A Bayesian hierarchical model for size spectra

Jeff S. Wesner1,✉, Justin P.F. Pomeranz2, James R. Junker3,4, Vosjava Gjoni1, and Yuhlong Lio5

1 University of South Dakota, Department of Biology, Vermillion, SD 57069  
2 Colorado Mesa University,…  
3 Great Lakes Research Center, Michigan Technological University, Houghton, MI 49931  
4 Louisiana Universities Marine Consortium, Chauvin, LA 70344  
5 University of South Dakota, Department of Mathematics, Vermillion, SD 57069

✉ Correspondence: [Jeff S. Wesner <[Jeff.Wesner@usd.edu](mailto:Jeff.Wesner@usd.edu)>](mailto:Jeff.Wesner@usd.edu)

# Abstract

A fundamental pattern in ecology is that smaller organisms are more abundant than larger organisms. At the individual level, this pattern is known as the individual size distribution (ISD) or community size spectrum, which describes the frequency distribution of all individuals in an ecosystem, regardless of taxon. This distribution arises from a power law distribution, such as the Pareto distribution, and a major goal of size spectra analyses is to estimate the ISD power law exponent. However, while numerous methods have been developed, they have focused almost exclusively on estimating the exponent from single samples. Here, we develop an extension of the truncated Pareto distribution within the probabilistic modeling language Stan. We use it to estimate multiple ISD exponents simultaneously with a hierarchical modeling approach. The most important result is the ability to examine hypotheses related to size spectra within a single generalized (non)-linear mixed model.

Keywords: *Bayesian, body size spectra, hierarchical, Pareto, power law, Stan*

# Introduction

In any ecosystem, large individuals are typically more rare than small individuals. This fundamental feature of ecosystems generates a remarkably common pattern in which relative abundance declines with individual body size, generating the individual size distribution ISD (or community size spectrum) (Sprules and Barth 1983; White et al. 2008)(Sprules et al. 1983, White et al. 2008). More formally, the ISD is a frequency distribution that can be approximated by a bounded power law with a single free parameter , corresponding to the following probability density function (Edwards et al. 2020)(Edwards et al. 2020):

where is the body size (e.g., mass or volume) of an individual regardless of taxon, is the smallest individual attainable and is the largest possible individual (White et al. 2008)(White et al. 2008). is a constant equal to:

This model is also known as the bounded power law or truncated Pareto distribution. The terms “bounded” or “truncated” refer to the limits of and . Without those limits, the function is a simple power law. Each term in the equations above comes directly from the data except for the exponent , which must be estimated from a statistical model.

The exponent is often described by its “steepness”, with more negative values (i.e., “steeper”) indicating higher abundance of large relative to small individuals, and vice versa. These patterns of size frequency are an emergent property of demographic processes (e.g., age-dependent mortality), ecological interactions (e.g., size-structured predation, trophic transfer efficiency), and physiological constraints (e.g., size-dependent metabolic rates) (Andersen and Beyer 2006, White et al. 2008)(Andersen and Beyer 2006, White et al. 2008). As a result, variation in across ecosystems or across time can indicate fundamental shifts in community structure or ecosystem functioning. For example, overfishing in marine communities has been detected using size spectra in which was steeper then expected, indicating fewer large fish than expected (Blanchard et al. 200x). Shifts in have also been used to document responses to acid mine drainage in streams (Pomeranz et al. 2019; Pomeranz et al. 2020)(Pomeranz et al. 2019, 2020), and changes in response to land use (Martínez et al. 2016)(**martinez2016?**), resource subsidies (Perkins et al. 2018)(Perkins et al. 2018), and temperature (Pomeranz et al. 2022)(Pomeranz et al. 2022).

Given the ecological information it conveys, the data required to estimate size spectra are deceptively simple; only a single column of data are needed, in which each data point is a single measure of the body size of an individual. As long as the body sizes are collected systematically and without bias towards certain taxa or phenotypes, there is no need to know any more ecological information about the data points (e.g., taxon, trophic position, age, abundance). However, despite the simple data requirement, the statistical models used to estimate are diverse. Edwards et al (2017)(Edwards et al. 2017) documented 8 different analytical methods. Six of these involved binning, in which the body sizes are grouped into size bins (e.g., 2-49 mg, 50-150mg, etc.) and then counted, generating values for abundance within each size bin. This allows to be estimated using simple linear regression. Unfortunately, the binning process also removes most of the variation in the data, collapsing information about 1000’s of individuals into just 6 or so bins. Doing so can lead to the wrong values of , sometimes drastically so (White et al. 2008, Edwards et al. 2017/2020)(White et al. 2008, Edwards et al. 2017, 2020).

