

**Genome annotation,
with implications for
biomarkers**

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A central problem for 21st century science is annotating the human genome and making this annotation useful for the interpretation of personal genomes. My talk will focus on this problem. I will describe an overall framework for data integration that brings together different evidence to annotate features such as binding sites and ncRNAs. Much of this work has been carried out within the ENCODE and modENCODE projects, and I will describe my approach interchangeably both in human and various model organisms (e.g. worm). I will further explain how many different annotations can be inter-related to characterize transcription in the intergenic space, build regulatory networks, and identify fusion genes. This work has clear implications for biomarker discovery.

Biography

Mark Gerstein is the Albert L Williams professor of Biomedical Informatics at Yale University. He is co-director the Yale Computational Biology and Bioinformatics Program, and has appointments in the Department of Molecular Biophysics and Biochemistry and the Department of Computer Science. He received his AB in physics summa cum laude from Harvard College and his PhD in chemistry from Cambridge. He did post-doctoral work at Stanford and took up his post at Yale in early 1997. Since then he has published appreciably in scientific journals. He has >400 publications in total, with a number of them in prominent journals, such as Science, Nature, and Scientific American. His research is focused on bioinformatics, and he is particularly interested in large-scale integrative surveys, biological database design, macromolecular geometry, molecular simulation, human genome annotation, gene expression analysis, and data mining.