

Bayesian inference on a 3D polymer model for epigenetic data

The spatial conformation of chromatin within the nucleus is of the uttermost importance for transcriptional regulation and therefore for phenomena such as cell differentiation. In particular, epigenetic modifications play a crucial role as they are believed to affect the spatial folding and the accessibility of the genome to transcription factors and proteins.

Understanding and quantifying the interplay between the intrinsic polymeric nature of the chromatin fiber and its 3d folding in space that we have on one side and the 1d DNA sequence and its epigenetic content on the other remains an open challenge.

Here, we propose a magnetic polymer model with inhomogeneous, genomic-sequence dependent, external fields to describe said epigenetic modifications. Furthermore, we introduce a novel numerical method to perform approximate posterior inference on the free parameters of the model.

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