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Development of Standard-Length Prediction Model Based on the Morphometrics of Shortfin Scad (*Decapterus macrosoma*) from the Karangantu Archipelagic Fishing Port, Banten

Naufaldi Arizky, Muh Herjayanto, Erik Munandar

Department of Fisheries Science, Faculty of Agriculture, University of Sultan Ageng Tirtayasa, Banten, Indonesia

*Correspondence Author: erik.munandar@untirta.ac.id

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ABSTRACT

The morphometric truss system is a widely used method for analyzing variations in fish body shape. However, its application remains limited for predicting standard length in specimens with incomplete body morphology. This study aims to develop a predictive model for estimating the standard length of shortfin scad (*Decapterus macrosoma*) based on morphometric truss characteristics as a solution for morphological estimation when fish specimens are not intact. The research was conducted at the Fisheries Science Study Program Laboratory, University of Sultan Ageng Tirtayasa. One hundred shortfin scad specimens were collected from the Karangantu Archipelagic Fishing Port (PPN Karangantu). Measurements were taken from 24 truss points, which were classified into four body regions: head (A), anterior body (B), posterior body (C), and caudal peduncle (D). The analysis employed simple and multiple linear regression, and model performance was evaluated using MAE, MSE, RMSE, and R^2 metrics. The multiple linear regression results indicated that the anterior body and posterior body groups exhibited the highest coefficients of determination ($R^2 > 0.97$), the lowest error values, and residuals approximating a normal distribution. In contrast, the caudal peduncle group showed the weakest predictive performance. These findings affirm that morphometric truss characteristics of the anterior and posterior body regions are the most effective quantitative indicators for predicting standard length in shortfin scad. The proposed model has significant potential to enhance the reliability of fisheries stock data, particularly under conditions involving morphologically incomplete specimens.

INTRODUCTION

Shortfin scad is a small pelagic fishery resource commonly found in marine waters and typically inhabits these environments in schools. According to White et al. (2013), there are three species of scads distributed across Indonesian waters: redtail scad (*Decapterus kurroides*), mackerel scad (*D. macarellus*), and shortfin scad

(*D. macrosoma*). Species *D. macrosoma* is characterized by an elongated, fusiform body that appears round in cross-section but resembles a torpedo in overall shape (Umar et al., 2019). This species is the most widely favored among Indonesian consumers and is locally known as "layang bengol deles" or "layang abu-abu". Due to its high market demand, large-scale fishing has been conducted to support supply needs. Shortfin scad has been recorded as one of Indonesia's most abundant commodities landed across all traditional fish landing sites (TFL), with a total catch volume reaching 25,937 tons in 2023. The estimated economic value of this catch amounts to approximately IDR 335 billion. One such TFL location is in Banten Province, where 1.2 tons of shortfin scad were landed (BPS, 2024).

The high and intensive production of shortfin scad landings in Banten Province occurs primarily at the Karangantu Archipelagic Fishing Port (PPN Karangantu). This situation necessitates practical management efforts to ensure stock sustainability and maintain marine ecosystem stability. One key management activity involves collecting size data for fish stock assessments. However, a significant challenge arises from the frequent landing of fish in incomplete physical conditions, which compromises the accuracy of standard length (SL) measurements. This leads to data bias in stock assessments and may result in serious errors in estimating fish biological parameters, ultimately affecting decision-making in fisheries resource management. Currently, fish stock assessments in Indonesia are guided by the Maximum Sustainable Yield (MSY) policy framework (Juniko et al., 2018). MSY assessments employ various methods, most relying on parameters commonly used in fish population dynamics studies. One such critical parameter is the standard length. SL measurement provides fundamental morphological information at the individual level and is a key index for estimating biomass, age structure, growth acceleration, and mortality (Barua et al., 2022).

