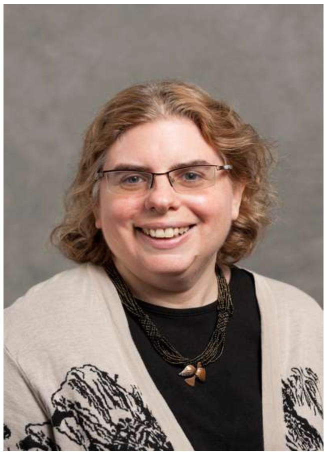

Lenore J. Cowen

Tufts University

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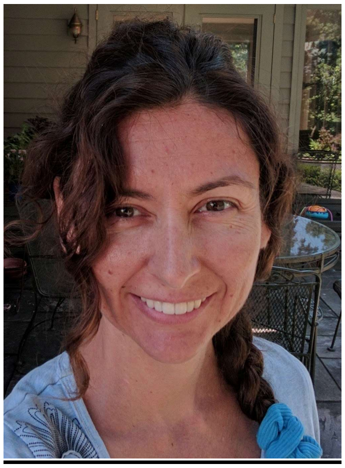
Bio-Sketch

Dr. Lenore J. Cowen is a Professor in the Computer Science Department at Tufts University. She also has a courtesy appointment in the Tufts Mathematics Department. She received a BA in Mathematics from Yale and a Ph.D. in Mathematics from MIT. After finishing her Ph.D. in 1993, she was an NSF Postdoctoral Fellow. and then joined the faculty of the Mathematical Sciences Department (now the Applied Mathematics and Statistics department) at Johns Hopkins University, where she was promoted to the rank of Associate Professor in 2000. Lured by the Boston area, and the prospect of making an impact in a growing young department, she joined Tufts in September, 2001. Dr. Cowen has been named an ONR Young Investigator and a fellow of the Radcliffe Institute for Advanced Study. Her research interests span three areas: Discrete Mathematics (since high school), Algorithms (since 1991 in graduate school) and most recently Computational Molecular Biology, where she focuses on predicting protein function, from structural and biological network information. She is on the Editorial Board of the IEEE/ACM Transactions of Computational Biology and Bioinformatics (TCBB). She is married to a computer systems geek, and Is the proud Mom of two teenage daughters.



Tamsen Dunn

Illumina

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Bio-Sketch

Tamsen Dunn is a genomic algorithms scientist at Illumina, Inc. Her research interests include disruptive and emerging technologies, open source software, open science, sequencing data analytics, simulations and algorithms, autonomous systems, robotics, somatic variant calling and oncology. She currently leads the Pisces Project at Illumina. Pisces is the default somatic variant caller on many of Illumina's sequencing platforms, such as the MiSeq and BaseSpace, and is available on github. Before joining Illumina, Tamsen worked on various disruptive technology projects at Northrop Grumman Space Technology. Her graduate studies were done at the Center for Astrophysics and Space Sciences at the University of California at San Diego. Tamsen is a rock climber and avid out door enthusiast.

Nurit Haspel

University of Massachusetts Boston

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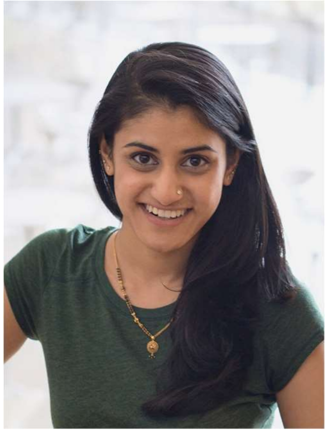
Bio-Sketch

Nurit Haspel received her BSc, MSc and PhD from Tel Aviv university in Israel. She later did a 2 year postdoctoral work at the Department of Computer Science at Rice University in Houston, TX and in 2009 she joined the department of Computer Science at UMass Boston where she is now an associate professor. Her research area is structural bioinformatics - the application of computational methods to solving key biological problems. Specifically, she develops and applies computational algorithms based on concepts taken from computational geometry, graph theory and robotics to model the structure, function and dynamics of proteins and biomolecular interactions. Other research interests include genomics, machine learning and statistical methods in bioinformatics.

Her research has been funded by grants from the National Science Foundation and the Massachusetts Green High Performing Computing Center.



