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Genome Assembly

Guest Editor:

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Deadline for manuscript submissions:
closed (30 April 2023)

Message from the Guest Editor

Dear Colleagues,

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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Message from the Editor-in-Chief

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