Modeling of Signal Transduction for Bacterial Chemotaxis Using the E-CELL Simulation System

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1 Introduction

We have modeled signal transduction for bacterial chemotaxis using the E-CELL system, a generic software for simulation of cellular processes [3]. Chemotaxis is the orientation of an organism in relation to the presence of a particular chemical. The chemotactic response of *E. coli* depends on the ability to modulate their flagellar motor in response to external stimuli. The flagellar motor has a switch protein which interacts with proteins called CheY. The CheY protein in a phosphorylated form is known to bind with the motor up to 20-fold more frequently than that in an unphosphorylated form. In this way, the phosphorylation controls bacterial response to external stimuli by regulating binding affinity of the CheY protein and the motor switch.

The external stimulus bound to a bacterial receptor works as a initial control element of cytoplasmic phosphorylation cascade. In case that the stimulus is an attractant, the phosphorylation flow is suppressed and, consequently, the motor rotates counterclockwise, resulting in smooth swim.

2 Simulation with the E-CELL system

We have simulated the phosphorylation cascade for bacterial (*E.coli*) chemotaxis with the attractant being aspartate (Fig. 1). In the E-CELL system, each reaction is defined as a set of substrates, products, catalysts, and kinetic constants. We use the following three kinetic types:

- Molecular binding, such as receptor-ligand interaction and CheY-motor binding, is modeled using 'EqReactor' type, which computes equilibrium state from the equilibrium constants.
- Autophosphorylation of proteins, such as CheA, CheB and CheY, is modeled using 'Michaelis-MentenReactor' type, which calculates the velocity using the Michaelis-Menten equation with the constants, Km and Kcat.
- Autodephosphorylation of the proteins is modeled using 'PlainReactor' type, whose velocity is proportional to the substrate's concentration.

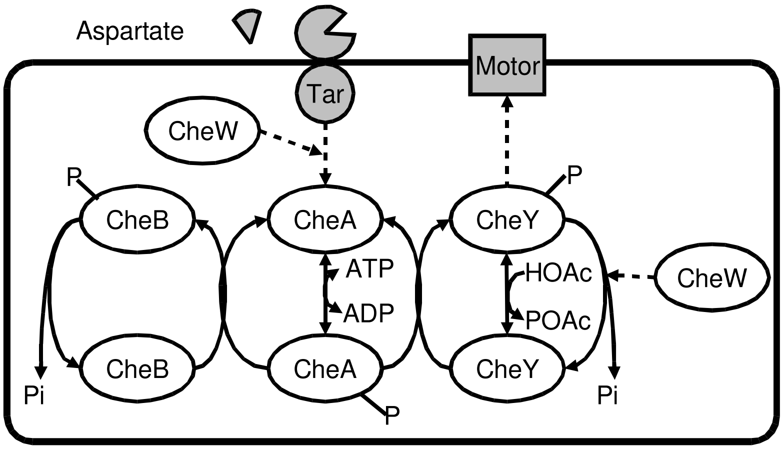

Figure 1: Signal transduction for bacterial chemotaxis.

3 Discussion

The E-CELL system allows us to perform virtual experiments on the bacterial chemotaxis model we have constructed. For example, mutants of the model can be created by making a particular protein always zero. The simulated behavior of each mutant, as well as the wild type, can then be compared with the results of laboratory experiments with indexes such as swimming direction, response time, and phosphate flux. We also compare our results with other simulation systems [1, 2].

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References

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