A Comparison of Fitting Growth Models with a Genetic Algorithm and Nonlinear Regression

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ABSTRACT A genetic algorithm (GA), an optimization procedure based on the theory of evolution, was compared with nonlinear regression for the ability of the 2 algorithms to fit the coefficients of poultry growth models. It was hypothesized that the nonlinear approach of using GA to define the parameters of growth equations would better fit the growth equations than the use of nonlinear regression. Two sets of growth data from the literature, consisting of male broiler BW grown for 168 and 170 d, were used in the study. The growth data were fit to 2 forms of the logistic model, the Gompertz, the Gompertz-Laird, and the saturated kinetic models using the SAS nonlinear algorithm (NLIN) procedure and a GA. There were no statistical differences for the comparison of the residuals (the difference between observed and predicted BWs) of growth models fit by a GA or nonlinear regression. The plotted residuals for the nonlinear regression and GA-determined growth values confirmed observations of others that the residuals have oscillations resembling sine waves that are not represented by the growth models. It was found that GA could successfully determine the coefficients of growth equations. A disadvantage of slowness in converging to the solution was found for the GA. The advantage of GA over traditional nonlinear regression is that only ranges need be specified for the parameters of the growth equations, whereas estimates of the coefficients need to be determined, and in some programs the derivatives of the growth equations need to be identified. Depending on the goal of the research, solving multivariable complex functions with an algorithm that considers several solutions at the same time in an evolutionary mode can be considered an advantage especially where there is a chance for the solution to converge on a local optimum when a global optimum is desired. It was concluded that the fitting of the growth equations was not so much a problem with the fitting methodology as it is with the form of the equation.

(*Key words*: broiler, growth equation, genetic algorithm, regression analysis, mathematical model)

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INTRODUCTION

Numerous growth equations have been developed to describe and fit the nonlinear sigmoid relationship between growth and time. Growth curves for poultry generally have the following characteristics: an accelerating phase of growth from hatching, a point of inflection in the growth curve at which the growth rate is maximum, a phase where growth rate is decelerating, and a limiting value (asymptote) mature weight (Wilson, 1977). The fitting of nonlinear growth equations is more difficult than for linear models. Traditional statistical methods for nonlinear models require a starting point to begin the optimization. Often the quality of the final solution is dependent upon the position of this starting point in the search space. For example, in fitting a growth model function with the SAS NLIN procedure, instead of listing regression variables, as is done with linear models, the nonlinear regression expression must be written, the parameter names declared, and initial parameter values specified. Coefficients and parameters are estimated through an iterative approach. The SAS manual (SAS Institute Inc., 1999) lists several iterative methods of computation that are used including steepest descent (gradient), Newton, Gauss-Newton, Marquardt, and multivariate secant (DUD) methods. The Marquardt method is a compromise between the Gauss-Newton and steepest descent methods (Marquardt, 1963). Some nonlinear regression models are difficult to fit, and there is no guarantee that the procedure picked can fit the model successfully (SAS Institute Inc., 1999).

The use of genetic algorithms (GA) is a recently developed optimization approach that can be used as an alternative to regression analysis to fit mathematical models (Goldberg, 1989; Michalewicz, 1992; Haupt and Haupt,

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Abbreviation Key: GA = genetic algorithm; SAS NLIN = SAS nonlinear algorithm.

TABLE 1. Initial values for nonlinear regression and parameter ranges for genetic algorithm calculations

	Nonlinear regression	Genetic algorithm	
Model	Initial estimate	Range of values	
Logistic (Rogers et al., 1987[1])			
Maximum response (A)	5845	5000	7000
Initial response (B)	9.34	7	10
Rate constant (K)	0.96	0.90	1.00
Predicted (N)	–676	–600	–800
Gompertz (Rogers et al., 1987)			
Maximum response, (A)	5800	5000	7000
Intercept (B)	58	50	70
Rate constant (K)	0.03	0.01	0.04
Saturation kinetics (Rogers et al., 1987)			
Maximum response (A)	5800	5000	7000
Intercept (B)	6.7	0	150
Rate constant (K)	4000	0	30000
Kinetic order (N)	3	0	4
Gompertz-Laird (Aggrey, 2002)			
Hatching weight (Wo)	44.6	40	50
Initial growth rate (L)	0.0908	0.08	0.10
Rate of decay (K)	0.0224	0.02	0.03
Logistic (Aggrey, 2002)			
Asymptotic weight (Wa)	2192.7	2000	2300
Exponential growth rate (K)	0.0422	0.03	0.05
Age at maximum growth (ti)	72.7	70	75

[1] Data are from Rogers et al. (1987) and are used by permission.

1998). A GA is a computational method modeled on the theory of biological evolutionary processes that can be used to find optimal solutions. For example, GA can be used to find the maximum and minimum of a function, to find an optimal route on a map, or to minimize the cost of products. In the problem set up, a GA estimation does require an estimate of the parameter range in which the solution values might be found for the problem. The choice of a starting point plays a significant role in finding a good solution to the problem with a large number of local optima. Genetic algorithms, with their many potential solutions approach, can search multiple points simultaneously and, therefore, can avoid being caught in a local optimum when a global optimum is sought.

