We would like to know the extent to which community properties are regulated/stable or changing over time, how and if they trade off with each other, and the extent to which they track or mask changes in functional and species composition. These questions have motivated Gotelli/Dornelas and Supp’s work (for example), but single-currency approaches can only ever offer limited perspective and can conflate qualitatively different phenomena. For example, knowing only that the total number of individuals in a community is increasing does not tell us whether the whole community is effectively being amplified – with coinciding increases in the total biomass and energy – or if it is shifting towards smaller-bodied species – which can sustain higher individual abundances without a net increase in energy use and witha *decrease* in standing biomass. A community-wide amplification might signal an overall increase in resource availability orthogonal to body size, while a size shift might signal a shift in *which functional groups* are best equipped to exploit an unchanging overall *amount* of resources.

We can get considerably more leverage on how and to some extent why communities are changing if we simultaneously track dynamics of *N*, *E,* and the size structure. The relative rates of change in N and E are often sufficient to distinguish important “syndromes” of community change (see flowchart). In some cases, where *N*  and *E* are either stable or changing in proportion to each other, we can look to the size spectrum and/or the rate of change in *M* to further distinguish between broad classes of phenomena. These different syndromes have logical interpretations in terms of the underlying biological processes that *could* generate them. They also likely differ in how prone they are to emerge from various types of random walks or to signal a strong, systematic process.

So far, we have not had a large body of timeseries of community-scale size data (with the notable exception of small mammals and some trees). However – following the approach in Thibault 2011 – it is entirely feasible to generate such a database for the communities in the Breeding Bird Survey. This allows us to evaluate the prevalence of these syndromes at a macroecological scale. Depending on the prevailing dynamics, we may also be able to leverage additional data sources to test hypotheses that would help explain or document the processes that generate the observed dynamics.

*Objectives and approach*

1. Develop syndromes framework
   1. Mathematical intuition relating syndromes to process
   2. Simulations to establish the extent to which we can distinguish between syndromes in realistic data
   3. Simulations to establish which syndromes are most likely to emerge from random walks at smaller scales
2. Extrapolate BBS size timeseries following Thibault et al 2011
3. Match observed dynamics in BBS to syndromes and/or null expectations
4. Follow-up analyses to test specific drivers of change in the BBS