Gene Mapping and Model Selection

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An initial step in linkage analysis often involves testing of markers throughout a genome for linkage to genes contributing to the trait. This involves selection of a model for the trait as a function of genotype and environment. The model may involve multiple, possibly interacting genes.

To map quantitative trait loci (QTL) in experimental genetics, Broman and Speed (2002, JRSSB) have suggested use of the Bayes Information Criterion (BIC) for model selection. However, the standard BIC penalty of $(k/2)\log n$ for choosing a model with k parameters when the sample size is n (Schwartz, 1968 *Ann. Math. Statist.*) appears to be inappropriate. In this talk I (i) give an asymptotic evaluation of BIC that is appropriate for linkage analysis viewed as a change-point problem, (ii) describe an alternative approach based on p-values and the logic of Bahadur efficiency, and (iii) show how these methods would function in examples from the literature.