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AN ENSEMBLE MACHINE LEARNING APPROACH FOR THE PREDICTION OF BODY WEIGHT OF CHICKENS FROM BODY MEASUREMENT

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ABSTRACT

This study aimed to develop an ensemble Machine learning (ML) model based on K-Nearest Neighbor (KNN), Random Forest (RF), Regression Tree (RT) and Support Vector Machine (SVM) for the prediction of body weight (BW) of chickens from their morphometric traits. The data of 100 Ross 308 broiler chickens (50 female and 50 male) from day 1 to 29 were used for predicting the BW of chickens using various body measurements such as body girth, body length, keel length, wing length and shank length. The data were randomly partitioned into training (80%) and testing (20%) datasets and *10*-fold cross-validation was employed to check the stability of the model. The predictive performance of the proposed ensemble method was evaluated and compared with individual ML models using evaluation criteria of adjusted coefficient of determination ($AdjR^2$), root mean square error ($RMSE$), mean absolute error (MAE) and mean absolute percentage error ($MAPE$). The proposed ensemble model outperformed all other ML methods used in the study, having very high predictive accuracy with $AdjR^2$ (0.999, 0.999), $RMSE$ (3.222, 5.465), MAE (2.332, 3.913) and $MAPE$ (0.941, 2.029) values for training and testing datasets, respectively. The results of the study revealed that the proposed ensemble model may help researchers and practitioners to accurately predict the BW of chickens from body measurements.

Keywords: Body weight, chickens, morphological traits, machine learning, ensemble method

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INTRODUCTION

Chicken, a domestic feathered bird, provides meat, eggs and feather to humans. It makes a substantial contribution to the domestic income and also provides a good supply of protein, minerals and essential vitamins. In poultry science, a significant consideration has been made to reveal the relationship between body weight and morphometric characteristics in describing species and breed standards. Chickens have high-level malleability against severe environmental conditions and play a crucial role as a basis of recurring income in growing rural economies and reducing poverty in underdeveloped states (Tadele *et al.,* 2018). Raising chickens is very prevalent among rural people because of the lesser investment and short-term income generation (Khieu, 1999). Chicken is the most common poultry species extensively raised globally and about 5 billion chickens have been raised annually as a food source for their eggs and meat (Mallick *et al*., 2020).

Body weight (BW) is one of the most significant and revealing features in selection and production, as well as animal performance as a whole. The prediction of BW of chicken is also important for a breeder in determining the correct amount of feed, health status and ideal dose of pharmaceuticals to treat animal disease. The use of linear body measurements of chickens could work as a basis in poultry and livestock production for the evaluation and selection of chickens for breeders. The morphological traits are known to be good indicators of market value and body growth of the chickens (Amao *et al.,* 2015). The BW and morphological traits of chickens, such as body length and shank length, have a great effect on the growth performances of broilers as these parameters directly affect slaughter yield at market age (Patbandha *et al.,* 2017).

Predicting the BW of farm animals with high predictive proficiency is a challenging problem for practitioners. Numerous traditional predictive methods have been used by researchers for predicting the BW of farm animals based on their morphological traits. Multiple linear regression (MLR) is one of the frequently used methods for BW prediction. Gueye *et al*. (1998) estimated the BW of indigenous chickens by employing MLR and the results showed that chest circumference (CC) and body length (BL) are the most suitable measures for BW prediction. Momoh and Kershima (2008) predicted the BW of local chickens by applying the regression analysis and found that male chickens showed a higher value of BW and body measurements than females. The study also revealed that CC and BL are the most appropriate measures for the prediction of BW. Ukwu and Okoro (2014) developed the prediction equations by using regression analysis to determine the relationship between BW and linear body parameters in Nigerian indigenous chickens. The study revealed that there exists a significant relationship between BW and linear body measurements and shank length (SL) is the most suitable predictor of BW.

Obike *et al*. (2019) predicted the BW of three chicken strains (Arbor Acre broiler, Noiler hybrid and Yoruba ecotype cockerel) by employing linear and quadratic functions and using the morphometric traits as predictors. The quadratic function showed the best accuracy, with breast width (BWD), body depth (BD), BL, drumstick (DS) and SL as the best predictors of BW. Hlokoe and Tyasi (2021) used stepwise regression to determine the BW in the Potchefstroom Koekoek chicken breed and concluded that a model including BG, WL, wither height (WH), toe length (TL), keel length (KL), BL and CC was the best. Negash (2021) employed stepwise regression for predicting the BW of Ethiopian Indigenous chickens from body measurements and reported SL as the best predictor for the BW. Moreover, the MLR equations that included the combination of four morphometric traits were found more suitable for predicting the BW of chickens.

