

Bias, confounding, and random error in whole-genome case-control studies

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Abstract:

In this talk I shall revisit the traditional problems which potentially beset the epidemiological case-control study in the context of whole-genome genetic association studies. Unmeasured confounding by population substructure has received considerable attention in the genetics literature, but selection bias and bias due to differential misclassification of "exposure" (here genotype) have been ignored until very recently. As with unmeasured confounding, addressing these problems is helped by the fact that tens or hundreds of thousands of genotypes are measured in such studies and the overwhelming majority of these will not be genuinely related to disease phenotype. I will discuss how "genomic control" methods, originally proposed as an approach to unmeasured confounding, can be extended to address bias. I shall also revisit the arguments for the use of multiple control groups in this context.