

# Package ‘dissCqN’

October 13, 2022

**Type** Package

**Title** Multiple Assemblage Dissimilarity for Orders  $q = 0-N$

**Version** 0.1.0

**Description** Calculate multiple or pairwise dissimilarity for orders  $q = 0-N$  (CqN; Chao et al. 2008 <[doi:10/fcvm63](https://doi.org/10/fcvm63)>) for a set of species assemblages or interaction networks.

**URL** <https://murphymv.github.io/dissCqN/>,  
<https://github.com/murphymv/dissCqN>

**BugReports** <https://github.com/murphymv/dissCqN/issues>

**Depends** R ( $\geq 4.0.0$ )

**Imports** parallel, stats

**Suggests** knitr, markdown, rmarkdown, SpadeR, vegan

**VignetteBuilder** knitr

**License** GPL ( $\geq 3$ )

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**Language** en-GB

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-10-14 11:50:05 UTC

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dissCqN

*Multiple Assemblage Dissimilarity***Description**

Multiple assemblage dissimilarity for orders  $q = 0-N$ .

**Usage**

```
dissCqN(
  mat,
  q = 0:2,
  pairwise = FALSE,
  compare.sub = NULL,
  shared.spp = FALSE,
  parallel = "no",
  ncpus = NULL,
  cl = NULL
)
```

**Arguments**

<code>mat</code>	A matrix with assemblages in rows and species or species interactions in columns. Alternatively, a list of matrices, which will be interpreted as interaction networks and used to construct an assemblage x interaction matrix.
<code>q</code>	Integer, the order(s) of $q$ for which to calculate dissimilarity. Can be any set of integers between 0 and $N$ (the number of assemblages in <code>mat</code> ).
<code>pairwise</code>	Logical, whether to calculate pairwise, rather than multiple assemblage, dissimilarity.
<code>compare.sub</code>	Subsets of assemblages to compare pairwise. These should be supplied as a list of two sets of assemblage names or indices. If only one set is supplied, this is compared to all other assemblages in <code>mat</code> . If more than two sets are supplied, only the first two are used. If NULL (default), all assemblages are compared.
<code>shared.spp</code>	Logical, whether to compare networks of shared species only (if <code>mat</code> is a list of networks).
<code>parallel</code>	The type of parallel processing to use, if any. Can be one of "snow", "multicore", or "no" (for none – the default). Passed to <code>pSapply()</code> .
<code>ncpus</code>	Number of system cores to use for parallel processing. If NULL (default), all available cores are used.
<code>cl</code>	Optional cluster to use if <code>parallel = "snow"</code> . If NULL (default), a local cluster is created using the specified number of cores.

## Details

Dissimilarity is calculated here for multiple species assemblages (or interaction networks) via the  $CqN$  generalisation of similarity indices (Chao *et al.* 2008, Jost *et al.* 2011). Increasing the value of  $q$  increases the 'depth' of the measure, that is, how much emphasis is placed on changes in relative abundance of the most common species. Setting  $q = 0$  represents the qualitative Sørensen index (Sørensen 1948), where rare and common species are treated equally.  $q > 0$  is more sensitive to common species, with  $q = 1$  representing the Shannon-based Horn index (Horn 1966) and  $q = 2$  the Simpson-based Morisita-Horn index (Morisita 1959, Horn 1966). For  $N > 2$ , indices are generalised to consider species shared across multiple assemblages (Diserud & Ødegaard 2007, eqns. 6.3-6.5 in Jost *et al.* 2011). For  $q \geq 2 \leq N$ , common species increasingly dominate the measure, and it can then be interpreted as the ratio of two probabilities of randomly sampling  $q$  individuals of the same species from the  $N$  assemblages, where 1) the individuals came from at least one different assemblage ( ${}^qG_D$ ) and 2) they all came from the same assemblage ( ${}^qG_S$ ) (Jost *et al.* 2011). Dissimilarity is thus:

$$1 - {}^qG_D / {}^qG_S$$

Pairwise dissimilarity can be calculated for all or a subset of the assemblages (or networks) in `mat`, in which case a dissimilarity matrix is returned (one for each value of  $q$ ). If comparing subsets, the names or indices of assemblages to compare should be supplied to `compare.sub`. Note that pairwise calculation may take a long time if  $N$  is large, in which case parallel processing may speed up results (e.g. `parallel = "snow"`).

If `shared.spp = TRUE` and `mat` is a list of interaction networks (as matrices), multiple or pairwise interaction dissimilarity will be calculated for networks of shared species only (see `netShared()`). This can be useful to help partition the different components of network dissimilarity, e.g. dissimilarity due to interaction 'rewiring' among shared species vs. that due to species turnover (Poisot *et al.* 2012).

