Online Appendix A: Additional data details.

This appendix provides additional details about data processing for some of the studies included in this investigation. Studies not listed below required no additional processing of the raw data.

Gonzalez & Descamps-Julien (2004)

Microcoms with the rotifer *Brachiorus calyciflorus* were not included in these analyses. Data reported in Gonzalez & Descamps-Julien (2004) are in units of mm^3 mL^{-1}; data in these analyses converted to g L^{-1} based on standard biovolumes.

Hector et al. (2010) (BioDepth)

Greece experiment was not included because first-year densities were low, suggesting that plants had not yet fully established. Switzerland experiment was not included because of missing data in third year of study.

Reich et al. (2006) (BioCON)

Early-season (June) samples were eliminated. 'Unsorted biomass' was eliminated. 2007-8 data from 9-species plots that were placed under rain-out shelters were eliminated.

Tilman (1996) (Biodiversity I)

Cover data were used for 1995 - 2001. Early-season (June) samples were eliminated. Data from weedy species were eliminated.

Tilman et al. (2006) (Biodiversity II)

Aboveground dry biomass data was used for 2001 - 2008. Early-season (June) samples were eliminated. Subsamples for 2007 data were averaged. Data from weedy species were eliminated.

Weigelt et al. (2010) (Jena)

Data are from the August / September samples in each year (one per year). 2004 was excluded because of missing data. All subsamples from a given plot and a given sampling occasion were averaged.

Weis et al (2007)

In the original study, the same monoculture EUs were used for both experiments.

Online Appendix B. Lack-of-fit testing for linear regressions

Table B1 below provides lack-of-fit tests for a linear regression model of the log of mean, SD or CV of yield vs. log species richness. Significant lack of fit is indicated by bold p-values. Degrees of freedom for F statistics are the same for all three tests associated with a single experiment. Lack-of-fit tests are not shown for Fox (2004), because the experiments in that study only included two levels of species richness.

Table B1. Lack-of-fit tests for linear regression models.

		$\hat{\beta}_{\mu}$		$\hat{\beta}_{\sigma}$		$\hat{\beta}_{CV}$	
Study	Experiment	F	p	F	p	F	p
Flombaun		$F_{2,80} = 2.27$	0.110	5.28	**0.007**	4.87	**0.010**
Gonzalez	1000	$F_{1,37} = 0.59$	0.446	1.37	0.248	3.08	0.087
Gonzalez	1001	$F_{1,37} = 0.76$	0.390	2.27	0.140	10.59	**0.002**
Gonzalez	1002	$F_{1,37} = 1.20$	0.281	1.55	0.220	0.77	0.384
Hector	Germany	$F_{3,59} = 0.87$	0.462	3.53	**0.021**	4.55	**0.006**
Hector	Ireland	$F_{3,59} = 3.26$	**0.028**	0.70	0.553	1.73	0.168
Hector	Portugal	$F_{3,59} = 0.24$	0.868	0.30	0.822	1.20	0.319
Hector	Sheffield	$F_{3,59} = 0.35$	0.788	0.18	0.907	0.37	0.773
Hector	Silwood	$F_{3,59} = 2.76$	**0.050**	1.34	0.267	0.83	0.480
Hector	Sweden	$F_{3,59} = 0.21$	0.886	0.23	0.874	2.04	0.120

Isbell		$F_{2,68} = 1.70$	0.190	0.17	0.841	6.24	**0.003**
Reich	113	$F_{2,70} = 0.27$	0.767	0.150	0.861	0.02	0.980
Reich	114	$F_{2,70} = 2.60$	0.081	3.59	**0.033**	0.21	0.813
Reich	115	$F_{2,70} = 1.10$	0.338	0.83	0.442	0.64	0.528
Reich	116	$F_{2,70} = 2.82$	0.066	3.16	**0.048**	0.07	0.930
Tilman I	E120	$F_{9,152} = 0.66$	0.742	0.96	0.478	0.69	0.715
Tilman II	E123	$F_{5,140} = 0.34$	0.884	1.21	0.306	0.22	0.953
van Ruijven	150	$F_{2,98} = 0.27$	0.760	0.83	0.437	0.54	0.587
Weigelt		$F_{4,76} = 0.91$	0.465	1.84	0.130	0.70	0.592
Weis	153	$F_{1,76} = 0.07$	0.797	0.20	0.655	0.80	0.375
Weis	154	$F_{1,76} = 0.11$	0.742	0.17	0.682	0.36	0.553
Zhang		$F_{3,114} = 0.19$	0.902	0.32	0.808	0.31	0.818

Online Appendix C: Mathematical proofs for eq. 1.

