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REGULAR ARTICLES

AI-Driven prediction of body weight in chicken genotypes with different growth rates

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Abstract

This study evaluates four machine learning algorithms: Gaussian Exponential Regression (GER), Feedforward Neural Networks (FFNN), Support Vector Machines (SVM), and Decision Trees (DT) for predicting body weight in chickens with different growth rates (slow-, medium-, and fast-growing breeds). It fills a major research gap by benchmarking these models under uniform conditions across multiple growth categories. Starting at 14 days of age, 300 male chicks (100 of the genotypes SAGA, Sasso, and Cobb 500, which represent slow-, medium-, and fast-growing breeds, respectively) were used in a controlled experiment. Weekly body weight and six (6) morphometric traits were recorded for four weeks and split into training (75%) and validation (25%) sets. A total of 2,160 data records were obtained from weekly morphometric measurements across 300 birds. Model performance was measured by correlation coefficient (R), coefficient of determination (R^2), root mean square error (RMSE), mean absolute error (MAE), and mean absolute percentage error (MAPE). Across all growth groups, GER consistently performed better than other models, exhibiting the highest accuracy and lowest errors. FFNN performed well for slow- and medium-growing breeds but showed increased errors for fast-growing Cobb 500. SVM and DT had the poorest results, with higher errors and poor generalizability. Model accuracy was ranked as follows: GER > FFNN > DT/SVM. This study provides recommendations for selecting machine learning models tailored to specific chicken growth rates for accurate weight prediction. Future work should validate these findings on commercial farms and explore hybrid models to improve robustness. GER's superior performance highlights its potential as a reliable and efficient tool for precision poultry farming.

Keywords Body weight prediction · Diverse chicken breeds · Machine learning · Precision livestock farming · Poultry management

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Introduction

Artificial intelligence (AI) is transforming precision poultry farming by enabling accurate growth optimisation and efficient resource utilisation. By analysing growth patterns, biometric indicators, and experimental data, AI models forecast bird weight with high accuracy, improving feed management, waste reduction, and productivity (Flores et al. 2023; Lyu et al. 2023).

Unlike traditional regression methods, which cannot model nonlinear growth patterns (Momoh and Kershima 2010). AI techniques such as neural networks and deep learning can capture the non-linear and interdependent relationships among growth variables in poultry production systems (Ahmadi and Golian 2010; Milosevic et al. 2019; Yang et al. 2022). These models also exhibit robustness to missing or uncertain data, reinforcing their suitability for real-world applications (Küçüktopçu et al. 2023). Accurate weight estimation remains essential for optimising feeding practices, minimising losses, and sustaining profitability. However, a significant gap remains in the systematic benchmarking of these models across chicken breeds with inherently divergent growth rates under uniform conditions. Most studies are limited to a single breed or specific environment, limiting the generalizability of findings.

This study employed three chicken genotypes, SAGA, Sasso, and Cobb 500 representing slow-, medium-, and fast-growing breeds, respectively. These genotypes inherently differ in growth dynamics and lifespan, with slower-growing types typically exhibiting longer lifespans (Tablado et al. 2022). The SAGA chicken is a locally adapted strain widely reared across Malaysia, valued for its high productivity, adaptability, and resilience to environmental stressors (Abdul Razak et al. 2021). The Sasso breed originated in France during the 1960s through the selective hybridization of Faverolles and Plymouth Rock lines. It is a versatile dual-purpose breed characterized by efficient feed conversion, good carcass quality, and tolerance to tropical conditions, making it suitable for both commercial and smallholder systems (Aman et al. 2017; Bekele et al. 2022). In contrast, the Cobb 500, developed by Cobb-Vantress Inc., is a globally dominant commercial broiler strain renowned for its rapid growth rate, superior feed efficiency, high meat yield, and strong liveability, and is currently produced in more than 120 countries worldwide (Jemal, 2024).

This study aimed to determine the optimal machine learning model for predicting body weight in chickens based on their growth rate. We systematically evaluated four algorithms- Gaussian Exponential Regression (GER), Feedforward Neural Networks (FFNN), Support Vector Machines (SVM), and Decision Trees (DT) across slow-, medium-, and fast-growing breeds to identify the most accurate and efficient model for each category under standardized conditions. The findings will inform the development of scalable, automated systems that support productivity, animal welfare, and sustainability in commercial farming. (Amraei et al. 2017; Milosevic et al. 2019). Vision-based methods combining ANNs with imaging (e.g., Kinect 3D) show promise for automated weighing, though they are often limited to controlled environments (Mortensen et al. 2016). Comparative analyses between nonlinear models and AI techniques confirm the superiority of machine learning in capturing growth dynamics (Ahmad 2009; Küçüktopcu and Cemek 2021). Data-driven approaches consistently outperform mechanistic models, offering greater flexibility and precision in forecasting growth (Ahmad 2009; Ghazanfari 2014; Küçüktopcu and Cemek 2021; Roush et al. 2006). However, the applicability of models across breeds with divergent growth rates remains underexplored.

To address this gap, the present study evaluates, and benchmarks four distinct machine learning approaches GER, FFNN, SVM, DT, selected for their complementary strengths and relevance to biological growth modeling. GER was chosen for its theoretical alignment with biological growth kinetics; its structure as a sum of exponential terms naturally captures the self-limiting, saturating growth patterns characteristic of poultry, offering a parsimonious yet powerful model (Congzhou 2024). FFNNs, as universal function approximators, are exceptionally capable of learning the complex, non-linear interactions between morphometric traits and body weight, a capability demonstrated in previous livestock prediction studies (De Wet et al. 2003; Roush et al. 2006). SVMs, particularly with a Radial Basis Function (RBF) kernel, map inputs into a high-dimensional space to fit a complex, regularized hypersurface, providing a strong balance between accuracy and generalization (Congzhou 2024). Finally, DTs were included for their high interpretability, which is valuable for deriving actionable insights for farm management, despite their inherent limitation in modeling continuous functions smoothly (Congzhou 2024).