Morphometric data collection has been widely applied in fisheries research to support growth studies, species identification, and the estimation of population parameters. External body measurements such as total length, standard length, snout or lip length, dorsal fin length, and caudal peduncle height have proven helpful for comparative analysis of fish body size (Setiawan, 2016; Salmanu, 2021). Among the available methods, the morphometric truss network is one of the most frequently utilized techniques for analyzing variations in fish body shape. However, the application of this technique remains limited when it comes to predicting the standard length of shortfin scad in cases where the body is incomplete. In response to this issue, the present study aims to develop a quantitative predictive model for estimating the standard length of shortfin scad using truss morphometric measurements. According to Kusumawati et al. (2017), linear regression methods effectively support standard length prediction for shortfin scad. Simple linear regression examines the correlation between a single independent variable and a dependent variable (Ginting et al., 2019), while multiple linear regression is applied when one or more predictor variables influence multiple interrelated response variables. Each group of morphometric characteristics is represented by a regression equation using the same set of predictor variables (Shofiyah, 2018).

The model developed and analyzed in this study is expected to offer a practical solution for accurately estimating standard length, particularly in cases where fish specimens are not intact. This approach is intended to enhance the reliability and validity of fish stock assessment data, particularly at the Karangantu Archipelagic Fishing Port (PPN Karangantu), thereby contributing to more informed fisheries management decisions.

METHOD

This research was conducted between May and June 2025. Fish measurements and data processing activities occurred at the Laboratory of the Fisheries Science Study Program, Faculty of Agriculture, Sultan Ageng Tirtayasa University. The tools used in this study included a laptop, mobile phone camera, cool box, 30 cm ruler, millimeter block paper, notebook, observation sheet, label paper, pens, and a digital caliper. The materials comprised 100 individuals of shortfin scad (*D. macrosoma*) as the test organisms and ice blocks to maintain fish freshness. Shortfin scad samples were obtained from the Karangantu Archipelagic Fishing Port (PPN Karangantu) in Kasemen District, Serang City, Banten Province.

Morphometric Truss Measurements

The morphometric truss measurement of shortfin scad (*D. macrosoma*) in this study followed the method established by Kusumaningrum et al. (2021), with modifications that included additional truss points on the snout region (Figure 1), as proposed by Pasisingi et al. (2023) (Table 1).

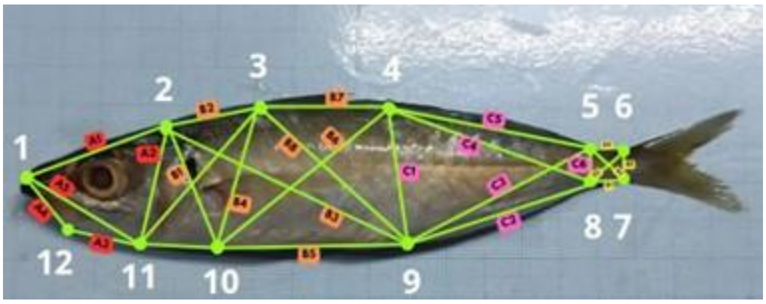

Figure 1. Truss morphometric Characteristic in Shortfon Scad. The truss code description can be seen in Table 1.

Table 1. Interpretation of Truss Morphometric Characteristics in Shortfin Scad.

No	Body Part	Truss Code	Distance Description
1	Head (A)	A1 (1 – 2)	Distance between the tip of the snout – Boundary point of the head

No	Body Part	Truss Code	Distance Description
2		A2 (2 – 11)	Distance between the boundary point of the head – Lower operculum point
3		A3 (11 – 12)	Distance between the lower operculum point – Base of lower jaw
4		A4 (1 – 12)	Distance between the tip of the snout – Base of lower jaw
5		A5 (1 – 11)	Distance between the tip of the snout – Lower operculum point
6	Anterior Body (B)	B1 (2 – 10)	Distance between the boundary point of the head – Base of ventral fin
7		B2 (2 – 3)	Distance between the boundary point of the head – Anterior base of dorsal fin
8		B3 (2 – 9)	Distance between the boundary point of the head – Anterior base of anal fin
9		B4 (3 – 10)	Distance between the anterior base of dorsal fin – Base of ventral fin
10		B5 (9 – 10)	Distance between the anterior base of anal fin – Base of ventral fin
11		B6 (4 – 10)	Distance between the anterior base of second dorsal fin – Base of ventral fin
12		B7 (3 – 4)	Distance between the anterior base of dorsal fin – Anterior base of posterior dorsal fin
13		B8 (3 – 9)	Distance between the anterior base of dorsal fin – Anterior base of anal fin
14	Posterior Body (C)	C1 (4 – 9)	Distance between the anterior base of posterior dorsal fin – Anterior base of anal fin
15		C2 (8 – 9)	Distance between the posterior base of anal fin – Anterior base of anal fin
16		C3 (9 – 5)	Distance between the posterior base of second dorsal fin – Anterior base of anal fin
17		C4 (4 – 8)	Distance between the anterior base of second dorsal fin – Posterior base of anal fin
18		C5 (4 – 5)	Distance between the anterior base of second dorsal fin – Posterior base of second dorsal fin
19		C6 (5 – 8)	Distance between the posterior base of second dorsal fin – Posterior base of anal fin
20	Caudal Fin (D)	D1 (7 – 8)	Distance between the posterior base of anal fin – Anterior base of lower finlet
21		D2 (6 – 8)	Distance between the posterior base of anal fin – Anterior base of upper finlet
22		D3 (5 – 7)	Distance between the posterior base of second dorsal fin – Anterior base of lower finlet
23		D4 (5 – 6)	Distance between the posterior base of second dorsal fin – Anterior base of upper finlet
24		D5 (6 – 7)	Distance between the posterior base of upper finlet – Posterior base of lower finlet

