

HICOMB 2018 Keynote Speaker

Computing Chromosome Conformation

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Abstract: Gene regulation – control of when, where, and at what level genes are expressed – is a fundamental part of cell development and identity. Gene regulation involves complex coordination of DNA architecture at multiple scales, from the individual DNA bases to the organization of whole chromosomes. Chromosomes in the eukaryotic nucleus are organized in a coordinated non-random configuration that has a substantial influence on the regulation of gene expression, and thus cell state and identity. Achieving a global full understanding of gene regulation requires a multi-scale understanding of the function of the genome in its developmental and structural context. In recent years, our ability to understand this organization has substantially increased due to a variety of high-throughput assays. Chromatin interactions can be interrogated globally using high-throughput sequencing based approaches including Hi-C in both populations of cells and more recently single cells. Localization in single-cells can also be interrogated using fluorescence imaging approaches that are increasingly high-resolution and high-throughput. Here I will discuss the computational challenges in analyzing and integrating these data types, and the resulting insights into our current understanding of how chromatin is organized. In addition, I will describe recent advances in software tools and infrastructure that help to facilitate the analyses of large-scale biological datasets.

Bio: James Taylor is the Ralph S. O'Connor Associate Professor of Biology and associate professor of computer science at Johns Hopkins University. Until 2014, he was an associate professor in the departments of biology and mathematics and computer science at Emory University. He is one of the original developers of the Galaxy platform for data analysis, and his group continues to work on extending the Galaxy platform. His group also works on understanding genomic and epigenomic regulation of gene transcription through integrated analysis of functional genomic data. James received a PhD in computer science from Penn State University, where he was involved in several vertebrate genome projects and the ENCODE project.