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Research article

Study on pig feed conversion ratio prediction based on machine learning

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Abstract: ***Objective:*** This paper explores the feasibility of using partial data to assess the pig feed conversion ratio (FCR) and identify the optimal method to predict the overall pig FCR throughout the entire growth period. ***Methods:*** Growth performance data, feed intake data, and the pedigree information of a total of 1084 pigs from 2021 to 2022 were used for the study. Four different machine learning methods (Random Forests (RF), Extreme Gradient Boost (XGBoost), Support Vector Regression (SVR), and linear regression (LR)) were compared with the baseline method that simply utilized the known portion of FCR as a proxy for the target prediction. The analysis utilized single-week data as well as different ranges of early-stage and late-stage growth period data. The Pearson correlation coefficient between the overall pig FCR estimated breeding values (EBVs) and the predicted EBVs was used as an indicator to evaluate the prediction accuracy under different scenarios. ***Results:*** The correlation between the FCR of each week and the entire duration FCR was weak, and the entire duration FCR may be affected by a combination of factors rather than just a single week. When using data from a single week to predict the entire duration FCR, RF showed the most stability and accuracy of all models. When using data from the first and second halves to predict the FCR over different time horizons, the predictive performance of all models declined as the prediction span increased. Among them, RF and SVR had better prediction performances across the time windows. Notably, when using the latter half of the data for prediction, the LR model had the best prediction performance. ***Conclusion:*** For the mid-term measurements, when only accuracy is considered, using the latter half of the data is recommended due to its higher representativeness. When the available data cover less than half of the growth period, RF performs better for the prediction, regardless of whether early or late data are used. In contrast, when the measurement data extend beyond the halfway point, a linear model is preferable to predict the overall FCR, as it better captures the representativeness of incomplete FCR data for the overall assessment.

Keywords: feed conversion ratio; genetic evaluation; machine learning; random forest; support vector regression

1. Introduction

Feed efficiency is a critical economic trait in swine production, thereby directly influencing production costs and profitability [1]. Traditional methods for evaluating feed efficiency rely on full-duration trials, which measure the feed intake and body weight gain throughout the entire growth cycle. However, this approach is time-consuming, costly, and imposes significant operational burdens on farms. To reduce measurement expenses, the industry has increasingly explored partial-duration trials, where feed efficiency is estimated based on data from specific growth phases. Nevertheless, the accuracy of such partial trials heavily depends on the selected measurement periods, and there remains a lack of systematic research to determine the optimal intervals, thus casting doubt on their reliability in practical applications.

In recent years, machine learning (ML) has gained prominence in agricultural research due to its robust capabilities in data modeling and predictive analytics [2–4]. By uncovering hidden patterns in historical datasets, ML models can establish correlations between feed efficiency across different growth stages, thus providing a data-driven approach to optimizing partial-duration measurement strategies. However, existing ML applications in swine feed efficiency prediction have primarily focused on full-duration data analyses [3,5], thus leaving a significant gap in research on model development and validation for partial-duration trials.

This study aims to leverage ML techniques to systematically assess the predictive accuracy of various partial-duration feed efficiency measurement schemes and identify the optimal time intervals for data collection. By comparing the performance of models trained on different growth phases and incorporating interpretability analyses, we seek to evaluate the feasibility of replacing full-duration trials with partial-duration alternatives. The findings will provide empirical support to optimize feed efficiency assessment protocols, thus facilitating precision livestock farming and cost-effective swine production.

2. Materials and methods

2.1. Data

2.1.1. FIRE raw record data

The dataset of this study originated from a large-scale breeding pig farm in China, and included growth performance measurements, feed intake data, and the pedigree information of a total of 1084 pigs during the period from 2021 to 2022. Considering the characteristics of data distribution (Figure 1) and statistical validity, and based on the principle of covering the longest possible time span and minimizing the loss of data, we finally determined the entire study period to be the 16th to the 24th week after the pigs were born. Pigs were in the late finishing period and exhibited rapid growth.

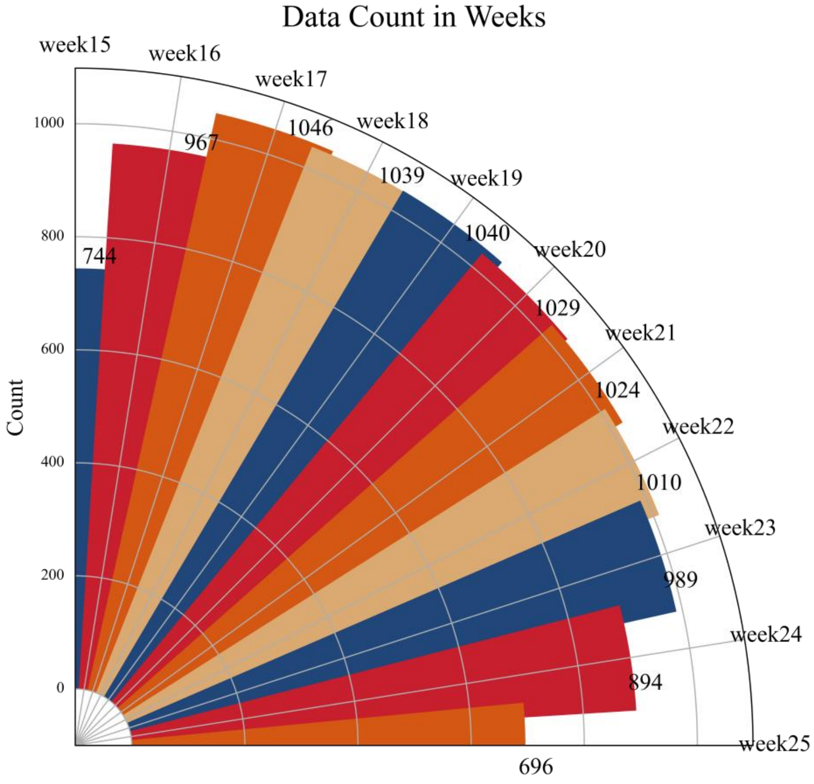


Figure 1. Data distribution.

Phenotypic data on pig feed intake were obtained by means of the Osborne Feeding Station Measurement System. The measuring equipment is set up in group houses with a capacity of 12 to 15 breeding pigs per pen.

The measurement process is as follows. Before the start of the measurement, the breeding facility accurately measures the weight of each pig. During the measurement phase, the pigs were provided ad libitum access to the formulated diet under automated feeding systems, and the feed intake levels were not individually restricted, but instead followed the nutritional requirement guidelines. It is important to note that when each pig entered the measuring equipment to feed, the measuring equipment was able to record the amount of food taken, the weight, and the time taken to feed by recognizing the ear tags of each pig. At the end of the measurement, the weight of the pig is measured again to ensure the accuracy and adequacy of the data. The pig performance measurement system provides an effective tool that allows us to dynamically track the feeding behavior of the pigs, and while obtaining more accurate behavioral data, it also lays the foundation for further ML model building and predictive analyses.

