

# Introduction of New Associate Editors

I am pleased to introduce the distinguished inaugural members of the Editorial Board.

Dan Gusfield  
Editor-in-Chief



**Raj Acharya** received the PhD degree from the Mayo Graduate School of Medicine/University of Minnesota in 1984. Since then, he has worked as a research scientist at the Mayo Clinic and at Thomson in Paris, France. He has also been a faculty fellow at the Night Vision Laboratory in Fort Belvoir, Washington D.C., and has been a NASA-ASEE faculty fellow at the Johnson Space Center in Houston, Texas. He was the chair of the Department of Computer Science and Engineering at the State University of New York-Buffalo from the fall of 1999 until the spring of 2001. He is currently the department head and a professor of computer science and engineering at the Pennsylvania State University. His main research thrusts are in the general areas of data mining, information fusion, and data warehouse design with applications to bioinformatics. He is the prime architect of the PCABC Cancer Bioinformatics

Datawarehouse project. His research concentrates on applying information fusion techniques and algorithms to the field of genomics and proteomics. He is also developing fractal models for the spatio-temporal organization of the DNA replication and transcription sites.



**Bonnie Berger** is a professor of applied mathematics at the Massachusetts Institute of Technology (MIT) and head of the Computation and Biology Group at the MIT Computer Science and Artificial Intelligence Laboratory (CSAIL). Professor Berger is also a member of the Program in Mathematics and Molecular Biology (PMMB), MIT's Computer Science and Systems Biology initiative (CSBi), as well as an affiliated member of the Harvard-MIT Division of Health Sciences and Technology (HST). Her major areas of research have been in applying mathematical and computational techniques to problems in molecular biology. In particular, the focus of her research has been on the following three core problem areas: comparative genomics, protein structural motif recognition and discovery, and molecular self-assembly and misassembly. She has coauthored more than 50 scholarly research articles and has been invited to

present at conferences in fields ranging from randomized algorithms and graph theory to computational molecular biology. She is an editor for the *Journal of Discrete Applied Math*. Professor Berger has won numerous awards and honors including a US National Science Foundation Career award, a Radcliffe Bunting Institute Science Scholarship, and the Biophysical Society's Dayoff Award for research among others. In 1999, she was named one of *Technology Review Magazine's* first TR100 for being a top young innovator of the 21st century. In 2004, she was elected a fellow of the ACM.



**Philip E. Bourne** (PhD) is a professor in the Department of Pharmacology at the University of California San Diego (UCSD), the senior advisor to the life sciences at the San Diego Supercomputer Center (SDSC), an adjunct professor at the Burnham Institute and the Keck Graduate Institute, codirector of the Protein Data Bank (PDB), an elected fellow of the American Medical Informatics Association, and the immediate past President of the International Society for Computational Biology. His current interests are in structural genomics, proteomics, apoptosis, cell signaling, data modeling, and scientific visualization. He is the author of more than 150 scientific papers and four books, one of which sold more than 120,000 copies. He has received two UCSD Connect Awards for new inventions in the areas of comparative protein structure analysis and shared visualization. Most recently, he was the recipient of the 2002 Sun Microsystems Convergence Award. He has founded two companies.

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tcbb@computer.org.



**Sorin Draghici** is director of the Bioinformatics Core at Karmanos Cancer Institute and an associate professor in the Department of Computer Science at Wayne State University. Dr. Draghici has published a best-selling book on microarray data analysis (*Data Analysis Tools for Microarrays*, Chapman and Hall/CRC Press), seven book chapters, and more than 60 peer-reviewed journal and conference papers. He is coinventor on four patent applications related to data analysis of microarray data. Dr. Draghici is a journal reviewer for *Trends in Genetics*, *Nucleic Acid Research*, *Bioinformatics*, *Genomics*, and 10 other international technical journals, as well as a regular US National Science Foundation panelist on computer science, biotechnology, and bioinformatics topics. His current research interests include data analysis of microarray data, early diagnostic tests based on DNA and protein microarrays, data mining in biological databases, and machine learning.



