We consider the problem of locating multiple interacting quantitative trait loci (QTL) influencing traits measured in counts. In many applications the distribution of the count variable has a spike at zero. Zero-inflated generalized Poisson regression (ZIGPR) allows for an additional probability mass at zero and hence an improvement in the detection of significant loci. Classical model selection criteria often overestimate the QTL number. Therefore, modified versions of the Bayesian Information Criterion (mBIC and EBIC) were successfully used for QTL mapping. We apply these criteria based on ZIGPR as well as simpler models. An extensive simulation study shows their good power detecting QTL while controlling the false discovery rate. We illustrate how the inability of the Poisson distribution to account for over-dispersion leads to an overestimation of the QTL number and hence strongly discourages its application for identifying factors influencing count data. The proposed method is used to analyze the mice gallstone data of Lyons, Wittenburg, Li, Walsh, Leonard, Churchill, Carey, and Paigen (2003). Our results suggest the
existence of a novel QTL on chromosome 4 interacting with another QTL previously identified on chromosome 5. We provide the corresponding R code.