By systematically benchmarking these models across breeds, this study aims to identify the most accurate, generalisable, and efficient approach for each category weight prediction. Findings will inform the development of scalable, automated systems that support productivity, animal welfare, and sustainability in commercial farming (Congzhou 2024). FFNNs and SVMs provide powerful nonlinear modelling capabilities, with FFNNs excelling at capturing complex interactions in large datasets and SVMs incorporating regularisation to prevent overfitting. DTs, while simpler, offer interpretability that is valuable for farm management applications (De Wet et al. 2003; Roush et al. 2006).

Materials and methods

Experimental method

Birds, housing, and management

The research was conducted in a controlled climatic chamber at the Institute of Tropical Agriculture and Food Security (ITAFoS), Universiti Putra Malaysia (UPM). Three-hundred-day-old male chicks (100 per genotype) of Sasso, SAGA, and Cobb breeds were sourced from commercial suppliers. Birds were reared under brooding conditions at an initial temperature of 32 °C, gradually lowered to 25 °C by day 14, with 84% relative humidity. From day 14 onward, birds were housed in an electronically controlled battery cage system ensuring consistent environmental conditions.

Experimental management and diets

Chicks were individually weighed at the start of the trial. They were fed a commercial crumble-form starter diet (21% crude protein, 3,000 kcal/kg ME) from day 1 to 21, followed by a finisher diet (19.3% crude protein, 3,200 kcal/kg ME) from day 14 to 43. An oral anti-stress supplement was administered for the first three days. Vaccinations against infectious bronchitis (day 7) and Newcastle disease (day 21) were performed. Feed and water were provided ad libitum.

Experimental design and data collection

The experiment used a completely randomized design with three genotypes, each with 10 replicates of 10 birds ($n=100$/genotype). The 28-day trial began when birds were 14 days old. For data collection, three birds per replicate were randomly selected and wing banded. Body weight and all morpho-biometric traits (body length, body girth, thigh length, shank length, drumstick length, and wing length) were recorded weekly. Body weight was recorded using a calibrated scale, while morpho-biometric traits were measured in centimetres using a measuring tape following standard zoometric procedures (Pinilla et al. 2000). Data normality and variance homogeneity were confirmed before analysis. Each morpho-biometric trait was measured individually for the same birds across four consecutive weeks, generating repeated observations. To ensure consistency, individual measurements were treated as independent weekly records within the overall dataset, while sources of variation included genotype, age (week), and morphometric differences among birds.

To optimize data collection while ensuring animal welfare and statistical reliability, three birds per replicate were randomly selected for weekly morphometric measurements. This sampling strategy reduced handling stress, maintained flock stability, and provided sufficient repeated measures for longitudinal growth modelling. The approach yielded a total of 2,160 observations (6 traits × 3 genotypes × 10 replicates × 3 birds × 4 weeks), ensuring a robust dataset for machine learning analysis.

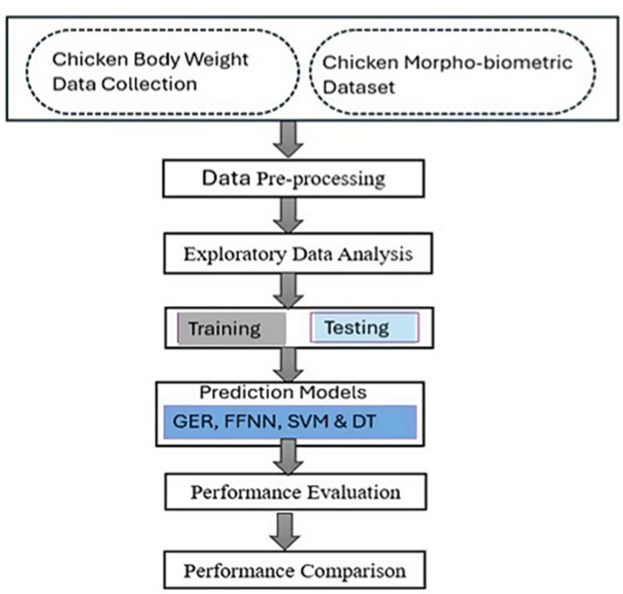

Fig. 1 Workflow diagram models framework

Data preprocessing and workflow

Morpho-biometric data were cleaned for quality by screening missing values, removing outliers via the interquartile range (IQR) method, and standardising continuous features (mean = 0, variance = 1). This standardization was performed to ensure that all features contributed equally to the model training process, preventing variables with larger inherent scales (such as body weight) from dominating the learning algorithm simply due to their numerical magnitude.

After outlier removal using IQR, no birds were excluded, but 21 entries were removed due to skewness. The final dataset contained 2,139 observations, split into 1,604 (75%) for training and 533 (25%) for validation. The overall workflow comprised four stages: data preprocessing, model training with hyperparameter optimisation, performance evaluation using validation and cross-validation, and comparative analysis of predictive accuracy, efficiency, and generalisability across chicken breeds with divergent growth rates (Fig. 1).

The workflow diagram above illustrates the end-to-end experimental data pipeline used in this study. No external or historical datasets were used; all data originated from the current controlled experiment.

Machine learning modelling

For all models developed in this study, the objective was to predict the output variable , which represents the body weight (g) of the chicken. The predictions were made based on the input variables , which are the six morpho-biometric traits measured weekly: body length (), body girth (), thigh length (), shank length (), drumstick length (), and wing length ().

