1290 Reactive N emissions from crops and pastures.
C. Wagner-Riddle* and K. Congreves, *University of Guelph, Guelph, ON, Canada*

1291 Measurement and mitigation of reactive nitrogen species from swine and poultry production facilities.
W. Powers* and M. Capelari, *Michigan State University, East Lansing.*

Reactive nitrogen (Nr) species include oxides of nitrogen (nitric oxide, nitrogen dioxide and nitrous oxide [N_2O]), anions (nitrate and nitrite) and amine derivatives (ammonia [NH_3], ammonium salts and urea). Of the different Nr species, air emissions from swine and poultry facilities are dominantly NH_3 followed by N_2O. Excreta emissions are NH_3, ammonium ions, and urea with trace amounts of nitrate and nitrite. Farm systems and practices that handle manure as a wet product without pH modification favor almost exclusive NH_3 production while systems and practices associated with dry manure handling and bedded systems emit more NH_3 and result in greater N_2O production than that produced in wet systems. Results from a turkey grow-out study estimated that just under 1% of consumed nitrogen was emitted as N_2O from housing, compared to just under 11% emitted as NH_3. Despite generally lower N_2O emissions from animal housing compared to crop field emissions, N_2O emissions from housing are greater than often estimated. Lagoon systems emit more N_2O than either slurry or deep pit swine systems. Deep pit swine buildings emit as much as two-thirds less N_2O than deep bedded swine systems and laying hen, broiler chicken and turkey buildings emit over 4 times as much N_2O as swine housing, on an animal unit basis. Critical control points for mitigation center on 1) reducing the amount of nitrogen excreted and therefore excreted nitrogen available for loss to air or water during housing, manure storage or following land application of manures, 2) capturing excreted nitrogen to prevent release of nitrogen-containing compounds to air, water or soil resources or 3) conversion/treatment of nitrogen-containing compounds to non-reactive nitrogen gas.

Key Words: air emissions, poultry, swine

1292 Modeling atmospheric reactive nitrogen.
J. O. Bash*[1], K. Foley[1], J. T. Walker[1], M. W. Shepard[2], K. E. Cady-Pereira[3], S. Napelenok[1], D. K. Henze[4], and E. J. Cooter[1], *[1]USEPA, Research Triangle, NC, [2]Environmental Canada, Toronto, ON, Canada, [3]Atmoshperic and environmental Research Inc., Lexington, MA, [4]University of Colorado, Boulder.*

Nitrogen is an essential building block of all proteins and thus an essential nutrient for all life. Reactive nitrogen, which is naturally produced via enzymatic reactions, forest fires and lightning, is continually recycled and cascades through air, water, and soil media. Human activity has perturbed this cycle through the combustion of fossil fuels and synthesis of fertilizers. The anthropogenic contribution to this cycle is now larger than natural sources in the United States and globally. Until recently, little progress has been made in modeling of the nitrogen cycle in the environment due to the complexity of and uncertainty in its transport and transformation between soil, water and atmospheric media. The lack of understanding of these multimedia transport processes is due to the typical focus of research on specific media and the difficulty in parameterizing the human dimension of anthropogenically fixed reduced nitrogen and input into the environment, primarily through mineral fertilizer application to crops, the largest source of environmental reactive nitrogen. Here we will focus on modeling of the atmospheric component of the nitrogen cascade, with an emphasis on ammonia, emerging measurement techniques, and the potential for model improvements using emerging measurements, existing networks and modeling. The USEPA's Community Mulitscale Air Quality (CMAQ) model will be evaluated against observational trends in nitrogen deposition and ambient air quality from 2002 to 2012 and the sensitivity of CMAQ to NH_3 emissions will be explored. These findings will be presented with an emphasis on how the sensitivity of the modeling system to animal husbandry emissions and how the representation of these emissions can be improved.

Key Words: nitrogen cycle, emissions, environment

BIG DATA IN ANIMAL SCIENCE: USES FOR MODELS, STATISTICS AND META-APPROACHES

1293 Modeling in animal science: an introduction to quantitative understanding and prediction.
J. Dijkstra*, *Animal Nutrition Group, Wageningen University, Wageningen, Netherlands.*

