

Appendix S4 Methods for the hierarchical analysis of response as a function of magnitude of the climate treatment.

Figure S4.1 Graphical representation of the hierarchical model's (a) structure and (b) functional relationship of analysis of effect size as a function of magnitude of treatment. θ . vector of parameters included in the analysis (a: maximum effect size and b: half-saturation constant), o: origin (native and non-native), t: terrestrial, a: aquatic, temp: temperature, prec: precipitation.

Supplementary methods for the hierarchical analysis

We explored the relationship between effect size (i.e., magnitude of performance response) and the treatment magnitude (i.e., degree of climatic change) within a hierarchical framework. For species *i* in study s (analyzed separately for negative and positive responses), the likelihood of observing that effect size was calculated as:

$$ES_{obs\ i,s} \sim Normal(ES_{i,s}, \sigma_i^2)$$

with process model:

 MT_s

 $ES_{i,s} = a_{origin (i),system (i),driver (i)} \overline{MT_s + b_{origin (i),system (i),driver (i)}}$

The variance associated with each effect size, σ_i^2 , was estimated as a combination of the observed variance in response size and an overall variance: $\frac{1}{\sigma_i^2} = \frac{1}{\sigma_{abs(i)}^2} + \frac{1}{\eta^2} \cdot \sigma_{abs(i)}^2$, the observed variance, was

calculated from the standard deviation (SD) or standard error reported in the original study for the response variable. To estimate the observed variance associated with each effect size, we ran 10,000 simulations calculating effect size from the mean response and reported SD. If measurements of variability around each effect size were not available (219 out of 755 observations), we then estimated this variance as $1/\sigma_{obs(i)}^2 \sim Gamma(0.01, 0.01)$. The overall variance, η^2 , was estimated from a distribution with non-informative priors, $1/\eta^2 \sim Gamma(0.01, 0.01)$.

The parameters, associated with the process model, for maximum effect size (parameter a) and the half saturation constant (parameter b) were estimated hierarchically as:

$$a_{origin,system,driver} \sim Normal(a1_{origin,system},\sigma_a^2)$$

 $a1_{origin,system} \sim Normal(a2_{origin},\sigma_{a1}^2)$ and $\sigma_a \sim Uniform(0,1000)$
 $a2_{origin} \sim LogNormal(0,10000)$ and $\sigma_{a1} \sim Uniform(0,1000)$

and

$$b_{origin,system,driver} \sim Normal(b1_{origin,system},\sigma_b^2)$$

 $b1_{origin,system} \sim Normal(b2_{origin}, \sigma_{b1}^2)$ and $\sigma_b \sim Uniform(0,1000)$
 $b2_{origin} \sim LogNormal(0,10000)$ and $\sigma_{b1} \sim Uniform(0,1000)$

We used non-informative priors for the hyperparameters, a^2 and b^2 , and the variances, σ^2 , and lognormal distributions for the overall parameters, a^2 and b^2 , to ensure positive values. This structure allowed us to make comparisons between native and non-native species at three levels: overall, parameters a^2_{origin} and

 $b2_{origin}$; within each system, parameters $a2_{origin,system}$ and $b2_{origin,system}$; and within system for each driver, parameters $a2_{origin,system,driver}$ and $b2_{origin,system,driver}$. Additional fixed (e.g., response type, latitude, or study duration) or random effects (e.g., study) did not improve the model fit (based on Deviance Information Criterion; Spiegelhalter *et al.* 2000); thus, results from the basic model were reported in the main text.

Reference

Spiegelhalter, D.J., Best, N., Carlin, B.P. & Linde, A.V.D. (2000). Bayesian measures of model complexity and fit. *J. Royal Statist. Soc. B*, 64, 583-639.