However, it has also been reported that often there exists multicollinearity, the association between explanatory variables, due to which the estimated parameters become biased and it becomes difficult to correctly find the influence of independent variables on the dependent variable (Jahan *et al*., 2013). To evade such problems, few studies have employed alternative techniques such as Principal Component Analysis (PCA) (Egena *et al*., 2014) for predicting the BW of chicken and Factor Scores in multiple regression (Yakubu *et al*., 2009) for predicting carcass weight of broiler. However, these traditional methods have not been found sufficient enough to model complex relationships. Moreover, after implementing PCA on the data, the original features turned into principal components are not as understandable and interpretable as the original features. Besides, the relationship between the BW and morphological traits is mostly nonlinear and hence MLR and traditional predictive models often fail to model this relationship correctly.

Novel Machine Learning (ML) algorithms can be applied to accurately model the nonlinear and complex relationship between the dependent variable and predictors. Machine learning is a subset of artificial intelligence that offers the system the capability to automatically learn and improve from experience without being explicitly programmed. The ML methods such as Artificial Neural Network (ANN), Multivariate Adaptive Regression Spline (MARS), K-Nearest Neighbor (KNN), Regression Tree (RT), Random Forest (RF) and Support Vector Regression (SVR) are popular methods for regression type problems.

Recently, many researchers have applied ML algorithms for the prediction of BW using linear body measurements of various animals. Mendes and Akkartal (2009) predicted the slaughter weight of broilers using RT and the study suggested body length, shank length and width as the most important predictors of slaughter weight. Faridi *et al.* (2012) employed SVR and ANN to predict the body and carcass weights of two broiler chicken strains (Ross and Cobb). The output variables were BW, empty BW, carcass, drumstick, breast, thigh and wing weight based on their intake of dietary nutrients. The study revealed that the SVR model achieved better accuracy and generalization than the ANN model. Tyasi *et al*. (2020a) predicted the BW of Hy-line silver brown chicken based on their biometric characteristics by using the MARS data mining algorithm and WL and BL were found the most important predictors of body weight.

Tyasi *et al*. (2020b) employed the Classification and Regression Tree (CART) for the prediction of body weight of Potchefstroom Koekoek Laying hens and their results demonstrated that WL, back length (BCL) and beak length (BKL) played an important role in predicting the BW. Tyasi *et al*. (2021) predicted the BW of Hy-line silver brown commercial layer and indigenous breed from 11 biometrical traits using Chi-square Automatic Interaction Detector (CHAID), Exhaustive CHAID (ECHAID) and CART and compared the predictive performance of these tree methods concluding that the CART was the best tree-based method with high predictive capability.

Celik *et al*. (2017) applied CART, CHAID, ECHAID, Multilayer Perceptron (MLP), MARS and Radial Basis Function (RBF) for predicting the BW of Mengali rams. The CART and MARS were applied to predict the BW of Turkish Tazi dogs by Celik and Yilmaz (2018). Huma and Iqbal (2019) used a generalized linear model (GLM), SVM, RF and RT to predict the BW of Balochi rams. Aytekin *et al*. (2018) applied the MARS data mining algorithm to predict live weight and fattening period in young bulls. Celik and Yilmaz (2017) used CHAID, ECHAID and CART to predict BW from morphological traits of three Kangal dog colors variety. The findings of these studies revealed that machine learning methods have promising potential and improve the predictive ability and hence these techniques may be considered as better alternatives to traditional statistical methods.

A significant development in machine learning algorithms has been achieved using ensemble methods. An ensemble method combines two or more machine learning algorithms into a single predictive model. This approach produces better predictions as compared to a single ML model as it reduces the variance and improves the model's accuracy (Ganaie *et al*., 2021). Liang *et al.* (2021) employed the stack ensemble technique for the genomic prediction of two animal datasets (Beef cattle and dairy cattle) and a plant dataset (Loblolly pine). The study revealed that ensemble methods improved the predictive capability of the models. An ensemble method with more accurate predictions can benefit poultry breeders to establish efficient selection plans in the enhancement of BW and attain multiple benefits such as economic boost and high financial contribution to livestock enterprise. However, ML and ensemble methods have scarcely been used for the prediction of BW of chickens based on their morphological characteristics.

The objective of the present study was to develop an ensemble machine learning model for accurate prediction of the BW of broiler chicken through morphometric characteristics such as body girth, body length, shank length, wing length and keel length. The ensemble machine learning model was developed by using popular supervised ML algorithms such as KNN, RF, RT and SVM. The data of 100 Ross 308 broilers were partitioned into training and testing datasets and *10*-fold cross-validation was used for robust modeling and prediction. The predictive capability of the models was compared through various evaluation measures on both training and testing datasets. To the best of our knowledge, no previous studies have used the ensemble machine learning method for the prediction of BW of broiler chickens from their linear body measurements.