2.1.2. Processing of weight anomaly data records

We developed a linear model of time versus weight using additional initial and ending weights recorded on the farm:

$$W_t = a + bt,$$

where W_t is the weight of the pig at the time of t, and a and b are the fitted parameters. This is done by calculating the residuals between the actual body weight recorded for each observation and the predicted body weight from this linear model. This method allows us to accurately detect any possible outliers or errors in the data. To ensure the accuracy of the data, the study deleted that portion of the data where the residuals were more than 3 standard deviations. Finally, these deleted weight data were populated by a moving average method (specifically, the average of 2 data before and after) to better smooth the data and retain the original trend information with reduced error.

2.1.3. Data processing of feeding anomaly records

The feeding data screening method used in the study was based on the screening criteria used to identify errors in electronic pig feeding trough data proposed by Casey and Dekkers [6] in their study (Table 1). The quality control process consisted of the following:

1) Defining feeding errors and counting the number of occurrences of each type of error;
2) Correcting for error-free feed intake per pig per day by fitting a linear mixed model with the number of errors, average daily gain, and body weight as covariates;
3) Calculating the number of errors per pig per day;
4) Calibrating the number of errors per pig per day; and
5) Calibrating the feed intake per day.

2.2. Research methodology

In order to comprehensively evaluate the predictive capability of different data segments for the entire growth period feed conversion ratio (FCR), this study designed prediction experiments for the following scenarios (Figure 2):

1) Use single-week data to predict the overall pig FCR: Explore the predictive effectiveness of single-week FCR measurements on the overall FCR.
2) Use mid-term data to predict FCR over different time ranges: Investigate the effect of extending the prediction range on FCR prediction accuracy.
3) Use partial growth period data to predict the overall FCR: Examine the impact of using reduced measurement periods on the prediction of the overall FCR.

Table 1. Screening criteria for feeding record data.

Error type	Related Variables	Record type	Screening Criteria
Low feed intake (FIV-lo)	Feed intake per visit (FIV)	All visits	FIV < -20 g
High feed intake (FIV-hi)		All visits	FIV > 2,000 g
Zero feed intake (FIV-0)		Visits with occupation time = 0 s	Abs (FIV) > 20 g
Low dwell time (OTV-lo)	Occupation time per visit (OTV)	All visits	OTV < 0 s
High dwell time (OTV-hi)		All visits	OTV > 3,600 s
High eating rate1 (FRV-hi-FIV-lo)	Feeding rate per visit (FRV)	Visits with 0 < FIV < 50 g	FRV > 500 g/min
High eating rate2 (FRV-hi-strict)		Visits with FIV >= 50 g and preceded or followed by a visit with FIV < -20 g	FRV > 110 g/min
High eating rate3 (FRV-hi)		Visits with FIV >= 50 g and not preceded or followed by a visit with FIV < -20 g	FRV > 170 g/min
Zero eating rate (FRV-0)		Visits with FRV = 0 g/min	OTV > 500 s
Low feeding rate (FRV-lo)		Visits with FRV /= 0 g/min	Abs (FRV) <= 2 g/min
Low forward weight difference (LWD-lo)	Leading weight difference (LWD)	All except last visit on feeder in test period	LWD < -20 g
High forward weight difference (LWD-hi)		All except last visit on feeder in test period	LWD > 1,800 g
Low backward weight difference (FWD-lo)	Following weight difference (FWD)	All except first visit on feeder in test period	FWD < -20 g
High backward weight difference (FWD-hi)		All except first visit on feeder in test period	FWD > 1,800 g
Low forward time difference (LTD-lo)	Leading time difference (LTD)	All except last visit on feeder in test period	LTD < 0 s
Low backward time difference (FTD-lo)	Following time difference (FTD)	All except first visit on feeder in test period	FTD < 0 s

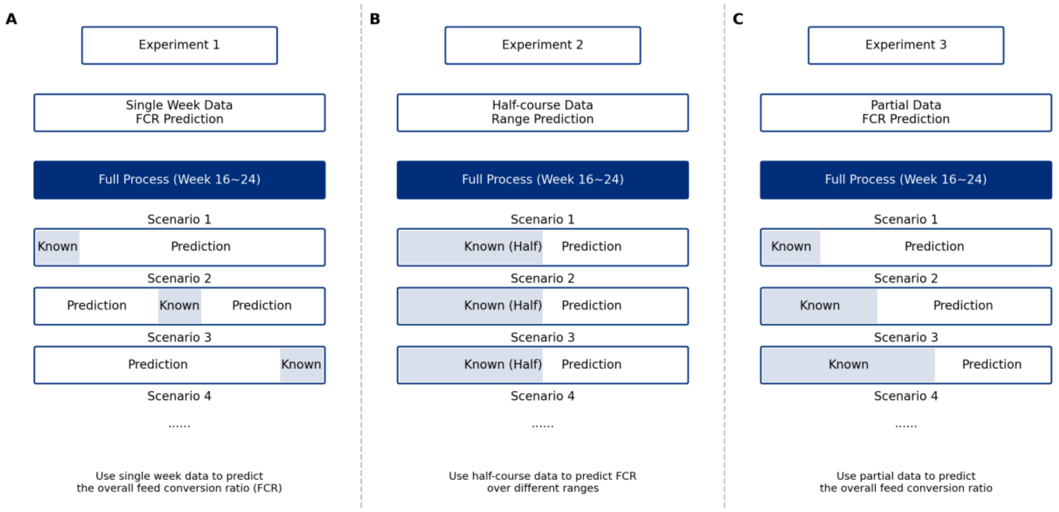


Figure 2. Flowchart of predicting overall pig feed convention ratio using weekly data.

2.3. *Predictive modeling*

We focused on evaluating commonly used and easily interpretable models in agricultural contexts. Therefore, the models used in this study included the following:

- Extreme Gradient Boosting (XGBoost);
- Random Forest (RF);
- Linear Regression (LR);
- Support Vector Regression (SVR); and
- Uncorrected mid-term data baseline (Standard) for comparison.

2.3.1. RF

RF is a powerful ML algorithm for classification and regression tasks. Specifically, for the regression task, it is called the RF Regressor (RFR). This method produces a final prediction by applying the average of the predictions from multiple Decision Trees.