As in the main text, let Y_i denote the biomass of species *i* in a group of *n* species. All variances, covariances and correlations below are taken with respect to the variation of Y_i over time or space. We first show that η = -1 when species achieve maximal asymmetry, such that the sum of species biomasses is constant. Suppose that $\sum_i Y_i = k$, where k is a constant. To show that η = -1, it suffices to show that $Corr\left(Y_i, \sum_{j \neq i} Y_j\right) = -1$ for all *i*. This follows simply as

$$\begin{aligned} Corr\left(Y_i, \sum_{j \neq i} Y_j\right) &= Corr\left(Y_i, k - Y_i\right) \\ &= \frac{Cov\left(Y_i, k - Y_i\right)}{\sqrt{Var\left(Y_i\right) Var\left(k - Y_i\right)}} \\ &= \frac{Cov\left(Y_i, k\right) - Var\left(Y_i\right)}{Var\left(Y_i\right)} \quad . \\ &= \frac{-Var\left(Y_i\right)}{Var\left(Y_i\right)} \\ &= -1 \end{aligned}$$

Next, we show that independence among species implies η = 0. Again, it suffices to show that $Corr\left(Y_i, \sum_{j \neq i} Y_j\right) = 0$ for all *i*. The proof is:

$$\begin{aligned}
Corr\left(Y_i,\sum_{j\neq i}Y_j\right) &= \frac{Cov\left(Y_i,\sum_{j\neq i}Y_j\right)}{\sqrt{Var\left(Y_i\right)Var\left(\sum_{j\neq i}Y_j\right)}} \\
&= \frac{\sum_{j\neq i}Cov\left(Y_i,Y_j\right)}{\sqrt{Var\left(Y_i\right)Var\left(\sum_{j\neq i}Y_j\right)}} \\
&= 0
\end{aligned}$$

where the last equality follows directly from independence.

Last, we show that $Corr\left(Y_i,Y_j\right)=1$ for all *i,j* implies η = 1. Yet again, it suffices to show that $Corr\left(Y_i,\sum_{j\neq i}Y_j\right)=1$ for all *i*. First we have

$$\begin{aligned}
Corr\left(Y_i,\sum_{j\neq i}Y_j\right) &= \frac{Cov\left(Y_i,\sum_{j\neq i}Y_j\right)}{\sqrt{Var\left(Y_i\right)Var\left(\sum_{j\neq i}Y_j\right)}} \\
&= \frac{\sum_{j\neq i}Cov\left(Y_i,Y_j\right)}{\sqrt{Var\left(Y_i\right)Var\left(\sum_{j\neq i}Y_j\right)}} \\
&= \frac{\sum_{j\neq i}\sqrt{Var\left(Y_i\right)Var\left(Y_j\right)}}{\sqrt{Var\left(Y_i\right)Var\left(\sum_{j\neq i}Y_j\right)}} \\
&= \frac{\sum_{j\neq i}\sqrt{Var\left(Y_j\right)}}{\sqrt{Var\left(\sum_{j\neq i}Y_j\right)}}
\end{aligned}$$

where the third equality follows from the fact that $Corr\left(Y_i, Y_j\right)=1$. Now, $Corr\left(Y_i, \sum_{j\neq i} Y_j\right)=1$ iff $\sum_{j\neq i}\sqrt{Var\left(Y_j\right)}=\sqrt{Var\left(\sum_{j\neq i} Y_j\right)}$, which is true if and only if $\left(\sum_{j\neq i}\sqrt{Var\left(Y_j\right)}\right)^2=Var\left(\sum_{j\neq i} Y_j\right)$. The desired equality follows as

$$\begin{aligned}\left(\sum_{j\neq i}\sqrt{Var\left(Y_j\right)}\right)^2 &= \sum_{j\neq i} Var\left(Y_j\right)+\sum_{j,k\neq i}\sqrt{Var\left(Y_j\right)Var\left(Y_k\right)} \\ &= \sum_{j\neq i} Var\left(Y_j\right)+\sum_{j,k\neq i} Cov\left(Y_j, Y_k\right) \\ &= Var\left(\sum_{j\neq i} Y_j\right).\end{aligned}$$

Online Appendix D. Simulation study of η

To examine the behavior of η, simulated data were generated according to the standard discrete-time Lotka-Volterra competition model. Denote the density of species *i*=1,...,*N*=10 at time *t* as $x_i(t)$. Species densities are governed by the iterative model

$$x_i(t+1) = x_i(t)\exp\left\{r_i\left(1-\frac{x_i(t)+\sum\limits_{i\neq j}\alpha_{ij}x_j(t)}{K_i}\right)+\varepsilon_i(t)\right\}$$

