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Machine Learning and Human Genetics for Causal Inference

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Human genetics provides a robust avenue for causal inference, avoiding the pitfalls of reverse causation thanks to the stable nature of the genome. Specifically, Mendelian randomization (MR) can leverage genetic information to assess causal relationships between risk factors and disease outcomes. For example, through MR, researchers have confirmed the detrimental impact of LDL cholesterol in cardiovascular diseases and discarded the protective role of HDL in the same set of conditions. Although its generality, applications of MR have been limited to the analysis of single risk factors and outcomes in isolation.

In this talk, I will show how one can integrate machine learning and MR to train aggregate predictors of disease risk from multiple risk factors, a new framework that we call Differentiable MR (DMR). At its core, DMR aligns genetic influences of composite risk factors with those of the disease under study, bringing principles of causality in disease risk assessment. Finally, my presentation also aims to showcase how the physicists' mindset can be channeled to tackle quantitative problems in other disciplines, with guiding examples in machine learning for biomedicine.

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