

# Methods

## Bird abundance data

We used data from the Breeding Bird Survey (Sauer et al. 2013) to evaluate trends in abundance, biomass, and energy use. BBS (BBS methods background). We explored trends in abundance, biomass, and energy use over the 30-year time period from 1989-2018. We selected these years to provide a temporal window sufficient to detect trends (Cusser et al. (2020)), while allowing for a substantial number of routes. To avoid irregularities caused by missing time steps, we restricted the main analysis to routes that had been in at least 27 of 30 years in this window ( $n = 739$ ), and compared these results to a more strict selection of routes that were sampled in every year ( $n = 199$ ). We take the route to be the “community” scale [Thibault et al. (2011); others]. We filtered the data to remove taxa that are poorly sampled through these methods, following (literally everyone). We accessed the data, and performed this preliminary cleaning and filtering, using the R package **MATSS** (Ye et al. 2020).

## Estimated size data

BBS contains abundances for all species along a route in each year, but does not include measurements of individual body size. We generated body size estimates for individual birds assuming that intraspecific size distributions are normally distributed around a species’ mean body size (following Thibault et al. (2011)). Using records of species’ mean and standard deviation body sizes from Dunning (2008), we drew individuals’ body sizes from the appropriate normal distributions. For species for which there was not a standard deviation recorded in Dunning (2008) (185 species affected, of 421 total), we estimated the standard deviation based on an allometric scaling relationship between mean and standard deviation in body mass ( $\log(\text{variance}) = -5.273 + (\log(\text{mass}) * 1.995)$ ); model  $R^2 .86$ ; see also Thibault et al. (2011)). For species with multiple records in Dunning (2008), we used the mean mean and standard deviation body sizes across all records (averaging across sexes, subspecies, and records from different locations). We performed this averaging after estimating any missing standard deviation measurements. For each individual bird observed, we estimated metabolic rate as  $10.5 * (\text{mass}^{.713})$  (Fristoe 2015, Nagy 2005, McNab 2009). For each route in a given year, we compute total energy use, total biomass, and total abundance by summing over all individuals observed on that route in that year. This method does not incorporate intraspecific variation in body size across geographies or over time (Dunning 2008, Gardner et al. 2011). However, it makes it possible to conduct macroecological studies of avian size distributions at a spatial and temporal scale that would otherwise be impossible (Thibault et al. 2011).

## Comparing abundance- and size- based currencies

Comparing trends across different currencies is a nontrivial statistical challenge. Because different currencies vary widely in their units of measure (e.g. abundance in the hundreds of individuals; total biomass in the thousands of grams), it is challenging to interpret differences in magnitude of slope across different currencies. Transformation and scaling using common approaches (such as a square-root transform or rescaling each currency to a mean of 0 and a standard deviation of 1; Gotelli et al. (2017); Dornelas et al. (2014)) destroys necessary information about the degree of variability within each currency.

Rather than attempting to compare slopes across currencies or to transform different currencies to a common scale, we use a simple null model to compare the observed dynamics for biomass and energy use to the dynamics that would occur in a scenario in which the species (and therefore, in this context, size) composition of the community was consistent throughout the timeseries, but in which total abundance varied over time consistent with the observed dynamics. For each route, we characterized the “observed” timeseries of total biomass and total energy use by simulating size measurements for all individuals observed in each time step and summing across individuals, using the method described above. We then created simulated timeseries for biomass and energy use incorporating observed changes in community-wide abundance over time, but

under a scenario of consistent species (and therefore size) composition over time. For each community, we characterized the timeseries-wide probability of an individual drawn at random from the community belonging to a particular species ( $P(s_i)$ ) as each species’ mean relative abundance taken across all timesteps:

$$P(s_i) = \frac{\sum_t^T \frac{n_{i,t}}{N_t}}{T}$$

where  $n_{i,t}$  is the abundance of species  $i$  in timestep  $t$ ,  $N_t$  is the total abundance of all species in timestep  $t$ , and  $T$  is the total number of timesteps. For each timestep  $t$ , we randomly assigned species’ identities to the observed number of individuals  $N_t$  by drawing with replacement from a multinomial distribution with probabilities weighted according to  $P(s)$  for all species. We then simulated body size measurements for individuals, and calculated total energy use and total biomass, following the same procedure as for the observed community. This estimates the dynamics for size-based currencies expected if the species (and size) composition of the community does not change over time, but incorporating observed fluctuations in total abundance. We refer to these dynamics as “abundance-driven” dynamics.

## Long-term trends

For each route, we evaluated the 30-year trend in biomass (or energy use) and compared this to the trend derived from the “abundance-driven” null model using generalized linear models with a Gamma family and log link (appropriate for strictly-positive response variables such as biomass or total metabolic flux). We fit four models to characterize 1) the trend in biomass (or energy use) over time and 2) whether this trend deviates from the trend expected given only changes in abundance:

1. **biomass ~ year \* source**, in which “source” refers to being either the “observed” or “abundance-driven” value. This model fits a slope and intercept for the observed trend in biomass (or energy use) over time, and a separate slope and intercept for the trend drawn from the abundance-driven, or null model, dynamics.
2. **biomass ~ year + source**. This model fits a separate intercept, but not slope, for the abundance-driven and observed dynamics.
3. **biomass ~ year**. This model fits a temporal trend, but does not fit separate trends for the observed and abundance-driven dynamics.
4. **biomass ~ 1**. The intercept-only model describes no directional change over time for either the observed or abundance-driven dynamics.

We selected the best-fitting model using AICc. In instances where multiple models had AICc scores within two AICc units of each other, we selected the simplest model within two units of the best score.

For each route’s best-fitting model, we extracted the predicted values for the first (usually 1988) and last (usually 2018) year sampled, for both the observed and null trajectories. We calculated the magnitude of change over time as the ratio of the last (2018) to the first (1988) value.

## Relating change in community structure to decoupling between abundance and size-based dynamics

Community dissimilarity metrics make the most sense when making pairwise comparisons. We compared the first and last five-year intervals in each timeseries, resulting in a “begin” and “end” comparison separated by a consistent window of time across routes (19-20 years). The use of five-year periods corrects for sampling effects (White (2004)), smooths out interannual variability, and, by including a relatively large proportion (1/3) of the total timeseries, partially mitigates the impact of scenarios where the start and end values do not align with the long-term trend.

Metrics:

Change in mean body size as the log ratio of mean body size in the last five years over the mean body size in the first five years.

ISD turnover (say turnover rather than overlap) by fitting GMMs (following Thibault), turning into scaled density functions, and calculating the area of overlap (following Read). Turnover is 1-overlap.

BCD to measure species turnover. Compare species composition in the first five years to the last five years.

Statistical comparison:

For mean body size, use the absolute log ratio because this will capture the *magnitude* of change. Fit an ordinary linear model. For turnover metrics, fit binomial GLM (because bounded 0-1). Compare fit of model fit to model\_type to an intercept only model. Explore contrasts using emmeans.

## References

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