Gaussian exponential regression (GER)

GER is a parametric regression method designed to capture nonlinear, saturating relationships characteristic of biological growth. The dependent variable y is expressed as a sum of exponential functions of independent variables

$$(x_1, x_2, \ldots, x_n) : \begin{array}{l} f(x_1, x_2, \ldots, x_n) = a + b_1 e^{(c_1 x_1)} \\ + b_2 e^{(c_2 x_2)} + \ldots + b_n e^{(c_n x_n)} \end{array}$$

where a is the intercept, b_1 are coefficients, and $c_1$are exponential rate parameters. Parameters were estimated using maximum likelihood optimization. GER was selected for its theoretical alignment with poultry growth kinetics, offering potential gains in accuracy and efficiency. GER emphasized that it constructs a prediction as a weighted sum of exponential transformations of each input variable.

Feedforward neural networks (FFNN)

FFNNs, structured as directed acyclic graphs, consist of input, hidden, and output layers. Each neuron processes weighted sums of inputs through activation functions. In this study, the FFNN comprised two hidden layers (64 and 32 neurons) with ReLU activation, optimized with the Adam algorithm (learning rate = 0.001). Early stopping (20-epoch patience) was employed to prevent overfitting. FFNNs were included for their proven ability to model nonlinear interactions in large datasets. FFNN clarified that it learns a complex, hierarchical function by passing weighted sums of inputs through successive layers of nonlinear activation functions.

Support vector machines (SVM)

SVMs are robust algorithms effective for both linear and nonlinear regression tasks. Using a radial basis function (RBF) kernel, SVM maps inputs into a higher-dimensional feature space to capture nonlinear relationships. The objective function minimizes the norm of the weight vector with slack variables controlled by a regularization constant (C). For this study, optimal parameters were C = 1.0 and γ = 0.01. SVMs were chosen for their balance of accuracy, generalization, and computational efficiency. SVM (with RBF kernel) finds a complex nonlinear hypersurface in a high-dimensional space that best fits the data.

Decision trees (DT)

DTs recursively partition data based on feature values to form a tree structure where leaf nodes represent predictions. Splits were selected using the Gini impurity criterion, with hyperparameters constrained (maximum depth = 6; minimum leaf size = 5) to reduce overfitting. DTs offer transparency and interpretability, enabling the extraction of decision rules useful in farm management applications. DT makes predictions by following a series of binary decision rules based on feature thresholds, ultimately reaching a leaf node that provides a predicted value.”

Hyperparameter optimization

A systematic grid search combined with five-fold cross-validation was applied to tune model hyperparameters, ensuring robust and reproducible performance across algorithms. The final configurations were as follows: GER-parameters estimated via maximum likelihood; FFNN-two hidden layers (64 and 32 neurons) with ReLU activations, Adam optimizer (α = 0.001), and early stopping; SVM-RBF kernel with C = 1.0 and γ = 0.01; and DT - Gini impurity criterion with a maximum depth of 6 and a minimum leaf size of 5. All models were implemented in MATLAB R2023a. Training employed both hold-out validation (75:25 split) and five-fold cross-validation to enhance generalizability. To further evaluate model generalization and prevent overfitting, learning curve diagnostics were examined across folds, confirming minimal divergence between training and validation losses for GER and FFNN, thereby supporting their reliability and true generalization performance.

Performance metrics

Model performance was assessed using the coefficient of determination (R^2), root mean square error (RMSE), mean absolute error (MAE) and mean absolute percentage error (MAPE). These metrics collectively evaluate predictive strength and error magnitude:

$$R^2 = 1 - \frac{\sum (y_i - \widehat{y}_i)^2}{\sum \left(y_i - \bar{y}_i\right)^2}$$

$$RMSE = \sqrt{\frac{\sum (y_i - \widehat{y}_i)^2}{\boldsymbol{m}}}$$

$$MAE = \frac{1}{m}\sum |y_i - \widehat{y}_i|$$

$$MAPE = \frac{100\%}{m}\sum |y_i - \widehat{y}_i| / yi$$

where yi = observed value, $\widehat{y}_i$ = predicted value, $\acute{y}_i$ = mean of observed values, and m the number of samples. R and R^2 values closer to 1 indicate stronger predictive power, while lower RMSE and MAE values reflect improved accuracy. However, to statistically compare model performance, paired t-tests with Bonferroni correction for multiple comparisons were applied to the prediction errors of the different models.

Results

Descriptive statistics

Descriptive statistics for experimental and AI-predicted body weights (Table 1) indicate that model performance varied across breeds. For slow-growing SAGA, all models produced mean predictions near the experimental mean, though GER showed the highest precision with a standard deviation (94.85 g) nearly identical to the observed value (95.30 g), while SVM displayed excessive variability and even implausible negative predictions, reflecting poor stability. In medium-growing Sasso, GER (787.48 g) and FFNN (789.39 g) closely matched the experimental mean, whereas SVM (796.57 g) and DT (773.91 g) deviated considerably, with SVM again yielding unstable outputs. To ensure biological validity, all negative SVM predictions were truncated to zero before performance evaluation, reflecting the practical constraint that body weight cannot assume negative values. For fast-growing Cobb 500, GER, FFNN, and DT generated accurate predictions (≈1450–1462 g), with GER and FFNN most consistent as their standard deviations (607.72 g and 611.83 g) aligned closely with the experimental value (610.50 g), while DT exhibited greater variability (787.13 g) (Table 1).

