



Quantitative Biology > Molecular Networks

# Dynamic phenotypes as criteria for model discrimination: fold-change detection in *R. sphaeroides*

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The chemotaxis pathway of the bacterium *Rhodobacter sphaeroides* has many similarities to the well-studied pathway in *Escherichia coli*. It exhibits robust adaptation and has several homologues of the latter's chemotaxis proteins. Recent theoretical results have been able to correctly predict that the chemotactic response of *Escherichia coli* exhibits the same output behavior in response to scaled ligand inputs, a dynamic property known as fold-change detection (FCD), or input-scale invariance. In this paper, we present theoretical assumptions on the *R. sphaeroides* chemotaxis sensing dynamics that can be analytically shown to yield FCD behavior in a specific ligand concentration range. Based on these assumptions, we construct two models of the full chemotaxis pathway that are able to reproduce experimental time-series data from earlier studies. To test the validity of our assumptions, we propose a series of experiments in which our models predict robust FCD behavior where earlier models do not. In this way, we illustrate how a dynamic phenotype such as FCD can be used for the purposes of discriminating between two models that reproduce the same experimental time-series data.

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