

# Final, Five-Year End, Editorial

Dan Gusfield

AS I end my five-year term as the Editor-in-Chief of *TCBB*, I want to thank all of the authors, editors, Steering Committee members, and IEEE Computer Society staff who together have made *TCBB* a top venue for high-quality research in computational biology and bioinformatics. I thank the associate editors in particular for volunteering so much of their time and energy. I also want to mention in particular the four inaugural members of the *TCBB* Steering Committee who continued on the board for all or most of my time as EIC: Russ Altman, Jacques Cohen, Evangelina Micheli-Tzanakou, and Chair of the committee Metin Akay. Their support of my efforts has been crucial. The support and work of the IEEE Computer Society staff has also been crucial, particularly Alicia Stickley, the one staff member who remained in place the whole five years. Finally, I thank Rangachar Kasturi who initially invited me to write the scientific part of the proposal to create *TCBB*, and Angela Burgess who, as Computer Society Publisher, provided critical help in many ways. It has been a pleasure working with all of you.

As one of my last official tasks, I am pleased to welcome six new associate editors to *TCBB*, who are experts in a wide range of topics from sequence analysis, microarray data analysis, clustering, phylogenetics, statistics, and more: Dan Brown, John Kececioglu, Yves Moreau, Sayan Mukherjee, Sven Rahmann, and Mike Steel. Bios for each of these new editors can be below.

Finally, I welcome the incoming Editor-in-Chief, Marie-France Sagot. Marie-France shares my conviction that the high quality and level of rigor of the papers in *TCBB* is its greatest asset. I know that *TCBB* is in excellent hands with Marie-France.

Thank you all again for your support of me and of *TCBB* during these five years.

Dan Gusfield  
*Outgoing Editor-in-Chief*



**Marie-France Sagot** received the BSc degree in computer science in 1991 from the University of São Paulo, Brazil, and a PhD and Habilitation degree in theoretical computer science in 1996 and 2000, respectively, from the University of Marne-la-Vallée, France. She was an appointed associate researcher at the Pasteur Institute in Paris from 1997 to 2001, before joining the French National Institute of Research in Computer Science and Control (INRIA) and the Laboratory of Biometry and Evolutionary Biology at the University of Lyon 1 and CNRS, France, where she currently is director of research and head of the BAOBAB-BAMBOO teams. Her main research interests concern computational biology, algorithmics, and combinatorics, and more specifically comparative genomics, chromosomal time and space dynamics, RNA structures, biological networks, and symbiosis. She cofounded the French

National Conference on Bioinformatics (JOBIM) and has been a member of the Steering Committee of the European Conference on Computational Biology (ECCB) since its beginning.



**Dan Brown** received the SB degree in mathematics with computer science from MIT in 1995, and the PhD degree in computer science from Cornell in 2000. Following a year of postdoctoral research working on the human and mouse genome projects at the Whitehead Institute/MIT Center for Genome Research, he joined the faculty of the David R. Cheriton School of Computer Science at the University of Waterloo in 2001, and has been an associate professor since 2007. He is the recipient of an early researcher award from the Ontario government. His work focuses on DNA sequence analysis and on probabilistic analysis of bioinformatics algorithms.



**John Kececioğlu** received the PhD degree in computer science from the University of Arizona in 1991. He did postdoctoral study at the Université de Montreal and the University of California, Davis, and then taught at the University of Georgia, before joining the University of Arizona in 2000 where he is an associate professor of computer science. He is the recipient of a US National Science Foundation CAREER Award, serves on the Editorial Board of *Algorithms for Molecular Biology*, is conference chair for RECOMB 2009, and has served on the Scientific Advisory Board of the Max-Planck-Institut für Informatik. His research is in the design, analysis, and implementation of algorithms for computational molecular biology.



**Yves Moreau** received the MSc degree in electrical engineering from the Faculté Polytechnique de Mons, Belgium, and an MSc degree in applied mathematics from Brown University, Rhode Island, USA, where he was a Fulbright grantee in 1992-1993. He received the PhD degree in electrical engineering from the University of Leuven, Belgium (K.U.Leuven) in 1998, in the areas of complex nonlinear systems, neural networks, and data mining. He is an associate professor of electrical engineering at the K.U.Leuven. In 2003-2004, he was a visiting researcher at the Center for Biological Sequence Analysis, Technical University of Denmark in Copenhagen. He is a principal investigator of the SymbioSys Center for Computational Systems Biology at the K.U.Leuven ([www.kuleuven.be/symbiosys](http://www.kuleuven.be/symbiosys) and [www.kuleuven.be/bioinformatics](http://www.kuleuven.be/bioinformatics)). He has been initially active in the areas of gene expression analysis and regulatory sequence analysis. Currently, the main focus of his research is on the development of analysis strategies for 1) the diagnosis of rare genetic disorders using comparative genomic hybridization arrays and next-generation sequencing and 2) the fusion of omics data and network analysis for the identification of disease genes underlying such disorders. Methodologically, his emphasis lies on probabilistic graphical models and kernel methods for the analysis of omics data. He is also cofounder of two spin-offs of the K.U.Leuven: Data4s, now Norkom ([www.norkom.com](http://www.norkom.com)), specializing in data mining for the financial industry and Cartagenia ([www.cartagenia.com](http://www.cartagenia.com)), specializing in IT solutions for clinical genetic diagnosis.



**Sayan Mukherjee** received the PhD degree from MIT in 2001, advised by Tomaso Poggio at the Center for Biological and Computational Learning and the Artificial Intelligence Laboratory. He was then a SLOAN postdoctoral fellow at the Broad Institute of MIT and Harvard. Since 2004, he has been a faculty member at Duke University with appointments in the Department of Statistical Science, Department of Computer Science, Department of Biostatistics and Bioinformatics, and the Institute for Genome Sciences & Policy. His research focuses on two complementary problems: 1) the biological problem of modeling complex (disease) phenotypes and 2) the methodological and theoretical problem of analysis and inference from high-dimensional (genomic) data. Both problems are instances of the fundamental problem of modeling uncertain and complicated natural processes. The objective of these models is to understand the mechanism giving rise to these processes both as an exercise in biological modeling as well as understanding fundamental mathematical properties of high-dimensional data.



**Sven Rahmann** is a professor for bioinformatics for high-throughput technologies and the chair of algorithm engineering, Computer Science Department, TU Dortmund. Before, he spent four months at HHMI Janelia Farm Research Campus as a visiting scientist. He led the Computational Methods for Emerging Technologies (COMET) group at Bielefeld University between 2004 and 2007. He wrote his doctoral thesis on oligonucleotide design for microarrays in the Computational Molecular Biology group at the Max Planck Institute for Molecular Genetics in Berlin, after studying mathematics and computer science with a focus on statistical methods in bioinformatics at the University of Göttingen, UC Santa Cruz, and the University of Heidelberg, where he wrote his Diploma (MSc) thesis at the German National Cancer Research Center (DKFZ) on word statistics in random texts.



**Mike Steel** studied mathematics at Canterbury and Massey Universities (New Zealand) and received the PhD degree in mathematics in 1989. From 1990-1993, he held various postdoctoral positions in Germany and New Zealand and was appointed to a tenured position at the University of Canterbury in 1994. He is currently a professor and director of the Biomathematics Research Centre at the University of Canterbury, and is a principal investigator in the Allan Wilson Centre for Molecular Ecology and Evolution.