About the Contributors

Limin Angela Liu, PhD, obtained her BSc degree from Tsinghua University, Beijing and her PhD degree from Carnegie Mellon University, USA. After postdoctoral research at Johns Hopkins University, USA, she became Associate Professor at Shanghai Jiao Tong University. Her recent work includes the establishment of an ab initio method for the prediction of transcription factor binding sites and a novel “tethered-hopping model” for describing the effects of protein-protein interactions on the formation and stability of ternary protein-DNA complexes.

Dongqing Wei, PhD, is the acting head of the Department of Bioinformatics and Biostatistics, College of Life Science and Biotechnology, Shanghai Jiao Tong University, Shanghai, China, the editor-in-Chief of the journal “Interdisciplinary Sciences - Computational Life Sciences,” and the chairman of the International Association of Scientists in the Interdisciplinary Areas (IASIA). Prof. Wei’s research is in the general area of structural bioinformatics. He is best known for his ground-breaking work on theory of complicated liquids. He, along with Prof. Gren Patey, has found that strongly interacting dipolar spheres can form a ferroelectric nematic phase. This was the first demonstration that dipolar forces alone can create an orientationally ordered liquid state. It is also the first time that the existence of a ferroelectric nematic phase has been established for a model liquid. This discovery solved a long standing problem in theoretical physics, and created a new direction in search for new liquid crystal materials (Phys. Rev. Lett. 68, 2043, 1992, cited about 180 times). In recent years, Prof. Wei has developed tools of molecular simulation and applied them to study biological systems with relevance to computer-aided drug design and structural biology. With more than 150 journal papers and greater than 2000 citations (Science Citation Index), he is becoming a leading figure in the area of structural bioinformatics.

Yixue Li, PhD, was born in Xinjiang, China. Currently, he is the director in Shanghai Center for Bioinformation Technology, vice director and a full research professor of Key Laboratory of Systems Biology at Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Dr. Li received his BSc. and Msc. degrees in theoretical physics from Xinjiang University, China, in 1982 and 1987, respectively, and his PhD degree in theoretical physics from the University of Heidelberg, Germany, in 1996. After Dr. Li got his PhD degree he worked as a bioinformatics research staff in European Molecular Biology Laboratory (EMBL) from 1997-2000, and came back to Shanghai, China in the middle of 2000. Dr. Li’s research interests include bioinformatics, systems biology and computational biology. Dr. Li has published more than 100 journal papers in various international scientific journals, such as Science, Nature Genetics, Nature Biotechnology, PNAS, Bioinformatics, NAR, Plos Computational Biology, Plos One, Molecular Systems Biology, Molecular Cellular Proteomics, Oncogene, BMC Bioinformatics, Genome Biology, et cetera, and his research results have been cited by more than 1500 researchers worldwide in books, theses, journal and conference papers. Dr. Li has served as an editorial board member for 5 scientific journals.

Huimin Lei, MD, obtained her degree from Inner Mongolia University of Science and Technology, China in 2004. She then became a lecturer and academic advisor for medical students at Baotou Health School,
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China. Since 2008, she became an Assistant Editor for the journal “Interdisciplinary Sciences – Computational Life Sciences” and an office administrator of Prof. Dongqing Wei’s lab at Shanghai Jiao Tong University. She has served on the organizing committees of several international conferences, including “Theory and Applications of Computational Chemistry – 2008” (TACC2008) and the annual “International Conference on Computational and Systems Biology” (ICCSB) meeting series.

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Giacomo Aletti, PhD, is a Mathematician. In 2001 he gained a PhD in Probability Theory and Mathematical Statistics working on set-indexed stochastic processes. His current research is devoted to both theoretical aspects and applications. The former ones concern metrics and topologies in different probability spaces, random reinforced urn models, survival analysis in set-valued stochastic processes and the general theory of stochastic geometric processes, while the latter are focused on modelling of social behaviour and biological phenomena, collaboration with medical research (applied/methodological statistics, e.g. statistical planning and modelling) and with numerical research for interdisciplinary approaches. Currently, he is Assistant Professor at Università degli Studi di Milano, Italy.

