Special Issue

Evolution of Gene Regulatory Networks

Message from the Guest Editors

Prediction of gene regulatory networks and gene function is currently among the most active topics in computational biology. The overwhelming accumulation of high-throughput sequencing data, capturing genomes and gene expression data for thousands of organisms species, requires us to invent novel bioinformatical approaches to efficiently process this data. Furthermore, it is becoming clear that the evolution of novel traits, such as organs, tissues, and metabolites, cannot be fully explained by genomic approaches since genomics might not reveal which genes work together to express a given trait. Consequently, current approaches use transcriptomics, proteomics, metabolomics and novel data processing and machine learning algorithms to try to infer the gene function and regulation. This Special Issue invites research articles, reviews, and short communications including but not limited to: methods to construct functional and gene regulatory networks, novel approaches to process high-throughput data to produce these networks, and comparative approaches that study the evolution of these networks.

Guest Editors

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Deadline for manuscript submissions

closed (30 April 2020)

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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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