

The geographical ecology of pond bacteria

April 21, 2015

Overview

We asked whether “Active” and “All” differ in primary aspects of alpha-diversity, beta-diversity, and geographical patterns: the taxa-area relationship (TAR), the distance-decay relationship in taxonomic and phylogenetic community similarity.

Study area

We analyzed environmental and bacterial community data from a survey of shallow ponds found east of Bloomington, IN. These ponds were constructed in the 1940s as wildlife refuge ponds, and are scattered throughout Brown County State Park, Yellowwood State Forest, and Hoosier National Forest. In the summer of 2013, we visited approximately 50 of these ponds and recorded their geographic locations. We sampled aspects of water chemistry, physical properties, and bacterial community composition.

Environmental data

We measured 19 environmental and geographic variables. These included elevation (m), geographical coordinates (lat-long; data: WGS84), temperature (C), Diameter(m), Depth(m), redox potential (ORP), specific conductivity or SpC (uS/cm), dissolved Oxygen (mg/L), total dissolved solids (g/L), salinity (p.s.u.=ppm), color - measured at absorbance = 660; an estimate of carbon in the water sample, chlorophyll a (ug/ml), dissolved organic carbon (mg/L), dissolved organic nitrogen (mg/L), and total phosphorus (ug/L).

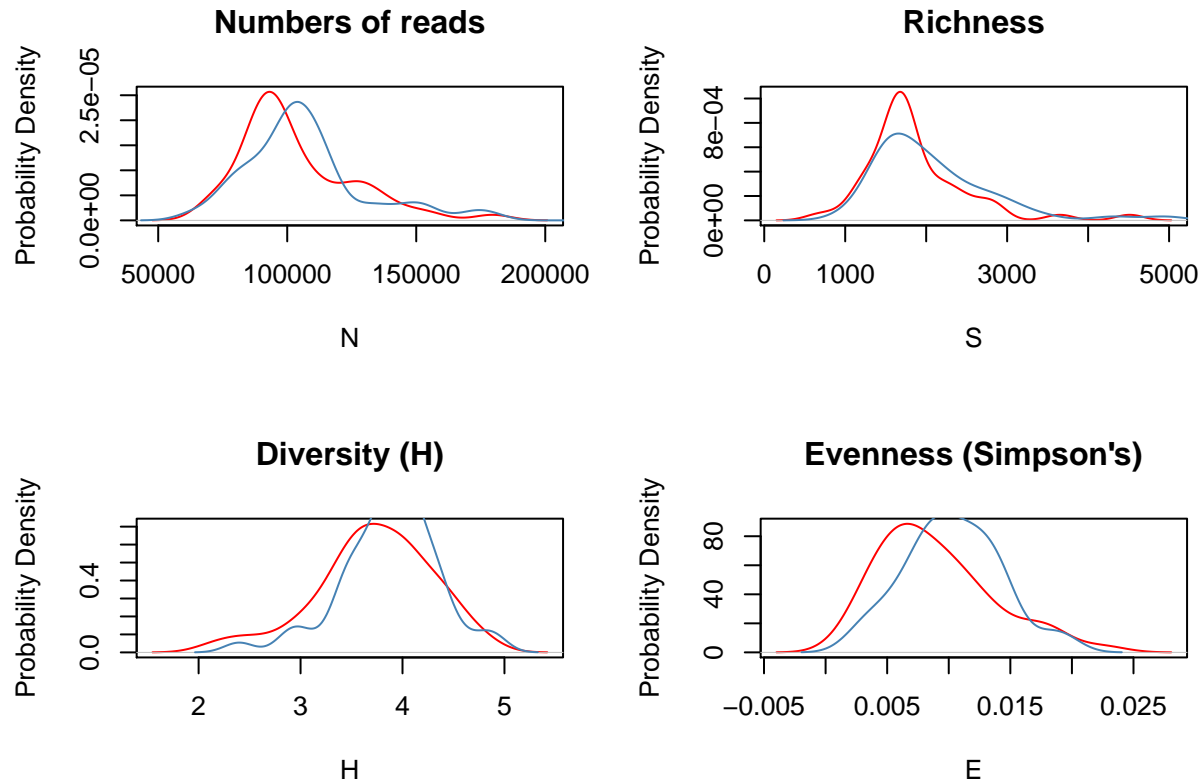
Microbial community data

In addition to measuring a suite of geographic and environmental variables, we characterized the diversity of bacteria in the ponds using molecular-based approaches. Specifically, we amplified the 16S rRNA gene (i.e., “DNA”) and 16S rRNA transcripts (i.e., “RNA”) of bacteria using barcoded primers on the Illumina MiSeq platform. We then used a `mothur` pipeline to quality-trim our data set and assign sequences to operational taxonomic units (OTU).

