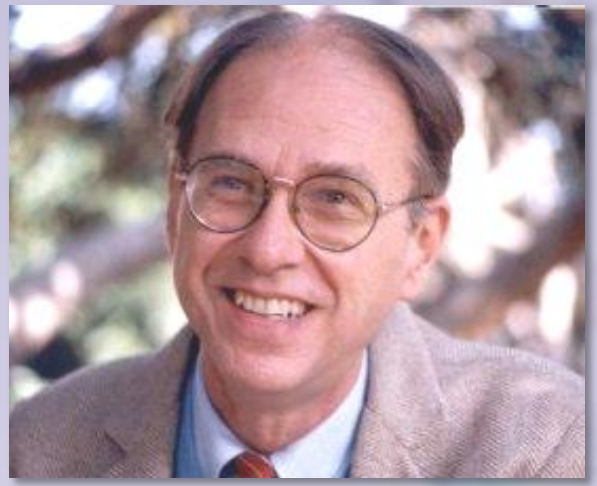
Tsinghua University

清华大学信息科学技术学院
清华信息科学与技术国家实验室
清华大学生物信息学教育部重点实验室

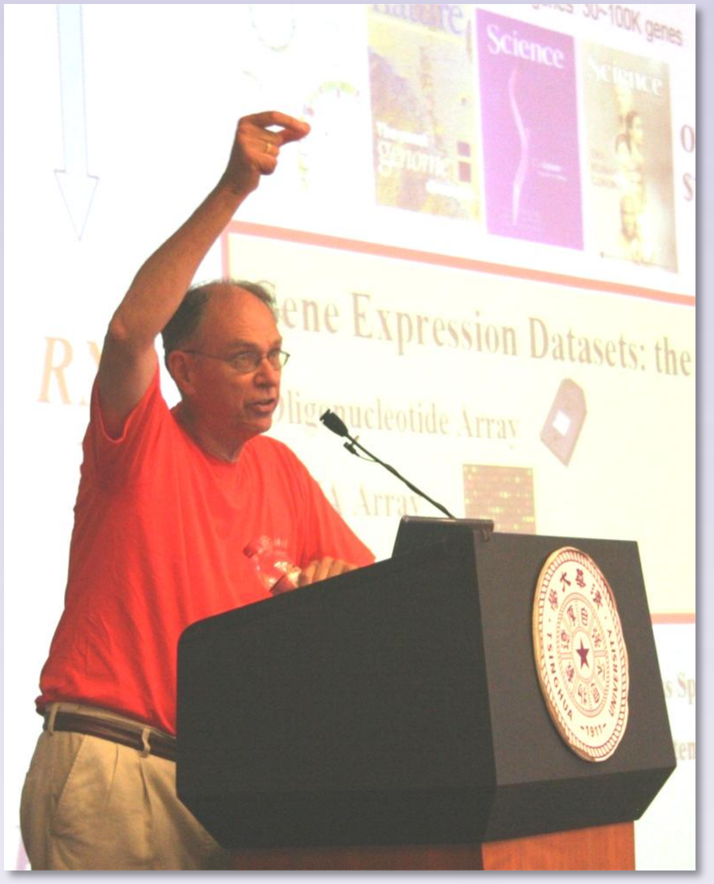
地点： 清华大学 FIT 多功能厅
时间： 2008年5月22日 （星期四）
上午 10:00-11:30

Michael S. Waterman 讲席教授组聘任仪式暨学术报告会

Michael S. Waterman 教授简介



Professor Michael S. Waterman holds an Endowed Associates Chair at University of Southern California. He received his Ph.D. in Statistics and Probability from Michigan State University. After that, he worked at Los Alamos National Laboratory and Idaho State University and joined University of Southern California in 1982. He was named a Guggenheim Fellow (1995), was elected to the American Academy of Art and Sciences (1995), and was elected to the National Academy of Sciences of the United States of America (2001). He is a Fellow of the American Association for the Advancement of Science and a Fellow of the Institute of Mathematical Statistics. In 2000, he became the first Fellow of Celera Genomics. In 2002, he received a Gairdner Foundation International Award. In 2005, he was elected to the French Académie des Sciences. As a professor of Mathematics, Computer Science, and Biology, he works in the area of Computational Biology and Bioinformatics, concentrating on the creation and application of mathematics, statistics, and computer science to molecular biology, particularly to DNA, RNA, and protein sequence data. He is the co-developer of the Smith-Waterman algorithm for sequence comparison and of the Lander-Waterman formula for physical mapping.



学术报告题目及内容

Title: Bioinformatics and Systems Biology

Speaker: Professor Michael S. Waterman

Abstract: This lecture provides a brief description of the growth of bioinformatics and an overview on some of the important problems in that period. With an introduction to the accomplishments that are closely linked to DNA sequencing and associated computational problems, each member of the Chair Professor Team is discussed in the context of his achievements.

讲席教授组其他成员简介

Professor Michael Q. Zhang received his Ph.D. in Physics from Rutgers University in 1987 and is now a professor in the Cold Spring Harbor Laboratory. He works in the area of computational biology and bioinformatics, focusing on the development of statistical and computational pattern recognition methods that can be combined with advanced biological experimental technologies to identify functional genetic elements within molecular sequences and pathways that control and regulate gene expression. His recent work focuses on the identification of genetic and epigenetic cis-regulatory elements, genome/chromatin organization, and gene regulation networks.

Professor Wing Wong is a professor of Statistics and of Health Research and Policy in Stanford University. His lab develops methods and software for the analysis of the data from high throughput genomics projects. He develops and enhances tools in exploratory data analysis, multivariate analysis, information theory, machine learning, Monte Carlo, graph theory, linear and nonlinear differential equations, and applies them to problems in computational biology and systems biology. Of particular interest is the combined use of experimental and computational analysis to clarify cis-regulatory mechanisms underlying several developmental processes.

Professor Jun Liu received his Ph.D. in Statistics from University of Chicago in 1991 and is now a professor of Statistics in Harvard University. He received the 2002 COPSS Presidents' Award that is given annually to a young individual in recognition of outstanding contributions to the profession of statistics. He works in the area of computational biology, bioinformatics, and statistical genetics, with particular interests in the application of Bayesian inference and Markov Chain Monte Carlo (MCMC) methods to deal with statistical missing data problems.

Professor Tao Jiang received his Ph.D. in Computer Science from University of Minnesota in 1988 and is now a professor of Computer Science in University of California, Riverside. His research interests include design and analysis of algorithms, computational biology and bioinformatics, and complexity of finite automata based models. His recent work focuses on efficient algorithms for comparison of annotated sequences, comparative plant/bacterial genomics, probe set design and cluster analysis for oligonucleotide fingerprinting of ribosomal RNA genes, search for transcription factor binding sites, and haplotype inference on pedigrees.

Professor Fengzhu Sun received his Ph.D. in Applied Mathematics from University of Southern California in 1994 and is now a professor of Mathematics and Biology in University of Southern California. He works in the area of computational biology and bioinformatics, statistical genetics, and mathematical modeling. His research interests include protein-protein interaction networks, single nucleotide polymorphisms (SNPs), gene expression, linkage disequilibrium (LD), and their applications in gene regulatory networks, the prediction of protein functions, and the identification of disease genes.

School of Information Science and Technology, Tsinghua University. Tsinghua National Laboratory for Information Science and Technology. Ministry of Education Key Laboratory of Bioinformatics.