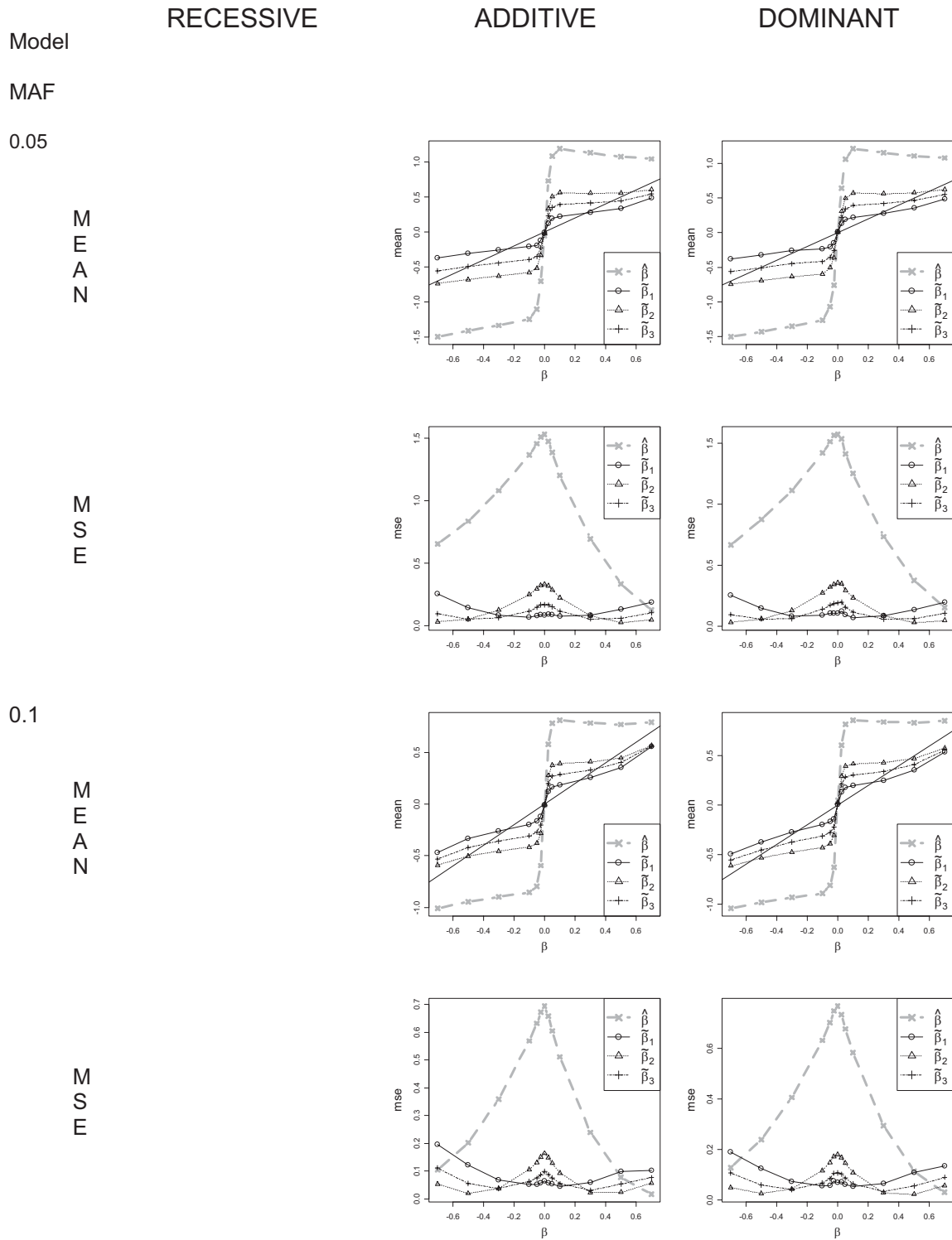


Supplemental Data

Estimating Odds Ratios in Genome Scans:

an Approximate Conditional Likelihood Approach

Arpita Ghosh, Fei Zou, and Fred A. Wright



0.5

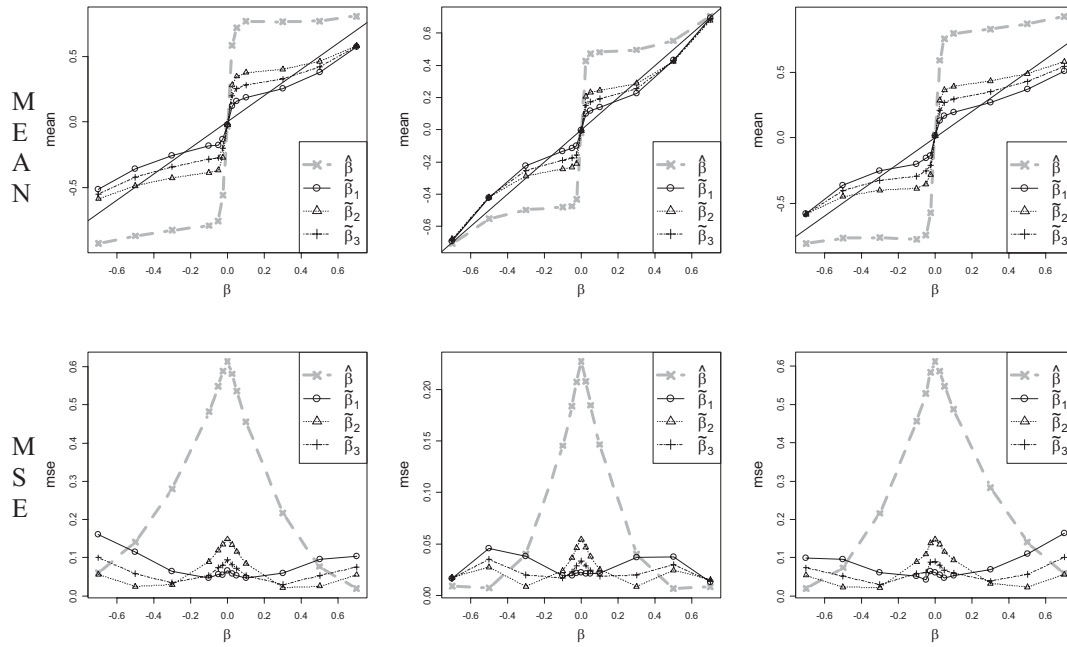


Figure S1. Expected Values and Mean Square Errors for the Estimators for the Three Models

MAF values are 0.05, 0.1 and 0.5 for additive and dominant models, and MAF = 0.5 for recessive models.

Model

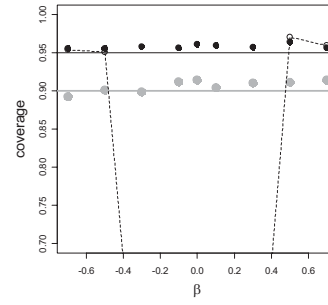
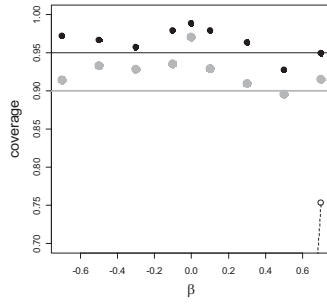
RECESSIVE

ADDITIVE

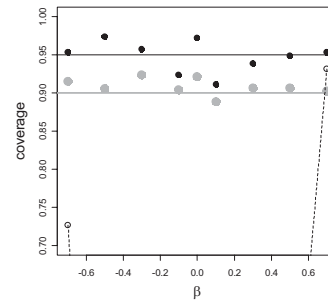
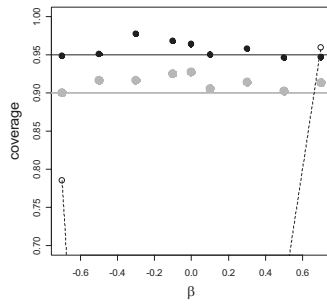
DOMINANT