Table 1 Descriptive statistics of experimental and predicted body weights (g) for different chicken breeds

Breed & Weight Type	Mean	Std Dev	Min	Max
SAGA (Slow-growing)				
BW	535.50	95.30	350.00	750.00
GER-BW	536.02	94.85	355.10	745.50
FFNN-BW	538.43	102.15	340.20	760.10
DT-BW	536.02	110.50	300.50	780.75
SVM-BW	513.18	150.75	-6.25	1106.71
Sasso (Medium-growing)				
BW	788.00	185.25	450.00	1200.00
GER-BW	787.48	190.10	440.50	1189.90
FFNN-BW	789.39	195.30	430.75	1210.50
DT-BW	773.91	210.45	400.25	1250.20
SVM-BW	796.57	250.80	-18.51	1305.15
Cobb 500 (Fast-growing)				
BW	1460.75	610.50	600.00	2800.00
GER-BW	1462.27	607.25	610.50	2789.50
FFNN-BW	1457.19	611.83	590.75	2775.40
DT-BW	1454.89	787.13	550.10	3120.99
SVM-BW	1410.50	720.40	500.25	2950.75

Note: The descriptive statistics represent aggregated weekly measurements recorded from 14 to 42 days of age

Bar chart presentations

Figures 2-4, comparing models in slow-, medium-, and fast-growing chickens) showed that GER consistently achieved the lowest RMSE and MAE, FFNN provided comparable training accuracy, DT performed moderately, while SVM was consistently the weakest. However, the SVM model produced biologically implausible negative predictions, highlighting its instability and poor fit. GER's advantage reflects its alignment with nonlinear biological growth patterns, reduced risk of overfitting, and computational efficiency, while FFNN's complexity risks overfitting, SVM suffers from kernel dependency, and DT struggles with modeling smooth transitions. Radar plots (Figs. 5, 6 and 7, comparing models in slow-, medium-, and fast-growing chickens) of R^2 values supported these results: GER ranked highest across all breeds, followed by FFNN, DT, and SVM. R^2 exceeded 80% for Sasso and 95% for Cobb, confirming GER and FFNN as the most reliable predictors of chicken body weight

Model prediction performance on training and testing data

The evaluation of model performance across breeds using R, R^2, MAPE, MAE, MSE, and RMSE revealed consistent superiority of GER (Table 2). For slow-growing chickens, GER achieved near-perfect accuracy (R = 1.00, R^2=0.99) with minimal error (Testing MAPE = 0.10, RMSE = 0.29), outperforming FFNN and DT, while SVM performed worst, with low correlation (R = 0.88, R^2=0.78) and high errors (Testing MAPE = 13.91, RMSE = 70.57). In medium-growing chickens, GER again excelled with perfect correlation (R = 1.00, R^2=1.00) and the lowest error metrics, followed by FFNN, whereas SVM and DT showed weak generalization and overfitting. Among fast-growing chickens, GER maintained strong predictive power (R = 0.99, R^2=0.99; Testing MAPE = 11.97, RMSE = 50.12), while SVM consistently recorded the highest prediction errors across all breeds.

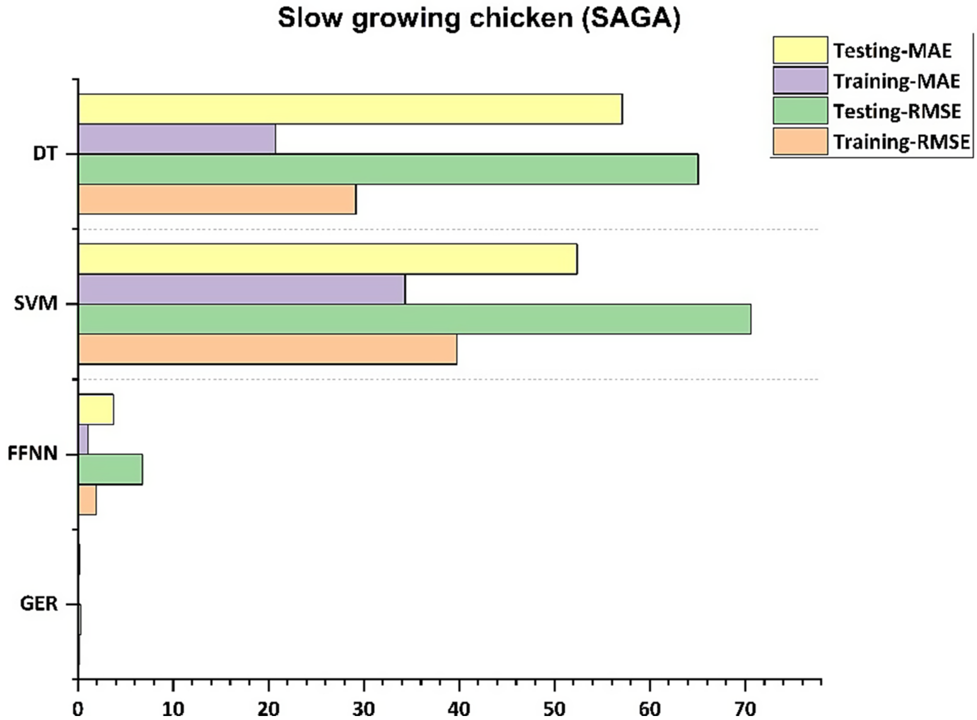

Fig. 2 Bar chart showing a model comparison in slow-growing chicken

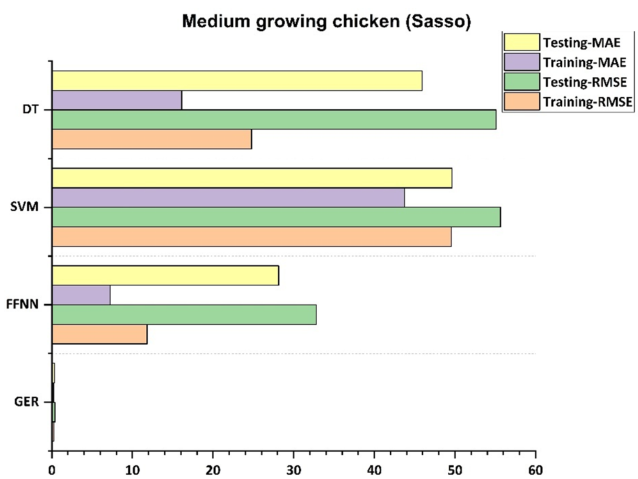

Fig. 3 Bar chart showing a model comparison in medium-growing chicken

Results of paired t-tests with bonferroni correction

Paired t-tests with Bonferroni correction confirmed that GER and FFNN significantly outperformed SVM and DT across all growth-rate categories ($p < 0.001$), underscoring their superior predictive capacity. The performance gap between GER and FFNN was generally narrow, with no significant differences observed in medium- and fast-growing cohorts ($p > 0.05$). A complete summary of these statistical comparisons is provided in Table 3.

