Statistical Inference of Chromatin 3D Structures from DNA Methylation Data

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Abstract: It has been hypothesized that, in complex genomes, a gene may be controlled not only by regulatory elements binding to its promotor, but also by distal enhancers and repressors. Molecular techniques have been developed to detect physical contacts between distant genomic loci, which support the hypothesis and validate the theory that communications between such elements are achieved through spatial organization of chromosomes to bring genes and their regulatory elements into close proximity. Although typical data used to understand the 3D structure are Hi-C based, recent work has shown that DNA methylation data obtained from primary patient samples can effectively recover the A/B compartment, the hallmark feature of chromatin 3D structure. In this talk, I will describe a statistical inference procedure for understanding the chromatin 3D structure. I will then discuss its application to a low-grade glioma (LGG) dataset to dissect long-range chromatin interactions and structural differences between two group of LGGs. Our results support the value of DNA methylation for understanding 3D structures, which show clear compartmentalization of active and inactive chromatins.