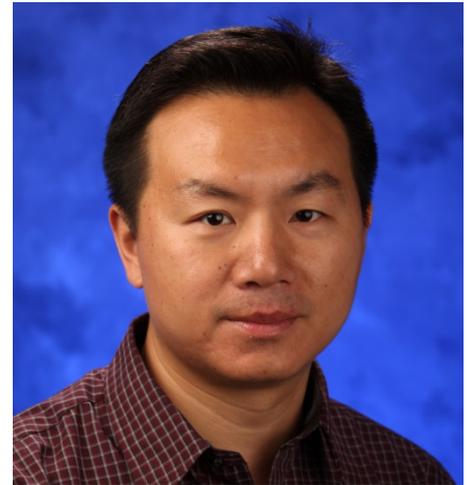


### BME Seminar Series

**Feng Yue, PhD**

Assistant Professor  
Department of Biochemistry and Molecular Biology  
Director, Bioinformatics Division  
Institute for Personalized Medicine  
Pennsylvania State University College of Medicine

**Date: Monday, October 16, 2017****Time: 1:30 pm****Location:** Traylor 709, East Baltimore Medicine Campus  
Video-teleconferenced to Clark Hall 110, Homewood Campus**Host:** Dr. Michael Beer

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## Genomic variations and its implications in cancer genomes

**Abstract:** In this work, we present an integrative framework for comprehensively identifying structural variation and investigating their effect on 3D genome structure. For the first time, we apply next-generation optical mapping, high-throughput chromosome conformation capture (Hi-C) techniques, and whole genome sequencing to detect SVs in up to 29 of normal and cancer cells. With this list of high-confidence SVs, we study their impact on genome organization, including the formation of novel topological associating domains (TADs) and enhancer hijacking events. Furthermore, we observe the disruption of TADs in cancer genomes is associated with changes in the gene expression, including many essential oncogenes. Our results underscore the importance of comprehensive structural variant identification and indicate that non-coding structural variation may be an underappreciated mutational process in cancer genomes.

**Speaker Bio:** Dr. Yue is an assistant professor in the Dept. of Biochemistry and Molecular Biology at Penn State School of Medicine, and also serves as the director of Bioinformatics division for the Penn State Institute for Personalized Medicine. He has been an active member of several large NIH funded consortia, including the ENCODE, Roadmap/Epigenomics, and 4D Nucleome projects.

He co-led the overall analysis effort for the mouse ENCODE consortium (Yue *et al.* Nature 2014). He was also a key contributor to the discovery of topologically associated domains (TADs, Dixon *et al.* Nature 2012). As a member of the 4D Nucleome consortium, he is working on integrative analyses and developing quality metrics for chromatin interaction datasets. His group built the highly popular 3D genome browser (<http://3dgenome.org/>), which has been visited by more than 40,000 users from over 100 countries.

His long-term goal is to study genomic/epigenomic regulation and 3D genome organization in human diseases, using a combination of high throughput experiments, computational modeling, and functional assays.