BioMed Research International

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Special Issue on

Translation of Multiomics Data to Biology and Clinic

CALL FOR PAPERS

Much efforts have been made to the genetic studies of complex traits/diseases, such as genome-wide association studies (GWAS) and de novo mutation (DNM) analyses. However, despite the rapid growing body of human genetic data, how to translate genetic discoveries to underlying biology and, one step further, to clinical applicability, for example, the development of new therapeutics, remains a big challenge. Possible reasons include the following: (1) the effects of individual variants are typically minute, (2) genetic loci exert their functions through a tissue-specific manner, and (3) the majority of disease-associated variants lie in the poorly characterized noncoding genomic regions. Meanwhile, the rapid growth of other omics data is expected to boost the interpretation of current genetic findings and help pinpoint the valid drug targets for treatment or prevention. For instance, epigenomics data are good resources to evaluate the regulatory function of noncoding variants and thus link them to skeptical genes. The large Genotype-Tissue Expression (GTEx) project provides a comprehensive collection of transcriptomics data, facilitating the eQTL studies and expression analysis in a tissue-specific way.

The field of translation of multiomics data to biology and clinic for complex diseases is at an exciting juncture: in particular, promising results are emerging by integrating multiple lines of evidence. However, the exploration in this field is still at initial stage, and there is spacious room for improvement. We welcome submission of research articles describing the computational methods for integrating of multiomics data. We especially welcome the discovery of novel druggable genes/pathways that are difficult to be detected based only on single-dimensional data, for human complex disorders through integrating multiomics data.

Potential topics include but are not limited to the following:

- Application of tissue-specific data to identify potential disease genes
- Computational methods for integration of multiomics data
- Convergence between regulatory and coding variants at "actionable" gene level
- Prediction of novel druggable genes/pathways by integrating multiple lines of evidence
- Search for potential drugs targeting the predicted genes/pathways through drug repositioning and other techniques

Authors can submit their manuscripts through the Manuscript Tracking System at https://mts.hindawi.com/submit/journals/bmri/bioinformatics/tmdb/.

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

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