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Special issue on the Third *q-bio* Conference on Cellular Information Processing

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Editorial

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

Summary: This Special Issue consists of 11 original papers that elaborate on work presented at *The Third q-bio Conference on Cellular Information Processing*, which was held on the campus of St. John's College in Santa Fe, New Mexico, USA, 5–9 August 2009.

The q-bio Conference has marked its third anniversary (in fact, as we are writing this, the fourth installment of the conference has concluded, the discussion of which is for the next Special Issue). It is fair to say that, in the three years since the inaugural event, the conference has established itself as a prominent meeting on the landscape of international systems biology gatherings. The conference fills an important gap in the field through its emphasis on quantitative, predictive modelling, high precision, physics-style experimentation, and theoretical quest for general principles of biological design. This year we began to see the students and postdocs of those who had presented at the earlier *q-bio* events, providing a glimpse of the impact of the conference on the community. The number of students at the affiliated *q-bio* summer school increased again; and attendance at the conference remained high despite the tough financial times. The 2009 conference attracted prominent biologists such as Bruce Alberts, Rita Colwell, and Michael Levin and it was encouraging to see these representatives of 'traditional' biology embrace the spirit of the meeting and the emerging field. The conference and the field owe Dr. Colwell a debt of gratitude, as her tenure as Director of the National Science Foundation is widely credited with the explosive growth of quantitative techniques in the life sciences – techniques without which *q-bio* science would be impossible.

This year the National Institute of General Medical Sciences (NIGMS) provided funding for nearly 100 travel awards that helped bring junior researchers to the event. As a result, the conference grew to include 27 invited talks, 22 contributed talks (twice as many as the year before!), 16 poster spotlights, and 110 contributed poster presentations (again, a record!). Over three quarters of all of the conference attendees presented, helping to sustain the uniquely dynamic and engaging atmosphere of the *q-bio* conference.

What's next for *q-bio*? There has been a significant investment in systems biology recently. For example, in the United States, there is now a network of National Cancer Institute (NCI) supported Cancer Systems Biology centers, a network of NCI-supported Physical Science-Oncology Centers, and a network of NIGMS-supported Systems Biology centers, all of which, clearly, explore quantitative and systems approaches to cellular regulatory processes. These investments signal a growing need for modelling and theory – the hallmarks of *q-bio*. But where will the modellers, theorists and quantitative experimentalists come from? As an event targeted towards early career scientists, with an affiliated summer school, *q-bio* is helping to create new communities of researchers that will fill the ranks. As a relatively small, agile event, it is also positioned to respond to the newly opening directions in systems biology, such as a merger of population biology, ecology and evolution with molecular and cellular biology and the newest biotechnology, where quantitative, systems approaches serve as glue. In short: *the future is bright for q-bio!* And, as organisers, we intend to keep it an event that breaks the frontiers of biology. The *Fifth q-bio Conference* is scheduled for August 10–13, 2011, in Santa Fe, New Mexico, USA with satellite meetings on August 14. The *Fifth q-bio Summer School* will open its doors on July 25, 2011. We will see you there!

The Special Issue at a Glance

As in previous years, the Special Issue is a snapshot of presentations at the *q-bio*. Even though the conference

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itself is almost equally split between computational and experimental contributions, the Special Issue is tilted towards theory and computation. It remains a challenge to recruit experimental contributions to the issue.

The eleven individual papers in this Special Issue speak for themselves. We encourage readers to inspect them directly, and the introductions below are deliberately brief. We have arranged the papers loosely into three themes: *Modelling, Theory, and Tools.*

Modelling: This section consists of four papers devoted to models of specific cellular systems. It starts with the work by Goldstein and co-workers, who continue their long-term program of developing a detailed mathematical model of events in IgE receptor signalling. Lipniacki and co-workers present a model of spatially-resolved kinase signalling in *Spatial Gradients in Kinase Cascade Regulation* to investigate effects of spatial dynamics of receptors on sensitivity to signals. This paper is followed by the contribution of Munsky, who presents a stochastic model of a synthetic genetic switch and investigates the conditions under which parameters of the system can be inferred from experiments. Finally, the section ends with a study of a biophysical model of cargo delivery through a cell membrane in the paper *Cell-Penetrating Peptides, Electroporation, and Drug Delivery* by Cahill.

Theory: Papers in this section focus on general properties of molecular networks that transcend specific modelling examples. Maienschein-Cline *et al.* (*Defining cooperativity in gene regulation locally through intrinsic noise*) and Igoshin and Narula (*Thermodynamic models of combinatorial gene regulation by distant regulatory elements*) independently explore different mechanisms for generation and approaches for analysis of combinatorial, cooperative transcriptional regulation. In the third paper of this section, Sinitsyn and Nemenman analyse effects that time dependence in kinetic parameters of a Michaelis-Menten reaction may have on experimentally observable molecular fluxes.

Tools: The four papers in this section describe computational and experimental tools for inference and simulation of biochemical reaction networks. The first paper (Enders *et al.*) presents an experimental platform that blends microfluidics with ion-mobility mass spectrometry for high-throughput real time profiling of cellular metabolic and protein states. The paper by Margolin *et al.*, presents a systematic definition of a statistical dependency in a multivariate context and uses the definition as the basis for an algorithm for reverse-engineering of cellular regulatory networks from high-throughput profiling data. Finally, the last two papers, Wolf *et al.*, and Yang *et al.*, explore computational techniques for solution of the chemical master equation that underlies stochastic biochemical processes using complementary numerical integration and kinetic Monte Carlo approaches.

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