

Using supercomputer to finish M1 Bioinformatics Exercise from Ogata Lab

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概要

The purpose of this period is using the supercomputer of Institute for Chemical Research, Kyoto University, to do M1 Bioinformatics Exercise.

In M1 Question, I mainly used python script to deal with data analysis, for example, *Transform an Amino Acid Sequence into RNA sequences; Search Restriction Enzyme Sites; Analysis KEGG GENOME and KEGG GENES relationship* and so on.

In this step, I used these datasets, such as: *bio/db/fasta/genome; /bio/db/fasta/genes; /bio/db/ideas; /bio/db/ideas/ko/*. And also downloaded several datasets from other sources into my personal dictionary, such as *KEGG PATHWAY dataset of E. coli; Amino acid sequence of ribosome biogenesis protein YsxC of E. coli O157; Osaka Bay 16S merged reads; Sequence Read Archive; Wine Quality Datasets*.

Now, I have totally finished the M1 Exercise and thank you for your supporting.