1176-92-359 **Collin B. Edwards*** (`collin.edwards@tufts.edu`), **Brooke Anderson**, **Rachel J. Dutton** and **Benjamin E. Wolfe**. *Simple, mechanism-based statistical models provide powerful tools for understanding microbial communities.*

Recent developments in data science have emphasized fitting flexible models to large data sets. However, for many topics in biology, powerful research can be carried out by fitting simple, parametric, mechanism-based models to data. Here I will demonstrate the value of using these mechanism-driven statistical models, using as a case study a series of analyses of competition and community succession of microbes in fermented foods. The constraints provided by less flexible mechanistic models reduced the quantity of data needed to fit them – this was important, as time series data of microbial communities is difficult to obtain. Further, because my statistical models represented biological mechanisms, model selection itself was a result that offered biological insight. Finally, because the statistical models captured real biological constraints and intuition, fitted models provided more accurate and precise predictions. My work highlights the continued value of carefully constructed statistical models in biological research as a compliment to the increasingly common big-data approaches. (Received January 25, 2022)