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Inferring the locations of DNA bound proteins from Hi-C data PAU FARRE, ELDON EMBERLY, Simon Fraser University — Eukaryotic DNA can be found in either a tightly packed state (heterochromatin) or an open conformation (euchromatin). Certain proteins that bind to the DNA are responsible for setting up these two types of states. They interact with each other, and generate spatially separated compartments in the DNA through the formation of loops. In this talk I will present a combination of analytic and simulation results for the effects of protein-protein interactions on the large-scale 3D structure of chromatin. Using these findings we have developed a maximum-likelihood method for inferring the distribution of DNA bound factors that can help refine and make new predictions for the locations of proteins responsible of structuring the chromosome.

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