

involves regressing residuals against predicted or other model variables. In this method, the model is unbiased if residuals are not correlated with predictions and the slope is not significantly different from zero. Predicted values can also be centered making the slope and intercept estimates in the regression orthogonal and thus, independent. This allows for mean biases to be assessed using the intercepts of the regression equations, and the slopes to determine the presence of linear biases. Mean square error of prediction (MSEP) and its square root (RMSEP) are commonly used methods of evaluation. In general RMSEP values less than half of observed SD may be considered having a good performance. The MSEP can be decomposed into error due to 1) overall bias of prediction, 2) deviation of the regression slope from unity, and 3) disturbance. Examples of the third category include concordance correlation coefficient (CCC), and the Nash-Sutcliffe index (NSE). The CCC can be represented as a product of 2 components (range from 0 to 1 and 1 indicates perfect fit): a correlation coefficient estimate that measures precision and a bias correction factor that indicates how far the regression line deviates from the line of unity. The NSE is a normalized statistic that determines relative magnitude of residual variance compared with observed data variance. During model evaluation, a combination of the methods described above should be used to gain insight on model performance. The hands-on exercises include coding a function to calculate RMSEP, NSE and CCC for a set of data, which will be provided to participants.

Key Words: model performance, modeling, prediction accuracy

10 Example models for ruminant digestion and metabolism .

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Mathematical models are a tool to examine existing theories, find gaps in knowledge and explain phenomena of nutrient digestion and metabolism. The model can then produce simulation data to examine model behavior and determine if predictions from such models make biological 'sense'. The objective of this session is to explore how concepts or theories of nutrient digestion, metabolism and lactation physiology are translated into mechanistic mathematical equations and combined into a whole animal model using the Molly model. Molly is a mechanistic model of a dairy cow composed of a digestive element and an animal element. The digestive element converts chemical composition of the diet to volatile fatty acids, microbial growth and absorbed nutrients using physical attributes of the diet such as proportions of large and small particles and water passage. The animal element converts products from the digestive element into tissues (protein), waste products, heat production or secreted products (milk, milk fat, etc.). In this session, representations of digesta passage, protein synthesis and milk production in Molly will be examined beginning with a conceptual diagram. Then differential equations representing these processes will be described. Finally, because Molly predicts changes in production processes over time, full lactation simulations will be demonstrated to show examples of how passage, protein accretion and milk synthesis change over time.

Based on these examples, participants will conduct a simulation exercise which uses concepts of milk synthesis in Molly that were explored previously to predict lactation performance. A compiled version of the Molly program which operates only in the Windows environment is available for download at <http://www.vmtc.ucdavis.edu/laboratories/metabolic/molly.cfm> and will be used in the simulation exercise. In the exercise, participants will observe effects of altering milk production processes on production of the dairy cow to understand how metabolic processes can be represented by mathematical equations to provide a conceptual framework that improves our understanding of animal biology.

Key Words: computer simulation model, dairy cow, metabolism

11 Meta-regression analysis of animal nutrition literature. R.

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Quantitative literature summary (meta-analysis) is often used to generate a more comprehensive understanding of system behavior than can be obtained from individual experiments. Although every data set is unique and often requires some individualized analysis, most meta-analytical data can be evaluated using weighted, mixed effect, regression in a 9-part procedure, described as follows. 1) Search criteria should be clearly defined. 2) The literature should be searched and all response variables, their standard errors, and all explanatory variables should be recorded. 3) Data should be evaluated for transcription errors and outliers. 4) Missing standard errors should be estimated by error propagation, where possible. 5) Standard errors from fixed-effect regression and mixed-effect regression should be standardized to remove statistical analysis effects, and weights should be calculated from these standardized standard errors. 6) Backward, stepwise regression should be performed, using fixed effects for all explanatory variables of interest, and random effects for study, laboratory, or location, as needed. 7) After a model is identified where all variables included are below a significance cutoff defined by the researchers, the parameters removed from the model should be iteratively re-tested for significance in the final model. This step helps ensure variables were removed for non-significance rather than accidentally removed due to model instability. 8) Parameter estimate correlation should be evaluated using variance inflation factors. Variance inflation factors above 10 are acceptable for parameters correlated by calculation but all other parameters should have variance inflation factors below 10. If parameter estimates have excessive correlation, the parameter with the highest variance inflation factor should be removed. 9) Researchers should iterate through steps 6 to 8 until a model is identified where all parameters are statistically significant and have acceptable covariation. Although this procedure might require adjustment for some applications, it provides a general framework for performing meta-regression analysis of animal nutrition literature. The workshop associated with this abstract will walk through this process using an example data set.

Key Words: meta-analysis, regression, methods