

Title

Species identity drives ecosystem function in a subsidy-dependent coastal ecosystem

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Electronic Supplementary Material

Appendix S1: Tukey HSD means comparison of species-specific consumption rates

Appendix S2: Supplemental model information for nested hierarchical model

Appendix S3: Field assay site map

Appendix S1

Table S1: Results from the Tukey post-hoc test for the One-way ANOVA of detritivore species consumption rates for all six species in laboratory mesocosms. Comparisons in bold font are significant ($P < 0.05$).

Species Comparison	95% Confidence Interval			
	Difference in Means	Significance	Lower Bounds	Upper Bounds
<i>M. Benedicti</i> - <i>M. minor</i>	-0.41	0.93	-1.89	1.07
<i>M. corniculata</i> - <i>M. minor</i>	2.51	0.00	1.03	3.98
<i>M. californiana</i> - <i>M. minor</i>	1.51	0.04	0.03	2.99
<i>A. perconvexus</i> - <i>M. minor</i>	0.31	0.98	-1.17	1.79
<i>P. rotundata</i> - <i>M. minor</i>	0.30	0.98	-1.17	1.78
<i>M. corniculata</i> - <i>M. benedicti</i>	2.91	0.00	1.44	4.39
<i>M. californiana</i> - <i>M. benedicti</i>	1.92	0.01	0.44	3.39
<i>A. perconvexus</i> - <i>M. benedicti</i>	0.72	0.59	-0.76	2.20
<i>P. rotundata</i> - <i>M. benedicti</i>	0.71	0.60	-0.76	2.19
<i>M. californiana</i> - <i>M. corniculata</i>	-1.00	0.28	-2.47	0.48
<i>A. perconvexus</i> - <i>M. corniculata</i>	-2.20	0.00	-3.67	-0.72
<i>P. rotundata</i> - <i>M. corniculata</i>	-2.20	0.00	-3.68	-0.72
<i>A. perconvexus</i> - <i>M. californiana</i>	-1.20	0.14	-2.68	0.28
<i>P. rotundata</i> - <i>M. californiana</i>	-1.21	0.14	-2.68	0.27
<i>P. rotundata</i> - <i>A. perconvexus</i>	-0.01	1.00	-1.48	1.47

Appendix S2

Supplementary Material for the paper ‘Species identity drives ecosystem function in a subsidy-dependent coastal ecosystem’ by Kyle A. Emery, Jenifer E. Dugan, R. A. Bailey and Robert J. Miller

Label the six intertidal detritivore species introduced in the **Methods** section as 1–6.

For each species combination, let x_i denote the number of species i present, for $i = 1, \dots, 6$. Thus $x_1 + x_2 + x_3 + x_4 + x_5 + x_6 = 12$ for every species combination.

Let j denote the number of different species present in a given species combination. This number is called the level of richness. For a monoculture, $j = 1$, and there is one value of i with $x_i = 12$, while $x_{i'} = 0$ if $i' \neq i$. For a duoculture, $j = 2$, and there are values i and i' with $x_i = x_{i'} = 6$, while the other x -values are zero. When $j = 3$ then three of the x -values are equal to 4 and the rest are zero. When $j = 4$ then four of the x -values are equal to 3 and the rest are zero. When $j = 6$ then $x_1 = x_2 = \dots = x_6 = 2$.

Here we give equations for the expectation of the response y on a given species combination in a given week under various models.

Model: Constant There is a constant c such that

$$y = c$$

for all species combinations in all trials. This means that there are no differences between species combinations, or between trials. This model has 1 parameter.

Model: Trial There are constants t_1, t_2 and t_3 such that

$$y = t_k$$

for every species combination in trial k . This model has 3 parameters.

Model: Richness There are constants r_1, r_2, r_3, r_4 and r_6 such that

$$y = r_j$$

for every species combination with richness level j . This has 5 parameters.

Because Richness levels 1 and 2 were done in Trial 1, Richness level 3 in Trial 2, and Richness levels 4 and 6 in Trial 3, the model **Trial** is a submodel of the model **Richness**.

Model: Identity There are constants a_1, a_2, a_3, a_4, a_5 and a_6 such that

$$y = a_1x_1 + a_2x_2 + a_3x_3 + a_4x_4 + a_5x_5 + a_6x_6$$

no matter what the level of richness or the trial. This has 6 parameters.

Model: Trial + Identity For every species combination in trial k ,

$$y = t_k + a_1x_1 + a_2x_2 + a_3x_3 + a_4x_4 + a_5x_5 + a_6x_6.$$

This has $3 + 6 - 1 = 8$ independent parameters, because we can add 1 to every a_i and subtract 12 from every t_k without changing the result.

Model: Richness + Identity For every species combination with level j of richness,

$$y = r_j + a_1x_1 + a_2x_2 + a_3x_3 + a_4x_4 + a_5x_5 + a_6x_6.$$

This has $5 + 6 - 1 = 10$ independent parameters.