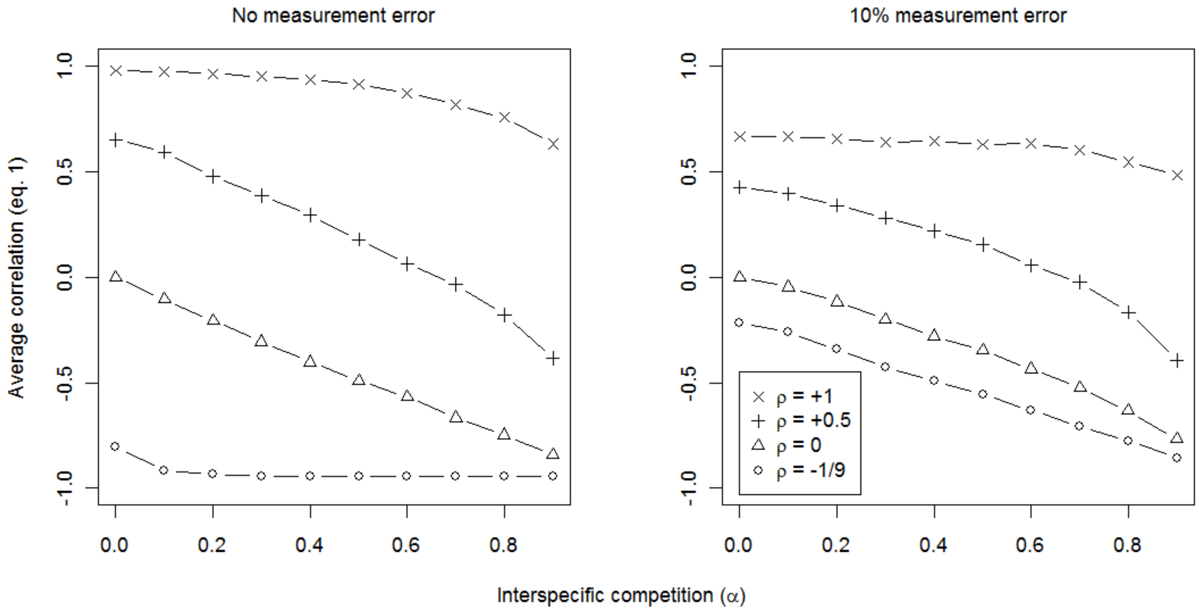
where r_i is the intrinsic rate of population growth of species *i*, α_{ij} measures the strength of interspecific competition of species *j* on species *i*, K_i is the carrying capacity of species *i*, and $\varepsilon_i(t)$ is an environmental perturbation. For simplicity, we assume that all species compete equally with one another ($\alpha_{ij} = \alpha$ for all *i,j* pairs), that each species has the same carrying capacity ($K_i = K$ for all species), and that this carrying capacity scales with α so that each species' equilibrium density is independent of α ($K_i = K^*\left(1+\alpha(N-1)\right)/N$, where K^*=1 is the total community-wide carrying capacity.) We allow species to differ in their intrinsic rates of growth by drawing r_i from a normal distribution with mean 1 and standard deviation 0.25. We draw $\varepsilon_i(t)$ from a normal distribution with mean 0, standard deviation 0.1, and correlation between $\varepsilon_i(t)$ and $\varepsilon_j(t)$ ($i \neq j$) equal to ρ. We assume that all environmental perturbations are serially independent. Finally, we allow for the possibility of measurement error by setting observations equal to the true densities $x_i(t)$ plus a normally distributed error term with mean 0 and standard deviation σ_m. Observations are truncated at 0, as negative densities cannot be measured.

We simulated data and calculated average observed correlations for two scenarios: a first scenario without measurement error, and a second scenario with σ_m = 0.01. Because the equilibrium density of each species is always K^*/N = 0.1, this corresponds to roughly 10% measurement error. For each scenario, we investigated four levels of correlated responses to the environment (ρ = -1/9, the largest possible negative correlation; ρ = 0, independence; ρ = +0.5, moderate positive correlation; and ρ = +1, maximum positive correlation). For each level of environmental correlation, we investigated values of interspecific competition in the range α = 0, 0.1, 0.2, ..., 0.9. Note that α = 0 corresponds to non-interactive species, and thus is equivalent to species reared separately (i.e., in monocultures). Finally, for each combination of ρ and α, we simulated 5000 time points and calculated the correlation on the basis of these data. Although 5000 time points are many more than one would find in any experiment, a long run of data generates a precise estimate of the expected value of η. Of course, experimental data sets will contain fewer time points, and thus will be less statistically precise than the results shown here.

