Regression tree analysis for predicting slaughter weight in broilers

Mehmet Mendeş¹, Erkut Akkartal²

¹Department of Animal Science. Çanakkale Onsekiz Mart University, Turkey
²Yeditepe University. Istanbul, Turkey

Corresponding author: Dr. Mehmet Mendeş. Department of Animal Science. Biometry and Genetics Unit. Çanakkale Onsekiz Mart University, Agriculture Faculty. Terziöğlu Kampüsü, Yeni Yerleşke, 17020 Çanakkale, Turkey - Tel. +90 286 2180018/1348 - Fax: +90 286 2180545 - Email: mmendes@comu.edu.tr

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ABSTRACT

In this study, Regression Tree Analysis (RTA) was used to predict and to determine the most important variables in predicting the slaughter weight of Ross 308 broiler chickens. Data for this study came from 224 chickens raised during three different seasons, namely spring (n=66), summer (n=66), winter (n=92). Second week body weight, shank length, shank width, breast bone length, breast width, breast circumference and body length were used to predict the slaughter weight. Results of RTA showed that among the seven independent variables only four were selected, namely; body weight, breast bone length, shank width, and breast circumference. These selected independent variables were more efficient than the others in predicting the slaughter weight. RTA indicated that the birds which had values of second week body weight >295.95 g, breast bone length >55.82 mm and breast circumference >14.18 cm or that of body weight ≤295.95 g, breast bone length >60.26 mm and shank width >8.32 mm could be expected to have higher slaughter weights.

Key words: Regression tree analysis, Body measurement, Slaughter weight, Multiple regression.

RIASSUNTO

REgRESSION TREE ANALySI S PER LA PReVISIONE DEl PESO DI MACellaZIONE NEI BROILER.

Nel presente studio è stata usata la Regression Tree Analysis (RTA) al fine di determinare le variabili di maggiore importanza per la previsione del peso medio di macellazione in broiler Ross 308. I dati sono stati raccolti da 224 polli allevati in differenti stagioni: primavera (n=66), estate (n=66), inverno (n=92). Nella seconda settimana sono stati rilevati: peso corporeo, lunghezza e larghezza della coscia, lunghezza ossea, larghezza e circonferenza del torace, lunghezza del corpo; tali rilievi sono stati utilizzati per la previsione del peso di macellazione. Attraverso la RTA sono state selezionate, sulle sette analizzate, quattro variabili indipendenti: peso corporeo, lunghezza ossea del torace, circonferenza del torace, larghezza della coscia. Queste variabili selezionate sono state più efficienti delle altre nel predire il peso di macellazione.

La Regression Tree Analysis ha indicato che da soggetti che nella seconda settimana mostrano valori di peso corporeo >295,95 g insieme a lunghezza ossea del torace >55,82 mm e a circonferenza del torace >14,18, oppure valori di peso corporeo ≤295,95 g insieme a lunghezza ossea del torace >60,26 mm e larghezza della coscia >8,32 mm, ci si può attendere pesi di macellazione più elevati.

Parole chiave: Regression tree Analysis (RTA), Misure corporee, Peso di macellazione, Regressione multipla.
Introduction

Experiments related to animal science are often conducted to develop a model to represent and explain the relationships between variables or to predict slaughter weight of animals by using some body measurements measured at early ages at given experimental conditions. For this purpose, many types of models have been developed, including multiple regression, multivariate multiple linear regression, discriminant analysis, logistic regression, neural networks and decision trees or classification and regression trees. Among these, multiple regression, discriminant analysis and logistic regression are commonly used in practice (Çamdeviren et al., 2005; Temel et al., 2005). However, some assumptions such as normality, constant variance, linearity, non-multicolinearity should be met in data to use these models (Draper and Smith, 1998). In practice, these assumptions are generally not met, which limits the flexibility of these methods to analyze such data. On the other hand, interpretation of analyses results might be difficult even if assumptions required by these models were met. In addition, evaluation of some complex relations will not be possible. It will be more obvious when working with large data sets, high numbers of independent variables and non-linear relations among the variables (Austin and Cunningham, 1981; Breiman et al., 1984; Austin et al., 1990, 1994; Clark and Pregibon, 1992; Hess et al., 1999; Muñoz and Felicísimo, 2004). In these cases, Regression Tree Analysis (RTA) can be used to analyze such data (Breiman et al., 1984; White and Sifneos, 2002). RTA has many advantages compared to traditional methods such as multiple regression, logistic regression, discriminant and cluster analyses. Because RTA is a non-parametric method, no assumptions are required about the underlying distribution of independent variables.