**Sandrine Dudoit** received the Bachelor's degree (1992) and the Master's degree (1994) in mathematics from Carleton University, Ottawa, Canada. She is an assistant professor of biostatistics in the School of Public Health at the University of California at Berkeley. Professor Dudoit first came to UC Berkeley as a graduate student and earned the PhD degree in 1999 from the Department of Statistics. For her doctoral thesis, she worked with Professor Terence P. Speed on the linkage analysis of complex human traits. From 1999 to 2000, she was a postdoctoral fellow at the Mathematical Sciences Research Institute, Berkeley. Before joining the faculty at UC Berkeley in July 2001, she underwent a year of postdoctoral training in genomics in the laboratory of Professor Patrick O. Brown, Department of Biochemistry, Stanford University. Her work in the Brown Lab involved the development of statistical methods for the design and analysis of DNA microarray experiments. Professor Dudoit's current research concerns the application of statistics to problems in genetics and molecular biology. Her areas of interest include the design and analysis of gene expression experiments using DNA microarrays, the identification of regulatory motifs in DNA sequences, and the genetic mapping of complex human traits. Her methodological research interests include loss-based estimation with cross-validation (prediction, density estimation, and variable selection) and multiple hypothesis testing. Professor Dudoit is also involved in the development of statistical software for genomic data analysis and is a core member of the Bioconductor Project ([www.bioconductor.org](http://www.bioconductor.org)).



**Dannie Durand** received the BS degree in physics from the Massachusetts Institute of Technology (MIT) and the MS and PhD degrees in computer science from Columbia University. She is an associate professor in the Departments of Biological Sciences and Computer Science at Carnegie Mellon University. Her research focuses on the evolution of genome organization and function in vertebrates. Dr. Durand is a David and Lucile Packard Foundation Science and Engineering fellow and a member of the ACM, AAAS, IEEE, ISCB, and Sigma Xi.



**Herbert Edelsbrunner** graduated from the Graz University of Technology in 1982 and was with the Department of Computer Science at University of Illinois at Urbana-Champaign from 1985 to 1999. He is an arts and sciences professor of computer science and mathematics at Duke University and the director of Raindrop Geomagic. His research areas are data structures and algorithms, computational geometry and topology, mesh generation, modeling and visualization, and computational structural molecular biology. He is author of more than 100 research articles. He published two textbooks in the general area of computational geometry and topology, the first in 1987 with Springer-Verlag and the second in 2001 with Cambridge University Press. In 1991, he received the Alan T. Waterman Award from the US National Science Foundation. He developed the theory and algorithms behind the popular alpha shapes software. In 1996, he cofounded Raindrop Geomagic, a company focusing on sophisticated 3D geometric modeling software. He specializes in the combination of computing and advanced mathematics to solve problems in applications. He bridges different disciplines within computer science, mathematics, and molecular biology. His methodology is to search out the mathematical roots of application problems and to combine mathematical with computational structure to get working solutions.



**Gary B. Fogel** received the PhD degree in biology from the University of California at Los Angeles in 1998 with a focus on the evolution and variability of histone proteins. He is currently the Vice President of Natural Selection, Inc.® in La Jolla, California. Dr. Fogel's current research interests focus on the application of evolutionary computation and computational intelligence to problems in the biomedical sciences and bioinformatics. He is currently investigating the use of evolved neural networks for gene expression analysis, gene recognition, drug activity prediction, as well as methods of evolutionary computation in RNA structure analysis, sequence alignment, and biomedical pattern recognition. Dr. Fogel has coedited a volume on *Evolutionary Computation in Bioinformatics* (Morgan Kaufmann, 2003) and serves as general chair of the Proceedings of the 2004 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, to be held in San Diego, California.



