Special Issue

Algorithms for Personal Genomics

Message from the Guest Editors

As genetic testing expands out of the research laboratory, into medical practice and the direct-to-consumer market, there is increasing public interest in efficient and private analysis of personal genomic variation for assessment of genetic risks, identification of relatives, for legal, forensic and historic purposes, and for multiple research purposes including haplotype reconstruction, analysis of rare variants and their combinations, and disease association with common variants.

This Special Issue aims to present novel algorithms for the analysis of personal genomes. Analysis can be at any stage of the data life cycle, from quality control to visualization, annotation, and interpretation at the individual, family, or cohort level. We also welcome methods for the integration of genomes with other data types such as multi-omics, Quantified Self and Electronic Health Records.

The emphasis is on algorithmic innovation. Ideally, the methods presented would involve brand new algorithms, significant changes to existing algorithms, or the repurposing of algorithms that were not previously applied in this field.

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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