

Statistical machine learning and computational biology
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Statistical machine learning is a field that combines algorithmic ideas with foundational concepts from probability and statistics. This combination makes statistical machine learning an essential tool for computational biology, in part because probabilistic notions are inherent in biology (arising, e.g., via thermodynamics, recombination and germline mutation) and in part because of the incomplete nature of most biological data sets. I will present several examples of applications of statistical machine learning to problems in biology, in the areas of protein functional annotation, protein structural modeling, protein structure prediction and multi-population linkage and association analysis.

Michael Jordan is Professor in the Department of Electrical Engineering and Computer Science and the Department of Statistics at the University of California, Berkeley. He received his Masters from Arizona State University, and earned his PhD in 1985 from the University of California, San Diego. He was a professor at the Massachusetts Institute of Technology from 1988 to 1998. He has published over 250 research articles on topics in computer science, statistics, electrical engineering, molecular biology and cognitive neuroscience. His research in recent years has focused on probabilistic graphical models, kernel machines, nonparametric Bayesian methods and applications to problems in computational biology, information retrieval and signal processing. Prof. Jordan was named a Fellow of the American Association for the Advancement of Science (AAAS) in 2006. He is a Fellow of the IMS, a Fellow of the IEEE and a Fellow of the AAI.