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Modeling the Entire Length of the Humerus from Transverse and Vertical Segment Lengths

Modelado de la Longitud Total del Húmero a Partir de las Longitudes de los Segmentos Transversales y Verticales

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SUMMARY: This study aims to develop predictive models for estimating the humerus total length (HTL) from dry humerus specimens using 19 transverse and vertical segment measurements, thereby contributing to applications in anthropometry, forensic medicine, and clinical practice. A total of 26 dry humeri (11 right, 15 left) of unknown age and sex from the Anatomy Department of Bolu Abant Izzet Baysal University were analyzed. The total humeral length was measured manually while 19 morphometric segments were measured using a digital vernier caliper. Each segment was measured three times and mean values were used for analysis. Normality was assessed via Shapiro-Wilk tests and right-left comparisons were performed using Independent Samples T-Test. Pearson correlation analysis was conducted to identify relationships between segment lengths and HTL. Two predictive models were constructed: multiple linear regression (MLR) with backward variable selection and multivariate adaptive regression splines (MARS). Model performance was assessed via coefficient of determination (R^2) and root mean square error (RMSE). No significant differences were observed between right and left humeri; therefore, analyses were performed collectively. Pearson correlation analysis indicated that 17 out of 19 segment measurements were significantly associated with HTL. The MLR model retained 9 measurements, achieving $R^2 = 0.984$ and RMSE = 2.937. The MARS model included 5 segments with interaction terms, yielding $R^2 = 0.994$ and RMSE = 1.755. The most influential measurements in MARS were ISUBH, DTUH, DTLH, PHTW, and SNUH. Both MLR and MARS models demonstrated high predictive accuracy for HTL, with MARS showing superior performance and efficiency. These models provide reliable tools for estimating humerus length in anthropometric, forensic and clinical contexts. Incorporating additional factors such as age, sex and body height in future studies may further enhance predictive performance.

KEY WORDS: Humerus morphometry; Bone length prediction; Anthropometry; Forensic identification; Clinical anatomy.

INTRODUCTION

Humans exhibit variations in their skeletal systems and in addition, bones themselves demonstrate a wide range of differences. Among these bones the humerus, being the longest bone of the upper limb is of great importance for the anatomical and functional integrity of the skeletal system (Singhal & Rao, 2011). The measurement of long bone lengths is used in anthropology and forensic medicine to estimate an individual's stature. In cases where the pelvis or skull is absent, morphometric analysis of an individual's long bones remains the best method for estimating living stature. Among the long bones of the upper limb, the humerus can be utilized for stature estimation. Therefore, defining humeral length from its segmental measurements is essential (De Mendonça, 2000; Premchand & Manjappa, 2014; Samoon *et al.*, 2019). An individual's stature is of vital importance, particularly in medico-legal contexts. Accordingly, in forensic anthropology projecting a person's height is a valuable step for identification in cases of missing persons (Salles *et al.*, 2009). Furthermore, knowing the humeral length is critical for orthopedic surgeons to make accurate plans for procedures such as fracture repairs, prosthesis placements, and deformity corrections (Greiner *et al.*, 2008). The aim of the present study is to derive a model for determining the humerus total length (HTL) from

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its parts. To improve the success of modeling, unlike similar studies, a total of 19 segment measurements were obtained in both the transverse and vertical planes. Indeed, the ability to estimate HTL from different segments may provide a broader perspective to the sciences of anthropology, forensic medicine and anatomy.

MATERIAL AND METHOD

The study was conducted on a total of 26 dry humeri (11 right and 15 left) belonging to the Department of Anatomy, Faculty of Medicine, Bolu Abant Izzet Baysal University. None of these bones exhibited any degeneration or loss of parts. The age and sex of the specimens were unknown. The total length of each humerus was measured and recorded as the dependent variable. HTL was defined as the distance between the most proximal point of the caput humeri and the most distal point of the trochlea humeri, measured manually using a measuring tape. The independent variables for modeling consisted of a total of 19 different measurements-both transverse and vertical segments-likely to be associated with HTL (Table I, Fig. 1). For each humerus, the lengths of these segments were measured using a precision digital vernier caliper. Each segment was measured three consecutive times by the same researcher and the mean value was calculated and recorded. All measurements were expressed in millimeters (mm). Ethical approval for the present study was obtained from Bolu Abant Izzet Baysal University Non-Interventional Clinical Research Ethics Committee with decision number: 2024/333.

