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Editors

Advances in Systems Biology

 Springer

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Preface

Systems biology takes a holistic view on biology and aims at elucidating design principles of whole biological systems rather than characterizing individual molecules or single events. It is generally believed that systems biology will transform biology from a descriptive to a predictive science, making it possible to understand, explain, and eventually engineer complex biological systems. In the past decades, we witnessed burgeoning development of various fields that mutually complement each other and together define the scope and methods of systems biology. This young and rapidly growing consortium of disciplines defies all attempts at rigid definition of its purpose and boundaries while continuing to evolve and develop new experimental tools and theoretical paradigms. Perhaps, the most definitive characteristic feature of systems biology is that it is a fundamentally interdisciplinary science that became a point of fusion of the traditional experimental biology with physics, chemistry, mathematics, computer science, and engineering. Inevitable cross-talk of distinct cultures, often a tumultuous and never an easy process, brought about the emergence of a new culture of modern quantitative biology.

The most recent advances and new developments in systems biology were presented and actively discussed at the 11th International Conference on Systems Biology which took place on 10–16 October, 2010 in Edinburgh. This meeting marked the tenth anniversary of the increasingly popular series of conferences initiated by Hiroaki Kitano in 2000 in Tokyo. The meeting in Edinburgh attracted the largest yet attendee number, which is sure to continue growing in the years to come. Reflecting the highly diverse interdisciplinary nature of systems biology, the scientific programme of the Conference featured eight plenary and 16 parallel sessions aiming at the fair representation of various contributing fields. As has become the tradition over the decade of ICSB conferences, particular attention was given to the developments in genomics, proteomics, metabolomics as well as mathematical modeling and computational tools. Special sessions were dedicated to the recent advances in neurobiology, biological rhythms and circadian clocks, and biological noise and cellular decision making. Strong emphasis was also given to the practical applications of systems biology in medicine, biotechnology, and

pharmaceutical industry. Following the trend of the previous meetings, ICSB 2010 witnessed continuously increasing coalescence of experimental and theoretical approaches that resulted in exciting, truly systems research projects presented at the Conference.

The present collection of articles has emerged from the contributions provided by the speakers of ICSB 2010 as well as by other leaders of systems biology who could not attend the meeting. As the biological systems themselves, this volume is the result of self-organization. Since each contributor chose the topic of their chapter independently from the others, the scope of this volume is a faithful and unbiased replica of the entire breadth and diversity of systems biology. At the same time, individual contributions naturally grouped together revealing the particularly exigent research directions that presently attract the most attention. These emergent clusters defined the sections of the present volume. Thus, traditionally strong interest remains focused on the identification, analysis, and modeling of networks that represent causative, correlative, and other relationships between various biological entities. Contributions by B. Andrews, J. Saez-Rodrigues, D. Armstrong, and their colleagues consider the use of the proteome-wide datasets as well as the development of high-throughput techniques for their acquisition. Chapters by B. Kholodenko and W. Kolch, E. Feliu, S. Schnell and their co-workers are devoted to the analysis and modeling of intracellular signaling networks. H. Kaltenbach and J. Stelling discuss in more abstract terms the theoretical aspects of modularity that is characteristic of biological networks.

Much interest is presently devoted to the understanding of cellular decision making, such as response and adaption to the environmental perturbations, cellular differentiation, and programmed cell death. Given the importance of these fundamental biological processes for the treatment of cancer and stem-cell-based regenerative technologies, to name just a few applications, this interest is well justified. Section 2 starts with a provocative discussion feature by D. Bray who posits that biological organisms, as simple as unicellular bacteria, carry acquired throughout the evolution information on optimal environmental conditions. The contributions by A. Levchenko, J. Fisher, D. Lutter, and others focus on cellular differentiation and apoptosis. Together they suggest that systems biology is finally getting into the position to tackle these exciting and exceptionally complex problems.

Section 3 considers spatial and temporal aspects of intracellular dynamics. Thus, D. Vavylonis and colleagues and A. Carlsson discuss systems properties of actin cytoskeleton, while M. Enculescu and M. Falke review modeling of morphodynamic phenotypes and dynamic regimes of cellular locomotion. More technically oriented contributions that present novel computational algorithms, software tools and theoretical methods are grouped into Sect. 4. Here E. Balsacanto, I. Sbalzarini, and their colleagues discuss global optimization and parameter identification in stochastic reaction networks. M. Blinov and I. Moraru present the rule-based modeling approaches that allow building larger models of complex reaction networks.

To conclude the volume, Sect. 5 discusses a broad spectrum of systems biology applications in medicine, biotechnology, and pharmaceutical industry. Discussion features by R. Phair, L. Kupfer, N. Benson, and their colleagues present the views from inside the industry on the advantages and pitfalls associated with the use of systems biology in drug design and development. Other contributors showcase practical applications of systems methods to the analysis of patient data and typical problems arising in biotechnology of microorganisms and livestock.

Finally, the Editors would like to express their sincere gratitude to Mrs. Fiona Clark who provided invaluable administrative support without which the effort of assembling this volume would be impossible.

Andrew B. Goryachev
Igor I. Goryanin

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