ELECTRONIC SUPPLEMENTARY MATERIAL

Evidence for the existence of a robust pattern of prey selection in food webs

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1 Empirical food webs

Table 1
Food webs studied. S is the number of trophic species in the food web and L is the number of trophic interactions.

Food web	S	L	L/S	L/S^2
Benguela (Yodzis, 1998)	29	203	7.00	0.241
Bridge Brook Lake (Havens, 1992)	25	106	4.28	0.171
Canton Creek (Townsend et al., 1998)	102	697	6.83	0.067
Caribbean Reef (Opitz, 1996)	50	556	11.12	0.222
Chesapeake Bay (Baird and Ulanowicz, 1989)	31	68	2.19	0.071
Coachella Valley (Polis, 1991)	29	262	9.03	0.312
El Verde Rainforest (Waide and Reagan, 1996)	155	1509	9.74	0.063
Grassland (Martinez et al., 1999)	61	97	1.59	0.026
Little Rock Lake (Martinez, 1991)	92	997	10.84	0.118
Northeast US Shelf (Link, 2002)	79	1400	17.72	0.224
Scotch Broom (Hawkins et al., 1997)	85	223	2.62	0.031
Skipwith Pond (Warren, 1989)	25	197	7.88	0.315
St. Marks Seagrass (Christian and Luczkovich, 1999)	48	221	4.60	0.096
St. Martin Island (Goldwasser and Roughgarden, 1993)	42	205	4.88	0.116
Stony Stream (Townsend et al., 1998)	109	829	7.61	0.070
Ythan Estuary (Hall and Raffaelli, 1991)	83	395	4.76	0.057

Aside from the specifics of their environment, there are additional factors which distinguish some food webs from the others and should be noted. First, two sets of food webs shared investigators in the compilation of the data: (i) Grassland, Little Rock Lake, and Scotch Broom (Martinez et al., 1999; Martinez, 1991; Hawkins et al., 1997) and (ii) Canton Creek and Stony Stream (Townsend et al., 1998). Second, Scotch Broom is a source web (Hawkins et al., 1997)—a food web generated by following all trophic links upward from a basal species—while the remainder are community food webs. Third, Canton Creek and Stony Stream (Townsend et al., 1998) are time-specific food webs, that is the data was collected one a single day, whereas the other foods webs are cumulative food webs composed of data collected multiple times and spanning multiple seasons.

2 Motif representation in the niche model

Unlike the generalized cascade model (Camacho et al., 2007), we were unable to derive analytical expressions to predict which motifs would be over- or under-represented in the niche model (Williams and Martinez, 2000). We can, however, use numerical simulations to demonstrate that the heuristic arguments presented in the manuscript do indeed agree with the predictions of the model. In Fig. 1, we show the results of numerical simulations of the niche model for motifs S1–S5. In addition, we show results of simulations of the niche model for motifs D1–D8 in Fig. 2.

From our simulations, it is clear that food webs generated by the the niche model are characterized by over-representation of motifs S1–S2 and under-representation of motifs S3–S5, just as in the generalized cascade model. In addition, they strongly agree with our heuristic arguments predicting over-representation of motifs D1, D2, and D6 and under-representation of motifs D3, D4, D5, and D8.

3 Motif representation in the nested-hierarchy model

Like the niche model, we were unable to derive analytical expressions to predict which motifs would be over- or under-represented in the nested-hierarchy model (Cattin et al., 2004). We can, however, examine numerical simulations to see how the nested-hierarchy model compares to the predictions of both the generalized cascade and niche models. In Fig. 1, we show the results of numerical simulations of the nested-hierarchy model for motifs S1–S5. In addition, we show results of simulations of the nested-hierarchy model for motifs D1–D8 in Figs. 2.