Table I. 19 transverse and vertical segments potentially associated with HTL.

HHW	Humeral Head Width
GTW	Greater Tubercle Width
LTW	Lesser Tubercle Width
ISW	Intertubercular Sulcus Width
GTH	Greater Tubercle Height
LTH	Lesser Tubercle Height
HHVH	Humeral Head Vertical Height
SNLH (B-E)	Surgical Neck Lower Height
SNUH (B-A)	Surgical Neck Upper Height
ISVH	Intertubercular Sulcus Vertical Height
ISUBH (F-A)	Intertubercular Sulcus Upper Border Height
ISLBH (G-E)	Intertubercular Sulcus Lower Border Height
DTUH (H-A)	Deltoid Tuberosity Upper Hight
DTLH (H-E)	Deltoid Tuberosity Lower Hight
EW	Epicondylar Width
CTTW	Capitulum + Trochlea Total Width
RCTW	Radial + Coronoid Fossae Total Width
OFW	Olecranon Fossa Width
PHTW	Posterior Humeral Trochlea Width

Statistical Analysis

Descriptive statistics for the measurements were calculated as mean (M), standard deviation (SD), median, 25th and 75th percentiles (first and third quartiles), frequency (N) and percentage (%). The normality of the numerical variables obtained from the measurements was assessed using the Shapiro-Wilk test, and they were found to follow a normal distribution. Initially, measurements from different bones with both right and left sides were compared using the Independent Samples T-Test. Prior to modeling, the relationship between HTL and segment measurements was preliminarily evaluated using Pearson correlation analysis. Two different models were constructed to predict HTL. The first model was a multiple linear regression (MLR) model with backward variable selection and the second model was a non-parametric Multivariate Adaptive Regression Splines (MARS) model. These two models were compared in terms of complexity, coefficient of determination (R^2) and model error (root mean square error, RMSE). A p-value of <0.05 was considered statistically significant. All analyses were performed using SPSS (ver. 23) and R programme with the «earth» package.

Fig. 1. Transverse and vertical humerus segments used in MLR and MARS models related to HTL.

RESULTS

A total of 26 humeri were examined in this study, including 11 right and 15 left humeri. Descriptive statistics for the measurements obtained from the right and left humeri are presented in Table II. Analysis of Table II revealed no significant differences between the right and left humeri for the measured parameters. Therefore, for the modeling analysis, all 26 dry humeri were included collectively, without distinguishing between right and left sides.

Prior to the modeling analysis, the relationship between the dependent variable, HTL and 19 different segment measurements was evaluated using Pearson correlation analysis and the results are presented in Table III. Examination of Table III indicated that only the LTW and ISW measurements did not show a significant linear relationship with HTL, whereas the remaining 17 measurements were significantly correlated with HTL.

Table II. Descriptive statistics of humerus measurements from the right and left sides.

	RIGHT			LEFT			
	N	**Mean (M)**	**SD**	**N**	**Mean (M)**	**SD**	**p***
HTL (A-E)	11	**309.31**	20.40	15	**319.38**	24.41	0.277
HHW	11	43.62	2.91	15	45.01	2.89	0.240
GTW	11	32.66	4.54	15	33.53	3.21	0.572
LTW	11	16.09	2.26	15	15.21	2.12	0.318
ISW	11	10.04	1.47	15	10.27	1.87	0.731
GTH	11	302.27	18.62	15	313.40	21.08	0.175
LTH	11	298.73	19.45	15	306.02	21.35	0.381
HHVH	11	295.35	20.53	15	302.29	21.12	0.411
SNLH	11	267.06	19.24	15	275.06	20.76	0.327
SNUH	11	41.66	3.82	15	40.02	2.81	0.217
ISVH	11	80.17	7.59	15	86.99	10.21	0.074
ISUBH	11	300.29	21.56	15	308.81	21.34	0.326
ISLBH	11	220.26	19.50	15	223.10	14.24	0.671
DTUH	11	137.31	11.54	15	144.50	16.20	0.222
DTLH	11	171.60	21.34	15	177.38	16.62	0.445
EW	11	58.24	4.97	15	61.30	4.83	0.128
CTTW	11	40.65	2.70	15	41.54	5.41	0.622
RCTW	11	31.71	3.27	15	30.97	3.23	0.573
OFW	11	26.23	2.41	15	26.72	2.05	0.583
PHTW	11	29.09	2.99	15	28.13	2.75	0.403

*: Significance between right and left sides.

