ON THE DESIGN OF GENE EXPRESSION STUDIES INVOLVING BIOLOGICAL AND TECHNICAL REPLICATION

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Microarrays are a powerful technology that measures the expression levels of many thousands of genes simultaneously. This has enabled great advances in the biological sciences including the discovery of the genetic basis of certain diseases. Statisticians can play a crucial role at the design stage of gene expression studies by suggesting designs that ensure the most effective allocation of available resources.

This presentation focuses on the statistical aspects of design for two-colour microarray experiments. We suggest optimal designs for gene expression studies based on statistical efficiency. In particular, the notion of admissibility is used to optimize separately for the effects of particular biological interest. This is especially relevant in the microarray context where analysis is typically carried out separately for those effects. Admissibility is discussed in detail for experiments involving independent biological replicates. Further to this, we consider issues that arise from the use of technical replication in which samples applied to different slides originate from the same biological extraction. The appropriate statistical model must then take into account the more complex error structure arising from the presence of technical replicates. The implications for optimal designs are discussed in the context of admissibility.