JDS Communications®
2025; 6:231–236
https://doi.org/10.3168/jdsc.2024-0622
Mini-Review
Genetics

Variance reduction and measurement errors in estimating lactation milk yields using best prediction: An analytical review

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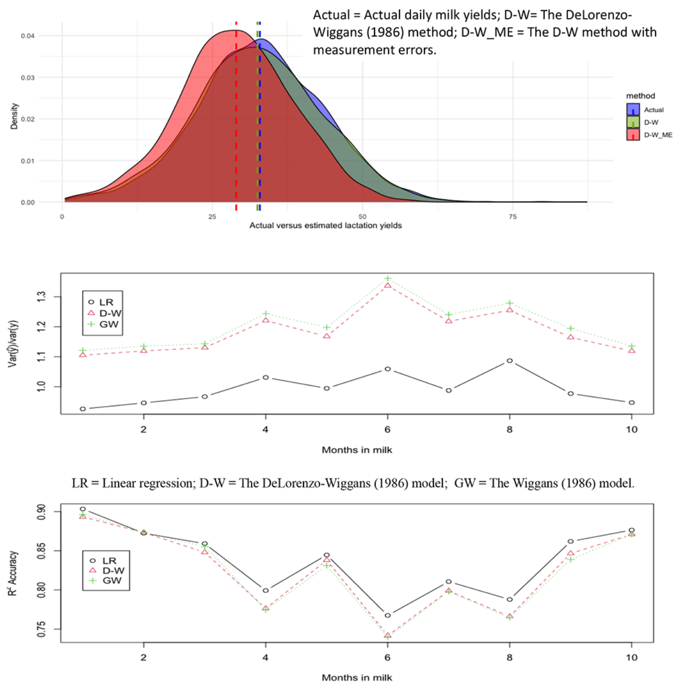
Graphical Abstract

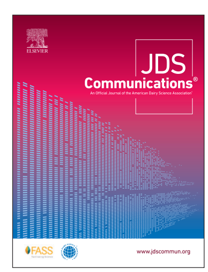


Summary

Since 1999, the best prediction (BP) method has been used in the United States to estimate unobserved daily and total lactation yields based on available test-day yields. Research shows that BP provides more accurate lactation yield estimates than previous methods. However, this method faces 2 major challenges. First, it reduces the variance of estimated yields relative to actual yields. This reduction in phenotypic variance is concerning for genetic evaluations, as it can lead to substantial underestimation of genetic variation. Second, measurement errors arise when projecting lactation yields from incomplete or inaccurate test-day records. These errors compromise the accuracy of lactation yield estimations by propagating through the calculation process, ultimately affecting the final genetic evaluation. This article provides an analytical review of BP, with a focus on addressing variance reduction and measurement errors.

Highlights

- Variance reduction is unavoidable in BP and linear regression models.
- Variance expansion factor and data collection ratio measures do not mitigate measurement errors.
- Measurement errors inherent in estimating daily milk yields are analytically explained.
- The challenges and possible solutions in dealing with measurement errors are illustrated.
- Alternative modeling strategies accounting for phenotypic errors are worth exploration.



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Variance reduction and measurement errors in estimating lactation milk yields using best prediction: An analytical review

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Abstract: Best prediction (BP) has been used in the United States to estimate unobserved daily and lactation yields from known test-day yields since 1999. This method has proven more accurate than its predecessors. However, it has 2 remarkable challenges in practice. First, BP reduces the variance of estimated yields compared with actual yields. Reduced phenotypic variance represents a concern because it can significantly underestimate genetic variations in genetic evaluations. Second, measurement errors occur in the projected lactation yields from incomplete or inaccurate test-day records. These errors can adversely affect the accuracy of lactation yield estimations and the subsequent genetic evaluations. This article provides an analytical review of BP, focusing on variance reduction and measurement errors. We demonstrate how variance reduction and measurement errors can be intrinsic to the method. Illustrative examples are presented, highlighting the practical challenges and possible solutions.