In animal science, continuous advances in technology, computing, and engineering result in the generation of data at a rapidly increasing rate. Mathematical models enable quantitative analysis and integration of data to study the behavior and complexity of biological systems. This review highlights several aspects of modeling in the context of understanding, predicting and modifying complex processes in farm animal systems, and offers a current perspective for animal scientists without requiring specialized knowledge of mathematics or bioinformatics. A mathematical model is an equation or set of equations which represents the behavior of a system, and can be viewed as an idea, hypothesis or relation expressed in mathematics. In animal science, the system may range from the molecules in cells up to herd or flock level, with any level of the system being composed of subsystems lying at a lower

level, or being a subsystem of higher level systems itself. In empirical models, experimental data are used directly to quantify relationships based at a single level. Alternatively, mechanistic models are process-based and seek to understand causation in the system of interest by describing a system level in terms of components and associated processes at subsystem levels. Furthermore, models may be static, capturing behavior of the system at a particular point in time, or dynamic, describing how quantities in the system change with time. Several key benefits have been attributed to modeling. First, models can provide an integrative, quantitative understanding of mechanisms and associated relationships between responses of a system at various levels. Second, building a model may pinpoint areas where data or knowledge are lacking, and may indicate priorities for further research and development. Third, models provide quantitative assessments of management practices for the animal production sector including policymakers. This aspect becomes particularly important when observations are hardly possible because of time scale (changes emerging after several years or decades only) or technical difficulty of measurements. Two areas are in need of further development. Emerging–omics data on genetic and metabolic regulatory networks at the molecular and cellular level require further modeling methodology efforts to integrate such data with processes at a higher system level. Second, further advances in understanding and prediction at integrated levels will be obtained on combination of models that differ in underlying methodology. Examples include the integration of mechanistic models of animal metabolism with linear programming and life cycle assessment models.

Key Words: modeling; animal science; system

1294 Traditional versus structure-based model development strategies. L. O. Tedeschi[*1], R. R. White[2], C. F. Nicholson[3], B. L. Turner[4], M. A. Fonseca[1], and M. D. Hanigan[2], *[1]Texas A&M University, College Station, [2]Virginia Tech, Blacksburg, [3]The Pennsylvania State University, University Park, [4]Texas A&M University-Kingsville, Kingsville.*

An important challenge in agriculture modeling is deciding how to mathematically represent biological phenomena. The objective of this paper is to compare more traditional model development methods (e.g., empirical models) with structure-based modeling (SBM) such as system dynamics (SD). Substantial overlap exists between traditional and SBM approaches, but there are important differences. The overall steps of the modeling process and scientific rigor are quite similar, but their focus and implementation can differ substantially. The steps of both modeling approaches often comprise the 1) identification of a problem (research objective), 2) formulation of the mathematical (and/or statistical) statements, 3) data collection (experimentation), 4) model evaluation and quantitative analysis relevant to the modeling objectives. SBM often differs from traditional approaches in each of these phases such as defining the problem as the replication of observed dynamic behavioral modes (e.g., s-shaped growth or oscillations) rather than situational point prediction or statistical estimation of parameters (step 1), giving more attention to system structure based on cause-effect relationships in terms of the stock-flow (i.e., level variables and rate variables) and feedback processes that generate observed behavior and visualizing these relationships in causal loop diagrams (CLD) and stock and flow diagrams (SFD) (step 2), and data collection that encompasses a broader range of sources (experimental, secondary, expert opinion, participatory exercises) and may include concepts hypothesized to be important but for which limited data are available (step 3). Model evaluation criteria can also differ due to the intrinsic nature of SBM as greater focuses are given to behavioral mode replication and feedback loop dominance analysis (step 4). In general, traditional modeling approaches focus on defining analytical functions and their statistical consistency with observed biological responses, whereas SBM focus on the mechanistic explanations for system behaviors and the feedback relationships that led to them. For example, a traditional modeling approach could use a saturating function to describe movement of a substrate across a membrane, whereas SBM would focus on feedback processes that represent decreasing affinity of the membrane for that substrate as concentration increases. Although they can differ substantially in their implementation, these 2 mathematical modeling strategies should be viewed as complementary rather than competing tools.

Key Words: modeling, simulation, methodology

1295 Big data analysis techniques. N. St-Pierre*, *Ohio State University, Columbus.*

The term ‘big data’ has recently entered our lexicon. Data scientists and statisticians have loosely defined big data as datasets with billions (10^9) of rows (tupples) of data. Hence, very few datasets in the animal sciences would qualify as true big data. At best, we deal with large datasets in the millions of tupples. Regardless, some of the same issues surrounding big data analyses are shared with large data: 1) near certainty of the presence of outliers, and 2) low signal to noise (irrelevant variables, subtle relationships, data imbalance, near collinearity). In large datasets, outliers are more than unidimensional: higher dimensions must be scrutinized. An example of this involved the characterization of feed composition data. Techniques used to address the low signal to noise issue can be classified into 2 groups: opaque techniques and black box techniques. The most prevalent techniques in the first group are: visualization through smoothing, regression, principal component analysis (PCA), decision trees, clustering methods, and multivariate adaptive splines (MARS). Black box techniques include neural networks, k-nearest neighbor

(KNN), K-mean, support vector machines and genetic algorithm. Each technique will be briefly explained using an example. With PCA, we first find a direction that has maximum variance. A second direction is then found, which has maximum variance of all directions perpendicular to the first. The process is repeated until there are as many directions (vectors) as original variables. Advantages of PCA are the dimension reduction and the ability to handle more predictors than observations. Disadvantages are that they often lack interpretation, and are linear models. Issues when only summary statistics are available (i.e., meta-analysis) will be explained, including the importance of properly weighing observations and accounting for the inherent blocking in the meta-design.