Our numerical simulations demonstrate that food webs generated by the nested-hierarchy model *generally* feature over-representation of motifs S1–S2 and under-representation of motifs S3–

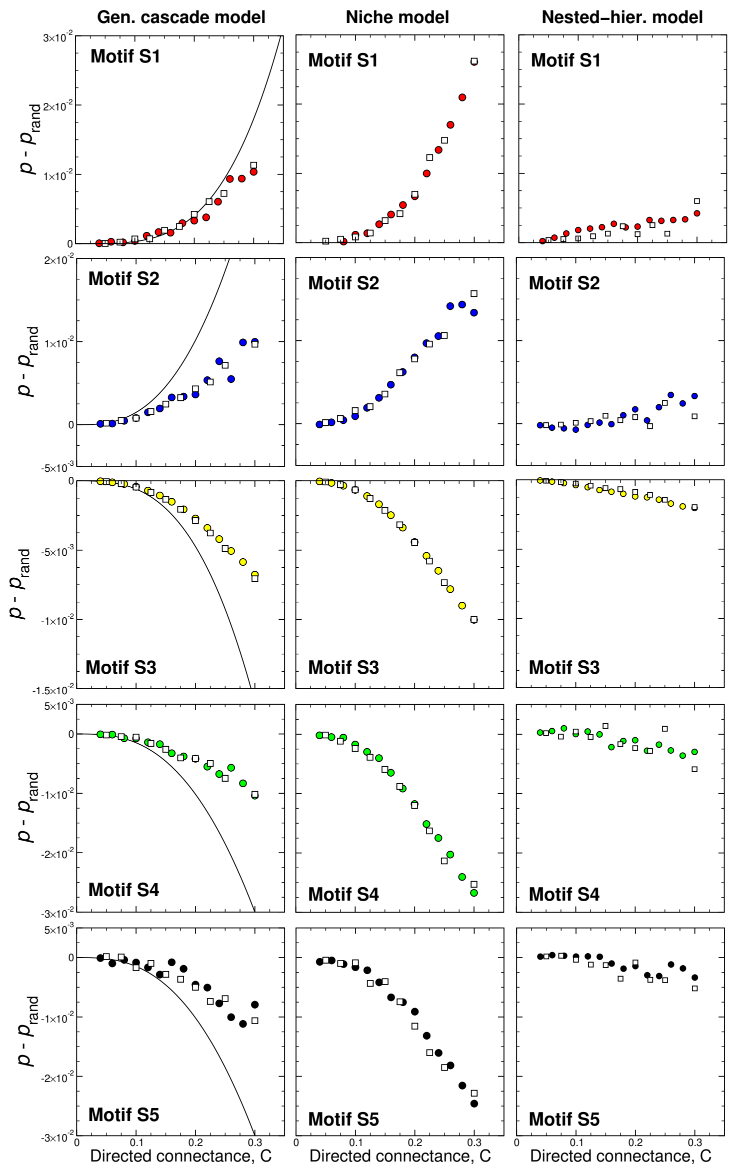

Fig. 1. Comparison between analytical expressions for $p - p_{\mathrm{rand}}$ (Camacho et al., 2007) and simulations of the generalized cascade model for motifs S1–S5. It is visually apparent that the analytical predictions compare well with the model-generated data. In the second and third columns, we show the same results for simulations of the niche and nested-hierarchy models, respectively. We observe that all three models exhibit the same qualitative behavior, however, the generalized and niche models are more quantitatively similar. All models generally predict over-representation of motifs S1 and S2 and under-representation of motifs S3, S4, and S5. The nested-hierarchy model, however, sometimes predicts under-representation of motif S2 and over-representation of motifs S4 and S5.. Filled circles are food webs with $S = 50$ and open squares food webs with $S = 100$. Each data point represents an average over 1000 model-generated food webs.

