

## Appendix E from X. Xiao et al., “A Strong Test of the Maximum Entropy Theory of Ecology” (Am. Nat., vol. 185, no. 3, p. E70)

### Bootstrap Analysis

We conducted a bootstrap analysis to examine whether the deviation of the empirical data from the distributions predicted by the maximum entropy theory of ecology (METE) was comparable to that of random samples drawn from the distributions themselves. In each community, we obtained the Lagrange multipliers  $\lambda_1$  and  $\lambda_2$  with empirically observed state variables  $S_0$ ,  $N_0$ , and  $E_0$ , which determined the form of the predicted patterns (eqq. [3]–[5]). We drew 500 bootstrap samples from the predicted distribution for each pattern. For the species abundance distribution (SAD), samples of size  $S_0$  were drawn from the upper-truncated log-series distribution defined by equation (3). For the individual size distribution (ISD), samples of size  $N_0$  were drawn from the distribution defined by equation (4). For the size-density relationship (SDR) and the intraspecific ISD (iISD), samples for each species given its abundance  $n$  were drawn from the exponential distribution defined by equation (5). The SDR of each sample community was then obtained by taking the average body size within a bootstrap sample for each species. Note that this sampling scheme assumes independence among values within each bootstrap sample. As a result, the values of the original state variables are unlikely to be preserved in the bootstrap samples. However, given that the discrepancy is not systematic and that the results of the bootstrap analysis are highly consistent both across samples and across communities (see fig. E2), we conclude that the assumption of independence should not qualitatively affect our results.

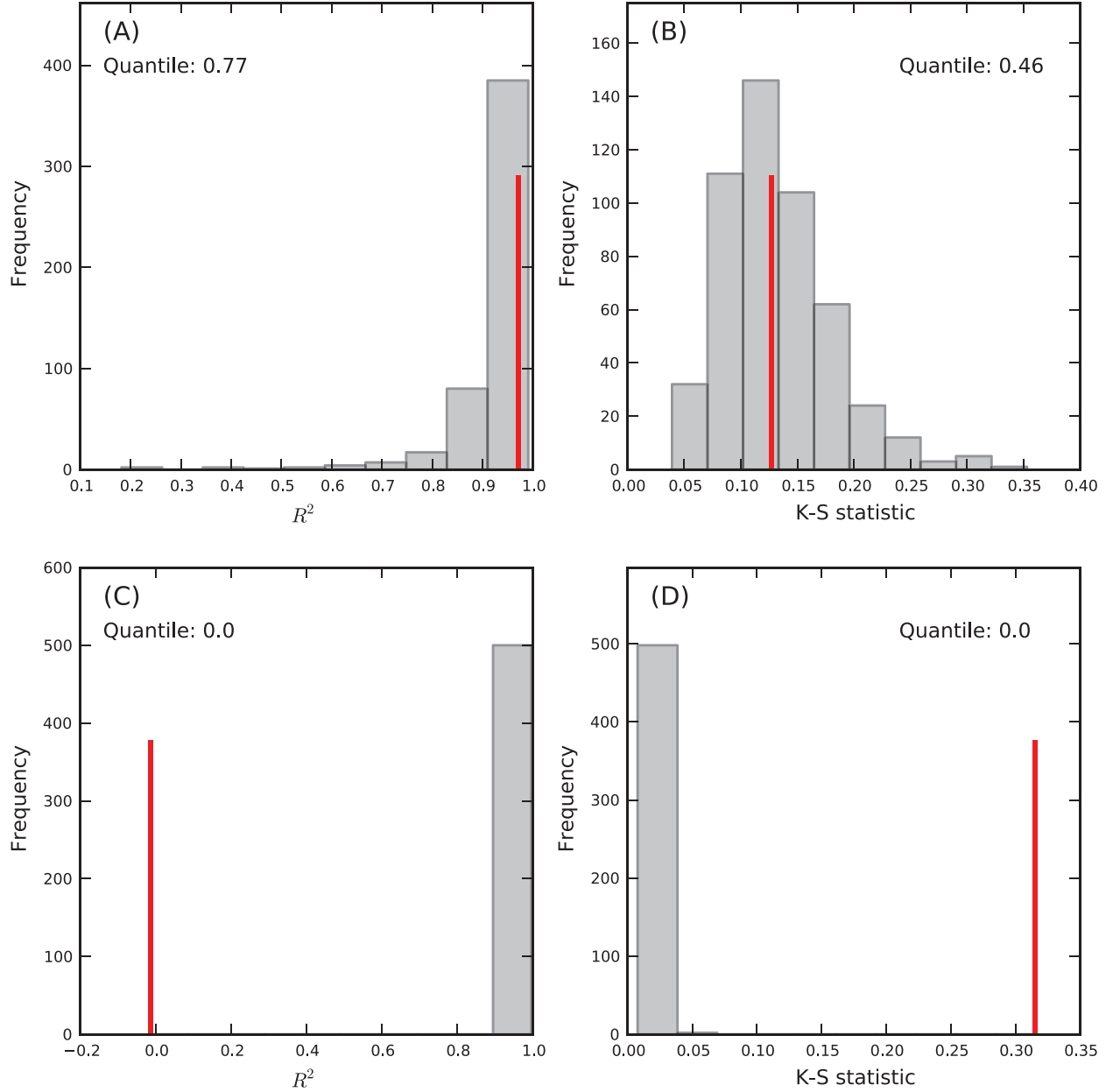
The deviation between empirical data or bootstrap samples and METE’s predictions were quantified using  $R^2$  and the Kolmogorov-Smirnov (K-S) statistic. The K-S statistic is defined as

