Appendices to:

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Appendix S1

SIMULATIONS INVOLVING ARTIFICIAL SURVEY DATA AT TIMES T1 AND T2

Introduction

This section reports the results of a simulation study carried out to determine if the new test of significance of the temporal beta change at individual sites (TBI) has correct type I error rates and is able to detect sites for which the response data had exceptionally high dissimilarities between time 1 (T1) and time 2 (T2). Simulations were done with random data generated in three different ways; six dissimilarity coefficients were used as TBI indices. Three different permutation methods were also compared.

Data generation methods

Two methods were used to generate random community-like data in matrices Mat1 and Mat2. The first one (gen.method=1) was to draw values at random from the Poisson distribution. The second method (gen.method=2) was to use random lognormal data.

The random Poisson deviates were generated with a probability of occurrence (lambda parameter of the distribution) of 0.8. The generated data were skewed and contained approximately 45% zeros. For the lognormal data, the normal distribution generating the deviates that are exponentiated to produce random lognormal data had mean = 0 and standard deviation = 2.0. The values were rounded to the nearest integer. The generated data were highly skewed and contained approximately 36.5% zeros. Random lognormal data are much more highly skewed than random Poisson data.

It may be of interest to ecologists to identify sites that are exceptional in the changes to their community structure on the one hand, and sites that are exceptional in the changes to their environmental conditions on the other hand. So, in a third series of simulations, quantitative environmental data will be generated through random normal deviates; they will represent environmental variables in simulations. Real quantitative environmental data are often not normally distributed, but in many cases then can be normalized using data transformations. Qualitative variables (factors) will not be used in the simulations. How to handle them is described in section "Application to physical environmental or community trait data" of the main paper.

Dissimilarity coefficients

Six dissimilarity coefficients were used in the simulation study. Among the coefficients that are often used to analyse community composition data, we used the chord, Hellinger and log-chord distances that have the Euclidean property (a useful property for PCoA ordination), and the percentage difference and Ružička dissimilarities, which are non-Euclidean dissimilarities and can produce negative eigenvalues and complex axes in PCoA. The Euclidean distance was also used because it is the most widely used coefficient to analyse environmental data tables transformed by

standardization or ranging. Its behaviour for the analysis of community composition data will be assessed against the coefficients specialized for this type of data.

Permutation methods

The three permutation methods are described in the main paper. Briefly, they are:

• Method 1 (permute.sp = 1) — Permute data separately in each column, but in the same way in both matrices.

• Method 2 (permute.sp = 2) — Permute data separately in each column. Do not force the permutations to start at the same point in the two matrices.

• Method 3 (permute.sp = 3) — Permute entire rows in each matrix separately.

Simulations to estimate type I error rates

These simulations will provide an assessment of the validity of the three testing methods. "A statistical testing procedure is valid if the probability of a type I error (rejecting H_0 when true) is no greater than α, the level of significance, for any α." (Edgington 1995, p. 37).

Simulation methods

Simulation series 1, community composition data, random Poisson deviates

Two subseries of simulations were carried out:

1.1. In the first subseries, the two matrices (mat.1 and mat.2, of size $n \times p$) contained random Poisson deviates, as described in the introduction of this Appendix; Fig. S1.1. Three permutation methods were used with 999 random permutations. See results in Table S1.1.

1.2. In this subseries of simulations, in addition to the random rata in mat.1a and mat.2a (called mat.1 and mat.2 in Fig. S1.1), a submatrix mat1.d containing zeros was added to mat.1a and a matrix mat2.d containing random Poisson deviates was added to mat.2a; see Fig. S1.2. Results with *p3* = 6 are shown in Table S1.2.

The objective of the second subseries was to show the effect on the tests of significance of having extra species in the data matrices showing strong difference between T1 and T2 (absent in **Mat.1** and present in **Mat.2**) but with only random differences among the sites. These extra species should have no effect on the TBI tests.

Simulation series 2, community composition data, random lognormal deviates

Two subseries of simulations were carried out:

2.1. In the first subseries, the two matrices (mat.1 and mat.2, of size $n \times p$) contained random lognormal deviates, as described in the introduction of this Appendix; Fig. S1.1. Three permutation methods were used with 999 random permutations. See results in Table S1.3.

2.2. In this subseries of simulations, in addition to the random rata in mat.1a and mat.2a (called mat.1 and mat.2 in Fig. S1.1), a submatrix mat1.d containing zeros was added to mat.1a and a matrix mat2.d containing random Poisson deviates was added to mat.2a; see Fig. S1.2. Results with *p3* = 6 are shown in Table S1.4.

The objective of the second subseries was the same as for subseries 1.2, with a different way of generating community composition-like data.

Simulation series 3, environmental data, random normal deviates

3. In this last series, quantitative environmental data were simulated using random normal deviates instead of species-like data. There were $n = 20$ sites and $p = 20$ variables in matrices **Mat.1** and **Mat.2**, as in Fig. S1.1. TBI tests were only computed with the Euclidean distance. The other distances investigated in the previous simulation series only make sense for community composition and other frequency-like data (Legendre & Legendre 2012, Chapter 7). The three permutation methods were used with 999 random permutations.

The data vectors were standardized as described in Appendix S5. Explanation: (a) the two data tables are joined into a single data matrix, **Y** = rbind(**Mat.1**, **Mat.2**), before standardization. In this way, the differences in values of each variable for a given pair of sites in the two tables will remain comparable to the differences of computed from the original unstandardized values; in this way, the distances computed between sites in T1 and T2 will be meaningful. This precaution is important when there are differences in means between T1 and T2. (b) Standardizing the variables insures that all variables will contribute the same variance to the calculation of the TBI indices; the variances will not depend on the physical units of the variables or other contingencies that make the variances unequal.

Results, type I error study

Results are presented in Tables S1.1 and S1.2 for random Poisson deviates, in Tables S1.3 and S1.4 for random lognormal deviates deviates, and in Table S1.5 for normal deviates.

The simulations produced the expected result that type I error was always correct. The three testing methods are thus valid following the definition shown above (Edgington 1995).

1. Examination of the tables of rejection rates of the null hypothesis (Table S1.1-S1.4) showed that the TBI tests had correct rates of type I error with the three permutational testing methods, for the two community-like data generation methods (Poisson and lognormal) and all dissimilarity indices used, and this for all significance levels (α) considered, from $\alpha = 0.01$ to $\alpha = 0.50$. Deviations from the nominal significance levels, shown at the top of each table, were very small. Simulations involving random environmental-like quantitative data (Table S1.5) also showed correct levels of type I error with the Euclidean distance used in the computation of TBI indices.

2. The tables of rejection rates were divided into separate matrices per data generation and permutation methods, and transformed into squared differences (or squared errors) between the rejection rates and the nominal significance levels α. The sum of the squared differences was computed for each matrix. Examination of the results (not shown in detail in this Appendix) showed no significant difference (Friedman's test) in type I error rejection rates between the data generation methods (Poisson or lognormal) or among the permutation methods.

3. The additional species that were present in **Mat.2** but not in **Mat.1**, did not affect the type I error rates of the TBI tests. The rejection rates in Tables S1.1 and S1.2 (random Poisson deviates), and those in Tables S1.3 and S1.4 (random lognormal deviates), were very similar. In Tables S1.2 and S1.4 (simulation subseries 2), the rejection rates produced by permutation method 2 were the closest to the nominal significance levels, as it was the case in Tables S1.1 and S1.3 (subseries 1).

Note — The percentage difference and Ružička dissimilarity indices differ only by their denominators. The tests of significance of these two indices produce the same p-value if they are run with the same series of permuted vectors. Since the random number generator was started at the same value at the beginning of all simulation runs, it is normal that the rejection rates found for these two dissimilarities in TBI simulations be the same in the report tables (Tables S1.1 to S1.4).

Simulations to compare power of *D* indices and permutation methods

Simulation methods

For the power simulations, some of the sites were generated with a strong difference between T1 and T2 whereas other sites only had random differences. The objective of these simulations was to determine (a) if some permutation methods produced more powerful tests than other methods for the two types of data (community composition and environmental), and (b) if some dissimilarity functions were better suited to identify sites with strong differences in community composition data between T1 and T2 than other dissimilarities.

Data generation proceeded as follows for community composition data. *n1* sites were assigned to a first group that differed in composition between T1 and T2, whereas *n2* sites only had random variation between T1 and T2. Refer to Fig. S1.3.

1. The *n1* sites received strong differences between T1 and T2, as follows:

• A first group of *p1* species received random abundance values in mat.1a.

• A second group of *p2* species received random abundance values in mat.2b

• In **Mat.1**, the *p2* species received the values of mat.2b times a contribution constant (parameter “contr") with values between 0 and 1; contr = 0.2 was used in the simulations with random Poisson deviates reported below. For the simulations with random lognormal deviates, contr was either 0.01 or 0.02, as described below.

• In **Mat.2**, the *p1* species received the values of mat.1a times the same contribution constant "contr" as in the previous paragraph.

The generated abundance-like values were either random Poisson or random lognormal deviates, as described at the beginning of this Appendix.

2. The *n2* sites received random abundance-like values, either Poisson or lognormal. Hence the differences between T1 and T2 were random for these sites (Fig. S1.3).

In the results reported below, $n1 = 5$, $n2 = 15$, $p1 = p2 = 10$. For random Poisson deviates, contr = 0.2. For the simulations with random lognormal deviates, contr was either 0.01 or 0.02, as described below. 1000 data sets were independently generated and analysed for each reported rejection rate (0.01, 0.05, 0.10) in Tables S1.6 and S1.7 reporting the results.

Simulation series 1, community composition data, random Poisson deviates

Two subseries of simulations were carried out:

1. In the first subseries, all matrices simply random Poisson deviates, structured following Fig. S1.3.

2. In addition, a submatrix mat1.d containing zeros was added to **Mat.1** and a matrix mat2.d was added to **Mat.2**, as in the subseries 2 simulations for type I error. See Fig. S1.4.

The objective of the second subseries was to show the effect on the tests of significance of having extra species in the data matrices showing strong difference between T1 and T2 (absent in **Mat.1** and present in **Mat.2**) but with only random differences among the sites. These extra species should have little effect, if any, on the TBI tests of significance.

Simulation series 2, community composition data, random lognormal deviates

Two subseries of simulations were carried out.

1. Random lognormal deviates. The contributions of the mat.2b data to the mat.1b data, and of the mat.1a data to the mat.2a data, was determined by contr = 0.01.

