Supporting Information

Berlow *et al.* 10.1073/pnas.0806823106

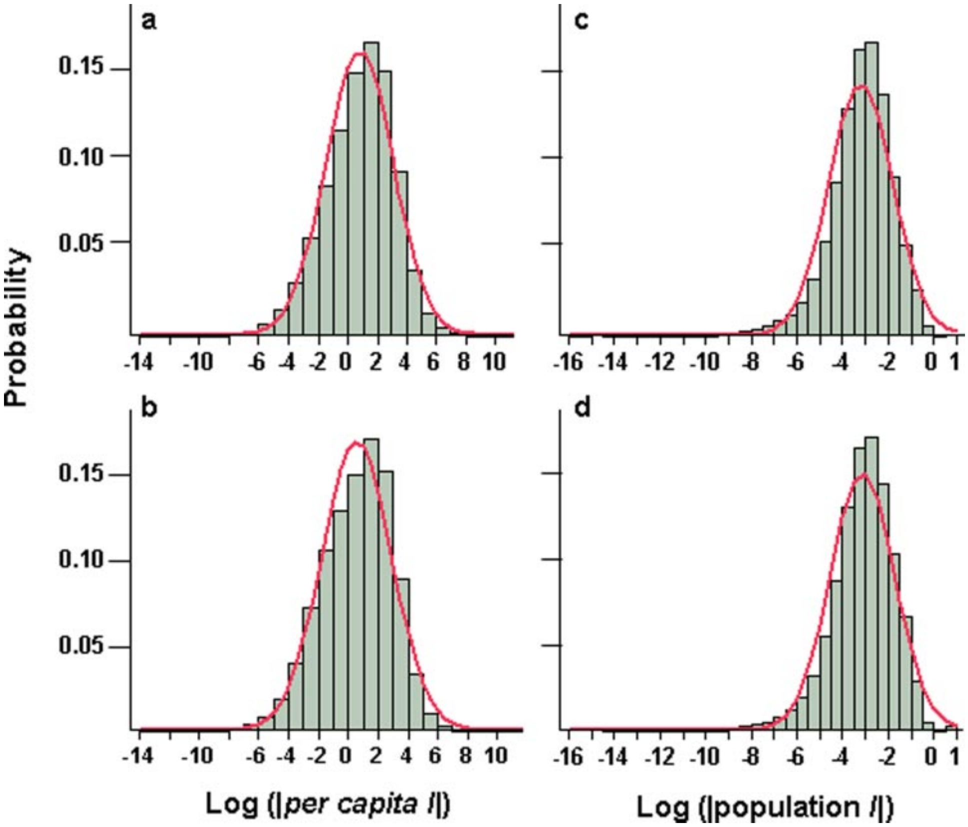

Fig. S1. Emergent variation in interaction strengths. (*a*-*b*) The distribution of $\log_{10}$ (per capita *I*) for (*a*) positive and (*b*) negative interactions. (*c*-*d*) The distribution of $\log_{10}$ (population *I*) for (*c*) positive and (*d*) negative interactions. $n = 114{,}114$ positive interactions for *a* and *c*, $n = 139{,}918$ negative interactions for *b* and *d*. The red line is a fitted normal distribution.