$$D_n = \sqrt{n} \sup |F_n(x) - F(x)|, \quad (\text{E1})$$

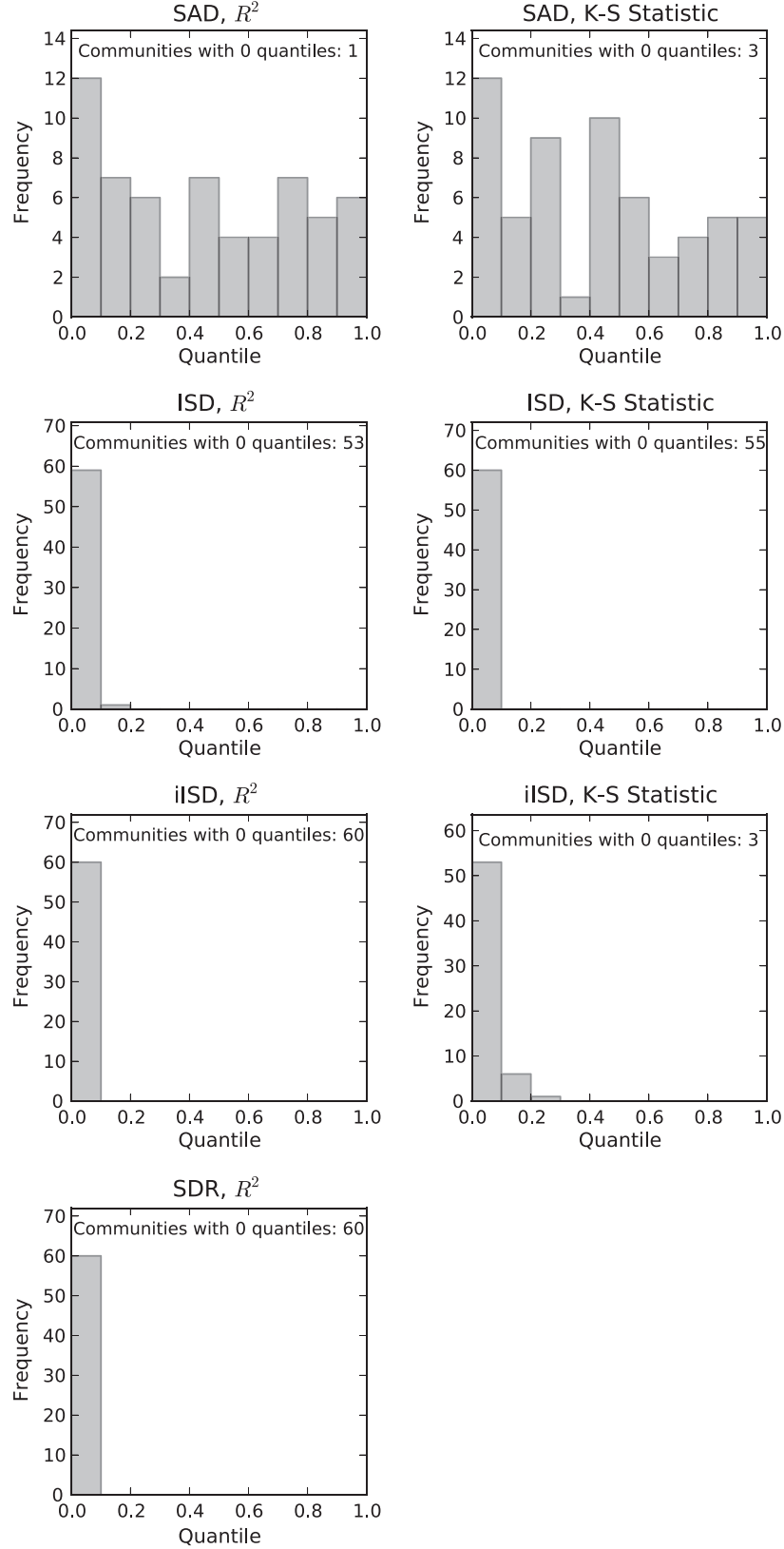
where  $n$  is the sample size,  $F_n(x)$  is the empirical cumulative distribution function, and  $F(x)$  is the reference (predicted) cumulative distribution function. Therefore, the K-S statistic directly measures the largest discrepancy in shape between two distributions across multiple points. Note that the statistic is defined for distributions only and thus cannot be applied to the SDR. However, since the SDR and the iISD are closely related (see “Methods”), the iISD results can provide insights for the SDR. Figure E1 illustrates the comparison between the empirical data and the bootstrap samples for the SAD and the iISD when evaluated with the two statistics, using data from one community (University of California, Santa Cruz, Forest Ecology Research Plot [UCSC FERP]) as an example.