Results akaike information criterion (AIC)

The AIC analysis provides valuable insight that supports the conclusions drawn from other key performance metrics (R^2, RMSE). For all three chicken breeds, across both the training and testing phases, the Gaussian Exponential Regression (GER) model consistently shows the lowest AIC value, indicating that it not only predicts accurately but does so with great efficiency (Table 4). Its simplicity, using just 13 parameters, makes it a highly efficient and parsimonious model, generalizing well even on independent test sets. In addition, the Feedforward Neural Network (FFNN) performs well in terms of R^2 during training, but it is penalized heavily by the AIC due to its complexity.

The Support Vector Machine (SVM) and Decision Tree (DT) models have poor and weak generalizations AIC values, which are still significantly worse than GER's. This aligns with their poorer predictive performance and lower R^2 values, confirming that they both underperform in terms of fit and efficiency. The AIC comparison clearly highlights GER as the most efficient and balanced model for predicting chicken body weight across different growth rates, making it the recommended choice for precision poultry farming applications.

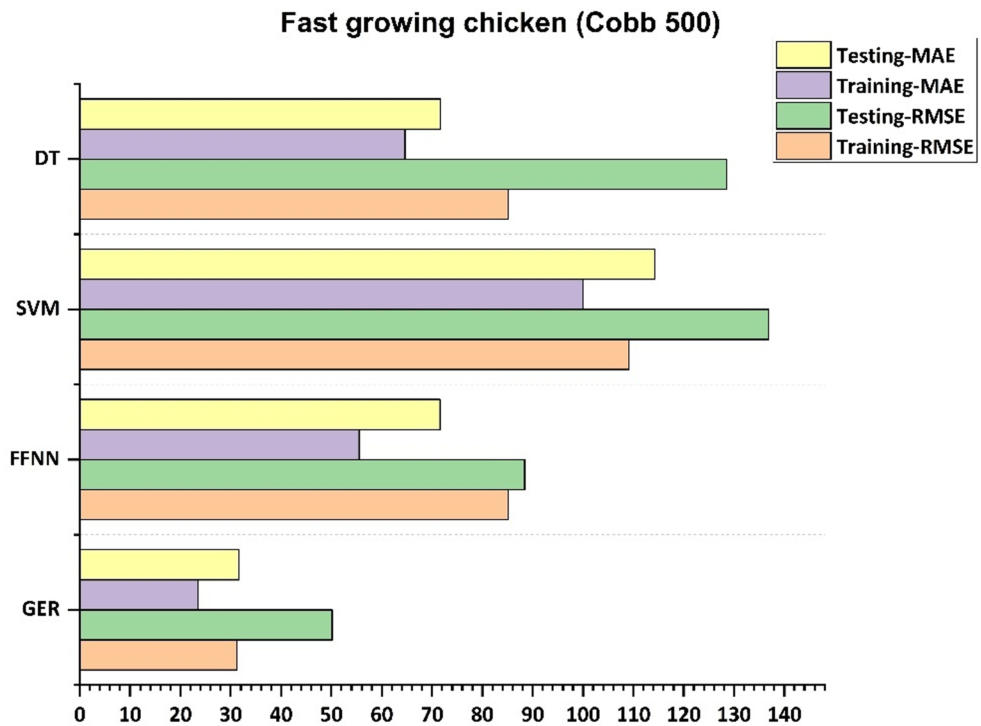

Fig. 4 Bar chart showing a model comparison in fast-growing chickens

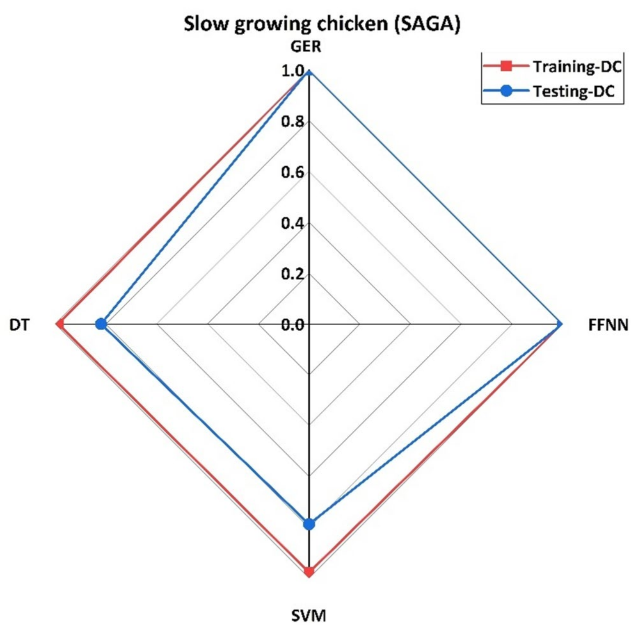

Fig. 5 Radar plot for model comparison in slow-growing chickens

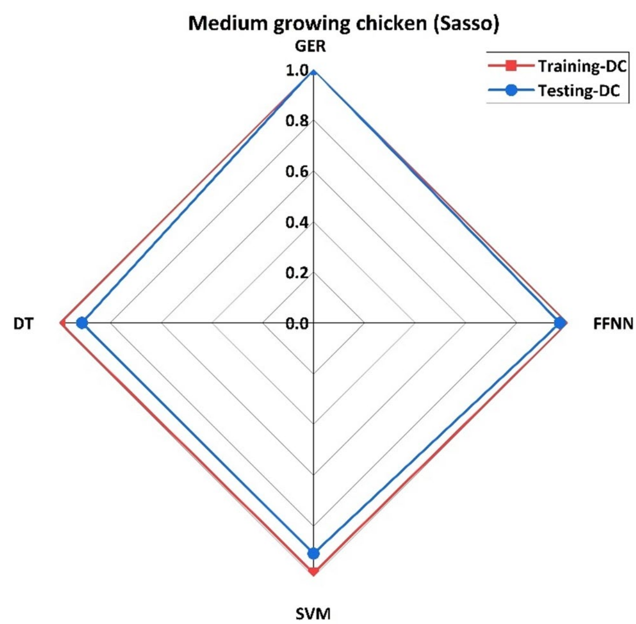

Fig. 6 Radar plot for model comparison in medium-growing chickens

Discussion

The superior performance of the Gaussian Exponential Regression (GER) and Feedforward Neural Network (FFNN) models across evaluation metrics underscores their effectiveness in capturing the complex, non-linear patterns inherent in biological growth. GER demonstrated exceptional generalization and