Hamilton Institute
&
Department of Biology, NUIM

Evolutionary Design Principles of Bacterial Chemotaxis

Dr. Jens Timmer

FDM & Dept. of Mathematiocs & Physics,
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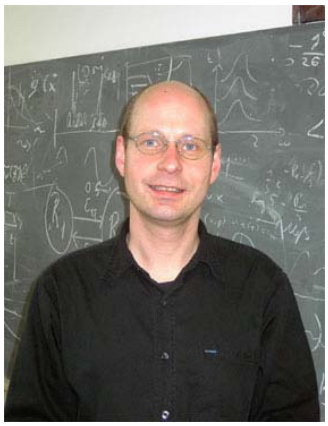
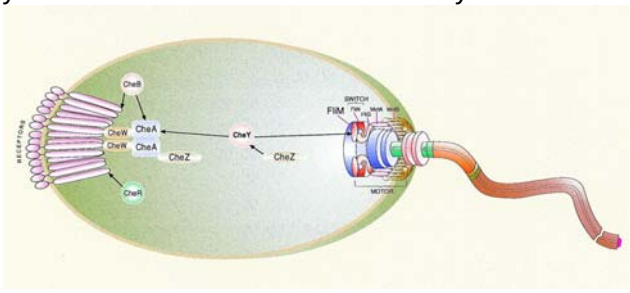
Thursday, August 25th, 2005



Abstract

Cellular biochemical networks have to function in a noisy environment. Especially networks involved in gene regulation or signal transduction allow only for small output tolerances. Thus, the underlying network structure is expected to have evolved for inherent robustness against perturbations. We report combined theoretical and experimental analysis to investigate an optimal design for bacterial chemotaxis. We experimentally identify intercellular variations in expression levels of the involved proteins as the main source of perturbations and apply computer simulations to quantify the robustness of several hypothetical chemotaxis pathway topologies against such gene expression noise. We show that the experimentally established topology is one of the smallest sufficiently robust structures. Our Systems Biology approach suggests that this pathway has evolved to show an optimal chemotacic performance while minimising the cost of resources associated with high levels of protein expression.



Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

Time: 1.00 - 2.00pm (followed by tea/coffee)

Travel directions are available at www.hamilton.ie

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Systems Biology of the JAK-STAT signalling pathway

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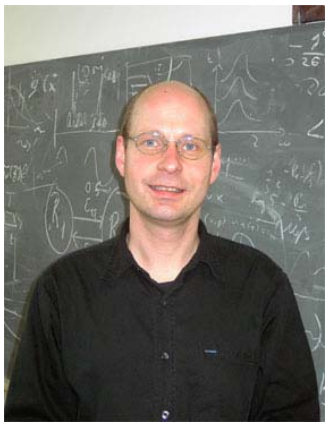
Friday, August 26th, 2005



Abstract
Considerable progress has been made in identifying the molecular composition of complex signaling networks. However, to reveal the systems properties, quantitative models based on experimental observations have to be developed. We investigate the core module of the JAK-STAT pathway of the Epo-receptor. Based on time resolved quantitative measurements of the receptor activity, unphosphorylated and phosphorylated STAT-5 in the cytoplasm, we estimate the parameters in differential equations describing the pathway.

The analysis shows that the so far believed assumption of a feed-forward cascade to describe the pathway is not compatible with the experimental data. A generalization of the model that includes nucleocytoplasmatic cycling is suggested. The final model is validated by successfully predicting the outcome of a new experiment. From this model, we infer the time courses of the unobserved STAT-5 populations and show that, on a systems level, fast nucleocytoplasmatic cycling of STAT-5 serves as a remote sensing system to couple gene activation to receptor activity.

Note Venue and Time

Venue: Ehrlich Suite, (Middle Floor), Institute of Immunology, BioResearch Building, NUI Maynooth

Time: 12.00 - 1.00pm Friday, August 26th, 2005

Travel directions are available at www.nuim.ie

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