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PREFACE

The eighth q-bio conference: meeting report and special issue preface

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William S Hlavacek¹, S Gnanakaran¹, Brian Munsky^{2,7}, Michael E Wall², James R Faeder³, Yi Jiang⁴, Ilya Nemenman⁵ and Orna Resnekov⁶

¹ New Mexico Consortium, Los Alamos, NM 87544, USA and Theoretical Biology and Biophysics Group, Theoretical Division and Center for Nonlinear Studies, Los Alamos National Laboratory, Los Alamos, NM 87545, USA

² New Mexico Consortium, Los Alamos, NM 87544, USA and Information Sciences Group, Computer, Computational, and Statistical Sciences Division and Center for Nonlinear Studies, Los Alamos National Laboratory, Los Alamos, NM 87545, USA

³ Department of Computational & Systems Biology, School of Medicine, University of Pittsburgh, Pittsburgh, PA 15213, USA

⁴ Department of Mathematics and Statistics, Georgia State University, Atlanta, GA 30303, USA

⁵ Department of Physics and Department of Biology, Emory University, Atlanta, GA 30322, USA

⁶ 255 La Canada Road, Hillsborough, CA 94010, USA

⁷ Current address: Department of Chemical and Biological Engineering, Colorado State University, Fort Collins, CO 80523, USA

This Special Issue, edited by Ilya Nemenman, celebrates the Eighth q-bio Conference, which took place in Santa Fe, New Mexico from August 13 to 16, 2014. It consists of a commentary, two reviews, and five primary reports, which represent ideas and work discussed at the meeting.

The q-bio Conference is an annual event with about 200 participants that aims to advance predictive modeling and theoretical understanding of cellular regulatory and other biological systems in coordination with quantitative experimentation. In 2014, the conference featured 17 invited talks, including an opening banquet talk from Alan S Perelson of Los Alamos National Laboratory ('How modeling viral infections can save lives') and a closing banquet talk from William Bialek of Princeton University ('Are we asking the right questions?'). At the opening banquet, Dr Perelson was presented with the Second q-bio Award in recognition of his contributions to our understanding of viral dynamics. The program also featured 7 tutorials, 25 contributed talks, 16 poster spotlight talks, and 118 poster presentations, which were selected by the conference's program committee on the basis of submitted abstracts. Most presenters at the meeting were junior researchers (graduate students, postdoctoral researchers, and Assistant Professors), which is a reflection of the organizers' ongoing efforts to build and nurture a strong q-bio community. Please refer to the online program for additional details about the 2014 conference (<http://q-bio.org>) and to past meeting reports for information about earlier conferences [1–9].

The q-bio Conference is affiliated with the Annual q-bio Summer School, which takes place at multiple campuses before the conference. The 2014 Summer school was held on two campuses, the University of

California, San Diego (UCSD) and the University of New Mexico (UNM), Albuquerque. These campuses together attracted approximately 70 student participants, a mix of graduate students and postdoctoral researchers who came from more than 50 different institutions. The UCSD school focused on computational and experimental synthetic biology, whereas the UNM school covered stochastic gene regulation, cell signaling, membrane dynamics, cancer dynamics, and biomolecular simulations. All together, around 50 faculty participants gave lectures. The faculty participants were drawn from research institutions around the world, although a majority came from UCSD, UNM and Los Alamos National Laboratory. A large percentage were affiliated with the San Diego Center for Systems Biology (SDCSB) or the Center for Spatio-temporal Modeling of Cell Signaling (STMC), which are two of the National Centers for Systems Biology supported by the National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH). Numerous computer labs complemented the lectures, and students had opportunities to participate in experimental labs. Importantly, summer school students worked individually or in teams on short research projects under the mentorship of summer school faculty.

Below, we briefly comment on each paper included in the Special Issue.

The paper 'Using noise to control heterogeneity of isogenic populations in homogenous environments' is from a group of four 2014 q-bio Summer School student participants (Paulina Symańska, Nicola Gritti, Johannes M Keegstra and Mohammad Soltani—who attended the UNM school) and their faculty mentor (Brian Munsky). The report stems from the authors' summer school project and describes how noise in

gene expression in individual cells can be leveraged to drive a population cells to desired phenotypic states via a control law reminiscent of Maxwell's demon. School projects typically do not lead to publications, but multiple times, students have managed to publish on their school projects [10–12].

The commentary paper 'DARPA's Big Mechanism program' from Paul R Cohen describes an ambitious and thought-provoking project to build models for cancer-relevant cellular regulatory systems automatically through natural language processing. Dr Cohen, the Program Manager spearheading the project at the Defense Advanced Research Projects Agency (DARPA), described the goals of the project during a special evening session at the conference, which spurred lively philosophical discussions about modeling. Given the high level of interest in the project among the attendees, Dr Cohen was invited back to report on the status of the project at the 2015 q-bio Conference. Interest apparently remains high as Dr Cohen's paper consistently held the top spot for 'most read' papers tracked at the *Physical Biology* Web site in the 30 days following its publication.

