Stony Brook University
The Graduate School

Doctoral Defense Announcement

Abstract

Study of the topological properties of bacterial metabolic network

By

Tin Yau, Pang

We considered the bacterial metabolic system as a complex network, studied the mapping of regulatory network onto metabolic pathways, and examined how the evolution jointly shapes their connections and giving rise to scaling laws. In particular, we proposed and studied the "toolbox model" that explains the dynamics of bacterial coevolution of metabolic and regulatory networks.

The toolbox model explains how evolutionary forces shape the scaling of the number of transcriptional factors (TFs) in bacterial genomes, where TFs are genes that monitor the expression of other genes. It has been known that the number of TFs in bacterial genomes scales quadratically with the number of genes in bacterial genome. For example, a small bacterium with a thousand genes has around 1% of the genes to be TFs, but a large bacterium with ten thousand genes, the TFs can constitute as high as 10%. This is surprising since naively one would predict the number of genes in every functional category should scale linearly with the total number of genes. The toolbox model explains this by making use of the fact that, bacteria can acquire useful genes over horizontal transfer and discard useless ones. When a bacterium receives a useful gene pathway that performs a particular function, it is assumed to evolve new TFs to monitor its expression. When the genome size of a bacterium gets large, the size of an additional pathway gets shorter since it can reuse the genes already present, and discard the redundant ones. But for the additional TFs, they maintain their constant size and do not depend on the genome size, hence the TFs and other genes have different scaling. We studied toolbox model by simulations and compared the results with the empirical data. The toolbox model was then solved analytically, which helps one to understand how the topology of the metabolic network affects the scaling and why it is quadratic. To simplify the analysis, we approximated the metabolic network in various ways, from as simple as complete graph to network from real data, in order to understand how the network topology affects the model scaling and dynamics.

Date: August 09, 2013
Time: 16:00
Place: Physics, P-119

Program: Physics
Dissertation Advisor: Sergei Maslov