(Source: modified from Kusumaningrum *et al.* 2021 and Pasisingi *et al.* 2023)

Simple Linear Regression

Simple linear regression was used to determine the extent of the relationship and causal effect between a single independent and dependent variable (Anto et al., 2025). The model was formulated according to Walpole (1995) as follows:

$$Y = a + bX$$

Information:
Y = Standard length of Shortfin Scad
X = Truss morphometric characters
a = Constant
b = Coefficient of regression

Multiple Linear Regression

Multiple linear regression was applied to predict the response variable based on multiple independent variables (Harlan, 2018). The formulation used follows Adiguno et al. (2022):

$$Y= a + b_1X_1 + b_2X_2 + ... + b_nX_n...$$

Information:
Y = Dependent variable (predicted value)
X = Independent variable
a = Constant (Y value if X1, X2, ..., Xn = 0
b = Coeffission of regression (increasing or decreasing value)

Mean Absolute Error (MAE)

MAE calculates the average of the absolute differences between the actual standard length and the predicted values generated by the regression model. This metric accurately represents model performance (Suryanto & Muqtadir, 2019). The MAE is calculated using the following equation:

$$\text{MAE} = \frac{1}{n}\sum_{i=1}^{n}|\text{fi} - \text{yi}|$$

Information:
MAE = *Mean Absolute Error*
fi = Actual standard length
yi = Predicted value
n = Amount of dataa

Mean Squared Error (MSE)

MSE calculates the average of the squared differences between actual and predicted values. A lower MSE indicates a smaller deviation, reflecting better model accuracy (Robial, 2018). It is calculated as:

$$\text{MSE} = \sum \frac{(\hat{y} - y)\text{^}2}{n}$$

Information:
MSE = *Mean Square Error*
$\hat{y}$ = Predicted value
y = Actual value
n = Amount of data

Root Mean Square Error (RMSE)

RMSE evaluates the magnitude of prediction error in estimating the actual values. It gives a standard interpretation of prediction accuracy (Fadilah et al., 2020) and is computed as (Prapcoyo 2018):

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

Information:
RMSE = *Root Mean Square Error*
$\hat{y}$ = Predicted value
y = Actual value
n = Amount of data

Coefficient of Determination (R^2)

The coefficient of determination (R^2) quantifies the proportion of variance in the dependent variable (standard length) explained by the independent variables (truss points) in the regression model (Hair et al., 2011). Statistical computation was performed using Python software.

Residual Normality Test

The normality test was conducted using histogram plots to evaluate whether the residuals from the regression model followed a normal distribution. This test influences the validity of statistical inference (Tolosang, 2018). All analyses were carried out using Python.

RESULT AND DISCUSSION

Simple Linear Regression

The results of simple linear regression analysis for each truss morphometric variable against the standard length (SL) of shortfin scad are presented in Table 2. Based on the table above, the results of the simple linear regression analysis between individual truss morphometric point variables and Standard Length (SL) indicate that 11 variables exhibit high coefficients of determination. These are observed at truss points A2, A5, B1, B4, B6, B7, B8, C1, C3, C4, and C5, with R^2 values ranging from 0.8037 to 0.9342. The variables with high coefficients are predominantly found in the anterior body group (B) and posterior body group (C).

