

# Chromatin Folding Project: Summer 2017

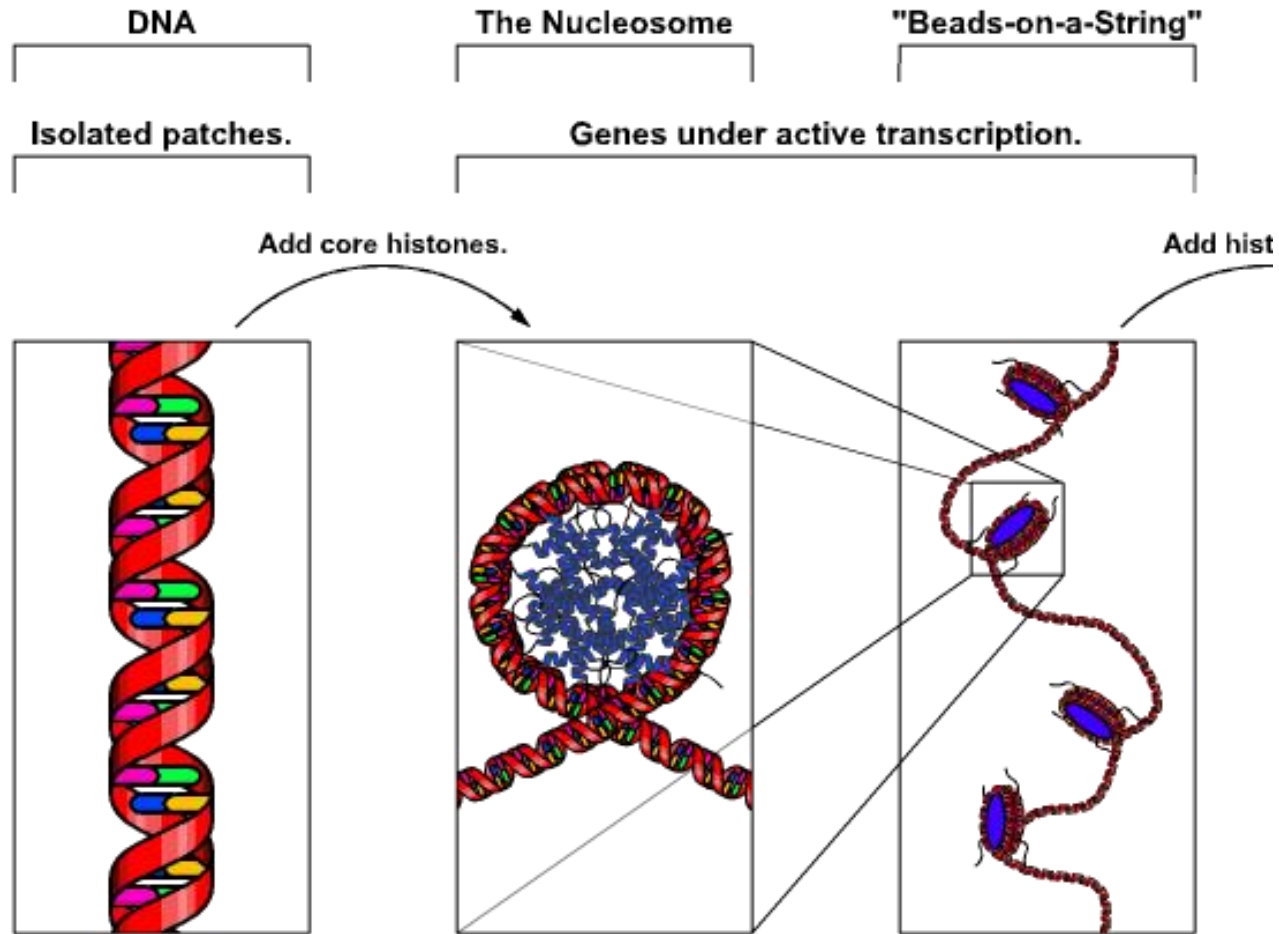
