

國立中央大學

統計研究所

學術演講

主 講 人：蔡政安 教授（國立臺灣大學農藝學系）

講 題：**Gene Set Correlation Analysis and Visualization Using Gene Expression Data**

時 間：**109年6月9日（星期二）上午11：00 ~ 12：00**

地 點：中央大學鴻經館M429室

茶 會：**上午 10：30 ~ 11：00** 地 點：鴻經館 510 室

ABSTRACT

Gene set enrichment analyses (GSEA) provide a useful and powerful approach to identify differentially expressed gene sets with prior biological knowledge. Several GSEA algorithms have been proposed to determine whether such functionally related gene sets express differentially (enrichment and/or deletion) in variations of phenotypes. GSEA provides a direct approach to the analysis of gene sets of interest and the results are relatively easy to interpret. In this talk, I will introduce a general strategy of gene set correlation analysis (GSCA) that simultaneously measures within and between gene sets variation to identify sets of genes enriched for differential expression and highly co-related gene sets. In addition, a graphical technique is used for visualizing and simultaneously exploring the associations of between and within gene sets and their interaction and network.

◎敬請張貼

歡迎參加◎