

國立中央大學

統計研究所

學術演講

主 講 人：高振宏 研究員（中央研究院統計科學研究所）

講 題：Statistical Methods for QTL mapping and Hotspot Detection

時 間：109年3月10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

Many biologically and economically important traits in organisms are quantitative, not qualitative. These quantitative traits may include the traditional traits (such as yields and quality in rice, weight and body fat percentage in animals, diabetes and hypertension in human) or molecular traits (such as gene expression and protein levels). Genes controlling quantitative traits are called quantitative trait loci (QTLs). The QTL hotspots are the genomic regions enriched in QTLs, and statistically, they harbor a significantly higher number of QTLs than expected by random chance. As the QTL hotspots can lead to identifying genes that affect the traits of interest, and further help to build networks among QTL hotspots, genes and traits, the QTL hotspot detection at genome-wide level has been an important task to understand the complex genetic architectures of quantitative traits in broad areas of genes, genomes and genetics studies. Statistical methods of QTL mapping and hotspot detection as well as the related issues are presented and discussed. Simulation study and real examples are used for illustration.

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