**Nir Friedman** received the BSc degree in mathematics and computer science from Tel-Aviv University in 1987, the MSc degree in mathematics and computer science from the Weizmann Institute of Science in 1992, and the PhD degree in computer science from Stanford in 1997. From 1996 until 1998, he was a postdoctoral scholar in the computer science division of the University of California at Berkeley. Since the fall of 1998, he has been a faculty member at the School of Computer Science and Engineering at the Hebrew University, Jerusalem, Israel. Dr. Friedman's major research interests involve learning and inference with probabilistic models and their applications to computational biology. In particular, his group has examined analysis of gene expression data for understanding human disease, pathway reconstruction, and understanding of regulatory circuits. Dr. Friedman is on the editorial board of several

journals; he also served in the program committee of numerous conferences, and was the program cochair of the Proceedings of the 18th Conference on Uncertainty in Artificial Intelligence, 2002.



**Mark Gerstein** received the AB degree in physics from Harvard College in 1989 and the PhD degree in chemistry and biophysics from Cambridge University in 1993. He did postdoctoral work at Stanford University and took up his post at Yale University in early 1997. Since then, he has received a number of young investigator awards (e.g., from the Navy and the Keck Foundation) and has published appreciably in the biological science journals (more than 150 papers in total; current publication list can be found at <http://bioinfo.mbb.yale.edu/papers>). He is the Albert L. Williams associate professor of Biomedical Informatics at Yale University. He is in the Department of Molecular Biophysics and Biochemistry and the Department of Computer Science at Yale University. His research is focused on bioinformatics, and he is particularly interested in large-scale integrative surveys, biological database design,

macromolecular geometry, molecular simulation, genome annotation, gene expression analysis, and Bayesian approaches for data mining.



**Roderic Guigo** (PhD) leads the Genome Bioinformatics Laboratory at the Institut Municipal d'Investigació Mèdica in Barcelona. He is also a professor at the Universitat Pompeu Fabra and coordinates the bioinformatics and genomics program within the recently created Center for Genomic Regulation. His research focuses on computational gene prediction. He is the author of one of the first general purpose gene finding programs, and he has contributed to the development of standards for the evaluation of the accuracy of gene prediction programs. He has also participated in the analysis consortiums of numerous eukaryotic genomes.



**Alfred O. Hero III** received the PhD degree from Princeton University (1984) in electrical engineering. Since 1984, he has been with the University of Michigan, Ann Arbor, where he is a professor in the Department of Electrical Engineering and Computer Science and, by courtesy, the Departments of Biomedical Engineering and Statistics. His recent research interests have been in the areas of statistical signal and image processing, networks, and bioinformatics. He has served as an associate editor for the *IEEE Transactions on Information Theory* (1995-1998, 1999) and the *IEEE Transactions on Signal Processing* (2002). He was chairman of the Statistical Signal and Array Processing (SSAP) Technical Committee (1997-1998) and treasurer of the Conference Board of the IEEE Signal Processing Society. He is currently president-elect of the IEEE Signal Processing Society (2004-2005). He is an IEEE fellow and has received

the 1998 IEEE Signal Processing Society Meritorious Service Award, the 1998 IEEE Signal Processing Society Best Paper Award, and the IEEE Third Millennium Medal.



**Tao Jiang** received the BS degree in computer science and technology from the University of Science and Technology of China, Hefei, People's Republic of China in July 1984, and the PhD degree in computer science from the University of Minnesota in November 1988. He was a faculty member at McMaster University, Hamilton, Ontario, Canada from January 1989 to July 2001. He joined the University of California at Riverside as a professor of computer science and engineering in September 1999. He is also a member of the UCR Genomics Institute, Center for Plant Cell Biology, Shanghai Center for Bioinformatics Technology, and Beijing University Center for Theoretical Biology. Tao Jiang's recent research interest includes algorithms, computational molecular biology, computational complexity, and computational aspects of information gathering and retrieval. He has published actively in all major

theoretical computer science and computational biology journals and conferences, and served on program committees for many international conferences as well as review panels for several funding agencies. He is presently serving on the editorial boards of the *International Journal of Foundations of Computer Science*, the *Journal of Combinatorial Optimization*, the *Journal of Computer Science and Technology*, and the *Journal of Bioinformatics and Computational Biology*.