## Value

A numeric vector of dissimilarities, or a pairwise dissimilarity matrix (or list of matrices), for the orders of  $q$ .

## References

- Chao, A., Jost, L., Chiang, S. C., Jiang, Y.-H., & Chazdon, R. L. (2008). A Two-Stage Probabilistic Approach to Multiple-Community Similarity Indices. *Biometrics*, **64**(4), 1178–1186. doi: [10/fcvm63](https://doi.org/10.1111/j.1541-0420.08063.x)
- Diserud, O. H., & Ødegaard, F. (2007). A multiple-site similarity measure. *Biology Letters*, **3**(1), 20–22. doi: [10/bwhfx6](https://doi.org/10.1098/rsbl.2006.0166)
- Horn, H. S. (1966). Measurement of "Overlap" in Comparative Ecological Studies. *The American Naturalist*, **100**(914), 419–424. doi: [10/b62ct5](https://doi.org/10.1086/28255)
- Jost, L., Chao, A., & Chazdon, R. L. (2011). Compositional similarity and beta diversity. In A. E. Magurran & B. J. McGill (Eds.), *Biological Diversity: Frontiers in Measurement and Assessment* (pp. 66–84). Oxford University Press.
- Morisita, M. (1959). Measuring of interspecific association and similarity between communities. *Memoirs of the Faculty of Science, Kyushu Univ., Series E (Biology)*, **3**, 65–80.

Poisot, T., Canard, E., Mouillot, D., Mouquet, N., & Gravel, D. (2012). The dissimilarity of species interaction networks. *Ecology Letters*, **15**(12), 1353–1361. doi: [10/f4dv37](https://doi.org/10/f4dv37)

Sørensen, T. (1948). A method of establishing groups of equal amplitude in plant sociology based on similarity of species and its application to analyses of the vegetation on Danish commons. *Kongelige Danske Videnskabernes Selskabs Biologiske Skrifter*, **5**, 1–34.

## Examples

```
# Sample community data from SpadeR package (three assemblages, 120 species)
data(SimilarityMultData, package = "SpadeR")
d <- SimilarityMultData$Abu

# Multiple-assemblage dissimilarity for q = 0:2
(CqN <- dissCqN::dissCqN(t(d)))

# Compare to empirical CqN values from SpadeR::SimilarityMult()
sim <- SpadeR::SimilarityMult(d, datatype = "abundance", nboot = 1)
CqN_2 <- 1 - c(
  "C0N" = sim$Empirical_richness["C0N(q=0,Sorensen)", "Estimate"],
  "C1N" = sim$Empirical_relative["C1N=U1N(q=1,Horn)", "Estimate"],
  "C2N" = sim$Empirical_relative["C2N(q=2,Morisita)", "Estimate"]
)
stopifnot(all.equal(CqN, CqN_2))

# Pairwise dissimilarity matrices
dissCqN::dissCqN(t(d), pairwise = TRUE)
```

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intMat

*Assemblage x Species Interaction Matrix*


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## Description

Generate a matrix of assemblages x species interactions from a set of networks.

## Usage

```
intMat(net, shared.spp = FALSE, ...)
```

## Arguments

**net** An interaction network, or list of networks, supplied as matrices.  
**shared.spp** Logical, whether to use networks of shared species only.  
**...** Arguments to [netShared\(\)](#) (if `shared.spp = TRUE`).

## Value

A matrix with assemblages in rows and species interactions in columns.

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`netShared`*Networks of Shared Species*

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**Description**

Generate interaction networks comprising only the shared species across two or more networks.

**Usage**

```
netShared(net, pairwise = TRUE, compare.sub = NULL)
```

**Arguments**

<code>net</code>	A list of two or more networks to compare, supplied as matrices.
<code>pairwise</code>	Logical, whether to compare networks pairwise (default), rather than considering species shared across multiple networks.
<code>compare.sub</code>	Subsets of networks to compare pairwise. These should be supplied as a list of two sets of network names or indices. If only one set is supplied, this is compared to all other networks in <code>net</code> . If more than two sets are supplied, only the first two are used.

**Value**

A list of networks of shared species. If comparing pairwise, this will be of length  $n1 * n2 * 2$  (with  $n1$  and  $n2$  being the numbers of networks in each set), or if considering multiple networks, the length of the original list.

**Note**

If comparing networks pairwise, and subsets are not specified, the output will contain network self-comparisons (redundancy).

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