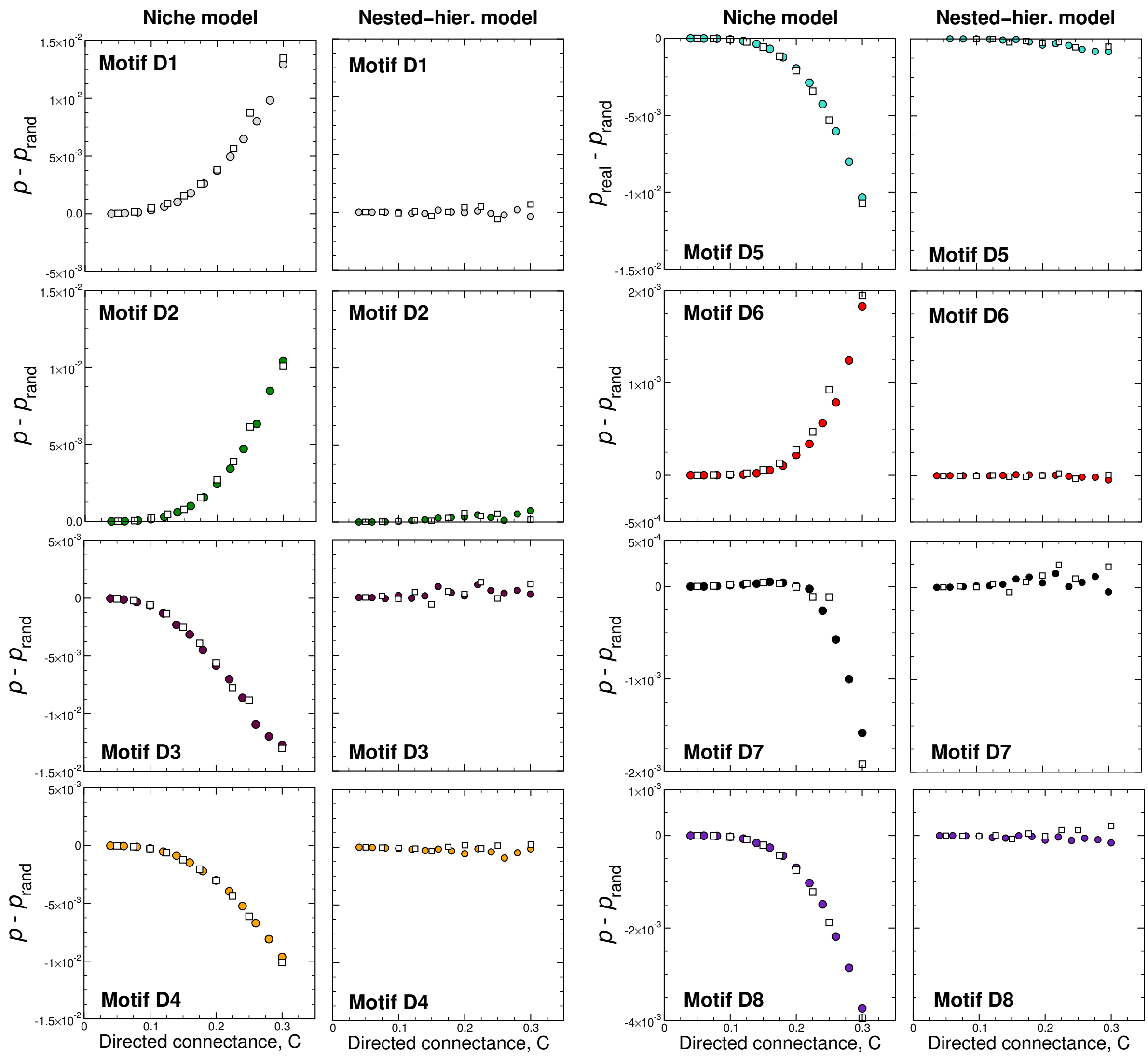

Fig. 2. Comparison between numerical simulations of $p - p_{\rm rand}$ of motifs D1–D8 for the niche and nested-hierarchy models, the first and second column respectively. We omit the generalized cascade model because it does not produce any double links. The niche model clearly generates food webs with over-representation of motifs D1, D2 and D6 and under-representation of motifs D3, D4, D5, and D8. For the nested-hierarchy model, however, we typically observe $p - p_{\rm rand}$ much closer to 0, implying that the model-generated and randomized food webs are quantitatively quite similar. In addition, we find that, with the exception of motif D2 and D5, the nested-hierarchy predicts either over- or under-representation, with no discernible trend. Filled circles are food webs with $S = 50$ and open squares are food webs with $S = 100$. Each data point represents an average over 1000 model-generated food webs.

