Current Developments in RNA Sequence Analysis

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**Supplement Aims and Scope**

This supplement is intended to focus on RNA sequence analysis. Topics of interest include, but are not limited to, the following:

- Data preprocessing and mapping
- Gene expression
- Novel genes and transcripts discovery and De novo transcript assembly
- Alternative splicing
- RNA editing
- Single nucleotide variation discovery
- Fusion gene detection
- Coexpression networks
- Pathway and master regulator analysis

Bioinformatics and Biology Insights aims to provide researchers working in this complex, quickly developing field with online, open access to highly relevant scholarly articles by leading international researchers. In a field where the literature is ever-expanding, researchers increasingly need access to up-to-date, high quality scholarly articles on areas of specific contemporary interest. This supplement aims to address this by presenting high-quality articles that allow readers to distinguish the signal from the noise. The editor in chief hopes that through this effort, practitioners and researchers will be aided in finding answers to some of the most complex and pressing issues of our time. At the discretion of the guest editors other articles on other relevant topics within the scope of the supplement may be included.

RNA sequencing (RNA-Seq) has been revolutionizing the research on the transcriptome. Due to its high sensitivity and accuracy, it has allowed researchers across the whole world to detect expression changes across the transcriptome with unprecedented visibility. With RNA-Seq, researchers now can study both known and novel features. And the studies of transcript isoforms, gene fusions, single nucleotide variants, and allele-specific gene expression all become easier and not limited by prior knowledge any more. Over the years, researchers across the world have been bringing up new algorithms and packages to address the RNA-Seq data analysis challenges and expanding RNA-Seq into new applications. In this section, we have six research groups sharing their latest research.

Assumpção et al demonstrated the use of high-throughput sequencing of the miRnome to investigate field effects in gastric cancer. They successfully identified multiple miRNAs significantly changed in tumor adjacent tissues compared to the antrum without tumor tissue.

Feltus et al provided a snapshot of Big Data transfer across networks, which is often overlooked by many biologists. Given the power of genomics, biology is an emerging “Big Data” discipline that will soon enter the exabyte data range. Their review article discussed several key aspects of the data transfer.
process biologists need to know to frame genomics-oriented needs to enterprise IT professionals.

Gudenas et al analyzed the long noncoding RNA (lncRNA) profile in individuals with intellectual disability (ID) from the BrainSpan developmental transcriptome dataset. By integrating their results, they made a prioritized list of potential ID-associated lncRNAs based on the developing brain gene coexpression network and genetic structural variants found in ID probands.

Zhang et al mapped out the landscape of alternative splicing studies in plants by collecting analysis results from 17 species. They have discovered the shortages of previous results. They concluded that to make analyses across different projects comparable, it is very important to have a standard protocol for the analysis.

Han et al presented a detailed overview of the applications of RNA-Seq and the challenges to be addressed, such as data preprocessing, differential gene expression analysis, alternative splicing analysis, variants detection, allele-specific expression, pathway analysis and co-expression network analysis. They also brought up some essential principles for computational methods.

Teng et al gave an overview on the genetics of schizophrenia, a serious psychiatric disorder that affects 1% of general population and places a heavy burden worldwide. In their review article, the advantages of RNA-Seq for transcriptome analysis, the accomplishments of RNA-Seq in SCZ cohorts, and the applications of RNA-Seq for schizophrenia research using induced pluripotent stem cells were thoroughly discussed.

With the development of sequencing technologies, which could result in higher sensitivity, longer reads and lower cost, we believe that RNA-Seq will become more and more important for research and clinical diagnosis. We also have no doubt that bioinformatics scientists will continue to play a key role in addressing the analysis challenges of RNA-Seq studies and helping RNA-Seq expand its applications.

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Dr. Jianping Zhang is a Bioinformatics Specialist at The Rockefeller University. He completed his PhD at State University of New York at Stony Brook and has previously worked at Cold Spring Harbor Laboratory and MD Anderson Cancer Center. He now works primarily in differential gene expression, alternative splicing, protein interactions with DNA, pathway analysis and master regulator analysis in neurological disorders. Dr. Zhang is the author or co-author of 16 published papers and has presented at more than ten conferences.

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