VARIANCE COMPONENT ESTIMATION IN MICROARRAY EXPERIMENTS INVOLVING POOLING

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One of the issues associated with the design and analysis of microarray experiments is the question of whether, and under what conditions, the pooling of RNA samples prior to hybridization can be beneficial. The primary motivations for pooling are to reduce variability and improve cost effectiveness. Disadvantages include difficulty in estimating appropriate variance components, and loss of information on individuals. However, in many experiments, such as developmental studies involving extraction of tissues from mouse embryos, the amount of available RNA per individual is limiting. Therefore, an approach involving either pooling of embryo tissue or RNA amplification is necessary.

We discuss the implications of pooling and/or amplification on statistical inference in microarray experiments. The problem of variance component estimation is presented in a composite sampling framework, allowing for imperfect mixing of pooled samples. A technique for obtaining variance component estimates via nonlinear least squares is described.