In the United States, it has been a long tradition for dairy farms to participate in a milk recording program in which their cows' milk production is measured and documented monthly (Volker, 1981). Typically, a cow is milked twice or more frequently on a test-day. Still, not all these milkings are weighed, primarily as a strategy to curtail costs associated with DHIA supervisor visits (Putnam and Gilmore, 1968). Instead, test-day milk yields (**MY**) are estimated from partial yields. Then, estimated test-day MY are used to impute unknown, non-test-day MY and extrapolate lactation MY up to 305 d (VanRaden, 1997; Cole et al., 2009). This same strategy is also used to estimate daily and lactation yields for milk fat and protein and to project SCC.

In February 1999, best prediction (**BP**) was officially adopted to estimate unobserved daily and lactation yields based on known test-day yields (VanRaden, 1997). Studies have shown that this method is more accurate than its predecessors for estimating 305-d yields (e.g., Norman et al., 1999). For estimating unknown daily or lactation MY, BP presupposes that their population means and (co)variances terms are known or estimated a priori, often taken to be the herd means from the previous year. Therefore, an unknown test-day or 305-d MY equates to the corresponding population average MY plus the covariance between the known and unknown MY, multiplied by the inverse of the variance for the known test-day MY and multiplied again by the known test-day deviations. A lactation MY is then obtained by aggregating all the known and estimated daily MY up to 305 d.

Alternatively, lactation MY can be directly modeled as the unknown quantity in BP. Let $\tilde{y}$ be an actual 305-d MY and $\tilde{\boldsymbol{x}}$ be a vector of actual MY measured on test-days, both pertaining to the same animal. The BP approach estimates 305-d MY as follows (VanRaden, 1997):

$$\tilde{y} = \mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\tilde{\boldsymbol{x}} - \boldsymbol{\mu}_x\right), \quad [1]$$

where $\boldsymbol{c}$ is a covariance vector between 305-d and test-day MY, $\mathbf{V}$ is the variance-covariance matrix between test-day MY, and μ_y and $\boldsymbol{\mu}_x$ are the population averages for 305-d MY and test-day MY, respectively. Here, for the sake of notation convenience, we omit the subscript index for individual animals.

Using projected lactation MY from the BP approach presents 2 major challenges in genetic evaluations: variance reduction and measurement errors. First, the BP approach can be viewed as a simple linear model with the regression coefficient defined by the known variance and covariance a priori. From the statistical viewpoint, variance reduction is inevitable with linear regression (**LR**) models, recognized long ago as the intrinsic phenomenon of regression known as "regression toward zero" (Galton, 1886). In estimating lactation MY from test-day MY, BP tended to have a smaller projected MY variance than actual MY variance (Weller, 1988; VanRaden et al., 1991). In practice, LR is not "perfect," and there is a nonzero variance of errors or residual effects. Consider a simple LR with an intercept: $y = a + bx + e$. The following inequality holds as long as $\hat{b}$ is equal (or approximately) to b and $Var(e) \geq 0$:

$$Var\left(\hat{y}\right) = \hat{b}^2 Var\left(x\right) \leq Var\left(y\right) = b^2 Var\left(\mathrm{x}\right) + Var\left(e\right). \quad [2]$$

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In contrast, multiplicative correction factor (**MCF**) models can inflate the variance of estimated daily MY from partial daily MY. For example, the commonly used DeLorenzo-Wiggans (**D-W**; DeLorenzo and Wiggans, 1986) model implements local LR each without an intercept on various milking interval classes. Without an intercept, the predictor variable(s) must account not only for the variability related to its specific influence on the dependent variable but also for its overall mean. This often requires larger coefficients because each predictor must scale more considerably to fit the data points. Consequently, the range of predicted values can be substantially wider, amplifying the variance of the predictions. The George Wiggans (**GW**; Wiggans, 1986) model, another widely used MCF approach, also inflates estimated yield variance. The GW model assumes a linear relationship between proportional daily MY and milking interval time. The reciprocal of the linear function of milk interval time defines the multiplicative correction factors for estimating test-day MY. While LR with an intercept tends to shrink the estimates, it, in turn, inflates multiplicative correction factors, thus leading to overestimated test-day MY in general.

