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Forecasting Apple Production of Jammu & Kashmir Using Non-Linear Growth Models

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Abstract

Apple is the principle fruit crop of Jammu and Kashmir and accounts for 51 per cent of total area of 2.72 lac hectare under all temperate fruits grown in this state. This paper emphasis on forecasting apple production of Jammu & Kashmir using non-linear approach. Different non-linear growth models viz. Logistic, Gompertz and Monomolecular models have been used for modelling of J&K's total apple production during the period 1974-75 to 2016-17. It was observed that Monomolecular and Logistic models performed better followed by Gompertz model for this dataset based on various goodness of fit criteria viz. Coefficient of determination (R2), Root mean square Error (RMSE), Mean absolute error (MAE) and Mean absolute percentage error (MAPE). Finally, J&K' total apple production for 2017-18 to 2019-20 has been forecasted by using the Monomolecular and Logistic models.

Keywords: *Apple production, Forecasting, Growth models*

I. INTRODUCTION

Jammu and Kashmir is northern most state of India with an area of 2, 22,236 sq. km. About 70 percent of total state population depends on agriculture for their raw livelihood. Horticulture in recent years has emerged as an important sector of Jammu and Kashmir. Apple is commercially the most important temperate fruit and is fourth among the most widely produced fruits in the world after banana, orange and grape. Nonlinear growth models have

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widely been used to measure agricultural growth in terms of growth rate (Joshi and Saxena, 2002; Sarma, 2005; Patil et al., 2009; Rajarathinam et al., 2010). These are also employed in modeling (Iquebal and Sarika, 2013) and forecasting production, productivity (Panwar et al., 2014), area, etc. of various commodities. Wani et al (2015) fitted different regression models for fodder yield estimation of Grewia optiva in Jammu Shiwaliks. In the present investigation, three realistic nonlinear growth models viz. Monomolecular, Logistic and Gompertz have been used. Prajneshu and Chandran (2005) discussed in details about these models and their uses. A special feature of these models is that they are Mechanistic models in which parameters have specific biological interpretation.

MATERIALS AND METHODS

Let *y(t)* denote the response variable at time *t*, *e.g.* agricultural production, or productivity and *r* is the intrinsic growth rate. *K* signifies the resources yet to be achieved. Some important nonlinear growth models are (Seber and Wild, 2007):

(I) Monomolecular Model:

This model is given by

$$y(t) = K - (K - y_0)\exp(-rt) \qquad (1)$$

Where y_0 is the value of $y(t)$ at $t = 0$

(II) Logistic Model:

This model is given by

$$y(t) = \frac{K}{\left[1 + \left(\frac{K}{y_0} - 1\right)\exp(-rt)\right]} \qquad (2)$$

This model has sigmoid type of behavior

(III) Gompertz Model:

This model also has sigmoid type of behavior and is found quite useful in biological work. It is given by

$$y(t) = K\exp\left[\ln\left(\frac{y_0}{K}\right)\exp(-rt)\right] \qquad (3)$$

The above models are deterministic in nature. An error term is added on the right hand side of each one of these, thereby making these as 'Nonlinear statistical models' (Draper and Smith, 1998). The error term is assumed to be independently and identically distributed with equal variances. Goodness of fit (GOF) of fitted models is examined by computing Coefficient of determination (R^2), Mean absolute error (MAE), Root mean square Error (RMSE) and Mean absolute

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percentage error (MAPE) using the following formula:

$$R^2 = 1 - \left[\sum_{t=1}^{n} (y_t - \hat{y}_t)^2 \Big/ \sum_{t=1}^{n} (y_t - \bar{y})^2 \right] \quad (4)$$

$$MAE = \sum_{t=1}^{n} |y_t - \hat{y}_t| \Big/ n \quad (5)$$

$$RMSE = \sqrt{\sum_{t=1}^{n} (y_t - \hat{y}_t)^2 \Big/ n} \quad (6)$$

$$MAPE = \frac{100}{n} \sum_{t=1}^{n} \left| \frac{y_t - \hat{y}_t}{y_t} \right| \quad (7)$$

where y_t is the actual observation for time period t, $\hat{y}_t$ the predicted value for the same period and $\bar{y}$ is the overall sample mean of observations.