MAF

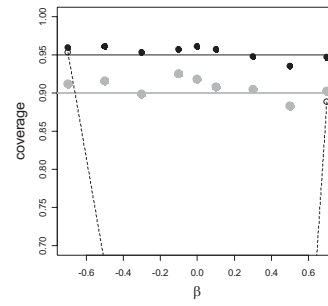
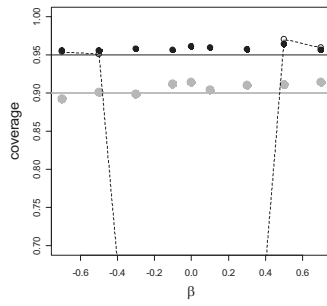
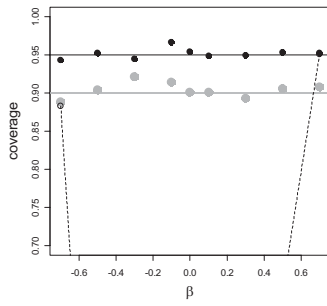
0.05



0.1



0.5



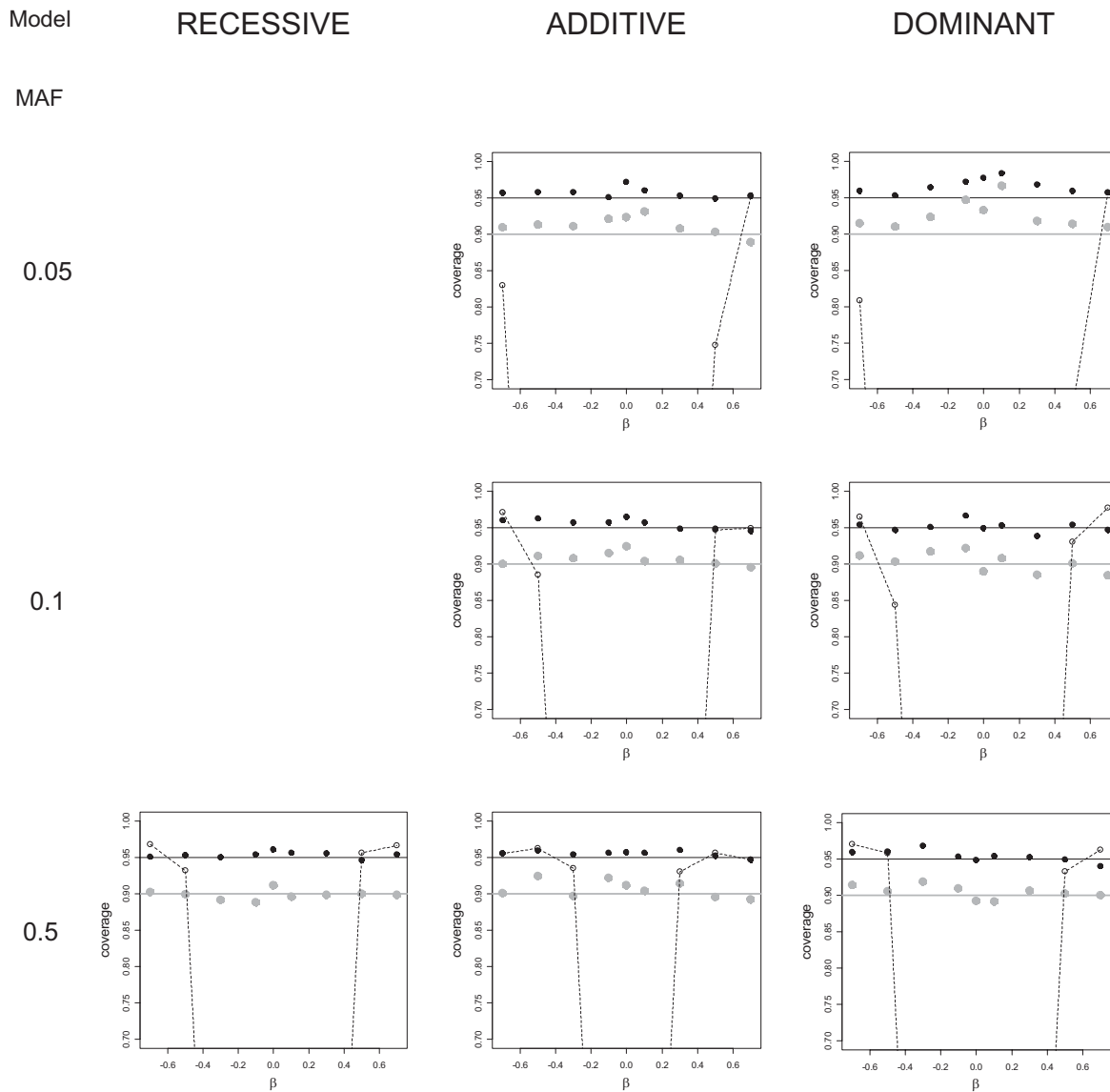


Figure S2. Estimates of the CI Coverage Probability Plotted Against for the Three Models

