

Systems Medicine

The Next Generation of Computer-assisted Precision Medicine

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Recent advances in modern OMICS technology allow measuring the expression of all kinds of biological entities (genes, proteins, metabolites, miRNAs, etc.) at low cost and in high-throughput. Computational challenges for analyzing such big data emerge, ranging from the low signal to noise ratio to high model complexity, which render simple statistical questions arbitrarily complicated. We will discuss several bioinformatics tools for de-isolating biological networks and multiple OMICS data types: de novo pathway enrichment, in vitro high-throughput screening (HTS) data integration, time-course network enrichment, cancer subtyping, and breath analysis. Using Huntington's disease patients' expression data we will employ a guilt-by-association approach to illuminate the power of molecular networks to identify novel disease mechanisms. We will then extend this principle to study HTS data gained from large-scale drug screens, siRNA knock-down and CRISPR/CAS9 knock-out screens, as well as microRNA screens. In addition, we will show how to unravel temporal systems-level response patterns using whole-genome time-series gene expression profiles of lung cells after Influenza infection. We discuss how this kind of computational network biology has strong potential to enable precision medicine by classifying breast cancer subtypes utilizing complex combo-features gained from combining networks with multiple OMICS data. Finally, we will show how modern image analysis technology can be used for non-invasive precision medicine by profiling metabolic patterns in human breath from COPD and lung cancer patients.