

Assembly and annotation pipeline for microorganism genomes from sequence to gene networks

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Microorganisms of natural and technogenic ecosystems represent an inexhaustible pool of metabolic pathways for the utilization of some compounds and the biosynthesis of others. Modern experimental technologies of genetics and microbiology provide an effective search in microbiological collections for new strains of microorganisms promising for biotechnological applications, as well as full sequencing of their genomes. As a result of experimental studies, large amounts of genetic data are generated. Their analysis requires the involvement of modern information and computer technologies, which make it possible, on the basis of genomic information, to reconstruct the gene networks that control the production of target substances.

This paper proposes a software pipeline for assembly, annotation of sequenced genomes of microorganisms and reconstruction of their gene networks. The pipeline includes the following steps: 1) Quality control and sequence cleaning (FastQC, Trimmomatic [1]); 2) on the side of the genome (Spades [5]); 3) Assembly quality analysis (Quast [3]); 4) genome annotation (Prokka); 5) probable identification of the organism (ProTaxon); 6) search for enzymes (Blast, Prokka); 7) reconstruction of gene networks (ANDSystem [2, 4]).

The developed pipeline was used on the data of the collection of microorganisms of the Kurchatov Genomic Center. To date, 1005 genomes have been processed. The average genome length was 6,045,404 bp. The average number of genes in the genome is 5545. KEGG gene networks and metabolic pathways were reconstructed for all analyzed genomes.

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