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Fortunato Bianconi, PhD, was born in 1981. He received his Ph.D. degree in Information Engineering from University of Perugia, Italy in 2010, where he also received the MSc (Laurea) in Information and Communication Technology Engineering in 2006. He worked at University of California San Francisco as Junior Specialist at El-Samad Systems Biology Lab (2008-2009). His research interests are mainly related to systems biology, with a focus on the application of theoretical and mathematical tools from control engineering to the study of genetic networks. His research focuses on the systems biology of cancer.

Ghislain Bidaut, PhD, holds a doctorate in bioinformatics from the Université de la Méditerranée, with a focus on gene expression analysis and pattern recognition for his research work done with Michael Ochs’s group (Fox Chase Cancer Center). Later on, he was a postdoctoral fellow at the University of Pennsylvania (Chris Stoeckert’s group) working on large scale data integration in stem cell research. He did a second postdoctoral internship at the Institut Pasteur (Benno Schwikowski’s group) before joining the CRCM in January 2008 to run the Integrative Bioinformatics group. He is now focusing on large scale network analysis and heterogeneous data integration, databases and LIMS, and multiparametric flow cytometry analysis to discover novel prognostic markers in cancer.

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Christoph Brockel, PhD, leads the Translational and Bioinformatics function within Research Business Technologies at Pfizer Inc. since 2008. He is responsible for computational solutions that support target identification, interpretation of data to form mechanistic hypotheses and translational research within Pfizer. Prior to his current role, he was the head of US bioinformatics at Sanofi-Aventis and responsible for the development and application of gene expression and pathway analysis platforms. He has a Ph.D. in biophysics from the Université Louis Pasteur in Strasbourg, France.

Paola Causin, PhD, is an Aerospace Engineer. In 2003 she earned a PhD in Numerical Analysis, during which, she worked in the field of the numerical simulation of fluid-dynamics with applications to continuum mechanics problems. During her post-doctoral work, she was involved in an European Research Project working on fluid-structure interaction problems applied to physiological flows. Currently, she is Assistant Professor of Numerical Analysis at Università degli Studi di Milano, Italy. Her present scientific interests
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Jake Y. Chen, PhD, is an associate professor of informatics and computer science at the Indianapolis joint campus of Indiana University and Purdue University, where he teaches database systems, bioinformatics, and computational systems biology. He is the founding director of the Indiana Center for Systems Biology and Personalized Medicine, an associate editor of BMC Systems Biology, an ACM senior member, an IEEE senior member, and the central Indiana section chair of the IEEE Engineering in Biology and Medicine Society. He has more than 80 scientific publications that span broadly over biological data management, biological data mining, bioinformatics, systems biology, and personalized medicine. He has given more than 100 invited talks nationwide in bioinformatics. He also has six years of biotech R&D research and management experience, and has been active in high-tech entrepreneurship in both Silicon Valley and Indiana.

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Benjamin B. Currall is nearing completion of his graduate studies at Creighton University’s School of Medicine. He has studied under the tutelage of both Drs. Richard Hallworth and David Z. He is researching the structure-function relationship of prestin, the mammalian motor protein. These studies have included research in bioinformatics (examining sequence analysis), function (using electrophysiology), and structure (protein-protein interactions using molecular biology and advanced microscopy) of this unique motor protein. Before attending Creighton, Mr. Currall operated a therapeutic drug monitoring laboratory designing drug analysis methods using mass spectrometry at an HIV research clinic in Los Angeles. Mr. Currall received his BS in Biology and BA in Philosophy degrees at Santa Clara University.

