Han Liang, J Comput Sci Syst Biol 2013, 6:4
http://dx.doi.org/10.4172/0974-7230.S1.004

OMICS Group Conferences
Accelerating Scientific Discovery

International Conference on
Integrative Biology Summit
August 05-07, 2013 Embassy Suites Las Vegas, NV, USA

From complete catalogs to "Actionable" shortlists: Integrative analysis for next-generation sequencing data

Han Liang
The University of Texas, USA

Next-generation sequencing has become a revolutionary tool for cancer research. However, there is still a big gap between complete catalogues of genomic alternations identified from NGS studies and "actionable" shortlists for further functional investigation. Using my two recent studies (RNA-seq in gastric cancer and exome-seq in endometrial cancer), I will discuss how to identify "driver" genes underlying the tumorigenesis. In the first study, we performed a comprehensive analysis on the whole-transcriptome of gastric cancer, and developed a multilayer and integrative analytic framework for identifying potential therapeutic targets from RNA-seq data (Kim et al., Cancer Research 2012). In the second study, we developed an integrated systems-biology approach to identifying driver somatic mutations from whole-exome sequencing data, which combines bioinformatics prioritization, a high-throughput approach to generating mutants and high-through cell viability assays (Liang et al., Genome Research 2012).

Biography

Liang received Ph.D. training from the Quantitative and Computational Biology program at Princeton University in 2006. As a postdoctoral researcher, Dr. Liang completed three years of research on computational and evolutionary genomics at the University of Chicago. Currently, Dr. Liang is an Assistant Professor in the Department of Bioinformatics and Computational Biology at the University of Texas MD Anderson Cancer Center and he is also a faculty member in Graduate Program in Structural & Computational Biology & Molecular Biophysics in Baylor College of Medicine. His research interests include the analysis of next-generation sequencing data, the integration of cancer genomics data, microRNA regulation, and the evolutionary process of tumor cells.

HLiang1@mdanderson.org