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Reverse-engineering Chromatin Folding via The Gaussian Polymer Model MANJUL APRATIM, Physics and Astronomy, Rutgers, The State University of New Jersey, SWAGATAM MUKHOPADHYAY, Cold Spring Harbor Labs, ANIRVAN SENGUPTA, Physics and Astronomy, and BioMaPS Institute, Rutgers, The State University of New Jersey — Recent technological advancements in techniques exploring chromatin conformation, such as 3C and its derivatives, provide us with information about contact frequency between chromatin segments. There is an urgent need for systematic methods of reconstructing folding patterns of the chromatin from such data. Dekker et al have previously summarized this experimental data in the form of a so-called 'spatially averaged' conformation around which fluctuations occur. This would be accurate for regions where the chromatin is mostly frozen around one structure, but rather misleading for more dynamic euchromatin. To address the ill-posed problem of reconstruction of probability distribution from pairwise contact data, we propose a minimum relative entropy approach, which reduces to finding an interacting polymer model that reproduces the contact strengths, and allows for both very dynamic as well as frozen structures depending upon the indicated degree of interaction. While comparing contact frequencies computed from this model to observed data, we introduce the minimal number of interactions required as determined by criteria controlling model complexity. This technique allows us to reproduce known interactions for several biologically important regions like the beta-globin locus.

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