It was hypothesized that the nonlinear approach of using GA to define parameters of growth equations would better fit the growth equations than use of nonlinear regression.

MATERIALS AND METHODS

Data

The BW data and growth models were based on research results reported by Rogers et al. (1987) and Aggrey (2002). Growth data used in this study were average values of male BW for a 168-d period (Rogers et al., 1987) and of male BW for a 170-d period (Aggrey, 2002). Birds used in the study conducted by Rogers et al. (1987) were Petersen × Arbor Acres, and those in the study by Aggrey (2002) were from an unselected, randomly mated Athens-Canadian poultry population. Specific husbandry of those birds can be found in those respective papers.

Growth Models

The growth models examined and fit were as follows:

- Logistic model, (Rogers, et al., 1987)

$$W = n + (A - n)/(1 + B \times Y^t)$$

where n = the predicted response as t (time) approaches the negative asymptote, A = the maximum response, B relates initial BW to potential response, and Y = time constant.

- Gompertz model, (Rogers, et al., 1987)

$$W = A \exp[-\log(A/B) \exp(-Kt)]$$

where W = the weight to age (t) with 3 parameters: A = asymptotic or maximum growth response, B = intercept or weight when age(t) = 0, and K = rate constant.

- Saturation kinetics model (Rogers, et al., 1987)

$$W = (bI + At^s)/(I + t^s)$$

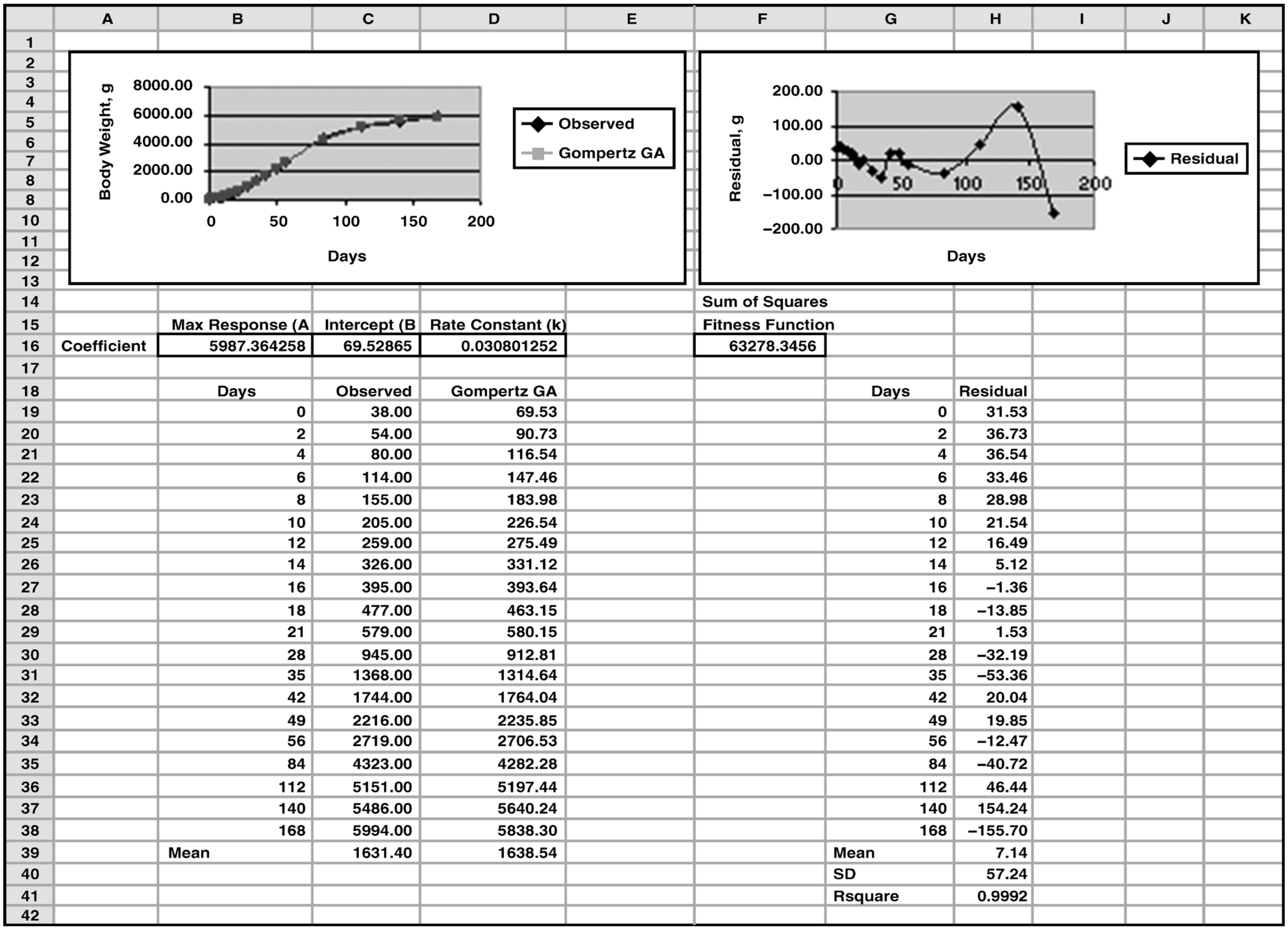
where W = the response of the chick, b = response intercept, A = maximum response, I = nutrient rate constant, and s = kinetic order of the response as t approaches zero.