Table III. Simple correlations between HTL and 19 different segment measurements.

			p*
HTL (A-E)	**HHW**	0.607	**0.001**
	GTW	0.661	**0.001**
	LTW	-0.003	0.990
	ISW	0.349	0.081
	GTH	0.963	**0.001**
	LTH	0.982	**0.001**
	HHVH	0.950	**0.001**
	SNLH	0.969	**0.001**
	SNUH	0.422	**0.032**
	ISVH	0.727	**0.001**
	ISUBH	0.983	**0.001**
	ISLBH	0.910	**0.001**
	DTUH	0.621	**0.001**
	DTLH	0.758	**0.001**
	EW	0.629	**0.001**
	CTTW	0.753	**0.001**
	RCTW	0.615	**0.001**
	OFW	0.504	**0.009**
	PHTW	0.541	**0.004**

*: Pearson correlation analysis.

Multiple Linear Regression (MLR) Model with Backward Variable Selection

Since 17 of the 19 segment measurements showed significant simple linear correlations with HTL, MLR analysis was initially employed for the modeling process (Fig. 2). Considering the backwardvariable selection method in model construction, the final model results are presented in Table IV. Examination of Table IV shows that, among the 17 segment measurements with significant simple correlations, 9 were retained in the MLR model, while the remaining variables were excluded. The explanatory power of this model, as indicated by the coefficient of determination (R^2), was 98.4 %, and the model's prediction error, based on the root mean square error (RMSE), was calculated as 2.937.

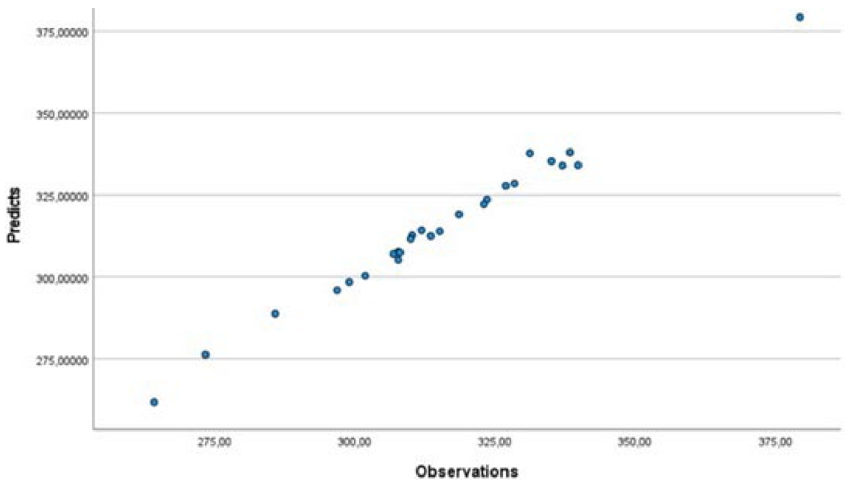

Fig. 2. Agreement between observed and predicted values in the multiple linear regression (MLR) model with backward variable selection.

Table IV. Measurements significantly associated with HTL in the multiple linear regression (MLR) model with backward variable selection.

	Regression	**Standard Error**	**p^{*}**
Constant (C)	-3.189	10.583	0.767
GTW	-0.904	0.338	**0.017**
ISW	1.286	0.412	**0.007**
SNLH	0.527	0.172	**0.007**
SNUH	1.491	0.272	**0.001**
ISVH	0.542	0.149	**0.002**
ISLBH	0.478	0.166	**0.011**
DTUH	0.183	0.055	**0.004**
OFW	-1.002	0.400	**0.023**
PHTW	-1.247	0.308	**0.001**

*: Multiple linear regression (MLR) model with backward variable selection.