In the Graphical Abstract (middle figure), we compared the estimated to actual daily MY variance ratios obtained from 3 methods: D-W, GW, and LR. Estimated test-day MY from the D-W and GW models had larger variances on average (10.7%–11.8%) than actual test-day MY variances, whereas LR resulted in a variance reduction (7.4%). Despite these differences, the R^2 accuracies (Wu et al., 2023a,b) of estimated daily MY were within a comparable range for the 3 methods (Graphical Abstract, lower figure). The R^2 accuracy was higher for the early lactation months than in later months because the variance of daily MY was the highest at the onset of milking and decreased afterward.

When unknown lactation MY are projected from estimated test-day MY instead of actual test-day MY, the potential errors are yet to be dealt with. These measurement errors are expected to increase as the proportion of sampled milk intervals decreases. Statistically, measurement errors refer to the difference between a measured or actual value of a predictor or explanatory variable, which can be inherent in the measurement process. Measurement error can be divided into 2 categories: random and systematic (Taylor, 1999). The former are measurement errors that make measurable values randomly inconsistent when repeated measurements are taken. The latter errors are not determined by chance but are introduced by repeatable processes inherent to a biased system. Hence, random errors have a zero mean, but systematic errors do not, as the latter effects are not reduced when observations are averaged. For example, when estimating daily MY, systematic errors can arise due to the nonrandom treatments of many secondary variables or factors, such as DIM, milking frequencies, milking months or seasons, and milking intervals.

A hypothetical situation is shown in the Graphical Abstract. In this example, derived from a Holstein farm milking record dataset (Wu et al., 2023b), measurement errors arose because a pre-adjustment of the effects due to months in milking and parities was made in the training but ignored in the testing. We randomly selected two-thirds of the data to train the D-W model and then tested for estimating test-day MY in the remaining data. The measurement errors were, on average, 4.0 kg, ranging from 3.01 kg (10th test-day) to 5.00 kg (third test-day). Measurement errors decreased R^2 accuracies (0.634–0.834) compared with R^2 accuracies without measurement errors (0.760–0.900).

In the United States, projected lactation yields from incomplete or partial lactation records were treated as having error variances greater than completed yields, and they received less emphasis in genetic evaluations (Wiggans and VanRaden, 1991). In reality, projected lactation yields had less variance than completely recorded yields (VanRaden et al., 1991). Weller (1988) found that the sire and error variances of projected yields were less than the corresponding variances of complete yields, especially for projections made early in lactation. He proposed adjusting coefficients of mixed-effects model equations to make the model assumptions match their actual distributions. In practice, such adjustments were not computationally trivial, yet the improvement in the accuracy of genetic evaluations was slight (Weller, 1988). Moreover, it was equally possible that other model effects, such as permanent environmental and herd-sire interaction effects, also have reduced variance in projected records, which are yet not considered.

Alternatively, VanRaden et al. (1991) proposed using expansion factors to rescale the variance of projected MY. The idea resembles a reversed BP such that the actual total MY, denoted by t, is the best predictor of the expanded record q (VanRaden et al., 1991). Expansion factors can be calculated using phenotypic correlations or genetic standard deviations. In the former case, for instance, a theoretical expansion factor using only phenotypic information is proposed as follows:

$$x = \sqrt{\frac{Var\left(t\right)}{Var\left(p\right)}} = \frac{1}{Corr\left(p,t\right)}, \quad [3]$$

where $Corr(p,t)$ is the phenotypic correlation between p and t. The above holds because $Cov(p,t) = Var(p)$. When $Var(p) \leq Var(t)$, we always have $x \geq 1$.