**Simon Kasif** is a professor of bioengineering, bioinformatics, and computer science and the codirector of the Center for Advanced Genomic Technology (CAGT) at Boston University. He is also affiliated with the Genome Center at the MIT/Harvard Broad Institute. He previously held teaching and research positions at Johns Hopkins University, Princeton University, the University of Illinois, Chicago, the NEC Research Institute, and the Cambridge Research Laboratory. He is also a consultant to a number of large industrial organizations. The Computational Genomics Laboratory he is directing conducts basic research in functional genomics, comparative genomics, new biotechnology, assignment of function to newly sequenced genes, and applications of machine learning to bioinformatics. Dr. Kasif helped design the system Glimmer, one of the most widely used gene finders for prokaryotic genomes built at TIGR, the

system MUMMER, one of the earlier whole genome comparative genomics systems (also built at TIGR), and helped develop a new protocol for finishing genomes using efficient multiplex PCR used at several genome centers. Dr. Kasif was a participant in the public Human Genome Consortium where he and his collaborators at the MIT Genome Center performed the first large segmental duplication analysis of the human genome. Dr. Kasif and his group pioneered and helped popularize the application of Bayesian networks to modern computational biology. The applications of the work performed by the lab includes basic biology, identification of functional elements in genomes, understanding their role in biological systems, host/environment-pathogen interactions, analysis of variability on different evolutionary scales, regulations in cancer pathways, and improving the cost and accuracy of advanced biotechnology techniques.



**Lydia E. Kavraki** received the BS degree in computer science from the University of Crete in Greece, and the PhD degree in computer science from Stanford University. She is the Noah Harding Professor of computer science and bioengineering at Rice University. She also holds a joint appointment in the Department of Structural and Computational Biology and Molecular Biophysics at the Baylor College of Medicine. Her research contributions are in physical algorithms and their applications in robotics, computational structural biology, and bioinformatics. Her robotics research focuses on motion planning, assembly planning, and manipulation. In structural computational biology, Dr. Kavraki works on computer-assisted drug design, the modeling of protein flexibility and receptor-ligand interactions, and the large-scale functional annotation of proteins. A unifying theme in her work is the investigation of algorithms and system architectures for solving complex geometric problems with physical constraints that arise in the real world. She has authored more than 100 peer-reviewed journal and conference publications, has coedited one book and is one of the authors of a robotics textbook to be published in 2004. Dr. Kavraki has been the recipient of the Association for Computing Machinery (ACM) Grace Murray Hopper Award. She has also received a US National Science Foundation CAREER award, a Sloan Fellowship, the Early Academic Career Award from the IEEE Society on Robotics and Automation, and has been included in the list of Top 100 Young Innovators of the MIT Technology Review Magazine. For more information on Dr. Kavraki's work, go to <http://www.cs.rice.edu/~kavraki>.



**Junhyong Kim** is the Edmund J. and Louise W. Kahn Endowed Professor of Biology with a joint appointment in the Department of Computer and Information Science at the University of Pennsylvania. He is a member of the Penn Genomics Institute and Penn Center for Bioinformatics. He is a council member of the Society for Systematic Biology, associate editor of *Systematic Biology*, and is on the editorial board of *Molecular Development* and *Evolution and Genomics and Informatics*. His research focuses on computational and experimental approaches to comparative genomics with an emphasis on computational phylogenetics, comparative development, and neurogenomics.



**Thomas Lengauer** (PhD) is the director at the Max-Planck Institute for Informatics in Saarbrücken, Germany. His background is in math (PhD degree, Berlin, Germany, 1976) and computer science (PhD degree, Stanford, 1979). He has been engaged in research in computational biology since the beginning of the 1990s. His major fields of research are protein structure and function prediction, computational drug screening and design as well as bioinformatics for understanding and curing diseases. Previously, he held the positions of a full professor at the University of Paderborn, Germany (1984-1992) and of a director of the Institute for Algorithms and Scientific Computing at the German National Research Center for Computer Science in Sankt Augustin, Germany (1992-2001). Dr. Lengauer has contributed concepts and/or direction to several German research programs on computational biology, is a founding member of the International Society for Computational Biology (ISCB), a member of the steering board of the international conference series RECOMB, and he currently heads the steering board of the European bioinformatics conference series ECCB. In 2003, he received the Konrad Zuse Medal of the German Informatics Society and the Karl Heinz Beckurts Award. He is a member of the German Academy of Natural Scientists Leopoldina.



