Yongsheng Bai, J Comput Sci Syst Biol 2014, 7:5
http://dx.doi.org/10.4172/0974-7230.S1.006

OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Summit on
Integrative Biology
August 04-05, 2014 Hilton-Chicago/Northbrook, Chicago, USA

Decoding next-generation sequencing data using custom-built computational and quantitative methods

Yongsheng Bai
University of Michigan, USA

In recent years, various next-generation sequencing (NGS) technologies have been assisting researchers in all kinds of genome projects. Non-model organism genomes are being sequenced with ease and tools are at hand to identify novel transcripts, splice junctions, and genetic variants for any organism with a sequenced genome. RNA-Seq, or whole transcriptome shotgun sequencing, has improved expression profiling. The key advantage of RNA-Seq is that it provides a more comprehensive view of the transcriptome with a single experiment than microarrays, including the ability to detect splice variants, splice junctions, and completely novel transcripts. Sequencing of all the coding regions in the genome (Exome) or targeted exome capture is considered a cost effective alternative to complete whole genome sequencing and is becoming an effective strategy in identifying genetic variants including single nucleotide polymorphisms (SNPs), insertions and deletions (INDELs), and large structural variations (SVs) in genetic disease research. Several novel NGS bioinformatics analysis pipeline algorithms and statistical methods, to whose development I contributed and which are used to extract information from mouse and human genome data, will be presented.

Biography

Yongsheng Bai received his PhD in Quantitative Biology from The University of Texas at Arlington in 2007. He has more than 10 years experience in bioinformatics and published his research work in many scientific journals and conferences. His current research interests lie in the development and refinement of bioinformatics algorithms/software and databases on NGS data, development of statistical model for solving biological problems, bioinformatics analysis of clinical data, as well as other topics including, but not limited to, large-scale genome annotation and comparative omics.

yongshengbaicool@gmail.com