Meanwhile, data collection rating (**DCR**) was proposed and used by farmers and breeders to determine the relative data information quality in relation to the standard, supervised plan encompassing 10 monthly tests (VanRaden, 1997). For a nonstandard milking plan, the DCR is defined as the squared correlation between predicted and actual lactation MY multiplied by 100 and divided by the squared correlation for a standard milking plan (VanRaden, 1997). Under this framework, a rating of 100 is reserved for the standard plan (Powell and Norman, 2006). Now, consider applying the DCR to address projected lactation MY from estimated test-day MY (denoted by $\hat{y}$) compared with those projected from actual full-day test-day MY (denoted by $\tilde{y}$). Let y represent the actual lactation MY. Following VanRaden (1997), the DCR is the following:

$$\text{DCR} = \left(\frac{r\left(\hat{y},y\right)}{r\left(\tilde{y},y\right)}\right)^2 \times 100 = \frac{Var\left(\hat{y}\right)}{Var\left(\tilde{y}\right)} \times 100. \quad [4]$$

This holds assuming $Cov\left(\hat{y},y\right) = var\left(\hat{y}\right)$ and $Cov\left(\tilde{y},y\right) = Var\left(\tilde{y}\right)$, meaning that the errors are not uncorrelated with the actual lactation yields.

The following adjustment uses DCR as the expansion factor to rescale the variance of projected lactation MY from estimated test-day MY to be comparable to the variance of projected lactation MY from wholly sampled test-day MY:

$$\hat{y}^{*} = \bar{\hat{y}} + \sqrt{\frac{100}{\mathrm{DCR}}} \times \left(\hat{y} - \bar{\hat{y}}\right). \quad [5]$$

Here, $\bar{\hat{y}}$ stands for the mean of $\hat{y}$, $\hat{y}^{*}$ is the adjusted value of $\hat{y}$, and $x = \sqrt{\frac{100}{\mathrm{DCR}}}$ is the expansion factor. In management, DCR provides a conceptual tool to gauge the expected data information or variation obtained from a particular test plan compared with a standard benchmark. For instance, Norman et al. (1999) showed that, based on Canadian monthly supervised milking data, DCR was 97, 95, and 90, respectively, for 2 of 3, 1 of 2, and 1 of 3 milkings. Some breed associations have also selected certain minimum levels of DCR as a criterion for selecting cows.

Arguably, neither the expansion factor nor DCR represents a precise mitigation to measurement errors in the projected lactation MY from partially obtained test-day MY. VanRaden (1997) noted that the expected values of tests for partial and complete days were not equal even if the morning and evening MY were adjusted to a 24-h basis using correction factors for the number of milkings and milking intervals. He posited that the variance of a test-day yield imputed from a partial day ought to exceed that of a full day, attributing this to the incremental measurement errors introduced.

We consider measurement errors in 2 hypothetical scenarios to investigate their effects on the BP approach. First, suppose the BP equation is established using actual lactation and test-day MY, free of measurement errors. Then, measurement errors can be present when estimating lactation MY from estimated test-day MY with errors. Let $\hat{\boldsymbol{x}}$ and $\tilde{\boldsymbol{x}}$ be the vectors of estimated and actual test-day MY, respectively, and let $\boldsymbol{v}$ be a vector of differences between them, quantifying the corresponding measurement errors. That is,

$$\hat{\boldsymbol{x}} = \tilde{\boldsymbol{x}} + \boldsymbol{v}. \quad [6]$$

Without observing actual test-day MY $\left(\tilde{\boldsymbol{x}}\right)$, the lactation MY is estimated from $\hat{\boldsymbol{x}}$ as follows:

$$\begin{aligned} \hat{y} &= \mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right) \\ &= \mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\tilde{\boldsymbol{x}} + \boldsymbol{v} - \boldsymbol{\mu}_x\right) \\ &= \mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\tilde{\boldsymbol{x}} - \boldsymbol{\mu}_x\right) + \boldsymbol{c}'\mathbf{V}^{-1}\boldsymbol{v}, \end{aligned} \quad [7]$$

where the third term on the right side, $\boldsymbol{c}'\mathbf{V}^{-1}\boldsymbol{v}$, represents a systematic error term in the projected lactation MY.