Results of the simulation are shown in fig. D1. Several results are clear. First, when species do not interact (α = 0) the magnitude of η increases as species respond more similarly to environmental perturbations. Second, when species do interact (α > 0), increasing the strength of interspecific competition decreases η. Thus, the difference between η in monoculture (α = 0) and η in polyculture (α > 0) provides an assessment of the extent to which interspecific interactions decrease correlations in species abundances. If species responses to environmental perturbations are negatively correlated (ρ <0), the lower limit of -1 on η may reduce the effect that competition has on reducing species correlations. However, evidence of negatively correlated responses to environmental fluctuations are not found in the data analyzed here (fig. 4).

Finally, measurement error reduces the magnitude of η. In this simulation, species' average abundances were the same regardless of the strength of interspecific competition. If, as is often the case in the experiments studied here, the densities of individual species are higher in monoculture than in many-species mixtures, then measurement error could have a larger effect in mixtures and thus exaggerate the apparent effect of competition on correlations among species.

Online Figure D1.



Online Appendix E. Additional figure.

Online Figure E1.

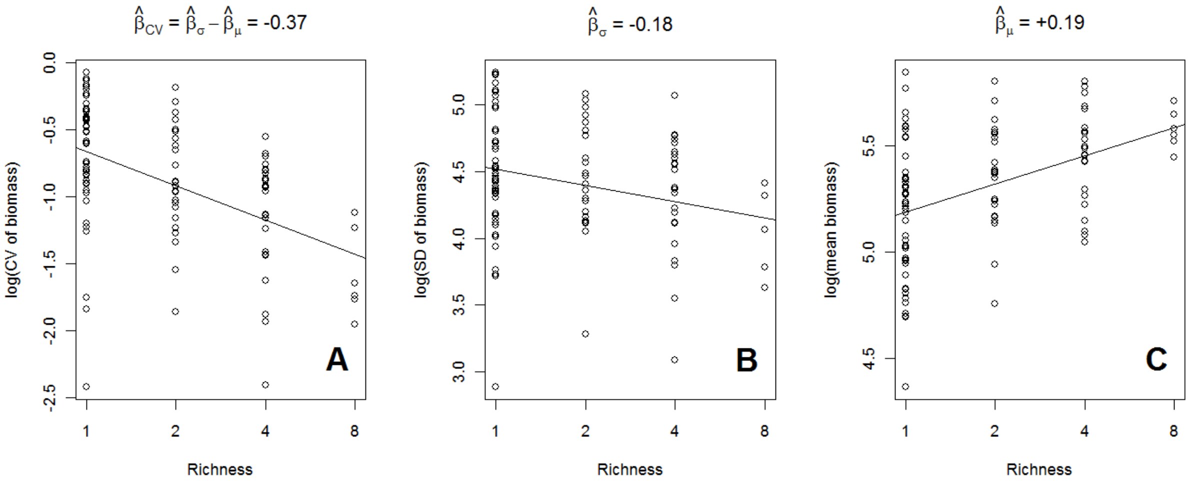


Figure legends

Online Figure D1. Species syncrhony among 10 simulated species as calculated by η from eq. (1). Left: species synchrony without measurement error. Right: species synchrony for data measured with 10% measurement error. In both panels, the case of $\alpha = 0$ corresponds to no interaction among species and represents correlations that could arise from species reared separately in monoculture. The parameter ρ is the correlation of species responses to environmental fluctuations.

Online Figure E1. Illustration of the relationship $\hat{\beta}_{CV} = \hat{\beta}_{\sigma} - \hat{\beta}_{\mu}$ for data from van Ruijven & Berendse (2005). (A): CV of biomass yield vs. species richness for individual experimental plots. (B): SD of biomass yield vs. species richness. (C): Mean biomass yield vs. species richness. All scatterplots and regressions are on a log-log scale. (Labels on the horizontal axis are given on an untransformed scale for convenience.) For these data, increasing species richness was associated with an increase in community stability ($\hat{\beta}_{CV} = -0.37$) caused by both a decrease in variance ($\hat{\beta}_{\sigma} = -0.18$) and an increase in mean yield ($\hat{\beta}_{\mu} = +0.19$).