An improved alternative to binning and linear regression is to fit the body size data to a power law probability distribution (White et al. 2008, Edwards et al. 2017/2020)(White et al. 2008, Edwards et al. 2017, 2020). This method uses all of the data without binning and directly estimates using maximum likelihood (Edwards et al. 2017)(Edwards et al. 2017)*.* However, at present it is only possible to fit the models to single data set using maximum likelihood. To our knowledge there is no current method to fit ISD models to multiple groups of ISD’s, such as data collected from multiple sites or multiple years. Instead, hypothesis testing with individual size distributions is typically done in two steps (e.g., Pomeranz et al. 2022)(Pomeranz et al. 2022). First, estimates are obtained individually from each collection (e.g., each site or year, etc.). Then, these estimates are used as response variables in a linear model to examine how they relate to predictor variables (Edwards et al. 2020)(Edwards et al. 2020). A downside to this approach is that it treats values as independent samples, even if they come from the same sites or times. It also removes information on sample size (number of individuals used to derive . As a result, the approach not only separates the data generation model from the predictor variables, but it is also unable to take advantage of partial pooling during model fitting.

Here, we develop a Bayesian model that uses the truncated Pareto distribution to estimate in response to both fixed and random predictor variables. The model extends the maximum likelihood approach developed by Edwards et al. (2020)(2020) and allows for a flexible hierarchical structure, including partial pooling, within the modeling language Stan (Stan Development Team 2022)(Stan Development Team 2022).

# Methods

## Translating to Stan

We first translated the probability density function described by Edwards et al. (2020)(Edwards et al. 2020) into Stan by converting it to a log probability density function (lpdf). Stan is a probabilistic modeling language that is capable of fitting complex models, including those with custom lpdf’s. The resulting lpdf is below:

which is coded in Stan as follows:

functions{  
real paretocustom\_lpdf(real x, real b, real xmin, real xmax){  
if(b != -1)  
return(log((b+1) / ( xmax\^(b+1) - xmin\^(b+1))) + b\\*log(x));  
else  
return(log(log(xmin) - log(xmax)) + b\\*log(x));  
 }  
}

We call this the distribution, which we can now use to estimate of given a data set. For example, an intercept-only model would look like this:

where is the th individual body size, is the size spectrum exponent, and are as defined above, and is the intercept with a prior probability distribution. In this case, we specified a Normal prior since is continuous and can be positive or negative, but this can be changed as needed.

The simple model above can be expanded to a generalized linear mixed model by including fixed predictors () and/or varying intercepts ():

with one or more regression parameters for one or more fixed predictors , and one or more varying intercepts . We specify separately because it is needed to account for the non-independence of body sizes. In other words, each body size is clustered within each site and so they are not independent and identically distributed. The addition of a varying intercept for each sample accounts for this non-independence. We demonstrate how excluding the sample-specific varying intercept can lead to overdispersion below. Prior distributions are given as for the parameters and varying intercept and for , but these can also be changed as needed.

The model above assumes that each body size represents a single individual such that the data set might have many repeats for individuals of the same size (e.g., = {0.2, 0.2, 0.2, 0.4, 0.4, 0.5, 9.8}). However, when individual body sizes are repeated in a data set, they are often accompanied by a count or density, such that the data set above might instead consist of two columns with = {0.2, 0.4, 0.5, 9.8} and = {3, 2, 1, 1}. To analyze this more compact data set, Edwards et al. (2020)(Edwards et al. 2020) developed a modification of the log probability density function to include :

which is coded in Stan as follows:

functions{  
 real paretocounts\_lpdf(real x, real lambda, real xmin, real xmax, real counts){  
 if(lambda != -1)  
 return(counts\*(log((lambda+1) / ( xmax^(lambda+1) - xmin^(lambda+1))) + lambda\*log(x)));  
 else  
 return(counts\*(log(log(xmin) - log(xmax)) + lambda\*log(x)));  
 }  
}

We refer to this as , such that the model can be fit using:

Aside from adding , the model is the same as presented above. These models ( and ) allow us to test how the size distribution exponent, , varies in response to continuous or categorical predictors and to include hierarchical structure as needed.