- Logistic model (Aggrey, 2002)

$$Wt = Wa/[1 + \exp(-K(t - ti)]$$

where Wt = the BW at time t, Wa is the asymptotic BW, K is the exponential growth rate, and ti is the age at the inflection point.

- Gompertz-Laird model (Aggrey, 2002)



	A	B	C	D	E	F	G	H
14						Sum of Squares		
15		Max Response (A	Intercept (B	Rate Constant (k)		Fitness Function		
16	Coefficient	5987.364258	69.52865	0.030801252		63278.3456		
17								
18		Days	Observed	Gompertz GA			Days	Residual
19		0	38.00	69.53			0	31.53
20		2	54.00	90.73			2	36.73
21		4	80.00	116.54			4	36.54
22		6	114.00	147.46			6	33.46
23		8	155.00	183.98			8	28.98
24		10	205.00	226.54			10	21.54
25		12	259.00	275.49			12	16.49
26		14	326.00	331.12			14	5.12
27		16	395.00	393.64			16	−1.36
28		18	477.00	463.15			18	−13.85
29		21	579.00	580.15			21	1.53
30		28	945.00	912.81			28	−32.19
31		35	1368.00	1314.64			35	−53.36
32		42	1744.00	1764.04			42	20.04
33		49	2216.00	2235.85			49	19.85
34		56	2719.00	2706.53			56	−12.47
35		84	4323.00	4282.28			84	−40.72
36		112	5151.00	5197.44			112	46.44
37		140	5486.00	5640.24			140	154.24
38		168	5994.00	5838.30			168	−155.70
39		Mean	1631.40	1638.54			Mean	7.14
40							SD	57.24
41							Rsquare	0.9992
42								

FIGURE 1. Genetic algorithm spreadsheet setup for fitting the Gompertz equation with GeneHunter. Data are from Rogers et al. (1987) and are used by permission.

$$Wt = Wo \exp [(L/K)(1 - \exp(-Kt)]$$

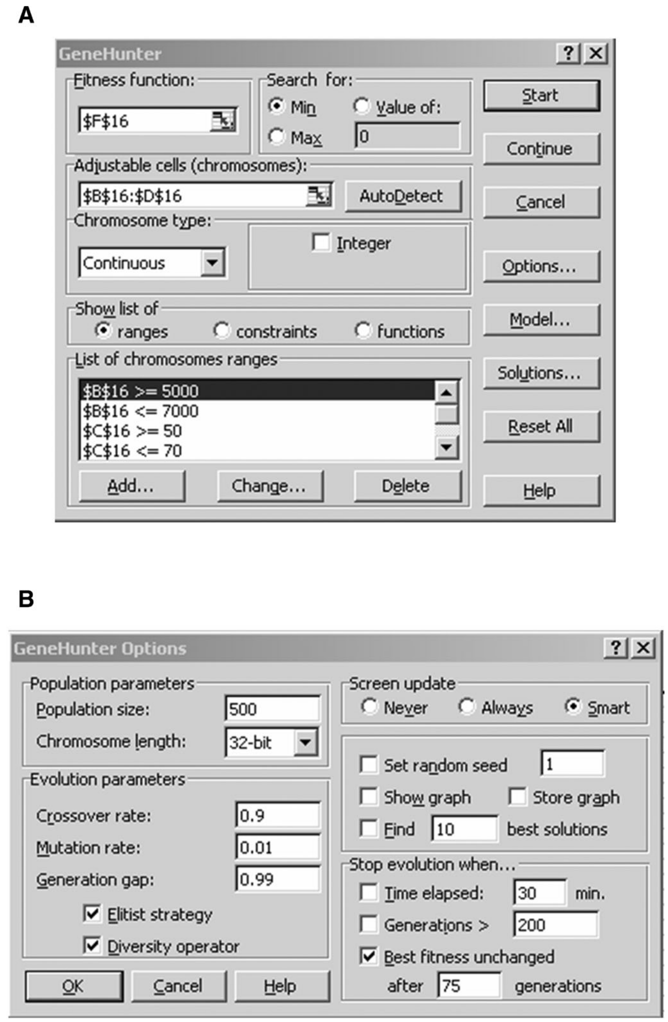
where Wt = the bird weight at time t, Wo = the initial (hatch) weight, L = the instantaneous growth rate (per d), and K = the rate of the exponential decay of the initial specific growth rate.

