Special Issue

Pipeline Tools for Next Generation Sequencing Analysis

Message from the Guest Editor

The use of Next Generation Sequencing (NGS) technologies in the interrogation of hypotheses has become increasing common in medical and biological research. With the advent of multiplexing technologies, the increase in sequence output from NGS machines and the development of novel applications for NGS, the complexity of high-throughput sequencing experiments has increased coordinately. The analysis of data from this diverse range of NGS applications requires a complex interaction between generic NGS data processing and application specific software tools while maintaining the high levels of reproducibility required in research. The use of pipelines and workflows in the analysis of NGS applications offers not only a high-throughput, automated processing and analysis of the data but a mechanism to enhance reproducibility and establish best practices in the analysis of NGS application types.

In this Special Issue, the contributing authors will present the most recent developments in pipelines and workflows for the analysis of both established and emerging NGS sequencing applications and technologies.

Guest Editor

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Deadline for manuscript submissions

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Editor-in-Chief

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