

Quantitative Comparison of Abundance Structures of Generalized Communities

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Abstract: The community, the assemblage of organisms co-existing in a given space and time, has the potential to become one of the unifying concepts of biology, especially with the advent of high-throughput sequencing experiments that reveal genetic diversity exhaustively. In this spirit we show that a tool from community ecology, the Rank Abundance Distribution (RAD), can be turned by the new MaxRank normalization method into a generic, expressive descriptor for quantitative comparison of communities in many areas of biology. To illustrate the versatility of the method, we analyze RADs from various generalized communities, i.e. assemblages of genetically diverse cells or organisms, including human B cells, gut microbiomes under antibiotic treatment and of different ages and countries of origin, and other human and environmental microbial communities. We showed that normalized RADs enable us to use quantitative approaches, like clustering, ordination or classification, for analysis and comparison of different samples that help to understand structures and dynamics of complex communities. The approach is essentially non-parametric and allows for the direct quantitative comparison of complex RADs without deconstruction and model fitting. By applying this method RADs can be used as an analytic tool to generate easily interpretable results, and also as a basis for quantitative models. [1]

Keywords: RADs; Rank Abundance Distribution; normalization

References

[1] M. Saeedghalati, F. Farahpour, B. Budeus, A. Lange, A. M. Westendorf, M. Seifert, R. Küppers, D. Hoffmann, "Quantitative comparison of abundance structures of generalized communities: from B-Cell receptor repertoires to microbiomes," *PLoS Comput. Biol.* 13 (2017). DOI:10.1371/journal.pcbi.1005362