Sample size calculation for assessing differential expression analysis in RNA-seq data

講者:李俊毅教授 嘉義大學應用數學系

Abstract

Sample size determination is an important issue in the experimental design of biomedical research. For RNA-seq experiments, we proposed two methods for calculating the required sample size, assuming the counts for each gene come from the Poisson or negative binomial distributions. However, these methods are limited in terms of accommodating covariates. To deal with this issue, the speaker will introduce the proposed an estimating procedure based on the generalized linear model.

時間:104年01月07日(三)15:00-16:30

地點:醫學綜合大樓前棟三樓會議室

對象:全校教職員及三院同仁

承辦單位:臺北醫學大學生物統計研究中心 連絡電話:2735-7873報名:請上學術活動網(三院及學生)教職員學習發展系統(教職員)