Coarse-graining biochemical complexity

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The First **Q-bio**

Conference Information P

August 8-11, 2007 | Santa Fe

http://cnls.lanl.gov q-bio@cnls.lanl

First q-bio Conference on Cellular Information Processi This conference is intended to advance predictive mo genetic regulatory systems. The emphasis is experimentation for the purposes of understanding particular regulatory systems and of elucidating gene information processing.

The single-track program will include invited talks theoretical researchers as well as shorter talks, pos demonstrations selected from contributed submissio banquets, six sessions covering a range of topics, ar sessions.

There will be an opportunity for selected participants presentations made at the conference to a special is journal indexed by ISI and PubMed.

Lodging is available for participants on the campus of St. John's College, which should facilitate interactions and stimulating informal discussions about quantitative biology. Space is available for 200 participants. In the event that registration demand exceeds capacity, preference will be given to individuals selected to present contributed talks or posters. Abstracts should be submitted for review via the conference web site.

First q-bio Summer School on Cellular Information Processing

This school is designed for researchers new to modeling cellular regulatory systems. It will take place in Los Alamos from July 23 to August 7. Participants will attend daily lectures about signal transduction, gene regulation and stochastic effects in biochemical networks and work in small teams on selected research projects. Tuition includes conference registration.

Abstract submission April 15, 2007 Summer School registration April 15, 2007 Early registration June 1, 2007

"Trevel associts for graduate students and politicus may be available. Here information and applications are available on the conference worksite.

Organizing Committee, Jerenny S. Edwards (University of New Mexico); James R. Faeder, William S. Hlavsoek, Yi Jiang, Itya Nemenman, and Michael E. Wat (Los Alamos National Laboratory).

Advisory Committee: William Bialek (Princeton University): Byron Goldstein, John E. Pearson, William H. Press, Davol H. Sharp, and P.el.J. Univefer (Los Alarnos National Lab); Michael A. Savageau (University of California, Davis)



The First **q-bio** Conference on Cellular Information Processing

Center for Nonlinear Studies

August 8-11, 2007 | Santa Fe, New Mexico, USA

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Deadlines:

Abstract submission Summer School registration Early registration April 15, 2007 April 15, 2007 June 1, 2007

*Travel awards for graduate students and postdocs may be available. More information and applications are available on the conference website.

Speakers Include:

Adam P. Arkin Lawrence Berkeley National Laboratory

Topic

- Animal learning, multiscale or power-law memory: world is complex
- Predictability, complexity, and learning. NeCo 2001: what is complexity (of a time series)?
- Coarse graining biochemical networks: how to deal with complexity?



Slide 2



Biochemical complexity:

Example - IgE receptor (From Faeder, Hlavacek, et al.)



354 species / 3680 reactions



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Why such complexity?



Slide 4



10+ reactions/species

(an example with a relatively short RHS)

XDOT(1) = (1.0*km1*X(8)*X(0)-2.0*kp1*X(7)*X(1))/1.0+(1.0*km1*X(10)*X(0)-2.0*kp1*X(9)*X(1))/1.0 +(1.0*km1*X(28)*X(0)-2.0*kp1*X(33)*X(1))/1.0 +(1.0*km1*X(35)*X(0)-2.0*kp1*X(17)*X(1))/1.0 +(1.0*km1*X(40)*X(0)-2.0*kp1*X(36)*X(1))/1.0 +(1.0*km1*X(43)*X(0)-2.0*kp1*X(37)*X(1))/1.0 +(1.0*km1*X(46)*X(0)-2.0*kp1*X(38)*X(1))/1.0 +(1.0*km1*X(49)*X(0)-2.0*kp1*X(39)*X(1))/1.0 +(1.0*km1*X(56)*X(0)-2.0*kp1*X(55)*X(1))/1.0 +(1.0*km1*X(60)*X(0)-2.0*kp1*X(117)*X(1))/1.0 +(1.0*km1*X(66)*X(0)-2.0*kp1*X(24)*X(1))/1.0 +(1.0*km1*X(67)*X(0)-2.0*kp1*X(77)*X(1))/1.0 +(1.0*km1*X(68)*X(0)-2.0*kp1*X(72)*X(1))/1.0 +(1.0*km1*X(69)*X(0)-2.0*kp1*X(78)*X(1))/1.0 +(1.0*km1*X(70)*X(0)-2.0*kp1*X(75)*X(1))/1.0



Slide 5



And, on top of this, everything is stochastic and dynamic!

