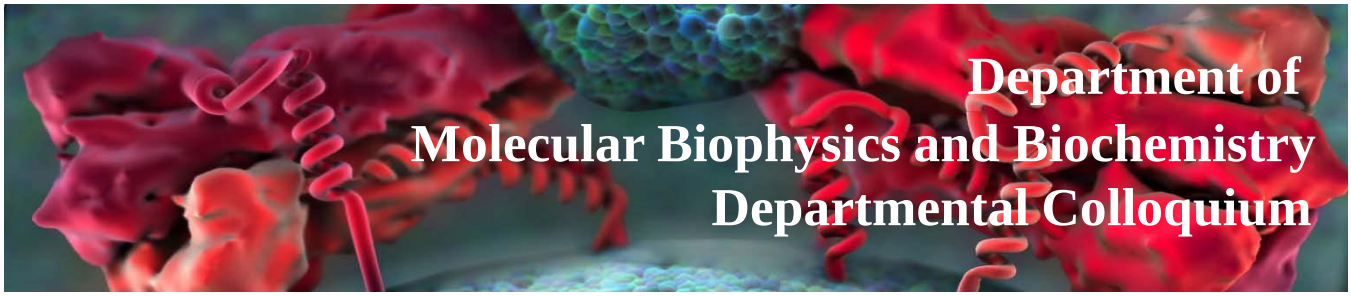

Leonid Mirny, Ph.D.

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Genomes in 3D

DNA of the human genome is two meters long and is folded into a structure that fits in a cell nucleus. Recently developed Chromosome Conformation Capture technique (Hi-C) provides comprehensive information about spatial genome organization and its reorganization during the cell cycle. I will present our analysis of Hi-C data and polymer modeling of chromosome organization for human, yeast and bacteria. In interphase, organization of human chromosomes is characterized by multi-level domain architecture, which correlates with sequence features and local chromatin states. In metaphase, the organization is homogeneous, common to all chromosomes, and is consistent among cell types, suggesting a general principle of metaphase chromosome structure. Using polymer simulations we built 3D models of metaphase chromosomes and suggested mechanisms of chromosome folding.

Monday, November 11, 2013

Bass 305

3:45 Tea 4:00 Seminar

Host: Karla Neugebauer

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