A common practice in Poultry Science is to compare new treatments to a control or between treatments tested in planned experiments. The overall F-test from an ANOVA of the data allows the researcher to reject or not the null hypothesis. Multiple comparison (MC) tests are then used to test the difference between subgroups of treatments and “making a decision about which test to use is not an easy task” (Demirhan et al., 2010, Journal of Statistical Computation and Simulation). In this work, we review several MC tests and study the influence of the number of repetitions and failures of assumptions on the power of tests using a simulation study (Poddlich et al., 1998, Bioinformatics), considering different variances and number of repetitions. The same type of procedures is used to analyze several real data sets.

**Key Words:** multiple comparison tests, statistical power, type i error, repetition, heterogeneity of variance

Statistical analyses are important methods for interpreting results of agricultural experiments for scientific writing, which should clearly communicate the particulars of the research being described in a way that it can be precisely repeated. Probabilities (p-values) are often described in articles in Poultry Science and related journals to compare treatment means to each other and to compare regression coefficients to zero. Most published data are subjected to ANOVA or regression models using the GLM (general linear models) procedures of the SAS (Statistical Analysis Software) program to determine the probabilities that means are different. Different statistical models and programming statements may lead to quite different conclusions. Several ANOVA and regression models are reported here. Data from an experiment with 2 independent variables (x1 and x2) and one dependent variable (y) were analyzed. Designs with 2 or more factors are frequent players in the world of experimental design. The computational burden of the attendant ANOVA is somewhat eased by the presence of statistical packages. Contrary to expectation, it is not clear from texts or the Manual(s) how the package(s) can be used to find components of the interaction effects, whether the factors are qualitative or quantitative factors. We show how SAS can be persuaded to calculate these components (A × B, etc., when A is a qualitative and B is a quantitative factor, and Linear A × Linear B, etc., when both A and B are quantitative factors). The procedure can be adapted to fit other packages which have provision for contrast calculations. The choice of an appropriate statistical model is important because conclusions from the subsequent analyses depend on the particular model used.

**Key Words:** ANOVA, regression, qualitative and quantitative factors, A× linear B, linear A× linear B contrasts

The term bioavailability means the degree to which a nutrient in a particular source can be absorbed and utilized for its required purposes by an animal. Bioavailability is expressed as a percent of an established “reference standard,” which is usually the form that was used to assess an animal’s dietary requirement for that nutrient. Experimental approaches (i.e., bioassays) to determine bioavailability must carefully considered unique nutritional characteristics of each nutrient source. The source’s purity, chemical structure, physical characteristics, accompanying carrier and metabolic steps necessary for utilization all interact to determine its bioavailability. These factors also interact to determine the shape of the relationship between the dietary level (dose) of a source and the response variable chosen to indicate its successful utilization. Thus, the experimental design of the bioassay and the statistical approach to analyze the results must be informed by the unique nutritional characteristics of the source being evaluated as well as the reference standard. For example, the design and statistical analysis of a bioassay used to compare a nutrient source that is chemically identical to the reference standard but differs in particle size or carrier attributes will often differ from the design and analysis used to assess a nutrient source that follows differing absorptive and metabolic pathways than the reference standard. Examples of the latter include seleno-DL-cystine vs sodium selenite and methionine-hydroxy analog vs D, L methionine. In each of these comparisons, either the test source or the reference source has multiple chemical forms. Each form has very different absorptive and metabolic paths and there is no reason to expect that their dose response relationships should be similar. Statistical processes for unbiased selection of the best fit models that describe the test source and also the reference standard should be employed to determine the bioavailability at the dietary level at which it will be fed in practice.

**Key Words:** bioassay, statistics, nutrition, reference standard, ingredient

This contribution focuses on applying mathematical models based on systems of ordinary first-order differential equations to synthesize and interpret data from egg production experiments. Models based on linear systems of differential equations are contrasted with those based on non-linear systems. Regression equations arising from analytical solutions to linear compartmental schemes are considered as candidate functions for describing egg production curves, together with aspects of parameter estimation. Extant candidate functions are reviewed, a role for growth functions such as the Gompertz equation suggested, and a function based on a simple new model outlined. Structurally, the new model comprises a single pool with an inflow and an outflow. Compartmental simulation models based on non-linear systems of differential equations, and thus requiring numerical solution, are next discussed and aspects of parameter
estimation considered. This type of model is illustrated in relation to
development and evaluation of a dynamic model of calcium and phos-
phorus flows in layers. The model consists of 8 state variables represent-
ing calcium and phosphorus pools in the crop, stomachs, plasma, and
bone. The flow equations are described by Michaelis-Menten or mass
action forms. Experiments that measures Ca and P uptake in layers fed
different calcium concentrations during shell-forming days are used
to evaluate the model. In addition to providing a useful management
tool, such a simulation model also provides a means to evaluate feeding
strategies aimed at reducing excretion of potential pollutants in poultry
manure to the environment.

