Toward big data analysis in the Baikal microbiome study

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The Baikal microbiome study is being conducted in Limnological Institute of SB RAS, the study is based on the next-generation sequencing data analysis. As a result, the study generates a big volume of metagenomic data. A seasonal monitoring of Baikal microbiome requires the study of thousands of samples.

The process of metagenomic data processing is multi-stage, *e.g.* an analysis of amplicons can include up to 50 consecutive steps. This requires microbiologist can plan and execute a pipeline of the processing, consisting of command-line utilities *like* Mothur or QIIME, scripts of the Python programming language, statistical processing with R modules. Additionally, the execution of the pipeline requires interaction with a storage and management software of metagenomic data. At the current state of the automation of the analysis, microbiologist is not always able to cope with the complex task independently.

In this work, we present an environment that supports visual planning and parallel execution of pipelines of the metagenomic data analyses. Visual planning is implemented as a plug-in module of Rapid miner system, and the parallel execution is provided by instrumental system Orlando. The big data storage facility based on Hadoop infrastructure. The environment under construction simplifies the research activity of microbiologist , making the metagenomic analysis to be more accessible for biologists without in-depth programming and data science skills.