

海洋性プランクトン群の進化と生態についての研究

Research in evolution and ecology of marine planktonic communities

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研究成果概要

In regard to my project:

- I try to decipher which NCLDV's viruses (also named Megavirales) present in the epipelagic oceans infect eukaryotic hosts, conducting co-occurrence association analyses. For such task I am using a matrix containing the abundance information of both 18S rRNA genes and polymerase B marker genes, the former corresponding to eukaryotes and the later to viruses. Since typical correlation analyses are prone to strong biases caused by compositional effects, approaches considering the nature of the data are being used.

To conduct this research project I make use of the SuperComputer System of Institute for Chemical Research, Kyoto University. I am using the software SparCC¹ that considers compositional effects on datasets, and very recently I have started using fastspar which is the c++ implementation of SparCC¹. In the coming days for the same purpose I will start using CoNet² which combines several correlation methods and weighting strategies.

References

1 Friedman J, Alm EJ: Inferring correlation networks from genomic survey data.

PLoS Comput Biol. 2012; 8(9): e1002687

2 Faust K and Raes J. CoNet app: inference of biological association networks using Cytoscape [version 2; referees: 2 approved] F1000Research 2016, 5:1519 (doi: 10.12688/f1000research.9050.2)