

“Penalized Maximum Likelihood Estimation of Genetic Covariance Matrices”

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Abstract

Multivariate estimation of genetic parameters considering more than a few traits is inherently problematic due to substantial sampling variation. We consider the scope for ‘regularization’ of estimates within a maximum likelihood framework by penalizing the likelihood. For quantitative genetic analyses, partitioning of phenotypic covariances into their causal components is a major source of sampling errors. Hence penalties designed to ‘borrow strength’ from estimates of the phenotypic covariance matrix, which is estimated more precisely than any of its components, can yield ‘improved’ estimates of genetic parameters. We propose several options and associated strategies to determine the appropriate stringency of penalization, and present simulation results demonstrating their impact on sampling variances and bias of estimates, as well as results from an application to beef cattle data.