

**Michigan State University**  
**Science at the Edge**  
***Engineering Seminar***

**October 11<sup>th</sup>, 2013**

11:30 a.m., Room 1400 Biomedical and Physical Sciences Building  
Refreshments served at 11:15 a.m.

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Stanford University School of Medicine

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

**Abstract**

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.

**Bio**

Michael Snyder is the Stanford Ascherman Professor, Chair of Genetics and the Director of the Center of Genomics and Personalized Medicine. He received his Ph.D. from the California Institute of Technology and 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. These technologies have been used for characterizing genomes, proteomes and regulatory networks. Seminal findings from the Snyder laboratory include; the discovery that much more of the human genome is transcribed and contains regulatory information than was previously appreciated, and a high diversity of transcription factor binding occurs both between and within species. 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 co-founder of several biotechnology companies including; Protometrix (now part of Life Technologies), Affomix (now part of Illumina), Excelix, and Personalis, and he presently serves on the board of a number of companies.

For further information please contact Prof. Christina Chan, Department of Chemical Engineering and Materials Science at krischan@egr.msu.edu

*Persons with disabilities have the right to request and receive reasonable accommodation. Please call the Department of Chemical Engineering and Materials Science at 355-5135 at least one day prior to the seminar; requests received after this date will be met when possible.*