Regression calibration, among the many with varied complexity, can be used to mitigate covariate measurement errors (Prentice, 1982). The idea is to apply iterated expectation, assuming nondifferential error (i.e., when the measurement error is unrelated to the outcome). That is,

$$\begin{aligned} E\left(y \mid \hat{\boldsymbol{x}}\right) &= E\left(E\left(y \mid \hat{\boldsymbol{x}}, \tilde{\boldsymbol{x}}\right) \mid \hat{\boldsymbol{x}}\right) \\ &= E\left(E\left(y \mid \tilde{\boldsymbol{x}}\right) \mid \hat{\boldsymbol{x}}\right) \\ &= E\left(\mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\tilde{\boldsymbol{x}} - \boldsymbol{\mu}_x\right) \mid \hat{\boldsymbol{x}}\right) \\ &= \mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(E\left(\tilde{\boldsymbol{x}} \mid \hat{\boldsymbol{x}}\right) - \boldsymbol{\mu}_x\right). \end{aligned} \quad [8]$$

The above regression calibration method relies on knowing $E\left(\tilde{\boldsymbol{x}} \mid \hat{\boldsymbol{x}}\right)$, which may not always be possible. Instead, approximations are typically used, as follows:

$$E\left(\tilde{\boldsymbol{x}} \mid \hat{\boldsymbol{x}}\right) \approx \boldsymbol{\mu}_{\tilde{x}} + \mathbf{C}_{\tilde{x}\hat{x}}\mathbf{V}_{\hat{x}}^{-2}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_{\tilde{x}}\right), \quad [9]$$

where $\boldsymbol{\mu}_{\tilde{x}}$ is the mean of $\tilde{\boldsymbol{x}}$, $\boldsymbol{C}_{\tilde{x}\hat{x}}$ is the covariance matrix between $\tilde{\boldsymbol{x}}$ and $\hat{\boldsymbol{x}}$, and $\mathbf{V}_{\hat{x}}^{2}$ is the variance-covariance matrix of $\hat{\boldsymbol{x}}$. All these variances and covariances are assumed to be known, or their values are estimated a priori.

In the second scenario, we assume the BP equation is constructed with projected lactation MY from estimated test-day MY; both are subject to measurement errors. Let $\boldsymbol{c}^{*}$ be a vector of covariance between test-day MY and lactation MY. Let $\mathbf{V}^{*}$ be the variance-covariance matrix between test-day MY. Here, we reserve the notations of $\boldsymbol{c}$ and $\mathbf{V}$ as the covariance vector and variance-covariance matrix for BP without measurement errors. Furthermore, we denote $\boldsymbol{a}$ and $\mathbf{B}$ as the vector and matrix to contain their differences as follows:

$$\boldsymbol{a} = \boldsymbol{c}^{*} - \boldsymbol{c}, \quad [10]$$

$$\mathbf{B} = \mathbf{V}^{*} - \mathbf{V}. \quad [11]$$

Then, the BP equation with measurement errors can be expressed as follows:

$$\begin{aligned} \hat{y}^{*} &= \mu_y + \boldsymbol{c}^{*\prime -1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right) \\ &= \mu_y + \left(\boldsymbol{c} + \boldsymbol{a}\right)'\left(\mathbf{V} + \mathbf{B}\right)^{-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right). \end{aligned} \quad [12]$$

Noting $(\mathbf{V} + \mathbf{B})^{-1} = \mathbf{V}^{-1} - \mathbf{V}^{-1}(\mathbf{V}\mathbf{B}^{-1} + \mathbf{I})^{-1}$ (Henderson and Searle, 1981), we expand the above BP equation as follows:

$$\begin{aligned} \hat{y}^{*} &= \mu_y + \left(\boldsymbol{c} + \boldsymbol{a}\right)'\left(\mathbf{V}^{-1} - \mathbf{V}^{-1}\left(\mathbf{V}\mathbf{B}^{-1} + \mathbf{I}\right)^{-1}\right)\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right) \\ &= \left[\mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right)\right] + \varepsilon_{\hat{y}}. \end{aligned} \quad [13]$$

