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Entropic effects in chromatin folding

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How DNA is organized in three dimensions inside the cell nucleus and how this organization affects the ways in which cells, access, read and interpret genetic information are among the most challenging questions in cell biology. Thanks to the recent development in molecular, genomic and computational approaches based on chromosome conformation capture technology (such as 3C, 4C, 5C and Hi-C) we are able to tackle a question regarding whether or not entropic forces are driving the relative positioning of chromatin fibers (represented as self-avoiding polymers) in the cell nucleus.
The idea that nonspecific forces (like "entropic centrifuge") can be a major driver of chromatin organization has been well formalized but a direct verification from real data is still missing.
Since a high GC content in the sequence is known to correlate with increased flexibility and decompaction of the chromatin fiber we suggest that integrating the information about contact probability and GC content will enable us to gain a better insight on the role of entropic forces in the self organization of chromosomes within nuclei.

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