



# Department of Biomedical Informatics Special Seminar



**Won-min Song, PhD**

Associate Professor, Icahn Institute of Genomics and  
Multiscale Biology, Ichan School of Medicine at  
Mount Sinai, NY

## Multi-scale network modeling of complex genetic diseases

**Tuesday, June 25, 2024**

**4:00pm - 5:00pm**

### Join Zoom Meeting:

<https://stonybrook.zoom.us/j/97308280160?pwd=pGUBKnk7M1n7abyTwCGPJdmf1GN9uQ.1>

**Meeting ID: 973 0828 0160    Passcode: 578458**

**Abstract:** Large-scale, sequencing-centric efforts (e.g. - The Cancer Genome Atlas (TCGA) and Accelerating Medicines Partnership - Alzheimer's Disease (AMP-AD)) have transformed researches on complex genetic diseases such as cancers and neurodegenerative diseases. Through the generation coordinated genomic, epigenomic and clinical data, these efforts have opened up new avenues to systematically characterize genetic, genomic, and proteomic features of aberrant molecular landscapes and exploit their unique therapeutic potentials in currently unmet clinical needs. However, identifying the mechanisms and regulators of the disease etiology presents significant challenges. Genetic diseases are often driven by interactions amongst aberrant functional molecules across different cellular (e.g. cell types), spatial (e.g. cellular neighborhoods) and molecular (e.g. multi-omics) domains. These necessitate a holistic modeling framework to succinctly capture the network of inter-wined interactions from the multi-faceted molecular readouts. In this seminar, I will share the ongoing efforts ranging from method development, disease modeling to mechanism and therapeutic discoveries through such integrative molecular modeling.

**BIO:** I am a computational biologist versed in integrative multi-omics large-scale data analysis to identify disease mechanisms and therapeutic strategies by leveraging state-of-art network modeling. I have previously established the statistical mechanics of embedded networks in complex manifolds to translate the network embedding as an effective modeling of the complex real-world networks. This line of research extended to develop a new gene interaction network inference framework, Multiscale Embedded Gene co-Expression Network Analysis (MEGENA), to infer multi-scale interaction networks identifying from loose to compact modules of genes and their key drivers. MEGENA is recognized as a top 10% cited article from PLoS computational biology in 2015 (as of May, 2021). Based on these, data-driven gene regulatory network models integrating mutational, epigenetic, and genomic alterations/regulations have been constructed for complex genetic diseases such as cancers, influenza infection and asthma. These network models have informed key pathways and potential regulators exploited in the disease etiologies, thereby nominate therapeutic strategies targeting the exploited mechanisms. Currently, I have extended the integrative network modeling framework to incorporate the cell-level molecular data from single-cell sequencing to dissect the interplay among diverse cells in the disease tissues.

Lab website: <https://labs.icahn.mssm.edu/songlab/>

Keywords: Cancer genetics, Genomics, Influenza Virus, Alzheimer's Disease, Systems Biology, Bioinformatics