
Whole-cell modeling of *E. coli*: from simulation to discovery

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Abstract:

Francis Crick first called for a coordinated worldwide scientific effort to determine a “complete solution” of the bacterium *Escherichia coli*. We have been working for some years now to complete a model of *E. coli* that takes into account all of the known functions of every well-annotated gene, in order to better understand and predict the behavior of this scientifically-relevant and industrially-significant model organism. I will discuss our ongoing efforts to improve this model, most recently with new modeling added to better describe growth rate control, transcription unit architecture and tRNA metabolism. I will then highlight our newest “whole-colony” models, a multi-scale modeling effort in which every individual within a simulated colony is running the latest version of the whole-cell model, to calculate population-level emergent behaviors based on molecular interactions and events as the colony responds to the sudden introduction of antibiotics.

Reading List:

[Paper 1](#)

[Paper 2](#)