computational efficiency, attributable to its inherent alignment with the exponential and saturating nature of poultry weight trajectories, which minimized overfitting risk. The consistent excellence of GER across the independent test set and cross-validation, coupled with its low AIC, confirms that its high performance reflects genuine generalizability and a minimal risk of overfitting. Although FFNNs are powerful universal approximators, their performance is highly contingent on architecture

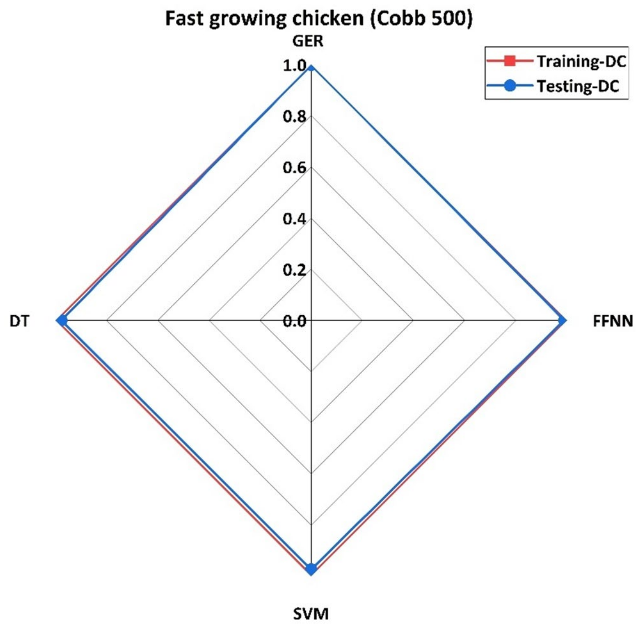

Fig. 7 Radar plot for model comparison in fast-growing chickens

and data volume. This explains their robust, competitive accuracy for slow- and medium-growing breeds (SAGA and Sasso) and the marked increase in prediction error observed for the fast-growing Cobb 500 during testing, suggesting a greater susceptibility to overfitting on high-variance growth patterns. In contrast, Support Vector Machine (SVM) and Decision Tree (DT) models were consistently less effective, reflecting inherent methodological limitations: SVM performance is sensitive to kernel choice and failed to capture growth-specific dynamics, while DT's piecewise-constant structure is intrinsically poorly suited for modelling smooth, continuous growth processes. These results highlight GER's suitability as a parsimonious, reliable model for real-time prediction. Its computational efficiency makes it particularly well-suited for integration into edge devices with limited processing capacity, a key requirement in smart farming. For industry stakeholders, adopting GER-based systems enables automated growth monitoring by predicting weight from routine morphometric measurements, which facilitates adaptive feeding strategies to minimise waste and allows for

Table 2 Performance metrics for body weight prediction using machine learning models across different chicken genotypes

