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Body Weight Prediction using Recursive Partitioning and Regression Trees (RPART) Model in Indian Black Bengal Goat Breed: A Machine Learning Approach

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ABSTRACT

Background: Live body weight (BW) of livestock animals is truly mirror image of all activities of genetics, nutrition, production, reproduction and health status. Thus, the knowledge of calculating BW is of great importance to the producer and critical for goat farming and business. However, there is an unavailability of suitable scales, leading to inaccuracies in decision-making. The present work aimed to predict the live BW of Indian Black Bengal goat using certain morphometric data.

Methods: The live BW and eight body measurement data from 1427 disease free, non- pregnant goats aged 25.87±10.47 months with 2.78±1.21 number of parity were collected. The data were first subjected to stepwise regression analysis to achieve the best-fitted model *for* BW prediction by comparing coefficient of determination (R^2) and determining the combination of body dimensions that explained variation in the dependent variable. Further, Recursive Partitioning and Regression Trees (RPART) model, a machine learning tool was deployed to predict BW using certain body measurements.

Result: The results of stepwise regression model clearly indicated that heart girth (HG) and punch girth (PG) measurements influenced live BW mostly, but thse predictive capabilities (Low R^2) of this statistical model were low. The stepwise regression model could not satisfactorily predict BW due to the problem of multicollinearity. Out of eight independent variables, the most important variables emerged from RPART were only HG and PG based on the largest reduction in overall sums of squares error. RPART generated a decision tree with minimal expected error to precisely predict live BW. Hence, RPART model was found to provide better predictive result than stepwise regression model in accurately predicting BW from body measurement variables in Black Bengal goats.

Key words: Black Bengal goat, Body weight prediction, Machine learning, Recursive partitioning, Regression trees model, Stepwise regression model.

INTRODUCTION

Goat farming is one of the principal animal husbandry components all over the world. In Asia and Africa, goat farming has huge potential for economic upliftment for marginal and landless farmers (Devendra, 2015). Small to medium scale goat farming has become an emerging opportunity for rural youths in Indian subcontinent. Not only in Asia and Africa, dairy goat farming has bright prospect in North, Central and South America and the Caribbean islands (Lu and Miller, 2019).

Body measurements of goats are imperative within the scope of reflecting the breed standards (Verma *et al*., 2016) and have significant relationship with animal's live body weight (BW) for determining breed standards, selection criteria and the prices of the goats (Eyduran *et al*., 2017; Abd-Allah *et al*., 2019). There are large variations in BW and functionality among different goat breeds. BW of a goat is important for a number of reasons, related to breeding (selection), feeding and health care. BW has direct relationship with feed conversion ratio and maintenance efficiency in goat breeds (Kusminanto, 2020). The prediction of BW and its relationships to other morphological measurements produces appreciable knowledge for breeding strategy with regard to meat production per animal (Yilmaz *et al*., 2013; Iqbal *et al*., 2013). BW is truly is mirror image of all activities of genetics, nutrition, production, reproduction and health status. Thus, the knowledge of calculating BW is of great importance to the producer and critical for management as well as economic point of view

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in goat rearing, management and business. However, this fundamental knowledge is often unavailable to those working in goat farming sector, due to unavailability of scales, leading to inaccuracies in decision-making.

Traditional statistical techniques have been utilized in determining BW in livestock. Some of the models aggregate observed morphometric data to make estimates of expected outcomes. Certain body morphometric traits have been utilized to formulate such equations using regression models for predicting BW dynamics in cattle (Siddiqui *et al*., 2015), sheep (Cam *et al*., 2010) and goats (Moaeen-ud-Din *et al*., 2006; Adhianto *et al*., 2020; Sun *et al*., 2020). It is known that statistical models aim to identify relationships between variables, but the predictive capabilities (in terms of their accuracies) of these statistical models are low. These usual regression procedures cannot evaluate the multicollinearity between independent factors; hence it can lead to biased outcomes (Raja *et al*., 2012; Ruhil *et al*., 2013). Multiple linear regression model (MLR) looks at the linear relationship between the dependent and set of independent variables. Sometimes, this relationship may be nonlinear or complex in nature and as a consequence, the estimates of MLR may be biased. Besides, MLR may suffer from the problem of multicollinearity (strong correlation among independent variables) which often exists between independent variables (Iqbal *et al*., 2021).

