMD check
# but they are still interesting.

## Not run:

## abs = FALSE
set.seed(123)
NCT_c = NCT(est_1, est_2, paired = TRUE, abs = FALSE, test.edges = TRUE,
            edges = list(c(1,2),c(3,6)), test.centralities = TRUE,
            centralities = c("strength"), nodes = "all", it=10)
summary(NCT_c)

## Finally, an example how to test for differences in centrality (e.g., expectedInfluence)

set.seed(123)
NCT_d = NCT(est_1, est_2, paired = TRUE, abs = FALSE, test.edges = TRUE,
            edges = list(c(1,2),c(3,6)), test.centralities = TRUE,
            centralities = c("expectedInfluence"), nodes = "all", it=10)
summary(NCT_d)

## End(Not run)

```

---

plot.NCT

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*Print method for NCT*


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### Description

Print method, prints the NCT output, plot method plots the output, summary method returns a summary of the output.

**Usage**

```
## S3 method for class 'NCT'  
print(x, ...)  
  
## S3 method for class 'NCT'  
plot(x, what = c("strength", "network", "edge", "centrality"), ...)
```

**Arguments**

x	output of NCT
...	for now ignored
what	defines what has to be plotted: results pertaining to test on invariance of global strength ("strength"), network structure ("network"), edge strength ("edge"), or specific centrality measure ("centrality")

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summary.NCT	<i>Summary method for NCT</i>
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**Description**

Summary method for NCT

**Usage**

```
## S3 method for class 'NCT'  
summary(object, ...)
```

**Arguments**

object	output of NCT
...	for now ignored



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