CPH Seminar in Precision Medicine

"Visualizing Human Genome in Time and Space"

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The high order nuclear organization of eukaryotic genome plays significant roles in important cellular functions such as gene regulation and cell state determination. The influx of new details about the higher-level structure and dynamics of the genome requires new techniques to model, visualize and analyze the full extent of genomic information in three dimensions. We created the first model-view framework of eukaryotic genomes, *Genome3D* (http://genome3d.org), to enable integration and visualization of genomic and epigenomic data in a three-dimensional space. Recently, we integrated various genomic databases with Genome3D software, providing a multi-scale genome information visualization system to explore and navigate eukaryotic genome in 3-dimension. The new system, iGenome3D, provides a wide spectrum of tools, ranging from model construction to spatial analysis, to decipher the relationships between 3D conformation of the genome and its functional implication. The incorporation of literature allows users to quickly identify key features from PubMed abstracts for genes in the displayed 3D genome structure. The seamless integration of UCSC Genome Browser allows genetic and epigenetic features from the 2D browser to be visualized in 3D genome structure. iGenome3D can also output 3D genome model in various forms, including one that allows these models to be explored in modern virtual reality environments such as Oculus. Eukaryotic genomes can be analyzed from a completely new angle in iGenome3D that enables researchers to make new discoveries from a truly multi-scale exploration.

Friday, March 3, 2017. 12p – 1p. UCT.1414

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