

Fourth-corner correlation is a score test statistic in a log-linear trait-environment model that is useful in permutation testing

Cajo J. F. ter Braak

Appendix S3. Permutation schemes based on the inflated data.

The five permutation schemes of the main text start from the layout of the data as a sites-by-species data table. In this appendix, two more schemes are described that start from an inflated data table. The description is for the case with a single trait and a single environmental variable.

With count data, individual organisms can be distinguished. In, what I call, the fully inflated table, each row represents an individual and lists two values: a trait value and an environmental value, which are the value of the trait of the species to which the individual organism belongs and the environmental value of the site in which it has been sampled, respectively. An example of this table is given in Fig. 1c of Dray & Legendre (2008). The fourth-corner correlation is precisely the Pearson correlation between the trait and the environmental variable in this fully inflated table. The observations in this table may not be independent so using the standard statistical test on the nullity of the correlation may not be right. Perhaps permutation is a way out. Dray and Legendre (2008) also considered permuting individuals (e.g. permuting their trait values while keeping the values of environmental variable fixed) but dropped the idea because it would lead to tests with highly inflated type I error rates. I included this scheme (referred to as scheme infl.ind) to verify this.

The weighted inflated table, as I call it, is the table with as many rows as there are nonzero entries in the abundance table $\mathbf{Y}$. Each row of this table lists the trait value, the environmental value and the relative count of the corresponding entry. The relative count is y_{ij}/y_{++} and is considered as the weight of the row. An example of this table is given in Fig. 1b of Dray & Legendre (2008). The fourth-corner correlation is precisely the weighted Pearson correlation between the trait and the environmental variable in this weighted inflated table. The scheme that randomly permutes the trait values while keeping the environmental values and the weights fixed has not been considered in Dray and Legendre (2008). This scheme (referred to as scheme infl.nz.cell.t, as it permutes the trait across the nonzero cells) looks at first sight similar to permutation model 1 of Dray and Legendre (2008) which permutes at random the cell entries (including zeroes) within columns of table $\mathbf{Y}$, but it is essentially different. First, the cell method does not include zeroes. Second, Model 1 destroys both the $\mathbf{Y-t}$ link and the $\mathbf{Y-e}$ link (see Appendix A of Dray & Legendre 2008) whereas the cell scheme destroys the $\mathbf{Y-t}$ link, but keeps the $\mathbf{Y-e}$ link intact. Similarly, a scheme infl.nz.cell.e can be defined, which randomly permutes the environmental values while keeping the trait values and the weights fixed. This scheme gives p values that differ slightly from those of the scheme infl.nz.cell.t and but the difference is not big enough to include this scheme explicitly in the reported result. Schemes that do not drop the zero entries from the vectorized data, so that the number of rows in the inflated data is equal to nm , were evaluated also, but results are not reported as they behave similar to when zeroes are dropped.

Scheme infl.nz.cell.t turns out to be so conservative in the three scenarios that do not include random variation that interacts with the observed trait or environment, that it almost controls the type I error rate in the two scenarios that do include this random variation. In order to examine whether this approximate error control holds for other parameter settings as well, I reran the simulations with the size of the coefficients b_{zx} , b_{ze} , b_{xt} and b_{te} set to 1 (where they were 0.2 in Fig. 1). In Fig. 1 $n=m=30$. In order to see what happens with unequal n and m , I set $n=50$, $m=20$. Further I decreased μ_0 from 30 to 10 to reduce the computation time for scheme infl.ind.

Table S1 present the type I error rates (false positives that incorrectly reject the true null hypothesis) at the 5% nominal level.

The results are shown graphically in Fig. S1 which has the same layout as Fig. 1 of the main text. Recall from the main text that “Except in the bottom-right panel in Fig. 1 (*i.e.*, non-null (alternative) model where $b_{te} \neq 0$), the ideal test in terms of type I error rates follows the 1:1 line. Lines above this line indicate liberal tests that have elevated Type I error rate (too many rejections at a specified nominal level, *e.g.* the horizontal dashed line at 0.05) and lines below the 1:1 line indicate conservative tests that have too few rejections at a specified nominal level. A test is said to control the type I error, if its type I error rate is at most the nominal level (Goeman and Solari 2010), that is, if its lines in Fig. 1 are all at or below the 1:1 line.”

The scheme infl.ind follows the 1:1 line only in the Poisson scenario. In the other null scenarios it is far too liberal (Fig. S1) as predicted by Dray & Legendre (2008).

The scheme infl.nz.cell.t is far too conservative in the scenarios that do not include random variation that interacts with the observed trait or observed environment (top row of Fig. S1). It is far too liberal in the other null scenarios.