2. The contribution parameter (contr) had the value 0.02.

The contribution parameter was adjusted to produce different rejection rates among the three permutation methods. That was obtained with the contribution values contr = [0.01, 0.02] that were used to generate the values in mat1b and mat2a. With contr = 0, the differences between **Mat.1** and **Mat.2** for the first 5 sites were so strong that all methods rejected H_0 with very high rates and identified the first 5 sites as exceptional; differences among the permutation methods were not clearly shown.

Simulation series 3, environmental data, random normal deviates

For simulation involving data simulating pseudo-environmental variables, the construction of the data matrices followed the same method as in simulation subseries 1 above, except that the data were random normal deviates standardized as described in Appendix S5.

In the results reported below, there were $n1 = 5$ and $n2 = 15$ sites, $p1 = p2 = 10$ variables. The contribution parameter was chosen to be contr = 0.05. 1000 data sets were independently generated and analysed for each reported rejection rate (0.01, 0.05, 0.10) in Tables S1.8 reporting the results.

Results, power study

Results are presented in Tables S1.6 and S1.7 for simulated community composition data and in Table S1.8 for simulated environmental data.

Differences among D and permutation methods, community composition data

Power is the ability to detect an effect when one is present in the data. In the simulations reported here, we know that rather large effects were present in all data sets because the simulation function had generated it in the data.

From the simulation results for community composition data (simulation series 1: Table S1.6, Fig. S1.5; simulation series 2: Table S1.7, Fig. S1.6), we can make the following observations, working from the bottom of the graphs up:

1. All simulations involving the Euclidean distance for the computation of TBI indices had dismally low power (triangles pointing down). TBI indices computed with the Euclidean distance hardly ever detected the presence of exceptional sites in the species-like data files simulated with Poisson or lognormal deviates. The Euclidean distance should not be used for TBI tests of community composition data.

2. The tests of significance of TBI indices carried out with permutation method 3 (black dashed lines) had much lower power than the tests produced with permutation methods 1 and 2 (blue and red lines). The power of this permutation method improved at nominal significance level 0.10, but even then power was lower than that of permutation methods 1 and 2. For the significance levels (0.01 and 0.05) routinely used in tests of significance, the power for detecting exceptional sites in data that contained an effect was much lower than with permutation methods 1 and 2. Permutation method 3 should not be used with community composition data.

3. For data generated with Poisson or lognormal distributions, the most powerful TBI tests were computed with the percentage difference (aka Bray-Curtis) and Ružička dissimilarities, followed by the group {Hellinger, log-chord} distances which produced very similar results with species-like data simulated with Poisson random deviates, and log-chord distances for community data simulated with lognormal deviates. TBI tests based on the chord dissimilarity had the lowest power among the distances that produced usable tests. The log-chord distance was expected to be the most appropriate (and thus produce more powerful tests that the chord or Hellinger distances) with lognormally distributed data since the log transformation, which is the first transformation in the calculation of that distance, makes the random data normal before the chord transformation is computed.

4. Permutation methods 1 (blue lines) and 2 (red lines) can both be used, with a small advantage for method 1 in results of Poisson simulations, and equivalent powers for methods 1 and 2 in simulations based on lognormal deviates.

5. When sites had entirely different species compositions between T1 and T2, the TBI test had maximum power: it always rejected H_0 at significance levels of 0.05 and 0.10, and in 98.7% of the cases at level 0.01. This situation was produced by setting the contribution parameter to the value contr=0 for the generation of data in submatrices mat1b and mat2b (see Fig. S1.3). These rejection rates were obtained with all dissimilarity indices tested: percentage difference, Ruzicka, chord, Hellinger and log-chord distances.

The best combination for TBI tests of community composition data with maximum power is to use the percentage difference or the Ružička indices with permutation methods 1 or 2. These two dissimilarities can also be decomposed into species losses (*B*/*den*) and gains (*C*/*den*), which can be used to examine the processes of losses and gains at the site level and to produce B-C plots.

Differences in power for simulated environmental data

For standardized environmental variables (simulation series 3, Table S1.8), the only distance tested in the simulation study was the Euclidean distance. The results show a marked advantage of

permutation method 1, which had higher power than the other two methods to detect effects that were present in simulated data. It would be the method of choice for this type of data.

Additional simulations, differences in power associated with different values of n1 and n2

Power to detect an effect in statistical tests is well-known to be a function of three parameters: the importance of the effect to be detected, the significance level α, and the number of observations n. Additional simulations were conducted to detect the effect on power of the number of exceptional sites (*n1*) and the number of sites with random variation (*n2*) in the study. Community composition was simulated using random lognormal deviates.

1. The number of sites n was 20 in all simulations, with the number of affected sites *n1* = varying from 1 to 19; *n2* = (n – *n1*). The simulations used the percentage difference index, permutation method 1, and contr = 0.02, 1000 independent simulations and permutation method 1 with 999 permutations.

The results show that for tests of significance at level alpha = 0.05, optimal power was obtained with *n1* = 1 to 9 in simulations (Fig. S1.7a). *n1* should not be larger than n/2. Tests carried out with *n1* equal to or larger than n/2 can still be used but they have lower power.

2. For *n1* = n/4, simulations were repeated for different values, with n = {8,16,24,32,40,48,56,64} and *n1* = {2,4,6,8,10,12,14,16}. Again, the simulations used random lognormal data, the percentage difference index, contr = 0.02, 1000 independent simulations and permutation method 1 with 999 permutations.

Rejection rates are reported in Fig. S1.7b for three significance levels alpha: 0.01, 0.05 and 0.10. Power remained constant over all values of n investigated.

In summary, power of the test performed with permutation method 1 was high when the effect was strong, and as long as the proportion of sites with an effect was smaller than n/2 (Fig. S1.7a). For a fixed proportion of affected sites, power did not increase when the total number of sites n in the study was larger (Fig. S1.7b).

References

Edgington, E. S. (1995) *Randomization Tests, 3rd edn.* Marcel Dekker, New York.

Legendre, P. & L. Legendre. (2012) *Numerical ecology, 3rd English edn*. Elsevier Science BV, Amsterdam.

Table S1.1. Type I error rates of the test of the TBI *D* indices shown in the first column: rejection rates (i.e. number of rejections of H_0 divided by the number of simulations, which was 1000) of the TBI test when there were no exceptional sites in the simulated data. The data were drawn from a random Poisson distribution; n = 20 sites, p = 20 species (Fig. S1.1). Three permutational methods were used with 999 random permutations. Simulation series 1: data at all sites and both times came from the same statistical population, hence H_0 was true.

	Permutation	Nominal significance levels						
	methods	0.01	0.05	0.10	0.20	0.30	0.40	0.50
% difference	1	0.000	0.034	0.108	0.208	0.275	0.335	0.491
% difference	2	0.009	0.048	0.094	0.192	0.298	0.398	0.497
% difference	3	0.008	0.049	0.097	0.195	0.289	0.385	0.493
Ružička	1	0.000	0.033	0.108	0.208	0.275	0.333	0.492
Ružička	2	0.009	0.047	0.093	0.190	0.296	0.397	0.498
Ružička	3	0.008	0.050	0.099	0.199	0.291	0.388	0.497
Chord	1	0.000	0.042	0.075	0.200	0.292	0.383	0.475
Chord	2	0.011	0.052	0.099	0.196	0.298	0.404	0.503
Chord	3	0.009	0.053	0.100	0.195	0.297	0.398	0.492
Hellinger	1	0.000	0.042	0.100	0.175	0.300	0.367	0.517
Hellinger	2	0.011	0.050	0.101	0.199	0.301	0.411	0.505
Hellinger	3	0.010	0.050	0.101	0.197	0.295	0.400	0.500
Log-chord	1	0.000	0.050	0.117	0.183	0.300	0.375	0.483
Log-chord	2	0.011	0.052	0.101	0.198	0.301	0.408	0.506
Log-chord	3	0.010	0.052	0.102	0.196	0.297	0.395	0.503
Euclidean	1	0.000	0.025	0.094	0.200	0.319	0.400	0.494
Euclidean	2	0.007	0.046	0.092	0.194	0.290	0.390	0.488
Euclidean	3	0.007	0.046	0.091	0.195	0.289	0.381	0.480

Table S1.2. Type I error rates of the test of the TBI *D* indices shown in the first column. See caption of Table S1.1. The data were drawn from a random Poisson distribution; n = 20 sites. Simulation series 2: for the basic *p1* = 20 species, data at all sites and both times came from the same statistical population. In addition, T2 had *p3* = 6 species more than T1 (Fig. S1.2). For these 6 species, there were no differences among the sites besides random variation; hence H_0 was still true.

	Permutation	Nominal significance levels						
	methods	0.01	0.05	0.10	0.20	0.30	0.40	0.50
% difference	1	0.017	0.042	0.092	0.183	0.267	0.425	0.541
% difference	2	0.008	0.054	0.086	0.176	0.269	0.383	0.494
% difference	3	0.007	0.043	0.091	0.192	0.292	0.388	0.496
Ružička	1	0.017	0.042	0.091	0.183	0.267	0.425	0.541
Ružička	2	0.009	0.048	0.095	0.199	0.302	0.401	0.505
Ružička	3	0.007	0.043	0.090	0.191	0.290	0.386	0.494
Chord	1	0.000	0.062	0.112	0.212	0.312	0.450	0.525
Chord	2	0.010	0.051	0.100	0.205	0.307	0.406	0.509
Chord	3	0.009	0.045	0.093	0.197	0.299	0.399	0.497
Hellinger	1	0.000	0.075	0.112	0.213	0.312	0.375	0.550
Hellinger	2	0.010	0.049	0.099	0.202	0.305	0.403	0.504
Hellinger	3	0.009	0.043	0.091	0.194	0.292	0.392	0.497
Log-chord	1	0.000	0.075	0.100	0.238	0.312	0.400	0.550
Log-chord	2	0.010	0.050	0.100	0.203	0.304	0.406	0.503
Log-chord	3	0.009	0.045	0.094	0.194	0.294	0.397	0.497
Euclidean	1	0.008	0.050	0.100	0.208	0.300	0.383	0.508
Euclidean	2	0.011	0.050	0.095	0.189	0.289	0.384	0.484
Euclidean	3	0.006	0.043	0.097	0.191	0.293	0.391	0.491

Table S1.3. Type I error rates of the test of the TBI *D* indices shown in the first column: rejection rates (i.e. number of rejections of H_0 divided by the number of simulations, which was 1000) of the TBI test when there were no exceptional sites in the simulated data. The data were drawn from a random lognormal distribution; n = 20 sites, p = 20 species (Fig. S1.1). Three permutational methods were used with 999 random permutations. Simulation series 1: data at all sites and both times came from the same statistical population, hence H_0 was true.

