

# CoOccurrence – a FORTRAN program for species co-occurrence analysis Version 2.0

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## 1. Introduction

The study of species co-occurrences has a long tradition in ecology (Weiher and Keddy 1999). Particularly the long lasting and still ongoing discussion around community assembly rules (Diamond 1975, Diamond and Gilpin 1982, Gilpin and Diamond 1982, Connor and Simberloff 1979, 1983, 1984, Gotelli and McCabe, 2002, Ulrich 2004) has inspired the development of statistical tools to infer non random patterns in community assembly (Gotelli and Graves 1996, Gotelli 2000, 2001).

Community assembly is often studied in terms of nestedness (Atmar and Patterson 1986, Wright et al. 1998, Ulrich and Gotelli 2007) and non-random patterns of species co-occurrences (Diamond 1975, Gotelli 2000, 2001) and the respective standard software is widely used: The *Nestedness Temperature Calculator* (Atmar and Patterson 1995), *EcoSim* (Gotelli and Entsminger 2002, and *Nestedness* (Ulrich 2006).

The present program *CoOccurrence* implements two nestedness and three common co-occurrence metrics :The discrepancy metric of Brualdi and Sanderson

(1999), NODF (Almeida-Neto et al. (2008), the species combinations score (Pielou and Pielou 1968), the C-score (Stone and Roberts 1990), and the checkerboard score (Gotelli 2000). While most of these metrics are also implemented in *Nestedness* and *EcoSim*, the present program is particularly designed for the study of multiple matrices for instance in null model analysis, for the analysis of the statistical behaviour of certain metrics, and in studies of neutral models.

## 2.1. Presence absence –metrics

### *Nestedness*

*CoOccurrence* contains the discrepancy metric *BR* and *NODF*. The first counts the number of discrepancies (absences or presence) that must be erased to produce a perfectly nested matrix (Brualdi and Sanderson 1999). This is done for rows and columns separately and the lower value is taken. NODF is a matrix wide count of species associations for rows and columns and separates the importance of columns (NODFcolumns) and rows (NODFrows) for the total degree of nestedness (Almeida-Neto et al. 2008).

*Co-occurrence* : Incidence metrics

The present program implements five measures of co-occurrences:

1. The species combinations score (COMBO) screens the columns of the presence absence or abundance matrix for unique species combinations (Pielou and Pielou 1968). Hence, it counts the number of species that always co-occur.

2. The checkerboard score (Gotelli 2000) screens the matrix for checkerboards. These are 2\*2 submatrices of the structure

$$\begin{matrix} 1 & 0 & & 0 & 1 \\ 0 & 1 & & 1 & 0 \end{matrix} \text{ or } \begin{matrix} 0 & 1 & & 0 & 1 \\ 1 & 0 & & 1 & 0 \end{matrix}$$

. The score is a simple count of the number of such submatrices.

3. The C-score (Stone and Roberts 1990) is the average number of checkerboards for two species  $i$  and  $j$ . The score is calculated from

$$CS = \sum_{i,j} (N_i - N_{ij})(N_j - N_{ij})$$

where  $N_i$  and  $N_j$  are the row totals (numbers of occurrences) of species  $i$  and  $j$  and  $N_{ij}$  is the number of co-occurrences of both species.

4. A correlation test calculates the average Spearman rank order correlation between all species pairs and compares this with the null expectation.

5. The variance test of Schluter (1984) compares the variance of row totals ( $s^2_{\text{row}}$ ) with the mean variance of  $N$  columns ( $s^2_{\text{column}}$ ). For a random matrix the quotient  $s^2_{\text{row}}/s^2_{\text{column}}$  should be  $\chi^2$  distributed with  $N$  degrees of freedom.

For comparing matrices of different size and shape the metrics have to be standardized. This is done by dividing the effect size through the expected value.

$$\text{Metric}_{\text{Standardized}} = \frac{\text{Obs} - \text{Exp}}{\text{Exp}}$$

#### Co-occurrence : Abundance metrics

CoOccurrence calculates six indices that might

quantify the pattern of co-occurrence in abundance matrices.

