

# 國立中山大學應用數學系

## 學術演講

講者：曾建城 教授

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講題：Integration of experimental data or analytical  
pipelines for improved precision medicine

時間：2016/5/26（星期四）14:10 ~ 15:00

地點：理學院四樓理 SC 4009-1 室

茶會：15:00 於理 SC 4010 室（系辦公室）

### 摘要

With the rapidly increasing amount of experimental data, biological databases and bioinformatic pipelines to analyze them, effective information integration is becoming critical to extract meaningful knowledge and improve disease understanding towards precision medicine. In this talk, I will present three recent studies from my lab on different aspects of omics data integration. In the first paper, we have developed a MetaSparseKmeans approach to combine multiple transcriptomic studies for disease subtype discovery. In the second study, we turned to combine multi-level omics data using an overlapping group lasso technique for disease subtyping. Finally, we performed a comprehensive comparative study to evaluate 15 fusion transcript detection pipelines from paired-end RNA-seq data. A meta-caller was developed to integrate information from the top callers to improve the performance. Through these studies, I wish to provide a general introduction of omics data integration and showcase its importance and usefulness in achieving precision medicine via bioinformatic approaches.

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