RTA is a more useful method than the traditional methods especially when there are large complex data sets and high number of independent variables (Breiman et al., 1984; Talmon, 1986; Beckman et al., 1995; Chaudhuri et al., 1995; Steinber and Colla, 1995; Honeycutt and Gibson, 2003; Çamdeviren et al., 2005). However, Breiman et al. (1984) reported that Regression Trees could be notably more accurate in the case of nonlinear problems, while the traditional regression models would probably work better for linear data. Although RTA was originally designed for large data sets, it can also be used on small data sets. At the same time, RTA is not affected by high correlations between independent variables (multi-collinearity problem), outliers, levels of measurement of independent variables and missing values. Moreover, RTA accounts for higher order interactions among the independent variables which lead to obtaining more detailed information about their effects. One of the other advantages of the RTA is to present results of the analysis in a visual form. This helps both researchers and readers to understand and interpret the results more easily (Breiman et al., 1984; De’ath and Fabricius, 2000; Çamdeviren et al., 2005).

RTA has been widely used for both prediction and classification in many fields of science such as medicine, industry, and engineering (Çamdeviren et al., 2005). The use of this method in animal science is not common and no studies are available on poultry science. However, the RTA, which has many advantages over the traditional methods, may be commonly and efficiently used in animal science studies. In this study we used RTA to predict slaughter weights by using some variables observed in the second week of the Ross 308 broilers, which were grown during three different seasons, to determine the most effective variables of slaughter weight.
Material and methods

Animals and experimental conditions

Data for this study came from 224 Ross 308 broiler chickens raised during three different seasons, namely spring (n=66), summer (n=66), and winter (n=92). Water and feed were provided ad libitum, on 23h light and 1h dark regime, throughout the 6-week trial period. Birds were offered a starter diet, from hatching to 3 weeks, a grower diet from 4 to 5 weeks, and a finisher diet at the last week of the trial. The starter, growth and finisher diets included 24.09% crude protein and 2818 kcal/ME, 25.32% crude protein and 2892 kcal/ME, and 22.38% crude protein and 2912 kcal/ME, respectively. Body weight (BW, g), shank length (SHL, mm), shank width (SHW, mm), breast bone length (BBL, mm), breast width (BRW, mm), breast circumference (BRC, cm) and body length (BL, cm), all measured at the second week of age, were the variables used to predict slaughter weight of birds. SHL, SHW, BBL, BRW and BL traits were measured using digital caliper, BRC was measured using tape measure.

Statistical analysis

Regression Tree Analysis (RTA) is a binary decision tree. It is structurally very simple and easy to visualize. The tree is constructed by splitting the whole data into nodes or sub-groups by using all the independent variables. RTA begins with a single node (root node) that contains all of the observations in the sample and then is branched into mutually exclusive child nodes. This process goes on until the requirements of homogeneity index are met. The purpose of RTA is to produce terminal nodes, which are homogeneous with respect to the target variable (Breiman et al., 1984; Bevilacqua et al., 2003; Çamdeviren et al., 2005). RTA finds the best possible variable to split the node into two child nodes. In choosing the best splitter, the program seeks to maximize the average “purity” of the two child nodes. The Least Squared Deviation (LSD) method was used as a measure of the homogeneity of nodes (Breiman et al., 1984; Karaliç, 1992; Dietterich, 1998; Torgo, 1998; Bevilacqua et al., 2003). For scale dependent variables, the risk value is estimation of the within nodes variance. For each node k, \( R(k) \) represents within node variance or risk value of node k. \( R(k) \) is computed as

\[
R(k) = \frac{1}{N(k)} \sum_{i \in k}^n (Y_i - \bar{Y}(k))^2
\]

where, \( N(k) \) is the number of observation in node k, \( Y_i \) is the value of the target variable, and \( \bar{Y}(k) \) is the mean of node k. However, risk value depends on the unit of dependent variable. Therefore, risk value must be adjusted accordingly.

