Small RNA Bioinformatics

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Message from the Guest Editors

The present Special Issue of Genes aims to gather research on the topic of small non-coding RNAs (sncRNAs) bioinformatics, including the analysis of large-scale data, novel methodology, and databases.

MicroRNAs (miRNAs) are near 22 nucleotide long non-coding RNAs which have been proven to be important regulators of many biological processes, both physiological and pathological. Discovered in 1993, miRNAs were recognized as a full class of molecules in 2000, and were proven to be shared by many eukaryote organisms. Since the early 2000s, bioinformatics has always accompanied all steps of miRNA research, including structure inference, profiling and target recognition. New-generation sequencing technologies have boosted the small non-coding RNA research and provide high-throughput datasets which strongly benefit from bioinformatics. miRNAs are part of a larger class of molecules called small non-coding RNAs (sncRNAs for short), which also includes (but is not limited to) piwi-interacting RNAs (piRNAs), small nucleolar RNAs (snoRNAs) and small interfering RNAs (siRNAs).

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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