1. A strong version of abundance checkerboards are 2x2 submatrices of the form

$$\begin{pmatrix} a & b \\ c & d \end{pmatrix}; (a > b, a > c, d > b, d > c) \vee (a < b, a < c, d < b, d < c)$$

The metric  $CA$  is a count of the number of abundance checkerboards in the matrix. This metric can be standardized with regard to matrix size by

$$CA_{\text{ST}} = \frac{4CA}{m(m-1)n(n-1)}$$

High values of  $CA$  point to species segregation.

2. A strong version of the number of species aggregations  $AA$  is a count of aggregated 2x2 submatrices of the form

$$\begin{pmatrix} a & b \\ c & d \end{pmatrix}; (a > b, a > c, d < b, d < c) \vee (a < b, a < c, d > b, d > c)$$

Again a standardized metric has the form

$$AA_{\text{ST}} = \frac{4AA}{m(m-1)n(n-1)}$$

Low values of  $CA$  point to species segregation.

3. A measure of the strength of the checkerboard pattern is

$$SA_{\text{ST}} = \frac{4 \sum \sqrt{(a-c)^2 + (b-d)^2} / (a^2 + b^2 + c^2 + d^2)}{m(m-1)n(n-1)}$$

4. The variance test of Schluter (1984) is a matrix wide metric of species segregation or aggregation.

This test compares the variance of row totals  $V$  with the sum of the column variances  $W$ . If all columns are random draws from the same metacommunity the value  $U=V/W$  should be  $\chi^2$  distributed with  $n$  degrees of freedom. Low values of  $U$  point to species segregation.

5. Chao et al (2008) extended the Morisita index of similarity for two communities to a matrix wide metric for  $n$  communities of the form

$$MA = \frac{\sum_{i=1}^m [(\sum_{j=1}^n p_{ij})^2 - \sum_{j=1}^n (p_{ij})^2]}{(n-1) \sum_{j=1}^n (p_{ij})^2}$$

This metric is also a possible metric of matrix wide species segregation. Low values of *MA* point to species segregation.

6. The Mantel test identifies non-congruence between two matrices. To assess whether a matrix is not random the program calculates the mean Mantel correlation between the matrix and the null model matrices (see below). Note that the Mantel test does not identify whether an observed matrix is more aggregated or segregated than observed.

### 3. Data structure

*CoOccurrence* needs one main plain text data file of the following structure. The columns of the matrix are sites, the rows species. Hence the matrix below contains 20 species distributed over 12 sites. The data file has to be a simple ASCII file with data delimited by one or more spaces. Accepted are either abundance or presences absence data of the integer (In) or real format (Fn.k) The first row contains site names, the first column species names. The file has therefore the same format that is needed for *EcoSim* (Gotelli and Entsminger 2002). The number of species is not limited, the maximum number of sites is about 150.

Alternatively, you may run *CoOccurrence* in a batch. In this case the input files must have a structure as shown above and the driver file contains only the names of the data files. The first line has to be a comment line.