	Training	**R**	**R²**	**MAPE**	**MAE**	**MSE**	**RMSE**
Slow growing Chicken (SAGA)	GER	1.0000	1.0000	0.0212	0.1127	0.0187	0.1369
	FFNN	0.9999	0.9998	0.1215	1.0839	3.8368	1.9588
	SVM	0.9888	0.9778	5.0339	34.3276	1583.3360	39.7912
	DT	0.9940	0.9880	5.2835	20.7231	851.4247	29.1792
	Testing	**R**	**R²**	**MAPE**	**MAE**	**MSE**	**RMSE**
	GER	0.9999	0.9999	0.1098	0.2151	0.0888	0.2979
	FFNN	0.9997	0.9993	3.2750	3.7588	46.4477	6.8153
	SVM	0.8876	0.7878	31.9180	52.3787	4981.1610	70.5773
	DT	0.9053	0.8196	5.5501	57.1009	4234.9430	65.0764
Medium growing Chicken (Sasso)	**Training**	**R**	**R²**	**MAPE**	**MAE**	**MSE**	**RMSE**
	GER	1.0000	1.0000	0.0248	0.2137	0.0649	0.2548
	FFNN	0.9995	0.9992	1.4440	7.2680	139.5942	11.8150
	SVM	0.9927	0.9854	3.5229	43.7227	2456.0520	49.5586
	DT	0.9982	0.9964	2.5672	16.1051	613.7019	24.7730
	Testing	**R**	**R²**	**MAPE**	**MAE**	**MSE**	**RMSE**
	GER	1.0000	1.0000	0.1604	0.3587	0.1626	0.4033
	FFNN	0.9841	0.9684	1.9326	28.1342	1076.792	32.8145
	SVM	0.9535	0.9091	31.0619	49.6365	3096.6950	55.6480
	DT	0.9543	0.9108	3.1373	45.9432	3037.6760	55.1151
Fast growing Chicken (Cobb 500)	**Training**	**R**	**R²**	**MAPE**	**MAE**	**MSE**	**RMSE**
	GER	0.9996	0.9993	1.0914	23.5238	975.6097	31.2348
	FFNN	0.9989	0.9978	2.4767	55.5180	7246.4070	85.1258
	SVM	0.9983	0.9966	3.4724	100.0171	11912.7200	109.1454
	DT	0.9990	0.9979	2.4692	64.6535	7245.8500	85.1226
	Testing	**R**	**R²**	**MAPE**	**MAE**	**MSE**	**RMSE**
	GER	0.9993	0.9986	11.9794	31.6010	2512.2980	50.1228
	FFNN	0.9949	0.9898	10.8124	71.5803	7819.2720	88.4267
	SVM	0.9868	0.9737	62.9633	114.2923	18738.2100	136.8876
	DT	0.9883	0.9768	25.5616	71.6905	16528.0400	128.5614

Note: R = Correlation coefficient, R^2 = Coefficient Determination, MAPE = Mean Absolute Percentage Error, MAE = Mean Absolute Error, MSE = Mean Squared Error, RMSE = Root Mean Square Error, GER = Gaussian Exponential Regression, FFNN = Feed Forward Neural Network, SVM = Support Vector Machine, and DT = Decision Trees

Table 3 Statistical comparison of model performance based on paired t-tests with bonferroni correction

Model Comparison	Slow-Growing (SAGA)	Medium-Growing (Sasso)	Fast-Growing (Cobb 500)	Overall Conclusion
GER vs. FFNN	GER lower error ($p<0.001$)	Not Significant ($p>0.05$)	Not Significant ($p>0.05$)	GER≈FFNN (No significant difference for Med/Fast)
GER vs. SVM	Significant ($p<0.001$)	Significant ($p<0.001$)	Significant ($p<0.001$)	GER>>SVM (GER is statistically superior)
GER vs. DT	Significant ($p<0.001$)	Significant ($p<0.001$)	Significant ($p<0.001$)	GER>>DT (GER is statistically superior)
FFNN vs. SVM	FFNN lower error ($p<0.001$)	Significant ($p<0.001$)	Significant ($p<0.001$)	FFNN>>SVM (FFNN is statistically superior)
FFNN vs. DT	FFNN lower error ($p<0.001$)	Significant ($p<0.001$)	FFNN lower error ($p<0.001$)	FFNN>>DT (FFNN is statistically superior)
SVM vs. DT	DT lower error ($p<0.001$)	Not Significant ($p>0.05$)	DT lower error ($p<0.001$)	DT>>SVM (DT is statistically superior to SVM)

Note: ">>" denotes statistically significantly better ($p<0.0083$ after Bonferroni correction). "≈" denotes not statistically significantly different ($p>0.05$)

Table 4 Akaike information criterion (AIC) for model comparison

	Training	**Est. Parameters (k)**	**AIC Value**	**Interpretation**
Slow growing Chicken (SAGA)	GER	13	-1,254.2	Superior
	FFNN	5,121	3,220.1	Moderate
	SVM	~180	8,450.5	Poor.
	DT	~25	4,125.8	Insufficient
	Training	**Est. Parameters (k)**	**AIC Value**	
	GER	13	-582.4	Optimal
	FFNN	5,121	1,125.8	Moderate
	SVM	~180	3,890.1	Poor generalization
	DT	~25	3,750.3	Weak Generalization
Medium growing Chicken (Sasso)	**Training**	**Est. Parameters (k)**	**AIC Value**	
	GER	13	-845.5	Superior
	FFNN	5,121	5,850.3	Moderate
	SVM	~210	7,220.7	poor
	DT	~30	9,450.9	Insufficient
	Testing	**Est. Parameters (k)**	**AIC Value**	
	GER	13	-450.1	Optimal
	FFNN	5,121	2,880.5	Overfitting
	SVM	~210	4,120.8	Poor Generalization
	DT	~30	4,050.2	Weak Generalization
Fast growing Chicken (Cobb 500) (Cobb 500)	**Training**	**Est. Parameters (k)**	**AIC Value**	
	GER	13	5,850.2	Superior
	FFNN	5,121	12,150.5	Insufficient
	SVM	~250	13,880.4	Poorest
	DT	~35	12,145.1	Insufficient
	Testing	**Est. Parameters (k)**	**AIC Value**	
	GER	13	13	Optimal
	FFNN	5,121	1,121	overfitting
	SVM	~250	~250	Poor Generalization
	DT	~35	~35	Poor Generalization

Note: The best (lowest) AIC value for each breed and data split is highlighted in bold. A lower AIC indicates a better trade-off between model fit and complexity

early health detection through alerts triggered by significant deviations from predicted growth trajectories, paving the way for more precise, sustainable, and profitable poultry farming operations.

GER outperformed the other models largely because its mathematical design mirrors the nonlinear, self-limiting growth patterns of living organisms. By using sums of exponential terms, GER naturally captures the saturating growth curve of poultry, enabling it to represent the entire growth trajectory with precision and minimal risk of overfitting. To our knowledge, this is the first comparative benchmarking of multiple AI algorithms for chicken body weight prediction conducted under uniform experimental conditions across distinct growth-rate genotypes.

