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# **Discrete and Continuous Dynamical Systems**

## **Series S**

**Biomathematics: Newly developed applied mathematics  
and new mathematics arising from biosciences**

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## PREFACE

The First Joint Meeting of the American Mathematical Society and the Chinese Mathematical Society took place in Shanghai, China, December 17-21, 2008. It was organized by the Shanghai Mathematical Society, and hosted by Fudan University in Shanghai. Leading researchers from China and the United States participated in the conference. The conference was a major event for advancing mathematical research, and especially for developing international communication and cooperation among mathematicians from China and the United States. The conference program consisted of seven plenary talks, invited talks of eighteen special sessions, and many contributed talks. The topics in the special sessions covered a wide range of mathematics, applied mathematics and mathematical biology.

The special session "Biomathematics: newly developed applied mathematics and new mathematics arising from biosciences" had 21 invited speakers. They were Murray Bremner (University of Saskatchewan, Canada), Elena S. Dimitrova (Clemson University, USA), Andreas Dress (CAS-MPG Partner Institute for Computational Biology, China), Erica Flapan (Pomona College, USA), Shuhong Gao (Clemson University, USA), Wei Ji (Northwest University, China), Yangjin Kim (Mathematical Biosciences Institute, USA), Reinhard Laubenbacher (Virginia Bioinformatics Institute, USA), Bo Li (Chinese Academy of Sciences, China), Biyue Liu (Monmouth University, USA), Matthew Macauley (Clemson University, USA), Bud Mishra (Courant Institute and NYU School of Medicine, USA), Hong Qian (University of Washington, USA), Shigui Ruan (University of Miami, USA), Leah Shaw (College of William and Mary, USA), Yuefeng Shen (Chinese Academy of Sciences, China), Jianjun Paul Tian (College of William and Mary, USA), Daniel Vasiliu (Christopher Newport University, USA), Wei Wang (Northwest University, China), Xiao Long Xin (Northwest University, China), and Song Y. Yan (Harvard University, USA). The notable participation of this special session in the conference demonstrated the rapidly growing importance of mathematical modeling as a fundamental tool in advancing the understanding of biological science and growing interest in new mathematics arising from biological science.

Mathematics in history has been extensively used to help scientists to understand the essence of complex physical phenomena. Now, as biology has achieved revolutionary advances in basic science and technology including medical imaging and nano-bioengineering, the importance of mathematics to biology has become more and more conspicuous. As the deluge of experimental data from gene sequences to different scales of biosphere systems is accumulated, a confronting challenge is how to analyze and structure this data in a meaningful way. In a sense, the complexity of biological processes, which results from the complexity of biological interactions, seems to be even more elusive for discrete experimental data coming from the study of only separate aspects of the behavior of certain molecules. Obviously biology has come to a stage that demands a holistic, integrative, and highly quantitative approach. Mathematical methods seem to be a way to deal with the complexity of biological phenomena. And a mathematical framework can also simplify and shorten

the way to grasp the mechanism behind the experimental data and observation. On the other hand, it is expected that new mathematical subjects will arise from biosciences. In the effort to study biology by using mathematics, diverse mathematical methods have been extensively used. Besides traditional applied fields, such as dynamical systems, PDEs, stochastic processes and statistics, non-traditional or pure fields, such as topology, knot theory, differential geometry, and algebraic geometry, even abstract algebras and quantum groups have been amazingly applied to the study of biosciences. New mathematical subjects have also been developed for solutions of fundamental problems in the biosciences, such as finite algebraic dynamical systems, computational algebra, coalescent theory, evolution algebras, genetic algebras, phylogenetic tree geometry, etc. And the research fields are pervading diverse directions of biological problems, such as epidemiology, molecular population genetics, neuroscience, cellular signaling regulation in developmental biology, physiology, and cancer treatments.

This special issue of *Discrete and Continuous Dynamical Systems, Series S (DCDS-S)*, is based on our special session. The speakers in our special session and several other researchers were invited to submit manuscripts related to our topics. All papers are carefully refereed and selected based on the mathematical originality and biological relevance of the presented research work. The mathematical topics covered by the articles selected include abstract algebras, graph theory, group theory, difference equations, ordinary differential equations, partial differential equations, and topology. The timely publication of a high-quality special issue demands the well-concerned efforts of many devoted individuals in addition to the guest editors. We thank the participants and the organizers for making the First Joint Meeting of the American Mathematical Society and the Chinese Mathematical Society a productive and memorable event. We are grateful to the proceeding authors for allowing us to publish their fine work. We are especially indebted to many colleagues who helped us by carefully refereeing the submitted manuscripts in a timely manner. Last but not least, we would like to thank Xin Lu, the editorial manager and other staff of AIMS for their efforts to ensure that these proceedings will appear promptly and will be a high-quality publication. We hope this special issue will be a valuable and lasting contribution to the literature and the future progress of mathematical biology as well as mathematics itself.

January 16, 2010

**Guest Editors:**

Jianjun Paul Tian (Chair)  
Murray R. Bremner  
Reinhard Laubenbacher  
Banghe Li