

DEPARTMENT OF STATISTICS AND BIOSTATISTICS

**Peter Lobel**

Center for Advanced Biotechnology and Medicine
Robert Wood Johnson Medical School

*Accounting for Subcellular Distribution-A Draft
Map of the Mammalian Organelle Proteome*

September 14, 2016

3:20 - 4:20pm

Light refreshments will be served

**110 Frelinghuysen Road
Hill Center, Room 552**

Abstract: Accurate knowledge of the intracellular location of proteins is important for numerous areas of biomedical research including assessing fidelity of putative protein-protein interactions, modeling cellular processes at a system-wide level and investigating metabolic and disease pathways. Many proteins have not been localized, or have been incompletely localized, partly because most studies do not account for entire subcellular distribution. Thus, proteins are frequently assigned to one organelle while a significant fraction may reside elsewhere. As a step towards a comprehensive cellular map, we used subcellular fractionation with classic balance sheet analysis and isobaric labeling/quantitative mass spectrometry to assign locations to >6000 rat liver proteins. We provide quantitative data and error estimates describing the distribution of each protein among the eight major cellular compartments: nucleus, mitochondria, lysosomes, peroxisomes, endoplasmic reticulum, Golgi, plasma membrane and cytoplasm. Accounting for total intracellular distribution improves quality of organelle assignments and assigns proteins with multiple locations. We also demonstrate the utility of this approach in identification of candidate disease genes underlying previously unsolved human hereditary disorders.

Bio Peter Lobel is Associate Director of the Center for Advanced Biotechnology and Medicine (CABM) and Professor of Biochemistry and Molecular Biology at Rutgers Robert Wood Johnson Medical School. Lobel and colleagues have developed proteomic approaches to characterize components of the lysosome and to investigate the role of lysosomal proteins in human disease. This research enabled discovery of the basis for two fatal hereditary childhood neurodegenerative diseases, late infantile neuronal ceroid lipofuscinosis and Niemann-Pick type C2 disease.

