

3D GENOME RECONSTRUCTION FROM PARTIALLY PHASED HI-C DATA

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The three-dimensional (3D) genome structure plays an important role in gene regulation. One of the main approaches to infer the 3D genome structure is from contact matrices that record interactions between different regions (loci) of the genome. In the case of diploid organisms the contact data is often unphased, which means that one cannot differentiate between contacts for homologous chromosomes. This talk is about partially-phased population contact data. Partially-phased contact data means that for some loci one can assign contacts to a maternal or paternal homolog. We study the identifiability of 3D genome reconstruction from partially phased contact data. Moreover, we suggest a reconstruction method built on semidefinite programming and homotopy continuation.

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