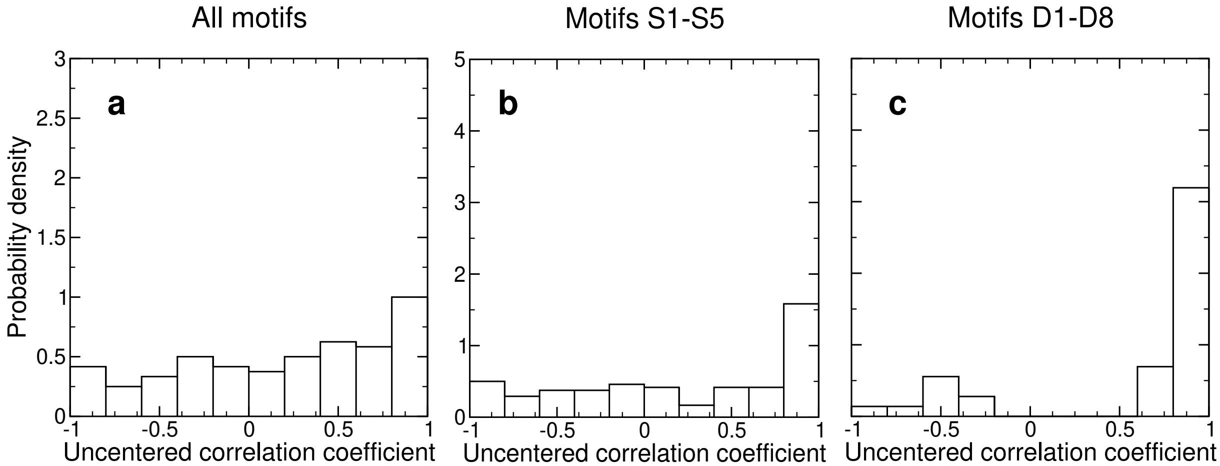

Fig. 3. Probability density for the uncentered correlation coefficient between pairs of empirical food webs for **a**, all motifs, **b**, motifs S1–S5, and **c**, motifs D1–D8. It is visually apparent that each of the distributions is highly skewed toward high values of the correlation coefficient. This is expected given that the empirical z-score profiles exhibit conserved patterns of over- and under-representation. In **c**, we only show the correlation between the food webs which have double links.

S5, just as in the generalized cascade and niche models. For motifs D1–D8, however, we find very different behavior from that predicted by the niche model. We find very little difference between food webs generated by the nested-hierarchy model and their randomizations (Figs. 2).

4 Bayes' rule for model selection

We show in Figs. 4 and 5 the probability densities of uncentered correlation coefficients between z-score profiles of empirical food webs and model-generated food webs with the same S and z. In Fig. 4, we observe that the generalized cascade, niche, and nested-hierarchy models exhibit high positive correlations with the empirical data for motifs S1–S5, as expected from earlier results. The random cascade model, in contrast, exhibits a very broad distribution of uncentered correlation coefficients, also as expected because the empirical food webs do not show random patterns of over- and under-representation. The differences between the models, however, becomes clear upon examining Fig. 5. Here we see that the niche model is *very* strongly correlated with the empirical data. The nested-hierarchy model, instead shows a very broad distribution of correlation values. Even though the nested-hierarchy model still typically generates model food

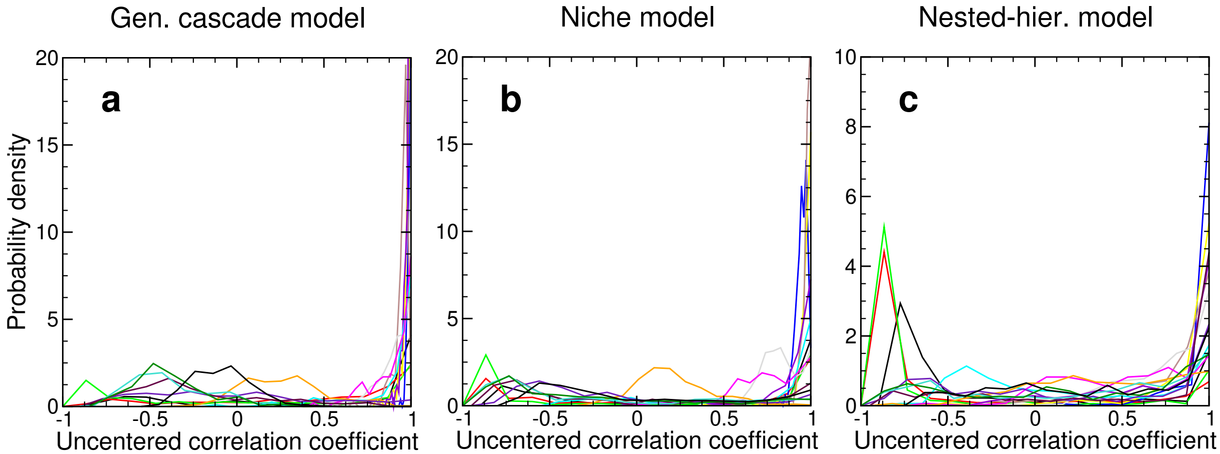

Fig. 4. Probability density for the uncentered correlation coefficient between all empirical food webs and model-generated food webs for motifs S1–S5 for the **a**, generalized cascade, **b**, niche, and **c**, nested-hierarchy models. It is visually apparent that all models generally show high positive correlation with the empirical food webs. This result is expected since all models predict the same over- and under-representation for motifs S1–S5.

webs which are positively correlated to the empirical data, the performance is much worse than for the niche model.

