

Poster: Polymer modelling to investigate yeast's 3D chromosome organization in S phase and Mitosis

In Eukaryotes, DNA is tightly packed into a polymer-like structure called chromatin. Chromatin self-organization remains an elusive phenomenon whose impact is extensive in several cells' fundamental processes.

In our project, we focus on the specific problem of how chromatin folding couples with DNA replication dynamics. Taking into account chromosomes' conformation properties is in fact crucial to fully characterize the one dimensional process of eukaryotic genomes' replication.

While the molecular actors and mechanisms involved in DNA replication on one side and in genome folding on the other start to be well characterized independently, the interplay of the two remains elusive. For this reason, we used polymer modelling to fill this gap by implementing a polymer class capable of replicating itself starting from several origins of replication.

The developed computational framework allowed us to simultaneously describe 3D chromatin folding and 1D replication dynamics and address specific biological problems.

In particular, we adapted the model to describe *Saccharomyces cerevisiae*'s chromosomes during S phase, focusing on the hypothesized co-localization of sister forks (*Kitamura et al.*, *Saner et al.*). From our simulated Hi-C maps, we predicted two different scenarios for contact enrichment around the origin of replication: entropic compaction due to bubbles' topology and active extrusion of newly replicated sister chromatid (chromatin fountains).

We also adapted our simulations to describe mitotic chromosomes to exploit the SisterC data by *Oomen et al.*. We showed that even with a minimal set of parameter, it is possible to recover some structural properties of yeast mitotic chromosome, such as cohesin loops mediated compaction (*Costantino et al.*) and loose alignment between the two sister chromatids.

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