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The packing of mammalian chromosome: a phase transition perspective

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时间：5月17日（星期四）15:00—16:30
地点：北京大学物理大楼中212教室

摘要：高毅勤，北京大学化学与分子工程学院 “长江计划”特聘教授，北京大学生物动态光学成像中心研究员，国家杰出青年科学基金获得者。1993年本科毕业于四川大学化学系，1996年在中科院化学所获得硕士学位， 2001年获得加州理工学院博士学位，导师为Rudolph A. Marcus教授（1992年诺贝尔化学奖）。2001年—2004年间在加州理工学院和哈佛大学做博士后研究（导师为Marcus和Martin Karplus教授，2013年诺贝尔化学奖）。2005年-2009年，美国得克萨斯农工大学化学系助理教授。2010-现今，北京大学化学与分子工程学院教授。研究领域为理论和计算化学。课题组主要研究方向包括：染色质结构和生物功能，生物分子的溶液构象，生物酶催化机制和化学反应中的溶剂化效应。曾获Pople Medal，日本化学会Keynote Lecturer奖，美国Searle Scholar，Dreyfus新教授奖和Clauser Prize等。担任ACS Central Science, Chemistry of Materials, Journal of Chemical Physics，Chem. Phys. Lett., Interdisciplinary Sciences, 物理化学学报等期刊的编委。

报告人简介： In this talk, a multi-scale approach that has been applied to understand the function of spatial organization of DNA into chromosomes. Using molecular dynamics simulations we showed that DNA structure can be significantly affected by epigenetic modifications such as DNA methylation, the distribution of which shows disease (e.g., cancer)-dependent scale-invariant behavior in various biological samples. We then utilized Hi-C data to construct models for autosomes of different types of human cells and show that the epigenetic markers are strongly related to the 3-D chromosome structure. The high-order structure of chromosome is thus thought to be strongly affected by the DNA sequence. The distribution of dinucleotides along the linear genome also shows a power-law behavior, which can be explained by the multi-scale clustering of dinucleotides and the human genome can be viewed roughly as a A-B block co-polymer. We try to make a connection of such a property of genome to the higher-order chromosome structure formation, including topologically associated domains (TADs) and compartments. Finally, we will discuss the tissue-specific organization of the chromosome structure in differentiation, development, and disease, in which segregation/mixing of DNA segments of different properties characterized by CGI (CpG islands) distribution and transcription factor binding play important roles.

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