	Permutation	Nominal significance levels						
	methods	0.01	0.05	0.10	0.20	0.30	0.40	0.50
%difference *D*	1	0.014	0.064	0.121	0.193	0.293	0.386	0.486
	2	0.010	0.051	0.101	0.199	0.300	0.403	0.504
	3	0.007	0.045	0.079	0.173	0.254	0.362	0.476
Ružička *D*	1	0.014	0.064	0.121	0.193	0.293	0.386	0.486
	2	0.010	0.051	0.101	0.199	0.300	0.403	0.504
	3	0.007	0.045	0.079	0.173	0.254	0.362	0.476
Chord *D*	1	0.000	0.038	0.100	0.188	0.251	0.388	0.513
	2	0.012	0.051	0.101	0.195	0.298	0.401	0.498
	3	0.008	0.031	0.085	0.176	0.278	0.370	0.468
Hellinger *D*	1	0.000	0.050	0.100	0.175	0.263	0.375	0.562
	2	0.012	0.052	0.102	0.201	0.303	0.398	0.498
	3	0.007	0.036	0.072	0.165	0.270	0.381	0.496
Log-chord *D*	1	0.000	0.025	0.076	0.213	0.313	0.425	0.512
	2	0.011	0.054	0.103	0.197	0.299	0.399	0.497
	3	0.008	0.036	0.081	0.163	0.264	0.374	0.479
Euclidean *D*	1	0.000	0.050	0.112	0.188	0.312	0.413	0.500
	2	0.009	0.051	0.100	0.202	0.303	0.403	0.502
	3	0.018	0.048	0.100	0.183	0.273	0.390	0.503

Table S1.4. Type I error rates of the test of the TBI *D* indices shown in the first column. See caption of Table S1.3. The data were drawn from a random lognormal distribution; $n = 20$ sites. Simulation series 2: for the basic $p1 = 20$ species, data at all sites and both times came from the same statistical population. In addition, T2 had $p3 = 6$ species more than T1 (Fig. S1.2). For these 6 species, there were no differences among the sites besides random variation; hence H_0 was still true.

	Permutation methods	Nominal significance levels						
		0.01	0.05	0.10	0.20	0.30	0.40	0.50
%difference *D*	1	0.022	0.061	0.105	0.210	0.294	0.389	0.500
	2	0.009	0.055	0.100	0.195	0.299	0.404	0.501
	3	0.008	0.046	0.114	0.193	0.275	0.386	0.462
Ružička *D*	1	0.022	0.061	0.105	0.210	0.294	0.389	0.500
	2	0.009	0.055	0.100	0.195	0.299	0.404	0.501
	3	0.008	0.046	0.114	0.193	0.275	0.386	0.462
Chord *D*	1	0.017	0.061	0.100	0.222	0.300	0.411	0.517
	2	0.009	0.048	0.098	0.197	0.295	0.395	0.497
	3	0.014	0.059	0.106	0.179	0.269	0.359	0.485
Hellinger *D*	1	0.017	0.055	0.111	0.194	0.273	0.368	0.501
	2	0.012	0.049	0.095	0.196	0.295	0.399	0.491
	3	0.005	0.061	0.094	0.184	0.280	0.374	0.501
Log-chord *D*	1	0.022	0.072	0.116	0.194	0.273	0.401	0.506
	2	0.009	0.048	0.096	0.192	0.290	0.398	0.491
	3	0.005	0.043	0.103	0.198	0.295	0.391	0.506
Euclidean *D*	1	0.017	0.056	0.133	0.194	0.322	0.405	0.505
	2	0.011	0.050	0.100	0.197	0.299	0.393	0.501
	3	0.004	0.050	0.107	0.186	0.303	0.400	0.480

Table S1.5. Type I error rates of the test of TBI indices computed using the Euclidean distance. Simulation series 3: the data were drawn from a random normal distribution; n = 20 sites, p = 20 variables. Three permutation methods were used with 999 random permutations. Data at all sites and both times came from the same statistical population, hence H_0 was true.

	Permutation	Nominal significance levels						
	methods	0.01	0.05	0.10	0.20	0.30	0.40	0.50
Euclidean *D*	1	0.007	0.050	0.100	0.193	0.321	0.421	0.528
	2	0.009	0.049	0.096	0.204	0.304	0.410	0.500
	3	0.010	0.050	0.112	0.209	0.304	0.392	0.495

Table S1.6. Power analysis of TBI *D* indices shown in the first column, random Poisson data. There were *n1* = 5 exceptional sites in the simulated data. The results in the table are the mean rejection rates of the TBI test for these 5 sites, computed as the number of rejections of H_0 divided by the number of simulations, which was 1000. (A) Data with *p1* and *p2* species only (Fig. S1.3). (B) *p3* = 6 extra species with values of 0 in Mat.1 and random Poisson deviates in all sites of Mat.2 (Fig. S1.4); H_0 is true for these *p3* species.

		(A) p1 and p2 species			(B) p1, p2 and p3 species		
	Permutation	Significance levels			Significance levels		
	methods	0.01	0.05	0.10	0.01	0.05	0.10
%difference *D*	1	0.341	0.787	0.859	0.478	0.858	0.900
	2	0.370	0.699	0.897	0.377	0.765	0.878
	3	0.000	0.256	0.686	0.000	0.212	0.716
Ružička *D*	1	0.341	0.787	0.859	0.478	0.858	0.900
	2	0.370	0.699	0.897	0.377	0.765	0.878
	3	0.000	0.256	0.686	0.000	0.212	0.716
Chord *D*	1	0.355	0.511	0.600	0.381	0.580	0.720
	2	0.350	0.400	0.493	0.355	0.425	0.527
	3	0.000	0.211	0.418	0.000	0.190	0.396
Hellinger *D*	1	0.377	0.577	0.711	0.421	0.660	0.840
	2	0.350	0.541	0.699	0.357	0.574	0.722
	3	0.000	0.214	0.529	0.000	0.191	0.526
Log-chord *D*	1	0.355	0.600	0.711	0.401	0.620	0.800
	2	0.350	0.492	0.660	0.355	0.523	0.694
	3	0.000	0.212	0.497	0.000	0.191	0.477
Euclidean *D*	1	0.000	0.000	0.000	0.000	0.000	0.020
	2	0.000	0.001	0.006	0.000	0.002	0.012
	3	0.000	0.000	0.002	0.000	0.002	0.009

Table S1.7. Power analysis of TBI *D* indices shown in the first column, random lognormal data. There were 5 exceptional sites in the simulated data. The results in the table are the mean rejection rates of the TBI test for these 5 sites, computed as the number of rejections of H_0 divided by the number of simulations, which was 1000. Data with *p1* and *p2* species only (Fig. S1.3). There were no extra species in these simulations (*p*3 = 0). The contribution parameter of these simulations varied: (A) contr = 0.01, (B) contr = 0.02.

		(A) contr = 0.01			(B) contr = 0.02		
	Permutation	Significance levels			Significance levels		
	methods	0.01	0.05	0.10	0.01	0.05	0.10
%difference *D*	1	0.875	0.975	1.000	0.463	0.849	0.962
	2	0.872	0.997	1.000	0.472	0.865	0.982
	3	0.000	0.387	0.971	0.002	0.354	0.770
Ružička *D*	1	0.875	0.975	1.000	0.463	0.849	0.962
	2	0.872	0.997	1.000	0.472	0.865	0.982
	3	0.000	0.387	0.971	0.002	0.354	0.770
Chord *D*	1	0.625	0.675	0.713	0.301	0.313	0.338
	2	0.668	0.668	0.681	0.360	0.360	0.360
	3	0.000	0.301	0.601	0.002	0.284	0.345
Hellinger *D*	1	0.612	0.737	0.850	0.315	0.401	0.529
	2	0.657	0.714	0.824	0.363	0.419	0.586
	3	0.000	0.303	0.639	0.003	0.285	0.381
Log-chord *D*	1	0.676	0.887	0.912	0.401	0.638	0.750
	2	0.714	0.902	0.939	0.403	0.659	0.766
	3	0.000	0.306	0.756	0.002	0.296	0.532
Euclidean *D*	1	0.012	0.025	0.062	0.012	0.025	0.062
	2	0.000	0.003	0.038	0.000	0.003	0.018
	3	0.002	0.022	0.048	0.002	0.018	0.044

Table S1.8. Power analysis of TBI indices computed using the Euclidean distance, random normal data. There were 5 exceptional sites in the simulated data. The results in the table are the mean rejection rates of the TBI test for these 5 sites, computed as the number of rejections of H_0 divided by the number of simulations, which was 1000. Data with p1 and p2 species only. There were no extra species in these simulations ($p3 = 0$). contr = 0.05.

		contr = 0.05		
	Permutation	Significance levels		
	methods	0.01	0.05	0.10
Euclidean *D*	1	0.627	0.772	0.843
	2	0.251	0.449	0.657
	3	0.033	0.182	0.310

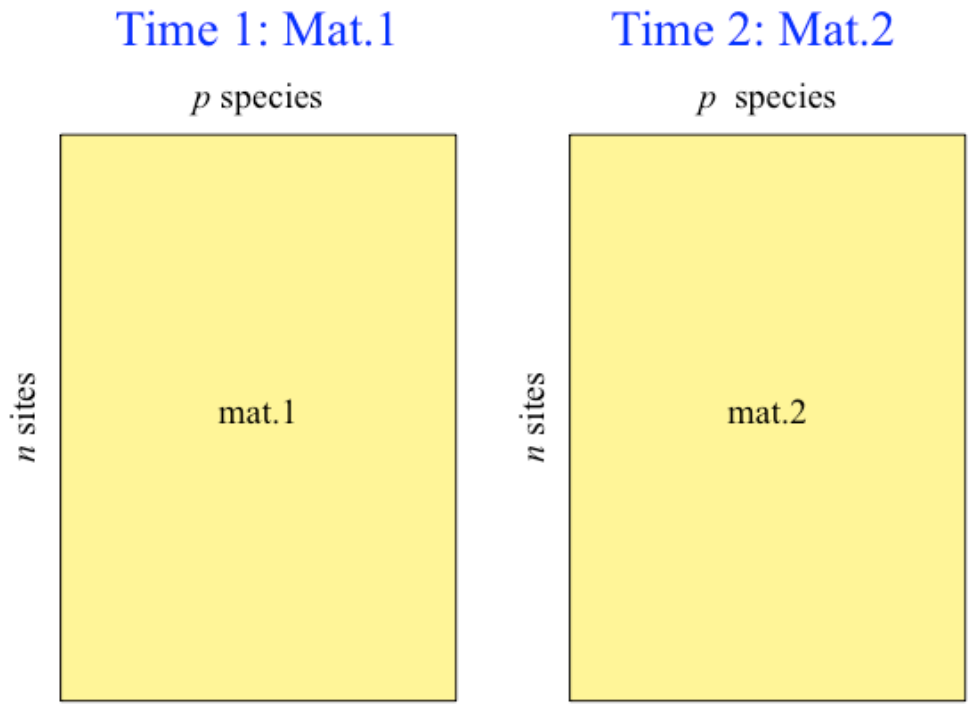

Fig. S1.1. Two data matrices (**Mat.1** and **Mat.2**) used in the type I error simulations. Sections mat.1 and mat.2 were filled with random numbers, so that H_0 was true. Note: **Mat.1** and **Mat.2** contain only one section each here; they will contain more sections in the next figures.

