

10. Data Analytics What Can New Analyses Techniques Bring for Better Farm Results 2

Title presentation

An alternative Interpretation of residual feed intake by phenotypic recursive relationships in dairy cattle

Author(s)

X-L Wu, K.L. Parker Gaddis, J. Burchard, H.D. Norman, E Nicolazzi, E.E. Connor, J.B. Cole and J. Durr

Institution for which the first author of this abstract is working

Council on Dairy Cattle Breeding, Bowie, MD 20716, USA.

Abstract

Feed efficiency is an important trait for genetic improvement programs because feed costs comprise a large portion of costs associated with dairy production. In the past decades, there has been an increasing interest in the use of residual feed intake (RFI) as a measure of net feed efficiency in meat and lactation animals. Studies on RFI often use a two-stage approach. First, an energy sink model treats feed intake as a linear regression of essential energy sinks, such as metabolic body weight, energy-corrected milk, and body weight change. It may also account for some additional covariates or factors. The residuals are taken to be the phenotypes of RFI. Then, the computed RFI phenotypes are fitted as the response variable in a quantitative genetic model to estimate the genetic values and relevant genetic parameters for net feed efficiency. Combining these two modeling stages leads to a one-step approach that eliminates the need to compute the residuals as the RFI phenotypes. However, the energy sink model, defined by a standard linear regression, is not statistically selfcontained concerning the model assumptions about the regressor variables. Besides that, the statistical features of RFI linear regression model have not been addressed adequately. Re-arranging the energy sink model suggests an alternative interpretation of RFI as a phenotypic recursive system between dry matter intake and energy sinks. In this technical note, we propose a Bayesian recursive structural equation model as a flexible, one-step solution to predict RFI and estimate relevant genetic parameters simultaneously. Relevant topics such as accounting for heterogeneous relationships between dry matter intake and energy sinks and extending to genomic prediction are also discussed. Extending the model to handle errors-in-variables is also relevant, but it remains a topic for future studies.