### 4. Program run

First, the program asks for the files names. The default output file names are *CoOccurrence.txt* and *Matrix.txt*. You get the default values after returning *enter*. If you don't give the name of the data file and

```
S 1 2 3 4 5 6 7 8 9 10 11 12
a 0.00 0.00 1.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 1.00 0.00
b 1.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 1.00 1.00
c 0.00 0.00 1.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
d 1.00 0.00 1.00 0.00 0.00 0.00 0.00 1.00 1.00 0.00 0.00 0.00
e 1.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 1.00 0.00
f 0.00 1.00 0.00 0.00 0.00 0.00 0.00 0.00 1.00 1.00 0.00 1.00
g 1.00 1.00 1.00 0.00 1.00 0.00 1.00 1.00 0.00 1.00 1.00 0.00
h 0.00 0.00 1.00 1.00 1.00 1.00 0.00 1.00 0.00 0.00 0.00 0.00
i 1.00 1.00 0.00 1.00 0.00 0.00 0.00 1.00 1.00 0.00 0.00 0.00
j 0.00 0.00 0.00 0.00 0.00 1.00 1.00 1.00 0.00 1.00 1.00 0.00
k 0.00 0.00 1.00 1.00 1.00 1.00 1.00 1.00 0.00 0.00 0.00 0.00
l 1.00 1.00 0.00 1.00 1.00 1.00 0.00 0.00 1.00 0.00 1.00 1.00
m 0.00 1.00 1.00 1.00 1.00 1.00 0.00 1.00 1.00 0.00 0.00 0.00
n 0.00 1.00 1.00 0.00 0.00 1.00 1.00 1.00 0.00 1.00 0.00 0.00
o 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 0.00 0.00 1.00 0.00
p 1.00 1.00 1.00 1.00 0.00 1.00 1.00 1.00 1.00 0.00 1.00 0.00
q 0.00 0.00 1.00 1.00 0.00 0.00 1.00 1.00 0.00 0.00 1.00 0.00
r 1.00 1.00 1.00 0.00 1.00 1.00 0.00 1.00 0.00 0.00 0.00 0.00
s 0.00 1.00 0.00 1.00 1.00 1.00 1.00 1.00 1.00 0.00 0.00 0.00
t 0.00 1.00 0.00 1.00 0.00 1.00 1.00 1.00 1.00 0.00 1.00 0.00
```

\* Comment

```
Test1.txt
return enter the program expects a batch
Test2.txt
run and a file name with the data files.
Test3.txt
```

```
Test4.txt
Next, the program asks for the model
Test5.txt
```

for randomization. In the case of incidence matrices you have five possibilities: A null model with fixed row and column constraints (input: s) using the independent swap algorithm (Gotelli 2000, 2001), no constraints (equiprobable row and columns, input: e), or fixed row (input: f) or fixed column (input: c) constraints only. For details of the null models used see Gotelli (2000, 2001). The independent swap model uses ten times the matrix size (10\*rows\*columns) single swaps to generate a randomized matrix.

The fifth null model (o) assigns species with a probability according to the number of site occurrences. This model is therefore identical to the Random 1 model of Patterson and Atmar (1986) and Wright et al. (1998).

In the case of abundances you have 16 null models divided in to two groups; one that reshuffles whole cell contents within the matrix and one that resamples according to predefined constraints:

1. *PM* reshuffles populations within the non-empty cells of the total matrix. The model alters total row and column relative abundances.

2. *PC* reshuffles populations within the non-empty

cells of each column. The model retains total row species richness but alters total row relative species abundances.

3. *PR* reshuffles populations within the non-empty cells of each row. The model retains total column species richness but alters total column relative species abundances.

4. *OA* resamples originally occupied cells proportional to observed row and column totals until the total number of individuals in the matrix is reached. *OS* does not retain observed row and column total abundances.

5. *OF* resamples originally occupied cells proportional to observed row and column totals until for each row and column total abundances are reached.

6. *IR* resamples the matrix proportional to observed row and column totals until total species richness is reached.

7. *IS* resamples the matrix proportional to observed row and column totals until for each row and column total species richness is reached. This model also preserves matrix wide species richness.

8. *ISA* resamples the matrix proportional to observed row and column totals until for each row and column total species richness is reached.

9. *ISR* sequentially resamples each row proportional to observed column totals until the respective row total species richness is reached. This model also preserves matrix wide species richness.

10. *ISC* sequentially resamples each column proportional to observed row totals until the respective column total species richness is reached. Again this model preserves matrix wide species richness.