This Special Issue also includes two review papers covering long-standing focus areas of the q-bio Summer School (stochastic gene regulation and cell signaling). The paper 'From analog to digital models of gene regulation' from Brian Munsky and Gegor Neuert, both of whom have lectured in the summer school on the subject of their paper, summarizes fundamental concepts in modeling and experimental characterization of stochastic gene regulation. These concepts are routinely taught at the summer school. The review paper 'Modeling for (physical) biologists: an introduction to the rule-based approach' from Lily A Chylek, Leonard A Harris, James R Faeder and William S Hlavacek, all of whom have lectured on this topic at the summer school, provides an introduction and extended tutorial for an interaction-based approach to modeling that is well suited for representing, for example, the dynamics of post-translational modifications of proteins in cell signaling systems.

The 2015 Special Issue includes several primary research articles. The paper 'Nonspecific transcription factor binding can reduce noise in the expression of downstream proteins' from M Soltani, P Bokes, Z Fox and A Singh reports analytical and numerical results that characterize how decoy binding sites for transcription factors influence the noisiness of gene expression. The paper 'Model reduction for stochastic CaMKII reaction kinetics in synapses by graph-constrained correlation dynamics' from Todd Johnson, Tom Bartol, Terrence Sejnowski and Eric Mjolsness reports a method for obtaining reduced forms of stochastic models. The paper 'The role of the bi-compartmental stem cell niche in delaying cancer' from Leili Shahriyari and Natalia L Komarova reports a theoretical analysis indicating that compartmentalization of a stem cell niche limits mutational load. The paper

'Model for adhesion clutch explains biphasic relationship between actin flow and traction at the cell leading edge' from Erin M Craig, Jonathan Stricker, Margaret Gardel and Alex Mogilner presents a mechanical model for cell migration focusing on actin-adhesion-myosin self-organization at the leading edge, as well as experiments that tested model predictions.

We appreciate every contribution made to this Special Issue, which reflects the spirit of the 2014 q-bio Conference. Of course, with the conference program consisting of more than 150 presentations, the papers collected here are just a small sample of the exciting science discussed at the meeting. We encourage you to attend the next q-bio Conference, which will be held at Vanderbilt University from July 27–30, 2016. The recently concluded 2015 q-bio Conference, held August 5–8 on the campus of Virginia Tech, will be featured in a future special issue, which will be co-edited by William Mather and Ilya Nemenman. If you attended the 2015 conference, please consider contributing to the next Special Issue. The deadline for submitting a manuscript is November 15, 2015. Potential contributors are strongly encouraged to contact one of the Editors to obtain submission approval. A call for contributions is posted at the q-bio wiki site (<http://q-bio.org>).

The 2014 q-bio Conference was the last conference to be hosted (for at least some time) at St. John's College in Santa Fe, the original location of the meeting and the site where it was held annually from 2007–2014. The conference location now moves from year to year. What prompted this change? The hope of the founding organizers is that the conference, by moving to different locations, will serve to strengthen q-bio research at the institutions hosting the event and that the conference will become more accessible to different local constituencies, which could help spur the adoption or popularization of q-bio approaches in biological fields where such approaches are presently not seen or uncommon. The successful meeting in Blacksburg, Virginia (organized by Yang Cao, Silke Hauf, William Mather, John Tyson and Jianhua Xing), provides an early indication that this hope will be fulfilled. The future success of the conference now depends on members of the q-bio community stepping forward to serve as local organizers. A review board consisting of past organizers (namely, the authors of this report) has been established and proposals to host the conference are now accepted annually. The next deadline for submitting a proposal is September 30, 2015. A call for proposals is posted at the q-bio wiki site (<http://q-bio.org>). Please consider submitting a proposal.

Please also consider participating in the q-bio Summer School (as a student or lecturer) and presenting your best work at the q-bio Conference. The most effective way to secure a place on the program is to submit an abstract reporting work aligned with the mission of the conference, which is to advance

predictive understanding of biological systems through integration of modeling and quantitative experimentation. The organizers are also keenly interested in promoting the development of experimental and computational methods, software, theory, and technology that enable quantitative biology. We invite you to provide input into future conference programs. If you have suggestions for invited speakers or wish to call attention to areas of quantitative biology deserving of greater recognition at the conference, please contact a member of the conference's program committee. Currently, the Chair of the program committee is Aleksandra M Walczak of the École Normale Supérieure in Paris. Dr Walczak is assisted by an outgoing Co-Chair, James R Faeder of the University of Pittsburgh, and an incoming Co-Chair, David J Schwab of Northwestern University. A listing of all current members of the program committee is available online (<http://q-bio.org>). Finally, we welcome nominations, including self-nominations, for positions on the program committee. Service on the committee entails reviewing nominations of invited speakers and submitted abstracts.

We look forward to seeing you at a future q-bio event!

The members of the local organizing committee of the 2014 q-bio Conference were William S Hlavacek (Chair), S Gnanakaran, Brian Munsky and Michael E Wall. The members of the program committee for the 2014 q-bio Conference were James R Faeder (Chair), S Gnanakaran, William S Hlavacek, Yi Jiang, Andre Levchenko, Brian Munsky, Ilya Nemenman, Orna Resnekov, Thomas S Shimizu, Lev S Tsimring, Aleksandra M Walczak, Michael E Wall, Bridget S Wilson and Anton Zilman. The lead organizers of the 2014 q-bio Summer School, who were aided by many others, were Jeff Hasty and Lev S Tsimring (at the UCSD campus) and William S Hlavacek and Brian Munsky (at the UNM campus).

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