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Statistical Genetics of Human Complex Traits

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Deadline for manuscript submissions:
closed (20 December 2023)

Message from the Guest Editor

Complex traits, including those of common diseases, are affected by many genetic variants. Over the past decade, genome-wide association studies (GWAS) have successfully identified hundreds of thousands of genetic variants that are associated with a broad range of complex traits and diseases. Although GWAS provide unprecedented opportunities to understand the genetics underpinning complex traits, current challenges lie in how to interpret and apply GWAS discoveries in research and clinical settings. These challenges have motivated the generation of innovative statistical methods and new datasets such as functional genomics and multi-omics data. To understand the biological mechanisms through which genetic variants exert their effects on phenotypes, analytical approaches that integrate GWAS data with transcriptomic or epigenomic data have been proposed to detect genes and regulatory elements relevant to these traits. Furthermore, the prediction of individual's disease risk by polygenic risk score is another exciting application of GWAS data. This Special Issue focuses on advances in the development and application of statistical methods for human complex traits.

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Message from the Editor-in-Chief

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