The computer used for this study was a Dell Workstation PWS340 with 2.53 GHz Intel Pentium 4 CPU (central processing unit) and a Microsoft Windows 2000 operating system. Each growth model was formulated on Microsoft Excel spreadsheets with 2 spreadsheets for each growth model representing the data to be fit by regression analysis and by GA. The significant digits for the development of the PROC NLIN and GA models were based on the significant digits for BW published in the 2 papers mentioned previously.

The nonlinear regression method was PROC NLIN of the SAS package. The initial values for each of the nonlinear regression models were based, respectively, on the published SAS methods of Rogers et al. (1987) and the estimated model coefficients determined by Aggrey (2002). The GA package used was GeneHunter (Ward Systems Group, 1995). The GA ranges were heuristically estimated from the values associated with the estimated coefficients of the nonlinear regression. The specific starting values and ranges for the 2 procedures are shown in Table 1.

GA

The GA works with a fixed-size population of possible solutions for a problem, called individuals, which are evolving in time. A GA uses 3 principal genetic operators: selection, crossover, and mutation. During each step (called a generation) in the reproduction process, the individuals in the current generation are evaluated by a fitness function, which is a measure of how well the individual solution solves the problem. Then each individual solution is reproduced in proportion to its fitness; higher fitness means a greater chance to participate in mating (cross-over) and to produce an offspring. A small number of newborn offspring (i.e., new solutions) undergo the action of the mutation operator. After many generations, only those individuals (solutions) with the best genetics (from the point of view of the fitness function) survive. The best individual provides an optimum or near optimum solution to the problem.



GeneHunter

Fitness function: $F$16

Search for: ● Min ○ Max ○ Value of: 0

Adjustable cells (chromosomes): $B$16:$D$16

Chromosome type: Continuous

☐ Integer

Show list of: ● ranges ○ constraints ○ functions

List of chromosomes ranges:
$B$16 >= 5000
$B$16 <= 7000
$C$16 >= 50
$C$16 <= 70

GeneHunter Options

Population parameters
Population size: 500
Chromosome length: 32-bit

Evolution parameters
Crossover rate: 0.9
Mutation rate: 0.01
Generation gap: 0.99
☑ Elitist strategy
☑ Diversity operator

Screen update: ○ Never ○ Always ● Smart

☐ Set random seed 1
☐ Show graph ☐ Store graph
☐ Find 10 best solutions

Stop evolution when...
☐ Time elapsed: 30 min.
☐ Generations > 200
☑ Best fitness unchanged after 75 generations

FIGURE 2. (A) Input data for genetic algorighm (GA) (GeneHunter) determination. (B) Genetic algorithm (GeneHunter) options.

Genetic algorithms are essentially probabilistic. In contrast, traditional optimization methods are essentially deterministic. The probabilistic nature of evolutionary computations allows them to explore areas in the search space that may appear improbable at first glance. Bad solutions (individuals) are not thrown out from the population. Instead, they have some finite probability of mating and of giving future generations some genetic features that could be very useful in creating true elite offspring. Thus, the GA avoids local optima and can find a true global solution to the problem.

The deterministic character of the traditional optimization techniques is the main reason they some times settle on a local optimum. Sometimes, the elite individuals in a GA population may also get stuck at the local optimum. However, the GA always has a good chance of escaping this local optimum because of the mutation, diversity operators, or both.

GA Example. The setup approach for fitting a fitness function for the GA was based on a polynomial approximation example demonstrated in the GeneHunter software package (Ward Systems Group, 1995).

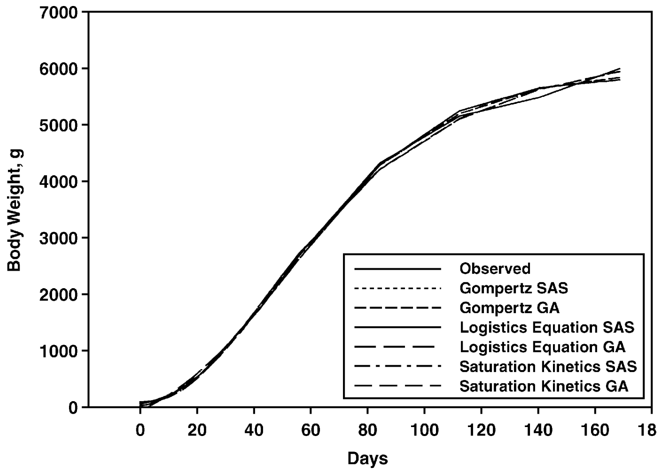


FIGURE 3. Sigmoid growth curves determined by SAS NLIN (SAS) and a genetic algorithm (GA) for Gompertz, logistic, and saturation kinetics growth curves using male growth data from Rogers et al. (1987). Data are from Rogers et al. (1987) and are used by permission.

