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*Research Note*

## **Computation of Compound Growth Rates in Agriculture: Revisited\***

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### **Abstract**

Growth rates are widely employed in the field of agriculture as these have important policy implications. The usual parametric approach for growth rate analysis is to assume multiplicative error in the underlying nonlinear geometric model and then fit the linearized model by 'method of least squares'. The deficiencies of this approach have been highlighted. It has been argued that nonlinear estimation procedures should be employed for fitting the model and then only the growth rates should be computed. A methodology has been discussed to compute the compound growth rate by using growth models, viz. monomolecular, logistic and Gompertz. Further, as an illustration, the total foodgrain production of our country during the period 1980 to 2001 has been considered and its growth rate has been computed.

### **Introduction**

If there is one concept that has been used maximum number of times during the past four decades or so in research papers published, particularly in the discipline of agricultural economics, it is undoubtedly the 'computation of compound growth rates' (*see*, for example, Panse, 1964; Dey, 1975; Reddy, 1978; Narain *et al.*, 1982; Kumar and Rosegrant, 1994; Kumar, 1997; Joshi and Saxena, 2002; Singh and Srivastava, 2003). In fact, one full issue of *Indian Journal of Agricultural Economics* (Vol. 35, No. 2) in 1980 was devoted exclusively to presentations of its various aspects.

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\* This paper is drawn from the Ph.D. thesis of the second author under the guidance of first author, submitted to Indian Agricultural Research Institute, New Delhi, in 2004.

The authors are grateful to the anonymous referee for valuable comments.

However, the procedure being followed for computation of growth rates has a number of serious lapses and therefore the conclusions drawn are not statistically sound. Accordingly, the aim of the present paper is to highlight the discrepancies in computation and suggest more efficient procedures that may be adopted to achieve the task.

### **Current Procedure for Computing Compound Growth Rate and Its Deficiencies**

If  $y_t$  denotes the observation (e.g. agricultural production, productivity, or area) at time  $t$  and  $r$  is the compound growth rate, model employed for estimating  $r$  is based on Eq. (1):

$$y_t = y_0 (1 + r)^t \quad \dots(1)$$

The usual practice is to assume a multiplicative error-term  $\exp(\varepsilon)$  in Eq. (1) so that the model may be linearized by means of logarithmic transformation, giving Eq. (2):

$$\ln(y_t) = A + Bt + \varepsilon \quad \dots(2)$$

where,  $A = \ln(y_0)$ , and  $B = \ln(1 + r)$ . Eq. (2) is then fitted to data using “method of least squares” and goodness of fit is assessed by the coefficient of determination  $R^2$ . Finally, the compound growth rate is estimated by Eq. (3):

$$\hat{r} = \exp(\hat{B}) - 1 \quad \dots(3)$$

As mentioned above, this procedure is beset with many pitfalls. Firstly, let us consider the basic model, as given in Eq. (1); it is nothing but the famous Malthusian model proposed towards the end of the eighteenth century. A well-known drawback of this model is that the response variable  $y_t$  tends to infinity as  $t \rightarrow \infty$ , which cannot happen in reality. Therefore, continuing to sticking to only this model does not make much sense, particularly when several other more realistic models exist in literature.

Secondly, as pointed out by Ratkowsky (1990, p. 12), assumption of multiplicative error tends to be valid when variability of response variable  $y_t$  increases with increasing values of  $y_t$ . However, this assumption is usually made only for mathematical convenience and its proper justification has hardly ever been provided. The third drawback is that there is no way to compute standard errors of estimates of original parameters, viz.  $y_0$  and  $r$  appearing in Eq. (1) from the corresponding values of the transformed model given in Eq. (2). Lastly, goodness of fit of linearized model given by Eq. (2) is assessed on the basis of  $R^2$ . In this context, Kvalseth (1985) has pointed

out that eight different expressions appear for  $R^2$  in the literature. Different computer packages employ different formulae for computation of  $R^2$  and hardly any effort is made to find out as to which particular formula has been employed in the computer package one is using! Furthermore, one most frequent mistake occurs when goodness of fit of even the original nonlinear model given by Eq. (1) is assessed by reporting the same value of  $R^2$  as has been obtained for the linearized model, given by Eq. (2). In fact, it is not at all possible to get  $R^2$  for Eq. (1) from that for Eq. (2). Scott and Wild (1991) have given an example where two models were almost identical visually when two different transformations were applied to attain linearity but had widely different values of  $R^2$ . In short,  $R^2$  is not the correct measure of goodness of fit of nonlinear model given by Eq. (1).

