
The 117th iCeMS SEMINAR

**Wed 12 Sep 2012
10:00–11:00**

Fluctuations in epigenetic switches and landscapes

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Venue: 2nd floor Seminar Room (#A207)
iCeMS Complex 1, Kyoto University

Construction of the sound theoretical framework of gene expression has been strongly desired to quantitatively understand processes in eukaryotic cells. In this seminar, I will explain our recent efforts toward this goal. We first discuss the stochastic dynamics of the core-gene network of mouse embryonic stem (ES) cells. Phenotypic heterogeneity of cultured population of ES cells is explained by the slow switching dynamics of Nanog expression. With this slow switching, dynamics of the gene network is regarded as a sequence of transitions among transient cell states. Effects of the slow switching dynamics on the pathway of transitions and on the cell-fate decision are discussed by using the calculated epigenetic landscapes. A possible mechanism of the slow switching dynamics of gene expression is the dynamical change of chromosome organization. By using the haploid budding yeast cell as an example, we explain the molecular dynamics simulation of chromosomes to understand the correlation between the chromosome structures and the gene expression patterns. We discuss fluctuations of the genome around the averaged structure inferred from the 3C data.

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