How results from large scale genetic analysis inform on disease

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ABSTRACT: The staggering increase in the size of genome-wide association and next generation sequencing studies has yielded thousands of robust associations. In this talk, I will present methods for leveraging the results of genetic studies to understand a range of outcomes including: the impact of intermediate phenotypes such as lipid levels on coronary artery disease; how genome-wide patterns of association can be leveraged to learn about what functional elements and cell types are relevant to phenotypic outcomes.