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## Indo-American Kavli Frontiers of Science

### Third Indo-US Frontiers of Science Symposium

Indo-US Science and Technology Forum  
U.S. National Academy of Sciences

March 1-4, 2009 - Agra, India

Cellular mechanisms for encoding information [-Presentation](#)

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The genome of an organism is both a parts list and an instruction manual, which together largely encode the functioning of the organism. In terms of information content, the genome is primarily a string of letters or base pairs in DNA, whose sequence specifies function. Sequencing projects in recent years have achieved much success in enumerating the genes encoded in the genome, determining how genes work in concert during normal cellular function, and how this functioning can go awry during disease. However, the proper functioning of the genome is also intimately connected to its physical structure. The genome is physically organized as chromosomes, which are precisely structured, hierarchical but dynamic assemblages of DNA and proteins. Chromatin structure thus offers an additional means of encoding information about biological function that is not directly dependent on DNA sequence. This "epigenetic" layer of encoding involves modification of DNA and histone proteins that are associated with DNA, as well as higher order structural features [1]. This encoding is more challenging to decipher as it is not directly reflected in the digital DNA sequence. In a remarkable feat of recursion, the genome encodes the entire cellular machinery required to duplicate itself during cell division, and to ensure faithful

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partitioning of replicated chromosomes to daughter cells. The segregation of chromosomes, which is essential for normal growth and development of all organisms, is also strongly affected by the physical organization of chromosomes and their spatial arrangement in the cell. Talks in this session will address the how the higher order organization of chromosomes underlies gene regulation and chromosome segregation.

1. Genomic views of chromatin. Dana J Huebert and Bradley E Bernstein, *Curr. Opin. Genet. Dev.* (2005) 15: 476–481

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