UNIVERSITY OF DELAWARE

CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY

CBCB SEMINAR
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BIOINFORMATICS SEMINAR

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UNRAVELING THE MECHANISM OF 3D GENOME FOLDING BY HIGH-THROUGHPUT FISH

The emerging model is that metazoan genomes are arranged into a nested hierarchy of structural features, driven by a division of labor amongst the few architectural proteins that we know of. In particular, CTCF and cohesin are essential for chromatin looping during interphase while recent work from our lab and others suggests that other factors may be important instead for larger-scale chromosome folding. However, many aspects of genome folding and nuclear positioning remains unknown. This highlights our need to identity additional factors to determine how these molecular machines cooperatively guide the genome through the cell cycle and development. To this end, we have combined two technologies that use fluorescent *in situ* hybridization (FISH). The first is a technology for high-throughput FISH (Hi-FISH), and the other, called Oligopaints, is a new type of probe that reduces the cost and increases the resolution of FISH. Using a combination of these tools, we are conducting imaging-based screens for novel architectural proteins in both *Drosophila* and human cells. I will present recent data from these screens, introducing novel factors that are providing new insights into the mechanisms underlying chromatin folding and nuclear positioning during interphase.

BIOGRAPHY

Dr. Eric Joyce is a geneticist and an imaging technologist who has pioneered the development of Oligopaints for visualizing a few Kb of DNA to entire chromosomes in single cells. Eric received his PhD from Rutgers University under the supervision of Dr. Kim McKim working on meiotic recombination. Following his post-doctoral training with Dr. Ting Wu at Harvard Medical School, he was recruited in 2016 by the Department of Genetics to the University of Pennsylvania as an Assistant Professor and core member of the Penn Epigenetics Institute. Eric's lab aims to understand how the structure and position of chromosomes within the nucleus is established and inherited across cell divisions. This includes previous work to integrate genomic-based assays and imaging. Recently, his group applied his Oligopaints technology to discover that the expression of genes at topological boundaries are particularly sensitive to pathological cohesin dysfunction such as in cohesinopathies like Cornelia De Lange Syndrome. He and his team frequently collaborate with other national and international groups as experts for 3D genome organization and chromatin structure.

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