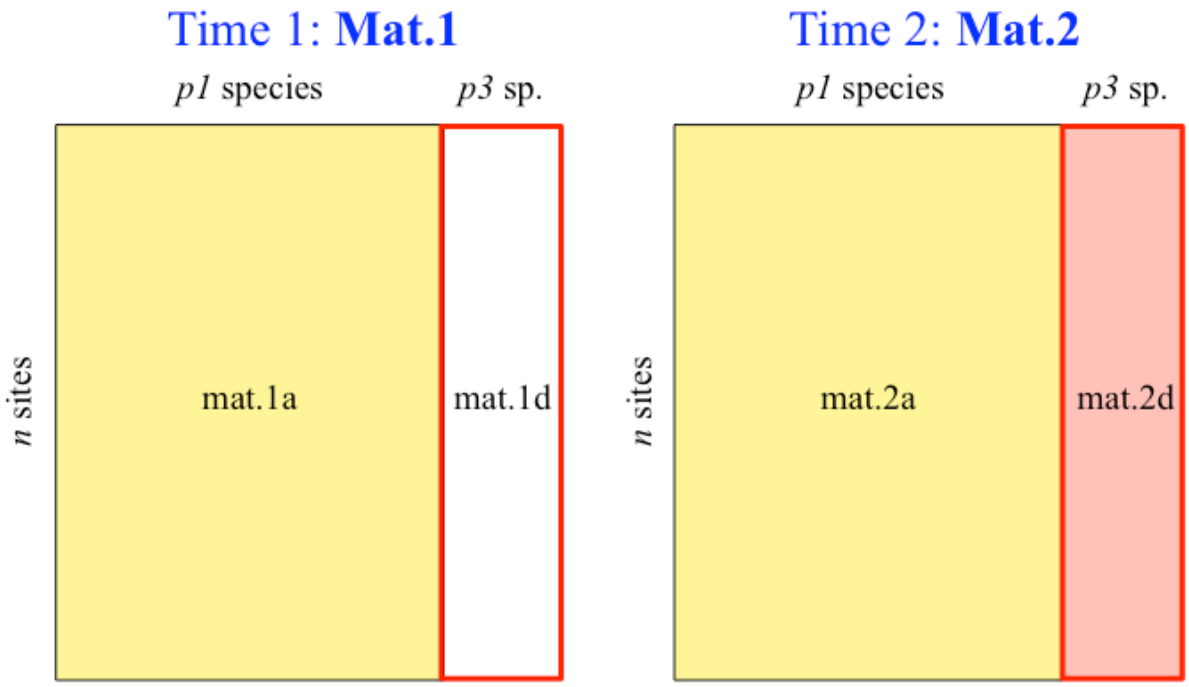

Fig. S1.2. Two data matrices (**Mat.1** and **Mat.2**) used in the type I error simulations; mat.1a and mat.2a contained random numbers, as in Fig. S1.1. In the simulations of subseries 2, mat.1d (white, containing zeros) and mat.2d (pink, containing random numbers) were joined to mat.1a and mat.2a.

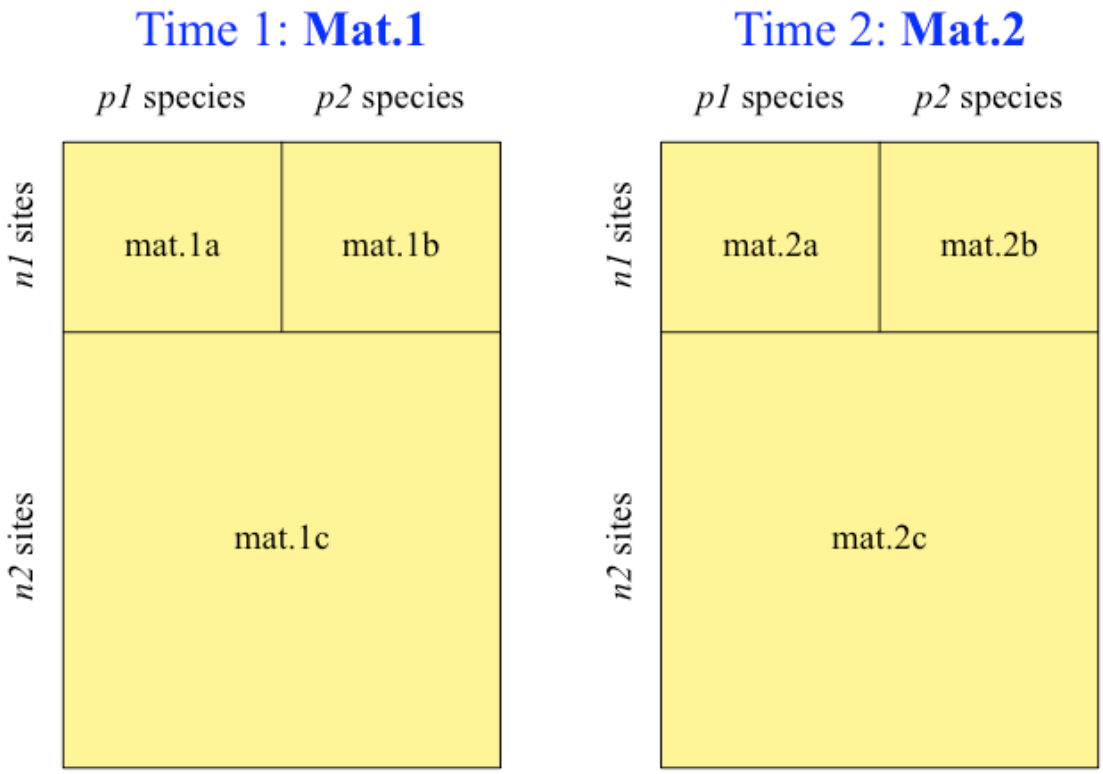

Fig. S1.3. Two matrices (**Mat.1** and **Mat.2**) used in the power simulations. Abundances in mat.1a and mat.2b were generated independently using either random Poisson or random lognormal deviates. Submatrix mat.1b received a fraction of the abundances in mat.2b and mat 2a received a contribution of the abundances in mat 1a. The values of these contributions are described in the text and depend of the random data generator used. Submatrices mat.1c and mat.2c received random deviates drawn from the same statistical population.

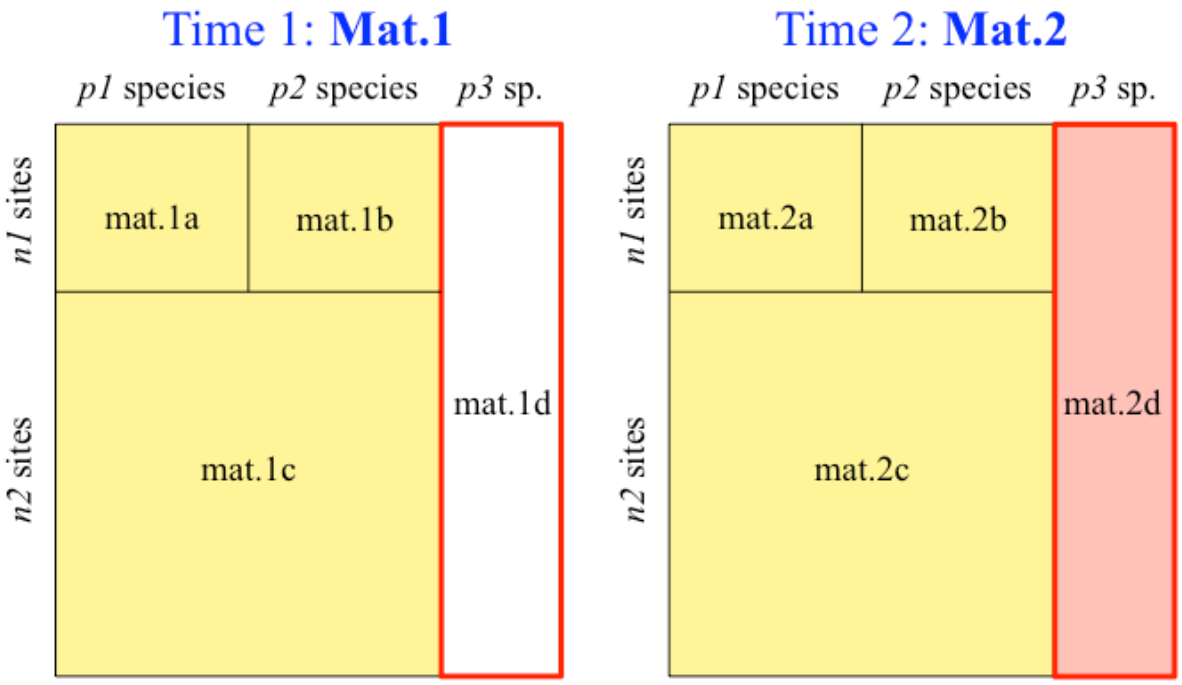

Fig. S1.4. Two matrices (**Mat.1** and **Mat.2**) used in additional power simulations with random Poisson error. In these simulations, mat.1d (white, containing zeros) and mat.2d (pink, containing random numbers) were joined to mat.1a-b-c and mat.2a-b-c. H_0 was true for the *p3* species in mat.1d and mat.2d.