Shilpa Nadimpalli Kobren

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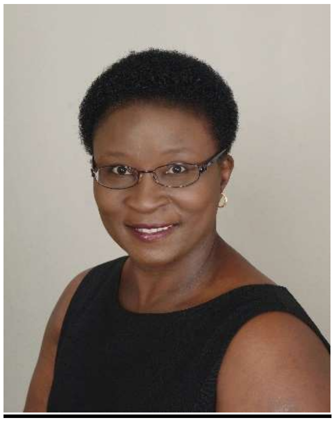
Bio-Sketch

Shilpa N. Kobren received her B.S. in Biology & Computer Science from Tufts University, where she worked on protein structural alignment problems with Dr. Lenore Cowen. She is currently a Ph.D. candidate at Princeton University working under Dr. Mona Singh. Her dissertation has focused on developing novel computational approaches to detect and interpret protein interaction and cellular network perturbations across species and within individuals in a population. Shilpa is a recipient of an NSF Graduate Research Fellowship, Google Anita Borg Memorial Scholarship, Siebel Scholarship, and Princeton Gordon Wu Fellowship.



Dr. Margaret Okomo-Adhiambo, DVM, PhD, MPH

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Bio-Sketch

Dr. Margaret Okomo Adhiambo is a Health Scientist and Bioinformatics Lead at the Office of Informatics, NCIRD, CDC. She holds a doctorate in Veterinary Medicine from the University of Nairobi, a PhD in Cell and Molecular Biology from the University of Nevada-Reno, and a Master of Public Health (Applied Epidemiology) from Emory University. Dr. Okomo has over 15 years' experience in conceiving, implementing and directing scientific studies aimed at detection, control and prevention of infectious diseases. She has extensive experience and knowledge of methodologies used to manage and analyze scientific data from complex studies related to a broad range of public health topics. In her current position, she provides scientific advice and leadership in the development and implementation of novel bioinformatics solutions for scientific data management and analysis, and their application to the federal government's policies on vaccines, therapeutics, diagnostics, emergency response preparedness and laboratory capacity building. Dr. Okomo has published over 50 scientific articles, including book chapters and technical reports, and has presented over 40 conference abstracts. She lives in Atlanta, GA, with her husband and three children.

Dagmar Ringe

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Bio-Sketch

My laboratory is focused on two broad areas of biomedical research: the structural basis for the catalytic power of enzymes and the prevention and treatment of age-related neurodegenerative diseases. The unifying theme that combines these two is the development of methods for the identification of function for proteins of unknown function and methods for drug design.

Together with my colleague Prof. Gregory Petsko, we have employed a combination of X-ray crystallography, site-directed mutagenesis, kinetics, organic synthesis and computational methods to identify active sites and to probe the mechanisms of action of enzymes and the role of protein dynamics in protein function. My own research was focused for some time on pyridoxal phosphate-dependent enzymes. I determined the first structures of most of the different family members in the broad class of PLP-utilizing proteins, and worked out detailed mechanisms of action for them and their interactions with inhibitors and inactivators. I contributed many of the original studies that established the structural basis of enzymic catalytic power, and the role of protein dynamics in protein function. Greg Petsko and I developed most of the techniques now in use for trapping unstable enzyme intermediates and determining their structures by crystallography, and were the first to apply them to many enzymes.

The above approaches are now being used to develop screens and multiple drug design methods, such as experimental and computational fragment based screening, and computational approaches to identification of binding sites and lead compounds.

Jérôme Waldispühl

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Jérôme Waldispühl conducts research in computational molecular biology with a strong emphasis on RNA & protein sequence/structure analysis and prediction. He also contributed to pioneer applications of crowdsourcing and human-computing techniques in bioinformatics.

Jérôme received a PhD in Computer Science from École Polytechnique (France) in 2004 under the mentorship of Jean-Marc Steyaert. From 2005 to 2006, he was a post-doctoral researcher with of Peter Clote in the department of Biology at Boston College. In 2006, he moved to the Massachusetts Institute of Technology where he was and instructor in applied mathematics under the mentorship of Bonnie Berger. In 2009, he joined the School of Computer Science at McGill University as an assistant professor, and got promoted associate professor with tenure in 2015.