## Testing the models

The and lpdf’s give the same results, differing only in how the data are aggregated. For simplicity, we demonstrate model performance here for the distribution, since the empirical data we used (see *Case Study* below) contains counts of individual body sizes. First, we tested for parameter recovery using data simulated from a bounded power law with known values of . Second, we fit the model to fisheries trawl data presented in Edwards et al. (2020)(Edwards et al. 2020) to estimate the hypothesis that declines over time.

## Parameter recovery from simulated data

To ensure that the models could recover known parameter values, we simulated ten data sets from a bounded power law:

where is the individual body size from the th simulation, is a unique draw from a distribution, and all other variables are the same as defined above. We set =1 and = 1000, and simulated = 1000 values from each of 10 ’s ranging from -2.2 to -1.2. To generate , we rounded each simulated value to the nearest 0.001 and then tallied them.

We estimated the ten values in two ways. First, we fit a separate intercept-only model to each of the ten data sets. Second, we fit a varying intercepts model (Gelman et al. 2014). The structure of this model is where each group represents and offset from the mean value of lambda.

Finally, we simulated data for a regression model with a single continuous predictor and a varying intercept: , where = -1.5, = -0.1, and was 0.3 for n = 3 groups. The predictor was continuous with 3 values (-2, 0, 2) and two replicates per value per group for n = 18 ’s. After solving for from these known parameter values, we simulated 300 individuals from each using the procedure above, with = 1 and = 100. We fit this model 20 times to measure variation in parameter recovery among model runs.

## Sample Size

We examined sensitivity to sample size (number of individual body sizes) across three values (-2, -1.6, -1.2). For each , we varied the number of simulated individuals from 2 to 2048, representing a sequence with ranging from 1 to 11. Each of the 11 densities was replicated 10 times resulting in 110 datasets of individual body sizes. We fit each data set using separate intercept-only models and then plotted the resulting values as a function of sample size.

## Case Studies

To examine model performance on empirical data, we re-ran a previously published analysis from of Edwards et al. (2020). In Edwards’ study, size spectra exponents were first estimated separately for each sample using maximum likelihood. Then the modeled exponents were used as response variables in linear regression models. The goal was to test for linear changes in size spectra over three decades using bi-yearly size data of marine fishes collected from the International Benthic Trawl Survey (IBTS). The data set and original model results are available in the sizeSpectra package (Edwards et al. 2017)(Edwards et al. 2017). We tested the same hypothesis as Edwards et al. (2020)(Edwards et al. 2020), but instead of using a two-step process we fit a single model using the lpdf (Eq. X).

## Model Fitting

We fit each of the above models in rstan (Stan Development Team 2022)(Stan Development Team 2022) using 2 chains each with 1000 iterations. All models converged with ’s <1.01. If a known parameter value fell inside the 95% Credible Intervals, we considered parameter recover successful. For the replicated regression model, we also tallied the number of times that the known value fell outside of the highest posterior density interval (HPI; out 20 runs).

## Data Availability Statement

All data and code are available at <https://github.com/jswesner/stan_spectra> (to be permanently archived on acceptance).

# Results

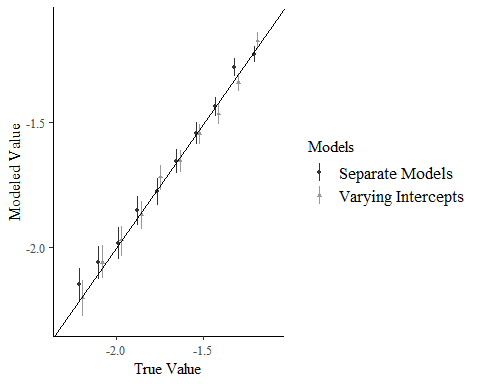
## Parameter Recovery

For models fit to simulated individual data set, all credible intervals included the true value of and posterior medians were no more than 0.05 units away from the true value (Table 1). Similarly, when the same data set was fit using a varying intercepts model, the posterior median intercept and group standard deviation were nearly identical to the true values (Table 1).

Table X. Parameter recovery.