11. *IT* resamples the matrix proportional to observed row and column totals until for each row and

```

C:\Users\ulichw\Documents\Projects\CoOccurrence.exe
*****
* Program Co-occurrence: Version 1; 12.05.2008
* Copyright Dr. Werner Ulrich
* The author does not take responsibility for correct
* program run or any damages caused by the program.
*****
Name of input file with extension. File has to have EcoSim format.
If batch run leave blank.
test.txt
Name of output file (with extension), default = Cooc.txt
Substructure analysis (yes/no), default = no
no
Name of matrix file (with extension), default = Matrix.txt, or type: no

Null model for randomization:
Fixed row and column constraints sequential swap (s),
no constraints (equiprobable row and columns)(e),
fixed row and equiprobable column constraints (f),
fixed column and equiprobable row constraints (c),
random sampling according to observed frequencies of occurrence (o),
random sampling from a lognormal distribution (l),
random sampling from the observed total abundance distribution (a)
a
Number of iterations for computing standard deviations of the null model
Default=100

test.txt Species: 20 Sites: 24 Nestedness: -0.468
Runtime of program: 0hh 0min 39sec
Fortran Pause - Enter command<CR> or <CR> to continue.

C:\Users\ulichw\Documents\Projects\Abundance\CoOccurrence.exe
*****
* Program Co-occurrence: Version 1; 12.05.2008
* Copyright Dr. Werner Ulrich
* The author does not take responsibility for correct
* program run or any damages caused by the program.
*****
Name of input file with extension. File has to have EcoSim format.
If batch run leave blank.
mat1.txt
Presence-absence (p)(default) or additional abundance analysis (a)
a
Abundances: using ranked data for metrics calculation (yes/no); default = no
Name of output file (with extension), default = Cooc.txt
Out.txt
Substructure analysis (yes/no), default = no
Name of matrix file (with extension), default = Matrix.txt, or type: no

Null model for randomization:
Fixed row and column constraints sequential swap (s),
no constraints (equiprobable row and columns)(e),
fixed row and equiprobable column constraints (f),
fixed column and equiprobable row constraints (c),
random sampling according to observed frequencies of occurrence (o),
abundance swap (pn),
abundance swap within columns (pc),
abundance swap within rows (pr),
resampling with total abundance fixed (ia),
resampling with row/column abundances fixed (it),
resampling site by site with column abundances fixed (itc),
resampling species by species with row abundances fixed (itr),
resampling with total species richness fixed (ir),
abundance swap with row/column abundances fixed (oi),
resampling with occurrences and total abundance fixed (oa),
resampling with occurrences and row/column abundances fixed (of),
resampling with row/column species richness fixed (is),
resampling with row/column species richness and total abundance fixed (isa),
resampling site by site with column species richness fixed (isc),
resampling species by species with row species richness fixed (isr),
resampling with row/column species richness and abundances fixed (if)
ia
Number of iterations for computing standard deviations of the null model
Default=100
10
mat1.txt Species: 77 Sites: 30 Nestedness: 1.258
Runtime of program: 0hh 1min 27sec
Fortran Pause - Enter command<CR> or <CR> to continue.

```

column total abundances are reached. This model also preserves matrix wide abundance.

12. *ITR* sequentially resamples each row proportional to observed column totals until the respective row total is reached. This model also preserves matrix wide abundance.

13. *ITC* sequentially resamples each column proportional to observed row totals until the respective column total is reached. Again this model preserves matrix wide abundance.

14. *IA* resamples the matrix proportional to observed row and column totals until the matrix wide

File	In	SimIn	StdDevIn	Z-In	StIndex	SkewIn	L95%CI	U95%CI
Checkerboard	0	0.00	0.00	0.00	0.0000	0.00	0.00	0.00
Combinations	3	1.63	1.35	1.01	0.0050	1.04	0.00	6.00
C-Score	10.56	11.47	1.41	-0.64	0.0000	0.36	9.18	14.43
BR	50	52.18	4.66	-0.47	-0.0055	0.16	44.00	62.00
Correlation	0.21	0.26	0.03	-1.65	-0.0665	0.20	0.20	0.32
Variancetest	2.77	2.38	0.21	1.84	0.0103	0.34	2.00	2.85
NODF	77.25	77.09	2.08	0.07	0.0067	-0.72	73.02	80.38
NODFcolumns	75.64	74.21	3.00	0.48	0.0554	-0.79	66.38	79.32
NODFrows	79.58	81.28	2.52	-0.67	-0.0906	-2.63	75.93	84.87

abundance is reached. This is the least constraint model.

