

# IMCB Invited Speaker



**Speaker : Prof. Hyungwon Choi**  
*Assistant Professor, Saw Swee Hock School of Public Health,  
National University of Singapore*

Date : 31 March 2014, Monday

Time : 11:00AM - 12:00PM

Venue : IMCB Seminar Room 3-46, Level 3, Proteos, Biopolis

Host : Dr. Jayantha Gunaratne

## Seminar :

### **Bioinformatics analysis of quantitative proteomics data with application to interaction mapping studies**

Mass spectrometry (MS) is a widely used experimental platform for systems-level proteomics. Despite growing applications, MS data are redundantly large and complex and thus bioinformatics tools for efficient data extraction and rigorous downstream statistical analysis play a critical role in sensible interpretation of the resulting data. In this talk, the existing computational pipeline for two basic modes of quantitative proteomic analysis will be reviewed: labeling-based ratio quantitation (e.g. SILAC) and label-free quantitation (spectral counts, peptide/fragment intensity, swath). Using these approaches, a robust open-source laboratory information management system called Prohits-SAINT will be introduced, which consists of computational tools to store, manage, and statistically analyze affinity purification – quantitative MS (AP-qMS) data generated for mapping protein complexes. Using the AP-qMS data for PP2A human phosphatases, it will be demonstrated that rigorous statistical analysis by interaction scoring and advanced bi-clustering algorithm can identify high confidence interaction networks, identifying direct targets for functional validation in the newly charted interactome.

## About the Speaker :

Hyungwon Choi obtained Ph.D. in biostatistics from University of Michigan (2009), where he developed computational and statistical algorithms for analyzing high-throughput -omics datasets. During post-doctoral training at UM, he developed a wide variety of statistical software packages for proteomic data analysis, including protein identification and quantitation, site localization of post-translational modifications, protein-protein interaction scoring and network clustering. In 2011 he joined National University of Singapore as assistant professor in biostatistics, where his research has focused on developing MS data processing pipeline and pathway-oriented statistical models for proteomics and metabolomics data in clinical applications.