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Wei Ding received his PhD from the State University of New York at Stony Brook in 1998. After working as a Fogarty Fellow in the National Center for Biotechnology Information (NCBI), he joined the Bioinformatics group at the Schering-Plough Research Institute (now Merck Research Laboratories) in 1999. He is also an adjunct professor in the Department of Biological Sciences at Kean University. His research interests include biomarker discovery, development and validation, -omics data mining and analysis, and systems
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Wenqing Feng obtained her PhD degree from Rutgers University in 1997, in the area of NMR structure determination of proteins. Prior to joining the Department of Drug Metabolism and Pharmacokinetics at Schering-Plough in 1999, Wenqing was a postdoctoral fellow in the Department of Structure Chemistry at Schering-Plough Research Institute. Her expertise resides in using NMR methods to solve problems of the pharmaceutical industry, including structure identification of organic molecules, quantitation, and NMR-based metabonomics. She chaired the North Jersey NMR group of American Chemical Society from 2006-2007, and a session in Eastern Analytical Symposium, 2008. Wenqing is currently a Principal Consultant at Accela Sciences, LLC.

Pascal Finetti earned a Master’s degree in Biochemistry at the Université de la Méditerranée (Marseille) in 1998. Next, he joined the group of Dr. Daniel Birnbaum as lab technician in the Molecular oncology laboratory at Institut Paoli-Calmettes (Marseille) where he has worked under Pr. Bertucci’s supervision until now. He manages an oligonucleotide-based microarray platform he set up in 2004 with the aim to profile tumors for the discovery of their taxonomy and markers. Furthermore, he is involved in research programs of the department to analyse large-scale genomic data at the RNA and/or DNA level.

Jean-François Ganghoffer, PhD, is a full Professor in Applied Mathematics and Mechanics of Materials. He received his PhD from Ecole des Mines in Nancy, France in 1992, and worked afterwards as a research fellow at CNRS. He was appointed to full Professor in 2000 at the Institut National Polytechnique de Lorraine, in Nancy. His present interests include biomechanics, covering growth of biological tissues and mechanobiology of the cell, symmetries in continuum mechanics, and the mechanics of fibrous materials. He has also been active in the fields of mechanics of interfaces, nonlocal mechanics, higher order gradient damage and plasticity. He is the author or coauthor of about 80 scientific publications and as many Conference papers.
Maxime Garcia holds a master’s degree in bioinformatics. During 2008, he followed an internship at Technological Advances for Genomics and Clinics (TAGC), working on the TranscriptomeBrowser. He joined the Integrative Bioinformatics team at the Centre de Recherche en Cancérologie de Marseille (CRCM) in March 2009 for his final internship. In November 2009, he began his PhD training on discovering biomarkers in breast cancer by interactome-transcriptome integration (ITI project). He is responsible for welcoming CRCM’s new students. He is also the webmaster of a student association (Hippo’Thèse) involved within his doctoral school (Ecole Doctorale des Sciences de la Vie et de la Santé).

Tian Ge is a PhD student in the School of Mathematical Sciences and Centre for Computational Systems Biology at Fudan University, Shanghai, People’s Republic of China. He received his bachelor’s degree in Mathematics from Fudan University in 2009. He will be a joint PhD student in the Centre of Scientific Computing at the University of Warwick, United Kingdom from 2010 to 2012 under a scholarship from the State Scholarship Fund. His research interests include computational neuroscience, systems biology and dynamical systems.

Richard Hallworth, PhD, was born in the United Kingdom, raised in Australia, and educated at the University of Melbourne, where he obtained bachelors and masters degrees in mechanical engineering. After a period working in the semiconductor industry, he moved to the United States, where he obtained the PhD degree in neuroscience from Baylor College of Medicine in Houston, Texas. After post-doctoral research in Houston and Chicago, he was appointed as Assistant Professor in the Department of Otolaryngology-Head and Neck Surgery of the University of Texas Health Science Center at San Antonio, Texas. He is now professor in the Department of Biomedical Sciences, Creighton University, in Omaha, NE.

