

Special Issue

RNA-Seq: A Versatile Approach to Study Biological Processes

Message from the Guest Editor

Large progress has been made in data generation and processing leading to simplification and wider use of RNA-seq. Genome-guided transcriptome assembly is generally devoted to annotate genomes by defining transcribed regions and gene models with alternative splicing events, while *de novo* assembly may generate full-length transcript sequences for any living organism. Many broad range sequencing projects have already been conducted or are still underway to characterize very taxonomically distant species.

In this SI, standard research articles and reviews will highlight progresses made in RNA-seq analysis. Major topics such as transcriptome assembly and quantification will be reviewed, and light will be shed on the possible evolution of RNA-seq. Papers focusing on third-generation read-based RNA-seq will be particularly welcomed. Articles dealing with state-of-the-art approaches to identify splicing events and differentially expressed genes/transcripts/isoforms to study biological networks or to classify samples or transcripts with machine learning-based approaches will also be considered.

Guest Editor

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