Recently, data mining and machine learning algorithms are becoming popular modelling and prediction tools among practitioners due to their ability to model complex relationships and high predictive accuracy. Artificial Neural Networks (ANNs) are a commonly used branch of Machine Learning (ML) methods that are used to correlate input parameters to corresponding output data. Application of ANNs in medical fieldis available in literatures (Hall, 2009; Tasdemir *et al*., 2011; Litjens *et al*., 2017; Wang *et al*., 2021). Few studies have successfully applied these ML methods in livestock sciences (Nasirahmadi *et al*., 2017; Cominotte *et al*., 2020). Different deep learning (DL) models performance in the regression task like Convolutional Neural Networks (CNNs), recurrent attention models and recurrent attention models with CNNs have been explored and found that CNNs could achieve the highest performance in predicting BW of beef cattle (Gjergji *et al*., 2020) and Hereford cows (Ruchay *et al*., 2021). ML methods have been implemented in order to predict BW of Harnai sheep (Ali *et al*., 2015), Pakistani goat breed (Celik *et al*., 2018), Balochi sheep (Huma and Iqbal, 2019) and Beetal goats (Eyduran *et al*., 2017; Iqbal *et al*., 2021). To the best of the current knowledge, no previous study has used these ML methods for predicting BW of highly prolific, excellent meat-type Black Bengal goats (Das *et al*., 2018) in Indian subcontinent. There is dearth of literature related to BW measurement formula in this unique goat breed reared in its home tract. Therefore, the present work aimed to determine the best-fitted regression model using certain morphometric data for prediction of live BW and investigate the applicability of machine learning to improve on the prediction of BW in Black Bengal goat raising program in Eastern part of India. Additionally, we would like to compare machine learning model with the statistical regression model for the predictive analysis of live BW.

MATERIALS AND METHODS

Study area

The study area included 45 villages in 4 districts (Nadia, North 24 Paraganas, Hooghly and Murshidabad) of West Bengal, a state of Eastern India and 23 villages in 3 districts (West Tripura, South Tripura and Dhalai) of Tripura, a state of North-East India. Two-stage stratified random sample survey (consisting of village as strata-1 and animal within village as strata-2) was conducted to collect certain morphometric data on Black Bengal goats.

Animals

The Black Bengal goat breed was the experimental animal in the present study. In the villages, the goats were generally reared in small numbers from 2 to 5 per household. The goats were allowed for free grazing during the day on natural pasture, tree lopping and scavenging on kitchen waste when available without any supplementation. A total of 1427 disease free, non- pregnant goats aged 25.87±10.47 months with 2.78±1.21 number of parity were selected randomly in the villages for collecting data on various linear traits.

Ethical approval

The experimental protocol and animal care were met in accordance with the National guidelines for care and use of Agricultural Animals in Agricultural Research and Teaching.

Data and variables

Data of the present study were obtained from the previous publication (Haldar *et al*., 2014). BW (kg) of 1427 goats was recorded using a spring balance. To predict BW of Black Bengal goats based on set of independent variables, eight body measurements: head rump length (HRL), head rump curve length (HRCL), body length (BL), heart girth (HG), paunch girth (PG), wither height (WH), croup height (CH) and chest height (CHH) were recorded. The length, height and circumference measurements (centimeters) were taken using a measuring tape. All measurements were recorded on an individual data sheet from the non- pregnant goats in the morning before the animals were released for grazing. Each individual goat was sampled once only.

Statistical analysis

Data sorting

The obtained data were edited firstly and the outliers and the illogical data were removed from the dataset. The microsoft excel and neuro solution (http://www.neuro solutions.com) software were used to normalize and standardize the data. Finally, data collected on 1397 goats were used. As there was no evidence of location effect on

data set reported earlier (Haldar *et al*., 2014), data recorded on 1397 goats in two locations, *viz*. West Bengal and Tripura were pooled together and subjected to statistical analysis.

Stepwise regression analysis

In order to predict BW of Black Bengal goat from the various body measurements taken at field level the stepwise regression procedure was applied to find the variables which are affecting the body weight using multiple stepwise regressions (PROC PHREG; SAS 9.3, 2012). BW was regressed on body measurements following least square by stepwise regression analysis to compare R^2 and determine the combination of body dimensions that explained variation in the dependent variable. The model used was the stepwise regression (SR) model:

$$Y = \alpha + \beta_1 x_1 + \beta_2 x_2 + ... + \beta_i x_i \quad .....(1)$$

Where,

α = Intercept of the model.

