

# MAPPING QUANTITATIVE TRAIT LOCI UNDER THE MULTIVARIATE- $T$ MODEL

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The basic theory associated with standard variance-component models for QTL mapping in linkage analysis usually assumes multivariate normality. Robust score statistic based on the normality assumption has been proposed and showed to have the correct type-I error free of the true phenotypic distribution (Tang and Siegmund (2001)), however very low power has been observed when phenotypic distributions are far away from normal. Since the normality assumption is often violated in practice, we propose to use multivariate- $t$  distribution as an alternative. This assumption leads to a mathematically tractable statistic. We show that it keeps most of the desirable properties of the normal-based statistic with respect to parameter estimation, ascertainment correction, tail approximation, etc. Moreover, the proposed statistic is more robust to outliers and more powerful when phenotypic distributions are heavily-tailed and/or skewed. This is partially because the  $t$ -distribution fits the data better by using one additional parameter—the degrees of freedom. When the phenotypic distribution is near normal, the two statistics are about equivalent, so there is no loss of power by using the new statistic. Numerical results under various phenotypic distributions w/out ascertainment sampling are presented and substantial gain in power is observed. Several data-transformation techniques including Copula, log-transformation are also discussed and compared to the proposed method.