The specific process of using the RF algorithm for predicting the whole hog FCR is as follows:

1) **Data splitting**: Divide the dataset into training set and test set. In this experiment, we uniformly use the five-fold cross-validation method to divide the training set and the test set. To prevent data leakage and to ensure unbiased performance estimation, five-fold cross-validation was performed at the individual animal level. The same validation strategy was applied to all other methods.
2) **RF model training**: Use the training set data to construct an RF model, which consists of multiple decision trees. Each decision tree is constructed based on a randomly selected subset of features and randomly selected training samples. The core steps of an RF regression include:

   a. Bootstrapping: For each tree in the training set, we randomly draw N samples from the training set; however, each time the samples are drawn, they are put back into the training set, which means that some samples may be repeatedly drawn, while other samples may not.
   b. Random subset feature selection: When constructing any node of the decision tree, the RF algorithm randomly selects a subset of features from the entire set of features and finds the optimal split point solely based on that subset.
   c. Train multiple decision trees: Use the set of samples obtained from the self-sampling and the corresponding random subset of features to train multiple decision trees.
   d. Make predictions: For each test sample, the predictions are separately made by each decision tree; then, the predictions of all the trees are averaged to get the final prediction.

3) **Model tuning**: Optimize the performance of RF models by adjusting the model's parameters such as the number of trees, maximum depth, splitting criterion, etc. Model validation and comparison are performed using methods such as cross-validation.
4) **Prediction and evaluation**: Predictions are made on the trained RF model using the test set data and the predictions are compared with the true values.

2.3.2. XGBoost

XGBoost is an optimized gradient boosting ML algorithm known for its high performance, flexibility, and speed. It obtains accurate models by means of gradient boosting and can be used to solve classification and regression problems. XGBoost can find the optimal splitting node by the greedy algorithm and complete model training faster on large datasets by parallel processing.

The use of the XGBoost algorithm to predict the whole hog FCR can be specifically categorized into the following process:

1) **Data splitting**: Divide the dataset into the training set and the test set. In this experiment, we uniformly use the five-fold cross-validation method for splitting.
2) **XGBoost model training**: The training set data is used to construct the XGBoost model. XGBoost uses a gradient boosting algorithm to improve the performance of the model by iteratively adding tree models. Training for XGBoost consists of the following steps:
   a. Initialization: Initially, all sample points will have the same weights, and it is straightforward to use this weight to predict the outcome.
   b. Creating the first model: A decision tree model is constructed, and this model is used to make predictions on the training set.
   c. Calculating the error: The difference between the model's prediction and the true value is computed (the residuals or the gradient).
   d. Creating new model: Builds a new model on top of the error in an attempt to correct the prediction error from the first step.

   e. Update weights: Updates the weights of the samples using the model that has already been learned.
   f. Repeat steps b-e: Performs them recursively until a specific stopping rule is met (e.g., the number of models reaches a specific number or the addition of a new model doesn't significantly improve the performance).
   g. Combine all the models: Combines all the models together that predict unknown data through a voting mechanism or through averaging.

3) **Model tuning**: Optimize the performance of the XGBoost model by adjusting the model parameters, such as the learning rate, the number of trees, the maximum depth, and the regularization parameter. Model validation and comparison can be performed using methods such as cross-validation.
4) **Prediction and evaluation**: The trained XGBoost model is predicted using the test set data, and the prediction results are compared with the true values to determine the predictive accuracy of the model.

2.3.3. LR

The process of using LR to predict the entire duration FCR is as follows:

1) **Data splitting**: Divide the dataset into the training set and the test set. In this experiment, we uniformly use the five-fold cross-validation method for splitting.
2) **Feature normalization**: Normalization of selected features to eliminate differences in magnitude between different features.
3) **LR model training**: A LR model is constructed using data from the training set. A LR model assumes a linear relationship between the features and the target variable and predicts the target variable by fitting a linear equation. Then, the coefficients of the model are estimated by minimizing the difference between the target variable and the model's predicted values. We use the commonly used Ordinary Least Squares (OLS) method to solve for the optimal model coefficients. OLS fits a linear equation by minimizing the sum of squares of the residuals to obtain the optimal coefficient estimates.
4) **Model evaluation**: The trained LR model was predicted using the test set data, and the predictions were compared with the true values. The Pearson correlation coefficient is used as a performance metric to evaluate the model to determine the predictive accuracy of the model.

2.3.4. SVR

SVR is an extension of Support Vector Machines (SVMs) and has a wide range of applications for solving regression problems. The main idea is to specify a range of ε (epsilon) such that errors within this range are accepted and only errors outside this range are penalized. Thus, SVR is naturally robust to noise.

The process of using SVR to predict the entire duration FCR is as follows:

1) **Data splitting**: Divide the dataset into the training set and the test set. In this experiment, we uniformly use the five-fold cross-validation method for splitting.
2) **Feature normalization**: Normalization of selected features to eliminate differences in magnitude between different features.
3) **Model training**: First, define a linear model:

$$f(x) = w^T x + b$$

where w and b denote the parameters of the model, and a dot product in the latitude with the input vector x forms the regression model. LR squares the prediction error for each sample. On the other hand, SVR uses a loss function called "ε-intensive", or ε-insensitive loss function, which is concerned with the choice of ε. If the prediction error is within ε, then the prediction is considered correct, and the error is 0. If the prediction error exceeds ε, then the error is the difference between the actual value and the predicted value, minus ε. The optimization objective uses a mean square error loss, which squares the prediction error for each sample. The optimization objective is to minimize the prediction error of the model, and at the same time, to make the model as simple as possible to prevent overfitting. Thus, the optimization objective is as follows:

$$\min \frac{1}{2} | |w| |^2 + C \sum_{i=1}^{n} \xi_i$$

where ξ_i represents the prediction error, and C is a parameter used to control the balance between model complexity and error.

4) **Model evaluation**: The trained LR model was predicted using the test set data and the predictions were compared with the true values. The Pearson correlation coefficient is used as a performance metric to evaluate the model to determine the predictive accuracy of the model.

2.3.5. Hyperparameter Optimization

In this study, we adopt a cross-validation scheme for data partitioning, specifically, the original training data is partitioned into a training set and a test set. During the Optuna hyperparameter optimization process, we further extract 15% of the data from the training set as the validation set. This careful segmentation allows us to accurately evaluate the model's performance during the subsequent hyperparameter optimization process, thus ensuring that our resulting model has a high generalization ability.

We configure the search space for each model accordingly. The main hyperparameters that determine RF optimization (Table 2) in this study include the number of estimators, the maximum depth of each decision tree, and the minimum number of samples required at each node (min samples split). These parameters are given explicit ranges of values in the predefined search space: number estimators from 100 to 500, max depth from 10 to 50, and min samples split from 2 to 10, thus guaranteeing a finite and precise optimization operation.