We converted the test statistics within each community into quantiles so that results can be pooled across communities. The quantile for each pattern in a community was calculated for each of the two statistics as the proportion of bootstrap samples that had larger deviations from METE’s prediction (i.e., lower value of  $R^2$  or higher value of K-S statistic) than the empirical data. For example, figure E1A shows that 77% of the bootstrap SADs have a lower  $R^2$  than the empirical SAD in the community UCSC FERP. For the iISD, where bootstrap samples were independently generated for each species, the quantile of the K-S statistic for a given community was calculated as the average quantile across all species having 10 or more individuals, weighted by their abundances.

Comparisons between the empirical data and the bootstrap samples for the four ecological patterns across all 60 communities are summarized in figure E2. Results from the two statistics are qualitatively consistent (although note again that the K-S statistic cannot be applied to the SDR, which is not a probability distribution). While the bootstrap analysis confirms that METE provides a satisfactory characterization for the empirical SAD but not for the empirical SDR or iISD, it shows that the empirical ISD cannot be fully accounted for by METE’s prediction, despite the relatively high  $R^2$  within and across communities for this pattern (see fig. 2B and the supplementary figures).



**Figure E1:** Illustration of the comparison between empirical data and bootstrap samples using data from the University of California, Santa Cruz, Forest Ecology Research Plot as an example. *A* and *B* show the results for the species abundance distribution (SAD) when evaluated with  $R^2$  (*A*) and the Kolmogorov-Smirnov (K-S) statistic (*B*), while *C* and *D* show the results for the intraspecific individual size distribution (iISD). In each panel, the histogram represents the frequency distribution of the test statistic among the 500 bootstrap samples, while the red vertical line represents the test statistic of the empirical data. Note that for the iISD the K-S statistic was individually obtained for each species, and the illustration in *D* includes the results for only one species, *Pseudotsuga menziesii*.



**Figure E2:** Results of bootstrap analysis across all 60 communities evaluated with  $R^2$  and the Kolmogorov-Smirnov (K-S) statistic for the four patterns (except for the size-density relationship [SDR], where only  $R^2$  is available). The histogram in each panel is the frequency

distribution of the quantile values across the 60 communities for one pattern using one statistic ( $R^2$  or K-S statistic), where each quantile value represents the quantile of the empirical statistic among that of the 500 bootstrap communities. The number of communities where the quantile equals 0 (i.e., where the empirical data have a larger deviation from the predicted pattern than any of the bootstrap samples) is also given. Note that for the intraspecific individual size distribution (iISD), the quantile of the K-S statistic is a pooled value across all species with abundance  $>10$  in a community and thus can equal 0 only when the quantiles for all species are 0. ISD = individual size distribution, SAD = species abundance distribution.