Let \( S^2_c \) and \( S^2_y \) show error variance (or explained variance) and variance of dependent variable (or variance of root node), respectively. Thus, \( S^2_c \) can be calculated as

\[
S^2_c = \frac{\text{risk value}}{S^2_y}. \quad \text{Explained variance (} S^2_x \text{) will be } S^2_x = 1 - S^2_c.
\]

The LSD criterion function for split S at node k is defined as

\[
\Phi(S, k) = R(k) - P_L R(k_L) - P_R R(k_R)
\]

where,

\( P_L \) is the proportion of observations in parent node k classified in the left child node \( K_L \);

\( P_R \), the proportion of observations in parent node k classified in the right child node \( K_R \).

The split S is chosen to maximize the value of \( \Phi(S, k) \). This value, weighted by the proportion of all observations in node k, is the value reported as “improvement” in the tree (Talmon, 1986; Cappelli et al., 2002).
The tree building process continues until each partition consisting of one observation in each of the child nodes or all observations within each child node have the identical distribution of independent variables, making splitting. After the tree has been formed, it can be visualized by showing how the data set is partitioned. Every partition contains a rule which allows the relations between variables to be investigated (Breiman et al., 1984; Çamdeviren et al., 2005).

In this study, we used the ten-fold cross-validation as an error estimation method. The purpose of running multiple cross-validations is to get more reliable estimates of the independent variables. The cross-validation or a test sample produces a single, final tree (Dietterich, 1998; Kuhnt et al., 2000).

In this study we also compared the terminal nodes with respect to slaughter weight. Firstly, slaughter weight of each bird in each terminal node was determined. Then, the slaughter weight of birds in each terminal node was subjected to analysis of variance using the following model to test effects of terminal nodes \((\alpha)\):

\[
Y_{ij} = \mu + \alpha_i + \epsilon_{ij}
\]

Where \(Y_{ij}\) is a slaughter weight, \(\mu\) is the overall mean, \(\alpha_i\) is the fixed effect of terminal nodes \((i=1, 2, \ldots, 6)\), and \(\epsilon_{ij}\) is the residual error distributed as N\((0, \sigma^2)\).

SPSS for windows (ver. 15.0) statistical package program was used in analyzing the data.

**Results**

The descriptive statistics of independent variables are given in Table 1. Figure 1 (optimal tree) shows the predictions of slaughter weights by using the variables including second week body weight (BW), shank width (SHW), shank length (SHL), breast bone length (BBL), breast circumference (BRC), breast width (BRW), body length (BL), and breeding season. Node 0 is called the root node and it contains descriptive statistics related to slaughter weight (Figure 1). We computed Pearson-moment

| Table 1. Descriptive statistics for independent variables. |
|----------------------------------------------------------------------------------|
| **Variables** | **Winter (n=92)** | **Spring (n=66)** | **Summer (n=66)** | **Overall (n=224)** |
| SHW | 9.90 | 0.15 | 10.54 | 0.16 | 10.84 | 0.18 | 10.36 | 0.10 |
| SHL | 30.44 | 0.20 | 30.88 | 0.20 | 30.86 | 0.22 | 30.69 | 0.12 |
| BBL | 60.90 | 0.68 | 62.40 | 0.64 | 62.56 | 0.92 | 61.83 | 0.43 |
| BRW | 35.75 | 0.28 | 37.33 | 0.41 | 35.88 | 0.37 | 36.25 | 0.20 |
| BRC | 14.48 | 0.15 | 14.97 | 0.20 | 15.71 | 0.19 | 14.99 | 0.11 |
| BL | 98.67 | 1.16 | 97.44 | 1.15 | 104.85 | 1.52 | 100.13 | 0.76 |
| BW | 238.65 | 5.83 | 264.55 | 7.14 | 288.37 | 7.04 | 260.93 | 4.03 |
| BW6 | 1759.02 | 43.35 | 1914.38 | 51.60 | 1984.30 | 48.06 | 1871.17 | 28.01 |