The second term on the right-hand side of the above equation gives the error in the projected lactation MY:

$$\varepsilon_{\hat{y}} = \left[\boldsymbol{a}'\left(\mathbf{V}^{-1} - \mathbf{V}^{-1}\left(\mathbf{V}\mathbf{B}^{-1} + \mathbf{I}\right)^{-1}\right) - \boldsymbol{c}'\mathbf{V}^{-1}\left(\mathbf{V}\mathbf{B}^{-1} + \mathbf{I}\right)^{-1}\right]\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right). \quad [14]$$

Table 1. Ratios of variances (diagonal; in bold) and covariances (off diagonal) in the best prediction equations with versus without measurement errors[1,2,3]

Item	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}
V*/V										
x_1	**1.356**	0.996	1.024	1.016	1.027	1.008	1.022	1.012	1.031	0.997
x_2	0.996	**1.309**	0.991	0.985	0.974	0.968	0.980	0.971	0.980	0.960
x_3	1.024	0.991	**1.357**	1.004	0.983	0.975	1.002	0.977	0.980	0.982
x_4	1.016	0.985	1.004	**1.346**	0.992	0.989	1.019	1.001	1.011	0.987
x_5	1.027	0.974	0.983	0.992	**1.351**	0.988	1.013	0.985	1.002	0.988
x_6	1.008	0.968	0.975	0.989	0.988	**1.309**	1.000	0.961	0.985	0.972
x_7	1.022	0.980	1.002	1.019	1.013	1.000	**1.347**	0.986	1.006	0.994
x_8	1.012	0.971	0.977	1.001	0.985	0.961	0.986	**1.289**	0.986	0.975
x_9	1.031	0.980	0.980	1.011	1.002	0.985	1.006	0.986	**1.304**	0.991
x_{10}	0.997	0.960	0.982	0.987	0.988	0.972	0.994	0.975	0.991	**1.291**
c*/c										
y	1.020	0.974	0.995	1.016	0.993	0.986	1.013	0.989	0.989	0.982

[1] $x_1, \ldots, x_{10}$ = 10 test-days; y = lactation yield up to 305 d.

[2] **V*** = variances and covariances between test-day milk yields ($x_1, \ldots, x_{10}$) with measurement errors, compared with that without measurement errors (**V**).

[3] ***c**** = vector of covariances between lactation yields (y) and test-day milk yields ($x_1, \ldots, x_{10}$) with measurement errors, compared with that without measurement errors (***c***).

Then, the projected lactation MY, adjusted for the measurement errors, is as follows:

$$\begin{aligned}\hat{y} &= \mu_y + \boldsymbol{c}'\mathbf{V}^{-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right) \\ &= \hat{y}^* - \varepsilon_{\hat{y}}.\end{aligned} \qquad [15]$$

For illustration purposes, we simulated actual daily MY up to 305 d for 3,000 cows using the Wood lactation curve (Wood, 1967):

$$y_t = at^b e^{-ct}, \qquad [16]$$

where y_t was MY on time t in days. The model parameters were sampled from $a \sim TN(9.77, 2.23^2)$, $b \sim TN(0.18, 0.06^2)$, and $c \sim TN(0.004, 0.0007^2)$, where TN stands for a truncated normal distribution with all nonnegative values. The actual MY were simulated without including the error term. Then, random measurement errors were simulated on test-days mimicking the within-test-day repeatability model, $e_i \sim N\left(0, \frac{1-\rho}{\rho}\sigma_p^2\right)$, where $\rho = 0.75$ and σ_p^2 is the phenotypic variance. Each animal's observed test-day MY equaled the actual MY plus an error.

