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Algorithms and Workflows in RNA Bioinformatics

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Deadline for manuscript submissions:
closed (15 January 2021)

Message from the Guest Editors

Dear Colleagues,

RNA is central to the majority of cellular processes in all domains of life, and the number of noncoding RNAs is on par with those coding for proteins. Common to most RNAs is that their function is determined by structure. Computational methods to study RNA structure are therefore important tools for elucidating the function of RNAs. Furthermore, RNAs interact with other RNAs and also with proteins, forming complex regulatory networks. Assessing these computationally enables a holistic view on cellular regulation. This Special Issue in Genes on "Algorithms and Workflows in RNA Bioinformatics" addresses the methodological and algorithmic developments that help to efficiently analyze the huge amount of available data, to study the structure of RNA in great detail, and to elucidate RNA function and its integration into large cellular networks. Case studies are also welcome but should specifically address limitations/shortcomings of current computational approaches.

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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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