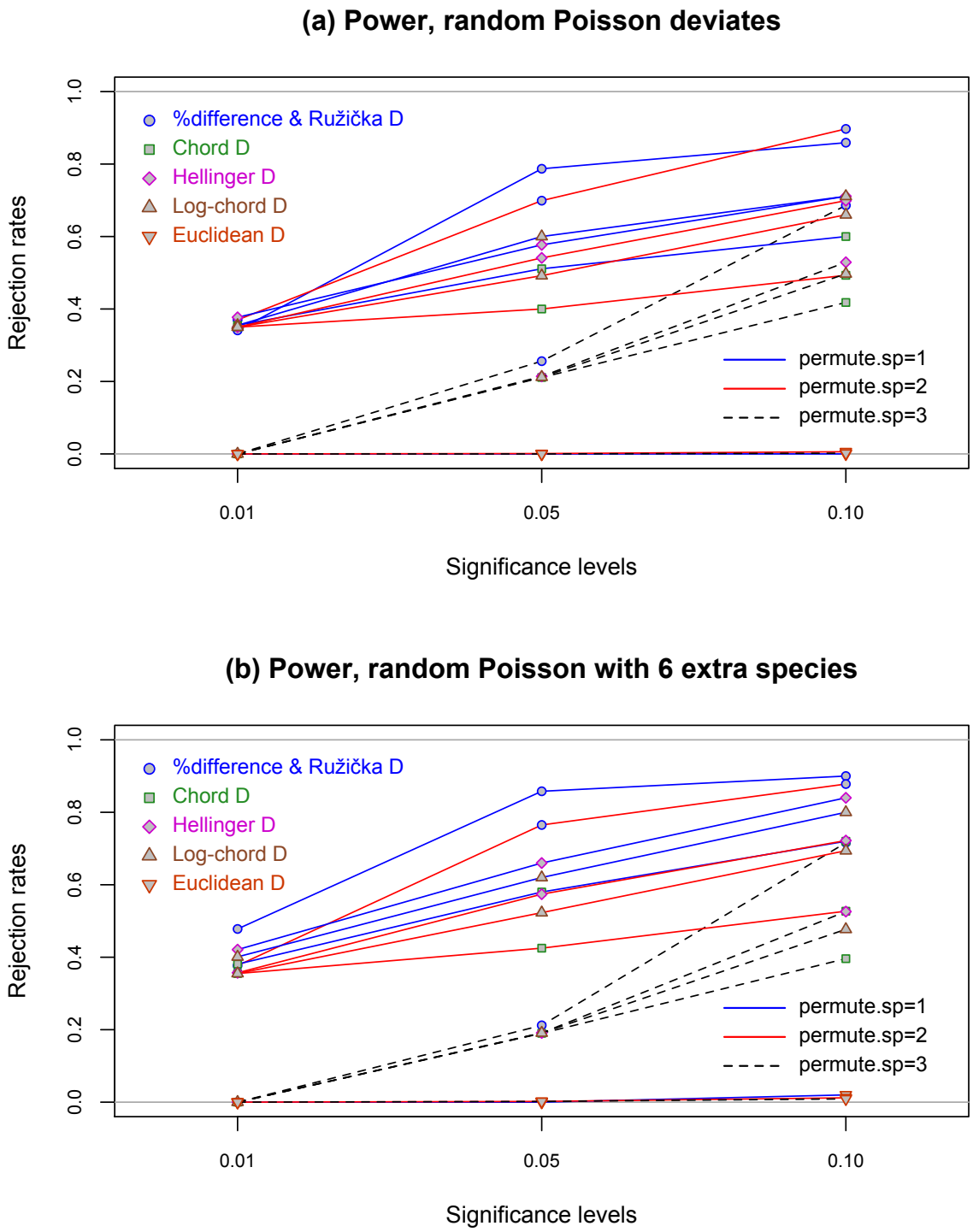

Fig. S1.5. Power study, random Poisson deviates. Rejection rates obtained with five dissimilarity coefficients and three permutation methods. Rejection rates are reported for three significance levels alpha: 0.01, 0.05 and 0.10 (abscissa).

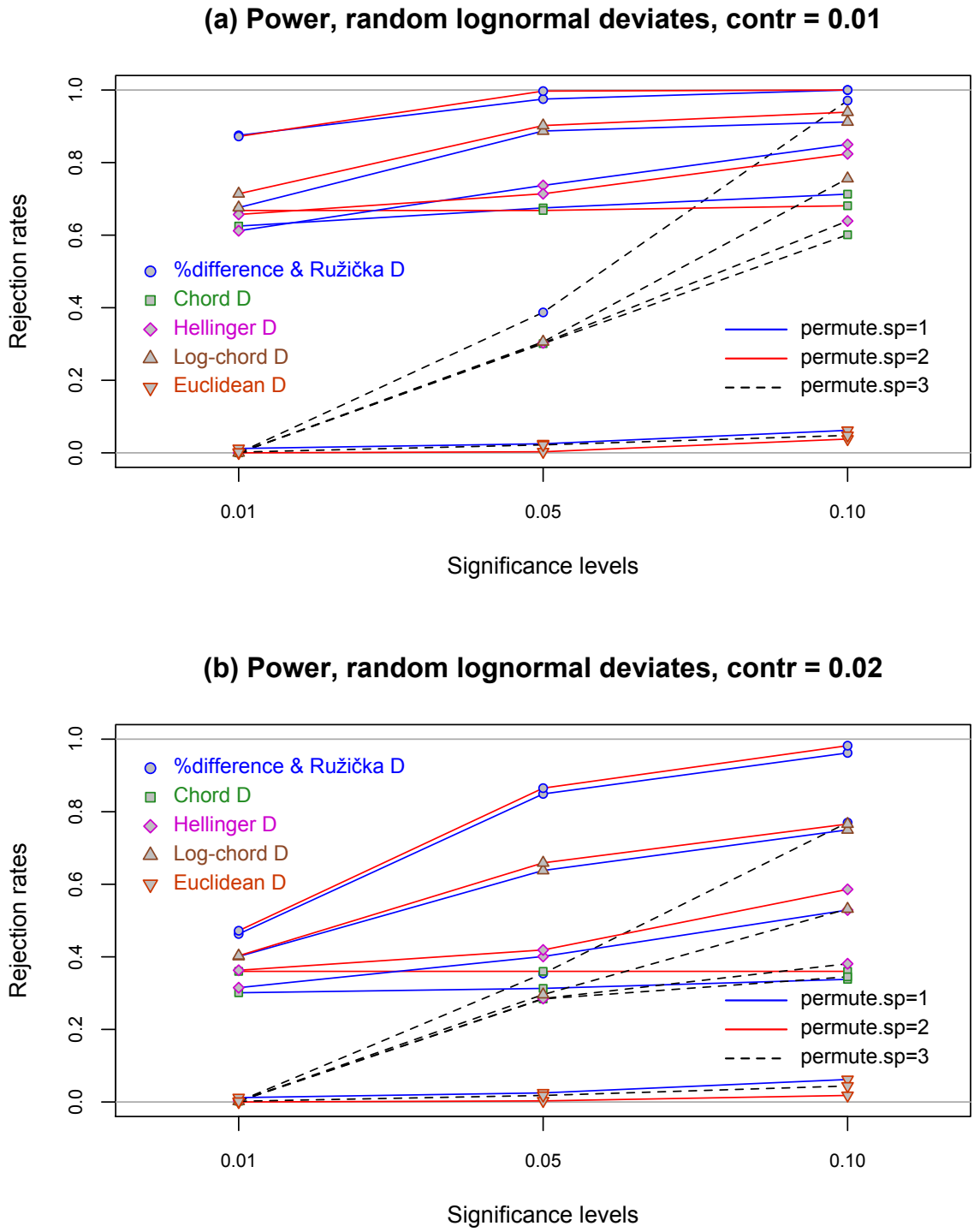

Fig. S1.6. Power study, random lognormal deviates. Rejection rates obtained with five dissimilarity coefficients and three permutation methods. Rejection rates are reported for three significance levels alpha: 0.01, 0.05 and 0.10 (abscissa).