FINDINGS

1.) No differences in distributions of observed N, S, Diversity, and Evenness

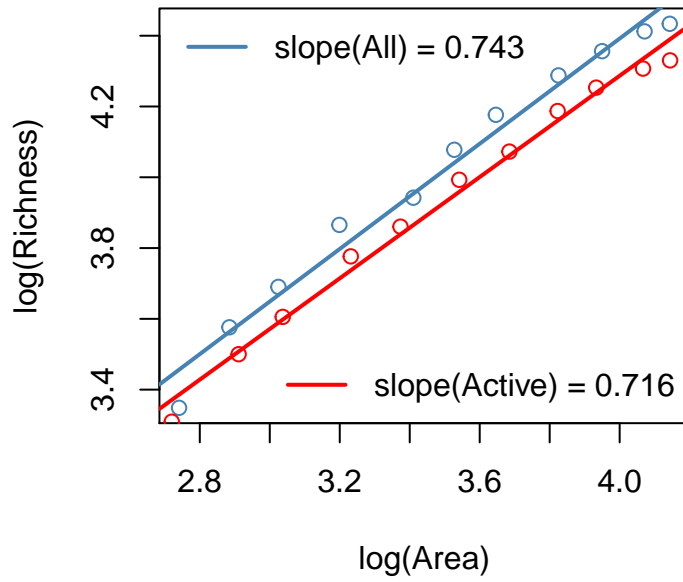
For each pond, we used the observed taxonomic richness (S), total number of gene reads (N), and number of gene reads per OTU (N_i) to estimate Shannon’s diversity index (H), and Simpson’s evenness (D/S).



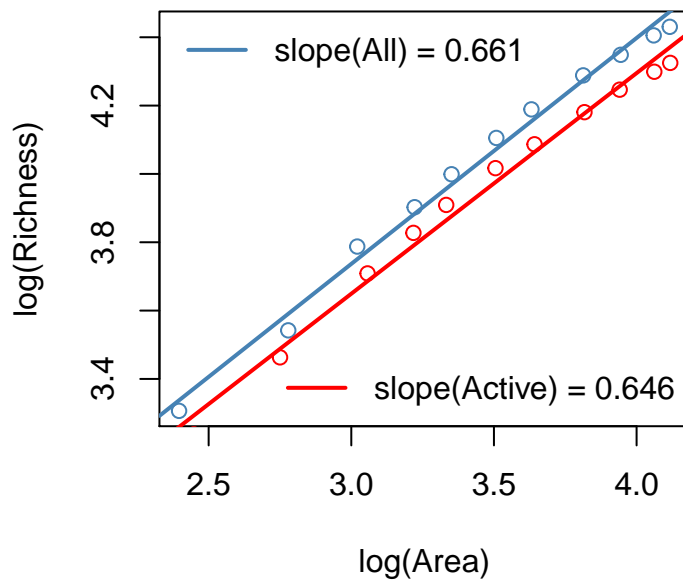
2.) No differences in slopes of taxa-area relationships

The species-area relationship describes the rate at which species are discovered with increasing area. The SAR is one of ecology's oldest and most intensively studied patterns. Arrhenius (1921) first described the general form of the *species-area relationship* (SAR) as a power-law: $S = cA^z$ where S is species richness and A is area. Arrhenius's formula predicts a rate of increase in richness that is approximately linear in log-log space. That is, $\log(S) = c + z\log(A)$, where z is the scaling exponent.

