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Computational analysis of cancer epigenome and transcriptome Wei Li Baylor college of medicine

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An elaborate system of epigenetic regulation is responsible for the complexity in higher eukaryotes. This regulatory system consists of diverse trans-acting factors, cis-acting regulatory sequences and the epigenomic background, such as histone modifications and DNA methylation. Recently, ChIP-seq, Bisulfite-seq and RNA-seq have evolved as powerful and unbiased approaches to study this genome-wide regulatory system. However, it also poses great challenges for the development of effective data analysis and integration algorithms, the key link between massive raw data and biological hypotheses. In the first part of my talk, I will briefly introduce a series of algorithms for second-generation sequencing data analysis, including Model Based Analysis of ChIP-seq (MACS), Bisulfite Sequence MAPping program (BSMAP), and Dynamic Analysis of Nucleosome Position and Occupancy by Sequencing (DANPOS). In the second part, I will present one case study on the role of SIRT7 in chromatin regulation and tumor formation in vivo.

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