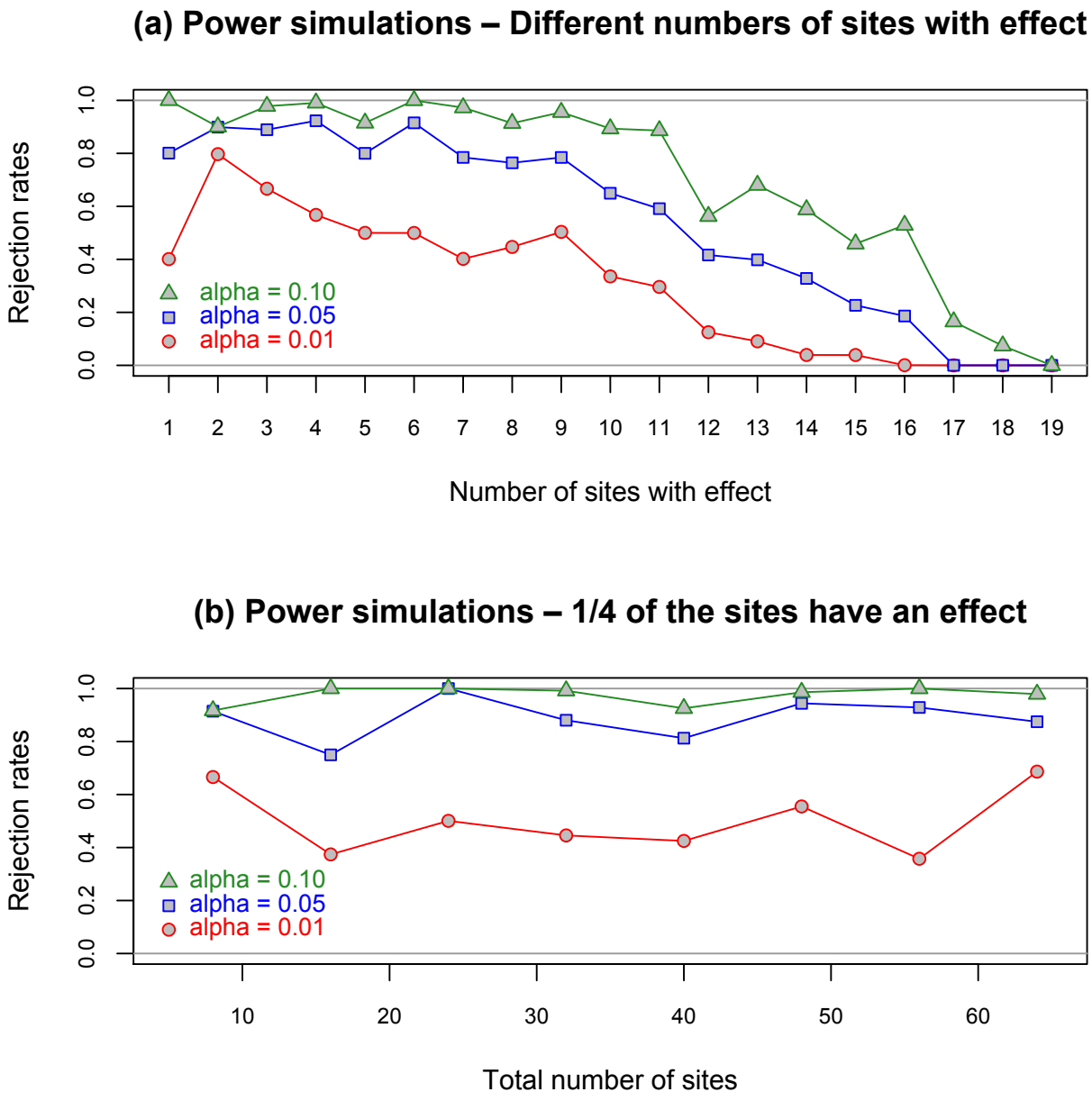

Fig. S1.7. Rejection rates of the TBI tests in power simulations. Rejection rates are reported for three significance levels alpha: 0.01, 0.05 and 0.10. (a) Different numbers of sites received an effect (abscissa, *n1* = 1 to 19), i.e. a difference in community composition between T1 and T2. There were 20 sites in total in each simulation. (b) The proportion of sites with an effect was kept constant, here *n1* = *n*/4, for different values of *n* (abscissa).

Appendix S2

DISCUSSION OF SOME ASPECTS OF PERMUTATION METHOD 1

Permutation method 1 is described in the Methods section of the paper. Some technical aspects of this permutation method are discussed here.

• By permuting the columns of each matrix separately, we produce realizations of H_0 corresponding to the idea that all sites come from the same statistical population and the variation observed among sites for each species is due to random sampling of the same statistical population. This type of permutation does not deny that species may be correlated to one another. If they are and all sites are drawn from a single populations, the variation observed within each species will still fluctuate as a result of random sampling.

• The permutations are done separately in Mat1 and Mat2, i.e. the values of a species at T1 and T2 are not combined and then permuted at random, because we want to preserve the differences per species, if any, between T1 and T2. The test is designed to identify sites where the difference between T1 and T2 is noticeably larger than that of most other sites in the study. If, on the contrary, one only wanted to identify a general difference between T1 and T2 in multivariate species [or other type of] data, i.e. a difference in the positions of the centroids of the T1 versus T2 data, one could use redundancy analysis (RDA) or Manova to achieve that; it is an entirely different question.

• In function TBI() with argument permute.sp = 1, each random permutation of a species is done in the same way in T1 and T2. The seed fed to the permutation function (which is sample() in R) used to permute the values in the columns of Mat1 is noted and used again to perform the permutations of Mat2.

• The data in both Mat1 and Mat2 are permuted. This is done because, if only one matrix (say, Mat1) was permuted, the dissimilarities under permutation, used to assess the reference dissimilarity for object *i*, would be computed by comparison with a fixed vector of values for that object at T2. The test would then not have access to the entire set of possible permutations, but this is necessary condition for the permutations to correctly represent H_0. As a consequence, the test would have reduced power.

Appendix S3

INSECTICIDE TREATMENTS IN MESOCOSMS

The Insecticide treatment invertebrate data

Observations on the abundances of 178 invertebrate species (macroinvertebrates and zooplankton) subjected to insecticide treatments in aquatic mesocosms (called "ditches") were used by van den Brink & ter Braak (1999) as an application example in their paper describing Principal Response Curves (PRC) analysis. The authors agreed to make the data available to researchers in the CANOCO program documentation and in the R package vegan (Oksanen et al. 2017).

The experiment involved twelve mesocosms, which were surveyed on eleven occasions. Four mesocosms served as controls (dose = 0) and the remaining eight were treated once with the insecticide chlorpyrifos, with dose levels of 0.1, 0.9, 6.0 and 44.0 µg/L in two mesocosms each. The data are log-transformed species abundances, $y_{tr} = \log_e(10y + 1)$. In their paper, the authors used the log-transformed invertebrate data in PRC analysis; PRC preserved the Euclidean distance among the observations.

The 12 mesocosms had been attributed at random to the treatments. However, to facilitate presentation of the results, they will be presented here in order of increased insecticide doses: {0, 0, 0, 0, 0.1, 0.1, 0.9, 0.9, 6.0, 6.0, 44.0, 44.0} µg/L. Results of the calculations with the R function TBI() are shown for the species abundance and occurrence data of this ecological application.

References

Oksanen, J., Blanchet, G., Friendly, M., Kindt, R., Legendre, P., McGlinn, D., Minchin, P. R., O'Hara, R. B., Simpson, G. L., Solymos, P., Stevens, M. H. H., Szoecs, E. & Wagner, H. (2017) *vegan: Community ecology package.* R package version 2.4-4. https://cran.r-project.org/package=vegan.

van den Brink, P. J. & ter Braak, C. J. F. (1999) Principal response curves: analysis of time-dependent multivariate responses of biological community to stress. *Environmental Toxicology and Chemistry* **18**, 138–148.

Results of calculations with R function TBI()

Pyrifos insect treatment data: compare survey #4 (one week after the insecticide treatment) to survey #11 (after full recovered from treatment). # Comments added to the output files.

```
library(vegan)
data(pyrifos)
survey4.order = c(38,39,41,47,37,44,40,46,43,48,42,45)
survey11.order = c(122,123,125,131,121,128,124,130,127,132,126,129)
```

1. Comparison based upon species abundance data, percentage difference D

```
( res1 <- TBI(pyrifos[survey4.order,], pyrifos[survey11.order,], method="%diff",
nperm=9999, permute.sp=1, BCD=TRUE, test.t.perm=TRUE, clock=TRUE) )
# Computation time = 51.634000  sec

-----
$TBI
 [1] 0.4332125 0.4490831 0.4048151 0.4593321 0.4958159 0.4392330 0.4884889 0.4851041
0.4740264 0.6205484 0.7345825 0.6721440

$p.TBI
 [1] 0.9305 0.8618 0.9827 0.7249 0.4664 0.8448 0.5350 0.6370 0.7404 0.0342 0.0001 0.0001

$p.adj
 [1] 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 0.3420 0.0012 0.0012

$BCD.mat
        B/(2A+B+C) C/(2A+B+C) D=(B+C)/(2A+B+C) Change
Site.1   0.1616465  0.2715660        0.4332125    +   # Untreated
Site.2   0.1973186  0.2517645        0.4490831    +   # Untreated
Site.3   0.2305092  0.1743059        0.4048151    -   # Untreated
Site.4   0.2643243  0.1950077        0.4593321    -   # Untreated
Site.5   0.2303800  0.2654359        0.4958159    +   # Treated, 0.1 microgram/L
Site.6   0.1980843  0.2411487        0.4392330    +   # Treated, 0.1 microgram/L
Site.7   0.2425404  0.2459484        0.4884889    +   # Treated, 0.9 microgram/L
Site.8   0.1854199  0.2996843        0.4851041    +   # Treated, 0.9 microgram/L
Site.9   0.1901665  0.2838599        0.4740264    +   # Treated, 6 micrograms/L
Site.10  0.3094316  0.3111168        0.6205484    +   # Treated, 6 micrograms/L
Site.11  0.3232546  0.4113279        0.7345825    +   # Treated, 44 micrograms/L
Site.12  0.1829121  0.4892319        0.6721440    +   # Treated, 44 micrograms/L

$BCD.summary   # Here the BCD summary is computed for the 12 mesocosms, not the 8 treated
 mean(B/den) mean(C/den)   mean(D)  B/(B+C)  C/(B+C) Change
   0.2263323   0.2866998 0.5130322 0.441166 0.558834    +

$t.test_B.C    # Here the tests is computed for the 12 mesocosms, not for the 8 treated
                mean(B-C)      Stat    p.param p.perm   p<=0.05
Paired t.test -0.06036748 -2.132286 0.05635548 0.0364          # Permutation test signif.

$BC
[1] NA
-----
```

2. Comparison based upon species occurrence (i.e. presence-absence) data, Sørensen D

```
( res2 <- TBI(pyrifos[survey4.order,], pyrifos[survey11.order,], method="sorensen",
nperm=9999, permute.sp=1, BCD=TRUE, test.t.perm=TRUE, clock=TRUE) )
# Computation time = 38.387000  sec

-----
$TBI
 [1] 0.4390244 0.4324324 0.4457831 0.4705882 0.4666667 0.4358974 0.5000000 0.4153846
0.4545455
[10] 0.6800000 0.7551020 0.6595745

$p.TBI
 [1] 0.8788 0.9134 0.7933 0.6390 0.6892 0.7769 0.4826 0.8964 0.9113 0.0001 0.0001 0.0001

$p.adj
 [1] 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 0.0012 0.0012 0.0012

$BCD.mat
        B/(2A+B+C) C/(2A+B+C) D=(B+C)/(2A+B+C) Change
Site.1   0.1463415  0.2926829        0.4390244    +   # Untreated
Site.2   0.1891892  0.2432432        0.4324324    +   # Untreated
Site.3   0.2048193  0.2409639        0.4457831    +   # Untreated
Site.4   0.2205882  0.2500000        0.4705882    +   # Untreated
Site.5   0.1733333  0.2933333        0.4666667    +   # Treated, 0.1 microgram/L
Site.6   0.1666667  0.2692308        0.4358974    +   # Treated, 0.1 microgram/L
Site.7   0.2105263  0.2894737        0.5000000    +   # Treated, 0.9 microgram/L
Site.8   0.1384615  0.2769231        0.4153846    +   # Treated, 0.9 microgram/L
Site.9   0.1363636  0.3181818        0.4545455    +   # Treated, 6 micrograms/L
Site.10  0.2800000  0.4000000        0.6800000    +   # Treated, 6 micrograms/L
Site.11  0.2857143  0.4693878        0.7551020    +   # Treated, 44 micrograms/L
Site.12  0.1276596  0.5319149        0.6595745    +   # Treated, 44 micrograms/L

$BCD.summary   # Here the BCD summary is computed for the 12 mesocosms, not the 8 treated
 mean(B/den) mean(C/den)   mean(D)   B/(B+C)   C/(B+C) Change
    0.189972   0.3229446 0.5129166 0.3703759 0.6296241    +

$t.test_B.C    # Here the test is computed for the 12 mesocosms, not for the 8 treated
               mean(B-C)      Stat      p.param p.perm   p<=0.05
Paired t.test  -0.1329727 -4.621706 0.0007383173  7e-04         *  # Both tests signif.

$BC
[1] NA
```

Appendix S4

SOUTH TIKUS ISLAND CORAL COMMUNITIES

South Tikus Island coral data

Brown and Suharsono (1990) surveyed coral communities (75 species) at 10 sites in the island of South Tikus, Indonesia, in the years 1981, 1983, 1984, 1985, 1987 and 1988. An El Niño event occurred in 1982–1983, which caused coral bleaching and death of coral colonies, and triggered changes in the composition of coral communities. They reported that "as many as 80-90% of corals died on the reef flats at the study sites, with the major casualties being branching species in the genera *Acropora* and *Pocillopora*".