In the optimization function, we specify the respective hyperparameters for the various models (Table 2–4) and train the models using the training set delineated above. The accuracy of the models on the subsequent validation set is explicitly used as an evaluation criterion for this step.

After a fixed number of evaluations are performed, the optimization process is completed and the optimal hyperparameter combination is obtained. Then, based on the determined optimal hyperparameter configurations, the previous model is retrained and rigorously validated on a set of independent tests set aside to comprehensively evaluate the expressiveness and generalization performance of the optimized model when dealing with unknown data. The results of this session relate to the generalizability and validity of the model in practical applications.

Table 2. Random Forest Hyperparameter Search Space.

Hyperparameter	Search Space
Number of estimators	10 ~ 150
Max depth	1 ~ 20
Min samples split	2 ~ 10

Table 3. Extreme Gradient Boosting Hyperparameter Search Space.

Hyperparameter	Search Space
Number of estimators	10 ~ 150
Max depth	1 ~ 25
Gamma	0 ~ 1
Min child weight	1 ~ 10
Subsample	0.5 ~ 1
Regularization factor alpha (Reg alpha)	0, 0.01 ~ 0.1, 1
Regularization factor λ (Reg lambda)	0, 0.1, 0.5, 1
Learning rate	0.01 ~ 0.1

Table 4. Support Vector Machine Hyperparameter Search Space.

Hyperparameter	Search Space
Kernel	Linear, poly, rbf
C	1 ~ 15
Degree	1 ~ 5
Gamma	Scale, Auto

2.4. Assessment of the effectiveness of model predictions

In order to compare the prediction effects between different models, the dataset is divided into a reference cluster and a validation cluster in this study. Using cross-validation, the data are randomly divided into reference cluster individuals as well as validation cluster individuals. We use two metrics, accuracy and stability, to measure the prediction effectiveness of different models. Prediction accuracy is the correlation between the actual entire duration FCR estimated breeding values (EBVs) of individuals in the validation cluster and the FCR predicted by the different models, and prediction stability is the standard deviation of prediction accuracy.

The benchmark for the predicted effect is the Pearson correlation coefficient between the breeding value directly calculated using the FCR measured at the half duration point and the true entire duration FCR. By comparing the predicted effects of the various models with the benchmark effect, the actual effect of using the halfway data for the entire duration prediction is derived.

EBVs in the experiments were calculated using the animal model BLUP with the following formula:

$$y_{ijk} = \mu + b_i + s_j + a_k + e_{ijk},$$

where y_{ijk} is the FCR at individual k, batch i, and station of measurement j, b_i is the incoming batch i, s_j is the fixed effect at station of measurement j, and a_k is the additive genetic effect at individual k.

All animal model calculations in the paper were performed using the DMUAI module of the DMU software.

3. Results

3.1. *Correlation of FCR between weeks*

To characterize the relationship between the FCR at each week and its effect on the full FCR, this study examined phenotypic breeding value correlations between the FCR of pigs at each week from weeks 16 to 24 and with the full FCR.

3.1.1. Phenotypic correlations

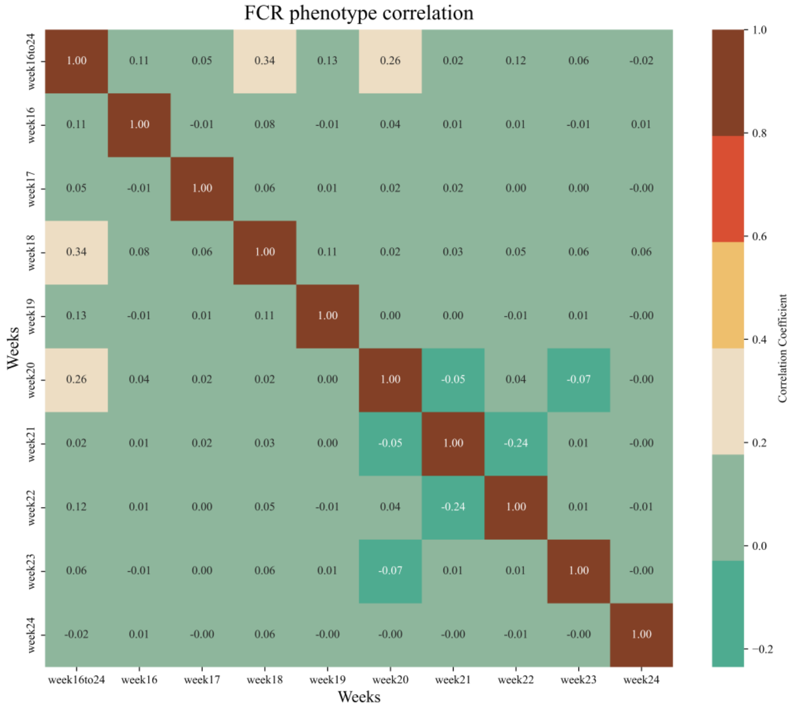
This study examined the phenotypic correlation coefficients of the weekly FCR in pigs from weeks 16 to 24 (Figure 3). The values of the correlation coefficients ranged from -1 to 1, with values close to 1 indicating a strong positive correlation, close to -1 indicating a strong negative correlation, and close to 0 indicating no or only a very weak correlation. As can be seen from the results, the correlation coefficients between most of the weekly periods were low, basically below 0.1. The FCR at weeks 18 and 20 exhibited moderate positive correlations (0.34 and 0.26, respectively) with the full-range FCR, suggesting that these weeks' FCR data may play a relatively important role in predicting the overall FCR performance. Among the weekly FCR values, we observed no significant positive or negative correlations, with all correlation coefficients being slightly above or below zero.

3.1.2. Breeding value correlations

This study examined breeding value correlation coefficients for the FCR of pigs between weeks 16 and 24 on a weekly basis (Figure 4). The values of the correlation coefficients ranged from -1 to 1, with values close to 1 indicating a strong positive correlation, close to -1 indicating a strong negative correlation, and close to 0 indicating no or only a very weak correlation.

