Special Issue

Bioinformatics of Disease Research

Message from the Guest Editor

Recent technological advances, including that of DNA sequencing, have enabled us to understand most of our diseases in terms of genetic information, which is stored as massive amounts of data. Thus, in modern medical research, computational methods in the analyses of such genetic data are essential. Nevertheless, in my opinion, the value of computational works based on pure public data still tends to be underestimated. It is true that there are works with less novelty, typically just applying existing tools to public data and/or just repeating very similar procedures to another dataset. However, there are also plenty of pure computational works reporting novel/significant biomedical discoveries based on a combination of public data on genomics/epigenomics. In this Special Issue, I would like to invite the submission of the latter kind of work, hoping that this Special Issue will become a showcase of valuable computational works even if they are based on public data only. Of course, we will also welcome manuscripts based on their own wet experiments if they are valuable in terms of the bioinformatics of disease research. We look forward to your submission.

Guest Editor

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Deadline for manuscript submissions

closed (10 May 2024)

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Genes

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Impact Factor 2.8
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mdpi.com/si/187781

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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?

Editor-in-Chief

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