EIC Editorial
Marie-France Sagot

In this issue, I announce the retirement of Professor Mike Steel who has been on the editorial board of TCBB since the end of 2008. He has contributed so much to make TCBB function and thrive and I would therefore like to express my very warm appreciation for his service and support.

I am happy to welcome the addition to the editorial board of TCBB of Professor Tatsuya Akutsu from the Bioinformatics Center of the Institute for Chemical Research, Kyoto University, Japan; Professor Rolf Backofen, chair for Bioinformatics at the University of Freiburg, Institute of Computer Science, Germany; Assistant Professor Michael Brudno from the University of Toronto, Toronto, Canada; Principal Researcher in Statistical Bioinformatics Dirk Husmeier from Biomathematics & Statistics Scotland, Edinburgh, Scotland; Professor Sushmita Mitra, head of the Machine Intelligence Unit at the Indian Statistical Institute, Kolkata, India; Professor Vincent Moulton, director of the Computational Biology Laboratory, School of Computing Sciences, University of East Anglia, United Kingdom; Professor Ora Schueler-Furman from the Hebrew University of Jerusalem, Israel; Professor Charles Semple from the University of Canterbury, Christchurch, New Zealand; and Professor Jörg Stelling from the Swiss Federal Institute of Technology (ETH) in Zürich, Switzerland. I am very much looking forward to working with them alongside the remaining Associate Editors in the coming years.

Further editorial board nominations will be announced in the next issues of TCBB.

Marie-France Sagot
Editor-in-Chief

Tatsuya Akutsu received the BEng and MEng degrees in aeronautics and the DEng degree in information engineering from the University of Tokyo in 1984, 1986, and 1989, respectively. From 1989 to 1994, he was with Mechanical Engineering Laboratory. From 1994 to 1996, he was an associate professor in the Department of Computer Science at Gunma University. From 1996 to 2001, he was an associate professor in the Human Genome Center, Institute of Medical Science, University of Tokyo. Since 2001, he has been a professor in the Bioinformatics Center, Institute for Chemical Research, Kyoto University. His research interests include bioinformatics and the design and analysis of algorithms.

Rolf Backofen studied computer science at the University of Erlangen, and received the PhD degree in computer science from the University of Saarland in December 1994, where he worked at the German Research Center for Artificial Intelligence (DFKI). He received his habilitation from the University Munich (LMU) in February 2000. He held the chair for bioinformatics at the University of Jena from November 2001 till June 2005. After declining an offer for a full professorship at the University of Linz in 2004, he became the holder of the chair for bioinformatics at the University of Freiburg, Institute of Computer Science. His research interests include post-transcriptional regulation, analysis and detection of noncoding RNAs, RNA-targeting, prediction and evaluation of alternative splice forms, simplified protein models, investigation of energy landscapes, and constraint programming. He is coauthor of the book Computational Molecular Biology: An Introduction (Wiley & Sons, Mathematical and Computational Biology Series, 2000).

Michael Brudno received the PhD degree from the Computer Science Department at Stanford University developing several approaches for comparison of genomic sequences, including the LAGAN Alignment Toolkit, “glocal” alignment algorithms for sequences with rearrangements, and whole genome alignments. His postdoctoral work at the Computer Science Division, University of California at Berkeley, primarily addressed the problem of whole genome assembly from shotgun read data. After his postdoctoral work, he was a visiting scientist at CSAIL (Massachusetts Institute of Technology) before starting as an assistant professor at the University of Toronto in January 2006.
Dirk Husmeier graduated in physics (Dipl.-Phys.) from the University of Bochum, Germany, in 1991, and received both the MSc degree in information processing and neural networks and the PhD degree in applied mathematics and neural computation from King’s College London in 1994 and 1997, respectively. After working as a postdoctoral research fellow in the Electrical Engineering Department at Imperial College London from 1997 to 1999, he joined Biomathematics and Statistics Scotland (BioSS) as a research scientist in October 1999. His former research interests included theoretical biophysics, statistical pattern recognition, supervised learning in neural networks, and Bayesian approaches to machine learning. His current research activities are in the field of computational biology and bioinformatics, especially focusing on statistical methods for phylogenetics and the reverse engineering of genetic networks.