Table 1 shows the ratio of variances and covariances when projecting lactation MY from test-day MY with versus without measurement errors. Measurement errors led to a significant increase in the variances of estimated test-day MY compared with actual variances. The variance ratios ranged between 1.289 and 1.356. Nevertheless, the covariances between lactation and test-day MY and between test-day MY changed only slightly, ranging from 0.960 to 1.020. Coincidently, VanRaden (1997) noted that covariances among tests for partial and complete days remained unaltered under the presumption of random and mutually independent measurement errors; only the projected MY variances increased. Best prediction compressed the variance of projected lactation MY, with the estimated variance being 74.4% of the actual lactation MY variance. Measurement errors also caused a significant shift in the mean of estimated lactation MY from actual lactation MY (Figure 1). Scatterplots of estimated lactation yields from partial yields against those from actual daily yields are shown in Figure 2. Rescaling the variance of estimated lactation MY to match the actual variance was straightforward, but it did not mitigate measurement errors. However, using the adjustment outlined in Equations 14 and 15 resulted in an exact alignment between the distributions of projected and actual lactation yields, yielding a correlation of 1 (Figure 1). This adjustment also perfectly matched the variance, as the actual MY were generated "ideally" from the Wood function without errors. In reality, however, lactation phenotypes do not precisely follow assumed lactation curves, and variance reduction may still occur.

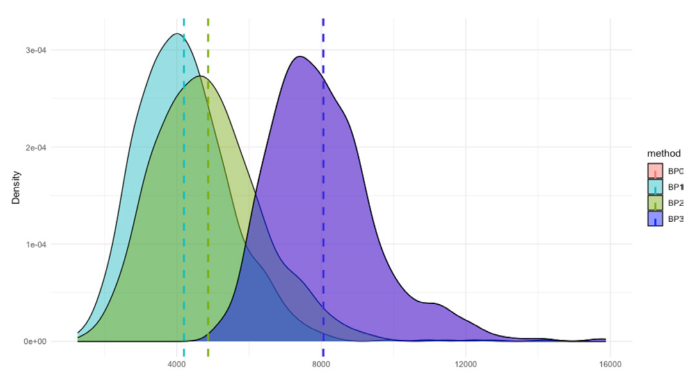

Figure 1. Comparing density plots of projected lactation milk yields obtained using best prediction (BP) under various scenarios. BP0 = lactation milk yields are estimated from actual test-day milk yields; BP1 = lactation milk yields are estimated from estimated test-day milk yields with measurement errors; BP2 = lactation milk yields are estimated from estimated test-day milk yields with measurement errors and rescaled to the same variance of actual lactation milk yields; BP3 = lactation milk yields are estimated from estimated test-day milk yields with measurement errors, and adjusted for measurement errors according to Equation 15. The density plots of projected lactation milk yields using BP0 and BP3 entirely overlap. The dashed lines represent means.

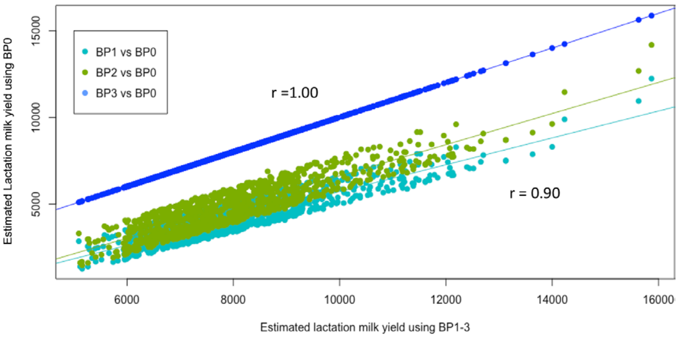

Figure 2. Scatter plots of estimated lactation milk yield using BP1, BP2, and BP3, respectively, against estimated lactation milk yield using BP0.