GA Spreadsheet Setup. An example of the spreadsheet setup for fitting the Gompertz equation using the Rogers data is shown in Figure 1. The fitness function for fitting the growth equations was a minimization of the sum of squares of the observed BW and the BW predicted by the growth equations. Fitness cell of the spreadsheet was the EXCEL function SUMXMY2 (array_x, array_y), where array_x was the observed BW and array_y was the predicted BW over the growth period. The fitness equation for the spreadsheet was located in Cell F16. Array_x was C19:C38 and array_y was D19:D38. Graphs of the observed and Gompertz BW and residuals were also located in the spreadsheet. Constants developed for the equations were located in cells B16:D16.

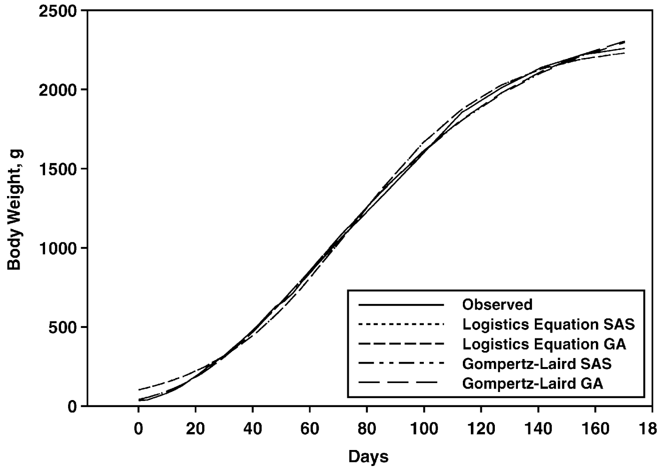


FIGURE 4. Sigmoid growth curves determined by SAS NLIN (SAS) and a genetic algorithm (GA) for logistic and Gompertz-Laird growth equations using male growth data from Aggrey (2002; data are used by permission).

TABLE 2. Resulting nonlinear regression and genetic algorithm coefficient calculations for growth equations based on male BW data[1]

Model	Nonlinear regression coefficient estimate	Genetic algorithm coefficient estimate
Logistic (Rogers et al., 1987)		
Maximum response (A)	5,871	5,872
Initial response (B)	9	9
Rate constant (K)	0.96	0.96
Predicted (N)	−735	−736
Gompertz (Rogers et al., 1987)		
Maximum response (A)	5,987	5,987
Intercept (B)	70	70
Rate constant (K)	0.031	0.031
Saturation kinetics (Rogers et al., 1987)		
Maximum response (A)	6,668	6,698
Intercept (B)	108	96
Rate constant (K)	13,057	11,832
Kinetic order (N)	2.3	2.2
Gompertz-Laird (Aggrey, 2002)		
Hatching weight (Wo)	44.7	44.7
Initial growth rate (L)	0.0888	0.0888
Rate of decay (K)	0.0220	0.0220
Logistic (Aggrey, 2002)		
Asymptotic weight (Wa)	2280.2	2279.9
Exponential growth rate (K)	0.0403	0.0403
Age at maximum growth (ti)	74.7	74.7

[1] Data are from Rogers et al. (1987) and Aggrey (2002) and are used by permission.

GA Input Interface. The GeneHunter graphical interface for inputs to the GA is shown in Figure 2a. As pointed out, the fitness function was located in F16, the inputs (adjustable cells) in B16:D16. Ranges for the parameters making up the equation are shown in the list of chromosome ranges.

Intuitively, the GA problem setup can be viewed to be similar to the set up for a linear program. That is, there is an objective equation to be maximized or minimized (or to find a specific value). The objective equation is subject to constraints, which may be in the form of traditional constraints (less than, equal to or greater than equations), a range of values, or functions.

GA Input Options. The selections used in the study for the GA Options are shown in Figure 2b. A GA functions by selective crossing of a population of potential solutions. In this case a set of potential solutions (population of solutions) was set at 500 with a chromosome length of 32 bits. The chromosome length determines the precision of the solution. The crossover rate was set at 0.9. The crossover is applied to parent individuals (solutions) from the current generation to produce 2 new offspring (or solutions). The crossover rate is the probability that crossover will occur. The mutation rate was set at 0.01. The mutation operator increases the variability of the population by a random process of changes in the population. The mutation rate is the probability of mutation. The generation gap was set at 0.99. The value of (1 − generation gap) indicates how many individual solutions will be kept from the previous generation. The Elitist strategy was chosen in which the value (1 − generation gap) determines the number of best (elite) individual solutions passing to the next generation without the crossover and mutation operators. Also the Diversity operator was chosen which is a form of slight mutation producing solutions that are only slightly changed as opposed to major changes in solutions that the mutation operator can produce.

