Rejoinder

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INTRODUCTION

I would like to thank the discussants for their remarks. I hope that readers will find that the discussion helps to clarify the ideas that I tried to present in my paper. Mostly, I have chosen not to use this opportunity to restate my opinion on minor points where I disagree with the discussants or where I would give different emphasis.

In this introduction I will pass quickly over a number of issues which can each be presented briefly. Issues requiring longer discussion will be laid out as separate sections.

C. R. Henderson died in March 1989. Searle (1989) is an obituary.

Following comments by Harville and Speed, I think that my presentation would have been easier to understand if I had given greater emphasis to the way the linear model (1.1) would be handled if the random effects were not to be estimated. The linear model could be rewritten as

$$y = X\beta + \varepsilon,$$

where $\varepsilon = Zu + e$. Now $\mathrm{Var}(\varepsilon) = (ZGZ^T + R)\sigma^2$ and it is convenient to denote $ZGZ^T + R$ by V. The generalized least-squares estimate

$$\hat{\beta} = (X^T V^{-1} X)^{-1} X^T V^{-1} y$$

is the same as the BLUP estimate as explained in Section 5.1.

As Harville and Thompson indicated, BLUP is often explained using a predictive formulation. Henderson frequently used such a formulation. (e.g., Henderson, 1973). Goldberger (1962) also used a predictive formulation. I find my presentation simpler, but I recommend that readers consider the alternative to see which they find easier to comprehend.

As pointed out by Spall, I did not clarify the distinction between smoothers and filters in my paper. His statement "it is a Kalman smoother . . . that produces the BLUP estimate of u based on data y" might leave readers thinking that the Kalman filter is not BLUP. In fact, the Kalman filter is the BLUP estimate of u based on the data up to time t, y_t.

NOMENCLATURE

One of the major barriers to discussion in this area is the variety of nomenclature.

- I have used the term BLUP where many other people would use the term *parametric empirical Bayes*.
- I refer to *random effects* within *mixed models* whereas Steffey and Kass refer to *unit-specific parameters* within *conditionally independent hierarchical models*.
- Much terminology is application specific.

I do not wholeheartedly support the term BLUP because it includes the idea of predicting, and I do not believe that estimates of random effects are predictors for any greater fraction of their usage than estimates of fixed effects are predictors.

In ore reserve estimation I find it silly to speak of predicting something that happened millions of years ago. In time series, it is common to differentiate between smoothing, filtering and prediction. BLUP can be used for all three—which suggests that it is not merely *prediction*.

In the absence of general agreement about terminology, I would appeal for greater tolerance of other people's terminology.

COMPUTATIONAL ISSUES

As Speed hinted at in his discussion, when I first started working on the paper I was involved in the task of designing a computating strategy for estimating the genetic merits of dairy cattle using BLUP. (My first draft of the paper was dated February 22, 1982.)

Up to that time, BLUP for large numbers of sires had been done using several different models, but BLUP for models requiring the solution of sets of simultaneous equations with equations corresponding to both male and female animals (often referred to as *animal models*) had only been used for small number of animals. Henderson (1975b) had proposed the model for use within single herds. The Australian Dairy Herd Improvement Scheme accepted my opinion that an animal model was computationally practical for large numbers of animals and has been using it for several years. Details of the computing strategy are given in Robinson (1986). See also Jones and Goddard (1990). A nonessential development was a method for solving the sets of up to one million simultaneous linear equations which is described in Robinson (1988). Many other genetic evaluation schemes with large