### **Suggested Procedure for Computing Compound Growth Rates**

The compound growth rates should be computed by first identifying the model that describes satisfactorily the path followed by the response variable over time. To this end, exponential model given by Eq. (1) may be replaced by more realistic growth models discussed below. A special feature of these models is that they are “Mechanistic models” in which parameters have specific biological interpretation unlike “Empirical models”, like polynomial or regression models.

### **Monomolecular Model**

This model describes the progress of a growth situation in which it is believed that the rate of growth at any time is proportional to the resources yet to be achieved, and can be given by Eq. (4):

$$dy/dt = r (K - y) \quad \dots(4)$$

where,  $r$  and  $K$  are the intrinsic growth rate and carrying capacity of the system, respectively. Integrating Eq. (4), we get Eq. (5):

$$y(t) = K - (K - y_0) \exp(-r t) \quad \dots(5)$$

where,  $y_0$  is the value of  $y(t)$  at  $t = 0$ .

### **Logistic Model**

This model postulates that in the beginning, growth takes place at an exponential rate, as in the well-known Malthusian model. Subsequently, a “deterrent force” comes into play because of the crowding effect and does not let the population (or biomass) grow beyond limits. The graph of this model is elongated S-shaped and, unlike the earlier model, has a point of

inflexion at half the carrying capacity. The differential equation of this model is given by Eq. (6):

$$dy/dt = r y (1 - y/k) \quad \dots(6)$$

Integrating Eq. (6), we get

$$y(t) = K / [1 + (K / y_0 - 1) \exp(-r t)] \quad \dots(7)$$

### Gompertz Model

This model has sigmoid type of behaviour and is found quite useful in the biological work. However, unlike logistic model, this is not symmetric about its point of inflexion. This model is given by the differential equation (8):

$$dy/dt = r y \ln(K / y) \quad \dots(8)$$

where, the symbol ‘ln’ denotes ‘natural logarithm’. Integration of Eq. (7) yields:

$$y(t) = K \exp[\ln(y_0 / K) \exp(-r t)] \quad \dots(9)$$

The above three models [Eqs (5), (7) and (9)] have been proposed deterministically. In order to apply these models to data, independently- and identically-distributed error-term with constant variance is assumed on the right hand side of Eqs. (5), (7), and (9), thus yielding the corresponding “statistical models”. It may be noted that in the Eqs (5), (7), and (9), parameters ( $r$ ,  $K$ ,  $y_0$ ) appear in a nonlinear manner. Thus, nonlinear estimation procedures, like ‘Levenberg–Marquardt’ algorithms, or ‘Does not Use Derivatives’ (DUD), are required to be employed for fitting the models. A good description of these procedures is given in Draper and Smith (1998). Fortunately, most of the software packages, like SPSS, SAS, SPLUS and GENSTAT, contain computer programs to accomplish the task. Subsequently, residual analysis may be carried out by employing “Run test” to examine the validity of assumption of independence of errors. Finally, goodness of fit of fitted models may be examined by computing a number of criteria, like mean square error (MSE), and mean absolute error (MAE).

After successfully identifying the best model for a data set, the last step is to compute the ‘compound growth rate’, which is given as:

$$d[\ln(y)]/dt, \text{ i.e. } y^{-1} dy / dt$$

For monomolecular, logistic, and Gompertz models, the annual growth rates pertaining to the period ( $t_i, t_{i+1}$ ) [ $i = 0, 1, \dots, n-1$ , where  $n$  denotes the number of data points], on using Eqs (4), (6), and (8), respectively are:

$$R_t^M = r [K / y(t) - 1] \quad \dots(10)$$

$$R_t^L = r [1 - y(t) / K] \quad \dots(11)$$

$$R_t^G = r \ln [K / y(t)] \quad \dots(12)$$

Taking arithmetic mean, the requisite compound growth rate over a given time-period may be obtained. However, it may be kept in mind that in “Nonlinear modelling”, convergence to biologically meaningful values is not always guaranteed. In such cases, the solution is to either study more advanced single-species growth models, such as Richards model and mixed-influence model, or apply non-parametric regression procedures (Chandran and Prajneshu, 2004).