We can use the results of Figs. 5 in Bayesian model selection analysis, to further discriminate between the two models of interest, the niche model and the nested-hierarchy model. We take the fraction of model-generated food webs with uncentered correlation coefficient satisfying an empirically observed event $\mathcal{R}$ as a measure of success of a given model M, where $\mathcal{R} = [0.75 \leq r \leq 1.0]$. Mathematically, Bayes' rule states

$$P\left(M|\mathcal{T}\right) = \frac{P\left(\mathcal{T}|M\right) P(M)}{\sum_{M'=1}^{2} P\left(\mathcal{T}|M\right) P(M)}\,, \tag{1}$$

where $P(M|\mathcal{T})$ is the posterior probability of selecting a model M given an observed event $\mathcal{T}$, $P(\mathcal{T}|M)$ is the probability of observing the event given a particular model, and $P(M)$ is the prior probability of selecting a model. Assuming no prior knowledge to differentiate between the two models, we select $P(M) = 0.5$. Because we have multiple food webs, we can perform this analysis iteratively to generate a posterior probability of selecting a model given *all* of the data. Using this process we find that, using the uncentered correlation coefficient as a basis,

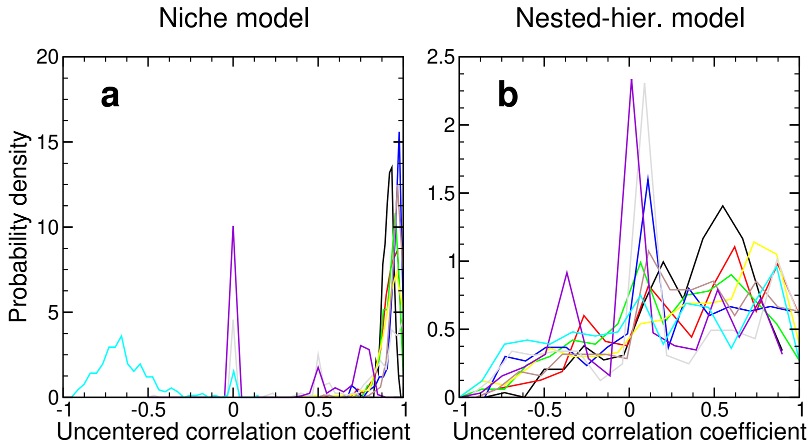

Fig. 5. Probability density for the uncentered correlation coefficient between the empirical food webs with double links and model-generated food webs for motifs D1–D8 for the **a**, niche and **b**, nested-hierarchy models. It is visually apparent that the niche model exhibits high positive correlation with the empirical food webs, while the nested-hierarchy model exhibits very broad distributions of uncentered correlation coefficient values. The niche model, unlike the other models, both qualitatively and quantitatively reproduce the empirically observed pattern of over- and under-representation for motifs D1–D8.

we would *always* select the niche model over the nested-hierarchy model because the posterior probability of the niche model is about 10^6 times larger than that of the nested-hierarchy model (Table 2). The ratio of these two posterior probabilities will remain the same even if other candidate models are added to consideration, as long as the two corresponding prior probabilities are equal.

Table 2
Bayesian model selection using the fraction of model-generated food webs with uncentered correlation coefficient satisfying an empirically observed event $\mathcal{R} = [0.75 \leq r \leq 1.0]$ for motifs D1–D8 as the measure of model success. It is clear that with this measure one would essentially *always* select the niche model.

Food web	$P(\text{Niche}\|\mathcal{R})$	$P(\text{Nested}\|\mathcal{R})$
Benguela	0.883	0.117
Bridge Brook Lake	0.747	0.253
Caribbean Reef	0.834	0.166
Coachella Valley	0.918	0.082
El Verde Rainforest	0.026	0.974
Little Rock Lake	0.859	0.141
Northeast US Shelf	0.947	0.053
Skipwith Pond	0.863	0.137
Ythan Estuary	0.771	0.229
All webs	0.999	1×10^{-5}

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