Statistical Analysis. The GA was run using the "continue" button of the software (Figure 2a) until there were no changes in the solution. After fitting the models to the data using SAS NLIN and GeneHunter, the residuals (difference between the predicted responses and the observed responses) were determined (Tables 1 and 2). A comparison was made between the residuals determined for the models fit by nonlinear regression analysis and by the GA.

The following hypothesis was tested for equality of variances (H_o: $\sigma^2_{\text{nlr}} = \sigma^2_{\text{ga}}$), where nlr and ga represent the nonlinear regression and GA methods, respectively. The SAS PROC MEANS statement was used to determine the corrected sums of squares for the nonlinear regression and GA models used in the following test statistic (TS),

$$\text{TS} = \frac{\text{corrected sum of squares}_{\text{large}}}{\text{corrected sum of squares}_{\text{small}}}.$$

The larger value was placed over the smaller value for determining the *F* statistic. The TS was compared with an *F* table with 19, 19 for the degrees of freedom for the Rogers et al. (1987) data and 27, 27 for the degrees of freedom for the Aggrey (2002) data. Significance was considered at $P \leq 0.05$.

RESULTS AND DISCUSSION

Model Parameter Results

The results of coefficients determined by nonlinear regression and GA are shown in Table 2. There were

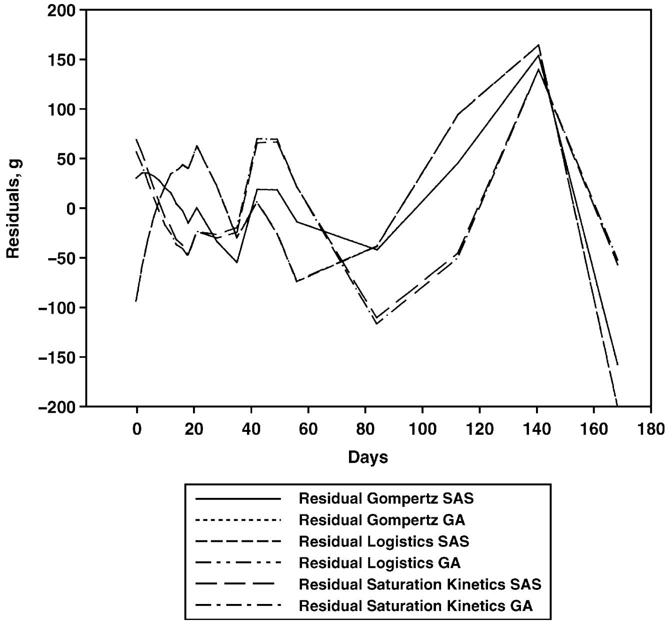


FIGURE 5. Residuals of the difference between observed male BW (Rogers et al. 1987 data) and BW determined from growth equations derived by SAS NLIN (SAS) and a genetic algorithm (GA). Data from Rogers et al. (1987) are used by permission.

no differences in the coefficient values for the Rogers Gompertz and Aggrey Gompertz-Laird growth equations. There was only a slight difference in the coefficients for the Rogers and Aggrey logistic growth equations. There was a difference for each of the coefficient values for the Rogers saturation kinetics growth equation. It should be pointed out that the length of time for running the GA was between 30 s and 19 min, whereas the SAS NLIN procedure was a matter of seconds. The slowness of the GA might be taken into consideration depending on the complexity of the problem and the advantages of the GA to provide a parallel iteration for solving complex problems. The slowness is due to the computationally intensive nature of the GA as it evaluates each potential solution over many different fitness cases. Improvement of the speed of the GA is being researched (Banzhaf et al., 1998).

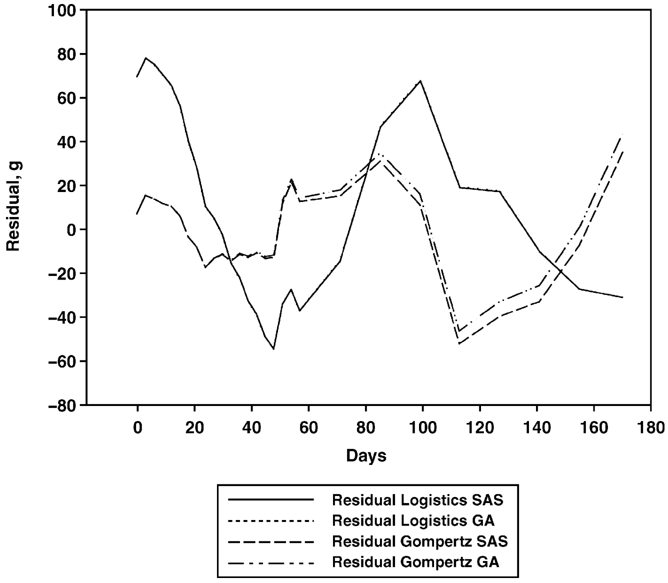


FIGURE 6. Residuals of the difference between observed male BW (Aggrey, 2002; data used by permission) and BW determined from growth equations derived by SAS NLIN (SAS) and a genetic algorithm (GA).