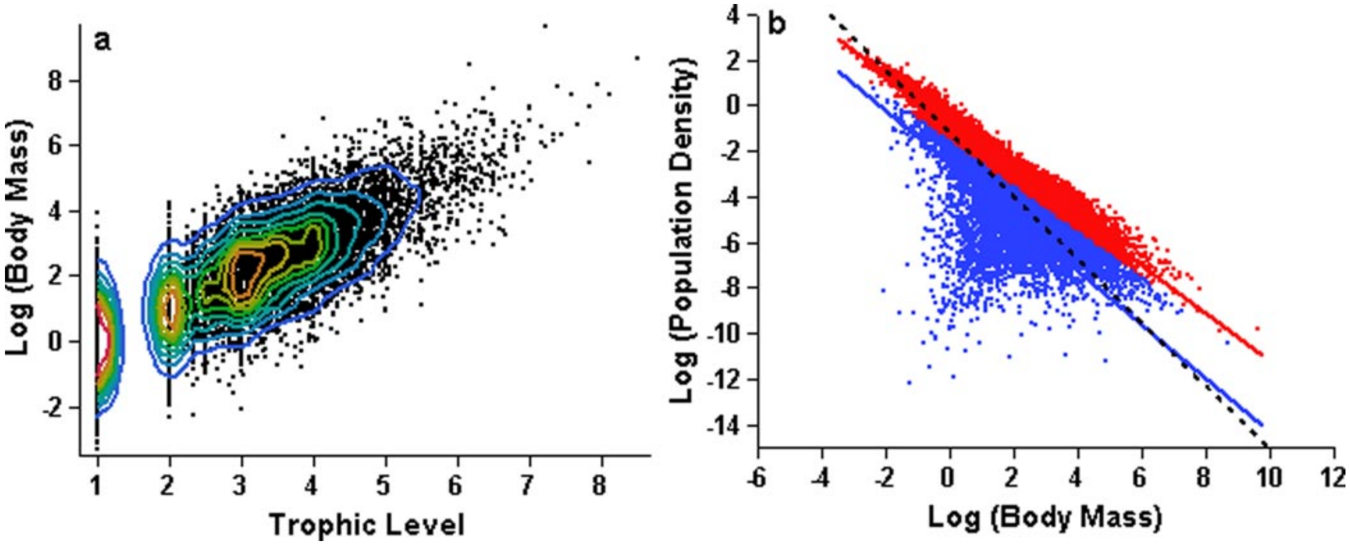

Fig. S2. Macroecological assumptions and emergent patterns. (*a*) Log_{10} body mass depending on trophic level across all food webs simulated. Contour lines are 10% density quantiles from blue (low) to red (high). (*b*) Emergent relationship between species mean density and mean body mass for all species. Different colors indicate upper (red) and lower (blue) 50% quantiles of mean B_R. RMA Regressions of $\log_{10}$ density vs. $\log_{10}$ body mass for each biomass quantile (from low (blue line) to high (red line)): slope $= -1.17$, -1.05, $R^2 = 0.36$, 0.96; error, $n = 6{,}058$ species for each quantile. The overall relationship (dotted black line) has a slope of -1.38 ($R^2 = 0.59$).