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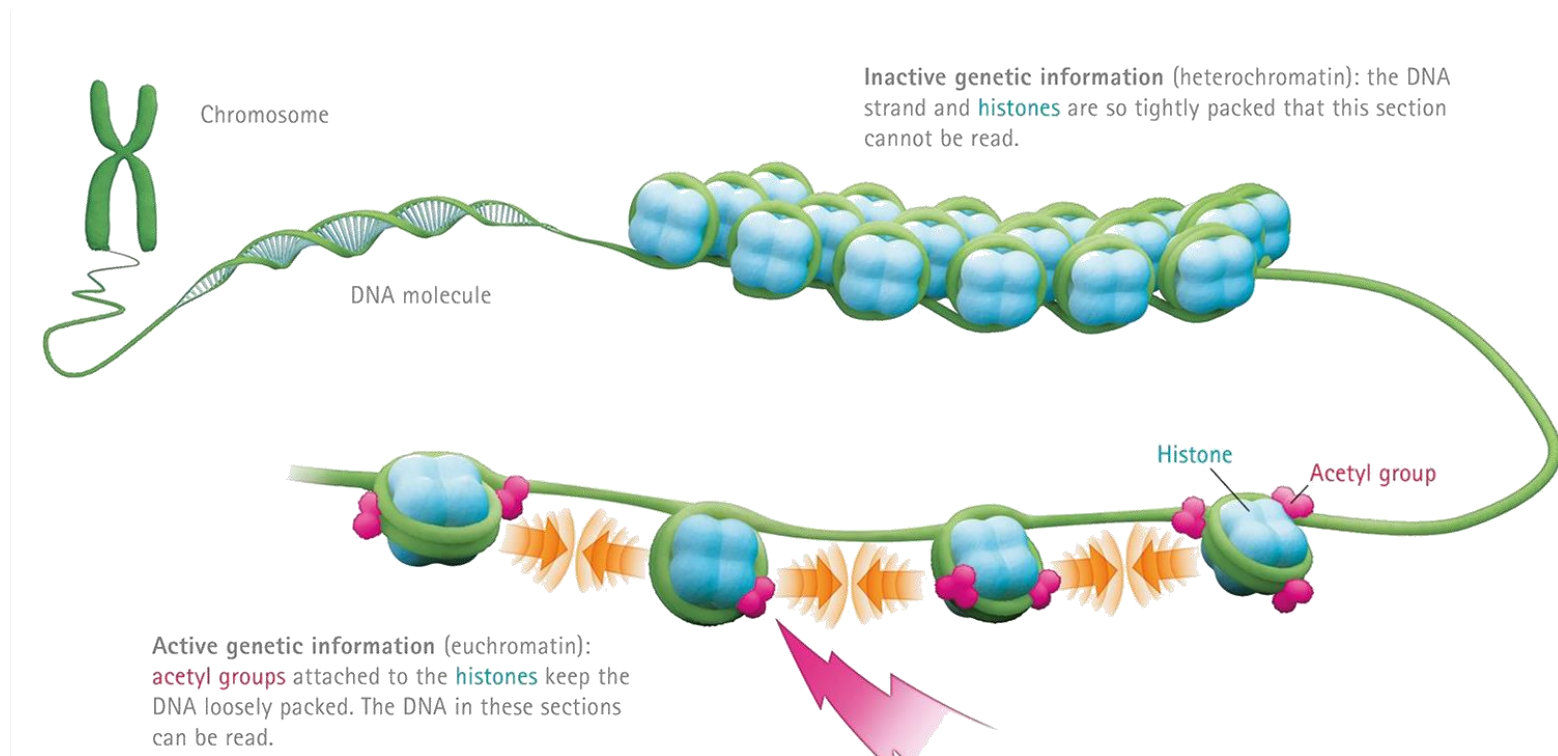
June 5, 2017