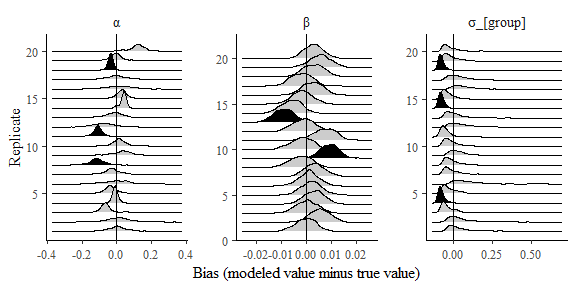
| Model | Parameter | True Value | q2.5 | q50 | q97.5 |
| --- | --- | --- | --- | --- | --- |
| Separate Models | λ | -2.20 | -2.22 | -2.15 | -2.09 |
| Separate Models | λ | -2.09 | -2.13 | -2.06 | -2.00 |
| Separate Models | λ | -1.98 | -2.05 | -1.99 | -1.92 |
| Separate Models | λ | -1.87 | -1.91 | -1.85 | -1.80 |
| Separate Models | λ | -1.76 | -1.83 | -1.78 | -1.72 |
| Separate Models | λ | -1.64 | -1.70 | -1.66 | -1.61 |
| Separate Models | λ | -1.53 | -1.59 | -1.54 | -1.50 |
| Separate Models | λ | -1.42 | -1.48 | -1.44 | -1.40 |
| Separate Models | λ | -1.31 | -1.31 | -1.28 | -1.24 |
| Separate Models | λ | -1.20 | -1.26 | -1.23 | -1.20 |
| Single Model with Varying Intercepts | α | -1.70 | -1.96 | -1.71 | -1.50 |
| Single Model with Varying Intercepts | σ\_[group] | 0.34 | 0.23 | 0.36 | 0.58 |

Using the varying intercept model to estimate group specific means yielded similar results as using separate models per group (Figure 1), demonstrating that a single model can be used to estimate multiple size spectra simultaneously.



Modeled estimates (median +/- 95% Credible Intervals of λ using either 10 separate models or a single model with ten varying intercepts.

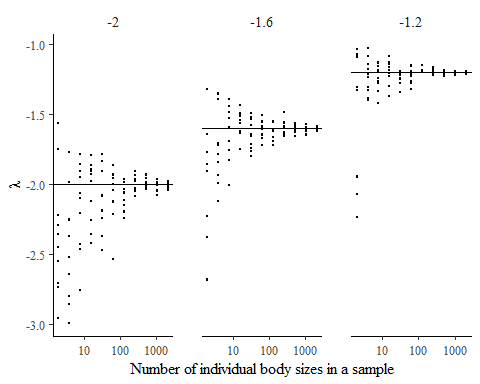
We also recovered regression parameters (intercept and slope ) along with the group-level sd () (Figure 2). Fitting this model 20 times indicated reliable fit. For example, out of 60 comparison (3 parameters x 20 replicates) the true value fell outside of the 95% HDI only once (Figure 2). Averaging the deviations (posterior median minus the true value) among the replicates indicated no bias in the modeled estimates (mean bias +/- sd: = 0 +/- 0.05, = 0 +/- 0.008, = 0.03 +/- 0.06).



Posterior distributions of n = 20 modeled estimates of alpha, beta, and sigma\_group for a linear regression estimating the size sepctrum exponent as a function of a continuous predictor. All data were simulated. Gray densities indicate that the HPI contains the true value, while black densities indicat the opposite. The vertical lines indicate true values.

## Sample Size

Variation in modeled estimates was high for samples containing less than 100 individual (Figure 2). For example, when the true value was -2, samples with just 8 individuals yielded estimates ranging from -2.7 to -1.7. By contrast, all samples with more than 300 individuals captured the true with less than 0.1 unit of error (Figure 3).



Estimates of λ across 11 different sample sizes (ranging from 2 to 2048 individuals) and three different true λ’s (-2, -1.6, -1.2). Ten separate models were fit for each of the 11 sample sizes. The horizontal lines show the true value of λ

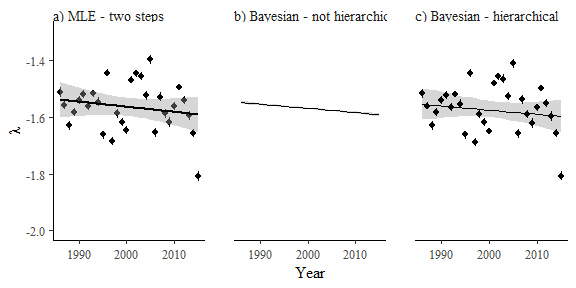
## Case Study

Using IBTS data with the Bayesian hierarchical regression, we found a negative trend over time. The ISD exponent of IBTS trawl data declined by ~0.001 units per year, but with a 95% CrI ranging from -0.005 to 0.002. These values were nearly identical to those reported by Edwards et al. (2020) using a two-step approach (Table 3).

