

**Appendix S2.** Correlation of native and exotic species richness: a global meta-analysis finds no invasion paradox across scales. Peng et al. *Ecology*.

## Materials and Methods supplement

### 1. Details on extracting latitude and longitude:

If a study identified study location by name only and did not provide concrete geographic data, we used Google Maps to estimate latitude and longitude. When the study area spanned a large region (e.g., California), we used the midpoint of the region. These midpoints were automatically calculated by using a Geographic Midpoint Calculator (<http://www.geomidpoint.com>).

### 2. Other details in the data collecting processes:

Many studies selected several sites (with specific coordinates) within a larger region. If they reported results separately for each site, we regarded results from each site as an individual case (Belote et al. 2008). For a minority of studies that attempted to explore the effects of artificial disturbances on NERRs, if they reported results of both undisturbed and disturbed (or both pre-disturbance and post-disturbance) plots, only undisturbed (or pre-disturbance) plots were used (McGranahan et al. 2012), and if studies reported temporal dynamic change of NERRs under a disturbance regime over time, we selected the earliest measurement (Meiners et al. 2002). Some studies, especially for nested design surveys, reported both cumulative diversity (gamma diversity) and mean diversity observed at a certain grain size (Jauni and Hyvönen 2012). Researchers generally focus on actual species counts rather than aggregated means when calculating NERRs (Deutschewitz et al. 2003, Belote et al. 2008, Chen et al. 2010). We therefore used only cumulative species richness counts as long as the sample plots were separate and independent of each other.

### 3. Effect size and model details:

The Pearson's product moment correlation coefficient ( $r$ ) from each case was normalized using Fisher's z transformation to use as an effect size:

$$z = \frac{1}{2} \ln \left( \frac{1+r}{1-r} \right), Var = \frac{1}{n-3}, \quad (\text{Eq. S1})$$

where  $n$  is the number of pairs of exotic and native species numbers of NERR for each case.

Results from studies that reported other coefficients, e.g., Spearman's rank correlation, were converted to Pearson's correlation coefficient according to Lajeunesse (2013). We constructed an inverse-variance weighted hierarchical mixed-effects meta-regression of  $z$  as a function of covariates of interest:

$$z_i = \zeta_i + \varepsilon_{z_i}; \varepsilon_{z_i} \sim N(0, s_{z_i}^2) \quad (\text{Eq. S2})$$

$$\zeta_i = \theta_j + \varepsilon_{\zeta_i}; \varepsilon_{\zeta_i} \sim N(0, \omega^2) \quad (\text{Eq. S3})$$

$$\theta_j = \beta_0 + \sum_{p=1}^P \beta_p X_{p_i} + \varepsilon_{\theta_j}; \varepsilon_{\theta_j} \sim N(0, \tau^2) \quad (\text{Eq. S4})$$

where  $z_i$  is the observed effect size for case  $i$ , which is normally distributed with mean  $\zeta_i$  and within-case variance  $s_{z_i}^2$ , where  $z_i$  and  $s_{z_i}^2$  are extracted from each case. The estimated true effect size for case  $i$ ,  $\zeta_i$ , is nested within study  $j$  and is normally distributed with mean  $\theta_j$  and among-case (i.e. within-study) variance  $\omega^2$ . Study-level effects  $\theta_j$ , were modeled fitting the intercept  $\beta_0$  and the coefficient  $\beta_p$  as a function of covariate  $X_p$ , with normally distributed errors with a variance of  $\tau^2$ .

#### 4. Model selection

In order to select a model that best explains the heterogeneity in effect sizes, we fit hierarchical mixed-effects multiple meta-regressions of  $z$  using all combinations of first-order covariates. Before fitting models, correlations between covariates were tested to exclude multicollinearity (none were highly correlated, all  $r < 0.25$ ). Model fit was compared using Akaike's information criterion corrected for small sample size (AICc). Models were considered equivalent to the best model (minimum AICc) when the difference in AICc is less than 2. We calculated marginal and conditional coefficients of determination ( $R^2$ ) (Nakagawa and Schielzeth 2013), as well as pseudo- $R^2$  for linear mixed-effects models as metrics of explanatory power. The pseudo- $R^2$  metric used was the proportion change in variance when fitting mixed-effects models relative to a random-effects only model.

#### 5. Species-area curve simulation

An important question was whether NERR increases with grain size purely because of statistical sampling properties on sampling rather than for biological reasons. We asked, to what extent to species area curves (SACs) explain patterns in the magnitude of NERR with increasing grain sizes? Assuming that the total species richness in a region was higher for native species

than exotic species, we hypothesized that the variation around the relationship of species richness and area (species area curve, SAC) would narrow approaching the asymptote, and if this were true, the NERR would get larger closer to the asymptote of the SAC. To test this, we simulated species area curves (SACs) for hypothetical communities with native and exotic species (45 native and 15 exotic species), in which species varied in probability of occurrence. We used 100 1 m<sup>2</sup> plots in our simulation, each with five randomly sampled (given probability of occurrence) individuals. In these simulations, we assumed that there were no spatial patterns in species distributions and that all plots were independent. We resampled plots at all possible extents, for example, sampling 10 m<sup>2</sup> extent (a collection of 10 plots) 100 times, creating a hypothetical SAC. We bootstrapped from this SAC, sampling native and exotic richness in 10 different plots at all possible grains, and calculated the NERR, iterating the process 10,000 times. We found no significant relationship between NERR and the grain size of the bootstrapped samples, suggesting that the relationship found in this study is a feature of biology rather than an artifact of sampling.

## References

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