Risk Value: 33390.83 Standard Error: 29535.84

*SHW: second week shank width, SHL: second week shank length, BBL: second week breast bone length, BRW: second week breast width, BRC: second week breast circumference, BL: second week body length, BW: second week body weight and BW6: slaughter weight.
Correlations between the variables to determine linear relations. Correlation analysis showed that slaughter weight had a high correlation with BW ($r=0.856; P=0.00$), BRC ($r=0.532; P=0.037$), BL ($r=0.507; P=0.039$), BBL ($r=0.499; P=0.041$), SHW ($r=0.365; P=0.047$), and SHL ($r=0.305; P=0.05$).

Firstly, the effect of each independent variable on the prediction of the slaughter weight was evaluated separately. For this, the importance of each variable was calculated. Because the BW reflected the highest slaughter weight, it was determined to be the most important variable, followed by BBL, SHW and BRC. Therefore, among the 7 variables, only 4 were selected. Using these 4 variables, we formed 6 terminal nodes. Each of these nodes was accepted as
a homogenous group. However, SHL, BRW, BL and breeding season were not found to be effective on predicting the slaughter weight based on optimal tree.

Table 1 shows the risk value and its standard error. Risk value shows the variance within the nodes and it can be used as model fitness criterion. Therefore, the model which has a lower risk value will be a better model. The variance of the root node or dependent variable is $S^2_y = (419.215)^2 = 175741.216$.

The unexplained variation in the slaughter weight is found to be

$$S^2_e = \frac{\text{risk value}}{S^2_y} = \frac{33990.830}{175741.216} = 0.19 = 19.0\%$$

The variation in dependent variable explained by the model is $S^2_x = 1 - S^2_e = 1 - 0.19 = 0.81 = 81.0\%$. It is concluded that 81.0% of the variation in slaughter weight can be explained by the independent variables which had a significant effect in forming the optimal tree.

As seen in the optimal tree (Figure 1), firstly, birds in Node 0 or root node were divided into two nodes, based on BW as Node 1 ($\leq 295.95$ g) and Node 2 ($>295.95$ g). As a result, BW was the most effective variable in predicting the slaughter weight. The mean slaughter weights of birds in Node 1 and Node 2 were predicted as 1765.701±31.37 g and 2103.211±46.65 g, respectively. The proportions of the birds in Node 1 and Node 2 in total are 68.8% and 31.2%, respectively. Mean slaughter weights for birds in Node 2 were higher than that of the Node 1. It is not sufficient, however, to use only BW to predict slaughter weight. In other words, birds in Node 1 and Node 2 were not homogeneous enough. Therefore, Node 1 and Node 2 generated by BW in the first step were divided into nodes again based on BBL value. It can be seen that BBL was the second most significant effect on the prediction of slaughter weight. Based on BBL values, 154 birds in Node 1 were divided into two new nodes: Node 3 ($\leq 60.26$ mm) and Node 4 ($>60.26$ mm). In addition, 70 birds in Node 2 were also divided into two new nodes: Node 5 ($\leq 55.82$ mm) and Node 6 ($>55.82$ mm).

