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Decoding epigenome with integrative "Omics" data analysis

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Decoding epigenome is a new and growing field of post-genomic research. With the advance in high-throughput sequencing technologies, large scale "omics" data including methylomes have been accumulated rapidly in the past few years. However, the cross-talk among epigenome, transcriptome and transcription factor binding remain largely unexplored. As an epigenetic on/off switch, DNA methylation plays essential roles in controlling chromatin configuration and gene expression. It has been recognized as an essential mechanism allowing genetically identical cells to exhibit distinct phenotypes. Recently, we developed genome-wide hairpin bisulfite sequencing technology and a series of computational tools to decode DNA methylation patterns. Integrative "omics" data analysis has been performed to understand the regulatory mechanisms underlying the DNA methylation dynamics. The novel insights gained from "omics" data analyses for stem cells and differentiated tissues will be discussed.

Biography

Hehuang Xie graduated from the University of Iowa with PhD in Genetics and a master degree in Computer Science in 2003. After his graduate studies, he received his Postdoctoral training in the field of bioinformatics at The University of Iowa and The University of Minnesota. In 2005, he joined the Cancer Biology and Epigenomics Program, Children's Memorial Research Center; Department of Pediatrics, Northwestern University as a research faculty. Currently, he is an Associate Professor at the Virginia Bioinformatics Institute.

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