Special Issue

Genome Assembly

Message from the Guest Editor

De novo genome assembly is one of the oldest problems in bioinformatics. One of the key complications of the assembly problem is that repetitive sequences induce several paths in the assembly graph by linking different genomic loci. As a result, multiple genome reconstructions are feasible, but only one is correct. The genome-path problem, as well as the huge advances in sequencing and genome-mapping technologies, have motivated the development of a variety of computational and experimental techniques for cracking genome sequences.

Research in genome sequencing and de novo assembly of complex genomes, metagenomes, and transcriptomes, as well as computational algorithms for haplotype-resolved assembly, sequence validation, repeat identification, sequence error correction, assembly-based variant calling, alignment-free methods, and genome finishing, are all covered in this Special Issue, "Advances in genome assembly," which is now open for submissions. The submission of experimental and bioinformatic articles, up-to-date reviews, and commentaries associated with the genome-assembly problem are also encouraged.

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Deadline for manuscript submissions

closed (30 April 2023)

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Message from the Editor-in-Chief

The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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