Table 2. Results of Simple Linear Regression Analysis

Comparison	**R²**
A1:SL	0,4811
A2:SL	0,8629
A3:SL	0,6436
A4:SL	0,5786
A5:SL	0,8433
B1:SL	0,906
B2:SL	0,3642
B3:SL	0,6332
B4:SL	0,8908
B5:SL	0,6043
B6:SL	0,9041
B7:SL	0,8428
B8:SL	0,9032
C1:SL	0,9179
C2:SL	0,7397
C3:SL	0,8037
C4:SL	0,9342
C5:SL	0,9331
C6:SL	0,5428
D1:SL	0,4016
D2:SL	0,4144
D3:SL	0,5649
D4:SL	0,3814
D5:SL	0,7122

Information: A: head, B: anterior body, C: posterior body, D: caudal fin, SL: standard length

The high R^2 values for these variables align with the interpretation proposed by Hair et al. (2011), which categorizes an R^2 value of 0.75 as strong, 0.50 as moderate, and 0.25 as weak. The R^2 value for each variable reflects the degree of association between the truss point and standard length, the closer the R^2 value is to 1, the greater the variable's contribution or association with standard length. This finding is consistent with the research by Sehangunaung et al. (2023), which stated that a higher percentage of the coefficient of determination indicates a greater contribution of the independent variable (X) to the dependent variable. Among the dominant groups, the highest R^2 values are found at truss point C4 (0.9342) and B1 (0.906).

Multiple Linear Regression

The results of the multiple linear regression analysis for the head (A), anterior body (B), posterior body (C), and caudal peduncle (D) groups representing each body segment of the shortfin scad about standard length are presented in Table 3.

Table 3. Results of Multiple Linear Regression Analysis

Group	R^2
Head (A)	0.9226
Anterior Body (B)	0.9722
Posterior Body (C)	0.9717
Caudal Fin (D)	0.8402

Based on Table 3, the multiple linear regression analysis demonstrates high coefficient values. According to Hair et al. (2011), a coefficient of determination (R^2) value of 0.75 or higher is considered strong, 0.50 is categorized as moderate, and 0.25 is regarded as weak. The high R^2 values in this study indicate a strong correlation between body parts and the standard length of the fish.

The high R^2 values associated with various body parts strongly correlate with the fish's standard length. This is consistent with the findings of Amatya (2021), who reported that truss measurements representing the head region provide a primary structural baseline for standard length. Therefore, truss points in the head region serve as initial and highly informative predictors, significantly contributing to the fish's body length. The body region exhibited the strongest relationship, with the highest coefficient of determination among all groups. Truss elements located along the body and tail span the longitudinal axis of the fish and directly capture variations in length that encompass a significant portion of the body's framework. This finding supports the strong correlation between truss measurements in these regions and standard length (Rawat et al., 2017).

Evaluation Metrics

The initial evaluation results of the linear regression model's performance in predicting the standard length of shortfin scad using square error (MSE), root mean square error (RMSE), and the coefficient of determination (R^2), based on truss morphometric measurements, are presented in Table 4. The performance of the linear regression model across each morphometric truss group demonstrated significant variation in predicting the fish's standard length. The anterior body group (B) yielded the best results, with an MSE of 4.7639 mm^2, RMSE of 2.1826 mm, and R^2 of 0.9722. The posterior body group (C) followed closely with an MAE of 1.7606 mm, MSE of 4.8225 mm^2, RMSE of 2.1960 mm, and R^2 of 0.9717. The head group (A) recorded an MAE of 2.7413 mm, MSE of 13.1663 mm^2, RMSE of 3.6285 mm, and R^2 of 0.9226. The caudal peduncle group (D) performed poorly, with the highest error values MAE of 3.7429 mm, MSE of 27.1925 mm^2, and RMSE of 5.2146 mm. The lowest R^2 value of 0.8402 indicates a high sensitivity to error and the weakest predictive ability.

