Editorial

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

This special issue consists of 12 original papers that elaborate on work presented at *The Second q-bio Conference on Cellular Information Processing*, which was held on the campus of St. John's College in Santa Fe, New Mexico, USA, 6-9 August 2008.

It is always somewhat scary to organise a second incarnation of an international scientific meeting after the first one has been universally praised with epithets like "a watershed moment", "the most energy in years", and "the best ... conference [in the field]" [1]. How would the second event compare? Would it be able to meet the expectations of the community, raised so high in the first year? Or would the conference start fizzling, like so many others do? When organising *The Second q-bio Conference on Cellular Information Processing* we had all of these fears. However, when the list of the speakers started to crystallise to include such luminaries as Robert Austin (Princeton University), Howard Berg (Harvard University), Thomas Pollard (Yale University), Lucy Shapiro (Stanford University), Peter Wolynes (UCSD), as well as many younger rising stars working in the quantitative biology field (or, as we call it, *q-bio*, see [2] for the history and the scope of the term), the fears started to fade. They disappeared completely when the conference received about 130 contributed submissions, almost all of which were deemed of high quality by the program committee, and were sorted into 11 contributed talks, 17 poster spotlight talks, and 99 poster presentations, to complement 33 invited talks and 14 tutorial presentations. As the program came together, and lodging at St. John's College filled to capacity (over 200 people participated at the conference), it became clear that the second *q-bio* would match the first.

The actual conference did not disappoint, being every bit as dynamic and exciting as the first one. Many fascinating results were presented, some approaching the *q-bio* ideal of combining experimental and modelling approaches with more general theoretical conclusions and predictions. To the collection of praises from 2007, Ido Golding (UIUC) added the epithet "my intellectual home". Naama Brenner (Technion) summarised the sentiment of many, complaining that there had been no bad sessions in the conference program, which had left no time for sightseeing in Santa Fe, a beautiful and culturally rich city. Clearly, such complaints were music to the organisers' ears. Similarly, *The q-bio Summer School*, which preceded the conference, was also successful, with most students stating that they had learned a lot. Some liked the school so much that they chose to come back again a year later. Others accumulated enough knowledge in the course of the two and a half school weeks to be able to write a serious research paper with the school faculty on the stochastic properties of complex enzymatic reactions, which appears in this special issue (de Ronde et al.). The organisers are particularly proud of this achievement, which signifies that the *q-bio* series is starting to have an impact beyond research, educating the next generation of quantitative biology researchers.

The Special Issue at a Glance

Just like a year ago, the idea of this special issue was to document a selection of the work presented at the conference in one place and to provide a snapshot of the *q-bio* field. And just like a year ago, this goal was only partially fulfilled: many excellent experimental results reported at *The q-bio Conference* have appeared elsewhere, and this special issue is biased toward the theoretical and computational end of the *q-bio* spectrum. We hope that, as time goes by and *q-bio* rises in prominence, this imbalance will disappear.

The twelve individual papers in this special issue speak for themselves. We encourage the readers to inspect them directly, and the introductions below are deliberately brief. We have arranged the papers loosely into four blocks: *Biophysics*, *Detailed modelling*, *General properties of biochemical networks*, and *Learning networks from data*.

Biophysics: The two papers in this block, *Simple model of the transduction of cell-penetrating peptides* by Cahill, and *Quantitative statistical description of integrin clusters in adherent cells* by Welf et al., develop models of the specific molecular systems, emphasising the tools of statistical physics, molecular biophysics, and soft condensed matter physics.

Detailed models and modelling tools: This is the largest block of papers in the special issue. Papers here address the need for tools that allow detailed kinetic modelling of large-scale molecular signalling and regulatory systems using modern knowledgebases and simulation tools (Ruebenacker et al., *Integrating BioPAX pathway knowledge with SBML models*), and they apply such toolboxes to modeling specific biological systems and producing experimentally testable predictions of their behavior. The systems analysed in the special issue dealt with the *ERK* nuclear translocation (Radhakrishnan et al.), as well as the *p53* and *NFκB* modules and their interactions (Hat et al. and Puszynski et al.)

General properties of biochemical networks: In these papers, the authors attempt to understand how constraints of various types affect information processing characteristics of biological networks and, more generally, the dynamics of these networks. The papers in this block include *Evolution of gene auto-regulation in the presence of noise* by Singh et al., *Quantifying evolvability in small biological networks* by Mugler et al., and *Interampatteness–a generic property of biochemical networks* by Nordling et al.

Learning networks from data: An important question in modern systems biology, confronted in many *q-bio* studies, is the question of learning the topology and the more specific kinetic parameters of biomolecular interactions using experimental data. Two papers in the *q-bio* special issue extend traditional tools, developed by the authors in prior publications, in the subfield of reverse engineering of genetic regulatory networks using gene expression profiles and similar data to increase the domain of applicability of the methods and to infer networks for specific, previously un-analysed systems: *Scalable learning of large networks* by Roy et al., and *Identification of gene interactions in fungal-plant symbiosis through discrete dynamical system modelling*. The work of de Ronde et al., *Mesoscopic statistical properties of multistep enzyme-mediated reactions*, addresses a somewhat different question of using fluctuation data to reverse engineer the kinetic network underlying activity of an enzyme. This article, as mentioned in the introduction of this editorial, is the work of the summer school students, which was stimulated by an open-ended homework problem posed in *The Second q-bio Summer School*.

What Does the Future Hold?

Nobody knows the complete answer to this question, but a few things are clear. As we are writing this editorial, *The Third q-bio Summer School* is in full swing, and *The Third q-bio Conference* is in the final preparation stages. The *q-bio* is now firmly established as an annual event; it has found its place on the map of systems biology conferences, assembled a regular group of dedicated followers, and it is still expanding its reach among both young students and senior established researchers. *The Fourth q-bio Conference* will take place in August of 2010, and a number of prominent scientists have already confirmed their participation. We will keep the tradition: the conference will again be preceded by a two-and-a-half-weeks long summer school. We hope to see you at either or both events.

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[1]   EDWARDS J., FAEDER J., HLAVACEK W., JIANG Y., NEMENMAN I., WALL M.: 'q-bio 2007: a watershed moment in modern biology', *Mol. Syst. Biol.*, 2007, **3**, (148)

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