It was predicted that the mean slaughter weights (1878.445±45.95) of birds with BW values $\leq 295.95$ g (Node 1) and BBL values $>60.26$ mm (Node 4) were higher than birds (1643.815±37.86) with BBL values $\leq 60.26$ mm (Node 3). Similarly, the mean slaughter weights of BW $>295.95$ g birds which had higher BBL values ($>55.82$ mm) were estimated higher than that of birds with low BBL values ($\leq 5.82$ mm). Based on SHW and BRC values, birds in Node 4 and Node 6 were divided into sub groups, but no new nodes were observed for birds in Node 3 and Node 5. For this reason, birds in Node 3 and Node 5 showed homogenous groups, called terminal nodes. Therefore, Node 3 and Node 5 were more efficient than the Node 4 and Node 6 in predicting the slaughter weight. In other words, BW and BBL values were the primary variables to predict slaughter weight. Node 4 and Node 6, on the other hand, were divided into new nodes, because it is not sufficient to use these two nodes to estimate slaughter weights of birds. New variables (SHW and BRC) were also needed. Based on SHW value, birds in Node 4 had 2 new nodes (Node 7 and Node 8). In addition, birds in Node 6 were divided into two new nodes (Node 9 and Node 10) based on BRC values. These findings showed that in addition to BW and BBL values, SHW value should also be used to predict the slaughter weight of birds with BW values $\leq 295.95$ g and BBL values $>60.26$ mm. However, BRC value should be used together with BW and BBL values for predicting slaughter weight of birds with BW values $>295.95$ and BBL values $>55.82$ mm. Based on SHW values, birds in Node 4 were divided into two nodes:
Node 7 (≤8.32 mm) and Node 8 (>8.32 mm). Birds in Node 6 were also divided into two nodes: Node 9 (≤14.18 cm) and Node 10 (>14.18 cm) based on BRC values. No sub-group separation in Node 7, Node 8, Node 9 and Node 10 was observed. Therefore, each one of these nodes was a terminal one. In this study, there were 6 terminal nodes including Nodes 3, 5, 7, 8, 9 and 10. The mean slaughter weights of the birds in Node 10 (2314.054±116.04) and Node 8 (2229.870±44.99) were predicted higher than that of the birds in Node 3, 5, 7 and 9. Nodes 3, 5, 7 and 9 formed a group of birds with low slaughter weight while the nodes 8 and 10 formed a group of birds with high slaughter weight. Node 3 is a group of birds with ≤295.95 g BW and ≤60.26 mm BBL values. Similarly, Node 5 is a group of birds with >295.95 g BW and ≤55.82 mm BBL values. Birds in Node 7 had ≤295.95 g BW, >60.26 mm BBL and >8.32 cm SHW values and Node 9 had >295.95 g BW, >55.82 mm BBL and ≤14.18 cm BRC values, respectively. On the other hand, Node 10 is a group of birds with >295.95 g BW, >55.82 mm BBL values and >14.18 cm BRC values. Birds in Node 8 nodes had ≤295.95 g BW, >60.26 mm BBL and >8.32 mm SHW values.

The slaughter weight means for terminal nodes were also compared by ANOVA to determine the differences among the nodes. The results of ANOVA indicated that the differences among the nodes were significant (P<0.01). Tukey Kramer multiple comparison test was used to determine different nodes. The highest slaughter weight means were for Node 10 and Node 8. However, the difference between two nodes was not significant (P>0.05). Thus, Node 10 and Node 8 were combined as a new group. Likewise, no differences were observed among Node 3, Node 5, Node 7 and Node 9 (P>0.05). Therefore, Node 3, Node 5, Node 7 and Node 9 were also combined as another group.

Discussion

Investigation of relations among variables in animal-based studies, which make predictions using the variables in early periods on slaughter weights, and also determine most effective variables in predictions on slaughter weights and the classification of animals, provides important findings for both production and, hence, breeding studies. The reliability of the results from the studies with such objectives is closely associated with the use of appropriate statistical methods in data analysis. Especially in cases such as the use of large data sets, a high correlation among independent variables (multi-collinearity problems), a high number of independent variables (both continuous and categorical) and the presence of non-linear relations among variables, the RTA method provides advantages to the researcher in both obtaining more reliable results and easier interpretation of them.