236 Interpreting experiments on egg production—Statistical
considerations. L. Billard,* E. Song, M. Y. Shim, P. Sodsee, S. E.
Aggrey, and G. M. Pesti, University of Georgia, Athens.

The effects of series of balanced dietary protein levels on egg production
and egg quality parameters in laying hens from 18 through 74 weeks of
age were investigated in this experiment. One hundred forty-four pul-
lets (Bovans) were randomly assigned to individual cages with separate
feeders and were then equally assigned to 3 different protein level series
with isocaloric diets. Diets were separated into 4 phases of 18–22, 23–32,
33–44 and 45–74 weeks. The protein levels of high protein (H) series
were 21.62%, 19.05%, 16.32% and 16.05%, respectively. Medium pro-
tein (M) and low protein (L) series were 2% and 4% lower in balanced
dietary protein. The results clearly demonstrated the balanced dietary
protein level was the limiting factor for body weight, average daily feed
intake (ADFI), egg weight, hen day egg production (HDEP) and feed per
kilogram eggs. Experiments designed to investigate strategies to opti-
mize the productivity of layers are relatively long-term and expensive
to conduct. However, as the cost of research increases, mathematical
models become valuable tools to answer research questions. A major
application of mathematical modeling is accurate estimation of produc-
tion performance, growth, and feed consumption for poultry research
and production. Different models have been proposed, with varying
degrees of success, to fit those curves. Despite advantages in predict-
ing economic traits, a diversity of models can result in mathematical
complexity and differences in interpretation. One of these models using
repeated measures is appealing. The approximation from overall mean
value (entire experimental period), adding 2% protein to the M series
will increase HDEP by 2.56%, egg weight by 2.84 g and decrease feed
intake per kilogram eggs by 127 g. Contrary to the idea of a daily amino
acid requirement, these results may be used to determine profit maxi-
mizing levels of balanced dietary protein (and therefore amino acids).

Key Words: layer, protein titration, egg production, mathematical
equation, repeated measure

237 Design and interpretation of high throughput genomic
analysis. A. Zhilkovsky,* Georgia State University, Atlanta.

In many applications of high throughput sequencing, sequenced samples
contain multiple distinct but sometimes very similar sequences. Issues
arising from several of such applications such as reconstructing viral
quasi species, transcriptome reconstruction from RNA-Seq reads, as
well as metagenomics, re-sequencing, and high quality scaffolding
assembly will be addressed. Error-prone replication of RNA viruses
with high mutation rate creates a diverse population of closely related
variants known as quasi species. By understanding the quasi species,
more effective drugs and vaccines can be manufactured saving the costs.

The case study of reconstruction IBV quasi species in chicken will be
described. Transcriptome reconstruction and quantification from RNA-
Seq reads is potentially much more accurate than expression arrays
because they can take in account individual transcript expression as well
discover unknown transcripts. Existing tools for analysis of RNA-Seq
data will be described.

Key Words: RNA-seq, transcriptome, metagenomics, quasi species,
chicken

238 From data to function: Resources for modeling poul-
try genomics data. F. M. McCarthy,* Mississippi State University,
Starkville.

New sequencing technologies enable us to generate genomic data not
only for each agricultural species but also individual genomes. However
using this data to understand how changes in the genotype affect phe-
tonotype is hindered by poor annotation. Via AgBase we provide data,
tools and training to enable poultry researchers to functionally model
their genomics data sets. We are developing new tools for functional
annotation and developing ontologies to support annotation and analysis
of anatomy and phenotypic data. For example, eGIFT (Extracting Gene
Information From Text) identifies key functional terms for a gene or
gene set based upon published literature and we are developing refer-
ence gene sets, standardized gene nomenclature and chicken anatomy
and phenotype ontologies. We also facilitate functional modeling by
simultaneously developing analysis tools to use these new data types
and adapting existing tools to cope with the larger data sets generated
by RNAseq experiments. Moreover, we are developing resources for
comparative genomics so that functional annotation for closely related
species can be leveraged to identify common traits. In this session I
will discuss some of the resources available at AgBase, give examples
of how we have used this data to model functional genomics data sets
and describe our ongoing efforts to provide genomics resources for the
poultry community.