**Arthur Lesk** received the AB degree in biochemical sciences from Harvard University, the MA degree from the University of Cambridge, and the PhD degree in physics and physical chemistry from Princeton University. His major contributions include discoveries of the relationship between changes in amino acid sequence and changes in protein structure, through analysis of the mechanism of evolution in protein families; the canonical-structure model for the conformation of the complementarity-determining regions of antibodies, and its application to prediction of structure and to analysis of antibody germ line genes (this work has supported the humanization of antibodies for clinical applications); mechanisms of conformational change in proteins; the tableau representation of folding patterns and its application to fold classification and recognition; and authorship of the first program to generate schematic diagrams of proteins by computer; and development of other algorithms in the field of protein structural analysis. Dr. Lesk is also the author of several scientific textbooks.



**Michal Linial** is a professor at the Hebrew University of Jerusalem, Israel (since 1990). She has an experimental and computational laboratory. On the biological facet, she is studying neuronal secretory system and developing cells by molecular, cellular, genomics, and proteomics methodologies. She is a member of the Otto Lewie for Molecular and Cellular Neuroscience in Jerusalem. Her expertise in the synapse led to the study of protein families, protein-protein interactions, and structural view on protein networks. The laboratory has mastered proteomics and genomics methodologies. The solid informatics approaches are used for large database storage and constant updating of several systems in view of classification, validation, and functional predictions. This is led by a small group of programmers and system experts. Professor Linial and her students have been active participants in the structural genomics consortium and she is a committee member of major bioinformatics and computational biology conferences. She is a participant of protein classification pilot experiments supported by NIH. She and her colleagues have created several global classification systems that are used by the biomedical and biology communities. In addition, they provided a system that rank proteins targets by their potential for revealing novel folds as well as optimal definition of clusters that is validated on current bioknowledge. All Web-based systems such as ProtoNet, PANDORA, and ProTarget are provided as an open source for investigators. The group is a member of the BioSapiens European Network of Excellence. She is involved in the committees of bioinformatics and computational biology and is a director of a new computational biology center in the Hebrew University. Linial is leading the first established educational program in computer science and life science for undergraduate-graduate studies in Israel and is involved in local teaching and training programs as well as in international schools.



**Webb Miller** is a professor in the Departments of Biology and of Computer Science and Engineering at the Pennsylvania State University. His main research interests are in developing methods to align vertebrate genome sequences and in using those methods to learn about the structure and functions of those genomes.



**Satoru Miyano** received the BS degree in 1977, the MS degree in 1979, and the Doctorate of Science degree, all in mathematics from Kyushu University. He is a professor in the Human Genome Center, Institute of Medical Science, The University of Tokyo. His research interest includes bioinformatics, discovery science, and computational complexity. Currently, he is intensively working for computational gene network inference methods, modeling and simulation of biological systems, and computational knowledge discovery from biological data.



**Bernard M.E. Moret** is a professor of computer science and of electrical and computer engineering at the University of New Mexico. His research centers on algorithm engineering: the design and application of high-performance algorithms to specific classes of problems. For the last five years, he has been applying algorithm engineering techniques to problems in computational molecular biology, with particular emphasis on phylogenetic reconstruction and comparative genomics ([compbio.unm.edu](http://compbio.unm.edu)). He is the past Editor-in-Chief and founding editor of the *ACM Journal of Experimental Algorithmics*. He directs the CIPRES project ([www.phylo.org](http://www.phylo.org)), funded by a large ITR grant from the US National Science Foundation to develop a national cyber infrastructure to support the reconstruction of the Tree of Life.



