

WEEKLY SEMINAR

Topic: Bioinformatics to Address the Challenges in Mass Spectrometry Data

Speaker: Tieliu Shi

The Institute of Biomedical Sciences, East China Normal University

Time: 15:30-16:30, 29 April 2014

Venue: Room 153, Geography Building, 3663 Zhongshan Road North, Shanghai
(华东师范大学中山北路校区, 地理楼 153 室)

ABSTRACT OF THE TALK

As one of the high throughput technologies, mass spectrometry has been widely used in biomedical researches, including protein identification, protein post-translation modification and biomarker discovery. However, this technology still has many limitations, and its data analysis has faced great challenges in deep elucidation of meaningful information. Bioinformatics plays important role in deciphering the MS data. In this talk, I will discuss how to use bioinformatics approaches to address those challenges in the MS data analysis.

BIOGRAPHY

Tieliu Shi, professor of Life Science school and Shanghai Key lab of Regulatory Biology, graduated from University of Louisville, US with MS degree in computer science in 1999 and PhD degree in molecular biology in 2000. He joined Shanghai Institute of Biological Sciences, Chinese Academy of Sciences in 2002 and has been conducting researches in Bioinformatics, especially in high throughput data analysis, including sequencing data, expression data and MS data. In the late of 2008, he moved to East China Normal University. He has published over 70 peer-reviewed papers.