Dynamics of Mathematical Models in Biology

Alessandra Rogato • Valeria Zazzu
Mario Guarracino
Editors

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Bringing Mathematics to Life

Editors

Alessandra Rogato
National Research Council
Institute of Biosciences and Bioresources
Naples, Italy

Valeria Zazzu
National Research Council
Institute of Genetics and Biophysics, ABT
Naples, Italy

Integrative Marine Ecology
Stazione Zoologica Anton Dohrn
Napoli, Italy

Mario Guarracino
Laboratory for Genomics, Transcriptomics
and Proteomics (Lab-GTP)
High Performance Computing
and Networking Institute (ICAR)
National Research Council (CNR)
Naples, Italy

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Preface

Despite Galileo's claim that mathematics is the language of nature, the two disciplines of mathematics and life sciences had been considered two planets belonging to two very far galaxies which would never meet. The two communities were vastly different and it seemed impossible for them to collaborate. Only recently when life scientists began producing experimental data at an unprecedentedly high pace, did it become clear that mathematical models were necessary to interpret such data and to structure them, with the ultimate goal of unveiling biological mechanisms, to making new discoveries, and to making predictions.

There are very few examples of events that bring the two communities together to discuss research questions. For this reason we decided to create a series of annual workshops to gather a multidisciplinary and international community. "Bringing Maths to Life" enabled the two communities of life scientists and mathematicians to exchange a bidirectional flow of ideas. The broad community of mathematician enabled life scientists to introduce new algorithms, methods, and software that may be useful to model life. Biologists enabled scientists to pose new challenges for mathematicians, thereby bringing to life novel opportunities for mathematicians to explore interesting problems. From this workshop many ideas and collaboration began. In the second year of the workshop, the *leitmotiv* had surrounded the concepts of time and dynamicity of nature. In the necessary simplifications applied during the modeling process, time is sometimes not accounted for in an attempt to avoid exponential complexity in computations. Nevertheless time imposed a different thought paradigm, which in turn created more elegant mathematical models.

The second workshop, held during October 19–21, 2015, in Naples (Italy) featured three main sessions. "Dynamics of genomes and genetic variation" was the topic of the first session. In this session, we discussed the molecular mechanisms and evolutionary processes that shape the structure and function of genomes and that govern genome dynamics. The session on "Dynamics of motifs" provided an overview of current methods for motif searching in DNA, RNA, and proteins, a key process to discover emergent properties of cells, tissues, and organisms. The third session was dedicated to the "Dynamics of biological networks." Networks representing complex biological functions and activities are useful to interpret

processes in the cell, and several mathematical models and algorithms are now available for their integration, analysis, and characterization. As mentioned above, in the necessary simplifications applied during the modeling process, time was often not accounted for in an effort to avoid exponential complexity in computations.

In this volume we collect many of the important ideas that derived from the workshop which are representative of the research questions that can be posed within such multidisciplinary applications. In the first chapter, Verena Thormann and colleagues describe the transcriptional regulation (when $1 + 1 \neq 2$). In the chapter “Differential Network Analysis and Graph Classification: A Glocal Approach”, a glocal approach to differential network analysis and graph classification is introduced by Giuseppe Jurmal and colleagues. Maria Pia Saccomanni and Karl Thomaseth discuss the identifiability of differential equation models that are used in systems biology. In the chapter “Boolean Dynamics of Regulatory Compound Circuits”, Elisabeth Remy et al. discuss the regulatory circuits and their dynamics. Target genes of homologous transcription factors are differentially analyzed by Elijah K. Lowe and colleagues. In the chapter “Reconstructing a Genetic Network from Gene Perturbations in Secretory Pathway of Cancer Cell Lines”, a pipeline for gene regulatory networks reconstruction is proposed by Marina Piccirillo et al., and in the chapter “Dissecting the Functions of the Secretory Pathway by Transcriptional Profiling” the functions of secretory pathways are analyzed starting from transcriptional profiling by Sonali Gopichand Chavan and colleagues. Saraunas Germanas et al. propose a Beta-Binomial model to detect rare mutations in NGS experiments. In the chapter “An Overview of Genotyping by Sequencing in Crop Species and Its Application in Pepper”, pepper genotyping by sequencing is discussed by Francesca Taranto et al. Irma Terracciano and colleagues describe in the chapter “Hybridization-Based Enrichment and Next Generation Sequencing to Explore Genetic Diversity in Plants” how to explore genetic diversity in plants. Lastly, in the chapter “DecontaMiner: A Pipeline for the Detection and Analysis of Contaminating Sequences in Human NGS Sequencing Data”, Ilaria Granata and colleagues describe a pipeline for the detection of sequences belonging to contaminating organisms in human NGS sequencing data.

We would like to acknowledge the work and support we have received for realizing this volume.

