Novel Approaches for High-Throughput Sequencing Data Analysis

Guest Editor:

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Message from the Guest Editor

Over the past two decades, High-Throughput Sequencing (HTS) technologies have been developed dramatically and have fundamentally reshaped the paradigm of biomedical researches. From bulk to single cells and from short to long reads, HTS has covered almost all aspects of biology involving nucleic acid, which includes RNA expression, RNA modification, RNA–protein interaction, RNA–DNA interaction, DNA sequencing, DNA modification, DNA–protein interaction, histone modification, chromatin 3D structure, chromatin accessibility, etc. While basic tools for HTS data processing and analysis have developed accordingly, more sophisticated approaches are needed for customized analysis, which reflects the biomedical problems experimenters are trying to resolve. Considering the large demands for novel, customized, and easy-to-use HTS data analysis approaches and to facilitate and accelerate biomedical research, we launched this Special Issue, "Novel Approaches for High-Throughput Sequencing Data Analysis", and welcome any submissions that fall within this scope.

Special Issue

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Message from the Editor-in-Chief

As the world of science becomes ever more specialized, researchers may lose themselves in the deep forest of the ever increasing number of subfields being created. This open access journal Applied Sciences has been started to link these subfields, so researchers can cut through the forest and see the surrounding, or quite distant fields and subfields to help develop his/her own research even further with the aid of this multi-dimensional network.

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