Table X. Slope values from a regression testing the relationship between the ISD exponent and year for IBTS trawl data (Edwards et al. 2020). The values are derived using the Bayesian hierarchical model presentd here or from the maximum likelihood approach described in Edwards et al. 2020).

| Model | Mean | q2.5 | q97.5 |
| --- | --- | --- | --- |
| Bayesian - one step | -0.001 | -0.005 | 0.002 |
| MLE - two steps | -0.001 | -0.005 | 0.003 |

An advantage of fitting the model in a single Bayesian hierarchical framework is that estimates for individual groups are pulled toward the mean via partial pooling. This is apparent in comparing the unpooled MLE estimates (Figure Xa) to the partially pooled Bayesian estimates in each year (Figure Xb).



Regression results from a) Edwards et al. (2020) using maximum likelihood and linear regression (two steps), b) the Bayesian model with a paretocounts lpdf (one step), but without varying intercepts, and c) the Bayesian model with varying intercepts. In a) the points represent maximume likelihood estimates calculated separately for each year. In c) they represent hierarchical varying intercepts calculated from the model. There are no points in (b) because the model does not estimate lambda for individual years.

# Discussion

The most important result of this work is the ability to analyze ISD exponents using fixed and random predictors in a hierarchical model. Our approach allows ecologists to test hypotheses about size spectra while avoiding the pitfalls of binning, which loses information and can lead to biased estimates of (White et al. 2008)(White et al. 2008). Maximum likelihood solves this problem by directly estimating the ISD, but testing hypotheses with maximum likelihood still requires a two-step process in which is estimated individually for each sample and the results are then used as response variables in linear or non-linear models (Edwards et al. 2020)(Edwards et al. 2020). Our approach merges these steps, allowing for the incorporation of prior probabilities and hierarchical structure.

The ability to incorporate prior information using Bayesian updating has two practical advantages over analysis with maximum likelihood. First, adding informative prior distributions can improve model fit by limiting the MCMC sampler to reasonable sampling space. In other words it would not be sensible to estimate the probability that is -1,234 or -9. Without informative priors, those values (and more extreme values) are considered equally likely and hence waste much of the algorithms sampling effort on unlikely values (e.g., Wesner et al. 2021)(Wesner and Pomeranz 2021).

Second, and most importantly, ecologists have much prior information on the values that can take. For example, Sheldon’s conjecture suggests that is -2.05 (Andersen et al. 2006), a value supported in pelagic marine ecosystems (Glazier et al. XXXX) and among forest trees (Enquist et al. I THINK?)[Perkins et al. (2019);]. However, benthic marine systems typically have shallower exponents (e.g., ~-1.4; Blanchard et al. 200X)(Blanchard et al. 2009), while freshwater stream ecosystems have values somewhere in between (-1.5; Pomeranz et al. 2022)(-1.5, Pomeranz et al. 2022). However, despite apparent variation among ecocystems, there is a strong indication that the values of are most likely to be somewhere between -2.05 and -1.4 for many ecosystems. As a result, a prior that places most of its probability mass on these values (e.g., seems appropriate. Such a continuous prior does not prevent findings of larger or smaller , but instead places properly weighted skepticism on such values.

Similar to priors, partial pooling from varying intercepts provides additional benefits, allowing for the incorporation of hierarchical structure and pulling estimates towards the global mean (Gelman et al. 2005, Qian et al. 2010)(Gelman 2005, **qian2010?**). In the examples shown here, the amount of pooling is relatively small because the sample sizes are large (>1000 individuals). However, the primary benefits of pooling (both from varying effects and skeptical priors) is in prediction (Gelman et al. 2005, Hobbs and Hooten 2015)(Gelman 2005, Hobbs and Hooten 2015). This becomes especially important when models are used to forecast future ecosystem conditions. We are unaware of efforts to forecast ISD’s, but such forecasts seem to be especially useful with modern long-term data sets like NEON (National Ecological Observatory Network) in which body size samples will be collected at the continental scale over at least the next 20 years (Loescher et al. 2016)(Kuhlman et al. 2016). In addition, because the effects of priors and pooling increase with smaller samples sizes, varying intercepts are likely to be particularly helpful for small samples. In other words, priors and partial pooling contain built-in skepticism of extreme values, ensuring the maxim that “extraordinary claims require extraordinary evidence”.

