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Statistical Computing in Medical Genetics: Current Approaches and Applications

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Message from the Guest Editor

The field of medical genomics aims to tackle complex questions relating to the etiology and pathology of disease, as well as response to treatment and interaction with environmental exposures. With the reducing cost of high-throughput technologies has come the ability to capture an extensive breadth and depth of “omic” data for clinical cohorts. Along with this has come the need to develop and apply powerful statistical computing approaches to address research questions.

In this Special Issue, we will cover the topic of statistical computing in medical genomics. The issue will highlight research that has applied new or alternate approaches in the field. There will be an emphasis on methods involving a) genomic data integration to identify biological processes and pathways involved in disease pathogenesis; b) variable selection methods for understanding gene–gene and gene–environment interactions; c) machine learning methods to identify genomic signatures predictive of disease outcomes.



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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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