

# **SEMINAR**

**Parag Mallick, Ph.D.**

**Dept. of Chemistry and Biochemistry  
University of California, LA**

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## **“Discovering Disease Markers and Mechanisms with Proteomics”**

Over the last few years a number of mass spectrometry-based quantitative proteomics methods have been developed that attempt to quantitatively and comprehensively identify the proteins present at different quantities in the samples compared. Such differences, in turn have been used to identify cellular functions and pathways affected by perturbations and disease, identify new components and changes in the composition of protein complexes and organelles and have led to the detection of putative disease biomarkers. We will first discuss the challenges of applying proteomics to identify putative markers. Next, we will describe computational proteogenomic methods for the discovery of disease specific SNPs and alternative splice forms for the annotation of the human genome. Lastly, we will discuss an emerging platform, based on proteotypic peptides, to enable high-throughput characterization of perturbations to cellular networks.

**Date: Friday, July 10**

**Time: 1:00 - 2:00pm**

**Location: Gilman Hall, Room 1352**

Presented by the L. H. Baker Center for Bioinformatics and Biological Statistics and  
the Computational and Systems Biology Summer Institute  
<http://www.bioinformatics.iastate.edu/seminars/index.html>