### An Illustration

As an illustration, the total foodgrain production of the country during the period 1980 to 2001 was considered. In the first instance, attempts were made to identify the model that best described this data set. For this, three nonlinear growth models, viz. monomolecular, logistic, and Gompertz, were tried. In order to apply these models to data, an independently– and identically–distributed error-term was assumed on the right hand side of respective Eqs (5), (7), and (9). Statistical Analysis System (SAS) software package, Version 8e was employed for data analysis. A number of widely separated initial values were tried to ensure ‘global convergence’ and the results have been reported in Table 1. In respect of monomolecular model, although convergence did take place, it was noticed that estimate of carrying capacity (K) was extremely high. Further, the standard errors of estimates of two parameters, viz.  $r$  and  $K$  were also very high. Thus, monomolecular model was found to be inappropriate for describing the data set under consideration. Subsequently, application of ‘Run test’ on residuals showed that, for both logistic and Gompertz models, assumption of independence of error-terms was not violated at 5% level. Thereafter, goodness of fit of models was assessed by computing MSE and MAE and the results have been reported in Table 1. A perusal of Table 1 indicates that, although logistic model had performed slightly better than Gompertz model for a given the data set, distinction between the two models was hardly significant and so both of them could be employed for computation of compound growth rates. For this, Eqs (11) and (12) were employed. These required the predicted values of  $y_t$ , which have been reported in the second and fourth columns of Table 2. The annual growth rates for the two models were also computed and have been given in the third and last columns of Table 2. Finally, on taking

**Table 1. Fitting of nonlinear growth models**

Parameter / Statistics	Growth model		
	Monomolecular	Logistic	Gompertz
r	0.0137 (0.0232)*	0.0625 (0.0243)	0.0381 (0.0241)
K	458.17 (484.37)	274.87 (61.63)	315.64 (118.09)
y <sub>0</sub>	122.95 (5.63)	123.53 (5.02)	123.25 (5.30)
<i>Goodness of fit statistics</i>			
MSE	-	58.42	58.72
MAE	-	5.82	5.83

\* Figures within the brackets indicate corresponding standard errors

**Table 2. Computation of compound growth rates**

Year	Growth model			
	Logistic		Gompertz	
	Predicted value of y <sub>t</sub>	Annual growth rate	Predicted value of y <sub>t</sub>	Annual growth rate
1980	127.79	0.0334	127.65	0.0345
1981	132.07	0.0325	132.04	0.0332
1982	136.36	0.0315	136.41	0.0320
1983	140.65	0.0305	140.76	0.0308
1984	144.93	0.0295	145.07	0.0296
1985	149.21	0.0286	149.34	0.0285
1986	153.45	0.0276	153.58	0.0274
1987	157.67	0.0266	157.77	0.0264
1988	161.85	0.0257	161.91	0.0254
1989	165.98	0.0248	166.00	0.0245
1990	170.06	0.0238	170.03	0.0236
1991	174.08	0.0229	174.00	0.0227
1992	178.04	0.0220	177.92	0.0218
1993	181.92	0.0211	181.77	0.0210
1994	185.72	0.0203	185.56	0.0202
1995	189.44	0.0194	189.28	0.0195
1996	193.08	0.0186	192.93	0.0187
1997	196.62	0.0178	196.51	0.0180
1998	200.07	0.0170	200.02	0.0174
1999	203.42	0.0162	203.46	0.0167
2000	206.67	0.0155	206.82	0.0161
2001	209.83	0.0148	210.11	0.0155

the arithmetic means, compound growth rates, on the basis of logistic and Gompertz models, were respectively obtained as 2.36% and 2.38%.

## Conclusions

Although, the correct computation of compound growth rates based on sound statistical procedures is of great significance, the methodology being followed has a number of deficiencies. When this methodology was proposed in 1964, there was no other choice, but during the past four decades, not only nonlinear estimation procedures have been developed but even software packages are also readily available to accomplish the task. Accordingly, in year 2005, there is hardly any justification for not using more realistic nonlinear growth models, like logistic and Gompertz models for computation of compound growth rates. Using these two models, the compound growth rates for the foodgrain production in India during the period 1980 – 2001 have been computed as 2.36% and 2.38%, respectively.

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