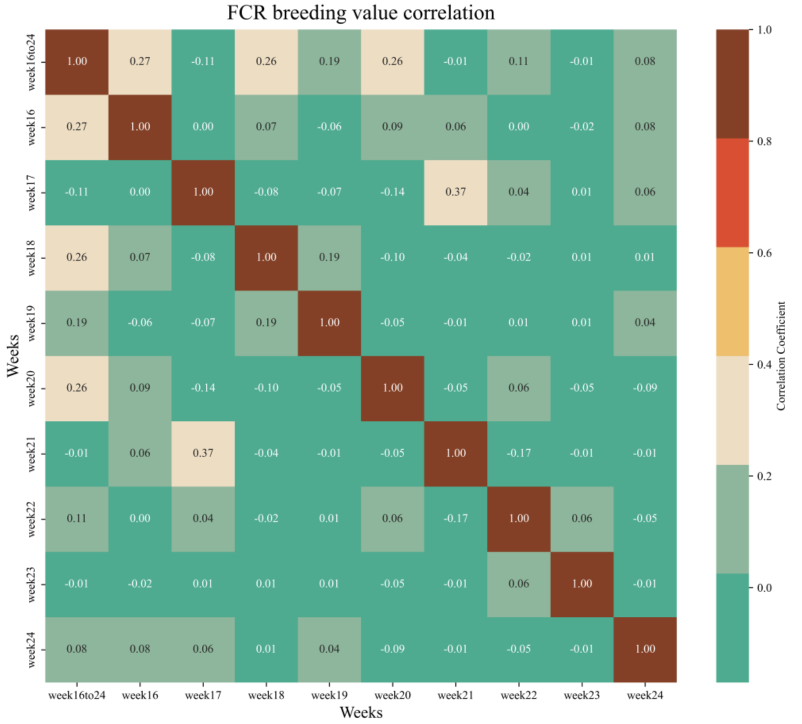
The highest correlation (0.27) between the weekly FCR and the full-range FCR (weeks 16–24) occurred at week 16, thus indicating a modest positive relationship. However, this relatively weak correlation suggests that the full-range FCR EBVs cannot be reliably predicted using the week 16 FCR alone.

Moderate positive correlations were also observed at weeks 18 and 20 (0.26), thus implying their potential influence on the full-range FCR, though the effects remain limited. Notably, weeks 17 and 21 exhibited a stronger positive correlation (0.37), possibly due to shared influencing factors. In contrast, weeks 21 and 22 showed a weak negative correlation (-0.17), thus suggesting that an increase in the FCR during one week might correspond to a decrease in the other.



	week16to24	week16	week17	week18	week19	week20	week21	week22	week23	week24
week16to24	1.00	0.11	0.05	0.34	0.13	0.26	0.02	0.12	0.06	-0.02
week16	0.11	1.00	-0.01	0.08	-0.01	0.04	0.01	0.01	-0.01	0.01
week17	0.05	-0.01	1.00	0.06	0.01	0.02	0.02	0.00	0.00	-0.00
week18	0.34	0.08	0.06	1.00	0.11	0.02	0.03	0.05	0.06	0.06
week19	0.13	-0.01	0.01	0.11	1.00	0.00	0.00	-0.01	0.01	-0.00
week20	0.26	0.04	0.02	0.02	0.00	1.00	-0.05	0.04	-0.07	-0.00
week21	0.02	0.01	0.02	0.03	0.00	-0.05	1.00	-0.24	0.01	-0.00
week22	0.12	0.01	0.00	0.05	-0.01	0.04	-0.24	1.00	0.01	-0.01
week23	0.06	-0.01	0.00	0.06	0.01	-0.07	0.01	0.01	1.00	-0.00
week24	-0.02	0.01	-0.00	0.06	-0.00	-0.00	-0.00	-0.01	-0.00	1.00

Figure 3. Correlation matrix between weekly feed conversion ratio.



	week16to24	week16	week17	week18	week19	week20	week21	week22	week23	week24
week16to24	1.00	0.27	-0.11	0.26	0.19	0.26	-0.01	0.11	-0.01	0.08
week16	0.27	1.00	0.00	0.07	-0.06	0.09	0.06	0.00	-0.02	0.08
week17	-0.11	0.00	1.00	-0.08	-0.07	-0.14	0.37	0.04	0.01	0.06
week18	0.26	0.07	-0.08	1.00	0.19	-0.10	-0.04	-0.02	0.01	0.01
week19	0.19	-0.06	-0.07	0.19	1.00	-0.05	-0.01	0.01	0.01	0.04
week20	0.26	0.09	-0.14	-0.10	-0.05	1.00	-0.05	0.06	-0.05	-0.09
week21	-0.01	0.06	0.37	-0.04	-0.01	-0.05	1.00	-0.17	-0.01	-0.01
week22	0.11	0.00	0.04	-0.02	0.01	0.06	-0.17	1.00	0.06	-0.05
week23	-0.01	-0.02	0.01	0.01	0.01	-0.05	-0.01	0.06	1.00	-0.01
week24	0.08	0.08	0.06	0.01	0.04	-0.09	-0.01	-0.05	-0.01	1.00

Figure 4. Correlation matrix of estimated breeding values between weeks of feed conversion ratio.

3.2. *Prediction of total FCR EBVs*

3.2.1. Single-week data to predict full FCR EBVs

In this experiment, we used five models—LR, RF, Standard, XGBoost, and SVR—with different weekly data from 16–24 weeks to predict the FCR over the whole period (Figure 5). The results are shown in Figure 4. The predictive accuracy of the standard model was the lowest of all models, and the decline in predictive accuracy of the baseline model was very pronounced, especially when predictions were made using data from 21–24 weeks. The results suggested that only using a single week of feed intake data to directly represent the full range of results is not a good strategy. Among a series of models, the RF model showed the most stability and accuracy among all models, thereby maintaining a prediction accuracy between 0.57 and 0.61 in each week

