Special Issue

Computational Analysis of RNA Structure and Function

Message from the Guest Editor

RNA is being intensively studied across all living organisms in numerous ways, ranging from analysis of its structure and folding properties to high-throughput sequencing (HTS) and its applications. Many trait and disease related mutations in higher eukaryotes are in non-coding regions of the genome and since most of the genome is transcribed into RNA, the mutations hold the potential impact structure and thereby function of the RNA molecules. In this Special Issue, we welcome work on computational strategies for analysis of RNA structure and function covering both algorithmic aspects, as well as bioinformatic analysis large-scale related data sets, as well as work on prediction of RNA structure and RNA interactions of single sequences.

Guest Editor

Prof. Dr. Jan Gorodkin
Center for non-coding RNA in Technology and Health, Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, 1165 Copenhagen, Denmark

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Deadline for manuscript submissions

closed (30 April 2018)

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Genes
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

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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?

Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham,
1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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