Table S1. Type I error rates and (in last row) power at the nominal 0.05 level of the chi-square method (chi2) and six permutation tests in the six scenarios of Fig. S1. The schemes ind and cell in this table are permutation schemes infl.ind and infl.nz.cell in Fig. S1. Value in bold represents the inflated error compared to the nominal level of 0.05.

<i>Scenarios</i>	<i>Permutation schemes</i>						
	chi2	ind	cell	rc	row	col	max
Poisson	0.05	0.05	0.00	0.05	0.05	0.05	0.03
negbin	0.58	0.58	0.00	0.05	0.05	0.05	0.03
ran.int	0.85	0.85	0.02	0.05	0.05	0.05	0.01
$b_{ze} = 1$	0.96	0.96	0.27	0.52	0.66	0.05	0.05
$b_{tx} = 1$	0.94	0.94	0.28	0.35	0.05	0.51	0.05
$b_{te} = 1$	1.00	0.99	0.91	0.97	0.98	0.84	0.84

The change in parameter settings in these simulations did not modify the qualitative results for the permutation schemes in the main text. The quantitative differences are:

- the type I error rate inflation in the new setting is more severe; all tests that were already too liberal are even more so in the new setting.
- there is now asymmetry between the row and the column scheme, the row scheme being even more liberal than the col scheme.

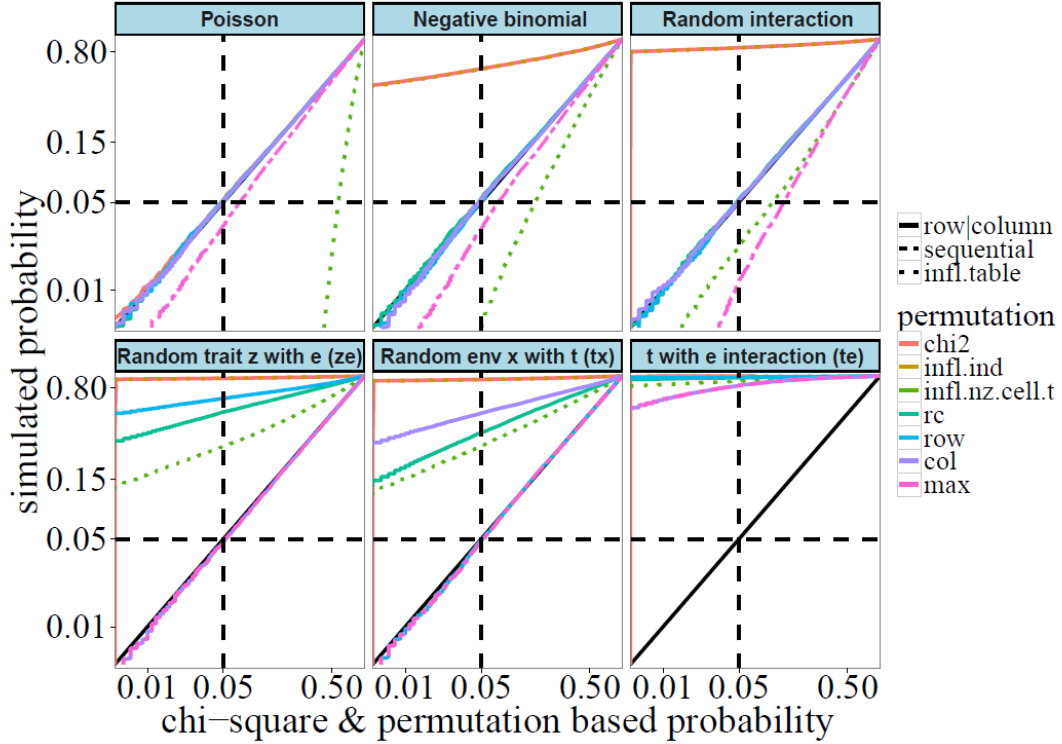


Fig.S1. Exceedance probability of the score test statistic of interaction in a Poisson log-linear model that also contains row and column main effects, as estimated from 10,000 simulated data sets, against the exceedance probability, as obtained from the chi-square distribution (chi2) and six different Monte Carlo permutation tests (999 permutations; permutation of the trait values in the full inflated table (infl.ind), permutation of the trait values in the weighted inflated table (infl.nz.cell.t), permutation of rows and column simultaneously (rc), of rows (row) and of columns (col) and the sequential combination of the row and col scheme in the max scheme, which takes the maximum of the p values of the row and the col scheme. The panels show results for six data generating scenarios, five of which represent typical deviations from the Poisson model (top left). All other models had negative binomially distributed response, without (top middle) and with further deviations (see text for details). The bottom right panel is the only model with a genuine non-zero interaction between the observed trait t and environment e . The variables z and x represent an unobserved (i.e. latent) trait and environmental variable, respectively. Parameter settings: $n=50$, $m=20$ and the coefficient of interaction (where nonzero) is 1.