

Integration of bioinformatics tools for metagenomic analyses

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Metagenomics is one of the fastest advancing fields in biology. It is driven by rapid development of high-throughput sequencing technologies on the one hand and continual advances in computational methods for large sequence data analysis on the other hand.

Rapid development of new algorithms aimed at metagenomic data analysis, however, makes it challenging for newcomers to the field to select the most suitable method/tool to analyze their own data fulfilling their specific tasks.

Using our experimental data on microbial communities that can generate electricity in microbial fuel cell systems, we show how to efficiently extract biologically relevant information from metagenome sequences employing a combination of existing bioinformatics resources.