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A maximum entropy model for chromatin structure PAU FARRE, ELDON EMBERLY, Simon Fraser University, EMBERLY GROUP TEAM — The DNA inside the nucleus of eukaryotic cells shows a variety of conserved structures at different length scales These structures are formed by interactions between protein complexes that bind to the DNA and regulate gene activity. Recent high throughput sequencing techniques allow for the measurement both of the genome wide contact map of the folded DNA within a cell (HiC) and where various proteins are bound to the DNA (ChIP-seq). In this talk I will present a maximum-entropy method capable of both predicting HiC contact maps from binding data, and binding data from HiC contact maps. This method results in an intuitive Ising-type model that is able to predict how altering the presence of binding factors can modify chromosome conformation, without the need of polymer simulations.

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