



**THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY**  
**Division of Life Science**

## *Systems Biology of Stem Cells*

by

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### **Abstract:**

Embryonic stem (ES) cells are characterized by their ability to self-renew and remain pluripotent. Transcription factors have critical roles in the maintenance of ES cells through specifying an ES-cell-specific gene expression program. Deciphering the transcriptional regulatory network that describes the specific interactions of these transcription factors with the genomic template is crucial for understanding the design and key components of this network. To gain insights into the transcriptional regulatory networks in ES cells, we use chromatin immunoprecipitation coupled to ultra-high-throughput DNA sequencing (ChIP-seq) to map the locations of sequence specific transcription factors. These factors are known to play different roles in ES cell biology. Our study provides new insights into the integration of these regulators to the ES cell-specific transcription circuitries. Collectively, the mapping of transcription factor binding sites identifies new features of the transcriptional regulatory networks that define ES cell identity. Using this knowledge, we investigate nodes in the network which when activated, will jump-start the ES cell-specific expression program in somatic cells.

**Date** : **18 October 2017 (Wednesday)**  
**Time** : **4:00 p.m.**  
**Venue** : **Lecture Theater C**  
**The Hong Kong University of Science & Technology**  
**Clear Water Bay, Kowloon**

*(Seminar Co-hosted by Dr. Angela Wu and Dr. Danny Leung)*

***All are Welcome!!***