Key Words: big data, principal component analysis, meta-analysis

1296 Evaluation of multilevel mixed effect models.

E. Kebreab*, *University of California, Davis, Davis.*

Simple mixed effect models have been extensively used in animal science literature. However, in some instances biological relationships require that models account for deviations of individual animals from that of the population. Furthermore, some animals might share similar genetic background because they are closely related (e.g., pig littermates) thus specification of animal within litter relationship (i.e., nested random effects) is necessary to model the hierarchical data structure. In some cases measurements taken on the same individual may not be independent (e.g., weekly BW measurements). This will result in models with heteroskedastic and serial correlated errors, which need to be evaluated and the errors minimized. Recent developments in statistical theory and computational power allow for specification of multilevel mixed effect models, especially nonlinear models. To demonstrate implementation of such models, an example is provided using data collected from an experiment with 40 pigs of 3 sexes originating from 17 litters and their BW measured weekly or every 2 wk up to 1,007 d. A multilevel mixed effects model was used within a growth function because it allows for estimation of all growth profiles simultaneously, and different sources of variation. Furthermore, variance in-homogeneity and within-animal correlation were introduced to the growth function. In the basic model, the variance was assumed to equal to identity matrix, i.e., the within-animal errors are independent, identical and random vectors. The basic model fit suggested that the within-animal variability increased with increasing BW and auto-correlation was also present. The variance-covariance matrix was then relaxed and decomposed into variance structure component and a correlation structure component that allows specification of model variance heterogeneity and serial correlation. Variance of the within-animal errors was modeled using a variance function, which when implemented reduced Bayesian Information Criteria (BIC) values to 8,950 compared to 9,861 for the basic model but did not remove the strong auto-correlation in the residuals. A continuous time autoregressive process of first order was applied to the within-animal errors because it deals with unequally spaced observations. This further reduced BIC to 7,146 due to removal of the serial correlated errors and thus inclusion of a continuous auto regressive process of first order is recommended when modeling frequently sampled growth data.

Key Words: multilevel mixed effect model, variance structure, autocorrelation

RUMINANT NUTRITION

1297 Effect of lactose inclusion in calf starters on rumen fermentation of weaned calves.

A. Saegusa*[1], K. Inouchi[2], M. Ueno[3], Y. Inabu[4], S. Koike[3], T. Sugino[4], and M. Oba[5], *[1]ZEN-RAKU-REN, Fukushima, Japan, [2]ZEN-RAKU-REN, Nishi-shirakawa, Japan, [3]Hokkaido University, Sapporo, Japan, [4]Hiroshima University, Higashi-hiroshima, Japan, [5]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to evaluate the effects of lactose inclusion in calf starters on ruminal pH and VFA profile. Sixty Holstein bull calves were raised on an intensified nursing program using milk replacer containing 28% CP and 15% fat, until 56 d of age. Calves were fed texturized calf starters containing lactose at 0% (Control), 5.0% (LAC5), or 10.0% (LAC10; $n = 20$ for each treatment) on a DM basis. All calf starters were formulated for 23.1% CP. All calves were fed treatment calf starters ad libitum from d 7 and their hay (Klein grass) intake was limited to 150 g/d (as fed). Ruminal pH was measured every 2 min using small ruminant rumen pH loggers (Dascor, CA) immediately after weaning (d 55 to 62) for 15 calves (5 calves per treatment), and 3 wk after weaning (d 77 to 80) for the other 45 calves (15 calves per treatment). Daily mean, minimum, maximum ruminal pH, and duration and area under rumen pH 5.8 were not affected by treatment for both periods (d 55 to 62 and d 77 to 80). However, Spearman's correlation coefficient (r_s) was 0.306 ($P < 0.05$) between lactose intake and minimum ruminal pH for d 77 to 80, indicating that actual lactose consumption may affect ruminal pH. In addition, hay intake was not affected by treatment, but it was positively correlated with daily mean ($r_s = 0.338$, $P < 0.05$) and maximum ruminal pH ($r_s = 0.408$, $P < 0.01$), and the variation in hay intake might have masked treatment effects on ruminal pH. Ruminal molar ratio of acetate (mean ± SE) was 40.6 ± 1.26 (Control), 42.8 ± 1.26 (LAC5), and 45.3 ± 1.26% (LAC10), molar ratio of propionate was 40.2 ± 0.98 (Control), 38.1 ± 0.98 (LAC5), 35.3 ± 0.98% (LAC10), and acetate/propionate ratio was 1.01 ± 0.06 (Control), 1.15 ± 0.06 (LAC5), 1.29 ± 0.06% (LAC10) on d 80, and the differences were significant