

Development of a Stochastic Pig Compositional Growth Model

A. P. Schinckel¹, N. Li², M. E. Einstein¹, and D. Miller²
Departments of ¹Animal Sciences and ²Agricultural Economics

Introduction

Several deterministic swine growth models have been developed which can be used to optimize the nutrition and management of the average pig within a population of pigs. Stochastic models incorporate the variation between pigs by modeling the compositional and live weight growth of numerous individual pigs. The objective of this research was to develop a simple stochastic compositional pig growth model.

Materials and Methods

Data from a Purdue University research trial was used as the example data set. High lean gain gilts were reared via all-in all-out procedures. Serial live weight and real time ultrasound measurements were taken at 21-day intervals starting at 49 days of age. Empty body protein and lipid mass were predicted from the live weight and serial ultrasound measurements.

The liveweight data were fit to alternate mixed nonlinear models. The best model based on residual standard deviation (RSD) and Akaike's Information Criteria (AIC) statistics was $WT_{it} = (C + c_i) (1 - \exp(-\exp(M' + m'_i) t^A)) + BW$, where WT_{it} is the weight of the i^{th} pig at t days of age; C , M' , and A are fixed population mean parameters; c_i and m'_i are random effects for the i^{th} pig; t is days of age and BW is birth weight (3.1 lb). The means and variances of the c_i and m'_i values and covariance between the c_i and m'_i values were calculated. Equations were developed from a set of c_i and m'_i values sampled from a large sample of c_i and m'_i values with the same distribution as the observed values. These values, when used in the nonlinear live weight function, reproduce a population of pigs with a distribution of individual live growth curves.

To produce this data, the live weight of a pig at each specific age is the predicted live weight (WT_{it}) plus a residual error term (e_{it}). The residual error term is a random effect produced by multiplying the RSD of the original equation by a value sampled from standard normal distribution (mean = 0, variance = 1).

Using the original live weight data, the predicted empty body protein (MTPRO) mass was fitted to live weight. Several mixed nonlinear functions were evaluated. The best fit was $MTPRO = C (f(LW)) + cp_i (f(LW))^D + e_{ij}$, where LW is live weight, $f(LW) = (1 - (\exp(b_0 + b_1 LW + b_2 LW^2)))$, C and D are fixed effects, cp_i is a random effect for the i^{th} pig, and e_{ij} is the residual error of the i^{th} pig at the i^{th} live weight. The value of D describes the relative magnitude of the between pig standard deviation relative to the mean MTPRO at a specific live weight. The value of D was 1.853, indicating that the predicted between pig coefficient of variation increased as live weight increased. In other words, the variation in MTPRO percentage increased as live weight increased.

The mean and variance of cp_i was calculated. The relationship of cp_i with live weight growth was evaluated via regression analysis. The best equation to predict cp_i was a function of predicted age at 242 lb ($D242$) and $D242^2$ with an R^2 of 0.0596. The distribution and relationship of cp_i to the live weight function was $cp_i = c\hat{p}_i + b_1 Z$, where $c\hat{p}_i$ is the value of cp_i predicted from the $D242$, $D242^2$ equation, Z is a random variable with a standard normal distribution, and b_1 is a coefficient calculated to produce cp_i with the same total variance as the original cp_i values.



The MTPRO mass at a specific weight is $c\hat{p}_i + \text{RSD } Z$, where the RSD is the residual standard deviation of the original equation and Z is a random variable with a standard normal distribution. Utilizing these relationships and a program that produces a distribution of the three predicted random effects (c_i and m'_i for live weight; c_p for protein to live weight function), a distribution of pigs can be produced to reflect the true variation in predicted compositional growth.

Several functions from a daily compositional growth model were utilized to predict daily lipid accretion and metabolizable energy intake (ME, Mcal): Total body lean mass (TBLEAN) = $6.8 (\text{MTPRO})^{.867}$, empty body weight (live weight minus gut fill) = $0.93 \times \text{on-farm live weight}$, and total body fat tissue mass (TBFAT) = empty body weight – TBLEAN. Also TBFAT = $a (\text{empty body lipid mass})^b$ where a and b are sex-population specific parameters. Thus, empty body lipid mass = $(\text{TBFAT}/a)^{1/b}$. Daily ME intake (Mcal/day) is a function of maintenance plus the energy cost of protein and lipid accretion: $\text{MEI, Mcal/day} = 0.255 (\text{LW, kg})^{.60} + (8.84 \text{ protein accretion, kg/d}) + (11.4 \text{ lipid accretion, kg/d})$

Prediction equations were developed for several common carcass backfat and muscle measurements. The predicted value of each carcass measurement was a function of carcass weight, fat-free lean or total carcass fat mass, sex, and lean of fat percentage plus $Z * \text{RSD}$, where Z is a value sampled from a standard normal distribution and RSD is the residual standard deviation of the prediction equation.

Results

The means, standard deviations and correlations of the serial live weights are shown in Table 1. The standard deviation in live weight increases with age and the serial correlation of serial live weights at the younger ages (49 to 70 days and 70 to 104 days) is lower than the correlations of the serial live weights after 153 days of age. The predicted standard deviation in carcass weight, fat-free lean mass, total carcass fat tissue mass, and all carcass measurements increase as the age at marketing increases (Table 2).

The stochastic model predicts a live weight growth curve for each individual pig. Also, each pig has an individual compositional growth curve including a predicted daily carcass fat-free lean and carcass fat tissue gain. For this reason, the stochastic model can be used to predict the live weight and carcass composition of groups of barrows and gilts marketed at different ages. The marketing strategy that maximizes the daily return for the grow-finish facility above daily feed costs can be identified. Stochastic models can be used to develop optimal sorting and marketing strategies and to evaluate the costs and returns of specific management decisions that effect variation.

Implications

This stochastic model can be used to develop marketing and Paylean use strategies that target specific mean and distribution of carcass composition end points. This stochastic model is a tool in which to refine vertically coordinated pork production systems.



Table 1. Predicted means, standard deviation and correlations of serial live weights

Age	Mean, lb	SD	Correlations				
			70	104	132	153	174
49	49.0	5.51	0.78	0.76	0.73	0.69	0.67
70	85.2	7.67		0.87	0.86	0.83	0.81
104	153.1	12.01			0.94	0.93	0.91
132	210.9	15.94				0.96	0.96
153	252.4	19.05					0.98
174	290.8	21.69					

Table 2. Mean and standard deviations for live weight and carcass measurements at alternative marketing ages

Age	146 days		160 days		174 days	
	Mean	SD	Mean	SD	Mean	SD
Live weight, lb	238.9	18.1	265.6	19.8	290.6	21.7
Hot carcass wt, lb	179.4	15.1	202.0	16.7	223.4	18.3
Fat-free lean, lb	94.0	8.1	103.1	8.8	111.3	9.7
Total carcass fat, lb	54.4	8.5	62.4	10.4	70.8	12.1
Fat depth, 10 th rib	0.82	0.11	0.88	0.13	0.94	0.15
10 th Rib loin muscle area, in ²	6.34	0.43	6.70	0.47	7.24	0.53
Optical probe fat depth, in	0.81	0.10	0.84	0.11	0.89	0.13
Optical probe muscle depth, in	2.06	0.12	2.13	0.12	2.20	0.13
Midline backfat last rib, in	0.93	0.16	1.00	0.17	1.06	0.18