MATERIALS AND METHODS

Data for the present study were collected from Ross 308, a greatly demanded broiler breed in the chicken farming sector raised specifically for meat, from a private poultry farm in Lahore, Pakistan. A one-day-old 120 chicks were randomly picked from the available stock and were kept in 10 different cages (each measuring 3×3 feet). The temperature during the trial period ranged between 24^0 to 32^0C and the light was provided consistently for 24h over the first week, 23h dim light and 1h darkness in the remaining weeks. All the chicks had free access to fresh and clean drinking water through drinking nipples. They were fed with the Pre-starter high-density (H.D) crumbs for the first 10 days, starter H.D crumbs for 11-24 days and finisher H.D crumbs after 25 days. The experiment continued for 5 weeks, from January 21 to February 18, 2020. In the meantime, a few chicks died and some ill chicks were removed from the experiment. Hence, a total of 100 healthy chickens (50 female and 50 male) were left. A total of 500 observations of body weight (BW), body length (BL), body girth (BG), keel length (KL), shank length (SL) and wing length (WL) were collected every week from day 1 to 29. The BW in grams (g) was measured using weight balance, whereas other body measurements in centimeters (cm) were recorded using typical tailor tape.

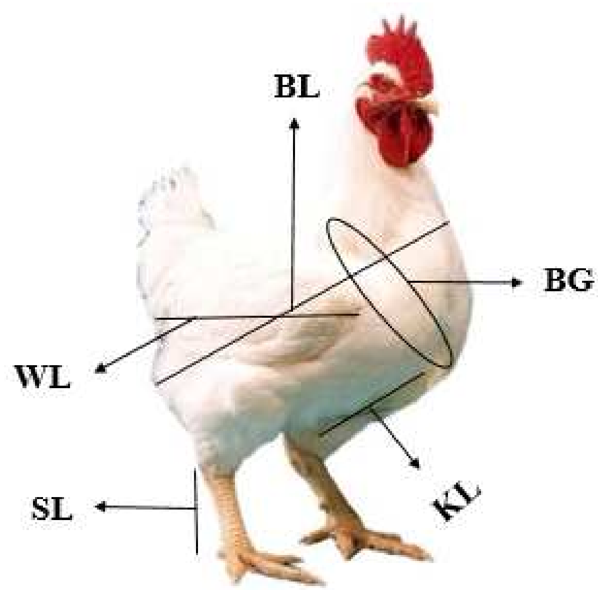

Figure 1. Morphological characteristics of chicken

Machine Learning Models:

Multivariate Adaptive Regression Spline: The multivariate adaptive regression spline (MARS), presented by Friedman (1991), is a kind of regression method. It is a non-parametric technique and can be considered as an extension of the linear models that automatically models interactions and nonlinearities among variables. The ideal MARS model is determined by a two-stage process; the forward pass and the backward pass. First, MARS builds a very large number of Basis Functions (BFs) where variables can interact with each other to better fit the data. In the backward pass, the model is sequentially pruned one by one, deleting the least effective term at each step until it finds the best sub-model. The performance of the sub-model can be compared by the generalized cross-validation (GCV) of Friedman (1991), which can be calculated as follows:

$$GCV = \frac{1}{n}\frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\left[1 - \frac{P(M)}{n}\right]^2},$$

where y_i and $\hat{y}_i$ are observed and predicted values of BW, n is the sample size, $P(M)$ represents the effective number of parameters which is a penalty measure for complexity and M represents the maximum number of BFs in the model.

Support Vector Machine: The method of Support Vector Machine (SVM) introduced by Vapnik *et al*. (1997) is an important and widely used supervised ML method that can be utilized for both regression and classification problems. Usually, regression-based SVM is termed Support Vector Regression (SVR). It is a computationally powerful and flexible technique with no prior assumptions for modeling purposes. The SVR model uses a threshold that is set by the experimenter. The basic idea is that the samples whose errors are within the intended threshold do not contribute to the regression process, whereas the samples whose errors are greater than the threshold contribute to the regression fit line. The SVR tries to fit the best line within an intended threshold. The SVR can take care of the problems such as small sample size, nonlinearity and high dimensionality of the dataset (Vapnik, 2010).

Regression Trees: Regression Trees (RT) proposed by Breiman *et al*. (1984) is one of the classical and most extensively used decision tree methods for building predictive models. The method of RT is considered a form of a decision tree that is intended to approximate real-valued functions. The RT are built through a procedure known as recursive-binary partitioning, which is an iterative procedure that splits the data into partitions, at each cut point, the sum of squared errors (SSE) is computed and compared across the variables. The variable with a minimum SSE is chosen as a root node. This procedure is continued until the stopping criterion is reached. The CART, CHAID and ECHAID are some regression tree methods commonly used by researchers.

