

Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing

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PREFACE

Selected papers from the Fourth Annual q-bio Conference on Cellular Information Processing

Conference Organizers and Guest Editors

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Summary

This special issue consists of 11 original papers that elaborate on work presented at the Fourth Annual q-bio Conference on Cellular Information Processing, which was held on the campus of St John's College in Santa Fe, New Mexico, USA, 11–14 August 2010.

Now in its fourth year, the q-bio conference has changed considerably over time. It is now well established and a major event in systems biology. The 2010 conference saw attendees from all continents (except Antarctica!) sharing novel results and participating in lively discussions at both the oral and poster sessions. The conference was oversubscribed and grew to 27 contributed talks, 16 poster spotlights and 137 contributed posters. We deliberately decreased the number of invited speakers to 21 to leave more space for contributed presentations, and the attendee feedback confirmed that the choice was a success.

Although the q-bio conference has grown and matured, it has remained true to the original goal of being an intimate and dynamic event that brings together modeling, theory and quantitative experimentation for the study of cell regulation and information processing. Funded in part by a grant from NIGMS and by DOE funds through the Los Alamos National Laboratory Directed Research and Development program, the conference has continued to exhibit youth and vigor by attracting (and partially supporting) over 100 undergraduate, graduate and postdoctoral researchers. The associated q-bio summer school, which precedes the conference each year, further emphasizes the development of junior scientists and makes q-bio a singular event in its impact on the future of quantitative biology. In addition to an increased international presence, the conference has notably diversified its demographic representation within the USA, including increased participation from the southeastern corner of the country.

One big change in the conference this year is our new publication partner, *Physical Biology*. Although we are very grateful to our previous partner, *IET Systems Biology*, for their help over the years in publicizing the work presented at the conference, we felt that the changing needs of our participants required that we find a new partner. We are thrilled that *Physical Biology* is publishing the q-bio proceedings this year. It has been a great collaboration, as evidenced by the high quality of this special issue.

What's next for q-bio? We are happy to report that NIGMS has recently extended the q-bio conference grant for the next three years, ensuring strong support for junior researchers who need financial assistance to participate in the event. The conference will retain its emphasis on cellular information processing, but will also build connections to other areas of modern biology and biotechnology, focusing specifically on ecology and evolutionary biology next year. Indeed, to fully understand biological information processing systems,

they must be studied in their ecological contexts. We will continue to honor distinguished contributors to the field in our opening banquets; the tradition started with Howard Berg, Bruce Alberts and Michael Savageau in previous years, and continues with Dennis Bray at the upcoming 2011 event. Starting in 2011, the conference will also venture into exploration of the social aspects of science. The future is bright for q-bio! We will see you at the Fifth Annual q-bio Conference on 10–13 August 2011, in Santa Fe, New Mexico, USA and at the Sixth Annual q-bio Conference in early August 2012.

The special issue at a glance

The special issue is a snapshot of presentations at the q-bio conference. As in previous years, it remains a challenge to recruit experimental contributions to the issue. Thus only one of the papers reports new experimental results, and the collection is tilted towards the computational end of the spectrum compared to the total q-bio presentations contributed.

The 11 individual papers in this special issue are each briefly introduced here. We have arranged the papers loosely to parallel the four pillars of q-bio: quantitative experiments, modeling, theory and tools.

Quantitative experiments

The single experimental paper is by Driscoll *et al*, ‘Local and global measures of shape dynamics’. This paper challenges the usual approaches to studying the motility of organisms (and behavior, more generally) and provides a fresh look at quantification of the motion of amoebae, which allows discovery of unexpected features involved in the motion generation.

Modeling

The largest section of the special issue consists of five papers devoted to models of specific cellular systems. It starts with the work by Wang and Raghavachari, who address the important emerging topic of micro-RNA regulation. Next, Wu and co-authors continue their quest to understand bacterial collective motility in ‘Self-organization in bacterial swarming: lessons from myxobacteria’. The next two papers, by Zhao *et al* and Szopa *et al*, deal with spatial aspects of signal transduction in the MAP kinase system and in kinase-receptor interactions, respectively. Finally, the modeling section ends with the work of Pan and Deem, who present a multi-scale differential equation and spin-glass model of recent zebrafish B cell genetic diversity experiments.

Theory

Papers in this section focus on general properties of molecular networks that transcend specific modeling examples. Kobayashi and Kamimura study a minimal network of chemical reactions needed to decode time-dependent environmental signals sensed through an ensemble of binary receptors. In ‘Deterministic characterization of phase noise in biomolecular oscillators’, Koepl and co-authors use perturbative analysis to develop a method for computing noise effects on the dynamics of biochemical oscillations.

Tools

The three papers in this section describe computational and experimental tools for inference and simulation of biochemical reaction networks. The first paper, by Yang and Hlavacek, presents an evaluation of simulation methods for rule-based models. Delmotte *et al* follow with new methods for analysis of protein interaction dynamics. Finally, Schmidt *et al* present a novel method for automated experimental design for inference of metabolic networks.

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