An integrated analytic model of bacterial chemotaxis

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***Short Abstract* — We present an analytic model of the full *Escherichia coli* chemotaxis system, including receptor complexes, signaling pathway, and the flagellar motor. This integrated model is applied to describe the observed behavior of both stimulated and unstimulated *E. coli* cells and to study the emergence of population level behavior from that of the single cell. The model successfully fits these multiple data sets with a minimal number of free parameters.**

I. Introduction

CHEMOTAXIS in *E. coli* has emerged as a model system for the quantitative study of cellular signal processing. The behavior of stimulated [1, 2] and unstimulated [3, 9] *E. coli* is well characterized at both the single cell and population levels by a wealth of experimental measurements. Previous theoretical work on chemotaxis has produced isolated models of the system's individual components: the receptors (*e.g.*, [5, 6]), the signaling pathway (*e.g.*, [4, 6]), and the flagellar motor [8]. However, these separate models have not yet been combined into a single description of the full chemotaxis system.

We present here a first attempt at an integrated analytic model of the full chemotaxis system. This single cell model is then combined with measurements of protein distributions across a population [4] to address chemotactic behavior at the population level. With a minimal number of free parameters, this integrated model is capable of reproducing both the stochastic fluctuations [3] of the single cell and the averaged dynamic response of the population [1, 2].

II. Methods and Model Description

Previous work has exploited the modularity of the chemotaxis system to fit isolated models of the receptors [5, 6] and pathway [4] to experimental data; we retain this approach when fitting the individual components of our integrated model.

A. Receptor complexes

Receptor complexes are modeled as strongly coupled, two state MWC clusters, similar to the model in [5]. For simplicity we assume that the free energy difference between the two states varies linearly in the methylation level of the complex. The receptor parameters are taken from fits to FRET measured responses to α-methylaspartate in [2].

B. Signaling pathway

As in [7], the signaling pathway is modeled using Michaelis-Menten kinetics to describe the (de)methylation steps of the receptors. One set of kinetic parameters is used and only [CheR] and [CheB] are varied. The power spectrum of the network output [CheY-P] is calculated using linear response theory.

C. Flagellar motor

The motor is modeled as a stochastic bistable system, expanding on the work of [8]. Transition probabilities are modulated by [CheY-P], according to parameters fit to the motor response observed in [8] and the motor power spectra [3].

III. Results

We apply the above model to both the single bacterium and a realistic [4] bacterial population. By varying [CheR] and [CheB], we find that this model is able to describe both the intrinsic noise levels measured in [3] and the observed dynamic responses to step [2] and pulse [1] input signals.

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