



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Modeling Linkage Disequilibrium for Polygenic Phenotype
Prediction

WEDNESDAY, February 19, 2020, at 2:00 PM
Jones 304, 5747 S. Ellis Avenue

ABSTRACT

Polygenic risk scores are crucial for understanding complex traits that are regulated by a large number of genetic markers and predicting disease risks. While traditional methods tend to discard linkage disequilibrium (LD) information, newer approaches take advantage of such information to enhance prediction results. Using LDpred, a Bayesian algorithm and simulated genotype data with LD structure, I here study how complex trait prediction behaves for polygenic traits with varying degrees of genetic heritability, both for individuals with the same ancestry as the training sample and for those with different ancestral background. Results show that the algorithm possesses strong predictive power on the same population but performs poorly while applied to a different population with distinctly different LD structure.