One major drawback to the Bayesian modeling framework here is time. Bayesian models of even minimal complexity must be estimated with Markov Chain Monte Carlo techniques. In this study, we used the Hamiltonion Monte Carlo (HMC) algorithm with a No-U-Turn Sampler (NUTS) via rstan (Stan Development Team 2022)(Stan Development Team 2022). Stan is substantially faster than other commonly used programs such as JAGS and WinBUGS, which rely on Gibbs sampling. For example, Stan is 10 to 1000 times more efficient than JAGS or WinBUGS, with the differences becoming greater as model complexity increases (Monnahan et al. 2017)(Monnahan et al. 2017). In the current study, intercept-only models for individual samples with 300 to 1500 individuals could be fit quickly (<2 seconds total run time (warm-up + sampling)) with as little as 1000 iterations and two chains. However, the IBTS regression models took >2 hours to run with the same iterations and chains. These times include the fact that our models used several optimization techniques, such as informative priors, standardized predictors, and non-centered parameterization, each of which are known to improve convergence and reduce sampling time (McElreath 2020)(McElreath 2016). But if Bayesian inference is desired, these run-times may be worth the wait. In addition, they are certain to become even faster with the refinement of existing algorithms and the introduction of newer ones like Microcanonical HMC (Robnik et al. 2022)(Robnik et al. 2022).

Understanding how body sizes are distributed in ecological communities has been a focus in ecology for over a century (Peters 1983). Individual size distributions or community size spectra are an important focus of size-based research, and represent a fundamental measure of ecosystem structure and function (Kerr and Dickie 2001, White et al. 2007, Perkins et al. 2019)(Kerr and Dickie 2001, White et al. 2007, Perkins et al. 2019). Most recently, ecologists have focused on testing theoretical predictions of how environmental changes affect ISD’s (Nelson et al. 2017, O’Gorman et al. 2017, Perkins et al. 2019, Pomeranz et al. 2022)(Nelson et al. 2017, O’Gorman et al. 2017, Perkins et al. 2019, Pomeranz et al. 2022). However, comprehensive analytical approaches to testing these hypotheses are lacking. We present a single analytical approach that takes advantage of the underlying data structures of individual body sizes (Pareto distributions) while placing them in a generalized (Non)-linear hierarchical modeling framework. We hope that ecologists will adopt and improve on the models here to critically examine hypotheses of size spectra or other power-law distributed data.

# Acknowledgements

This material is based upon work supported by the National Science Foundation under Grant Nos. 2106067 to JSW and 2106068 to JRJ. We especially thank Edwards et al. (2017) and (2022) for placing their code and data in easily accessible repositories.

# References

Andersen, K. H., and J. E. Beyer. 2006. [Asymptotic Size Determines Species Abundance in the Marine Size Spectrum.](https://doi.org/10.1086/504849) The American Naturalist 168:54–61.

Blanchard, J. L., S. Jennings, R. Law, M. D. Castle, P. McCloghrie, M.-J. Rochet, and E. Benoît. 2009. [How does abundance scale with body size in coupled size-structured food webs?](https://doi.org/10.1111/j.1365-2656.2008.01466.x) Journal of Animal Ecology 78:270–280.

Edwards, A. M., J. P. W. Robinson, J. L. Blanchard, J. K. Baum, and M. J. Plank. 2020. [Accounting for the bin structure of data removes bias when fitting size spectra](https://doi.org/10.3354/meps13230). Marine Ecology Progress Series 636:19–33.

Edwards, A. M., J. P. W. Robinson, M. J. Plank, J. K. Baum, and J. L. Blanchard. 2017. [Testing and recommending methods for fitting size spectra to data](https://doi.org/10.1111/2041-210X.12641). Methods in Ecology and Evolution 8:57–67.

Gelman, A. 2005. [Analysis of variancewhy it is more important than ever](https://doi.org/10.1214/009053604000001048). The Annals of Statistics 33:1–53.

Hobbs, N. T., and M. B. Hooten. 2015. [Bayesian models: A statistical primer for ecologists](https://doi.org/10.23943/princeton/9780691159287.001.0001). Princeton University Press.

