

Special Issue on  
**Scalable, Reproducible, Accessible Bioinformatics  
Computing for Genomic and Transcriptomic Data Science**

# CALL FOR PAPERS

With the significant reduction in cost for Next Generation Sequencing (NGS) in recent years, researchers now have access to sequencing technology that was previously only available to large-scale core facilities. However, sequencing instruments are not equipped with software to perform bioinformatics, and generating scientific value from the NGS data requires significant bioinformatics infrastructure and technical expertise.

Therefore, bioinformatics has become a bottleneck for broad applications of genomic sequencing in a range of biomedical fields of research. This special issue seeks original research that demonstrates development of novel bioinformatics online and offline platforms, databases, frameworks, toolkits, and meta-languages that enable researchers to seamlessly perform NGS data analysis. At the same time, the demonstrated solutions must be scalable with large amounts of data, reproducible outside the institution where they were originally developed, and ideally easily accessible by non-bioinformatics experts.

Any of the developed tools should meet the requirements above through example applications, including, but not limited to, one or more of the following: NGS data quality analysis, read mapping, genome assembly, variant annotation in transcripts, gene differential expression and transcriptomics, metagenomics analysis, and epigenetics. The goal of this special issue is to demonstrate bioinformatic solutions based on cutting-edge software technologies, enabling seamless access to analytical capabilities for Genomic Data Science, with broad applications from basic biology to clinical research.

Potential topics include but are not limited to the following:

- Cloud Computing 2.0 technologies (Kubernetes, Docker, NextFlow) and their applications to bioinformatics
- Frameworks enabling portability, scalability, and reproducibility of complex bioinformatics pipelines
- Bioinformatics web portals, databases, and platforms for genomic data analysis
- Visualization 2.0 (HTML5, Javascript-D3) for Next-Generation Sequencing (NGS) datasets
- Bioinformatics and Genomic Data Science learning platforms, enabling nonexperts to easily analyze complex NGS datasets

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/ijg/srab/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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**Submission Deadline**

Friday, 9 November 2018

**Publication Date**

March 2019