Various MAF values are shown (for recessive models, only MAF = 0.5 is depicted), as well as sample sizes of $n = 1000$ and $n = 2000$. Black dots correspond to 95% CIs; gray dots correspond to 90% CIs. The dashed curves represent coverage of standard 95% CIs that do not acknowledge the significance selection.

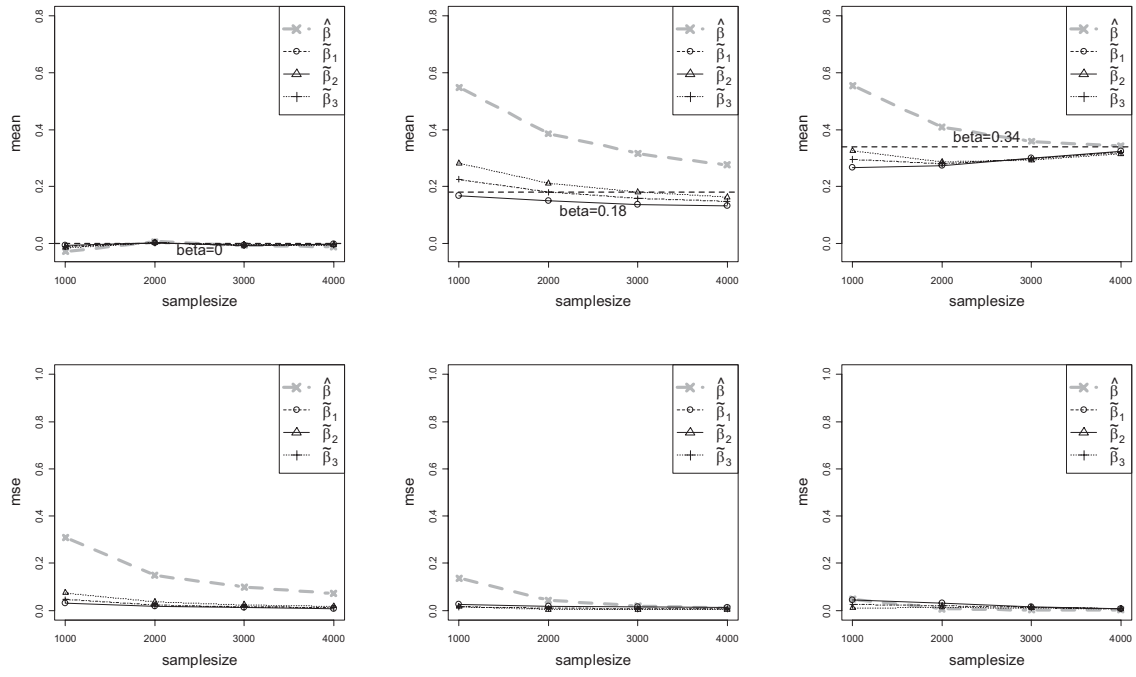


Figure S3. Expected Values and Mean Square Errors of the Estimators for the Additive Model with MAF = 0.25
 The results are plotted against sample size, for $\beta = 0, 0.18,$ and $0.34,$ corresponding to OR values 1.0, 1.2, and 1.4.

