

1153-62-436

**Wenxiu Ma\*** ([wenxiu.ma@ucr.edu](mailto:wenxiu.ma@ucr.edu)), Department of Statistics, University of California Riverside, Riverside, CA 92521. *Statistical and computational methods for analyzing chromatin spatial organization data.*

High-throughput methods based on chromosome conformation capture technologies have greatly advanced our understanding of the three-dimensional (3D) organization of genomes and demonstrated that genome architecture strongly influences gene regulation. However, methods to analyze the 3D chromatin spatial organization data are still in their infancy. In this talk, I will present an empirical Bayes hierarchical model to infer allele-specific chromatin contacts from diploid Hi-C data. We use zero-inflated Poisson to model the Hi-C contact frequency matrix with excessive zeros, and apply EM algorithm to infer the allelic contact maps and model the optimal allele-specific 3D structures simultaneously. Our method is able to reconstruct more accurate allele-specific chromatin structures compared to other existing allelic Hi-C analysis approaches. (Received September 03, 2019)