

## Molecular and Network Modelling in Biology

### Professor Bruce Tidor

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Singapore-MIT Alliance for Research and Technology (SMART)

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**Time:** 4pm to 5pm

**Venue:** Perseverance Room, Enterprise Level 5



### Abstract

Computational methods offer tremendous potential for understanding complex systems and applying design principles to their engineering. Applications include human disease on multiple scales, detailed understanding of signaling processes in cells, biotechnological applications, and therapeutic interventions. Reaching the full potential of this set of approaches requires managing many challenges, including designing efficient algorithms to make large-scale studies feasible, and effectively treating cases with missing and uncertain information. Here we explore the development of methods with the ability to manage and resolve some of these issues that frequently interfere with computational modelling of complex biological systems and show a number of recent applications.

### Biography

Bruce Tidor is Professor of Biological Engineering and Computer Science at MIT. His undergraduate degree is in Chemistry and Physics from Harvard College, and he then received a Marshall Scholar award to study at Oxford University's Wolfson College, where he earned an M.Sc. in Biochemistry. After completing his Ph.D. in Biophysics at Harvard, he moved to the Whitehead Institute for Biomedical Research, where he started his independent research as a Whitehead Fellow. In 1994 he was appointed to the faculty at MIT.

Dr. Tidor's research focuses on the analysis of complex biological systems at the molecular and cellular level. Using molecular modelling, theory, and computation, he explores the structure, function, and interactions of proteins and nucleic acids and the roles played by specific chemical groups in defining the stability, specificity, and reactivity of molecular interactions. This work advances our basic understanding of how molecules cause change in living systems and has important applications in the fields of drug development and enzyme engineering. Using cell-level models his group explores the relationship between network structure and biological function, with important applications in the fields of metabolic engineering, target identification, and synthetic biology. He is actively involved in applying knowledge from modelling studies to rational design.