What to do?

- Coarse graining! $out = f(in); x_{last} = f(x_{first})$
- Already are doing this (in deterministic context)



- Is this legitimate?
 - Is the functional form correct?
 - Are these events Poisson?
- How can simulations be done?
 - Simple SSA-Gillespie won't work (though recall Golding's talk)



Slide 7



Which coarse-graining method to use?

- Combining nodes
 - how?



- Fast rates vs. slow rates
 - Rates concentration dependent
 - May couple very different species types
- Momentum space RG
 - Does not decrease # of nodes
- Fast nodes vs. slow nodes
 - All couples, all same speed
- High abundance (relatively slow) vs. Low abundance (relatively fast): adiabatic approximation
 - That's what biochemists have been using
 - Stochasticity?





Why adiabaticity? (Kozdon, Faeder) FccRI (trimer) 2954 states **Relaxation time scales** of different species FceRI (dimer) 354 states EGFR 356 states 10-3 10-2 10-1 10-0 10² **10**¹ Time (seconds) Slide 9



Michaelis-Menten reaction: Deterministic coarse-graining



- Adiabatic approximation
 - Many enzyme turnovers for small fractional change in [P], [S]
- How to do coarse-graining with fluctuations?



Slide 10



MM with fluctuations

(Hwa, Bundschuh, Vanden-Eijnden, Ehrenberg, Szabo, Arkin, et al.)

- Mean = deterministic
- Var = mean for linear regimes (one step dominated)



• Is first statement correct? What about the bend area for the second?



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Michaelis-Menten reaction (or a pore): Stochastic coarse-graining



Functional integral over all paths - can get full MGF

(Simper version of Sinitsyn and Nemenman, 2007)

Slide 12



Adiabatic approximation

$$P(Q) \sim \int \prod [dN] [d\chi] \exp [i\chi \dot{N} + N_E H]$$

occupied Lagrange # enzymes multiplier # enzymes

Saddle point solution (exact due to linearity of S)

$$\frac{\partial H(N,\chi)}{\partial \chi_{cl}} = -i\dot{N}_{cl} = 0$$
Adiabatic solution



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Michaelis-Menten reaction: Periodic modulation of two rates





Example 1: Bulk fluxes

 $k_1 = 1.5 + R \cos \omega t;$ $k_{-2} = 1.5 + R \sin \omega t;$ $k_{-1} = k_2 = 1$ equilibrium, on average: $J_{cl} = 0$





Example 2: Noise in single molecule experiments



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Example 3: Nonperiodic correction to MM rate

$$S \xrightarrow{k_1 \ k_{-1}} SE \xrightarrow{k_2 \ k_{-2}} P$$

$$\dot{N}_{p} = J_{S \to P}^{cl} - J_{P \to S}^{cl} + \left(k_{2} + k_{-1}\right) \frac{\left(k_{1}\dot{N}_{S} + k_{-2}\dot{N}_{P}\right)\left(k_{2} + k_{-2}N_{P}\right)}{\left(k_{1}N_{S} + k_{-1} + k_{2} + k_{-2}N_{P}\right)^{3}}$$



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Conclusions

- Adiabatic coarse-graining of stochastic biochemical networks
- Nonzero mean corrections (pump effects) -- geometric nature
- Nonpoisson statistics
- Developing symbolic package for coarse graining (to be built into BioNetGen -- network simulation package from LANL, NAU, and now Pitt)



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