Random Forests: Random Forests (RF) developed by Breiman *et al*. (2001) are ensemble tree methods that can be utilized for both classification and regression problems. RF improves the predictive accuracy and controls the overfitting which was encountered while using the regression tree. The RF combines several decision trees in determining the final result instead of depending on individual trees. Each tree in RF is generated from a different sample of rows and at each node, different samples of features are selected for splitting and then each tree makes its distinct predictions; these predictions are then averaged to yield a single output.

K-Nearest Neighbor: The K-Nearest Neighbor (KNN) developed by Fix and Hodges (1951) is a simple, easy-to-implement and versatile supervised learning algorithm. Its construction depends upon the K closest sample from the training data. To predict the value of new input, KNN has to find out the K-nearest neighbors. The forecasted result is the median or means of the observed values of the K-Nearest neighbors. The idea of the KNN model is based on the description of the distance between different data points, and the most commonly used metric for this purpose is Euclidean distance.

Stacking Machine learning algorithms: Stacking is an ensemble machine learning technique, sometimes called stacked generalization, that can be used to improve the predictive capability of the models. It yields better performance than any single trained algorithm. This method involves training multiple ML algorithms and then combining the predictions of two or more ML algorithms. The base-level models generally consist of different ML algorithms and thus, stacking ensembles are heterogeneous. First, all other algorithms are trained based on a complete training dataset, and then the meta-model (combiner algorithm) is trained to make a final prediction using the predictions of the base-level models.

Model evaluation: Various evaluation measures have been utilized to assess the performance of ML algorithms developed in the current study for modeling and predicting the BW of chickens. These include:

i. Coefficient of determination (R^2):

$$R^2 = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{n}(y_i - \bar{y})^2}$$

ii. Pearson correlation coefficient (R):

$$R = \sqrt{R^2}$$

iii. Adjusted coefficient of determination ($AdjR^2$):

$$AdjR^2 = 1 - \frac{(1 - R^2)(n - 1)}{(n - m - 1)}$$

iv. Root mean square error ($RMSE$):

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}$$

v. Mean Absolute error (MAE):

$$MAE = \frac{1}{n}\sum_{i=1}^{n}|y_i - \hat{y}_i|$$

vi. Mean absolute percentage error ($MAPE$):

$$MAPE = \frac{1}{n}\sum_{i=1}^{n}\left|\frac{y_i - \hat{y}_i}{y_i}\right|$$

where n is the number of observations in the dataset, m is the number of predictors, $\bar{y}$ is the mean of all known values of BW, y_i and $\hat{y}_i$ represent the actual and predicted values of BW, respectively. The highest values of R, R^2 and $AdjR^2$ and lowest values of $RMSE$, MAE and $MAPE$ indicate a better fit for the model.

***k*-fold Cross-Validation:** The *k*-fold cross-validation, also called an out-of-sample test, is a resampling procedure used to evaluate ML models on a limited dataset. Cross-validation divides the data into k subsets of equivalent size, a part of the subsets is chosen as a training dataset which is used to fit a model, and the remaining is selected as a testing dataset which is used to estimate the adequacy of the model. Cross-validation is used to limit problems like over-fitting and generally results in a less-biased model as compared to the other methods. Mostly, *10*-fold cross-validation is used for this purpose. Cross-validation is a commonly used method among researchers and practitioners because it is simple to understand and easy to implement.

In the present study, the entire data were first split into two parts; the training dataset (80%) and the testing dataset (20%). The training dataset was used to train and tune the parameters of all the models using *10*-fold cross-validation. Once the models were built, the test dataset was used to evaluate the performance of all fitted ML models. The morphological characteristics of chicken are presented in Figure 1. The outline of the methodology used in this study is presented in Figure 2 and the framework of ensemble machine learning algorithms is reported in Figure 3. All the statistical analyses were performed using R 3.6.3 software (R Core Team, 2020)..