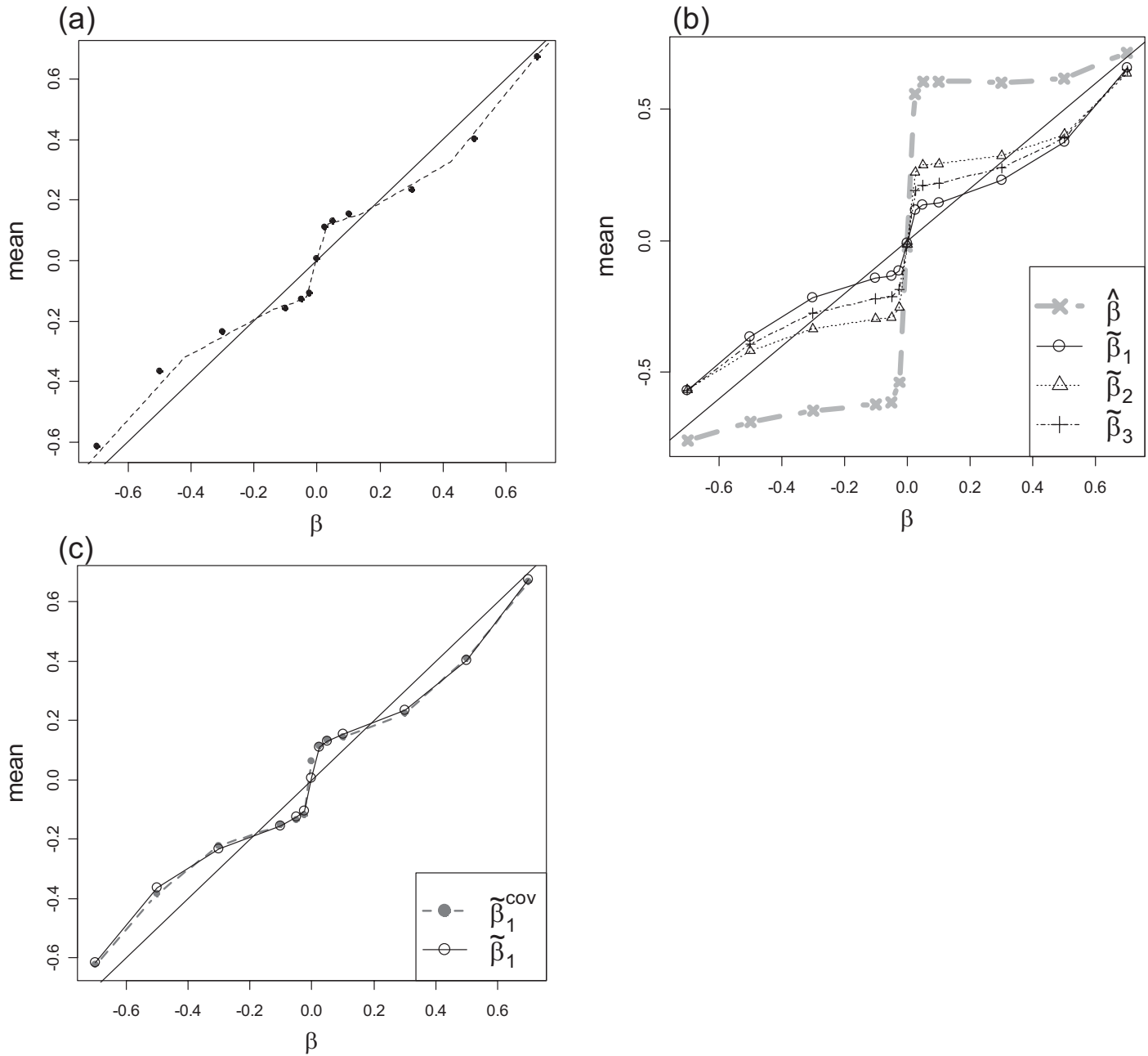


Figure S4. Properties of the Corrected Estimators Extend to Additional Settings

Throughout this figure we use the additive model, MAF = 0.25, and $n = 1000$ except where noted. (a) Expectations of $\hat{\beta}_1$ vs. β (plotted points) for $n = 1000$, overlaid with results for the same estimator versus β (dashed line) for $n = 2000$. The close correspondence is a consequence of the unifying treatment in terms of β . (b) Expectations of the estimators for $c = 5.5$ show that the qualitative behavior is similar to the behavior for $c = 5.0$. (c) Inclusion of both a discrete (2 degree-of-freedom) and a continuous (1 d.f.) covariate in the logistic regression modeling has essentially no effect on the behavior of our estimators.