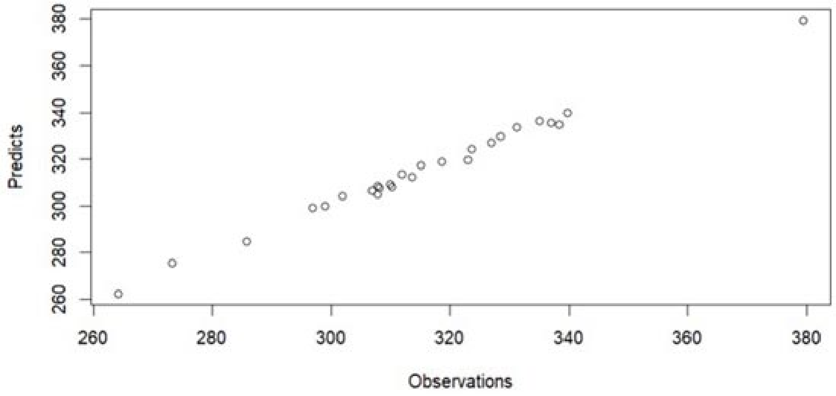

Fig. 3. Agreement between observed and predicted values in the multivariate adaptive regression splines (MARS) model.

Multivariate Adaptive Regression Splines (MARS) Model

To analyze nonlinear relationships and interaction structures, a MARS model was constructed using the same variables, and the results are presented in Table V. The basis functions (BF) listed in Table V represent the terms that were found to be statistically significant in the model. Examination of the model shows that, among the 19 independent variables, 5 (ISUBH, PHTW, SNUH, DTUH, and DTLH) were included, two of which contained interaction terms. These interactions occur when the ISUBH measurement exceeds 304, in combination with the SNUH and PHTW variables, respectively. Table V also indicates that the intercept in the model is 312.0, and when the conditions described in the "Conditions" column are met, the corresponding basis function value in the last column is calculated. The sum of all basis function values provides the predicted value of HTL (Fig. 3).

To illustrate the functioning of the model presented in Table V, the predicted value for the first sample in the dataset is explained in Table VI based on its measurements.

The MARS model demonstrated an explanatory power of 99.4 %, as indicated by the coefficient of determination (R^2). Assessment of the goodness-of-fit criteria showed a model error, measured by the root mean square error (RMSE), of 1.755, and a Consistent Akaike Information Criterion (CAIC) of 49.475. Internal validation was performed using cross-validation, yielding a generalized cross-validation (GCV) value of 20.8. Among the contributing variables, the most influential measurement, according to its importance, was ISUBH, followed sequentially by DTUH, DTLH, PHTW, and SNUH.

Table V. Predicted values for HTL using the multivariate adaptive regression splines (MARS) model.

Final Model: Predicted HTL = Constant Term (C) + BF1+ BF2 + BF3 + BF4 + BF5

Basis Functions (BF)	**Conditions**		+312 (C)
BF1	If "**ISUBH < 304**"	**Predicted HTL=**	-0.664 * (304 -ISUBH)
	Otherwise "**ISUBH > 304**")		+2.960 * (ISUBH -304)
BF2	If "**ISUBH > 304**"		+0.0535 * SNUH * (ISUBH - 304)
	Otherwise		0
BF3	If "**ISUBH > 304**"		- 0.14 * (ISUBH -304) * PHTW
	Otherwise		0
BF4	If "**DTUH > 140**"		+0.478 * (DTUH -140)
	Otherwise		0
BF5	If "**DTLH < 176**"		-0.373 * (176 -DTLH)
	Otherwise		0

Table VI. Prediction of HTL for a single sample using the multivariate adaptive regression splines (MARS) model-.

