



Department of Biomedical Informatics Special Seminar



Ferhat Ay, PhD

Institute Leadership Assoc. Prof. of Computational Biology
Center for Autoimmunity and Inflammation
Center for Cancer Immunotherapy
Center for Sex-based Differences in the Immune System

Host: Ramana Davaluri, PhD

**Professor Department of Biomedical Informatics
Director, Bioinformatics Shared Resource,
Stony Brook Cancer Center**

“Computational Methods for Studying the 3D Chromatin Structure of Human Genome”

Monday, April 29, 2024

12:00 pm – 1:00 pm

Location: Mart Building, Level 7M-0602

<https://stonybrook.zoom.us/j/95974160825?pwd=cjVIR1ZJUy9FcHVFdGtmUmxVc2UrUT09>

Meeting ID: 959 7416 0825 Passcode: 636537

Abstract: Our lab develops methods to understand the genetic and epigenetic bases of gene regulation mainly in human immune cells. We are particularly interested in the analysis and modeling of the 3D genome organization from high-throughput chromatin conformation capture data to understand its impact on genome function. I will discuss our recent work under three major areas of interest for us: (i) Developing computational methods for detecting chromatin loops from high-resolution contact maps; (ii) Annotating genetic variants in human immune cells through the lens of 3D genome; (iii) Discovering association between common genetic variants chromatin loops.

Bio: Ferhat Ay is the Institute Leadership Associate Professor of Computational Biology at the La Jolla Institute for Immunology (LJI) with adjunct appointments from UC San Diego (UCSD). Prior to LJI, he was a Research Assistant Professor at Northwestern University (2015) and a CRA Computing Innovation Fellow in the Department of Genome Sciences at the University of Washington (2011-2014). Ferhat completed his Ph.D. in Computer Science at the University of Florida (2007-2011) and his B.S. degrees in Computer Engineering and Mathematics both from Middle East Technical University (METU), Turkey, in 2007. His primary research areas are computational biology, immunology, epigenomics, and regulatory genomics. He serves as an Associate Editor for PLoS Computational Biology, Journal of Computational Biology, and as an Editorial Board Member for Genome Biology.