Jérôme was the recipient of a Tomlinson Scientist Award in 2012, and the Fessenden Professorship in Science Innovation in 2013.

Tandy Warnow

University of Illinois at Urbana-Champaign

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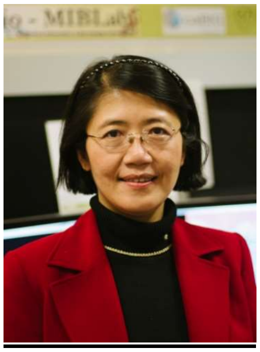
Bio-Sketch

Tandy Warnow is the Founder Professor of Computer Science, a member of the Carl R. Woese Institute for Genomic Biology, an affiliate in the National Center for Supercomputing Applications and in the departments of Statistics, Mathematics, Animal Biology, Entomology, and Plant Biology at the University of Illinois at Urbana-Champaign. Tandy received her PhD in Mathematics in 1991 at the University of California at Berkeley under the direction of Eugene Lawler. She received postdoctoral training with Simon Tavaré and Michael Waterman at the University of Southern California from 1991-1992, and at Sandia National Laboratories from 1992-1993. Tandy was on the faculty at the University of Pennsylvania from 1994-1999 and at the University of Texas from 1999-2014, before joining the faculty at the University of Illinois in 2014. Tandy received the National Science Foundation Young Investigator Award in 1994, the David and Lucile Packard Foundation Award in Science and Engineering in 1996, a Radcliffe Institute Fellowship in 2006, and a Guggenheim Foundation Fellowship for 2011. She was elected a fellow of the Association for Computing Machinery (ACM) in 2016 and of the International Society for Computational Biology in 2017.



May Dongmei Wang, Ph.D.

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Bio-Sketch

Dr. May Dongmei Wang is a full professor in the Joint Biomedical Engineering Department of Georgia Tech and Emory University, a Kavli Fellow, a Georgia Cancer Coalition Scholar, Georgia Tech Petit Institute Faculty Fellow, Director of Biomedical Big Data Initiative, and a Fellow of the American Institute for Biological and Medical Engineering (AIMBE). She earned BEng from Tsinghua University China, and MS and PhD from Georgia Institute of Technology. Her research is in Biomedical Big Data Analytics with a focus on Biomedical and Health Informatics (BHI) for predictive, personalized, and precision health (pHealth). In FDA-organized MAQC international consortium, she led the comprehensive RNA-Seq data analysis pipeline study. Dr. Wang published over 200 peer-reviewed conference and journal articles in referred journals (e.g. Briefings in Bioinformatics, BMC Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal of American Medical Informatics Association, Journal of Biomedical and Health Informatics-JBHI, Journal of Pathology Informatics, Proceedings of National Academy of Sciences-PNAS, Annual Review of Medicine, Nature Protocols, Circulation Genetics, IEEE Trans. on Biomedical Engineering-TBME etc.) and conference proceedings, and delivered more than 200 invited and keynote lectures. She received Outstanding Faculty Mentor Award for Undergraduate Research at Georgia Tech, and a MilliPub Award (for a high-impact paper that has been cited over 1,000 times) from Emory University.

Dr. Wang has served as an Emerging Area Editor for PNAS, Senior Editor for JBHI, an Associate Editor for TBME, and a panelist in NIH, and NSF review panels. She has helped organize ACM Bioinformatics, Computational Biology, and Health Informatics Conferences and IEEE International Conference on Biomedical and Health Informatics. Dr. Wang is elected as the Vice Chair for 2018 Gordon Research Conference (GRC) on Advanced Health Informatics, and has served in IEEE Big Data Initiative (BDI) Steering Committee. Dr. Wang is Georgia Tech Biomedical Informatics Program Co-Director in Atlanta Clinical and Translational Science Institute (ACTSI), and Co-Director of Georgia-Tech Center of Bio-Imaging Mass Spectrometry. Her research has been supported by NIH, NSF, CDC, Georgia Research Alliance, Georgia Cancer Coalition, Emory-Georgia Tech Cancer Nanotechnology Center, Children's Health Care of Atlanta, Atlanta Clinical and Translational Science Institute (ACTSI), and industrial partners such as Microsoft Research and HP.