

A Statistical Framework for the Integrative Analysis of Genetic Data with Biomedical Big Data



Abstract: Emergence of large scale genetic/genomic data and relevant biomedical big data provides unprecedented opportunities of investigating biological and clinical problems by integrating these datasets. In the talk, I will discuss our recent research works aiming to develop novel statistical approaches for integrative analyses of biomedical big data to facilitate understanding genetic basis of diseases. Specifically, we have developed multiple novel statistical methods for integration of genetic studies for multiple diseases and functional annotation data within a unified framework, based on network modeling and machine learning approaches. We showed that these approaches can be powerful to improve identification of disease-risk genetic variants and facilitate understanding of relevant biological mechanisms. In addition, we further implemented text mining of biomedical literature and utilized this information to improve these analyses. Finally, I will discuss exciting research projects that are currently ongoing in my lab, including animal GWAS for opioid use disorder and immuno-informatics.

About the Speaker: Dr. Dongjun Chung is an Associate Professor in the Department of Biomedical Informatics at the Ohio State University (OSU), and a member of the Pelotonia Institute for Immunology-Oncology (PIIO) at the OSU Comprehensive Cancer Center (OSUCCC)-James. His research mainly focuses on development of novel statistical and computational approaches for the integrative analysis of genetic data with biomedical big data and the immuno-informatics. He received his Ph.D. in Statistics from the University of Wisconsin at Madison and had postdoctoral training at Yale University.

Dongjun Chung, PhD
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Carmen Zoom