

Abstract Submitted
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A Probabilistic Graphical Model to Detect Chromosomal Domains¹ DIETER HEERMANN, ANDREAS HOFMANN, Institute for Theoretical Physics, Heidelberg University, 69120 Heidelberg, Germany — To understand the nature of a cell, one needs to understand the structure of its genome. For this purpose, experimental techniques such as Hi-C detecting chromosomal contacts are used to probe the three-dimensional genomic structure. These experiments yield topological information, consistently showing a hierarchical subdivision of the genome into self-interacting domains across many organisms. Current methods for detecting these domains using the Hi-C contact matrix, i.e. a doubly-stochastic matrix, are mostly based on the assumption that the domains are distinct, thus non-overlapping. For overcoming this simplification and for being able to unravel a possible nested domain structure, we developed a probabilistic graphical model that makes no a priori assumptions on the domain structure. Within this approach, the Hi-C contact matrix is analyzed using an Ising like probabilistic graphical model whose coupling constant is proportional to each lattice point (entry in the contact matrix). The results show clear boundaries between identified domains and the background. These domain boundaries are dependent on the coupling constant, so that one matrix yields several clusters of different sizes, which show the self-interaction of the genome on different scales.

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