β = Coefficient of predictor variables.

SR enters predictor variables in a stepwise manner; it will also fit specified models or perform forward selection of variables. At each step in the stepping process, an attempt was made to enter significant variables into the model and stop when no more predictors can be justifiably entered or removed from our stepwise model, thereby leading to a "final model."

Application of machine learning model

Data that were analyzed using regression models in the previous step were analyzed using a decision tree model known as Recursive Partitioning and Regression Trees (RPART) (Baldi and Brunak, 2002). This machine learning tool created a decision tree through some algorithm that classified members of the population by splitting it into sub-populations based on several dichotomous independent variables for predictive modeling in machine learning (Alpaydin, 2020). Decision Trees partitioned a data set into smaller subgroups and then fit a simple constant for each observation in the subgroup. The partitioning was achieved by successive binary partitions (recursive *partitioning*) based on the different predictors. The constant to predict was based on the average response values for all observations that fell in that subgroup. The total data set was divided into 70: 30 ratio for training and testing purpose indicating that out of 1397 observations 978 observations were used for training and rest 419 observations for testing.

Deciding on internal nodes/splits

The partitioning of variables was made in a top-down, *greedy* fashion that a partition was performed earlier in the tree that would not be changed based on later partitions. The model began with the entire data set, *S* and searched every distinct value of every input variable to find the predictor and split value that partitioned the data into different regions such that the overall sums of squares error were minimized.

Having found the best split, the data were partitioned into two resulting regions and the splitting process was repeated on each of the two regions. This process was continued until some stopping criterion was reached. What results was, typically, a very deep, complex tree that might produce good predictions on the training set, but was likely to over fit the data, leading to poor performance on unseen data.

Cost complexity criterion

There was often a balance to achieve in the depth and complexity of the tree for optimizing predictive performance on some unseen data. To find this balance, we typically grew a very large tree and then pruned it back to find an optimal subtree. We created the optimal subtree by using a cost complexity parameter (α) that penalized our objective function for the number of terminal nodes of the tree (T) as in Eq 1.

$$\text{Minimize } \{SSE+\alpha|T|\} \quad .....(2)$$

For a given value of α, the smallest pruned tree had the lowest penalized error.

RESULTS AND DISCUSSION

Regression analysis

The result of stepwise regression analysis is presented in Table 1. The ANOVA table for stepwise regression and the coefficients from stepwise regression model were given in the Table 2 and 3, respectively. Various body measurements were considered to construct the regression equation. In the present study, regression equations could not satisfactorily predict BW in Black Bengal Goat as coefficient of determination (R^2) in the regression models was very low.

The results clearly indicated that HG and PG influenced BW mostly, but with low degree of precision (as R^2 was 0.443 and 0.458). However, Habib *et al*. (2019) reported that regression equation involving HG and BL could predict live BW accurately in Black Bengal Goat. Previously, certain body morphometric traits have been utilized to formulate regression equations using step wise regression method for predicting BW dynamics in other goat breeds (Moaeen-ud-Din *et al*., 2006; Adhianto *et al*., 2020; Sun *et al*., 2020). Though stepwise regression model identified relationships between variables, the predictive capabilities (in terms of

Table 1: Biometrical relationship between body measurements and BW using stepwise regression.

Model	R	R^2	Adjusted R^2	Std. error of the estimate
1	.665[a]	.443	.442	3.54585
2	.677[b]	.458	.457	3.49840
3	.683[c]	.466	.465	3.47247
4	.684[d]	.468	.467	3.46747

a. Predictors: (Constant), HG.

b. Predictors: (Constant), HG, PG.

c. Predictors: (Constant), HG, PG, BL.

d. Predictors: (Constant), HG, PG, BL, HRL.

their accuracies) of this statistical model were low in the preset study. These usual regression procedures could not evaluate the multicollinearity between independent factors; hence it could lead to biased outcomes (Raja *et al*., 2012; Ruhil *et al*., 2013).

Recursive partitioning and regression trees (RPART)

As the results of stepwise regression could not satisfactorily predict BW, RPART, a machine learning tool has been deployed here to predict BW of Black Bengal goat based on some independent body measurements. The machine learning tool was used for improving prediction of BW of Black Bengal goats to evaluate the performance and capabilities on how it could provide BW information for the stakeholders of goat farming.