Table 4. Model Performance Evaluation Analysis

Group	MAE	MSE	RMSE	R^2
Head (A)	2.7413	13.1663	3.6285	0.9226
Anterior Body (B)	1.7205	4.7639	2.1826	0.9722
Poterior Body (C)	1.7606	4.8225	2.1960	0.9717
Caudal Fin (D)	3.7429	27.1925	5.2146	0.8402

Group B demonstrated the most optimal performance, with the lowest MAE, MSE, and RMSE values and the highest R^2, indicating very high predictive accuracy and consistency. Group C performed nearly as well, while Group A, although fairly accurate, was less precise. In contrast, Group D exhibited the weakest performance, marked by the most significant errors and the lowest R^2. These findings align with Susilawati & Muhamthir (2019), who emphasized that lower MSE values reflect better model classification; Romaita et al. (2020), who noted that the lowest MAE indicates the best forecasting results; and Bode (2017), who evaluated prediction accuracy based on RMSE values approaching 1.

Based on this analysis, the body and tail regions (Groups B and C) are confirmed as the primary contributors to accurate prediction models. At the same time, the caudal peduncle (Group D) shows limited predictive capacity due to its low structural variability. Consequently, future model development should prioritize truss morphometric features from Groups B and C, individually or in combination. While Group A remains relevant, Group D should be used only as a supplementary predictor rather than a primary one.

Residual Normality Test

A residual distribution histogram is used to assess the normality of errors in the regression model. This graph illustrates the distribution of prediction errors, defined as the difference between actual values and predicted standard lengths of shortfin scad generated by the regression model. The residual histogram for Group A (Figure 2) displays a distribution resembling a bell-shaped curve, indicating that the residuals are approximately normally distributed, with most errors concentrated around zero. This observation aligns with the findings of Lubis et al. (2025), who state that such histogram shapes usually suggest distributed residuals. The distribution reflects that model errors are random and lack systematic patterns, indicating a well-fitted regression model. Although there are a few deviations on the left side, around -15, suggesting the presence of minor outliers, these are not substantial enough to reject the normality assumption (Knief & Forstmeier, 2021). Overall, the linear regression model based on Group A's morphometric truss measurements satisfies residual normality and homoscedasticity assumptions.

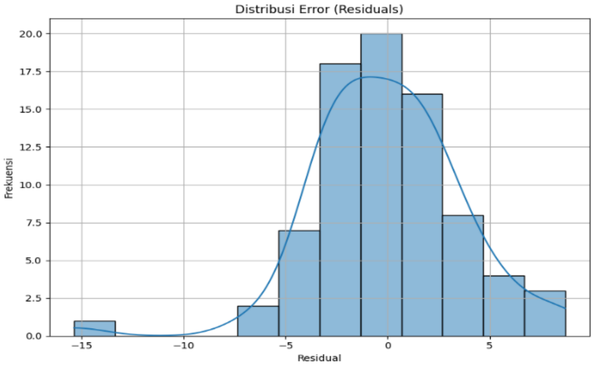

Figure 2. Distribusi Error (Residual) A

The residual histogram for Group B (Figure 3) displays a symmetrical distribution peaking around zero, resembling a normal distribution. Most residuals fall within the range of −2 to +2, indicating that the model predictions are pretty accurate and the errors are randomly distributed. This pattern suggests the absence of systematic bias and that most errors are minor in magnitude. A few extreme values on the right-hand side reflect slightly overestimated predictions, but these deviations are not substantial enough to compromise the overall reliability of the model. In summary, this distribution supports the conclusion that the linear regression model for Group B is stable and exhibits strong predictive performance (Zygmont, 2023).

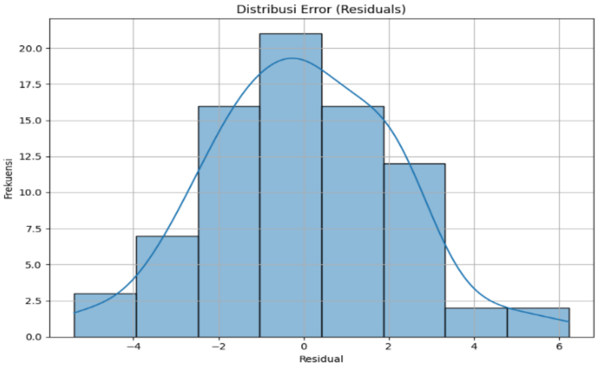

Figure 3. Distribusi Error (Residual) B

The residual histogram for Group C (Figure 4) shows that most prediction errors are concentrated around zero to positive values, with the distribution slightly skewed to the left. This suggests a tendency of the model to underestimate the actual standard length slightly. According to Medeiros et al. (2024), the model could benefit from refinement rather than a sign of failure. The asymmetry may result from morphological variation in the fish that is not fully captured by the model, particularly if non-linear patterns are present. Nevertheless, most residuals remain small and close to zero, indicating that the model is generally accurate (Feng et al., 2020). However, the distribution also signals the need for improvement to achieve more balanced predictions. As Nandy et al. (2020) suggested, adjustments to address suboptimal residual distribution can significantly enhance estimation accuracy.

