**Rank transformation in Haseman-Elston regression using scores for location-scale alternatives**

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The Haseman-Elston method is a simple regression approach for detecting genetic linkage to quantitative traits in sib-pair studies, where the squared phenotypic difference of two sib-pairs is regressed over the proportion of alleles identical by descent. Although this method and especially the extended new Haseman-Elston approach is quite robust, there might be some loss of power for non-normal distributed traits, as the assumption of linear regression is violated under the alternative hypothesis. Here, we propose a rank transformation approach, which either combine the information of a trend in locations and in scales or detect a trend for only a subset of the trait variables. As in most real applications usually genetic marker information is incomplete, this regression approach outperforms nonparametric trend tests, which assumes discrete groups of the dependent variables. Simulation results indicate a gain in power in comparison to recently suggested nonparametric methods.

## References

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