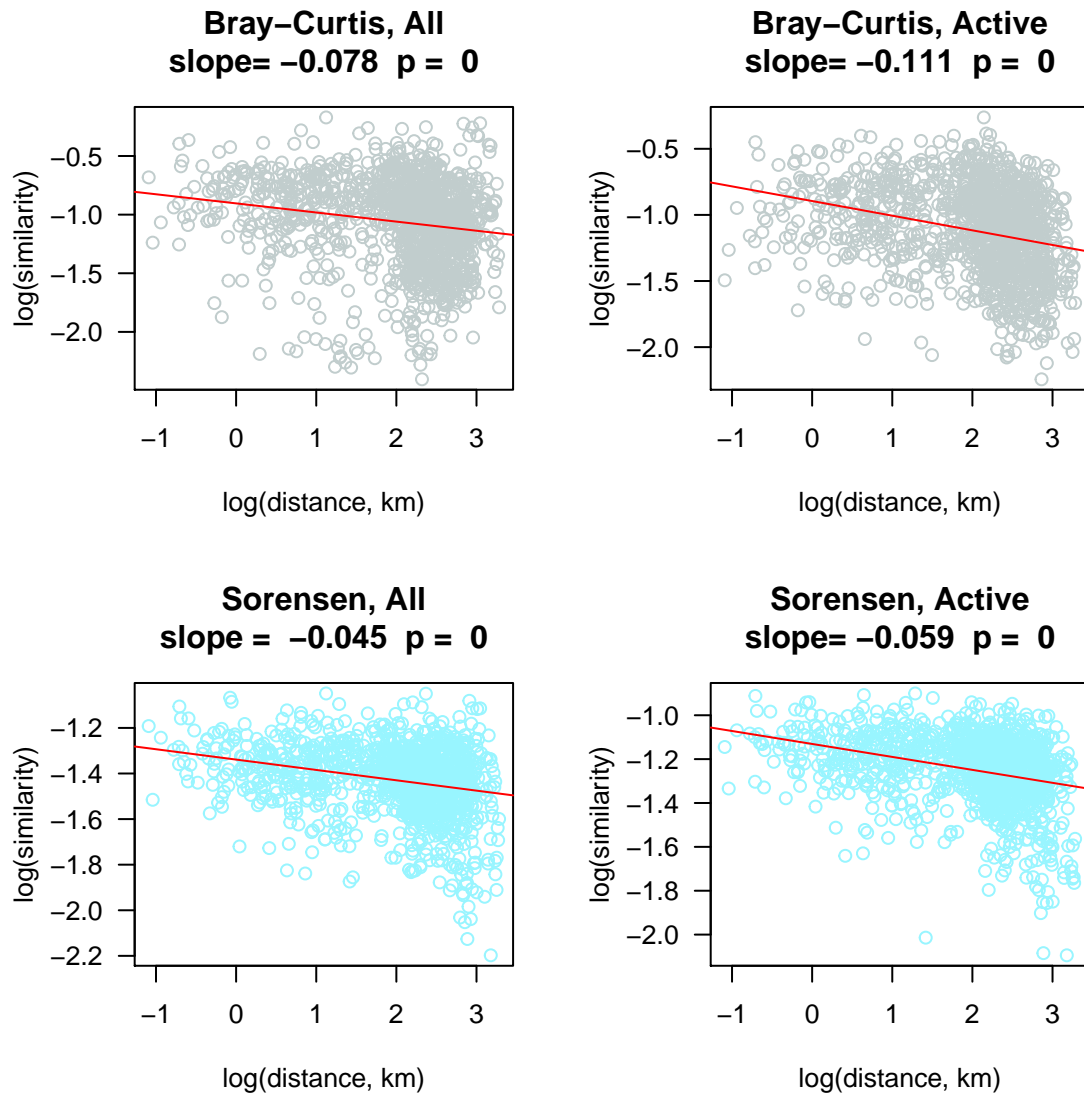
Taxa–Area Relationship aggregating area by distance



Taxa–Area Relationship aggregating area at random



3.) Slight differences in distance-decay relationships



Are the slopes of the DD's different?

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## [1] "Bray-Curtis: Difference in slope = -0.033 ; p = 0.014"
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## [1] "Sorensen: Difference in slope = -0.014 ; p = 0.026"
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4.) Little difference in community distance matrices between Active and All when using presence-absence; generally low similarity. Substantial differences between Active and All based on Bray-Curtis.

