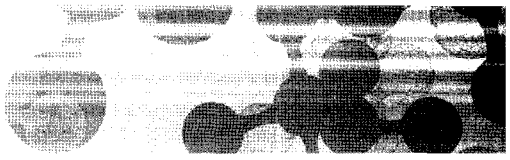

PL-1

Exploring Genomic Medicine Using Integrative Biology

Atul J. Butte

Stanford University School of Medicine, USA

The past 10 years have led to a variety of measurements tools in molecular biology that are nearly-comprehensive in nature. For example, microarrays are just one of at least 30 large-scale measurement or experimental modalities available to investigators in molecular biology. Instead of focusing on the cell, or the genotype, or on any single measurement modality, using integrative biology allows us to think holistically and horizontally. A disease like diabetes can lead to myocardial infarction, nephropathy, and neuropathy; to study diabetes in genomic medicine would require reasoning from a disease to all its various complications to the genome and back.enable such research,we have been studying the process of intersecting genome-scale data sets in molecular biology, such as those from genome scans, microarrays, proteomics, RNAi, and many others. I will show how we have computational tools that reason over these types of data to help enable discoveries in genomic medicine, with specific applications for obesity and diabetes mellitus. Though standards are increasingly being required and used for genome-scale data, representing the experimental context using a structured vocabulary has not yet happened, yet is a crucial set towards automated integrative biology. I will show how the largest unified biomedical vocabulary can now be used to represent microarray sample annotations and show examples of visualization, searching, and analysis using this coding that could not have been done before.I will end with a consideration of ways we can use genome-scale data to provide new ways to classify disease, and show how this broad recasting of disease nosology allows identification of new therapeutic opportunities, and of the specificity, or lack thereof, of disease biomarkers.