

Prof. Kasif is a Professor of Bioengineering, Bioinformatics and Computer Science at Boston University and is also affiliated with the Children's Hospital Informatics Program Harvard-MIT Division of Health Sciences and Technology (CHIP@HST).

Prof. Kasif is a co-founder and co-director of the Center for Advanced Genomic Technology (CAGT) with Charles DeLisi, co-founder of COMBEX: COMPUTATIONAL BRIDGE TO EXPERIMENTS PROJECT with Rich Roberts and Martin Steffen, www.combex.org, combex.bu.edu), and a member of the I2B2 Center (Informatics for Integrating Biology and Bedside) at Harvard Partners (www.i2b2.org). He was a participant in the Human Genome Consortium that produced the first public draft of the human genome.

His contributions to Computational Biology include the co-development of multiple systems and frameworks that include: Glimmer, one of the most widely used gene finders in the community (with Steven Salzberg and Art Delcher), Mummer, the first whole genome comparative alignment system (with Salzberg and Delcher), early advocacy of the use of Bayesian probabilistic networks in Computational Biology (1992), introduction of probabilistic functional linkage networks (with Stan Letovsky) for gene function prediction, and an early deployment of network signatures of disease (with Zak Kohane and Manway Liu) for diabetes as part of I2B2 activities. The most recent COMBEX project is a first of a kind community implementation of the Active Learning paradigm in biological computing. This project (in part) is funding community experiments which are explicitly prioritized based on their expected impact on increasing both the coverage and the accuracy of predictions produced by computational models.

In his previous life as a faculty in AI/CS at Johns Hopkins University Prof. Kasif contributed to several new concepts and popular systems in knowledge representation, constraints systems, probabilistic reasoning and machine learning.

Dr. Kasif has served the editorial boards of many journals in AI, Machine Learning, Constraint Systems, Computational Biology and Bioinformatics and and the co-author of numerous papers published in venues as such AI Journal, Foundations of Computer Science (FOCS), Nature, Nature Biotechnology, Nature Biochemistry, Nature/Embo Mol. Systems Biology, PLoS Biology, PLoS Genetics and Genome Research.