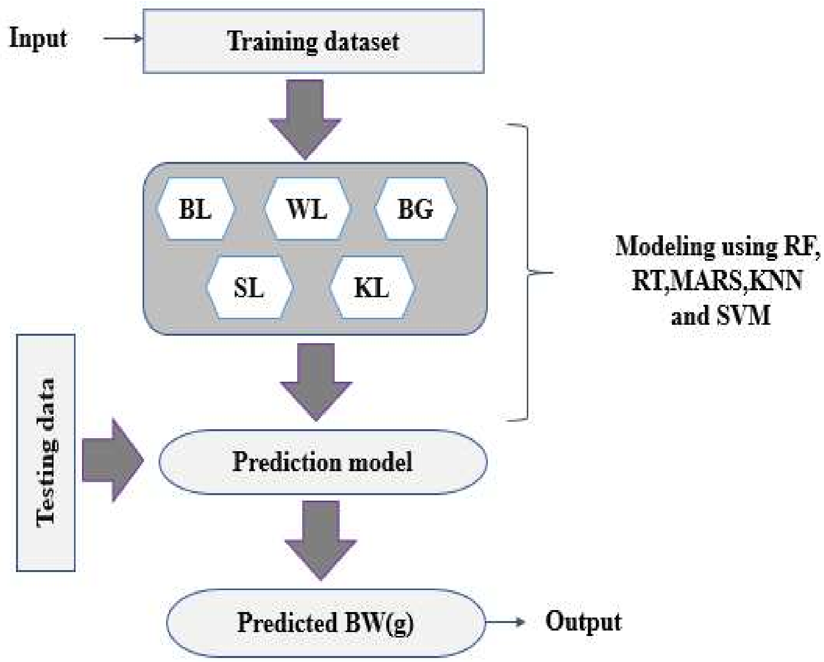

Figure 2. Methodology for predicting body weight (BW) of chicks by machine learning algorithms.

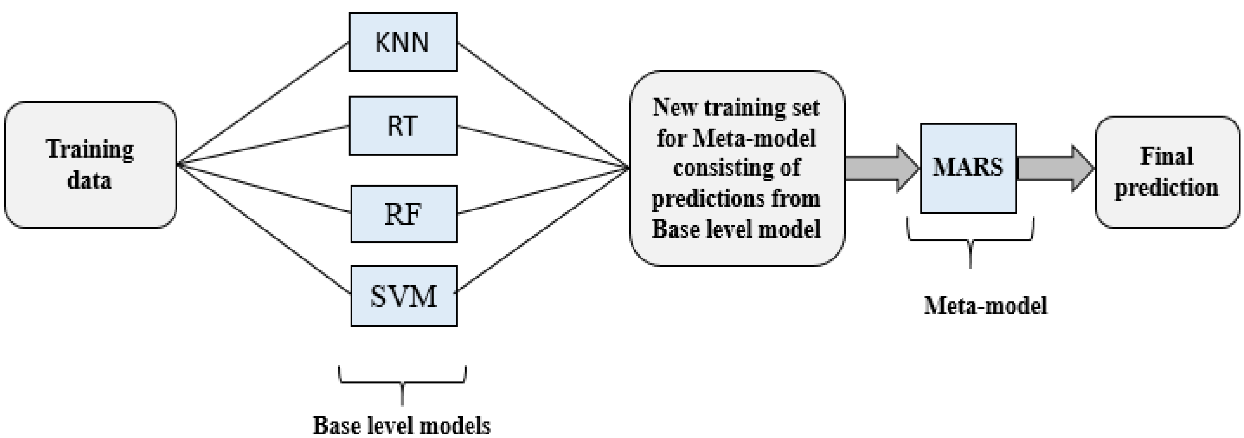

Figure 3. The stack ensemble framework.

RESULTS AND DISCUSSION

The descriptive statistics of the dependent and independent variables are reported in Table 1. The average BW of the chicken was 492.34 g with 511.06 standard deviation, whereas the coefficient of variation (CV) was found to be 104, indicating a greater degree of relative variability among body weights. Pearson's coefficient of correlation between all the variables is presented in Figure 4. Significant positive correlations were found between all the body measurements, with correlation coefficients ranging between 0.56 and 0.95. Body weight was found positively and strongly correlated with SL (0.92), WL (0.86), BG (0.8) and KL (0.8), whereas a weak correlation was found between BW and BL (0.56).

Table 1. Mean, standard deviation (SD) and coefficient of variation (CV).

Variables	Mean	SD	CV (%)
Body weight (grams)	492.34	511.06	104
Body girth (cm)	18.44	5.17	28.03
Body length (cm)	28.85	4.93	17.09
Wing length (cm)	12.69	5.71	44.99
Shank length (cm)	3.76	1.14	30.31
Keel length (cm)	4.73	1.95	41.23

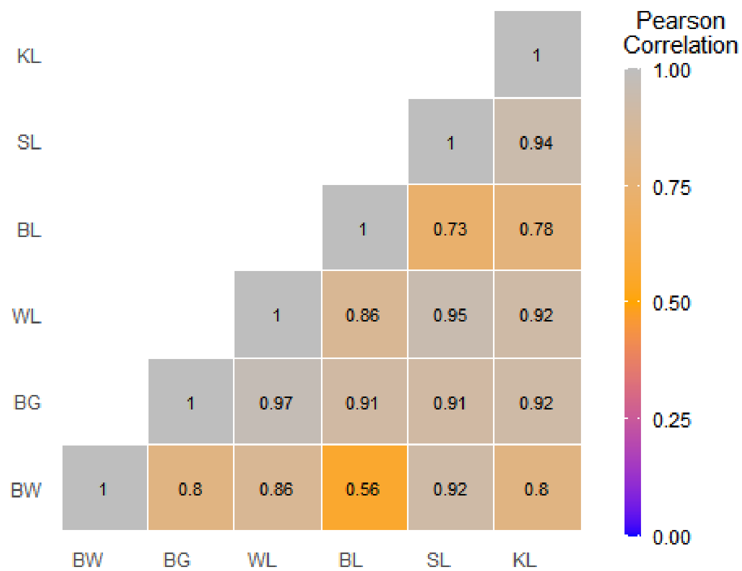

Figure 4. Pearson correlation coefficient between body weight and biometric body measurements for chicken.

