Prediction with Scores of Tiny Effects: Lessons from Genome-wide Association Studies

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Abstract

Although recent genome-wide association studies have led to the identification of many susceptibility loci for a variety of complex traits, the utility of these discoveries for predicting individualized risk has been modest. This talk will examine the potential utility of future risk models that may include additional susceptibility loci as well as non-genetic risk factors. In particular, we will describe methods for estimating number of underlying susceptibility loci for a trait and the distribution of their effect-sizes using data from recent genome-wide association studies. We will then show how such estimates can be used to assess the limits of performance of future prediction models including high-dimensional polygenic models that may include hundreds or thousands of SNPs. We will point out some of the intrinsic theoretical challenges for the general problem of prediction with scores of tiny effects. This is joint work with JuHyun Park and Mitchell Gail.

Keywords: Prediction; Risk models; Genome-wide association studies.

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