Rui-Ru Ji received a PhD in Molecular Biology and an MS in Computer Science, both from Purdue University in West Lafayette, Indiana. She joined Celera Genomics in 2000 and is one of the co-authors of the human and mouse genome publications in the journal of Science. In 2002, Rui-Ru moved to New Jersey and joined Purdue Pharma L.P. where she built the bioinformatic infrastructure for the Discovery Research site. In 2005, Rui-Ru joined Bristol-Myers Squibb. She has developed a number of algorithms for data analysis, including a novel methodology for dose response transcriptional profiling, a MANOVA-based approach for gene set enrichment analysis, and methods for analyzing co-expression network transcriptional modules. Her current interests include next-generation sequencing analysis, GWAS, copy number analysis, and miRNA. She is now working closely with scientists in the Oncology and Immunology areas to identify and validate new targets for therapeutic interventions.

Awdhesh Kalia, PhD, is an Associate Professor of Microbiology at the University of Louisville. His work addresses the following two questions: (1) what are the molecular and evolutionary forces that shape and maintain genetic diversity in bacterial species? And (2) how does genetic diversity in bacterial species shape the outcome of host-pathogen interaction? Dr. Kalia graduated from the All India Institute of Medical Sciences, New Delhi and underwent postdoctoral training at Yale University and Washington University School of Medicine. He is a recipient of the Ralph Powe junior faculty enhancement award from ORAU, and a Young Investigator award from the International Chemotherapy Congress. Dr. Kalia has authored or co-authored over 35 research articles and book chapters.

Bin Li, PhD, worked as an experimental biologist, holds three patents, and published eight international papers during his PhD training in China. In 1999, he came to the United States and switched to computational work during his postdoctoral training at the University of Washington in Seattle, publishing six papers on molecular dynamics simulations of biomolecules. In 2003, Dr. Li joined Institute for Systems Biology as a senior scientist to work on the systematic study of large biological networks, focusing on statistical analysis.
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**Wei Liu, PhD**, graduated from Peking University in Applied Chemistry in 1987. He then obtained his M.Sc. in Polymer Chemistry from the Institute of Chemistry of the Chinese Academy of Sciences in 1990. He studied protein structure and dynamics in solution using fluorescence spectroscopy at Louisiana State University starting in 1991, and obtained his PhD in Biophysics in 1996. He subsequently performed his postdoctoral training at the University of California, Berkeley, in the laboratory of Dr. Stu Linn, studying the DNA replication and repair process. He joined Wyeth Bioinformatics in 2000, and has been focusing on the integrative, cross-platform data-mining and text-mining analytics to help move forward the drug discovery programs at Wyeth. He moved to Wyeth Systems Biology in 2008, supporting multivariate phenotypic profiling of autophagy-inducing compounds, and the genome-wide RNAi knockdown studies to look for new opportunities in drug combinatorial therapy. He joined Agios Pharmaceuticals in 2010, and is now leading an integrated Informatics team to support the drug discovery and development programs in Cancer Metabolism.

**Yan-Hui Liu, PhD**, is a Senior Principle Scientist at Merck. She received her PhD from University of Michigan in 1996. After one and a half years of post-doctoral work at Schering-Plough Research Institute (SPRI), she joined Mass Spectrometry/Structural Chemistry group in 1997. Dr. Liu is currently working at Merck Research Laboratories on protein mass spectrometry to characterize recombinant proteins and antibodies for drug targets / therapeutic purposes. She is also working on applying proteomic methods for drug
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**Eric Meslin**, PhD, is the Founding Director of the Indiana University Center for Bioethics, Associate Dean for Bioethics and Professor of Medicine, Medical and Molecular Genetics, Public Health and Philosophy. On May 9, 2007, he was appointed a Knight of the National Order of Merit by the President of France. Prior to joining Indiana University in 2001, he had been Executive Director of the National Bioethics Advisory Commission (NBAC) appointed by President Bill Clinton, and a Program Director in the Ethical, Legal and Social Implications (ELSI) program at the National Human Genome Research Institute. He has been a consultant to the World Health Organization, the US Observer Mission to UNESCO, the Canadian Institutes of Health Research and sits on several boards and committees. Dr. Meslin received his BA in Philosophy from York University in Toronto, and both his M.A. and PhD from the Bioethics Program in Philosophy at the Kennedy Institute of Ethics at Georgetown University. He has held many academic positions, including at the University of Toronto (1988-96) and at Oxford University (1994-95). He has more than 100 publications on topics ranging from international health research to science policy.