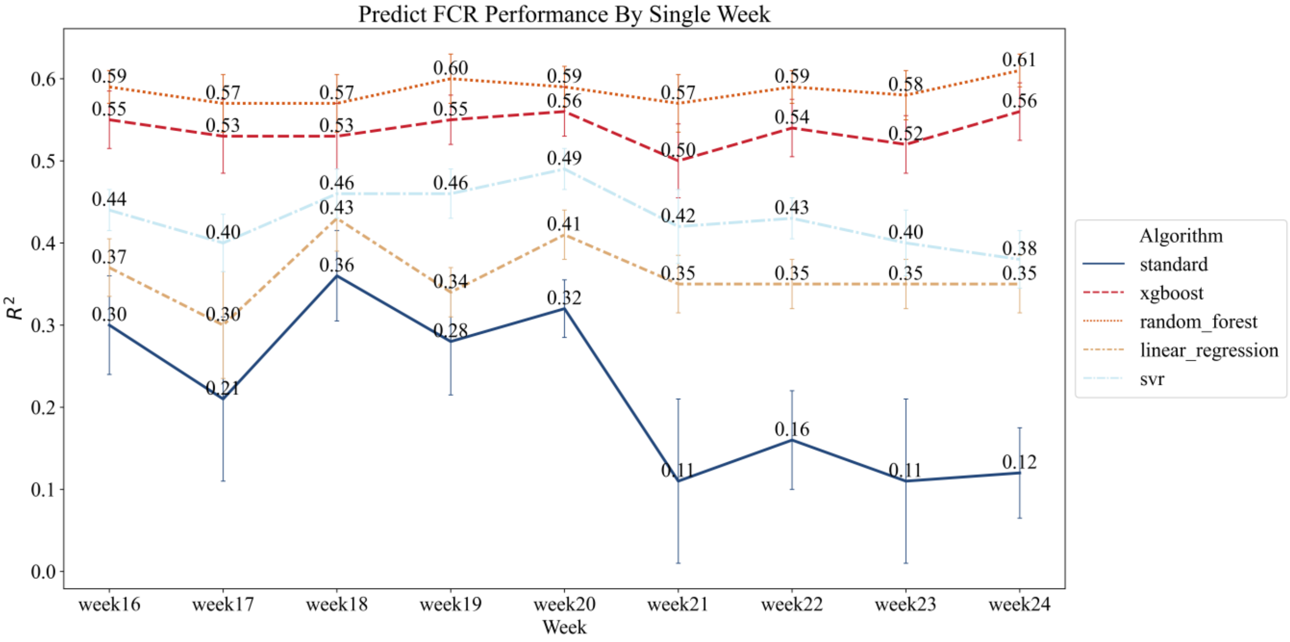
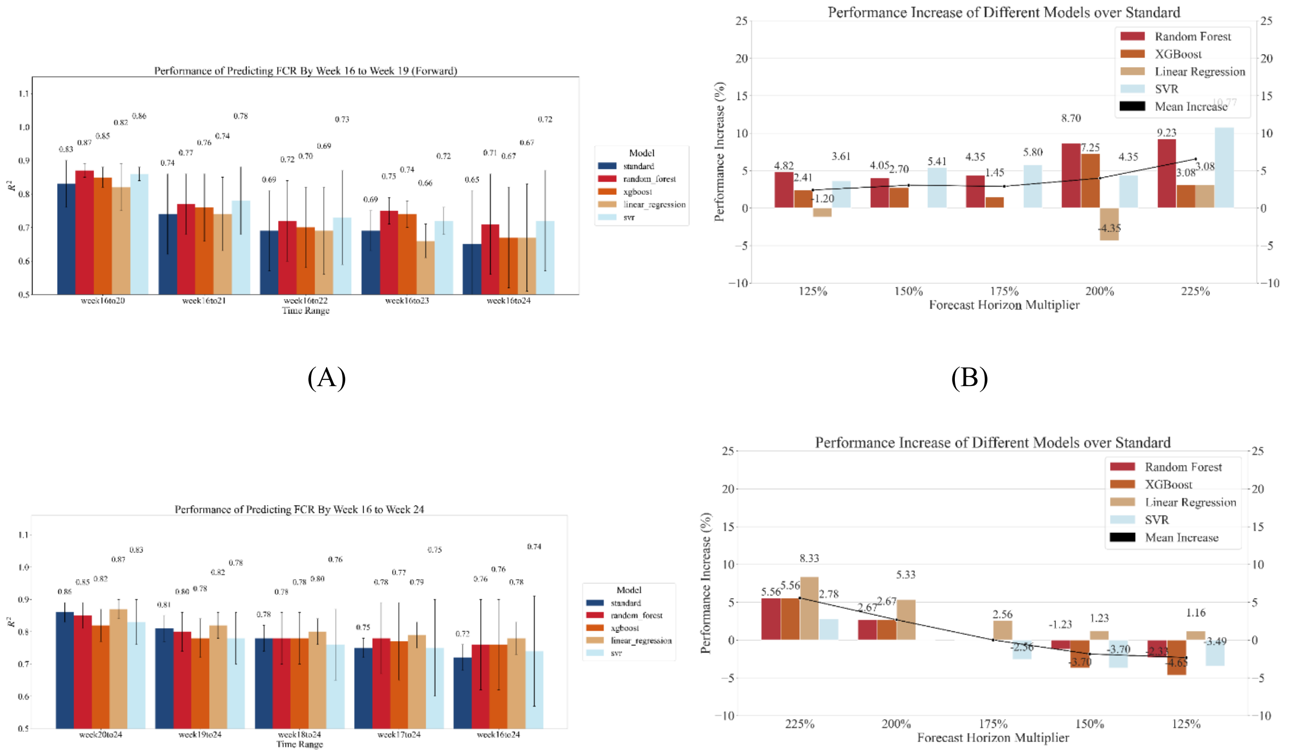


Figure 5. Predicting full range feed convention ratio by weekly data.

3.2.2. Predicting FCR EBVs from partial data

The aim of this experiment was to use partial data to predict the FCR EBVs for pigs at various time ranges up to the full range. For this purpose, ML models such as Standard, RF, XGBoost, and LR were used. The predictive accuracy of the different methods was assessed by calculating the average correlation coefficient (average performance metric) and the standard deviation of the correlation coefficients (stability metric) of the predicted values of each model for each time range (Figure 6). When predicting solely based on the first-half data, the standard model exhibited the lowest prediction accuracy among all models, along with a relatively high standard deviation in prediction errors. This suggests that using partial-cycle data to estimate the full-cycle FCR yields suboptimal results. Both RF and SVR consistently outperformed the baseline model and LR across all time windows. As the prediction horizon extended from 16–20 weeks to the full cycle (16–24 weeks), the performance of all models declined to varying degrees. When using late-stage data for the prediction, the LR model consistently outperformed all other models across all test periods, with its efficacy remaining stable within the 0.78–0.87 range. Additionally, the standard model demonstrated a higher predictive accuracy when utilizing late-stage data compared to early-stage data.



