

Diagnostics for censored mixed-effects models using the multivariate Student-t distribution

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In biomedical studies on HIV RNA dynamics, the viral loads generate repeated measures that are often subjected to (upper and lower) detection limits, and hence these responses are either left- or right-censored. Linear and non-linear mixed-effects censored (LMEC/NLMEC) models are routinely used to analyze these longitudinal data, with normality assumptions for the random effects and residual errors. However, the derived inference may not be robust when these underlying normality assumptions are questionable, especially presence of outliers and thick-tails. Motivated by this, Matos et al. (2013b) recently proposed an exact EM- type algorithm for LMEC/NLMEC models using a multivariate Student-t distribution, with closed-form expressions at the E-step. In this paper, we develop influence diagnostics for LMEC/NLMEC models using multivariate Student-t density, based on the conditional expectation of the complete data log-likelihood which eliminates the complexity associated with the approach of Cook (1977, 1986) for censored mixed-effects models. The new methodology is illustrated through an application to a longitudinal HIV dataset using the NLMEC framework. In addition, a simulation study is presented, which explores the accuracy of the proposed measures in detecting influential observations in heavy-tailed censored data under different perturbation schemes.

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