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Impact of Parallel and High-Performance Computing in Genomics

Guest Editors:

Dr. Zhong Wang

Dr. Suzanne Sindi

Dr. Alexander Sczyrba

Prof. Dr. Hong An

Prof. Dr. Alex Zelikovsky

Deadline for manuscript submissions:
closed (20 October 2019)

Message from the Guest Editors

Dear Colleagues,

In the past two decades, massive parallel next-generation sequencing techniques have also parallelized genomics projects. Human genome sequencing has evolved from sequencing a few individuals to the massive parallel sequencing of 100,000 individual people or single cells. Culturing and sequencing single microbes has been replaced by culture-independent, metagenomics sequencing. Genomic data generated from single projects has grown from a few megabases to hundreds of gigabases or even terabases.

This Special Issue focuses on various “big data genomics” strategies that employ parallel programming paradigms to analyze extremely large genomics datasets. Its scope includes, but is not limited to, traditional task parallelism (MP, MPI, GPU and FPGA), data parallelism (MapReduce, Spark), or the recent model parallelism (deep learning). We welcome submissions of reviews, research articles, and short communications. We also encourage the submission of manuscripts describing new ideas, in the form of “concept papers”.

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Guest Editors

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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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