In the present study, J&K's total apple production data (in Million tonnes) during the period 1974-75 to 2016-17 is considered. This data has been published by Directorate of Horticulture, Kashmir. Several sets of initial values for the parameters y_0, K and r have been tried and it is found that the final estimates remain the same.

RESULTS AND DISCUSSION

In the first instance, attempts were made to identify the model that best described this data set. Statistical software SPSS have been 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.

Table 1: Fitting of nonlinear growth models

Parameters	Growth Models		
	Monomolecular	**Logistic**	**Gompertz**
y_0	69.103	51.159	78.351
K	202.33	171.17	189.16
r	0.001	0.041	0.054
Goodness of fit statistics			
R^2	0.789	**0.794**	0.723
MAE	0.8208	**0.8155**	0.8299
RMSE	1.5710	**1.4527**	1.6721
MAPE	12.409	**11.629**	13.264

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It has been observed from table 1 that all the three models have been fitted well with the dataset. However, when we compared the models based on various GOF criteria, it was found that Monomolecular and Logistic models performed better than the Gompertz model. In case of MAE, RMSE and MAPE, the bold entries indicate the minimum values whereas for R2, the bold figure specifies the maximum value.

However, before taking final decision on suitability of model, assumption of independence of errors needed to be examined by employing Run test on residuals. The results of the test obtained in respect of the three models, are reported in **table 2.** As calculated value of Z-statistic, in each case, is less than the tabulated value, it can be concluded that null hypothesis of independence of errors was not rejected at 5% level of significance for any model.

An important assumption of regression analysis, either linear or nonlinear, is that the residuals from fitted model should be normal. The assumption of normality of errors is checked by Kolmogorov-Smirnov and Shapiro-Wilk tests on residuals are depicted in **table 3.** It is observed from the table that for all the three models, the residuals passed the test of normality.

Table 2: Run test

	Residuals from fitted models		
	Monomolecular	**Logistic**	**Gompertz**
Total Cases	43	43	43
No. of Runs	11	19	13
Value of Statistics	-0.954	-0.923	-0.983
Asympt. Sig	.421	.356	0.423

Table 3: Tests of Normality

Residuals from fitted models	**Kolmogorov-Smirnov**			**Shapiro-Wilk**		
	Statistic	**df**	**Sig.**	**Statistic**	**df**	**Sig.**
Monomolecular	0.076	43	0.200	0.960	43	0.142
Logistic	0.159	43	0.108	0.924	43	0.117
Gompertz	0.168	43	0.176	0.976	43	0.159

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Table 4: Forecasting apple production of J&K

Year	Production in million tonnes	
	Monomolecular	**Logistic**
2017-18	1597.978	1644.636
2018-19	1629.651	1713.755
2019-20	1661.289	1785.129

As it has been observed that Monomolecular and Logistic models perform better than Gompertz model, point forecasting of J&K's total apple production has been done by using these two models as represented in table 4.

CONCLUSION

Three nonlinear growth models viz. Monomolecular, Logistic and Gompertz have been employed for modeling time series data of J&K's total apple production. All the three models were fitted well for the dataset under study, however, based on different measures of in-sample forecasting accuracy, Monomolecular and Logistic models out perform the Gompertz model. The residuals from fitted models also obey the assumptions of independence and normality which are validated by run test and test of normality respectively. Finally, point forecasting of J&K's total apple production for the year 2017-18 to 2019-20 has been carried out by using the suitable models. It has been observed that the J&K's total apple production is likely to be increased with a slow and steady rate. Finally, the approaches advocated here are very general and may be used for forecasting of time series data of other crops as well.

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