

# IMS Public Lecture

FREE  
ADMISSION

**Speaker:** Professor Martin Tompa  
*University of Washington, USA*

**Date:** Wednesday, 19 July 2006

**Time:** 6:30 p.m. – 7:30 p.m.

**Venue:** LT33 (SoC 1, #02-36)  
School of Computing, NUS  
3 Science Drive 2,  
Singapore 117543

## The Role of Mathematics and Computer Science in Molecular Biology Research



### About the Speaker

Professor Martin Tompa graduated from Harvard University in 1974 and received his Ph.D. in Computer Science from the University of Toronto in 1978. For the next 7 years he was on the Computer Science faculty at the University of Washington, where he received an NSF Presidential Young Investigator Award in 1984, the inaugural year for these awards. From 1985 to 1989 he was on the staff of the IBM Research Division at the Thomas J. Watson Research Center, and became manager of its Theory of Computation group. In 1989 he rejoined the Computer Science faculty at the University of Washington, and in 1998 and 1999 received the first two ACM Undergraduate Teaching Awards.

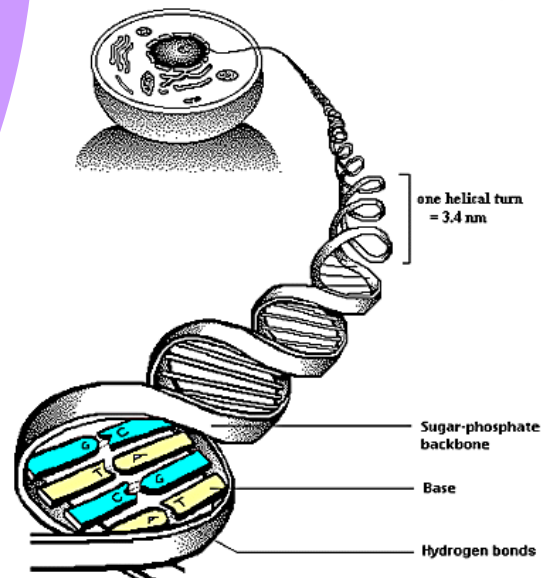
Professor Tompa's research interests are in computational complexity and computational molecular biology, with emphases on biological sequence analysis and regulatory analysis.

### Abstract

What role do mathematicians and computer scientists have to play in the genome projects that have revolutionized biology over the past decade? The speaker will try to give some indication by looking in some depth at two particular problems in the analysis of biological sequences. One is an overview of how the human genome was sequenced. The other is called "phylogenetic footprinting", and is a method for discovering functional regions of DNA by comparing the DNA sequences of multiple species.

No prior knowledge of mathematics, computer science, or molecular biology will be assumed.

### THE STRUCTURE OF DNA



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