The results of all the evaluation measures are reported in Table 2. For the training data, the coefficient of correlation between the observed and predicted BW for all the ML methods ranged between 0.981 - 0.999, with RF and RT providing the highest values. For the testing dataset, the correlation coefficient values between the observed and predicted BW were in the range 0.972 - 0.999, with the ensemble model providing the greatest value.

The RF achieved the minimum value of $RMSE$ among all ML methods for both training and testing datasets (3.232 and 5.698, respectively). The $RMSE$ value was the maximum for the SVR for both training and testing datasets (31.744 and 52.570, respectively), indicating its low performance amongst all other models. Moreover, the RF model attained the lowest value of MAE for the training (2.342) and the testing (4.161) data set, followed by RT, KNN and MARS. However, the SVR had the highest value of MAE for the training (27.797) and testing (35.219) data set. The $MAPE$ value was found to be minimum for the RF model for both the training and testing data set (0.949 and 2.032, respectively), followed by RT, KNN and MARS. The SVR again acquired the maximum value of $MAPE$ for the training (21.541) and testing (22.091) dataset, indicating its poorest predictive performance than other ML models.

The results obtained from the ensemble model are also reported in Table 2. The $RMSE$ values for training and testing data were found to be 3.222 and 5.465, respectively, which were the minimum among all other competing models. The MAE values acquired by the ensemble model were found to be minimum for both training and testing data sets (2.332 and 3.913, respectively). The ensemble model also achieved the lowest values of $MAPE$ for training and testing datasets (0.941 and 2.029, respectively). These findings showed that the ensemble model obtained the best results among all other ML models.

The observed BW (in g) of chickens and the fitted values of BW attained from all ML methods are reported in Table 3. The corresponding prediction errors (residuals) are also reported. The values of the residuals of all the algorithms varied from small to large except for the ensemble model. The residual values of the ensemble method were found to be the least, which also indicates its highest predictive capability among all other competing models.

Figure 5 shows the relative importance of the predictors for describing the BW of chickens. The most important predictor was found to be SL, accounting for 28%, followed by WL, with 21% of the total variation. BG and KL were also found to be significant predictors, with each showing almost 16% of the total variation. Whereas BL contributed a little in predicting the body weight with 11% of the total variation.

Figure 6 shows the outcomes of *10*-fold cross-validation for the best (ensemble) model for different evaluation measures. The values of the four evaluation measures remain almost the same for all 10 iterations, indicating the strength and stability of the model. Hence, the overall findings revealed that the ensemble model outperforms all other competing models in this study by accurately predicting the BW of chickens based on their morphological characteristics.

To check the significant difference between observed and predicted BW by the ensemble method, a two-sample t-test was applied. The predicted body weights were obtained on the testing data from the best (ensemble) model and the results of the t-test are reported in Table 4. A high *p*-value (0.996) of the t-test showed no significant difference between the observed and predicted weight, which further strengthens the argument that the ensemble model provided an accurate fit to the BW of broiler chicken.

Table 2. Comparison of results for different evaluation measures

Model	R	R^2	$AdjR^2$	$RMSE$	MAE	$MAPE$
			Training data (n=402)			
K-Nearest Neighbor	0.995	0.991	0.983	8.544	5.297	2.008
MARS	0.999	0.998	0.996	11.785	8.329	6.127
Random Forest	0.999	0.999	0.998	3.232	2.342	0.949
Regression Tree	0.999	0.999	0.991	6.037	4.534	2.712
Support Vector Machine	0.981	0.963	0.925	31.744	27.797	21.541
Ensemble Model	0.999	0.999	0.999	**3.222**	**2.332**	**0.941**
			Testing dataset (n=98)			
K-Nearest Neighbor	0.994	0.988	0.976	27.833	7.991	4.344
MARS	0.992	0.984	0.968	12.489	9.104	7.178
Random Forest	0.998	0.996	0.992	5.698	4.161	2.032
Regression Tree	0.997	0.995	0.990	6.236	4.885	3.009
Support Vector Machine	0.972	0.945	0.887	52.570	35.219	22.091
Ensemble Model	0.999	0.999	0.999	**5.465**	**3.913**	**2.029**

The bold values represent the values of the evaluation measures of the best-fitted model.

