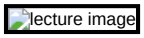

CCT Colloquium Series

Multiscale Modeling of DNA and Chromatin Folding

Thomas C. Bishop, Assistant Professor, Tulane University School of Public Health & Tropical Medicine
Dept. Env. Health Sciences
Johnston Hall 338
September 08, 2006 - 03:00 pm

Abstract:
A method of analyzing the structure and dynamics of DNA at basepair resolution is presented and applied to a 10ns all atom molecular dynamics simulation of a nucleosome (~130,000 atoms). The nucleosome is a protein-DNA complex and the structural basis for chromatin folding. Therefore, its structure and dynamic properties impact all genetic processes. The results are extended to rapidly assess nucleosome stability for entire genomes and the 3 dimensional folding of chromatin.

Speaker's Bio:
Tom Bishop is a computational molecular biologist. His primary research interest is the structure and dynamics of DNA and chromatin and how it relates to genetic function and disfunction (e.g. transcription, regulation, replication and repair). He studies molecular events in the hormone response mechanism as a model system for this research, and has developed a multiscale modeling approach that spans time, length and energy scales from those associated with all atom molecular dynamics simulations to those associated with a mathematical model derived from continuum mechanics. Dr. Bishop has received support for this research from the Louisiana Board of Regents, the National Science Foundation, and the National Institutes of Health. He maintains a state of the art molecular modeling laboratory with advanced molecular graphics and high performance parallel computing capabilities.

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