(A)

(B)

(C)

(D)

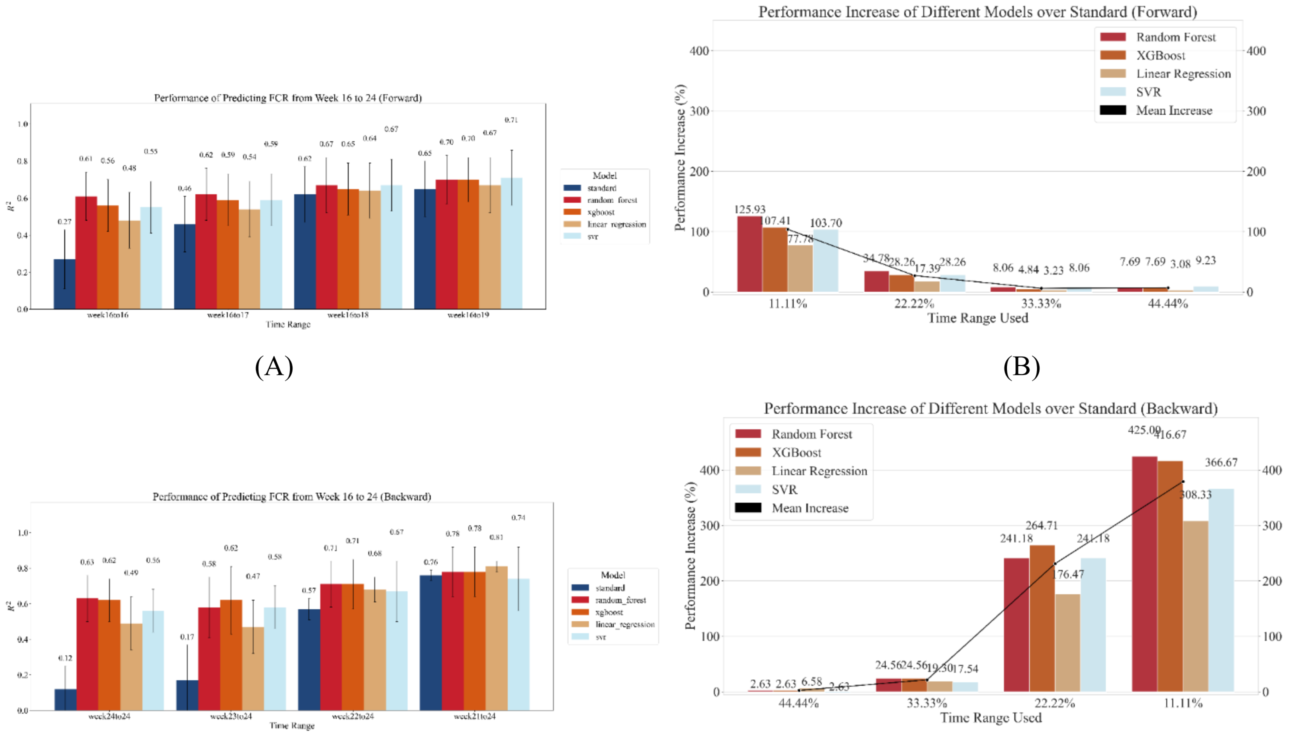
Figure 6. Performance of Predicting FCR by Partial Data. A. The accuracy results of FCR prediction using the first half of the data. B. The improvement of various methods relative to the baseline when predicting using the first half of the data. C. The accuracy results of the FCR prediction using the latter half of the data. D. The improvement of various methods relative to the baseline when predicting using the latter half of the data.

3.2.3. Prediction of entire duration FCR EBVs

The results (Figure 7) demonstrate the performance of the model to predict the entire duration (16–24 weeks) FCR using data from different time ranges. Predictions were made with five different models: Standard, RF, XGBoost, linear regression, and SVR.

When early-stage data were used for prediction, ML models (RF and XGBoost) consistently outperformed both the baseline model and LR in predicting the full-cycle FCR, regardless of the time window considered. Notably, we observed that as the temporal range of the input data decreased, the improvement in the predictive performance became more pronounced. For instance, when only using 16-week data, the baseline model achieved an accuracy of 0.34, whereas RF improved the prediction accuracy to 0.65. Similarly, for data spanning weeks 16–19, the baseline model yielded an accuracy of 0.69, while RF and XGBoost increased the accuracy to 0.75.

In contrast, when late-stage data were employed for prediction, both RF and XGBoost exhibited the best performance in the "week24to24" timeframe, with mean predictive accuracies of 0.63 and 0.62, respectively. As the prediction window expanded (e.g., "week21to24"), all models demonstrated improved performances, with LR showing the most significant enhancement, thereby reaching a mean accuracy of 0.81—substantially higher than that of the baseline model. However, when the temporal range was reduced, all models exhibited a decline in the predictive performance. Despite this, RF and XGBoost maintained relatively robust performances compared to other methods under reduced time spans.



(A) (B)

(C) (D)

Figure 7. Performance of Predicting Whole-Course FCR. A. The accuracy results of predicting the full-term FCR using the early-stage data. B. The improvement of various methods relative to the baseline when predicting the full-term FCR using the early-stage data. C. The accuracy results of predicting the full-term FCR using the later stage data. D. The improvement of various methods relative to the baseline when predicting the full-term FCR using the later stage data.

4. Discussion

The FCR, feed intake, and daily weight gain all are important economic traits of pigs. By accurately predicting these traits, we can dynamically understand the growth process and growth rate of pigs to effectively provide reference bases for pig production and selection of breeding boars, and ultimately maximize the economic benefits of pig farms.

He Yuqing et al. analyzed the feeding behavior data of 655 pigs and found that the feed intake was affected by genetic factors throughout the growth period, and that ML algorithms could more accurately predict pig weight gain [5]. In addition, Poulsen et al. showed that a prediction model that combined direct and indirect genetic effects could significantly improve the accuracy of predicting the pig growth rate [7]. Additionally, other research has demonstrated that combining ML with microbiome data can effectively predict growth and carcass traits in swine [8].

Duy Ngoc et al.'s measurement of the daily weight gain of fattening pigs over the whole period found that the heritability of average daily weight gain of Duroc boars at the 30–90 kg stage was highly similar to that of the whole period, which provides an important reference basis for early selection in breeding work [9]. These findings suggest that the pig growth traits can be better understood and utilized through scientific measurements and prediction methods to optimize the breeding strategies and improve the production efficiency.

4.1. Correlation analysis of FCR between weeks

4.1.1. Phenotypic correlation analysis

For the phenotypic correlation of the entire duration (16 to 24 weeks) FCR with each individual week, it can be noted that the FCR of week 18 and week 20 showed a moderate positive correlation (0.34 and 0.26) with the entire duration FCR, respectively. This suggests that the FCR data from weeks 18 and 20 may play a more important role in the full-length FCR. The phenotypic correlation coefficients of the entire duration FCR with the FCRs of the other weeks showed weak positive correlations, and these values were below 0.15.

We could not see any significant positive or negative correlations between the weekly FCRs, and all the correlation coefficients were slightly above or below zero, thus suggesting that differences in the FCR performance between weeks may be influenced by many other unstudied variables.

The only noteworthy thing may be the weak negative correlation (-0.24) shown between the FCRs of weeks 21 and 22, which may indicate that the FCRs of these two periods showed some kind of reverse trend under the influence of certain factors. These factors may include environmental changes, feed quality, etc [1].

Only very weak correlations were demonstrated between the full and single weekly FCRs, and between the FCRs of different weeks. This may imply that the fluctuations in the weekly FCR are mainly controlled by their respective specific genetic and environmental factors, rather than by effects between different weeks.

