Statistical methods for high-resolution chromosome conformation data analysis

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Abstract: High-throughput methods based on chromosome conformation capture technologies have enabled us to investigate the three-dimensional (3D) genome organization at an unprecedented resolution. However, high-resolution maps of chromatin interactions require costly, extremely deep sequencing and have been achieved for only a small number of cell lines. Without sufficient sequencing depth, the observed chromatin interaction maps are very sparse and noisy, which imposes great statistical and computational challenges. In this talk, I will present our recent work on enhancing the resolution of chromatin interaction maps and statistical denoising with thresholding.