

A dynamic linear model for genetic analysis of longitudinal traits

S. Forni^{*,**}, D. Gianola^{*,**,***,2}, G. J. M. Rosa^{dagger} and G. de los Campos^{*}

^{*} Department of Animal Sciences, and ^{**} Department of Dairy Science, University of Wisconsin, Madison 53706; and ^{***} Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, 1432 Ås, Norway

Abstract :

A Bayesian model for quantitative genetic analysis of longitudinal traits is presented. It connects the model known as the Kalman filter (KF) with the standard mixed model of quantitative genetics. The KF model can be implemented easily in a Bayesian framework because, under standard prior assumptions, all fully conditional posterior distributions have closed forms. An analysis of beef cattle growth data including comparisons with a standard multivariate model was performed to assess applicability of the KF to animal breeding. Models were compared using the deviance information criterion and the Bayes factor. Models in which a KF acted on additive genetic and maternal effects were favored by the deviance information criterion, although KF did not describe residual (co)variance adequately. The Bayes factor did not provide conclusive evidence in favor of a specific model. Fitting KF to longitudinal traits provides estimates of genetic value for a whole range of time points, assuming that there are genetic differences through time between and within individuals. Different model embeddings of the KF in a mixed model were demonstrated to provide a more parsimonious (co)variance structure than a standard multivariate specification for the quantitative genetic analysis of longitudinal data.

Key Word :

Bayes factor, beef cattle, deviance information criterion, growth, Kalman filter, longitudinal data

Volume 87, Number 12, December 2009