Out of eight independent variables the most important variables emerged from RPART were only HG and PG based on the largest reduction in overall sums of squares error (SEE) as shown in Table 4. The complexity parameter is presented in Table 5.

Table 2: The results of analysis of variance (ANOVA) table using stepwise regression.

Model	Sum of squares	df	Mean square	F	Sig.
1 Regression	13920.408	1	13920.408	1107.160	.000[b]
Residual	17526.866	1394	12.573		
Total	31447.274	1395			
2 Regression	14398.594	2	7199.297	588.234	.000[c]
Residual	17048.680	1393	12.239		
Total	31447.274	1395			
3 Regression	14662.445	3	4887.482	405.329	.000[d]
Residual	16784.828	1392	12.058		
Total	31447.274	1395			
4 Regression	14722.778	4	3680.694	306.129	.000[e]
Residual	16724.496	1391	12.023		
Total	31447.274	1395			

a. Dependent Variable: BW.
b. Predictors: (Constant), HG.
c. Predictors: (Constant), HG, PG.
d. Predictors: (Constant), HG, PG, BL.
e. Predictors: (Constant), HG, PG, BL, HRL.

Table 3: Stepwise regression model with their respective coefficients.

Coefficients[a]					
Model	Unstandardized coefficients		Standardized coefficients	t	Sig.
	B	Std. error	Beta		
1 (Constant)	-14.741	.993		-14.847	.000
HG	.539	.016	.665	33.274	.000
2 Constant)	-16.214	1.008		-16.093	.000
HG	.406	.027	.501	15.277	.000
PG	.136	.022	.205	6.251	.000
3 (Constant)	-17.374	1.030		-16.862	.000
HG	.349	.029	.431	12.015	.000
PG	.118	.022	.177	5.354	.000
BL	.110	.023	.131	4.678	.000
4 (Constant)	-18.023	1.069		-16.862	.000
HG	.322	.031	.398	10.238	.000
PG	.113	.022	.170	5.105	.000
BL	.107	.023	.128	4.566	.000
HRL	.048	.021	.061	2.240	.025

a. Dependent variable: BW.

Table 4: Variable importance of different body measurements from RPART.

HG	PG	BL	WH	HRL	CH	HRLC	CHH
10028.11	4816.65	2725.84	2500.75	2424.54	2118.94	837.33	2.99

To illustrate the point of selecting a tree with 7 terminal nodes, we could force RPART to generate a full tree by using CP=0 (no penalty resulted in a fully grown tree). As the tree grewdeeper towards 7 terminal nodes, there was diminishing return in error reduction as shown in Fig 1. Thus, we could significantly prune our tree and still achieve minimal expected error (Mean Absolute Error- 2.60431219).

Table 5: Complexity parameter (CP).

CP	Number of splits	Relative error	Apparent error	Apparent S.D.
0.279283	0	1	1.001721	0.042147
0.076875	1	0.720717	0.723666	0.035757
0.057528	2	0.643842	0.660606	0.036767
0.015581	3	0.586314	0.602843	0.033692
0.014804	4	0.570733	0.599067	0.033413
0.011545	5	0.55593	0.581679	0.032317
0.01	6	0.544385	0.571436	0.032407

Decision tree predicting goat BW using RPART model is presented in Fig 2. All observations went through this tree, were assessed at a particular node and proceeded to the left if the answer was “yes” or proceeded to the right if the answer was “no”. First, all observations that had HG less than 64 went to the left branch; all other observations wherein HG was more than 64 cm preceded to the right branch. Next, the branches were further partitioned by both HG and PG leading to *terminal nodes* which had predicted response value. The predicted BW under different measurements of HG and PG is shown in Table 6. For example, if PG was <63 cm and HG was<56 cm, BW of

