

**Local influence in pedigree data**

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The polygenic model has become an useful tool in the genetic analysis of quantitative traits. This model has been studied through variance components approach under normality of errors, which makes the inference vulnerable to outlying observations. In this work, the authors describe a method to assess the local influence in a minor perturbation of the model or data in the context of a pedigree study assuming that the observations follow a multivariate scale mixture of normal. This class of distributions have been an interesting alternative to obtain robust estimates against outlying observations. To illustrate the methodology, they use data from a brazilian heart study, involving 1,666 individuals from 81 families from the village of Baependi, in the state of Minas Gerais, Brazil.