Bachelorthesis Project Proposal

In the group of Aquatic Microbiology – AG Meckenstock

Supervisor: Lisa Voskuhl, Lisa.voskuhl@uni-due.de

Testing the habitat-heterogeneity hypothesis to the Pitch Lake water droplet communities

According to the habitat-heterogeneity hypothesis, species diversity increases with increasing habitat heterogeneity because more habitats are providing more niches that can be occupied [1-4]. In this research project, the student will test the habitat-heterogeneity hypothesis on water droplet microbial communities which we sampled from a natural oil seep and compare the results to the results from other habitats. The unique situation is here that the water droplets are absolutely closed ecosystems that do no exchange with the surrounding and we want to find out how that compares to other systems in order identify the influence of dispersal on community compositions.

Initial calculations on a subset of 36 droplets' Shannon indices indicated that the trend of the outcomes depends on order of summed up habitat diversities (Figure 1). Interestingly, the slope of both, decreasing (rhombus) and increasing (square, triangle, cross) diversities, was steeper until approximately 10 droplet communities, afterwards the Shannon diversity seemed to level out at a value of around four, displayed by the flattened slope of the mean graph (Figure 1: blue graph). These observations might indicate either that the water droplets are not all distinct enough from each other and by that not providing individual niches, or that due to the dispersal limitation of the Pitch Lake water droplet communities, potential responses to the heterogenic droplet habitats where hindered, because dispersal has been identified as relevant process for the identification of responses on community level [2].

The student will have to establish a R script for systematically testing 1) the effect of different diversity measures (e.g. observed richness, Shannon-index, Simpson index), 2) different orders of considered water droplet communities, and 3) chosen subsets of droplets (all droplets, only one droplet per side, only above salinity threshold, with comparable 16S rRNA gene copy numbers), on the hypothesis that the more (heterogenous) water droplet habitats are considered, the higher the observed community diversity index. At the end, the results will be compared to calculations from other habitats taken from literature research e.g. from [6].

In case of interest or questions please contact Lisa Voskuhl (lisa.voskuhl@uni-due.de).

Hands-on experiences on:

- Statistical calculation of ecological parameters such as diversity measures
- R programming
- Habitat-heterogeneity hypothesis and the Pitch Lake water droplet ecology
- Literature research

The offered bachelor thesis project addresses students who are interested in ecology and R-programming. Strong programming background is not required but rough basic knowledge on R and analytical way of thinking is very helpful. Thesis can be written in English or German language.

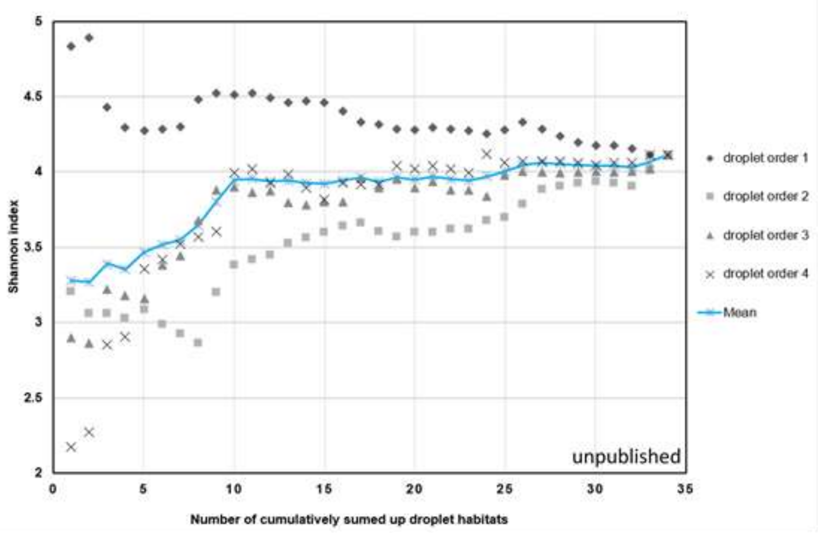

Figure 1 Testing the habitat-heterogeneity hypothesis on the Pitch Lake water droplet microbial communities. To this aim the Shannon diversity index (y-axis) was plotted of one randomly chosen single droplet community (x-axis). Afterwards I summed up another random droplet community to the first community and recalculated again the Shannon index of the merged community (now consisting of two droplet communities) and plotted this Shannon index again. Cumulatively, all tested 34 droplet communities were summed up to one community. The order by which the droplet communities were summed up to each other affected the course of the plot. Because of that, I calculated the Shannon index cumulatively for four random chosen orders of the droplets, displayed by the different symbols (legend), and calculated the mean diversity (displayed in blue) of the four separate calculated orders. Shannon index calculations and the summation of the droplet communities were conducted in R with the package phyloseq [5].

References

1 Armeli Minicante S, Piredda R, Quero GM, Finotto S, Bernardi Aubry F, Bastianini M, (...) and Zingone A, Habitat heterogeneity and connectivity: effects on the planktonic protist community structure at two adjacent coastal sites (the Lagoon and the Gulf of Venice, Northern Adriatic Sea, Italy) revealed by metabarcoding. Front Microbiol, 2019. 10(2736).

2 Hamm M and Drossel B, Habitat heterogeneity hypothesis and edge effects in model metacommunities. J Theor Biol, 2017. 426: p. 40-48.

3 Heidrich L, Bae S, Levick S, Seibold S, Weisser W, Krzystek P, (...) and Müller J, Heterogeneity–diversity relationships differ between and within trophic levels in temperate forests. Nat Ecol Evol, 2020. 4(9): p. 1204-1212.

4 MacArthur RH and MacArthur JW, On bird species diversity. Ecology, 1961. 42: p. 594-598.

5 McMurdie PJ and Holmes S, phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. PLoS One, 2013. 8(4): p. e61217.

6 Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Lozupone CA, Turnbaugh PJ, et al. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proc Natl Acad Sci U S A. 011; 108 Suppl 1:4516–4522. doi: 10.1073/pnas.1000080107 PMID: 20534432