

# Model Selection in Irregular Problems: Applications to Gene Mapping

David O. Siegmund, Ph.D.

Visiting Professor, Section on Statistical Genetics

## Abstract:

I discuss two methods of model selection for change-point like problems, especially those arising in genetic linkage analysis. The first is a method that selects the model with the smallest p-value, while the second is a modification of the Bayes Information Criterion (BIC). The methods are compared theoretically and on examples from the literature. For these examples, they are roughly comparable although the p-value based method is somewhat more liberal in selecting a multi-parameter model.

## References

Bogdan, M., Doerge, R. and Ghosh, J. K. (2003). How to modify Schwarz Bayesian information criterion to locate multiple interacting quantitative trait loci, to appear in *Genetics*.

Broman, K. and Speed, T. (2002). A model selection approach for the identification of quantitative trait loci in experimental crosses, *J. R. Statist. Soc. B* **64**, Part 4, 1-16.

Sen, S., Churchill, G. A. (2001). A statistical framework for quantitative trait mapping, *Genetics* **159**, 371-87.

Yi, N., Xu, S., and Allison, D. B. (2003). Bayesian model choice and search strategies for mapping interacting quantitative trait loci, *Genetics* **165**, 867-883.