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Research Area: Computational Biology

Although *Escherichia* has been studied for several decades, changes in the metabolic fluxes imposed by sustained restriction of bacterial growth are poorly understood. This research project will focus on modeling of the central metabolism of *E. coli* in the conditions of exponential growth and in the stationary state by the flux balance analysis. The modeling results will be compared with experimental data that characterized gene expression in these bacterial states. The obtained results will be used to identify limitations of the developed models and to reveal changes in the metabolic fluxes of *E. coli* in the stationary state. Simpheny software will be used to implement the task.

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