**Analysis**

We fit three separate general linear models representing the different hypotheses and data aggregations (i.e., lake-level size-abundance relationships and feeding group-level size-abundance relationships). First, we fit a global model with log10 abundance as the response variable and log10 biomass as the predictor variable. Second, to test the hypothesis that the size abundance relationship varies with lake trophic status, we fit a model to the same data as before but added an interaction between log10 biomass and lake trophic status. The data contained a single observation per lake (n = 1025 total observations). Finally, to test they hypothesis that the size-abundance relationship varies across zooplankton feeding groups and lake trophic status, we fit a third model with log10 abundance of each feeding group as the response variable and a three-way interaction between log10 biomass of each feeding group, feeding group identity, and lake trophic status. This model used the same raw dataset as before, but summarized log10 abundance and biomass per feeding group per lake rather than just per lake. That resulted in 2,704 total data points. All models assumed Gaussian likelihood. To ease interpretation of parameter estimates and improve model convergence, we centered log10 abundance and log10 biomass prior to fitting the model by subtracting the global mean of each variable from each observation.

We specified the models in R (version 4.2.0) using Bayesian inference via the *brms* package (Bürkner 2017), which translated the model structure to *rstan* (Stan Development Team 2022). *rstan* then sampled the joint posteriors using Hamiltonion Monte Carlo. We sampled 2000 iterations from each of 4 chains. After discarding the first 1000 iterations from each chain, we obtained 4000 total samples of the joint posterior distribution. We checked chain convergence using the Gelman Rubin statistic, ensuring that all *Rhat* values were <1.1 (Gelman and Rubin 1992). Finally, we checked model fit using posterior predictive plots (Conn et al. 2018). Below we use the joint posteriors to summarize the median and 95% credible intervals of parameters of interest, including derived quantities (e.g., marginal slopes) (Hobbs and Hooten 2015).

*Prior justification*

In each model, we specified an informative prior for the slope parameters as Normal(-0.75, 0.1), where the values represent the mean and standard deviation, respectively. For the intercept, we specified Normal(0, 1), a reasonable choice given that the response and predictors are centered at 0 and the data are log transformed. For the interaction parameters, we specified a fairly uninformative prior of Normal(0, 1). Finally, for sigma, we used the default prior in *brms* of half-Student\_t(3, 0, 2.5).