The Optimal Tree explained 81.0% of the variation in slaughter weights. That is, it can be concluded that 81.0% of the variation in the slaughter weights of birds can be explained by the second week body weight, breast bone length, shank width and breast circumference variables included in the model. Such a value indicates that estimations of slaughter weight by the Regression Tree Analysis are highly reliable. The significance of correlation coefficients between slaughter weight and second week body weight, breast bone length, breast circumference and shank width suggests that changes in these variables may significantly affect prediction of slaughter weight, which might be seen as another indicator of the robustness of RTA. On the other hand, it should be kept in mind that only the use of correlations between slaughter weight and other variables may not be sufficient to determine the factors affecting a dependent variable.
RTA showed that birds with values of BW>295.95 g, BBL>55.82 mm and BRC>14.18 cm or that of BW≤295.95, bb1>60.26 and SHW>8.32 mm could be expected to have higher slaughter weights. Conversely, the lowest slaughter weight was estimated for the birds in Node 3 which is a group of birds with ≤295.95 g body weight in the second week and ≤60.26 BBL values, birds in Node5 which is a group of birds with >295.95 g BW and ≤55.82 mm BBL values, birds in Node 7 with ≤295.95 g BW, >60.26 mm BBL and >8.32 cm SHW values, and Node 9 with >295.95 g BW, >55.82 mm BBL and ≤14.18 cm BRC values, respectively. Therefore, it can be expected that birds in these groups should have lower slaughter weights. Nevertheless, the mean of the slaughter weights in all terminal nodes (node 3, node5, node7, node8, node9, node10) constructed by the analysis of Regression Tree, was observed to be in the optimum acceptable limits for the enterprises producing for commercial purposes. Although only the body weight measurements are routinely evaluated by producers or breeders to estimate the body weight gains, determining the relations between body weight and other body measurements such as shank width, shank length, breast bone length, etc. provide useful information. Based on these relations, breeders may have a chance to revise their management practices as well as getting the chance for an early selection (Mendeş et al., 2005). Genetic companies may use these relationships to select the birds at an earlier stage within genetic lines, thereby decreasing generation interval and increasing profitability.

Many studies have investigated the relationships of slaughter weight with BW, SHW, SHL, BBL, BL, BRW and breeding season; and by utilizing these variables, tried to predict slaughter weight of Ross 308 broiler chickens. Based on the findings, we concluded that SHL, BL and breeding season were not effective in predicting slaughter weight. Hence, prediction of slaughter weight of birds from SHL, BL and season would not give reliable results. Contrarily, BW, BBL, SHW and BRC variables were found to be highly related, suggesting that these 4 vari-

Conclusions

In this study, we investigated the relationships of slaughter weight with BW, SHW, SHL, BBL, BL, BRW and breeding season; and by utilizing these variables, tried to predict slaughter weight of Ross 308 broiler chickens. Based on the findings, we concluded that SHL, BL and breeding season were not effective in predicting slaughter weight. Hence, prediction of slaughter weight of birds from SHL, BL and season would not give reliable results. Contrarily, BW, BBL, SHW and BRC variables were found to be highly related, suggesting that these 4 vari-

studies, the relations between body weight and some of the body measurements have been discovered and the results have been used in estimating future steps. Multiple regression models are widely used to estimate body weight of the animals in the future using their body measurements at early ages. Mahanta et al. (1998) demonstrated that there was a linear relation between body weight and shank length. Along with shank length, breast width, breast circumference, spine length and pelvis width are the other important body variables used in body weight estimations. Latshaw and Bishop (2001) investigated the relations between body weight and different body measurements in chickens from different breeds and diet programs. They reported that the best regression model to estimate body weight was BW=-93.0+68.5 (breast width)+48.5 (breast circumference)+62.8 (pelvis width). As one can see, breast circumference, which existed in Latshaw and Bishop’s (2001) model also exists in our model. The difference between the results may be due to the use of different statistical techniques in data analysis, different lines of chickens as experimental material, and varied experimental conditions.
variables are important in predicting slaughter weight. In the other words, these variables were more efficient than the others in predicting the slaughter weight of birds. 81.0% of variation could be explained by these 4 variables. In conclusion, the optimal tree shows that high slaughter weight can arise from two different combinations of variables (the birds which had values of BW>295.95 g, BBL>55.82 mm and BRC>14.18 cm or that of BWs295.95, bb1>60.26 and SHW>8.32 mm could be expected to have higher slaughter weights), and that the Regression Tree Analysis provides a means of identifying and developing different strategies for increasing slaughter weight.

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