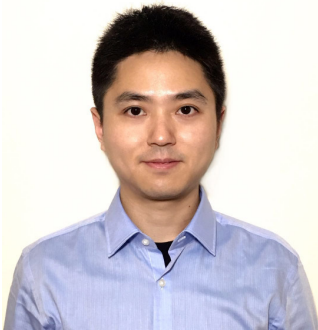


DEPARTMENT OF STATISTICS AND BIOSTATISTICS

Sijian WangDepartment of Statistics
Rutgers University*X-ray crystallography, protein data bank and
some statistical question***September 12, 2018****3:20 – 4:20pm**

Light refreshments will be served

**110 Frelinghuysen Road
Hill Center, Room 552**

Abstract: Protein is an important component of every cell in the body and is an important building block of bones, muscles, cartilage, skin, and blood. The knowledge of a high resolution atomic structure of a target protein is an essential pre-requisite for understanding biological activities of the protein and all structure-based biomedical research and structure-based drug design.

The Protein Data Bank (PDB) provides a rich resource on archive-information about the 3D shapes of proteins, nucleic acids, and complex assemblies that helps researchers understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease. The RCSB PDB hosted by Rutgers also takes in charge of curating and annotating PDB data.

Statistics plays an important role in many structure-related research. In this talk, I will describe some statistical applications and statistical questions when we analyze PDB data, including crystallization condition parsing, fitting and refinement of structure model, quality control of PDB structures, structure classification/clustering in PDB and automatic biological assembly annotation.

Bio: Dr. Sijian Wang has a Ph.D. in Biostatistics from The University of Michigan and a B.S. in Mathematics from Tsinghua University, China. He is currently an associate professor in the Department of Statistics and Biostatistics at Rutgers and is a resident faculty of Institute of Quantitative Biomedicine at Rutgers. His research interests include high-dimensional data analysis, proteomics, precision medicine, cancer genomics, bioinformatics, survival analysis, longitudinal data analysis and statistical modeling in health sciences.