Sushmita Mitra is the head and a full professor in the Machine Intelligence Unit, Indian Statistical Institute, Kolkata. From 1992 to 1994, she was with RWTH, Aachen, Germany, as a DAAD Fellow. She was a visiting professor in the Computer Science Departments at the University of Alberta, Edmonton, Canada, in 2004 and 2007; Meiji University, Japan, in 1999, 2004, 2005, and 2007; and Aalborg University Esbjerg, Denmark, in 2002 and 2003. Dr. Mitra received the National Talent Search Scholarship (1978-1983) from NCERT, India, the University Gold Medal in 1988, the IEEE TNN Outstanding Paper Award in 1994 for her pioneering work in neuro-fuzzy computing, and the CIMPA-INRIA-UNESCO Fellowship in 1996. She is the author of the books *Neuro-Fuzzy Pattern Recognition: Methods in Soft Computing and Data Mining: Multimedia, Soft Computing, and Bioinformatics* published by John Wiley, and *Introduction to Machine Learning and Bioinformatics* published by Chapman & Hall/CRC Press, besides a host of other edited books. Dr. Mitra has guest edited special issues of several journals, is an associate editor of the *IEEE/ACM Trans. on Computational Biology and Bioinformatics, Neurocomputing*, and is a founding associate editor of *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery (WIRE DMKD)*. She has more than 75 research publications in refereed international journals. According to the Science Citation Index (SCI), two of her papers have been ranked 3rd and 15th in the list of top-cited papers in Engineering Science from India during 1992-2001. Dr. Mitra is a senior member of the IEEE and a fellow of the Indian National Academy of Engineering and The National Academy of Sciences, India. She has served in the capacity of program chair, tutorial chair, plenary speaker, and as member of program committees of many international conferences. Her current research interests include data mining, pattern recognition, soft computing, image processing, and bioinformatics.

Vincent Moulton received the PhD degree in mathematics from Duke University in 1994 and did postdoctoral research work at the University of Bielefeld, the University of Canterbury, and Massey University. He was a senior lecturer in discrete mathematics at Mid Sweden University from 1999-2002 and a professor in bioinformatics at Uppsala University from 2002-2004. In 2004, he moved to the University of East Anglia, where he is a professor in computational biology. His research interests are in phylogenetics, computational biology of RNA, metabolic modeling, algorithms in bioinformatics, and the study of discrete structures such as graphs and finite metric spaces.

Ora Schueler-Furman is an assistant professor at the Hebrew University of Jerusalem, Israel. She is an expert on the structure-based computational manipulation of proteins and their interactions. She has cochaired the area of protein structure and function at major bioinformatics conferences, such as ISMB and ECCB, in the last years. She received her PhD degree in computational structural biology in 2000 from the Hebrew University in Jerusalem, Israel. She then joined the group of David Baker in the Department of Biochemistry in Seattle, Washington, where she developed tools for the accurate structural modeling of protein-protein interactions and their manipulation through computational design. In 2005, she returned to Israel and started her own group at the Hebrew University, which focuses on various aspects of the basic energetic and evolutionary principles that govern protein-protein interactions, in particular those mediated by peptides.
Charles Semple is a professor of mathematics at the University of Canterbury. A trained secondary school teacher, he taught for five years before returning to university and receiving his PhD degree in mathematics from Victoria University of Wellington in 1998. Initially a postdoctoral fellow, he has been on the permanent staff at the University of Canterbury since 2001. He is a principal investigator in the Allan Wilson Centre for Molecular Ecology and Evolution and, in 2010, he was awarded the New Zealand Mathematical Society’s Award for Mathematical Research. His research interests are combinatorics, algorithms, and mathematical biology, particularly phylogenetics and matroid theory.

Jörg Stelling received the PhD degree in 2004 from the Department of Mechanical Engineering, University of Stuttgart; his PhD thesis devised new methods for the analysis of robustness in complex biological networks. He joined the Swiss Federal Institute of Technology (ETH), Zürich, first as an assistant professor of bioinformatics in the Department of Computer Science before becoming an associate professor of computational systems biology in the new Department of Biosystems Science and Engineering in 2008. From 1989 to 1996, he studied biotechnology at the Technical University of Braunschweig, with an intermediary stay at the Ecole Normal Superieure d’Agronomie Montpellier. By the end of 1996, he started as a PhD student in the Systems Dynamics and Control Group at the University of Stuttgart, before becoming one of the first employees of the newly founded Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg. His current research interests are focused on the analysis and synthesis of biological networks using—and further developing—methods from systems theory and computer science.