ID de Contribution: **16**   Type: **Non spécifié**

Polymer model for reconstructing chromatin and generating SPTs

Chromatin organization is probed by chromosomal capture data,from which the encounter probability (EP) between genomic sites is represented in a large matrix. However, this matrix is obtained by averaging the EP over cell population, where diagonal blocks called TADs, contains hidden information about sub-chromatin organization. Our aim here is to elucidate the relationship between TADs structure and gene regulation. For this end, we reconstruct the chromatin dynamics from the EP matrix using polymer model and explore the transient properties, constrained by the statistics of the data. To construct the polymer, we use the EP decay in two steps: first, to account for TADs, we introduce random connectors inside a restricted region defining the TADs. Second, we account for long-range frequent specific genomic interactions in the polymer architecture. Finally, stochastic simulations show that only a small number of randomly placed connectors are required to reproduce the EP of TADs, and allow us to compute the mean first time and the conditional encounter probability of three key genomic sites to meet. These encounter times reveal how chromatin can self-regulate. The present polymer construction is generic and can be used to study steady-state and transient properties of chromatin constrained on 5C data.

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