

## THE UNIVERSITY OF GEORGIA DEPARTMENT OF STATISTICS

## Colloquium Series

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4:00 PM, Thursday, March 31, 2022 https://zoom.us/j/94182050005

## Ribosome footprint Differentiation and DNA Cyclizability Prediction

High throughput sequencing has become a standard technology in many assays in biomedical research. In this talk I present recent work on two problems namely, ribosome footprint profiling and DNA cyclizability prediction. Ribosome is a protein that binds along the transcript to facilitate translation. Knowing its footprint and abundance provides a measurement of translation efficiency and dynamics. I will discuss a statistical framework named RiboDiPA for differential pattern analysis for ribo-seq data. DNA bendability/cyclizability is a fundamental measure of DNA mechanics that virtually affects all cellular activities that involve DNA. A recently high throughput assay named loop-seq has been developed to quantify the DNA cyclizability. We show a tool named DNAcycP based on deep learning model that can predict DNA cyclizability with high fidelity.