Coral forms colonies which occupy surfaces, so that the data are not in numbers of individuals but in areal cover of each species. The sum of the species areal covers at a site may exceed 100% because coral colonies may overlap one another vertically. The Brown and Suharsono (1990) data have been used in several papers to demonstrate the application of multivariate methods for the analysis of beta diversity and the comparison of surveys across time, e.g. by Warwick et al. (1990), Anderson et al. (2011) and Chao and Chiu (1996). Following these papers, the data in the present application were treated as if they were species abundances. They were obtained from Appendix S1 of the Anderson et al. (2011) article.

References

Anderson, M. J., Crist, T. O., Chase, J. M., Vellend, M., Inouye, B. D., Freestone, A. L. et al. (2011) Navigating the multiple meanings of b diversity: a roadmap for the practicing ecologist. *Ecology Letters* **14**, 19–28.

Brown, B. E. & Suharsono. (1990) Damage and recovery of coral reefs affected by El Niño related seawater warming, in the Thousand Islands, Indonesia. *Coral Reefs* **8**, 163–170.

Chao, A. & Chiu, C.-H. (2016) Bridging the variance and diversity decomposition approaches to beta diversity via similarity and differentiation measures. *Methods in Ecology and Evolution* **7**, 919–928.

Warwick, R.M., Clarke, K.R. & Suharsono. (1990) A statistical analysis of coral community responses to the 1982–83 El Niño in the Thousand Islands, Indonesia. *Coral Reefs* **8**, 171–179.

Appendix S5

THE CHESAPEAKE BAY BENTHOS DATA

The Chesapeake Bay Benthic Monitoring Program data

The data set used in this example was extracted from the Maryland Data Sets of the Chesapeake Bay Benthic Monitoring Program (http://www.baybenthos.versar.com/data.htm), which is a portion of the Chesapeake Bay Program (http://www.chesapeakebay.net/). Detailed information about the sampling protocol is found on that web page. The data, available online, come in the form of numerous text files, one per group of variables and per year. Legendre & Gauthier (2014) compiled and formatted these files in a *Rdata* file for immediate analysis in R. The <ChesapeakeBay.Maryland.RData> data are available in a zipped file found in S5 of their paper. The file contains faunal data collected during surveys at 27 sites, spring and fall, during 13 years, i.e. from 1996 to 2008, for a total of 702 data rows. It also contains data frames describing sampling information, sediment, water quality, and geographic coordinates of the sites; these files all have corresponding data rows. These authors used the Chesapeake data in a series of practical exercises in R for ecologists who want to learn how to analyse space-time ecological data. The exercises are detailed in Appendices S2 and S3 of their paper.

The faunal data for all sites, years and seasons consist of the abundances of 205 benthic macrofaunal taxa (203 invertebrates and 2 chordates) identified in the sediment of 25 brackish-water sites of the bay. Table S5.1 shows how the species are split between seasons and salinity groups. The spring survey data contain 181 species and the fall data 142 species. Two freshwater sites (#36 and #79) were present in the database; they contained 105 species. These two sites were excluded from the present example, which focussed on 25 brackish sites where 155 species were identified.

A map of the 25 brackish sites used in Ecological application 3 of the main paper, plotted with the RgoogleMaps package, is shown in Fig. S5.1. Also shown are the results of calculations with the R function TBI(), for the species abundance and occurrence data of this ecological application.

Reference

Legendre, P. & Gauthier, O. (2014) Statistical methods for temporal and space-time analysis of community composition data. *Proceedings of the Royal Society B* **281**, 20132728.

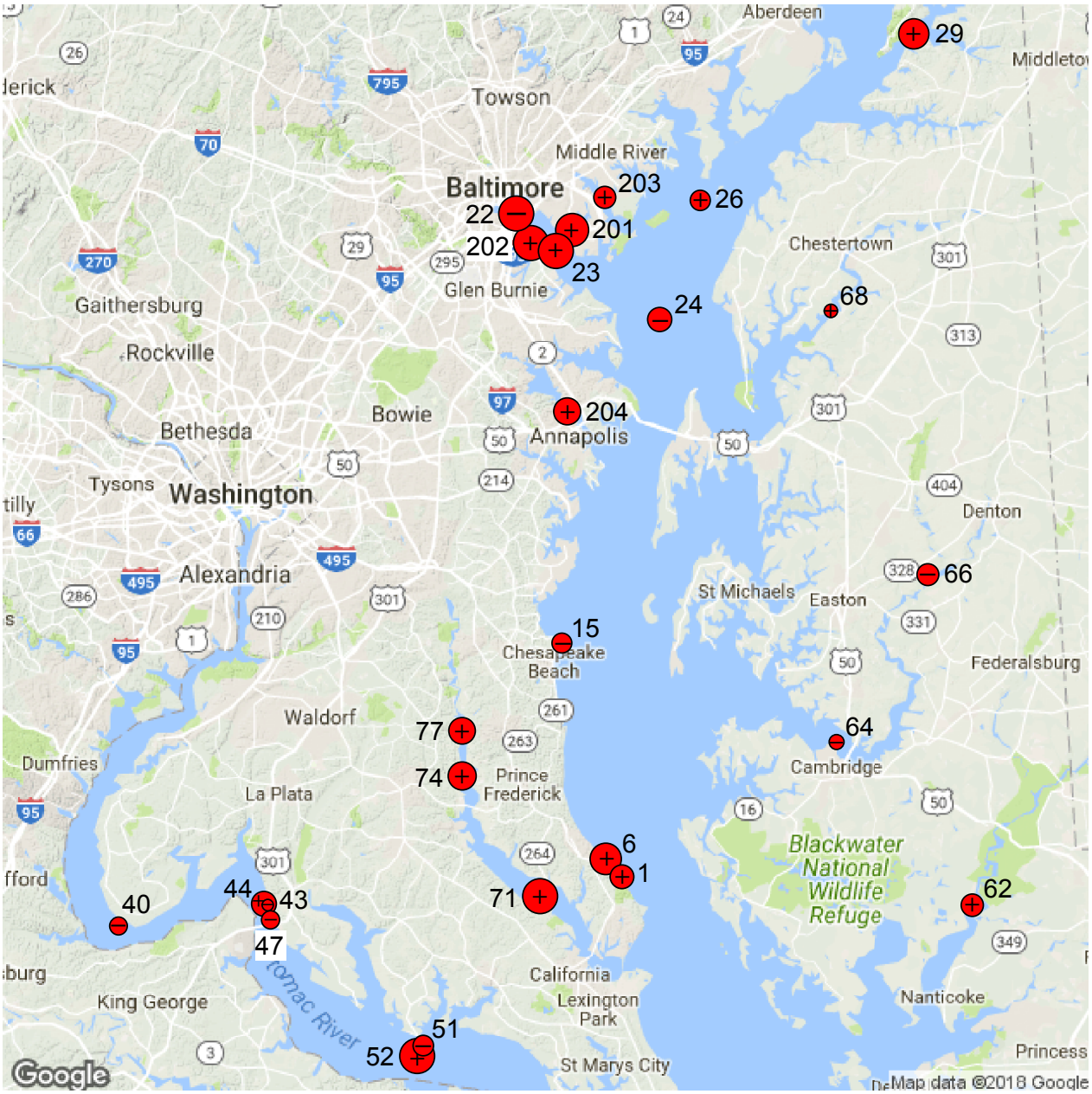

Figure S5.1. Map of the 25 brackish sites (red symbols) of the Chesapeake Bay ecological survey, produced with the RgoogleMaps package in R. Comparison of survey in years 2005 and 2008: point sizes are proportional to the TBI indices (percentage difference *D*). + signs indicate the 17 sites where *gains* in abundances-per-species dominated; – signs, the 8 sites where *losses* dominated.

Table S5.1. Number of species in subsets of the Chesapeake fauna data surveyed during 13 years, spring and fall. In total, 205 benthic species were found at the 27 survey sites.

	Spring	Fall	Spring and fall
Freshwater (2 sites)	93	58	105
Brackish (25 sites)	128	121	155
All survey sites (27 sites)	181	142	205

Results of calculations with R function TBI()

Compare Chesapeake Bay benthic fauna, 25 brackish sites, years 2005 and 2008, fall survey data.

