This special section includes five papers that were selected from the papers presented at the Eighth International Conference on Computational Systems Biology and fourth Translational Bioinformatics Conference (ISB/TBC 2014), which was held in Qingdao, China, 24-27 October, 2014. The five selected papers cover diverse topics, including cancer genomics, metagenomics, epigenomics, genetic and sequence analysis, biological data mining and analysis, etc.

In "An Independent Filter for Gene Set Testing Based on Spectral Enrichment", H. Robert Frost, Zhigang Li, Folkert W. Asselbergs, and Jason H. Moore studied the gene set testing issue. They developed a so-called spectral gene set filtering (SGSF) for independent filtering of gene set collections prior to gene set testing. The SGSF method as a filter statistic measures the statistical significance of the association between each gene set and the sample principal components. They demonstrated the efficiency of this method using simulated and real gene expression data.

In "Evolutionary Pressures on the Transcriptome", Dominique Chu and Anton Salykin studied decoding time relating to the codon usage bias (CUB) phenomenon. They considered a novel approach based on comparing mRNA with random synonymous variants to estimate the evolutionary pressures that have acted on the transcriptome. They found that over 70 percent of ORFs have been subject to a strong selection pressure for translation speed and that there is also a strong selection pressure for the avoidance of traffic jams. They also found that both homogeneous and very heterogeneous transcripts are over-represented. Their observations confirmed the validity of the Gromadski-Rodnina model.

In "Inferring Sequential Order of Somatic Mutations during Tumorgenesis based on Markov Chain Model", Hao Kang, Kwang-Hyun Cho, Xiaohua Douglas Zhang, Tao Zeng, and Luonan Chen explored sequence information of genomics to identify the temporal order of gene mutations in cancer initiation and development. They proposed a Markov chain model for estimating the sequential order of gene mutations during tumorigenesis from genome sequencing data. Moreover, they provided a new criterion to infer the order of patients to characterize the severity or stage of the disease, and also illustrated the potential clinic applications of their method by using several high-throughput datasets.

In "Identify Critical Genes in Development with Consistent H3K4me2 Patterns across Multiple Tissues", Nan Meng, Raghu Machiraju, and Kun Huang studied the H3K4me2 distribution patterns across six different cell lines from five major tissue types and embryonic stem cells. They defined a metric ‘tail length’ to quantitatively describe H3K4me2 distribution patterns around the TSS. They revealed 217 genes with ubiquitous long-tail H3K4me2 patterns in all the tested tissues and the embryonic stem cells. They further validated the importance of these genes using bioinformatics analysis.

In "Infer Metagenomic Abundance and Reveal Homologous Genomes Based on the Structure of Taxonomy Tree", Yu-Qing Qiu, Xue Tian, and Shihua Zhang developed a hierarchical taxonomy tree-based mixture model (HTTMM) for estimating the abundance of taxon within a microbial community by incorporating the structure of the taxonomy tree. In their model, genome-specific short reads and homologous short reads among genomes can be distinguished and represented by leaf and intermediate nodes in the taxonomy tree, respectively. They adopted an expectation-maximization algorithm to solve it, and also demonstrated their method using simulated and real-world data.

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