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Friday, April 10, 2026

12:00-1:00 pm

Morgridge Hall Seminar Room 7650

Zoom Meeting: 966 3372 9112

<https://uwmadison.zoom.us/j/96633729112?pwd=tHFc9i1dAAqmXe05uWtw8wXBIQZxGB.1>

Passcode: 621125

Semiparametric Neural Network Models for Testing and Estimating Heterogeneous Treatment Effects

Abstract: In this talk, we introduce deepHTL (deep Heterogeneous Treatment Learning), a semiparametric framework for testing and estimating heterogeneous treatment effects (HTE) using observational data where complex confounding exists. deepHTL incorporates three key components to deliver robust causal inference. First, we employ bagged deep neural networks to estimate high-dimensional nuisance functions, improving accuracy and addressing the instability commonly observed in standard DNNs with finite samples. Second, we estimate heterogeneous treatment effects through a bias-reduced semiparametric regression that leverages the refined nuisance estimates, mitigating the bias that often affects conventional R-learner approaches. Third, to rigorously assess whether treatment effect heterogeneity is present, we implement both a global kernel score test based on the Davies method and a cross-fitted permutation test, ensuring valid finite-sample inference.

Across extensive simulations designed to mimic confounding structures typical of clinical registry data, deepHTL achieves proper type I error control and yields more accurate individualized treatment effect estimates than existing methods. In an application to a lung transplant cohort data, we find strong evidence of heterogeneity in the effect of bilateral versus single lung transplantation on post-transplant FEV1, a key measure of lung function. These results may help guide patient selection and the allocation of scarce donor organs.

Bio: I am a professor in the Department of Biostatistics and Genetics at the University of North Carolina (UNC) – Chapel Hill. I have a diverse and strong multi-disciplinary background with extensive expertise in biostatistics, bioinformatics, and machine learning. I have a well-established publication record in high-dimensional omics data analysis, improved principal component analysis, and surrogate variable analysis for dealing with confounding variables in observational, genetic, and genomic studies. My research has appeared in various high-profile scientific and statistical journals, including Nature Genetics, Nature Communications, Biometrika, Annals of Statistics, Annals of Applied Statistics, American Journal of Human Genetics, NEJM, and JASA, among others.

I have extensive experience as a PI and co-I on many NIH grants, including multiple R01 grants. More relevant to this project, I have been closely collaborating with Dr. Xai (PI) on using multi-omics data from large cohorts and biobanks, evaluating cross-platform normalization methods for downstream integrated omics data analysis, blocking missing data imputation and fast eQTL analysis for correlated samples. I also have a strong collaboration record, and currently I am serving as the director of the Data Management and Analysis Core (DMAC) of the UNC Superfund Research Program (UNC SRP) and serving on the Biostatistics core of UNC CFAR (Center for AIDS Research).



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