Model: Richness*Identity There are constants a_{ij} for $1 \leq i \leq 6$ and every level j of richness such that, for every species combination which has level j of richness,

$$y = a_{1j}x_1 + a_{2j}x_2 + a_{3j}x_3 + a_{4j}x_4 + a_{5j}x_5 + a_{6j}x_6.$$

Because there is only one species combination involving all six species, and $x_1 = x_2 = x_3 = x_4 = x_5 = x_6 = 2$ for this, we only need one constant for level 6 of Richness.

So there are $6 + 6 + 6 + 6 + 1 = 25$ independent parameters.

Model: Species Combination Each of the 57 species combinations gives a different expectation of y , with no simple explanation of the 57 different parameters.

Figure 1 shows the hierarchy of models that we considered. Each box shows one of the models. The number in each box shows the number of independent parameters for that model.

Following the convention in Figure S2 of Perkins et al. (2015), models in solid boxes are those which are not the sum of smaller models. Sometimes such models are called *irreducible*.

If one model is lower in the diagram than another and is joined to the higher one by a line, or an upwards path of lines, then it is a special case of the higher one. For example, the Constant model is a special case of the Identity model with $a_1 = a_2 = a_3 = a_4 = a_5 = a_6$.

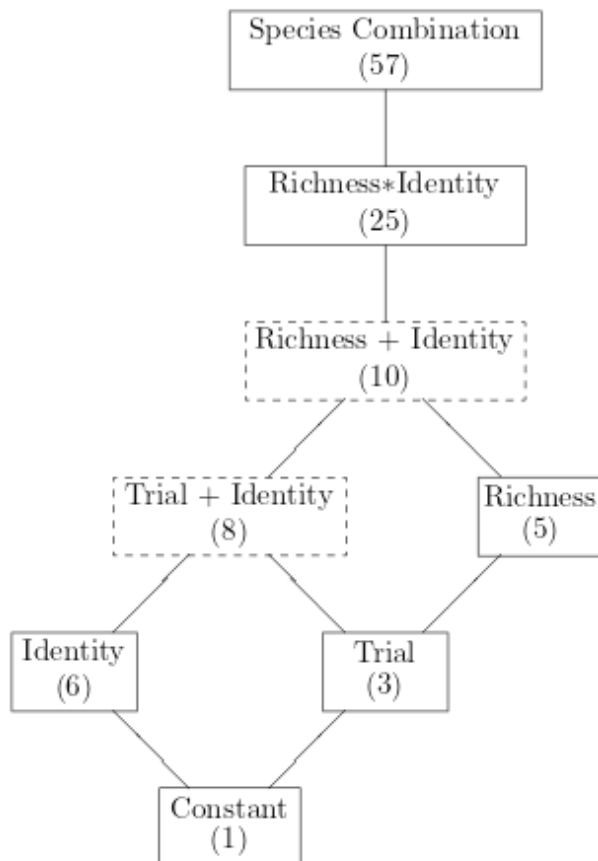


Figure 1: Hierarchy of models considered

This family of models gives the analysis-of-variance (ANOVA) table. This table includes only the irreducible models (but usually omits the Constant model). As explained by Reiss et al. (2011), each row of the ANOVA table corresponds not to a model but to the unique edge in the diagram that goes down from that irreducible model. The number of degrees of freedom shown in that row is the difference between the number of independent parameters for the model at the top of the edge and the number of independent parameters for the model at the bottom of the edge. In other words, it is the degrees of freedom for the extra information in the model at the top of the edge that is not contained in any smaller models.

Once we have the ANOVA table, hypothesis testing starts with the model with the largest number of parameters. At each stage, we consider the P-value for all edges leading downwards from the model that we are considering. If the P-value for an edge is large, then it is very likely that the simpler model at the bottom of that edge explains the data adequately, so we can move down that edge to that simpler model and carry on. If the P-value for an edge is very small, then we cannot simplify to the smaller model at

the bottom of that edge, so we do not do any further hypothesis tests below that. This procedure is explained by Grafen and Hails (2002).

For example, suppose that we are considering the model Richness*Identity. The next simpler model is Richness + Identity, and the edge between them corresponds to the row of the ANOVA table labelled

Richness * Identity (25) | Richness + Identity (10).

In Table 2, that P-value is 0.002, so, if we are requiring a significance level of 0.001, we can simplify the model to Richness + Identity. Now there are two edges down. The edge between Richness + Identity and Richness corresponds to dropping Identity from the model, but the corresponding P-value is less than 0.00001, so we cannot do that. The edge between Richness + Identity and Trial + Identity corresponds to dropping Richness, and the P-value for this is 0.2, which is relatively large, so we can simplify the model to Trial + Identity. And so on.

References

- Grafen, A. and R. Hails. 2002. *Modern Statistics for the Life Sciences*. Oxford University Press, Oxford.
- Perkins, D. M., R. A. Bailey, M. Dossena, L. Gamfeldt, J. Reiss, M. Trimmer and G. Woodward. 2015. Higher biodiversity is required to sustain multiple ecosystem processes across temperature regimes. *Global Change Biology* **21**:396–406.
- Reiss, J., R. A. Bailey, D. M. Perkins, A. Pluchinotta and G. Woodward. 2011. Testing effects of consumer richness, evenness and body size on ecosystem functioning. *Journal of Animal Ecology* **80**:1145–1154.

Appendix S3