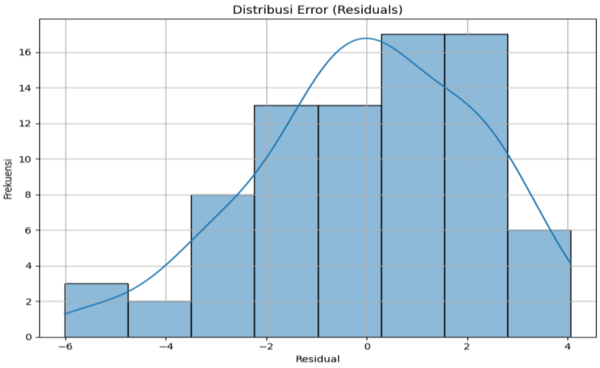

Figure 4. Distribusi Error (Residual) C

The residual histogram for Group D (Figure 5) displays a pattern resembling a normal distribution, with a sharp peak around zero and a relatively symmetrical spread. This indicates that the linear regression model has good predictive performance, with most predictions closely aligned with the actual values. The bell-shaped form also suggests that the errors are random and non-systematic, supporting the assumption of residual normality. Although a few outliers are present on both sides, their number is negligible and does not compromise the model's stability if the deviations are not extreme (Zygmont, 2023).

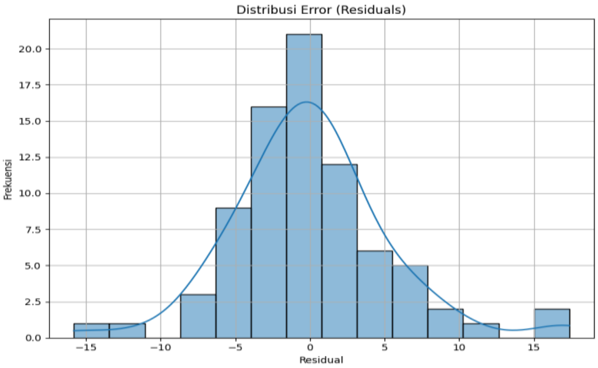

Figure 5. Distribusi Error (Residual) D

This interpretation suggests that the truss morphometric data used likely underwent an effective variable selection process, enabling the predictors to represent variations in the fish's body shape proportionally. This reflects a reasonably strong linear relationship between the predictor variables and standard length within the sampled population. Given its solid statistical performance, near-normal residual distribution, and the fulfillment of most regression assumptions, the linear regression model built on truss morphometric characteristics is considered highly reliable in predicting the shortfin scad's standard length.

CONCLUSION

The linear regression model developed using 24 truss morphometric landmarks to predict the standard length of shortfin scad (*D. macrosoma*) demonstrated that most variables exhibit a strong relationship with standard length, particularly the truss points located on the body (B1, B4, B6, B7, B8) and tail (C1, C3, C4, C5). The coefficient of determination (R^2) ranged from 0.8037 to 0.9342, indicating that the independent variables explain 80–93% of the variance in standard length. Truss point C4 recorded the highest R^2 value of 0.9342, followed by B1 with 0.906, reflecting a very strong correlation. Furthermore, the multiple linear regression model enhanced predictive accuracy, with the highest R^2 values observed in Group B (0.9722) and Group C (0.9717). Evaluation using MAE, MSE, and RMSE confirmed that Groups B and C had the lowest prediction errors, reinforcing the model's high precision. The residual normality test showed that the error distribution closely approximated a normal distribution, indicating that the model meets the assumptions of linear regression. Overall, the model is considered statistically sound and reliable for predicting the standard length of fish, particularly in cases where the body is incomplete.

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