Introduction:
3D genome architecture

CS/CME/Biophys/BMI 371

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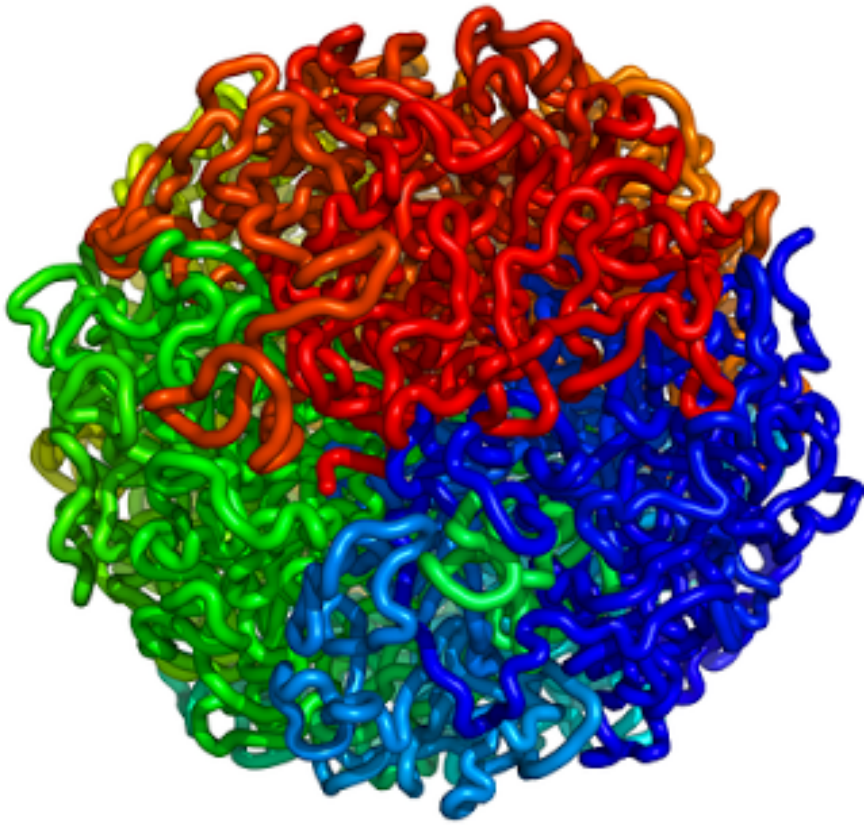
“3D genome architecture”

- Each human cell contains about 2 meters of DNA
- How is it packed into the nucleus?



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Why should we care?

- Every cell in your body contains the same DNA (i.e., the same genes)
- Yet the cells are very different from one another, because the genes are expressed differently (i.e., different quantities of protein get made from each gene)
- These expression differences are probably linked, in part, to the physical organization of the DNA
  - They're also related to chemical modifications of DNA (post-translational modifications)

How can we study 3D genomic architecture?

- One can use microscopy to observe actual physical locations of labels attached to the chromosomes, but resolution is relatively low
- Most of the available information comes from chromosome conformation capture techniques (e.g., Hi-C and TCC)
  - These techniques find DNA “contacts” (i.e., places where one DNA strand touches another)
  - To do this, they introduce chemical links between spatially proximate DNA strands, and then use DNA sequencing techniques to find out which parts of the chromosomes were linked
- Computational problem: reconstruct structure (and dynamics) from this partial information
  - Remember that chromosomal structure varies over time and from cell to cell

Background material

- Review paper
  - "Organization and function of the 3D genome" (Nature Reviews Genetics, 2016)
  - http://www.nature.com/nrg/journal/v17/n11/full/nrg.2016.112.html
- Original Hi-C paper
  - "Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome" (Science, 2009)
  - http://science.sciencemag.org/content/326/5950/289