

令和2年度 京都大学化学研究所 スーパーコンピュータシステム 利用報告書

巨大ウイルスの進化過程に関する研究
Analysis of the evolution of giant viruses

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研究成果概要

Used R , python , jupyter notebook , etc,to practice how to analysis the genetic files.

Learned how to conduct the OTU table from the metagenome sequencing files. We used cd-hit to cluster, and did alignment against silva database to annotate the otus we got. Next, we used the python package , pandas , to calculate the frequency of each otu . And we can use the R package , vegan , to calculate Bary-curtis dissimilarity and apply multidimensional scaling method using the Bary-curtis dissimilarity as the distance matrix. Then plotted a 2d-dimensional distance map to show the beta-diversity between samples.

I'm in the process of learning machine learning , so basically what I do everyday is using these biological tools to solve some problems for my further study.

For my main research – analysis of the evolution of giant viruses. I'm going to do sampling at serval sea spots, and sequencing. Then analyze the sequences I got. Maybe I will do genome mapping and alignments , try to find out the genetic interactions between the giant viruses and their hosts and explain why the genome size of giant viruses are so large, and how it become so large.

発表論文(謝辞あり)

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