4.1.2. Breeding value correlation analysis

From the results, the highest correlation coefficient of 0.27 between the entire duration (weeks 16 to 24) FCR and each individual week occurred at week 16, thus indicating that the FCR at week 16 has some positive correlation with the entire duration FCR. However, this correlation is relatively weak, so the full FCR is not well predicted by the FCR of week 16 alone. Among the correlation values for the other weeks, weeks 18 and 20 also showed a mild positive correlation (0.26). This shows that changes in the FCR during these weeks may affect the full FCR, but these effects may not be significant.

The correlation between the FCR at week 21 and the full FCR was almost zero at -0.01, thus indicating that the two are virtually uncorrelated. Similarly, the FCR at week 23 showed a very weak correlation with the full FCR (-0.01).

When analyzing the relationship between a single week and a common week, we saw a strong positive correlation (0.37) between the FCRs of week 17 and week 21, thus indicating that the FCRs of these two weeks may have shared influences. In addition, the FCR of weeks 21 and 22 showed a weak negative correlation (-0.17), thus indicating that an increase in the FCR in one of these two weeks may cause a decrease in the FCR in the other week.

This result shows us how the full (16 to 24 weeks) FCR EBVs correlate with each individual week's FCR. Although some weeks showed some correlations with the full FCR, these correlations were relatively weak and did not show a clear trend.

From these data, we can see that the full FCR may be influenced by a number of factors, not just one week alone. The overall FCR may be the result of a combination of factors, rather than something that can be independently determined by a single week [11].

Overall, the analysis of EBVs and phenotypic correlations provides us with an initial understanding of the complexity of the FCR, and we need to gain a deeper understanding of the genetic and environmental factors that underlie the FCR at each weekly level, and how they interact with full FCR. To do this, we may need to use more sophisticated statistical models to make accurate predictions of the pig FCR.

4.2. Analysis of the results of the prediction of FCR EBVs

The results suggested that only using a single week of feed intake data to directly represent the full range of results is not a good strategy. As Taylor suggested in his study, the FCR of pigs may be affected by a variety of factors such as time, growth stage, diet, and environmental changes, and these complex interrelationships and dynamics cannot be adequately captured by single-week data [12]. When early-stage data were used for predictions, the accuracy remained relatively low, while predictions based on late-stage data showed significantly higher accuracies. This discrepancy may be attributed to the greater influence of feeding intake and daily weight gain during the latter growth phase, which play a more dominant role in determining the overall feed efficiency.

Our results indicate that the predictive performance remains robust for short-term intervals (1–2 weeks), with marginal differences between early- and late-stage data, likely due to stable weekly growth rates during these phases. However, extending the prediction window beyond three weeks systematically reduced the accuracy across all methods, thus underscoring fundamental limitations in extrapolating partial-period data to the full-cycle FCR. Notably, late-stage measurements (weeks 21–24) achieved near-optimal accuracy ($R^2 \approx 0.80$), thus offering a viable balance between selection intensity and selection accuracy.

Among a series of models, the RF model showed the most stability and accuracy among all models, thereby maintaining a prediction accuracy between 0.57 and 0.61 in single week, and the study showed that the RF model excelled in predicting the growth trajectory of pigs [13,14]. The high accuracy obtained when using the FCR data of the last week for prediction of the entire trajectory may be caused by the fact that the animals in the last week were at their maximum body weight and highest feed intake, so the relative FCR data was higher in percentage. Additionally, the RF model is theoretically well-regarded for its powerful analytical capabilities [15]. Notably, RF consistently outperformed most of the other models in partial-data predictions (Figure 6,7). RF algorithms demonstrate notable superiority in partial-data settings due to their inherent robustness and adaptive mechanisms for handling missing information, thus making them particularly suitable for complex real-world datasets [16].

The XGBoost model has the next best prediction accuracy, and although the model itself has a higher complexity, it struggles to outperform RF in this task [17]. However, it still performed relatively better than the LR and SVR models. The XGBoost model performed well in predicting growth traits in pigs, especially when dealing with complex nonlinear relationships.

The SVR model performed worse than the RF and XGBoost models, but better than the LR and standard models. Its prediction accuracy consistently ranged from 0.38 to 0.49 across weeks. Moreover, the SVR model had some applications in predicting the feed efficiency and growth performance of pigs, although it did not perform as well as the RF and XGBoost models [18].

The LR model had the lowest prediction accuracy for single week data, which may be related to its lack of strength in capturing complex relationships in the data, but it performed better than the standard model. Moreover, it performed best to predict the full stage FCR EBVs when using data from 21–24 weeks. LR models often struggle to capture nonlinear relationships in data when dealing with complex growth data, thus resulting in lower prediction accuracies for most scenarios [3,19].

In summary, the RF model was robust in predicting pig growth traits and the FCR, followed by the XGBoost and SVR models, while the LR and standard models performed relatively poorly. These results suggest that choosing appropriate ML models is important to improve the prediction accuracy and optimize pig farm management.

A single week of data cannot effectively represent the FCR throughout the growth phase, while integrated learning models such as RF are better able to capture and utilize information from multiple weeks of data due to their model complexity, thus leading to better predictions.

The predictive frameworks and insights developed in this study, while derived from a specific population under controlled conditions, hold significant potential for broader applications. ML models, particularly ensemble methods such as RF, are inherently adaptable and can learn complex, non-linear relationships from data. This suggests that with appropriate retraining and validation, the methodology could be effectively transferred to predict the FCR in different swine breeds, alternative production systems (e.g., commercial versus nucleus herds), or varied management environments. However, the generalizability of the specific predictive models and the optimal measurement intervals identified herein may be constrained by contextual factors.

5. Conclusion

Based on the preliminary analysis of growth patterns and the FCR correlations across different pig breeds, and through the application of ML models to predict the overall FCR, this study provides theoretical support to select appropriate measurement stages and improve the representativeness of early-stage FCR measurements. The main conclusions are as follows:

1) For mid-term measurements, when only considering the prediction accuracy, the use of latter-half growth period data is recommended for the FCR evaluation due to its higher predictive power. However, since early-stage data can be obtained earlier in the growth cycle and ML methods (especially RF and SVR) can significantly improve the accuracy of the pig FCR evaluation, breeding practitioners should flexibly select appropriate measurement strategies

based on their specific circumstances.

2) When the available FCR measurement period is short (less than half of the total growth period), RF is recommended for the prediction, regardless of whether using early-stage or late-stage data. When the available FCR measurement period is longer (more than half of the total growth period), LR models are more suitable for predicting the overall FCR.

Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

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Conflicts of interest

The authors declare no conflict of interest.

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