1. Comparison based upon species abundance data, percentage difference D

```
( res.fauna.05.08.pcdiff = TBI(Y1, Y2, "%diff", pa.tr=FALSE, permute.sp=1, nperm=99999,
BCD=TRUE, test.BC=TRUE, test.t.perm=TRUE, clock=TRUE) )
# Computation time = 792.754000  sec

-----
$TBI
 [1] 0.6766467 0.5704698 0.9411765 1.0000000 0.6309524 0.7685950 1.0000000 1.0000000
 [9] 0.6960000 0.5777778 0.8632812 0.5081967 0.3229572 0.7083333 0.5164835 0.5843137
[17] 1.0000000 0.8983051 0.6385965 0.4244604 0.6256158 0.3846154 1.0000000 0.8020833
[25] 0.7611940

$p.TBI, nperm=9999
 [1] 0.3929 0.6419 0.0032 0.0033 0.4416 0.1919 0.0001 0.0001 0.3223 0.5884 0.0705
[12] 0.7248 0.9681 0.3324 0.7594 0.6169 0.0001 0.0381 0.4727 0.9135 0.5359 0.9165
[23] 0.0001 0.1564 0.2146

$p.adj, nperm=9999
 [1] 1.0000 1.0000 0.0672* 0.0672* 1.0000 1.0000 0.0025* 0.0025* 1.0000 1.0000 1.0000
[12] 1.0000 1.0000 1.0000 1.0000 1.0000 0.0025* 0.7239 1.0000 1.0000 1.0000 1.0000
[23] 0.0025* 1.0000 1.0000

$p.TBI, nperm=99999
 [1] 0.39289 0.64205 0.00322 0.00319 0.44089 0.19191 0.00002 0.00002 0.32282 0.58789
[11] 0.07023 0.72529 0.96808 0.33231 0.76022 0.61646 0.00001 0.03828 0.47287 0.91356
[21] 0.53649 0.91707 0.00001 0.15645 0.21396

$p.adj, nperm=99999
 [1] 1.00000 1.00000 0.06699 0.06699 1.00000 1.00000 0.00046 0.00046 1.00000 1.00000
[11] 1.00000 1.00000 1.00000 1.00000 1.00000 1.00000 0.00025 0.72732 1.00000 1.00000
[21] 1.00000 1.00000 0.00025 1.00000 1.00000
```

```
$BCD.mat
         B/(2A+B+C) C/(2A+B+C) D=(B+C)/(2A+B+C) Change
Site.1  0.167664671 0.50898204        0.6766467    +
Site.2  0.436241611 0.13422819        0.5704698    -
Site.3  0.029411765 0.91176471        0.9411765    +
Site.4  0.250000000 0.75000000        1.0000000    +
Site.5  0.053571429 0.57738095        0.6309524    +
Site.6  0.347107438 0.42148760        0.7685950    +
Site.7  0.950000000 0.05000000        1.0000000    -  * Abundances-per-species losses
Site.8  0.400000000 0.60000000        1.0000000    +  * 40% Ab.-per-sp. losses, 60% gains
Site.9  0.576000000 0.12000000        0.6960000    -
Site.10 0.100000000 0.47777778        0.5777778    +
Site.11 0.224609375 0.63867188        0.8632812    +
Site.12 0.483606557 0.02459016        0.5081967    -
Site.13 0.190661479 0.13229572        0.3229572    -
Site.14 0.229166667 0.47916667        0.7083333    +
Site.15 0.340659341 0.17582418        0.5164835    -
Site.16 0.482352941 0.10196078        0.5843137    -
Site.17 0.000000000 1.00000000        1.0000000    +  * All species gains
Site.18 0.135593220 0.76271186        0.8983051    +
Site.19 0.057894737 0.58070175        0.6385965    +
Site.20 0.316546763 0.10791367        0.4244604    -
Site.21 0.571428571 0.05418719        0.6256158    -
Site.22 0.161538462 0.22307692        0.3846154    +
Site.23 0.098039216 0.90196078        1.0000000    +  * All species gains
Site.24 0.005208333 0.79687500        0.8020833    +
Site.25 0.008955224 0.75223881        0.7611940    +

$BCD.summary
 mean(B/den) mean(C/den)   mean(D)   B/(B+C)   C/(B+C) Change
   0.2646503   0.4513519 0.7160022 0.3696222 0.6303778    +

$t.test_B.C, nperm=99999
               mean(B-C)      Stat    p.param  p.perm   p<=0.05
Paired t.test  -0.1867016 -1.826046 0.08031088 0.08221

$BC
[1] NA
-----
```

Note – The site names, Site.1 to Site.25, in the function output files correspond to the following site names on the map:

```
site.names
 [1] "S1"   "S15"  "S201" "S202" "S203" "S204" "S22"  "S23"  "S24"  "S26"
[11] "S29"  "S40"  "S43"  "S44"  "S47"  "S51"  "S52"  "S6"   "S62"  "S64"
[21] "S66"  "S68"  "S71"  "S74"  "S77"
```

2. Comparison based upon species occurrence (i.e. presence-absence) data, Sørensen D

```
( res.fauna.05.08.sor = TBI(Y1, Y2, "sorensen", pa.tr=FALSE, permute.sp=1, nperm=9999,
BCD=TRUE, test.BC=TRUE, test.t.perm=TRUE, clock=TRUE) )
# Computation time = 63.074000  sec

-----
$TBI
 [1] 0.4838710 0.4166667 0.6666667 1.0000000 0.2727273 0.1578947 1.0000000 1.0000000
 [9] 0.3846154 0.1818182 0.3600000 0.3333333 0.2500000 0.4000000 0.2500000 0.2857143
[17] 1.0000000 0.5238095 0.2592593 0.2592593 0.3333333 0.1538462 1.0000000 0.1304348
[25] 0.2592593

$p.TBI
 [1] 0.1533 0.3568 0.0259 0.0032 0.7316 0.9651 0.0001 0.0001 0.4021 0.9175 0.4696
[12] 0.5722 0.8212 0.3680 0.8236 0.7183 0.0001 0.1347 0.7819 0.8123 0.6038 0.9808
[23] 0.0001 0.9646 0.7098

$p.adj
 [1] 1.0000 1.0000 0.5180 0.0672? 1.0000 1.0000 0.0025* 0.0025* 1.0000 1.0000 1.0000
[12] 1.0000 1.0000 1.0000 1.0000 1.0000 0.0025* 1.0000 1.0000 1.0000 1.0000 1.0000
[23] 0.0025* 1.0000 1.0000

$BCD.mat
        B/(2A+B+C) C/(2A+B+C) D=(B+C)/(2A+B+C) Change
Site.1  0.06451613 0.41935484        0.4838710    +
Site.2  0.25000000 0.16666667        0.4166667    -
Site.3  0.16666667 0.50000000        0.6666667    +
Site.4  0.50000000 0.50000000        1.0000000    +
Site.5  0.09090909 0.18181818        0.2727273    +
Site.6  0.15789474 0.00000000        0.1578947    -
Site.7  0.87500000 0.12500000        1.0000000    -  * 87.5% species losses, 22.5% gains
Site.8  0.50000000 0.50000000        1.0000000    +  * 50% losses, 50% gains
Site.9  0.15384615 0.23076923        0.3846154    +
Site.10 0.09090909 0.09090909        0.1818182    +
Site.11 0.16000000 0.20000000        0.3600000    +
Site.12 0.22222222 0.11111111        0.3333333    -
Site.13 0.08333333 0.16666667        0.2500000    +
Site.14 0.20000000 0.20000000        0.4000000    +
Site.15 0.12500000 0.12500000        0.2500000    +
Site.16 0.14285714 0.14285714        0.2857143    +
Site.17 0.00000000 1.00000000        1.0000000    +  * All species gains
Site.18 0.38095238 0.14285714        0.5238095    -
Site.19 0.11111111 0.14814815        0.2592593    +
Site.20 0.11111111 0.14814815        0.2592593    +
Site.21 0.28571429 0.04761905        0.3333333    -
Site.22 0.03846154 0.11538462        0.1538462    +
Site.23 0.36363636 0.63636364        1.0000000    +  * All species gains
Site.24 0.04347826 0.08695652        0.1304348    +
Site.25 0.11111111 0.14814815        0.2592593    +

$BCD.summary
 mean(B/den) mean(C/den)   mean(D)  B/(B+C)  C/(B+C) Change
   0.2091492   0.2453511 0.4545004 0.460174 0.539826    +

$t.test_B.C
               mean(B-C)       Stat   p.param p.perm   p<=0.05
Paired t.test  -0.0362019 -0.6218665 0.5398928 0.5533

$BC
[1] NA
```

```
#                                  Appendix S6, R function
#
# An R function to standardize environmental data prior to TBI analysis.


#' Special standardization for environmental data prior to TBI analysis.
#'
#' After standardization, all variables will have the same weight (i.e. they will
#' all contribute the same variance) in the calculation of TBI indices.
#'
#' @param mat1 First data matrix, class matrix or data.frame.
#' @param mat2 Second data matrix, class matrix or data.frame.
#' @param non.neg=TRUE : make the data non-negative before scaling (recommended).
#'        non.neg=FALSE: keep standardized data with signs (due to centring).
#'
#' @return A list with the two matrices standardized as dexscribed above.
#'
#' @details
#' The two data sets are joined into a single data matrix, Y = rbind(Y.T1, Y.T2).
#' Y is standardized [Y.stand = scale(Y)], then it is separated into two tables of
#' the sizes of the original data matrices, before analysis with function TBI().
#'
#' Explanation:
#' (a) the two data tables are joined into a single data matrix, Y = rbind(Y.T1,
#' Y.T2), before standardization. In this way, the differences in values of each
#' variable for a given pair of sites in the two tables will remain comparable
#' to the differences ofcomputed from the original unstandardized values; in this
#' way, the distances computedbetween sites in T1 and T2 will be meaningful. This
#' precaution is important when there are differences in means between T1 and T2.
#' (b) Standardizing the variables insures that all variables will contribute the
#' same variance to the calculation of the TBI indices; the variances will not
#' depend on thephysical units of the variables or other contingencies that make
#' the variances unequal.
#'
#' Argument non.neg=TRUE makes the values non-negative to produce data without
#' negative signs. It does not change the results of the TBI tests.
#'
#' @author  Pierre Legendre \email{pierre.legendre@@umontreal.ca}, 2018
'scale.for.TBI' <-
    function(mat1,mat2,
             non.neg=TRUE)
    {
    mat1 <- as.matrix(mat1)
    mat2 <- as.matrix(mat2)
    dim.1 <- dim(mat1)
    dim.2 <- dim(mat2)
    if(!is.numeric(mat1)) stop("First data matrix not numeric")
    if(!is.numeric(mat2)) stop("Second data matrix not numeric")
    if(dim.1[1] != dim.2[1]) stop("Data sets have different numbers of rows")
    if(dim.1[2] != dim.2[2]) stop("Data sets have different numbers of columns")
    #
    tmp <- scale(rbind(mat1,mat2))
    if(non.neg) tmp <- tmp - min(tmp)
    mat1 <- tmp[1:n12,]
    mat2 <- tmp[(n12+1):(2*n12),]
    list(mat1=mat1, mat2=mat2)
    }
```