Table 3. A sample dataset of observed vs predicted values of body weight of chicks

Observed BW(g)	KNN		Regression Tree		Random Forest		Ensemble Model	
	Predicted BW(g)	Error	Predicted BW(g)	Error	Predicted BW(g)	Error	Predicted BW(g)	Error
38	37.66	0.34	39.82	-1.82	37.85	0.15	38.13	-0.13
104	106.54	-2.54	106.95	-2.95	106.59	-2.59	105.12	-1.12
223	211.00	12.00	209.52	13.48	216.43	6.57	219.72	3.28
701	712.03	-11.03	707.853	-6.85	706.32	-5.32	697.07	3.93
1396	1393.00	4.00	1390.00	6.00	1394.07	2.93	1397.32	-1.32

Gueye *et al*. (1998) estimated R^2 values of 0.69 and 0.67 for male and female indigenous chickens, respectively, of Senegal for predicting the BW by using MLR techniques. Udeh *et al*. (2011) predicted the BW in four strains of chicken using MLR methods and reported R^2 values in the range of 0.50 to 0.67. Egena *et al*. (2014) reported R^2 values of 0.602 and 0.684 for MLR and two-factor scores in MLR, respectively, in predicting BW of chicken. Tadele *et al*. (2018) reported R^2 value of 0.433 for stepwise MLR, using the data of male and female chickens raised in Ethiopia. Tadele (2019) employed MLR analysis to predict the BW of indigenous chicken and found R^2 value of 0.25. The R^2 estimates of all the methods in the present study were found to be greater than those reported in the aforementioned studies.

The reported R^2 value of 0.59 by Hlokoe and Tyasi (2021) using stepwise regression for the Potchefstroom koekoek chicken breed was smaller than the R^2 values of all the ML methods employed in the current study. Similarly, the R^2 values in the range of 0.58 to 0.74 and 0.59 to 0.69 for male and female chickens, respectively, using stepwise regression reported by Negash (2021) for Ethiopian Indigenous chickens were also smaller than R^2 values in the current study. The R^2 value of 1.00 reported by Tyasi *et al*. (2020a) for the Hy-line silver brown commercial layer breed using the MARS algorithm was greater than R^2 values in the present study. The values of R^2 (0.832) and $AdjR^2$ (0.828) for the CART algorithm reported by Tyasi *et al*. (2021) in predicting the live weight of the Hy-line silver brown commercial layer breed were smaller than those reported in the present study.

The $RMSE$ value of 0.084 for stepwise regression analysis (Tyasi *et al*. 2021) and 0.001 for MARS (Tyasi *et al*. 2020a) were lower than those found in the present research. Furthermore, the $RMSE$ values of 205.98 to 254.94 for male and 198.15 to 224.10 for female chickens reported by Negash (2021) were greater than the $RMSE$ values of this study. The value of $MAPE$ (4.227) for CART obtained by Tyasi *et al*. (2021) was higher the $MAPE$ values of RF (2.032), RT (3.009) and ensemble model (2.029) in the present study.

In contradiction to our findings, Gueye *et al*. (1998) reported that the body and the chest length are the most suitable predictors of BW. However, Nosike *et al*. (2017) findings that shank length is the most important body parameter for predicting the BW of broiler chicken strains were compatible with our results. Dzungwe *et al*. (2018) and Negash (2021) also reported the shank length as the most important predictor of the BW of the chicken.

Table 4. Two sample t-test for the difference between the observed and predicted body weights for the ensemble model.

Variable	t-test result	
	t-statistic	p-value
Body weight (g)	0.004	0.996
Number of observations	98	

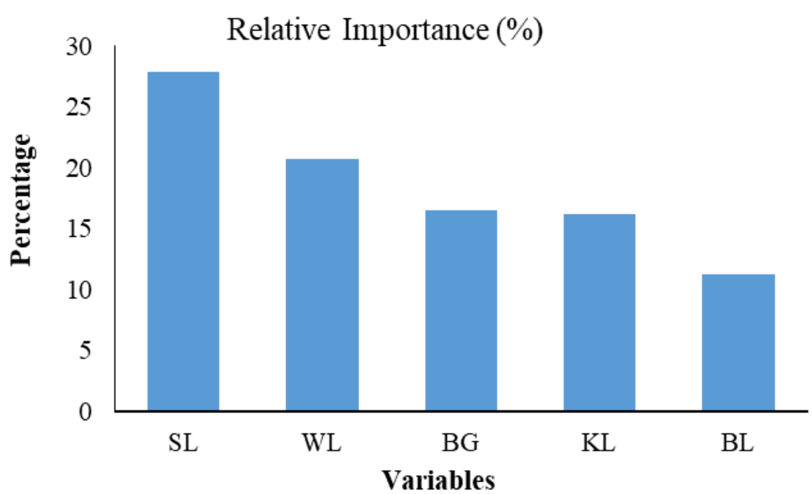

Figure 5. Relative importance of predictors.

