
Robust Confidence Intervals for Generalized Linear Models with an application to RNA-Sequencing Data

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Abstract

Confidence sets provide essential inferential summaries beyond point estimates in generalized linear models (GLMs). However, parametric interval construction critically depends on correct model specification. In high-throughput genomic data—such as RNA sequencing and other omics assays—model assumptions are often violated due to overdispersion, heteroskedasticity, and unobserved sources of variability. These factors can lead to serious undercoverage of nominal confidence levels. We propose a robust approach for constructing confidence intervals for regression parameters in GLMs. Our method is based on the inversion of hypothesis tests derived from sign-flipping of individual score contributions, combined with a bisection search algorithm for interval determination. We introduce two implementations of the procedure: an equitailed interval, which, given a level $1-\alpha$, balances one-sided p-values at level $\alpha/2$, and a symmetric interval, centered around the point estimate and defined by a joint condition on both tails. These frameworks inherit the properties of the flip-score test, guaranteeing asymptotic nominal coverage while remaining valid under variance misspecification. Simulation studies demonstrate the robustness and finite-sample accuracy of the proposed intervals across a range of model misspecifications. We further illustrate the method with an application to differential expression analysis in RNA-seq data. The proposed intervals provide a practical, distributionally robust alternative to conventional quasi-likelihood or Wald-based methods, particularly suited to the complex error structures of modern post-genomic datasets.

Keywords: Confidence sets, Generalized linear models, RNA seq, Semiparametric test, Sign flip, Variance misspecification

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