

*Institute of Computational and Theoretical Studies*

## *Colloquium*

# *Millisecond Dynamics of the RNA Polymerase II Backtracking Elucidated by Markov State Models*

**Dr. Lin-Tai Da**

Department of Chemistry  
The Hong Kong University of Science and Technology

**Date: 11 Feb 2014 (Tuesday)**

**Time: 11:00 a.m. – 12:00 p.m.**

**Venue: FSC 1014, Fong Shu Chuen Library Building  
Ho Sin Hang Campus, HKBU, Kowloon Tong**

### **Abstract**

Dynamics of the backtracking process in RNA polymerase II during transcription elongation is poorly understood. We built Markov State Models to obtain the metastable states involved in backtracking, as well as their thermodynamic and kinetic properties. Our results show that the backtracking occurs in a stepwise mode where four well-defined metastable states were observed. Unexpectedly, we found that the bending motions of Bridge Helix (BH) domain serves as a critical checkpoint adopting the highly conserved residue T831 as a sensing probe. If the base pair in the active site is unstable (e.g. mismatched), the continuously BH bending can examine the stabilities of the base pair and finally promote the RNA 3'-end nucleotide into a frayed form that leads to backtracking. We further investigated the backtracking propensities for different types of base pairs, which allowed identifying the dominant factors that regulate the preferences of the translocation (forward or backward).