Model Predicted Responses

The observed and predicted BW predictions for the models determined by nonlinear regression and GA are shown in Table 3 for data from Rogers et al. (1987) and Table 4 for Aggrey (2002). The results showed no difference in the values for weights predicted by either method for the logistic and Gompertz models. There was a perceptible difference in the predicted values for the saturation kinetics model, although there was no statistical difference ($P \geq 0.05$) in the residuals for the nonlinear and GA determined growth models (Table 5).

Statistically there was no significant difference in the variances for the 2 fitting methods (Table 5). The plotted sigmoid curves for the 2 sets of data showed that there is hardly a perceptible difference in the plotted growth equations (Figures 3 and 4).

Residual Analysis

It is apparent from the residuals representing the difference between the observed and model predicted responses in Tables 3 and 4 that there is considerable deviation in the model predicted responses from the observed growth responses. Although the R^2 values were quite high, the residuals show a discrepancy between the observed and model predicted responses. Although the GA fit the set equations equivalent to the parameters obtained by nonlinear regression, it is evident that finding a model that fits the observed data is still a goal that has not been achieved.

The plotted residuals for the 2 data sets show responses that have some oscillation in them (Figures 5 and 6). This oscillation, resembling a sine wave function, has been observed by Maruyama et al. (1998). In their studies, Maruyama et al. (1998) fit logistic, Gompertz, von Bertalanffy, Richards, Weibull, and Morgan-Mercer Flodin growth curves and found that all had a significant lack of fit. The residuals also had a sine wave nature to them. It appears that the fitting problem is not so much a problem with the fitting method as it is with the form of the equation being fit.

It was found that GA could successfully determine the coefficients of growth equations. A disadvantage of slowness in converging to the solution was found for the current GA software. The advantage of GA over traditional nonlinear regression is that only ranges need be specified for the parameters of the growth equations,

TABLE 3. Observed and predicted body weights with residuals determined by nonlinear regression and genetic algorithms[1]

		Logistics model				Gompertz model				Saturation kinetics model			
		Nonlinear regression		Genetic algorithm		Nonlinear regression		Genetic algorithm		Nonlinear regression		Genetic algorithm	
Age, d	Observed weight, g	Predicted	Residual	Predicted	Residual	Predicted	Residual	Predicted	Residual	Predicted	Residual	Predicted	Residual
0	38	–54	–92	–54	–92	70	32	70	32	108	70	96	58
2	54	–4	–58	–4	–58	91	37	91	37	110	56	98	44
4	80	49	–31	49	–31	117	37	117	37	119	39	108	28
6	114	105	–9	105	–9	147	33	148	34	136	22	126	12
8	155	165	10	165	10	184	29	184	29	162	7	153	–2
10	205	228	23	228	23	227	22	227	22	197	–8	189	–16
12	259	295	36	295	36	275	16	276	17	242	–18	235	–24
14	326	365	39	365	39	331	5	331	5	296	–31	291	–36
16	395	440	45	440	45	394	–1	394	–1	359	–36	355	–40
18	477	518	41	518	41	463	–14	463	–14	431	–46	429	–48
21	579	642	63	643	64	580	1	581	1	557	–22	557	–22
28	945	968	23	968	23	913	–32	913	–32	916	–29	920	–26
35	1,368	1,339	–29	1,340	–28	1,314	–54	1,315	–53	1345	–23	1,350	–18
42	1,744	1,751	7	1,752	8	1,764	20	1,764	20	1811	67	1,815	71
49	2,216	2,192	–24	2,193	–24	2,236	20	2,236	20	2284	68	2,286	70
56	2,719	2,647	–73	2,647	–72	2,706	–13	2,707	–13	2741	22	2,742	23
84	4,323	4,286	–37	4,286	–37	4,282	–41	4,282	–41	4214	–109	4,208	–115
112	5,151	5,246	95	5,246	95	5,197	46	5,197	46	5107	–44	5,102	–49
140	5,486	5,650	164	5,650	165	5,640	154	5,640	154	5,626	140	5,626	140
168	5,994	5,797	–198	5,797	–197	5,838	–156	5,838	–156	5,938	–56	5,943	–51
Model R^2		0.999		0.999		0.999		0.999		0.999		0.999	
Residual mean			0		0		7		7		4		0
Residual SD			75		75		57		57		57		57

[1] Data are from Rogers et al. (1987) and are used by permission.