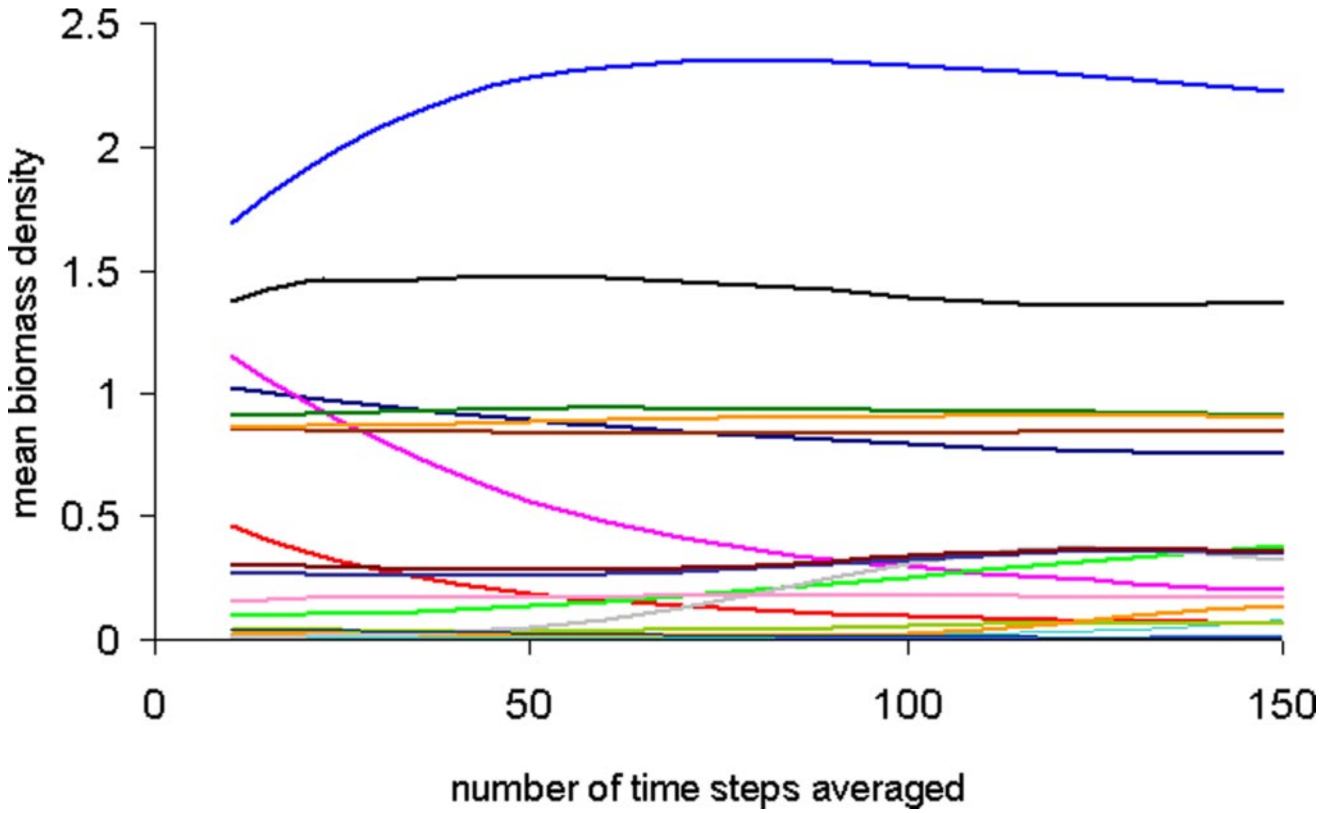

Fig. S3. Determining the time averaging window in an example 30 species niche-model food web. Mean biomass densities depending on the number of time steps averaged (starting after time step 50). Colors indicate different species

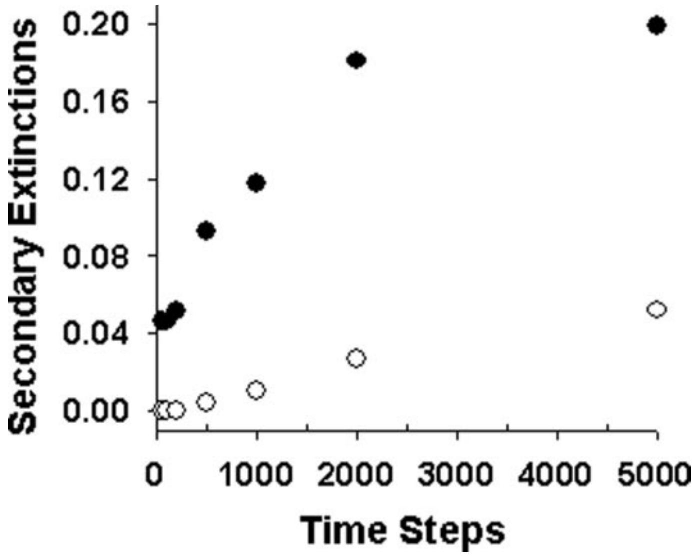

Fig. S4. Secondary extinctions over time. The proportion interactions where *R* removal caused secondary extinction of *T* for simulations of different length. Extinction thresholds were defined by either final *T* biomasses (solid symbols) or time-averaged *T* biomass (open symbols). One hundred different webs were used for each time series length. Cases where *R* or *T* did not persist in runs with *R* unmanipulated were excluded from the analysis.

Table S1. Explaining variation in log (|*I*|) for different simulation lengths

time steps	2° extinctions	*n*	R^2	*Intercept*	B_T^+	B_R
50	included	40868	0.48	−1.20	0.68	0.20
50	*excluded*	*38979*	*0.50*	*−1.19*	*0.69*	*0.21*
100	included	42910	0.58	−1.30	0.71	0.21
100	*excluded*	*40940*	*0.59*	*−1.27*	*0.72*	*0.21*
200	included	43390	0.68	−1.33	0.73	0.20
200	*excluded*	*41160*	*0.69*	*−1.29*	*0.73*	*0.20*
500	included	37202	0.75	−1.42	0.72	0.23
500	*excluded*	*33659*	*0.76*	*−1.38*	*0.73*	*0.22*
1000	included	36462	0.74	−1.44	0.71	0.28
1000	*excluded*	*31950*	*0.75*	*−1.42*	*0.71*	*0.27*
2000	included	25181	0.75	−1.32	0.70	0.35
2000	*excluded*	*20218*	*0.76*	*−1.33*	*0.70*	*0.34*
5000	included	19242	0.68	−1.20	0.65	0.46
5000	*excluded*	*14689*	*0.67*	*−1.22*	*0.63*	*0.46*

Multiple linear regression results predicting log (|*I*|) using log(B_T^+) and log(B_R) for different simulation lengths and with secondary extinctions included or *excluded* from the analysis. $P < 0.0001$ in all cases. n = number of interactions. B_T and B_R are the biomass of *T* with *R* present and the biomass of *R*. respectively

Other Supporting Information Files

SI Appendix