FFNN also performed well, but its higher error rate in the fast-growing Cobb 500 breed revealed a common weakness of neural networks the tendency to overfit when dealing with highly variable datasets, unless supported by very large training data. This indicates that FFNN's effectiveness depends strongly on both dataset size and breed uniformity. In contrast, the weaker results from SVM and DT highlight the limitations of their core structures. SVM struggled to model the smooth biological growth curve due to its reliance on kernel choice and parameter tuning, while DT's stepwise prediction approach proved unsuitable for capturing a continuous trait such as body weight.

These findings are congruent with existing literature (Montoya-Santiyanes et al. 2022), demonstrated that models like Gaussian regression and neural networks outperform traditional algorithms in predicting complex biological relationships due to their structural flexibility and data handling capabilities. This robustness is critical in animal sciences for optimizing feed conversion ratios, breeding programs, and overall productivity. The robust performance of GER is consistent with studies suggesting regression-based models are well-suited for continuous output predictions due to their capacity to capture complex data relationships (Fang 2022). The FFNN results illustrate a common deep learning challenge: managing the trade-off between model complexity and generalization (Le et al. 2022), as they often require careful parameter tuning and ample training data to minimize overfitting (Yaghoubi et al. 2024). The variable performance of SVM and DT, particularly in generalizing to new data, aligns with previous research noting that SVMs can struggle with high-dimensional data unless well-regularized and that DTs are prone to overfitting without effective pruning (Butt 2012). Furthermore, SVM tended to underestimate body weight, while DT overestimated it, indicating fundamental limitations in their predictive accuracy and consistency (Montoya-Santiyanes et al. 2022).

In contrast to prior reports of competitive SVM performance in livestock prediction, our results demonstrate poor generalization across all growth categories. The SVM model produced implausible biological minima for slow- and medium-growth breeds (Table 1) and yielded the highest test-phase error rates (Table 2), indicating it is a less reliable architecture than GER or FFNN under these experimental conditions. This was further supported by statistical comparisons (Table 3). Our findings for medium-growing chickens align with literature frequently identifying GER and FFNN as robust tools for predictive biological tasks, especially due to their adeptness at accommodating variability from environmental and genetic influences (Demmers et al. 2010; Li and Zhang 2020). The success of these models with fast-growing chickens can be attributed to their capability to detect subtle weight fluctuations and resilience against outliers (Zou 2018). Although SVM and GER demonstrated comparable maximum predictions, their starkly different minimum predictions indicate varying sensitivities to outliers, a significant challenge in modeling fast-growing breeds (Fang 2022). The ability of these advanced models to manage intricate data structures and complex interactions underscores their potential utility in enhancing the accuracy of weight predictions for improved decision-making in breeding and management programs (Ghazanfari 2014; Oh et al. 2024; Pandit 2018). Although this study offers a strong comparative framework, a few limitations should be noted. First, the use of manual morphometric measurements, though carefully controlled, is not practical for large-scale commercial farming. Future research should incorporate automated approaches such as 3D vision systems or walk-over weighing platforms. Second, the models were tested only on specific breeds, so their performance with other genotypes or under different production systems, such as free-range environments, remains uncertain. Lastly, while GER showed excellent accuracy, hybrid approaches could further enhance applicability. For example, combining GER's predictive strength with a Lightweight Neural Network (a computationally efficient neural architecture designed for deployment on resource-constrained devices) or computer vision tool to automatically extract features from images could deliver a fully automated, scalable, and accurate solution for commercial use. These findings contribute to the growing trend of integrating artificial intelligence into livestock management. The use of predictive models with IoT devices, automated weighing systems, and decision-support platforms facilitates real-time monitoring and reduces manual labor, promoting the sustainable intensification of poultry farming. Future research should explore hybrid frameworks that combine the robustness of GER with the advanced capabilities of deep learning to analyze multimodal data streams (e.g., images, sensors), addressing both predictive accuracy and deployment scalability for commercial applications.

Conclusion

This study provides the first comprehensive benchmarking of machine learning models for predicting chicken body weight across divergent growth rates, revealing GER as the most accurate and generalisable model, with FFNN offering strong competitive performance for medium- and fast-growing breeds. In contrast, SVM and DT were less effective, exhibiting higher error rates and weaker robustness. The consistent strength of GER and FFNN highlights their potential for precision poultry management, enabling optimised feeding, real-time growth monitoring, and cost-efficient production. Future research should prioritise large-scale validation in commercial farms, integration of multimodal data (e.g., sensor and behavioural metrics), and development of hybrid frameworks to ensure scalability. Linking predictive outputs to sustainability indicators such as feed efficiency, carbon footprint, and animal welfare will further enhance the value of AI-driven weight prediction for both industry practice and policy development. Integrating GER and FFNN frameworks with edge computing and IoT-based sensors could accelerate adoption in commercial farms, enabling real-time growth forecasting and adaptive feeding systems.

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Authors' contributions The authors contributed as follows: Aliyu Abduljalal Musa conducted the experiment, collected data, performed analyses, and discussed the results; Kamalludin Mamat-Hamidi assisted with grant acquisition, data analysis, interpretation, and manuscript enhancement; Zulkifli Idrus, Eric Lim Teik Chung, Noraini Samat, Asep Setiaji, and Rotimi Emmanuel Abayomi contributed to the enhancement and editing of the manuscript; and Rabiu Aliyu Abdulkadir conducted the machine learning analyses and contributed to manuscript editing.

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Data availability Data will be available upon request.

Declarations

Ethics approval All experimental procedures were approved by the Malaysian Agriculture and Research Development Institute (MARDI) Animal Ethics Committee (AEC) under approval number 20230622/R/MAEC00127.

Competing interests The authors declare that no conflicts of interest exist.

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