conferenceseries.com

5ᵗʰ International Conference on

Predictive, Preventive and Personalized Medicine & Molecular Diagnostics

December 01-02, 2016   Valencia, Spain

How to maximize the utility of big cancer genomic data?

Han Liang
The University of Texas MD Anderson Cancer Center, USA

The Cancer Genome Atlas (TCGA) project represents the largest effort to systematically characterize the molecular profiles of human cancers. A central question for the cancer research community is how to use these genomic and proteomic data effectively to deliver the clinical benefits to cancer patients. In my talk, I will first introduce some useful bioinformatics tools we recently developed for effectively analyzing and visualizing TCGA data including TCPA for cancer proteomics and TANRIC for long non-coding RNAs. Then I will present systematic analyses of the power of diverse TCGA molecular data in predicting patient survival times and of the sex effects across cancer types. Finally, I will focus on the biomedical significance and clinical relevance of RNA editing in human cancer. Together, my talk will cover three key aspects of big cancer genomic data: User-friendly bioinformatics tools, more systematic analyses and discovery of novel molecular drivers.

Biography

Han Liang has received his PhD in Computational Biology from Princeton University and Postdoctoral training in Computational Genomics at the University of Chicago. He is an Associate Professor and the Deputy Chair of the Department of Bioinformatics and Computational Biology at the University of Texas MD Anderson Cancer Center. His group has focused on the integrative analysis of cancer genomic data and the development of related bioinformatics tools. He has been very productive in terms of publications in leading journals at MD Anderson. He is the PI for multiple large government grants including NIH/NCI R01. He is the Founder and Chair of The Cancer Genome Atlas (TCGA) Pan-Cancer Clinical/Predictor Working Group and Co-Leader of the International Cancer Genome Consortium (ICGC) Pan-Cancer Whole Genome Analysis Project.

HLiang1@mdanderson.org

Notes:

J Pharmacogenomics Pharmacoproteomics
ISSN:2153-0645 JPP, an open access journal

Euro Personalized Medicine 2016
December 01-02, 2016

Volume 7, Issue 4(Suppl)

Page 42