**Joseph Nadeau** received the PhD degree in population biology from Boston University in 1978. He was a postdoctoral fellow with Jan Klein in the Immunogenetics Department, Max Planck Institute for Biology, Tübingen (1978-1980) and with Eva Eicher at the Jackson Laboratory (1980-1981). He was appointed associate staff scientist (1981-1985), staff scientist (1985-1991), and senior staff scientist (1991-1994) at the Jackson Laboratory, and then professor, Department of Human Genetics, McGill University, and medical scientist, Department of Medicine, Montreal General Hospital (1994-1996). He is currently the James H. Jewel professor and chair of the Genetics Department at Case Western Reserve University School of Medicine and codirector for the Center for Computational Genomics. He was a founding member of the International Mammalian Genome Society and a founding editor of *Mammalian Genome*.

He was founder and director of the Mouse Genome Informatics Project (1989-1994) and founder of the Mouse Gene Expression Database Project (1992-1994). He has served on review panels and advisory groups at the National Institutes of Health, the US National Science Foundation, and the Human Genome Database. He has consulted for GlaxoSmithKline, Pharmacia, Celera Genomics, Exelixis, NineSigma, and CellTech Chiroscience, and is on the Scientific Advisory Board of Galileo Genomics.



**Chiara Sabatti** received the BS degree and Masters degree in economics and statistics from the Bocconi University (Milan, Italy) in 1993. She received the PhD degree in statistics from Stanford University in 1998, and it is based on work on Markov Chain Monte Carlo algorithms. She consequently approached the field of genetics as a postdoctoral fellow in the Department of Genetics at Stanford University. Since 2000, she has been an assistant professor of human genetics and statistics at the University of California at Los Angeles. In her research, she develops statistical models and computational tools for high-dimensional data analysis, with special regard to data of genetic origin (as DNA sequences, expression arrays and genome screens, etc.).

**Marie-France Sagot** received the BSc degree in computer science from the University of São Paulo, Brazil, in 1991, the PhD degree in theoretical computer science and applications from the University of Marne-la-Vallée, France, in 1996, and the Habilitation from the same university in 2000. From 1997 to 2001, she worked as a research associate at the Pasteur Institute in Paris, France. In 2001, she moved to Lyon, France, as a research associate at the INRIA, the French National Institute for Research in Computer Science and Control. Since 2003, she has been the director of research at the INRIA. Her research interests are in computational biology, algorithmics, and combinatorics.



**Jeanette P. Schmidt** received the BSc degree in mathematics and statistics from the Hebrew University in Jerusalem and the PhD degree from the Weizman Institute of Science, Rehovot, Israel. She has been with the Incyte Corporation since 1997, serving most recently as vice president of Bioinformatics R&D, leading the bioinformatics research operations as well as product development. Prior to joining Incyte, Dr. Schmidt was an associate professor of computer science at the Polytechnic University, New York (1989-1997), where her research focused on computational biology. While on sabbatical from Polytechnical University, Dr. Schmidt spent a year at Stanford University in the Department of Biochemistry and the Section for Medical Informatics (1996-1997), supported by a grant from the US National Science Foundation. Dr. Schmidt previously held visiting professor positions at Rutgers University in New Jersey and at the Courant Institute of New York University, New York City.



**Ron Shamir** received the BSc degree in mathematics and physics from the Hebrew University and the PhD degree in operations research from the University of California at Berkeley. He is a professor at the School of Computer Science and the Raymond and Beverly Sackler chair in bioinformatics at Tel Aviv University. His expertise covers graph theoretic, probabilistic and complexity methods for design, and the analysis of algorithms. Since 1990, he is specializing in algorithms for problems in molecular biology. He was the founding director of the bioinformatics program at Tel Aviv University. His current research focuses on developing computational tools for gene expression analysis, DNA chips, comparative genomics, genetic and regulatory networks, and haplotyping. He is a member of the editorial board of several leading journals and series in computational biology, and on the steering committee of RECOMB. Dr. Shamir has published more than 120 scientific publications.



