Computational aspects of three-dimensional genomics

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Abstract: New sequencing technologies, so-called next-generation sequencing (NGS), is changing biological sciences drastically. With decreasing costs and rapidly increasing data yields, the focus is shifted from studying single genes to a broader approach involving entire genomes and epigenomes. The new sequencing technologies also put a new perspective on medicine and diagnostics, since genomic samples from patients will soon routinely be sequenced and studied. Recently, novel methods that allow for studying the three dimensional structure of chromatin in a genome-wide fashion have been developed. A recent method called hi-C involves chromosome conformation capture coupled to massively parallel sequencing. Due to the dynamic structure of interphase chromatin not all interactions detected by such techniques are due to functional biological interactions. We propose to use a statistical framework to detect real interactions in these types of data. We integrate known gene interaction data with three-dimensional genomic data to detect regions of the 3d-genome where functional interactions are found. We discuss the use of such methods in several settings, such as detection of transcription factories and the study of gene expression units.

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