The workshop has been organized by Alessandra Rogato (Institute of Biosciences and Bioresources), Valeria Zazzu and Enza Colonna (Institute of Genetics and Biophysics “Adriano Buzzati-Traverso”), and Mario Guarracino (High Performance Computing and Networking Institute and Institute for Higher Mathematics “F. Saveri”) from the Italian National Research Council (CNR), Italy. Gerardo Toraldo from the Department of Mathematics and Applications “Renato Caccioppoli,” University of Naples Federico II, contributed to the organization. The initiative has been supported by the Italian National Research Council (CNR), the Institute for High Mathematics “F. Saveri” (INDAM), the High Performance

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Naples, Italy

Alessandra Rogato

Valeria Zazzu

Mario Guarracino

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Contributors

Maria I. Arnone Stazione Zoologica Anton Dohrn, Naples, Italy

Marina Borschiwer Max Planck Institute for Molecular Genetics, Berlin, Germany

Concita Cantarella Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA) - Centro di ricerca per l'orticoltura, Pontecagnano Faiano (SA), Italy

Sonali Gopichand Chavan Institute of Protein Biochemistry, National Research Council (CNR-IBP), Naples, Italy

Claudia Cuomo Stazione Zoologica Anton Dohrn, Naples, Italy

Nunzio D'Agostino Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA) – Centro di ricerca per l'orticoltura, Pontecagnano Faiano (SA), Italy

Michele Filosi Fondazione Bruno Kessler, Trento, Italy

Cesare Furlanello Fondazione Bruno Kessler, Trento, Italy

Sarunas Germanas Institute of Mathematics and Informatics, Vilnius University, Vilnius, Lithuania

Ilaria Granata ICAR-CNR, Naples, Italy

Mario Guarracino Laboratory for Genomics, Transcriptomics and Proteomics (LAB-GTP), High Performance Computing and Networking Institute (ICAR), National Research Council (CNR), Naples, Italy

Audrone Jakaitiene Department of Human and Medical Genetics, Faculty of Medicine, Vilnius University, Vilnius, Lithuania

Giuseppe Jurman Fondazione Bruno Kessler, Trento, Italy

Elijah K. Lowe Stazione Zoologica Anton Dohrn, Naples, Italy

Beacon Center for Evolution in Action, Michigan State University, East Lansing, MI, USA

Alberto Luini Institute of Protein Biochemistry at National Research Council (CNR), Naples, Italy

Istituto di Ricovero e Cura a Carattere Scientifico SDN, Naples, Italy

Sebastian H. Meijnsing Max Planck Institute for Molecular Genetics, Berlin, Germany

Brigitte Mossé Aix Marseille Université, CNRS, Centrale Marseille, I2M, UMR 7373, Marseille, France

Seetharaman Parashuraman Institute of Protein Biochemistry, National Research Council (CNR-IBP), Naples, Italy

Marina Piccirilo Laboratory for Genomics, Transcriptomics and Proteomics (LAB-GTP), High Performance Computing and Networking Institute (ICAR) at National Research Council (CNR), Naples, Italy

Elisabeth Remy Aix Marseille Université, CNRS, Centrale Marseille, I2M, UMR 7373, Marseille, France

Samantha Riccadonna Centro Ricerca e Innovazione, Fondazione Edmund Mach, San Michele all'Adige, Italy

Prathyush Deepth Roy Institute of Protein Biochemistry at National Research Council (CNR), Naples, Italy

Maria Pia Saccomani Department of Information Engineering, University of Padova, Padova, Italy

Mara Sangiovanni ICAR-CNR, Naples, Italy

Francesca Taranto Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA) – Centro di ricerca per l'orticoltura, Pontecagnano Faiano (SA), Italy

Irma Terracciano Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA) - Centro di ricerca per l'orticoltura, Pontecagnano Faiano (SA), Italy

Denis Thieffry Computational Systems Biology team, Institut de Biologie de l'Ecole Normale Supérieure (IBENS), CNRS UMR8197, INSERM U1024, Ecole Normale Supérieure, PSL Research University, Paris, France

Karl Thomaseth Institute of Electronics, Computer and Telecommunication Engineering (IEIIT-CNR) c/o DEI, Padova, Italy

Verena Thormann Max Planck Institute for Molecular Genetics, Berlin, Germany

Kumar Parijat Tripathi Laboratory for Genomics, Transcriptomics and Proteomics (LAB-GTP), High Performance Computing and Networking Institute (ICAR) at National Research Council (CNR), Naples, Italy

Pasquale Tripodi Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria (CREA) – Centro di ricerca per l'orticoltura, Pontecagnano Faiano (SA), Italy

Alessandra Varavallo Institute of Protein Biochemistry, National Research Council (CNR-IBP), Naples, Italy

Roberto Visintainer Fondazione Bruno Kessler, Trento, Italy