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Jason Moore, PhD, is a Frank Lane Research Scholar in Computational Genetics, a professor of Genetics and Community and Family Medicine at Dartmouth Medical School, and the associate director of Bioinformatics of the Norris Cotton Cancer Center at Dartmouth Hitchcock Medical Center in Lebanon, NH. His research focuses on understanding the role of genetic information in predicting susceptibility to common human diseases. His research program aims to develop, evaluate, distribute, and apply powerful computer algorithms and software for identifying combinations of genetic and environmental factors that are associated with complex clinical endpoints.

Stuart Murray, PhD, completed his PhD research at the University of Newcastle-upon-Tyne, UK, studying the regulation of hormone receptors. His Post-doctoral research was carried out at the Albert Einstein College of Medicine, Bronx, NY. During his post-doctoral work, he identified and characterized basal transcription factors and studied the role transcription factors play in cellular differentiation. He then joined Wyeth Research’s Information Management group where he pioneered literature informatics by introducing text-mining technologies to Wyeth Research. Following a transition to the Systems Biology Group, he worked to fully combine literature analytics with bioinformatics analytics to create an integrated analytics platform. More recently, he has had the opportunity to join a dynamic biotechnology company to develop integrated analytics in cancer metabolism research.

Giovanni Naldi, PhD, is a Mathematician. He earned a PhD in Applied Mathematics in 1993. He has been a visiting Professor in institutions in Germany, Japan and USA. Since 2001, he is full professor in Numerical Analysis at University of Milano, Italy. He is Scientific coordinator of national and international research projects and Director of the ADAMSS (ADVanced Applied Mathematical and Statistical Sciences) Center of University of Milano; he serves on the editorial board of several international Journals. His research interests include numerical and theoretical analysis of mathematical models in physiology and neurophysiology, statistical models in epidemiology, wavelet bases for image processing and partial differential equations, numerical methods for kinetic equations, and mathematical models of cell chemotaxis.

Madhusudan (Madhu) Natarajan, PhD, is a Principal Scientist at Pfizer in the Quantitative Biotherapeutics Modeling group in Cambridge, MA. He uses systems biology approaches to develop mechanistic understanding of disease indications and leverages that provide insights to the design of biotherapeutics. Madhu’s initial training was in Electronics and Communication Engineering, and he went on to graduate studies in Biomedical Engineering and Neurobiology. He received his Ph.D. from Northwestern University, IL, where he investigated sources of sympathetic rhythm generation, which forms the basis of mammalian cardiovascular control. As a member of the research faculty in the Department of Pharmacology at the University of Texas Southwestern Medical Center (UTSWMC), Madhu was part of the Alliance for Cellular Signaling (AfCS) - a multi-investigator multi-university research collaboration whose goal was to comprehensively address how cells interpret signals in a context-dependent manner. His subsequent work at UTSWMC with Dr. Rama Ranganathan applied analysis of information transduction within proteins to engineer protein chimeras with novel function.
Wilfred Ndifon, PhD, is a Postdoctoral Fellow in Immunology at the Weizmann Institute of Science in Rehovot, Israel. His primary interest is in the development of immunologically grounded approaches to controlling the spread of disease.