Independent variables included in the final mars model	**Measurement value of the first humerus in the dataset**	**Model and calculation fort he prediction of HTL**
ISUBH	320.42	**Predicted HTL** = 312 + (2.96 * (320.42-304) + (0.0535 * 42.2 * (320.42-304)) - (0.14* (320.42-304) * 29.34) = **329.6**
PHTW	29.34	
SNUH	42.20	
DTUH	127.37	
DTLH	203.73	

DISCUSSION

In this study, a total of 26 humeri were used, including 11 right and 15 left. For each humerus, HTL and 19 different transverse and vertical segment measurements were obtained. Comparison of measurements from the right and left sides revealed no significant differences, indicating that the right and left humeri possess similar morphological characteristics. Consequently, modeling analyses were conducted collectively using all 26 humeri without distinguishing between sides. This finding is consistent with previous studies by Kastamoni *et al*. (2021), Singhal & Rao (2011), Tetiker *et al*. (2023), and Al *et al*. (2025), which reported that the right and left humeri exhibit similar structural features with no significant differences in measurements. However, studies conducted in India by Prashanth *et al*. (2019), and Samoon *et al*. (2019), identified statistically significant differences between right and left humeri, proposing separate regression equations for each side. Such discrepancies may be attributed to demographic and biological factors, including ethnicity, age group, lifestyle or bone development, vary across study populations.

Correlation analysis between HTL and the 19 segment measurements revealed significant linear relationships for 17 segments. This indicates a strong association between HTL and the morphometric segments of the humerus, suggesting that these segments are robust candidates for predicting HTL. Notably, high correlation coefficients observed between HTL and LTH, GTH, SNLH and ISUBH segments suggest that these regions exert a considerable influence on HTL. Previous studies by Singhal & Rao (2011), Samoon *et al*. (2019), Chandragirish *et al*. (2021), in the Indian population and Mutluay *et al*. (2020), in the Turkish population similarly reported significant correlations between HTL and various humeral segments in their modeling analyses. These findings support the statistical relevance of morphometric relationships among body segments and provide guidance for variable selection in the modeling process.

For HTL modeling, MLR analysis with backward variable selection was initially employed. Out of 17 candidate segments, 9 were retained in the final model. Among these, SNUH emerged as the most significant and positively associated predictor of HTL (b = 1.491), followed by ISW, ISVH, SNLH, ISLBH and DTUH. Premchand & Manjappa (2014) reported similar findings, noting a significant positive correlation between H2 segment length (analogous to SNUH) and HTL. Conversely, negative predictors including PHTW, OFW and GTW were observed, suggesting these segments may act as compensatory factors balancing HTL. The MLR model demonstrated an explanatory power of 98.4 % with a low RMSE of 2.937, indicating highly accurate and reliable predictions of HTL. These results confirm that the selected morphometric segments are valid and significant predictors, making the model suitable for both clinical and anthropometric applications. Similar studies by Singhal & Rao (2011), Esomonu *et al*. (2013), and Premchand & Manjappa (2014) have demonstrated the utility of segment measurements in predicting HTL, reporting strong predictive power with high explanatory capacity and low error.

To account for potential nonlinear relationships among variables, MARS analysis was employed as a second modeling approach. MARS is particularly effective and flexible for capturing nonlinear associations and interactions in multidimensional and complex datasets (Zhang *et al*., 2016). Recent literature by Eskandarinejad *et al*. (2025), highlighted MARS as functioning similarly to a machine learning technique. Analysis of the MARS model indicated that ISUBH was the most influential predictor, followed by DTUH, DTLH, PHTW and SNUH. The model achieved an explanatory power of 99.4 %, approximately 1 % higher than the MLR model, with a lower RMSE of 1.755, indicating superior prediction accuracy. Furthermore, MARS provides a more interpretable model due to its effectiveness over specific variable ranges. The model included five basis functions and five independent variables. A low CAIC value (49.475) indicated a parsimonious model with sufficient fit using fewer parameters, while a GCV of 20.8 demonstrated reliable predictive performance. Overall, the MARS model is both statistically significant and anatomically meaningful, providing a highly reliable tool for predicting HTL in clinical and anthropometric contexts. A comparable modeling strategy was previously applied to the femur in the same population, where both MLR and MARS models were constructed to estimate the entire femoral length from proximal and distal measurements (Sertel Meyvaci et al., 2025). That study reported similarly high explanatory power and confirmed that nonlinear modeling approaches such as MARS may provide improved predictive performance with fewer variables. The consistency between the femoral and humeral modeling outcomes strengthens the reliability of segment-based length estimation in long bones.