Note that the previously described decomposition of a project lactation MY is instructive but not a real-world example. The challenge is that the mitigation solution requires knowing the variance and covariance components, which may always be possible. A special case is one in which all the covariances due to measurement errors are zeros, such that, $\boldsymbol{c}^* = \boldsymbol{c}$ and $\mathbf{B} = Diag\left(\tau_1^{-1}\sigma^2_{\hat{x}_1} \quad \tau_2^{-1}\sigma^2_{\hat{x}_2} \quad \ldots \quad \tau_k^{-1}\sigma^2_{\hat{x}_k}\right)$ is a diagonal matrix with off-diagonal elements $\tau_1, \ldots\ldots, \tau_k$ equaling the ratio of the estimated over actual test-day MY. Then, an approximate adjustment can be formulated as follows:

$$\begin{aligned}\hat{y} &= \mu_y + \boldsymbol{c}'(\mathbf{V}^* - \mathbf{B})^{-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right)\\ &= \mu_y + \boldsymbol{c}'\left(\mathbf{V}^{*-1} + \mathbf{V}^{*-1}\mathbf{B}\left(\mathbf{V}^* - \mathbf{B}\right)^{-1}\right)\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right)\\ &= \left\{\mu_y + \boldsymbol{c}'\mathbf{V}^{*-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right)\right\} + \boldsymbol{c}'\left(\mathbf{V}^{*-1}\mathbf{B}\left(\mathbf{V}^* - \mathbf{B}\right)^{-1}\right)\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right).\end{aligned} \quad [17]$$

This holds because $(\mathbf{V}^* - \mathbf{B})^{-1} = \mathbf{V}^{*-1} + \mathbf{V}^{*-1}\mathbf{B}(\mathbf{V}^* - \mathbf{B})^{-1}$. In [17], $\hat{y}^* = \mu_y + \boldsymbol{c}'\mathbf{V}^{*-1}\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right)$ is the lactation MY projected from the estimated test-day MY with measurement errors, and $\delta = \boldsymbol{c}'\left(\mathbf{V}^{*-1}\mathbf{B}\left(\mathbf{V}^* - \mathbf{B}\right)^{-1}\right)\left(\hat{\boldsymbol{x}} - \boldsymbol{\mu}_x\right)$ is an adjustment term.

Some key distinctions between lactation MY models and test-day MY models for genetic evaluations are worth noting, as the methods discussed in this article are more relevant to lactation MY models. A lactation MY model leverages the high heritability of total lactation yield, providing assessments that are directly useful to dairy producers. Often, lactation models can better represent biological reality and the correlations among data points, especially at the extremes of days in milk, thus offering more accurate predictions of 305-d MY than test-day models with 3-term or 4-term Legendre polynomials. An advantage of test-day models is that they allow for multiple genetic effects. Nevertheless, lactation models fit a single genetic effect across the lactation, simplifying the computation. This is another issue to consider when handling large data sets, such as those with 100 million or more lactation records.

In conclusion, variance reduction and measurement errors are 2 major challenges when lactation MY projected from incomplete or inaccurate daily MY are used in genetic evaluations. In this review, we have analytically reviewed both topics. In dealing with the measurement errors, we have shown the analytical formulas, which are more illustrative than practical. In reality, precise mitigation of measurement errors can be challenging as no simple solutions are available. Alternative modeling strategies that account for phenotypic errors, such as measurement errors or response-in-error models (Buonaccorsi, 2010), merit further exploration. Bayesian modeling also offers valuable approaches for handling measurement errors in covariate and response variables (Bartlett and Keogh, 2018).

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Notes

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This study received no external funding.

No human or animal subjects were used, so this analysis did not require approval by an Institutional Animal Care and Use Committee or Institutional Review Board.

The authors have not stated any conflicts of interest.

Nonstandard abbreviations used: BP = best prediction; BP0 = lactation milk yields are estimated from actual test-day milk yields; BP1 = lactation milk yields are estimated from estimated test-day milk yields with measurement errors; BP2 = lactation milk yields are estimated from estimated test-day milk yields with measurement errors and rescaled to the same variance of actual lactation milk yields; BP3 = lactation milk yields are estimated from estimated test-day milk yields with measurement errors, and adjusted for measurement errors according to Equation 15; DCR = data collection rating; D-W = DeLorenzo-Wiggans model; GW = George Wiggans model; LR = linear regression; MCF = multiplicative correction factor; MY = milk yield.