# Chromatin



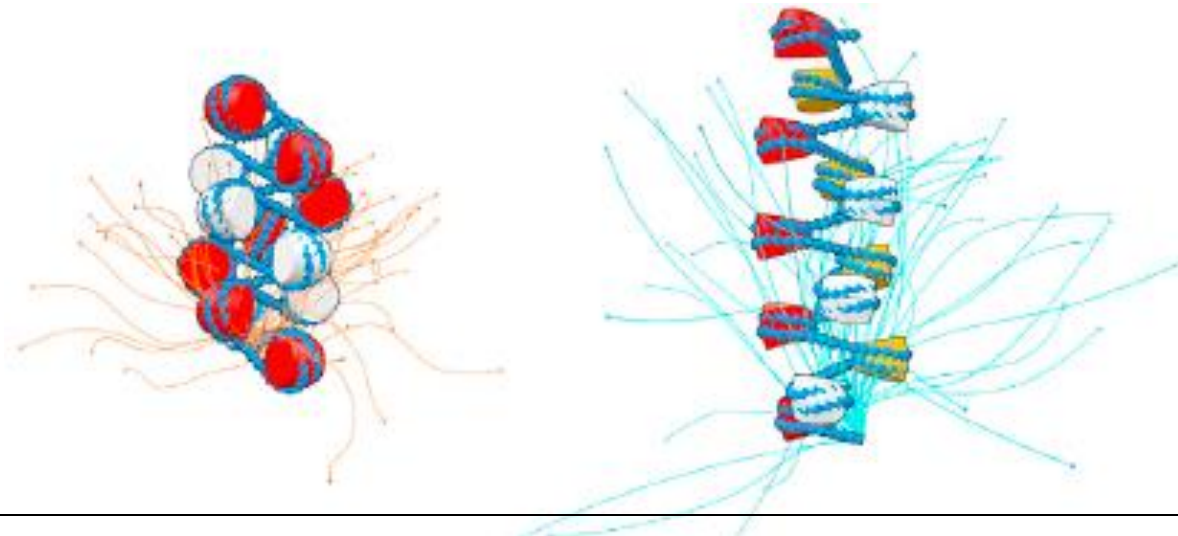
# Why are structures important?

- “Beads on a string” structures relate to expression of genes



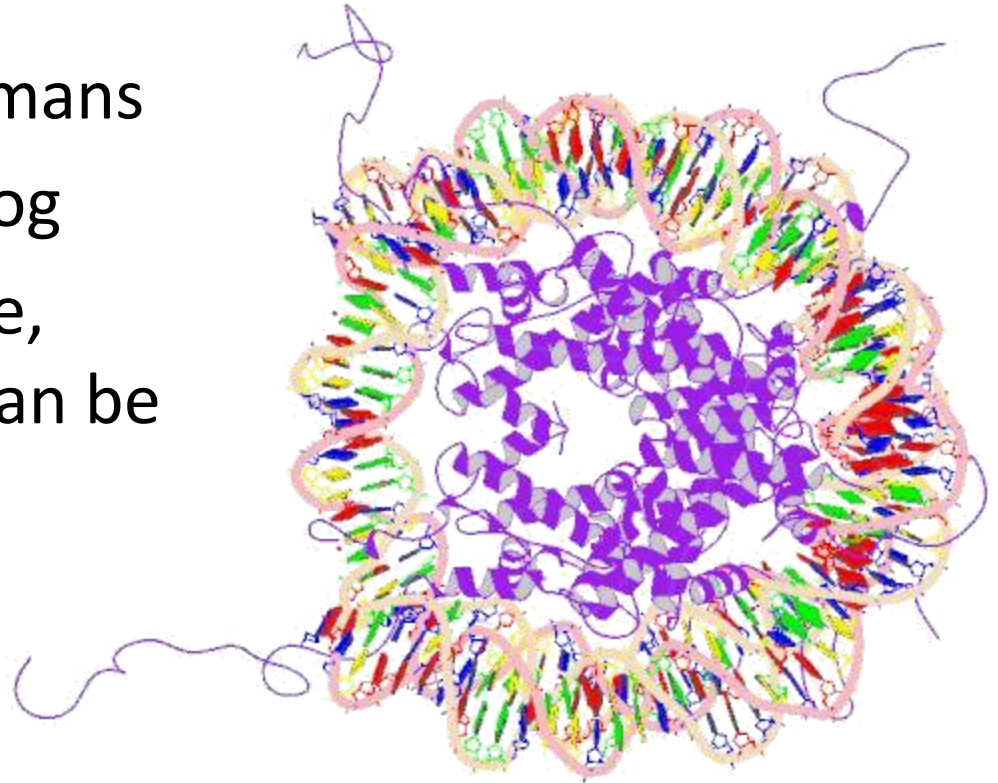
# Nucleosome interaction

- Needs further study
- Overlap not just between adjacent base pairs
- Having a “coefficient of overlap” can help simulations show what is favorable



# Known structure: 1kx5

- Sequence found in humans
- Comes from African frog
- Locations of phosphate, centers of base pairs can be used to determine coordinate frame



# Computing overlap - steps

- Treat nucleosome as polygonal cylinder
- Use phosphate or some atoms to find reference frame
- Given 2 nucleosomes, compute mid-frame
- Project polygons onto common frame
- Find overlap
- Enhance simulations with coefficient of overlap

# Thank you

- Work supported by NSF grant CCF-1559855
- Questions?