CONCLUSION

This study investigated the relationship between HTL and transverse and vertical segment parameters and developed two predictive models using MLR and MARS regression analyses. The findings indicate that both transverse and vertical measurements are strongly associated with HTL and contribute significantly to prediction models. In the MLR model, SNUH, followed by ISW, ISVH, SNLH, ISLBH and DTUH were positive and significant predictors, while PHTW, OFW, and GTW were significant negative predictors. In the MARS model, ISUBH, followed by DTUH, DTLH, PHTW and SNUH, emerged as the most influential segments. Both models exhibited high R^2 and low RMSE values, confirming reliable prediction of HTL. However, MARS demonstrated higher explanatory power and lower error with fewer variables, offering a more practical and efficient approach.

The developed models provide reliable and valid tools for anthropometric, forensic, clinical, and anatomical applications. Their use in cadaver studies, radiological measurements, or bone fragment assessments can improve measurement accuracy and operational efficiency. Future studies incorporating individual factors such as sex, age, and body height may further enhance the predictive power of these models.

Ethical approval

Ethical approval for this study was obtained from the Bolu Abant Izzet University Non-interventional Clinical Research Ethics Committee with decision number 2024/333. The study was conducted in accordance with the principles of the Declaration of Helsinki.

Conflict of interest

There is no conflict of interest among the authors regarding the publication of this manuscript.

Author(s) contribution(s):

SSM:Protocol/project development, planning, organization, design, data collection, manuscript writing/editing; HA: Data interpretation, statistical analysis and manuscript writing/editing; SD:Planning, organization, design, data collection, manuscript writing/editing.

SERTEL MEYVACI, S.; ANKARALI, H. & DEMIROGLU, S. Modelado de la longitud total del húmero a partir de las longitudes de los segmentos transversales y verticales. *Int. J. Morphol., 44(1)*:158-164, 2026.

RESUMEN: Este estudio tuvo como objetivo desarrollar modelos predictivos para estimar la longitud total del húmero (LTH) a partir de especímenes de húmero seco utilizando 19 mediciones de segmentos transversales y verticales, lo que contribuye a aplicaciones en antropometría, medicina forense y práctica clínica. Se analizaron 26 húmeros secos (11 derechos, 15 izquierdos) de edad y sexo desconocidos del Departamento de Anatomía de la Universidad Bolu Abant Izzet Baysal. La longitud humeral total se midió manualmente, mientras que 19 segmentos morfométricos se midieron con un calibrador Vernier digital. Cada segmento se midió tres veces y se utilizaron los valores medios para el análisis. La normalidad se evaluó mediante pruebas de Shapiro-Wilk y se realizaron comparaciones derecha-izquierda utilizando la prueba T de muestras independientes. Se realizó un análisis de correlación de Pearson para identificar relaciones entre las longitudes de los segmentos y la LTH. Se construyeron dos modelos predictivos: regresión lineal múltiple (MLR) con selección de variables hacia atrás y splines de regresión adaptativa multivariante (MARS). El rendimiento del modelo se evaluó mediante el coeficiente de determinación (R^2) y el error cuadrático medio (RMSE). No se observaron diferencias significativas entre los húmeros derecho e izquierdo; por lo tanto, los análisis se realizaron colectivamente. El análisis de correlación de Pearson indicó que 17 de las 19 mediciones de segmentos se asociaron significativamente con la LTH. El modelo MLR retuvo 9 mediciones, logrando $R^2 = 0{,}984$ y RMSE = 2,937. El modelo MARS incluyó 5 segmentos con términos de interacción, lo que produjo $R^2 = 0{,}994$ y RMSE = 1,755. Las mediciones más influyentes en MARS fueron ISUBH, DTUH, DTLH, PHTW y SNUH. Tanto los modelos MLR como MARS demostraron una alta precisión predictiva para la longitud del húmero, con MARS mostrando un rendimiento y una eficiencia superiores. Estos modelos proporcionan herramientas fiables para estimar la longitud del húmero en contextos antropométricos, forenses y clínicos. La incorporación de factores adicionales como la edad, el sexo y la altura en futuros estudios podría mejorar aún más el rendimiento predictivo.

PALABRAS CLAVE: Morfometría del húmero; Predicción de la longitud ósea; Antropometría; Identificación forense; Anatomía clínica.

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