

Building Risk Prediction Models from Genome Wide Association Data

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Abstract

Recent genome wide association studies have identified many genetic variants affecting complex human diseases. It is of great interest to build disease risk prediction models based on these data. In this presentation, we will present the statistical challenges in using genome wide association data for risk predictions, and discuss different methods through both simulation studies and applications to real-world data. This is joint work with Jia Kang and Judy Cho.