Random walks on (almost) six regular graphs as dynamics for the associations between chromosomes in 2n=40 mouse spermatocyte's meiotic nuclei

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Résumé

Meiosis is an extraordinary process that produces haploids and genetically diverse gametes in organisms of sexual reproduction. During one phase of these processes, called pachytene, chromosomes in synapse are attached to the nuclear envelope by both their ends, being able to move or glide upon the internal surface of it. Associations between chromosomes are made possible by overlapping chromosomal structures, which are revealed for example by means of immunocytochemical techniques applied to squashes (or spreads), which are nuclei in which the nuclear envelope has been removed and the spermatocyte's nucleus content projected to a flat 2D surface. An important issue at this point is to determine whether the observed association clusters are due to an underlying random processes.

We model the nuclear architecture of 2n=40 Mouse meiotic prophase nuclei by an (almost) six-regular graph, upon which different stochastic dynamics describing the evolution of the chromosome's positions can be tested.

Squashes are simulated by a percolation-diffusion process upon vertices of the graph and clustering probabilities of chromosomes are determined as aggregations of overlapping chromatin domains. Simple Laplace random allocation of nodes in an almost six-regular graph as well as other random principles are explored and confronted with experimental measurements.

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