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Statistical Methods for Genetic Epidemiology

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submissions:

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Message from the Guest Editors

Dear Colleagues,

Genetic epidemiology, an important area of public health research, has rapidly evolved in the last two decades. This Special Issue aims to highlight the latest advances in statistical methods in genetic epidemiology. We encourage researchers to share their original research on developing novel statistical, bioinformatical, and computational approaches or applying advanced statistical techniques to complex traits or diseases. Review papers addressing current advances in this field are also welcome. Topics of primary interest include, but are not limited to:

Family and twin studies;
Genome-wide association studies;
Population genetics;
Heritability and genetic correlation;
Polygenic risk score;
Gene–environment interaction;
Multi-omics study;
Imaging genetics;
Expression quantitative trait loci (eQTLs);
Mendelian randomization;
Epigenetic epidemiology;
Single-cell epidemiology.



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Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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