TABLE 4. Observed and predicted BW with residuals determined by nonlinear regression and genetic algorithms[1]

		Logistic model				Gompertz–Laird model			
		Nonlinear regression		Genetic Algorithm		Nonlinear regression		Genetic algorithm	
Age, d	Observed weight, g	Predicted	Residual	Predicted	Residual	Predicted	Residual	Predicted	Residual
0	37.00	107.08	70.08	106.88	69.88	44.68	7.68	44.67	7.67
3	41.74	120.12	78.38	119.91	78.17	57.82	16.08	57.81	16.07
6	59.19	134.64	75.45	134.42	75.23	73.60	14.41	73.60	14.41
9	79.94	150.80	70.86	150.57	70.63	92.26	12.32	92.27	12.33
12	102.96	168.75	65.79	168.51	65.55	113.99	11.03	114.02	11.06
15	132.13	188.64	56.51	188.39	56.26	138.94	6.81	139.01	6.88
18	170.18	210.64	40.46	210.39	40.21	167.24	−2.94	167.33	−2.85
21	206.56	234.92	28.36	234.66	28.10	198.92	−7.64	199.06	−7.50
24	250.71	261.65	10.94	261.39	10.68	234.00	−16.71	234.20	−16.51
27	285.27	290.98	5.71	290.73	5.46	272.43	−12.84	272.69	−12.58
30	324.92	323.08	−1.84	322.83	−2.09	314.10	−10.82	314.44	−10.48
33	372.83	358.08	−14.75	357.84	−14.99	358.87	−13.96	359.30	−13.53
36	417.41	396.10	−21.31	395.87	−21.54	406.54	−10.87	407.08	−10.33
39	469.13	437.25	−31.88	437.03	−32.10	456.90	−12.23	457.55	−11.58
42	519.72	481.57	−38.15	481.38	−38.34	509.67	−10.05	510.46	−9.26
45	577.27	529.10	−48.17	528.94	−48.33	564.59	−12.68	565.51	−11.76
48	633.59	579.80	−53.79	579.68	−53.91	621.34	−12.25	622.43	−11.16
51	667.18	633.61	−33.57	633.52	−33.66	679.64	12.46	680.89	13.71
54	717.17	690.38	−26.79	690.34	−26.83	739.15	21.98	740.59	23.42
57	786.35	749.93	−36.42	749.93	−36.42	799.58	13.23	801.21	14.86
71	1,069.28	1,055.30	−13.98	1,055.56	−13.72	1,085.09	15.81	1,087.72	18.44
85	1,326.49	1,373.43	46.94	1,373.90	47.41	1,358.06	31.57	1,361.78	35.29
99	1,589.71	1,657.67	67.96	1,658.22	68.51	1,601.54	11.83	1,606.35	16.64
113	1,859.26	1,878.85	19.59	1,879.33	20.07	1,807.89	−51.37	1,813.70	−45.56
127	2,015.44	2,033.15	17.71	2,033.48	18.04	1,976.30	−39.14	1,982.99	−32.45
141	2,142.31	2,132.79	−9.52	2,132.95	−9.36	2,109.99	−32.32	2,117.42	−24.89
155	2,220.54	2,193.95	−26.59	2,193.97	−26.57	2,213.97	−6.57	2,222.01	1.47
170	2,262.63	2,232.25	−30.38	2,232.16	−30.47	2,298.54	35.91	2,307.09	44.46
Model R^2		0.999		0.999		0.997		0.999	
Residual mean			9.49		9.50		−1.47		0.58
Residual SD			43.17		43.17		20.22		19.96

[1] Data are from Aggrey (2002) and are used by permission.

whereas estimates of the coefficients need to be determined, and in some programs the derivatives of the growth equations need to be identified. Depending on the goal of the research, solving multivariable complex functions with an algorithm that considers several solutions at the same time in an evolutionary mode can be considered an advantage especially when there is a chance for the solution to converge on a local optimum when a global optimum is desired.

TABLE 5. Statistical results for comparing residuals of growth equations calculated with nonlinear regression and genetic algorithms

Residual[1,2]	df	Corrected SS	*F* value[3]
Growth data from Rogers et al. (1987)			
R_LogisticSAS	19	107,490.21	1.000 NS
R_LogisticGA	19	107,488.69	
R_GompertzSAS	19	62,275.65	1.000 NS
R_GompertzGA	19	62,243.30	
R_SatKinSAS	19	62,478.80	1.009 NS
R_SatKinGA	19	61,926.17	
Growth data from Aggrey (2002)Growth Data			
R_LogSAS	27	50,293.25	1.000 NS
R_LogGA	27	50,324.25	
R_Gompertz-Laird SAS	27	11,034.89	1.025 NS
R_Gompertz-Laird GA	27	10,763.67	

[1] Residuals (R_model) represent the comparison of the BW prediction of each respective model minus the observed BW.

[2] SAS indicates the model was determined by the SAS nonlinear procedure (Proc NLIN). GA indicates that the model parameters were determined with a genetic algorithm. SatKin = saturation kinetics.

[3] *F*-test statistic for the hypothesis of equal variances for the residuals of the SAS models compared to the GA models was determined by putting the larger corrected sum of squares over the smaller corrected sum of squares (SS) and comparing to an *F* table with 19 df and 27 df for the data from Rogers et al. (1987) and Aggrey (2002), respectively. Data from Rogers et al. (1987) are used by permission.

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