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Report on Darren Wilkinson’s “Parameter inference for stochastic kinetic models of bacterial gene regulation,” also referred to as “the paper.” It is a chapter in the proceedings of the ninth Valencia meeting on Bayesian statistics [1].

Abstract

1 Introduction: Parameter Inference for Biological Models

Modern biology has progressed to the point of creating *in silico* models of entire cells. The potential benefit is enormous, because unlike real cells, which must be observed via microscopy or high-throughput methods, a simulated cell can regularly dump its entire internal state to a file. The obvious drawback is that simulations do not necessarily correspond to reality either in terms of their mechanisms or in terms of their results. One key limiting factor: even if the structure of biochemical networks is often well known, information about how interactions play out over time has not kept pace. If Protein A promotes Gene B, and we let them mix for five minutes, we still need to know whether to expect 10, 100 or 1000 new copies of mRNA B at the end. Wilkinson’s paper confronts a subproblem in this domain.

Chemical reactions are often modeled using ordinary differential equations (ODE’s), but Wilkinson’s exact subproblem has an extra complication that rules ODE’s out: natural stochasticity. Wilkinson’s model organism, the bacterium *Bacillus subtilis*, varies its behavior so that even if two bacteria begin in similar initial conditions, one may become mobile and the other may not. One explanation, pursued in the paper and

1.1

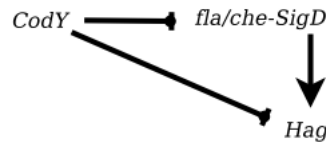


Figure 1: Regulatory relationships. *Hag* is the gene for *flagellin*, while *SigD* encodes σ^D .

References

- [1] Bernardo, J.M., Bayarri, M.J., Berger, J.O., Dawid, A.P., Heckerman, D., Smith, A.F.M., West, M.: Ninth Valencia international meeting on Bayesian statistics, Benidorm, Spain, 03-08.06.2010. Oxford U.P., Oxford (2012)