239 Utilization of phenotypic, full pedigree, and genomic infor-
mation for genetic evaluation in poultry. I. Misztal*, I. Aguilar', S.
Tsurtua', R. Rekaya', and S. E. Aggrey', 'Department of Animal and
Dairy Science, University of Georgia, Athens; 'Department of Poultry
Science, University of Georgia, Athens.

Currently, the genomic selection that exploits the SNP information is
performed in multiple steps and involves several approximations. It is
also hard to use for complicated models. A population-based relationship
matrix A can be modified to include genomically-derived relationships
and form a combined relationship matrix H. Use of H in BLUP allows
for the genomic selection in a single-step, for a single step genomic
BLUP (ssGBLUP). Experiences with field data in chicken, pigs and
dairy indicate that ssGBLUP is more accurate yet much simpler than
multi-step methods. Current limits of ssGBLUP are about 100,000
alleles, and 18-trait models involving 10 million of animals have
been run successfully. The inverse of H can also be used in existing
programs for parameter estimation but a properly scaled G is needed
for unbiased estimation. Also, as genomic predictions can be converted
to SNP effects, ssGBLUP is useful for GWAS. ssGBLUP makes the
use of the genomic information in BLUP and variance-component
programs a routine.

Key Words: SNP, GWAS, single-step BLUP

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240 Computational challenges in multiple line selection using genomic information in poultry. R. Rekaya*, I. Misztal¹, and S. E. Aggrey², ¹Department of Animal and Dairy Science, University of Georgia, Athens, ²Department of Poultry Science, University of Georgia, Athens.

With the advent of new technologies it is now possible to efficiently genotype animals for thousands of single nucleotide polymorphisms (SNP), generating high density markers maps. These high density maps can enable the identification of markers in population-wide disequilibrium with quantitative trait loci (QTL). Using groups of markers, the effects of genomic regions can be estimated and combined to form genomic estimated breeding values (GEBV). Several studies in the majority of animal species have shown that high accuracies for GEBV can be obtained in the absence of large numbers of progeny records. Two approaches are being used to estimate GEBVs: 1) single step procedure where phenotypic and genomic data are jointly considered in a general mixed linear model with modified relationship matrix and 2) a multi-step procedure where generally pseudo-records are regressed on a set of markers to estimate SNP effects followed by a validation step on animals not used in the first step. Several algorithms and methodologies ranging from simple regression models to Bayesian and machine learning procedure have developed to implement these methods. Differences between approaches and implementation methods are often small and data dependent. Although the basic methodological hurdles of using SNP information for genomic selection have been addressed, major practical and implementation issues are still not fully resolved. Issues such as admixed and crossbred populations in beef cattle, selective genotyping to reduce costs, especially in swine and poultry, and decay in accuracies as the time interval between training and validation animals increases are just to name few. In poultry and due to the short generational interval and limit economic value of any individual bird, following the dairy cattle example is likely not to be the best approach and different strategies should be pursued for multiple line genomic selection and perhaps some on selective genotyping.

Key Words: SNP, multiple line selection, selective genotyping, QTL, GEBV

241 Applying complex models to poultry production in the future: Economics and biology. H. Talpaz*, M. Cohen², B. Fancher², and J. Halley², ¹LIDM Software Systems Ltd., Herzliya, Israel, ²Aviagen Inc., Huntsville, AL.

The ability to determine the optimal broiler feed nutrient density which maximizes margin over feeding cost (MOFC) has obvious economic value. To determine optimal feed nutrient density, one must consider ingredient prices, meat values, the product mix being marketed and the projected biological performance. A series of 8 feeding trials were conducted to estimate biological responses to changes in energy and amino acid density. Eight different genotypes of sex-separate reared broilers were fed diets varying in energy (2723–3386 kcal ME/kg) and amino acid (0.89–1.65% digestible lysine with all essential amino acids being indexed to lysine) levels. Broilers were processed to determine carcass component yield at many different bodyweights (1.09 - 4.70 kg). Trials data generated were utilized in model constructed to discover the dietary levels of energy and amino acids which maximize MOFC on a per broiler or per broiler annualized basis (bird * number of cycles / year). The model was designed to estimate the effects of dietary nutrient concentration on broiler live weight, feed conversion, mortality, and carcass component yield. Estimated coefficients from the step-wise regression process are subsequently utilized to predict the optimal energy and amino acid concentration which maximizes MOFC. The effects of changing feed or meat prices across a wide spectrum on optimal energy and amino acid levels can be evaluated via parametric analysis. The model can rapidly compare both biological and economic implications of changing from current practice to the simulated optimal solution. The model can be exploited to enhance decision making under volatile market conditions.

Key Words: broiler, nutrient optimization model, parametric analysis, margin over feeding cost, carcass component yield