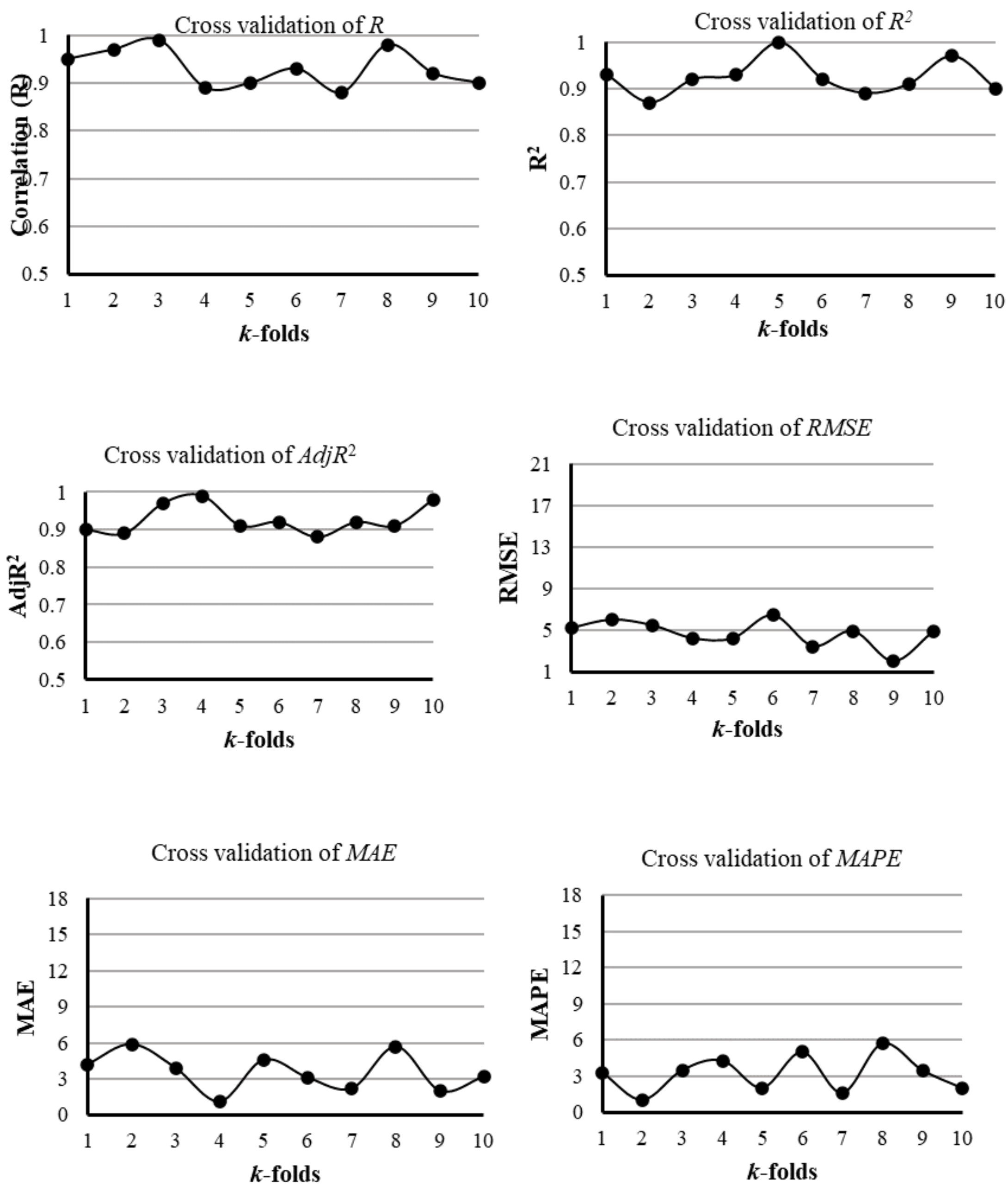

Figure 6. ***10*-fold cross-validation of R, R^2, $AdjR^2$, $RMSE$, MAE and $MAPE$ by ensemble model**

Conclusion: To increase the predictive capability of models, we ensembled the RF, SVR, RT and KNN models by using the MARS model as a Meta learner. The predictive performance of the ensemble model was compared with other ML models used in this study. The ensemble model was found to beat all other methods used in the current study in terms of better predictions and showed promising potential as it combined the prediction from various individual models. Hence, ensemble modeling can be used by researchers and practitioners for the accurate prediction of body weight from the morphometric traits of various farm animals when the relationship between the variables is multifaceted. The advantage of stacking is that it can utilize the skills of a variety of best-performing models on a regression task and build a model that has a better predictive capability than any single model. The results showed that the most important predictor in predicting the BW of chickens is shank length, followed by wing length. Moreover, it has been perceived that the predictive capability of the model was reduced when exposed to the test dataset. Hence, a researcher must also test the predictive capability of the model on an unseen dataset because a model that overfits the training dataset may fail to give satisfactory results on the testing dataset.

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