**Kimmen Sjölander** received the PhD degree in computer science from the University of California at Santa Cruz under David Haussler. She is an assistant professor in the Department of Bioengineering at the University of California at Berkeley. Her research focuses on statistical and machine learning approaches to inferring protein sequence, structure, and function relationships. Prior to joining the faculty at UC Berkeley, Dr. Sjölander was principal scientist of the Protein Informatics Group at Celera Genomics, responsible for the functional classification of the human genome. Dr. Sjölander received a CAREER Award from the US National Science Foundation, is a member of the California Institute for Quantitative Biomedical Research (QB3), and was a national fellow of the Program in Mathematics and Molecular Biology (PMMB).



**Steven Skiena** received the BS degree in computer science from the University of Virginia in 1983 and the MS and PhD degrees in computer science from the University of Illinois, Urbana-Champaign in 1985 and 1988, respectively. He is a professor of computer science at the State University of New York (SUNY) at Stony Brook. His research interests include computational biology, combinatorial algorithm design, and discrete mathematics. He is the author of four books, including *The Algorithm Design Manual* and *Calculated Bets: Computers, Gambling, and Mathematical Modeling to Win*. Dr. Skiena is a member of the ACM and recipient of the IEEE Computer Science and Engineering Undergraduate Teaching Award.



**Donna Slonim** received the PhD degree in computer science under Professor Ron Rivest in the theory of computation group at the Massachusetts Institute of Technology (MIT) Laboratory for Computer Science in 1996. Her doctoral research, in the area of computational learning theory, focused on problems of drawing conclusions from noisy or incomplete data. She is a research scientist in computational biology at Wyeth Genetics Institute, where she leads a team in the genomics group. Her current research focuses on developing methods for extracting meaningful biological and medical information from gene expression and other genomic data. Before joining Wyeth, she was a researcher in the Cancer Genomics group at the Whitehead Institute Center for Genome Research, where her work focused on analyzing gene expression data. Dr. Slonim also worked on computational problems related to genome mapping and was involved with the human, mouse, and rat mapping efforts at the Genome Center. Her other research interests include machine learning, sequence analysis, and understanding complex biological traits.



**Jens Stoye** studied computer science and theoretical physics at Bielefeld University, where he received the PhD degree in 1997 on a topic related to multiple sequence alignment. After postdoctorate positions at the University of California at Davis and the German Cancer Research Center in Heidelberg, he became a group leader in algorithmic bioinformatics at the Max Planck Institute of Molecular Genetics in Berlin. Since March 2002, Dr. Stoye has been a professor of genome informatics at Bielefeld University. He is the speaker of the Institute of Bioinformatics at Bielefeld University and the vice speaker of the Bioinformatics sections of the German Computer Society.



**Esko Ukkonen** has been a professor of computer science at the University of Helsinki since 1985, and since 2002, the director of a national Center-of-Excellence 'From Data to Knowledge' of the Academy of Finland. He has had visiting positions at the University of California at Berkeley and at the Universities of Freiburg and Bielefeld in Germany. He has published more than 100 original scientific articles. His research interests include algorithms and data structures, combinatorial pattern matching, and machine learning. He has worked on algorithmic problems in computational biology since the early 1980s. Dr. Ukkonen is a member of the Finnish Academy of Science and Letters. From 1999-2001, he was the chairman of the Finnish Society for Computer Science.

**Lisa Vawter** received the PhD degree in molecular evolution and population genetics from the University of Michigan in 1991. After a US National Science Foundation-NATO fellowship at the University of East Anglia and a Bunting Fellowship at Harvard, Dr. Vawter joined SmithKline Beecham (later Glaxo SmithKline) as a bioanalyst. She has worked as senior principal scientist in informatics at Aventis Pharma since 2001, where she specializes in phylogenetic algorithms and G protein-coupled receptors.



**Wing Hung Wong** is a professor of statistics and a professor of biostatistics at Stanford University. Before joining Stanford, he had held faculty positions at The University of Chicago, Chinese University, University of California at Los Angeles, and Harvard University. His research interests include mathematical statistics, Monte Carlo methods, and computational biology. His group has developed several methods and software for the analysis of microarray data, and is working on systematic approaches to understand gene regulation in development.