Computational Advances and Challenges in Proteomics

By

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Abstract

Over the past decade there has been significant progress with developing computational tools and methods for mass spectrometry based proteomics. Nevertheless, new challenges emerged and need to be carefully addressed. These include: 1) the ever increasing size of proteomics datasets requiring new approaches for estimation of peptide and protein identification error rates on a genome-wide scale; 2) exciting but challenging proteogenomics applications that seek to identify novel peptides currently not represented in reference protein sequence databases; 3) the need for robust computational algorithms for emerging proteomics strategies such as data dependent acquisition mass spectrometry. In my talk I will present our recent work in these areas.

Date: 8 January 2016 (Friday)
Time: 14:00
Venue: Room 6573 (Lift29-30)