Biostatistics Seminars
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Transfer Learning with False Negative Control Improves Polygenic Risk Prediction

Wednesday, October 25, 2023
3:30 pm – 4:30 pm - Room 1140
Hybrid Seminar (Dr. Jeng will present virtually from North Carolina)

Zoom Link:

https://mcgill.zoom.us/j/83361845814?pwd=anhrOHRXcWdMWG1uM2xSazFpQk1RQT09

Abstract:
Polygenic risk score (PRS) estimates an individual's genetic predisposition for a trait by aggregating variant effects across the genome. However, mismatches in ancestral background between base and target data sets are common and can compromise the accuracy of PRS analysis. In response, we propose a transfer learning framework comprising two steps: (1) false negative control (FNC) marginal screening to extract useful knowledge from base data, and (2) joint model training to integrate knowledge with target data for accurate prediction. Our FNC screening method efficiently retains a high proportion of signal variants in base data with statistical guarantees under arbitrary covariance dependence between variants. This new transfer learning framework provides a novel solution for PRS analysis with mismatched ancestral backgrounds, improving prediction accuracy and facilitating efficient joint-model training.

Bio:
Dr. Jeng is an Associate Professor in the Department of Statistics at North Carolina State University, specializing in statistical methods and computational tools for biomedical data analysis. Her work integrates high-dimensional minimax theory with large-scale genomic data to develop optimal methods for detecting genomic signals. Her methodologies have found practical applications in areas such as copy number variation detection, rare genetic variant identification, and polygenic risk prediction.

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