CDB SEMINAR

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16:00~17:00 A7F Seminar Room

Physical bases of 3D genome organization

* This seminar is a part of the Epigenetics Seminar Series 2017-2018.

Summary

Recent advancement of biochemical and microscopic observations have revealed the importance of three-dimensional (3D) genome structure and its dynamics for understanding DNA functions. In particular, it is beginning to be recognized that computational modeling of genome structure is indispensable for analyzing the observed data. In this talk, I will explain the physical bases of genome architecture that can be inferred from the computational modeling of genomes of budding yeast and human fibroblast.
Haploid budding yeast genome is comprised of 16 chromosome chains. Due to the small size of the nucleus, interactions between chromosomes and nuclear landmarks such as spindle pole body and nucleolus play important roles to constrain the interphase genome structure. The simulated chromosomes move flexibly under these constraints, and we discuss the correlation between the spatial distribution of genes and their regulation.
Human genome is organized in a largely different way from yeast because of its much larger system size. We propose a hypothesis that the phase separation mechanism to form the clustered regions of heterochromatin and euchromatin is a major driving force to determine the human genome structure. The experimentally observed compartment AB formation and nuclear lamina interactions were well explained with this phase-separation mechanism.

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