The three main aims when analysing data from a genome-wide association study are to detect causal variants, construct prediction models and understand genetic architecture. I will present improved methods for all three aims. Central to these new methods is a better understanding of how heritability is distributed across the genome; in particular, a new model for how heritability varies with factors such as allele frequency, linkage disequilibrium and functional annotations. I will show results from analyzing over 100 complex human traits; these include estimates of selection, of the total contribution of common and rare variants, of the relative importance of different types of genomic variants, and prediction models that those outperform rival methods. Although I primarily work on human data, I will also explain how these new methods can be applied and developed for use on livestock and plants.

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