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Systems biology and functional genomics for precision medicine: A data-driven and integrative approach

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Data-driven precision or genomic medicine is coming of age. It's increasingly easy to collect relevant "big data" from genomics to clinics. However, the interpretation of "big data" and translation into down-stream testable experimental hypotheses and patient-beneficial clinical applications or therapeutics remain difficult. In this talk, I will demonstrate how to leverage and integrate computational & systems biology analysis of cancer genomics data and genome-wide functional genomics screens by RNAi or CRISPR to identify novel driver-type therapeutic targets as well as predictive biomarkers to overcome drug-resistance and to treat aggressive human cancers. Specifically I will introduce a network-based systems biology framework to computationally infer disease drivers from large volumes of cancer genomics data and sophisticated statistical algorithms to deconvolute and analyze noisy high-throughput microarray or NGS-based functional genomics screening data. I will talk three application stories in details, two of which have successfully launched two clinical trials and one biomarker patent for specific subtypes of breast cancer.

Biography

Jiyang Yu received his Bachelor's degree in Computer Science from Zhejiang University, China in 2006. In 2008-2012, he did his PhD in Biomedical Informatics with Dr. Andrea Califano at Columbia University. After his PhD, he joined Pfizer Oncology as a Senior Scientist in Department of Precision Medicine. His PhD work has successfully launched two clinical trials and one biomarker patent in breast cancer. He has numerous publications in top journals including Cancer Cell, Genes & Dev, Leukemia, Cancer Research, Oncotarget and Bioinformatics, among others.

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