

Industry Panel at ACM BCB: Experiences from the trenches

Join us for a lively panel discussion to learn first-hand about career paths in industry. The panelists will describe their career paths, and discuss the most joyous and challenging parts of their jobs. In addition, the panelists will provide tips and best practices on training for, finding and succeeding in industry jobs.

Panelists

Chu-Fang (Bamboo) Lin
Principal Bioinformatics Scientist
Roche Diagnostics, Pleasanton, CA

Bamboo Lin is a Principal Bioinformatics Scientist at Roche, where she develops bioinformatics workflows and integrates computer science, statistics, and engineering to analyze NGS data. She enjoys working at the interface between the wet lab, product development, and business development.

Bamboo received a B.S. degree in Power Mechanical Engineering and a M.S. degree in Electrical Engineering, both from National Tsing-Hua University in Taiwan. She received her Ph. D. degree in Electrical Engineering from Pennsylvania State University, with a focus on developing machine learning algorithms for medical image analysis.

Bamboo has startup experience at Vizyontech Imaging, Inc., where she worked with a team to advance ultrasound imaging on breast cancer detection. In 2013, Bamboo made a career transition to the bioinformatics field with a passion for applying machine learning algorithms to solve bioinformatics problems and taking part in innovating medical technologies. She has been enjoying working in this challenging but very rewarding field.

Other than being a bioinformatician, Bamboo enjoys backpacking, swimming, and trail running.

Malika Mahoui
Senior Research Scientist
Eli Lilly and Company, Indianapolis, IN

Malika Mahoui is a Senior Research Scientist at Eli Lilly and Company. She Holds a PhD in Computer Science and an Mph in public health. Previously she held several academic positions at universities including her more recent faculty position with the School of Informatics at IUPUI. Her current research interests lie in the areas of data and text mining applied to health.

Sangtae Kim
Senior Bioinformatics Scientist
Illumina, San Diego, CA

Dr. Sangtae Kim is a senior bioinformatics scientist at Illumina. Prior to joining Illumina, he was a senior research scientist at Pacific Northwest National Laboratory. He received B.S. and M.S. in Computer Science at Seoul National University, and Ph.D. in Computer Science at University of California, San Diego.

Dr. Kim's early research efforts focused on computational proteomics, in particular developing algorithms for identification of peptides and intact proteins via mass spectrometry. He developed several software tools, including MS-GF+, a widely used database search engine for peptide

identification. At Illumina, he is focusing on improving DNA variant analysis to inform clinical decision making and medical research. Recently, he and his colleagues developed Strelka, a fast and accurate small variant caller for next-generation sequencing data.

Dr. Kim organized and co-chaired several conferences on computational proteomics, including the RECOMB satellite conference on computational proteomics. He was a coordinator of the bioinformatics interest group at the American Society for Mass Spectrometry (ASMS), and a member of the proteome informatics research group at the Association of Biomolecular Resource Facilities (ABRF) for organizing the community-wide studies. In 2015, he was highlighted in GenomeWeb as a young investigator doing promising work.

Henry van den Bedem

Senior Staff Scientist, Manager at SLAC National Accelerator Laboratory / Stanford University, CA

Henry's group is interested in uncovering the 3-D structure and dynamics of biomolecules, such as protein and RNA, from experimental data. They are creating, implementing and applying robotics-inspired, kinematics-based computational methods to automate accurate protein structure determination, identify and model polymorphism, and compute spatiotemporal, conformational distributions. A key challenge is that their systems are very high-dimensional and highly underdetermined, which requires sophisticated conformational search methods and complex optimization algorithms.

Enoch Huang, Pfizer

Head of Computational Sciences, Pfizer R&D

Cambridge, MA

Enoch S. Huang received an AB in Molecular Biology from Princeton and a PhD in Structural Biology from Stanford, where he was a NSF Pre-doctoral Fellow with Prof. Michael Levitt. He was a Jane Coffin Childs Fellow at Washington University School of Medicine. After starting his computational biology career at Cereon Genomics, he joined Pfizer's Cambridge laboratories in 2000. In 2001, he was appointed Head of Molecular Informatics and joined the site leadership team. In 2007 he accepted a global role as Head of Computational Sciences.

Enoch has been an Adjunct Assistant Professor of Bioinformatics at Boston University since 2001. He has served on external advisory boards for Drug Discovery Today, Brandeis University, the International Society for Computational Biology, the NIH "Illuminating the Druggable Genome" program, the Rochester Institute of Technology, and the Minnesota Supercomputing Institute. Enoch has also served on the program committees at the New York Academy of Sciences, the Massachusetts Biotechnology Council, and on NIH study sections. He has authored over 30 publications and released the Open Source software package PFAAT.

Moderator:

Soha Hassoun

Professor

Tufts University

Soha Hassoun is Professor at the Department of Computer Science at Tufts University. She holds secondary appointments in the Department of Electrical and Computer Engineering and also in the Department of Chemical and Biological Engineering at Tufts. Dr. Hassoun was a

recipient of the NSF CAREER Award, and several awards from ACM/SIGDA for her service, including the Distinguished Service Award in 2000 and 2007, and the 2002 Technical Leadership Award. She held executive and technical leadership positions for several conferences and workshops, including DAC, ICCAD, IWLS, and TAU. She was ICCAD Technical Program Chair in 2005, ICCAD Vice Chair in 2006, ICCAD Chair in 2007, DAC Technical Program Co-Chair in 2011 and 2012, DAC Vice Chair in 2013, and DAC Chair in 2014. She co-founded the International Workshop on Bio-Design Automation in 2009. She was an Associate Editor of the IEEE Transactions On Computer-Aided Design and of the IEEE Design and Test magazine. In 2013, she was recognized by the Electronic Design Automation Consortium as one of 33 luminaries in the field of Electronic Design Automation. She served on the IEEE Council on Design Automation, and was Director of Educational Activities for ACM's Special Interest Group on Design Automation for several years. She is a fellow of Tau Beta Pi, a senior member of IEEE, and a member of ACM and Eta Kappa Nu.