



Department of Mathematics  
The University of Hong Kong



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Hong Kong Baptist University

## Joint HKBU-HKU Seminar Series on Mathematical and Computational Biology

### What is the Origin of Cell Diversity?

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#### Abstract

Regulation of gene expression levels is dependent on the concentrations of multiple transcription factors, which are also products of genes. The complexity of interactive gene regulation is considered to be responsible for diversity of distinct cell types generated in the developmental process. The difference in cell property reflects difference in gene expression pattern. However, I have shown that the number of genes or interactions between genes does not affect the number of steady states of gene activity. Then, what is really responsible for increasing cell diversity, which should be the base of complexity of our body?

To answer this question, I introduce an idea to analyze gene networks, by which we can specify possible steady states of gene activity and derive important motifs from the linkage structure of gene interaction. The used principle is very simple: each gene should not show multiple different activities to a single set of expressions of controlling genes (i.e.: unique output to unique input). Based on this principle, we can reduce the complexity in behavior and understand the dynamics easily from the structure of gene networks. I analyzed real regulatory network by this method. 6 simple loops including 10 genes are derived as the responsible motifs for differentiation from a complex gene regulatory network governing early development of sea urchin including nearly 50 genes.

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Time: 2:30 – 4:30

Venus: Room 517, Meng Wah Complex, The University of Hong Kong, Pokfulam Road, Hong Kong.

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*All are Welcome*