

**Opening Black Boxes: Enhancing Statistical  
Rigor in Genomics Data Science**

**Jingyi Jessica Li, PhD**  
**Associate Professor**  
**Department of Statistics**  
**University of California, Los Angeles**

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**ABSTRACT**

The rapid development of genomics technologies has propelled fast advances in genomics data science. While new computational algorithms have been continuously developed to address cutting-edge biomedical questions, a critical but largely overlooked aspect is the statistical rigor. In this talk, I will introduce our recent work that aims to enhance statistical rigor by addressing three issues:

1. Large-scale feature screening (i.e., enrichment and differential analysis of high-throughput data) relying on ill-posed p-values;
2. Double-dipping (i.e., statistical inference on biasedly altered data);
3. Gaps between black-box generative models and statistical inference.