California State University, Fresno
Department of Biology
Co-sponsored by the Department of Biology and Research Infrastructure for Minority Institutions Program (RIMI)

Presents

Dr. Michael Snyder

Ascherman Professor and Chair of Genetics and the Director of the Center of Genomics and Personalized Medicine, Department of Genetics, Stanford University School of Medicine

Dr. Snyder received his Ph.D. training at the California Institute of Technology and carried out postdoctoral training at Stanford University. He is a leader in the field of functional genomics and proteomics, and one of the major participants of the ENCODE project. His laboratory study was the first to perform a large-scale functional genomics project in any organism, and has launched many technologies in genomics and proteomics. These including the development of proteome chips, high resolution tiling arrays for the entire human genome, methods for global mapping of transcription factor binding sites (ChIP-chip now replaced by ChIP-seq), paired end sequencing for mapping of structural variation in eukaryotes, de novo genome sequencing of genomes using high throughput technologies and RNA-Seq. He has also combined different state-of–the-art "omics" technologies to perform the first longitudinal detailed integrative personal omics profile (iPOP) of person and used this to assess disease risk and monitor disease states for personalized medicine. He is a cofounder of several biotechnology companies, including Protometrix (now part of Life Tehcnologies), Affomix (now part of Illumina), Excelix, and Personalis, and he presently serves on the board of a number of companies.

"Personalized Medicine: Personal Omics Profiling of Healthy and Disease States"

Personalized medicine is expected to benefit from the combination of genomic information with the global monitoring of molecular components and physiological states. To ascertain whether this can be achieved, we determined the whole genome sequence of an individual at high accuracy and performed an integrated Personal Omics Profiling (iPOP) analysis, combining genomic, transcriptomic, proteomic, metabolomic, and autoantibodyomic information, over a 38-month period that included healthy and two virally infected states. Our iPOP analysis of blood components revealed extensive, dynamic and broad changes in diverse molecular components and biological pathways across healthy and disease conditions. Importantly, genomic information was also used to estimate medical risks, including Type 2 Diabetes, whose onset was observed during the course of our study. Our study demonstrates that longitudinal personal omics profiling can relate genomic information to global functional omics activity for physiological and medical interpretation of healthy and disease states.

Friday, April 4th, 2014
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If you need a disability-related accommodation or wheelchair access, please contact Katie Williams at the Department of Biology at 278-2001, or e-mail katiew@csufresno.edu (at least one week prior to event).