Youlian Pan, PhD, is a Research Officer and Project Leader in the Knowledge Discovery group, Institute for Information Technology, National Research Council (NRC), Canada. Prior to joining NRC, Youlian was a Lecturer in Biology at Saint Mary’s University, Halifax, Canada; Postdoctoral Research Associate in Marine Biomedicine and Environmental Sciences at the Medical University of South Carolina, Charleston, USA; and Research Associate at the Institute of Oceanology, Chinese Academy of Science, Qingdao, China. He received his M.Sc. in computer science and Ph.D. in Biology from Dalhousie University, Halifax, Canada in 2002 and 1994, respectively. His research interests include bioinformatics, functional genomics, transcription regulation, systems biology, data mining, and machine learning. Currently, Youlian serves in numerous editorial boards of international journals, such as Current Bioinformatics, The Open Medical informatics, The Open Applied Informatics Journal, and The Open Bioinformatics Journal. Youlian also serves on numerous national and international research grant review panels.

Kristine Pattin, PhD, received her BS degree from Boston College in biology with a minor in environmental studies. In 2010, she received her PhD in genetics at Dartmouth College where she investigated approaches to ease the computational burden of detecting epistasis, or gene-gene interactions, in genome-wide studies. Specifically, she explored approaches that integrate expert knowledge from protein-protein interaction (PPI) databases into the analysis process. Other research experience has brought Kristine to work with IDEXX Laboratories in Westbrook, ME, in the area of laser immunodiagnostics and at Enanta Pharmaceuticals in Watertown, MA, in discovery biology. She is currently a research associate at Dartmouth College participating in the nation-wise eagle-I consortium for discovering and making research resources visible across the country.

Victoria Petri, PhD, is a Research Scientist at the Rat Genome Database (RGD), Bioinformatics Program, Human and Molecular Genetics Center, Medical College of Wisconsin. Before joining RGD, she was a post-doctoral fellow in the Chemistry Department at Northwestern University. She holds a diploma from a European Conservatory of Music, a Master in Library and Information Science from Columbia University and a Ph.D. in Biochemistry from Albert Einstein College of Medicine; her interests span many areas of research. At RGD, she has initiated and developed the pathway project; as such, she is interested in understanding how the structure-function correlations of biological macromolecules mold their reactions, recognitions, and interactions, as well as how these events entwine into complex molecular networks, how these networks integrate to shape the behavior of biological systems, and how malfunctioning in parts of the system can lead to the diseased phenotype.

George V. Popescu, PhD, received a PhD degree from Rutgers University in 2001. He is currently a senior researcher at the University Politehnica of Bucharest, Romania. He was with IBM TJ Watson Research Center between 2001 and 2004, performing research in the System Modeling and Optimization group. Between 2004 and 2006, he was a postdoctoral researcher at the Center for Excellence in Genomics Sciences at Yale University, New Haven. His main research interest is analyzing the complexity and dynamics of cell signaling and transcription networks. He is conducting research on stochastic modeling for epigenetics, chromosomal variation analysis and cellular differentiation. He is currently a member of the International Society for Computational Biology, Association for Computing Machinery and Society for Industrial and Applied Mathematics and has formerly been a member of IEEE and INFORMS.

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Jack A. Tuszynski, PhD, is the Allard Chair and a professor in the Department of Oncology. The major thrust of his computational biophysics group is in silico drug design for cancer chemotherapy applications and in vitro testing. His research interests are strongly linked to the protein tubulin and the microtubules assembled from it. Due to its prominent role played in eukaryotic cell division, tubulin is an important target for anti-cancer cytotoxic treatments. His on-going research aim is to identify variants of known compounds showing greater tubulin isotype-specific effects, which could potentially lead to more efficacious chemotherapy treatments with lower side effects. Other studies in his group have examined microtubule electrical, structural, and mechanical properties; proteins that bind to microtubules (MAPs); and the motor proteins in cells that travel along microtubules and actin filaments. The group is also developing physiologically-based models and simulations for pharmacokinetic and pharmacodynamic applications.

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