Kerr, S. R., and L. M. Dickie. 2001. The biomass spectrum: A predator-prey theory of aquatic production. Columbia University Press.

Kuhlman, M. R., H. W. Loescher, R. Leonard, R. Farnsworth, T. E. Dawson, and E. F. Kelly. 2016. [A New Engagement Model to Complete and Operate the National Ecological Observatory Network](https://doi.org/10.1002/bes2.1248). The Bulletin of the Ecological Society of America 97:283–287.

McElreath, R. 2016. Statistical rethinking: A bayesian course with examples in R and stan. Second. CRC Press.

Monnahan, C. C., J. T. Thorson, and T. A. Branch. 2017. [Faster estimation of Bayesian models in ecology using Hamiltonian Monte Carlo](https://doi.org/10.1111/2041-210X.12681). Methods in Ecology and Evolution 8:339–348.

Nelson, D., J. P. Benstead, A. D. Huryn, W. F. Cross, J. M. Hood, P. W. Johnson, J. R. Junker, G. M. Gíslason, and J. S. Ólafsson. 2017. [Experimental whole-stream warming alters community size structure](https://doi.org/10.1111/gcb.13574). Global Change Biology 23:2618–2628.

O’Gorman, E. J., L. Zhao, D. E. Pichler, G. Adams, N. Friberg, B. C. Rall, A. Seeney, H. Zhang, D. C. Reuman, and G. Woodward. 2017. [Unexpected changes in community size structure in a natural warming experiment](https://doi.org/10.1038/nclimate3368). Nature Climate Change 7:659–663.

Perkins, D. M., I. Durance, F. K. Edwards, J. Grey, A. G. Hildrew, M. Jackson, J. I. Jones, R. B. Lauridsen, K. Layer-Dobra, M. S. A. Thompson, and G. Woodward. 2018. [Bending the rules: Exploitation of allochthonous resources by a top-predator modifies size-abundance scaling in stream food webs](https://doi.org/10.1111/ele.13147). Ecology Letters 21:1771–1780.

Perkins, D. M., A. Perna, R. Adrian, P. Cermeño, U. Gaedke, M. Huete-Ortega, E. P. White, and G. Yvon-Durocher. 2019. [Energetic equivalence underpins the size structure of tree and phytoplankton communities](https://doi.org/10.1038/s41467-018-08039-3). Nature Communications 10:255.

Pomeranz, J. P. F., J. R. Junker, and J. S. Wesner. 2022. [Individual size distributions across North American streams vary with local temperature](https://doi.org/10.1111/gcb.15862). Global Change Biology 28:848–858.

Pomeranz, J. P. F., H. J. Warburton, and J. S. Harding. 2019. [Anthropogenic mining alters macroinvertebrate size spectra in streams](https://doi.org/10.1111/fwb.13196). Freshwater Biology 64:81–92.

Pomeranz, J. P. F., J. S. Wesner, and J. S. Harding. 2020. [Changes in stream food-web structure across a gradient of acid mine drainage increase local community stability](https://doi.org/10.1002/ecy.3102). Ecology 101:e03102.

Robnik, J., G. B. De Luca, E. Silverstein, and U. Seljak. 2022, December. [Microcanonical Hamiltonian Monte Carlo](https://doi.org/10.48550/arXiv.2212.08549). arXiv.

Sprules, W. G., J. M. Casselman, and B. J. Shuter. 1983. [Size Distribution of Pelagic Particles in Lakes](https://doi.org/10.1139/f83-205). Canadian Journal of Fisheries and Aquatic Sciences 40:1761–1769.

Stan Development Team. 2022. RStan: The R interface to Stan.

Wesner, J. S., and J. P. F. Pomeranz. 2021. [Choosing priors in Bayesian ecological models by simulating from the prior predictive distribution](https://doi.org/10.1002/ecs2.3739). Ecosphere 12.

White, E. P., B. J. Enquist, and J. L. Green. 2008. [On Estimating the Exponent of Power-Law Frequency Distributions](https://doi.org/10.1890/07-1288.1). Ecology 89:905–912.

White, E. P., S. K. M. Ernest, A. J. Kerkhoff, and B. J. Enquist. 2007. [Relationships between body size and abundance in ecology](https://doi.org/10.1016/j.tree.2007.03.007). Trends in Ecology & Evolution 22:323–330.

\*\*TBD