

On organizing a software platform for seeking biotechnologically important features in bacteria

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Motivation and Aim: Modern biotechnology combines approaches of genetic engineering with technologies of computer analysis and modeling of the molecular-genetic organization of microorganisms and computer design of experiments to construct superproductive strains with specified properties. Taken together, this leads to the development of genetic and metabolic engineering technologies for the design of superproducing strains of target products.

The aim of this work is to develop a software platform to assist in the cycle of research from the search for new promising for biotechnology species of microorganisms to the construction of superproductive strains of target products. The platform is based on the use of developed bioinformatic approaches: software for assembly and annotation of sequenced microorganism genomes, computer analysis and modeling of molecular-genetic organization of microorganisms.

Methods and Algorithms: We used a wide range of methods and approaches of bioinformatics analysis (genome assembly and annotation, search of functional sites within genomes, reconstruction of gene regulatory networks [1] and metabolic pathways), systems biology (automatic generation of mathematical and computational models of microbial metabolism and genetic regulation [2]) as well as approaches and technologies of software development (client-server and micro services architectures, databases etc.) to implement the platform.

Results and Discussion: We have developed a suit of instruments, which provide a microbial genome analysis chain starting from genome assembly, functional annotation, search for various functional regions (operons, promoters, transcription factor binding sites) within genome and more bioinformatics analysis through the reconstruction of various biological networks (associative gene networks, transcription regulation networks, metabolic pathways), to the construction and analysis of mathematical and computational models of molecular-genetics processes in microbes, which include flux balance models and dynamical models written in the form of ordinary differential equations.

Availability: <https://cgimu.sysbio.cytogen.ru>.

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References

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