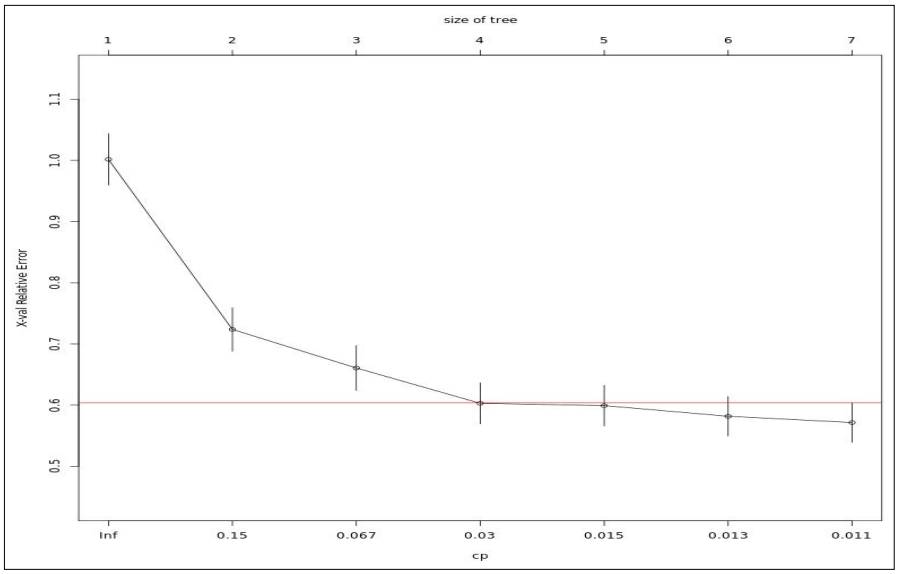


Fig 1: Pattern of error reduction under RPART.

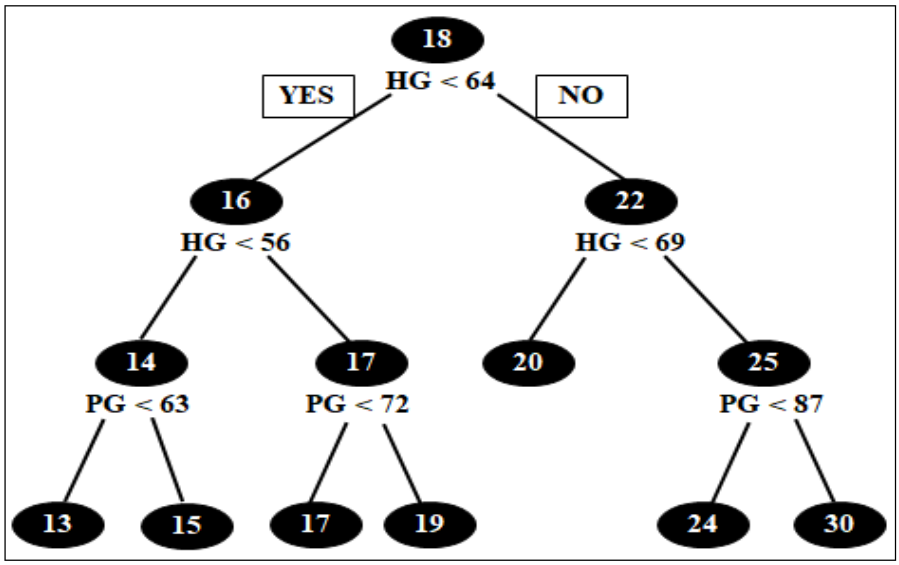


Fig 2: Decision tree predicting goat body weight using RPART model.

Table 6: Predicted BW under different measurements of HG and PG.

HG (cm)	PG (cm)	Predicted BW (kg)
<56	<63	13
<56	>63	15
>56	<72	17
>56	>72	19
<69 and <64	-	20
<69	<87	24
<69	>87	30

goat was13 kg and if PG was >63 cm and HG was <56 cm, BW of goat was 15 kg and so on.

Goat genetic resource is highly diverse in the world and body morphometrics are distinct from one breed to another (FAO, 2007). Though ML methods have been used in order to predict BW of Harnai sheep (Ali *et al*., 2015), Pakistani goat breed (Celik *et al*., 2018), Balochi sheep (Huma and Iqbal, 2019) and Beetal goats (Eyduran *et al*., 2017; Iqbal *et al*., 2021), the application of RPART machining learning tool for the prediction of BW using only two body measurements, *i.e.,* HG and PG in Black Bengal goats is the first time information.

CONCLUSION

Many researchers formulated regression equations for predicting BW in different goat breeds. However, regression model might not be a suitable measure for accurately predicting BW due to the problem of multicollinearity which often existsted between independent variables. Thus, the present study aimed at predicting BW of Black Bengal goats by different body measurement variables using a machining learning tool known as RPART. The present study showed that RPART model hold promise for precisely predicting BW of Black Bengal goats. Hence, RPART model could be considered as the method of choice for BW calculation from body measurement variables in Black Bengal goats.

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