15. *IF* is a two step algorithm that preserves row and column abundances and species richness. In the first step the algorithm converts the abundance matrix into a presence – absence matrix and reshuffles 2x2

submatrices of the form  $\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \vee \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$  to

$\begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix} \vee \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$ . In the second step it fills the non-empty cells according to algorithm *OF*.

Note that the program has the option to convert species abundances into ranks and perform all calculations with the rank abundances.

Next the program asks for the number of randomizations to compute the null model means and standard deviations, as well as upper and lower 95% confidence

Packed matrix: test.txt

	1.0	2.0	3.0	4.0	5.0	6.0	7.0	
1	1	1	1	1	1	1	1	7
2	1	1	1	1	1	0	0	5
3	1	1	1	1	1	0	0	5
4	1	1	1	1	0	1	0	5
5	1	1	1	0	0	0	0	3
6	1	1	0	0	1	0	0	3
7	1	1	0	1	0	0	0	3
8	1	0	1	0	0	0	0	2
9	0	1	0	0	0	0	0	1
10	1	0	0	0	0	0	0	1
	9	8	6	5	4	2	1	

Last packed randomized matrix: test.txt      No. of Swaps: 25000

	1.0	2.0	3.0	4.0	5.0	6.0	7.0	
1	1	1	1	1	1	1	1	7
2	1	1	1	1	1	0	0	5
3	1	1	1	1	1	0	0	5
4	1	1	1	1	1	0	0	5
5	1	1	1	0	0	0	0	3
6	1	1	0	1	0	0	0	3
7	1	0	1	0	0	1	0	3
8	1	1	0	0	0	0	0	2
9	1	0	0	0	0	0	0	1
10	0	1	0	0	0	0	0	1
	9	8	6	5	4	2	1	

limits. In most cases 100 such randomizations will be enough.

## 5. The output files

*CoOccurrence* produces two output files. The first file (*Cooc.txt*) contains basic information about the matrix and the measurements. First it gives species and site numbers, matrix fill, the total number of occurrences, and the null model algorithm. Then observed metric values, simulated values, the respective standard deviations, Z-scores, standardized values, skews of the null model distribution, and upper and lower 95% confidence limits of this distribution are provided. The second file *Matrix.txt* contains the packed original data matrix and the last randomized packed matrix. The examples above show both files. Due to the fixed output format (I5) the matrix file may have problems to proper print the values in the case of relative abundances as input values.

## 6. Null model properties

Different null models point to different degrees of randomness in the data. Matrix size and fill might also influence the results. The fixed row - fixed column model (sequential swap) appears to be the most conservative model while retaining the basic matrix properties during simulation. However, standard deviations of this model are often smaller than those of the other models increasing thus the probability of pointing to non-randomness. The equiprobable model, in turn, is the most liberal. Fixed row equiprobable column and fixed column equiprobable row constraints behave quite similar, which is not surprising due to the theoretical equivalence of matrix rows and columns. The lognormal sampling model appears to be robust against matrix fill but not against matrix size. Theoretically this model should behave similar to the fixed row - fixed column model.

There is no consensus about the question which

null model is best suited to account for passive sampling. Because the lognormal and the resample models are passive sampling models they should theoretically be preferred. However, we seldom know the underlying abundance distribution from which the individuals are drawn. Recent evidence (Ulrich and Gotelli 2007a, b) points to the fixed row - fixed column model to account best for passive sampling. However, there is still no comparative study. In my view the lognormal model and the fixed row - fixed column should be preferred.

## 7. Citing *CoOccurrence*

*CoOccurrence* is freeware but nevertheless if you use *CoOccurrence* in scientific work you should cite *CoOccurrence* as follows:

Ulrich W. 2006. *CoOccurrence* – a FORTRAN program for species co-occurrence analysis. [www.uni.torun.pl/~ulrichw](http://www.uni.torun.pl/~ulrichw)

## 8. System requirements

*CoOccurrence* is written in FORTRAN 95 and runs under Windows 9.x, XP, and Vista. The present version is limited to 300 sites, otherwise computation abilities are only limited by the computer's memory.

## 9. Acknowledgements

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