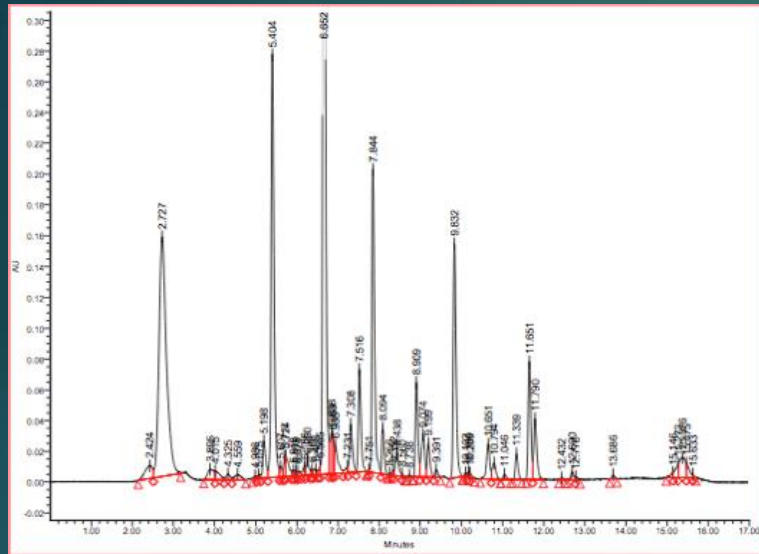


DEPARTMENT OF ECOLOGY & EVOLUTIONARY BIOLOGY

Fall 2016 Exit Seminar

“On the quantification of complexity and diversity from phenotypes to ecosystems”

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A cornerstone of ecology and evolution is comparing and explaining the complexity of natural systems, be they genomes, phenotypes, communities, or entire ecosystems. These comparisons and explanations then beget questions about how complexity should be quantified in theory and estimated in practice. Here I embrace diversity partitioning using Hill or effective numbers to move the empirical side of the field regarding the quantification of biological complexity. First, at the level of phenotypes, I show that traditional multivariate analyses ignore individual complexity and provide relatively abstract representations of variation among individuals. I then suggest using well-known diversity indices from community ecology to describe phenotypic complexity as the diversity of distinct subsidiary components of a trait. I show how total trait diversity can be partitioned into within-individual complexity (alpha diversity) and between-individual components (beta diversity) within a hierarchical framework. Second, I use simulations to demonstrate that naïve measures of standardized beta diversity such as turnover or local/regional dissimilarity are biased estimators when the number of sampled units (e.g., quadrats) is less than the “true” number of communities in a system (if it exists). I then propose using average pairwise dissimilarities and show that this measure is unbiased regardless of the number of sample units. Moreover, the measure is intuitively interpreted as the average proportional change in composition as one moves from one sample to the next. Finally, I apply a hierarchical Bayesian approach to the estimation of species abundances within and among samples, communities, or regions. This strategy accommodates difficult problems of bias and uncertainty in the estimation of the diversity of the underlying communities while providing integrated estimates of uncertainty. Moreover, multilevel hierarchies are possible. We can then use model comparison to determine whether patches/communities/habitats within regions or sets are distinct subcommunities of a metapopulation, or whether they are “arbitrary” distinctions from one contiguous system.

Friday, Nov 11, 2016; Room 307, SERF; 3:30 - 4:30PM. - Pre-talk reception: 3:00 PM in Dabney 568