

**Assessing genetic linkage and association with robust
components of variance approaches.**

Christopher I. Amos, Dakai Zhu, Eric Boerwinkle

SUMMARY

Simulation studies are used to explore the properties of procedures for estimating components of variance and constructing test statistics in genetic linkage studies of quantitative traits. We evaluated the bias and median squared error of estimates of the linked additive genetic variance obtained by regression, maximum likelihood and quasi likelihood estimation procedures. The quasiliikelihood and regression procedures provided unbiased estimates of the additive component of variance. Maximum likelihood procedures that assumed multivariate normality were biased for most sample sizes considered but had more precision for most generating models than regression or quasi likelihood methods did. Wald tests derived from quasi likelihood procedures had similar or greater power than Wald tests based upon estimators from maximum likelihood analyses. Quasi likelihood estimation may therefore be preferable whenever there is uncertainty about the generating distribution for the error variance, but the robustness of this approach is offset by its required computational complexity.

(Ann.Hum.Genet. (1996), **60**, 143-160)