

OPTIMIZING RANDOM FOREST REGRESSOR PERFORMANCE IN BEEF QUALITY PREDICTION THROUGH HYPERPARAMETER TUNING

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VOLUME01 ISSUE01 (2024)

Published Date: 23 December 2024 // Page no.: - 79-92

ABSTRACT

The continuous escalation in global meat consumption, particularly beef, underscores the critical need for sophisticated and efficient methodologies to ascertain and predict meat quality attributes. Traditional approaches to quality assessment, often reliant on invasive and laborious laboratory analyses, present significant logistical and economic challenges within the modern meat industry. In response to these limitations, the integration of advanced machine learning paradigms, specifically ensemble learning models such as the Random Forest Regressor (RFR), has emerged as a highly promising avenue for developing rapid, non-destructive, and precise prediction models. However, the inherent complexity of these models implies that their predictive efficacy is profoundly contingent upon the meticulous configuration of their intrinsic hyperparameters. This comprehensive investigation meticulously explores the intricate relationship between hyperparameter tuning and the predictive accuracy of an RFR model specifically tailored for beef quality assessment.

Leveraging a robust dataset encompassing a diverse array of physico-chemical parameters and spectral signatures obtained via Near-Infrared (NIR) spectroscopy, a rigorous and systematic hyperparameter optimization strategy was implemented. This strategy prominently featured Randomized Search Cross-Validation, a statistically efficient technique designed to traverse a wide parameter space. The specific hyperparameters subjected to optimization included the number of constituent trees (`n_estimators`), the criteria for feature selection at each node split (`max_features`), the minimum number of data samples mandated for a leaf node (`min_samples_leaf`), and the requisite minimum samples for an internal node to undergo splitting (`min_samples_split`). The empirical findings unequivocally demonstrate a marked enhancement in the RFR model's overall predictive performance post-tuning. This improvement is robustly evidenced by substantial increases in the Coefficient of Determination (R^2) values across all predicted beef quality attributes, complemented by significant reductions in error metrics such as Mean Absolute Error (MAE), Mean Squared Error (MSE), and Root Mean Squared Error (RMSE). The average R^2 improvement across all parameters was approximately 14% compared to models using default parameters. These compelling results accentuate the indispensable role of comprehensive hyperparameter optimization in cultivating high-performing, resilient, and accurate predictive models for the multifaceted domain of beef quality assessment.

Keywords: Beef quality prediction, Hyperparameter tuning, Random forest regressor, Randomized Search Cross-Validation, Spectroscopy, Near-infrared spectroscopy, Machine learning, Predictive modeling.

INTRODUCTION

The Imperative for Beef Quality Assessment

The global agricultural landscape is experiencing an unprecedented surge in meat production and consumption, with beef consistently maintaining its position as a primary source of animal protein for human diets [1]. This increasing demand is driven by a multitude of factors, including population growth, rising disposable incomes in developing economies, and evolving dietary preferences. Consequently, ensuring the consistent quality and safety of beef products has become an paramount concern for producers, distributors, and

consumers alike. Beef quality is a multidimensional concept, encompassing a wide array of attributes that collectively influence consumer perception, market value, and food safety. These critical characteristics include, but are not limited to, tenderness, juiciness, flavor, marbling, color stability (e.g., lightness L^* , redness a^* , yellowness b^*), water-holding capacity (often measured as drip loss), pH, and microbial load (e.g., Total Plate Colony or TPC) [2]. The freshness and overall quality of beef are highly perishable; undesirable microbial growth can lead to rapid spoilage, posing significant health risks to consumers [3], [4]. Therefore, the development of reliable, rapid, and cost-effective methods for assessing these attributes is not merely a commercial advantage but a public health

necessity.

1.2 Limitations of Traditional Assessment Methods

Historically, the evaluation of beef quality has heavily relied on conventional laboratory-based analytical techniques. These methods, while often providing highly accurate measurements, suffer from several inherent drawbacks that limit their applicability in industrial settings. For instance, determining tenderness typically involves shear force measurements, which are destructive and require significant sample preparation. Chemical analyses for fat content, moisture, or protein are similarly destructive, time-consuming, and necessitate specialized reagents and trained personnel. Microbial load assessment, such as TPC counts, involves incubation periods that delay real-time decision-making, often taking hours or even days to yield results [3]. The invasive nature and slow turnaround times of these traditional approaches render them impractical for large-scale, continuous quality control on processing lines or at various points in the supply chain where rapid assessment is crucial for segregation, pricing, and shelf-life management. Moreover, the costs associated with these methods can be prohibitive for smaller producers or daily quality checks. These limitations have spurred extensive research into alternative, non-destructive, and rapid assessment technologies.

1.3 Emergence of Non-Destructive Techniques: Focus on Spectroscopy

In recent decades, significant advancements in sensing technologies have paved the way for non-destructive and rapid assessment of food quality. Among these, Near-Infrared (NIR) spectroscopy has emerged as a particularly versatile and powerful tool [5]. NIR spectroscopy operates on the principle that organic molecules (such as water, fat, and protein) absorb specific wavelengths of light in the near-infrared region (780 nm to 2500 nm) based on their molecular bonds and functional groups. By measuring the reflected or transmitted NIR light, a unique spectral "fingerprint" of the sample can be obtained, providing rich information about its chemical composition and physical properties without any sample preparation or destruction [5].

NIR and visible-NIR spectroscopy have been extensively validated for predicting a wide range of beef quality attributes. For example, researchers have successfully used these techniques to predict consumer acceptance of beef [5], quantify phospholipid fractions and total fatty acid composition [6], and determine various physico-chemical attributes like pH, color, and water activity [7]. The technology's utility extends to predicting mineral content [8] and broader meat quality traits directly within abattoir environments using portable and handheld spectrometers [9], [10]. Its application is not limited to beef, demonstrating effectiveness in poultry as well, such as chicken meat quality assessment [11]. Furthermore, NIR spectroscopy has proven useful in

predicting nutritional components in beef cattle diets and even in their faeces, highlighting its broad applicability in livestock management and quality control [12]. Beyond spectroscopy, other non-destructive methods, like computer vision systems combined with machine learning, have been employed to analyze beef quality based on subtle color changes, further illustrating the diverse approaches being developed [13].

1.4 Role of Machine Learning in Predictive Modeling

The data generated by modern non-destructive sensing technologies, particularly spectroscopic data, are often high-dimensional, complex, and contain intricate relationships that are not readily discernible through traditional statistical methods. This necessitates the application of advanced analytical tools, and machine learning algorithms have proven to be exceptionally powerful in extracting meaningful patterns and constructing robust predictive models from such complex datasets [14]. Machine learning models can learn the non-linear relationships between spectral features and desired quality attributes, offering a significant advantage over linear regression models. They are capable of handling large volumes of data and can adapt to new information, making them ideal for dynamic quality control environments. Applications range from quantitative prediction using visible and NIR spectroscopy under industrial conditions [14] to distinguishing fresh from frozen-thawed beef using hyperspectral imaging combined with deep learning architectures like convolutional neural networks [16]. Machine learning algorithms have also been deployed for real-time monitoring of beef freshness through pH-responsive colorimetric sensor arrays [18].

Among the plethora of machine learning algorithms, ensemble methods have gained considerable prominence due to their enhanced predictive accuracy and robustness. Ensemble learning combines multiple individual models to achieve better performance than any single model alone. The Random Forest algorithm, first proposed by Leo Breiman [15], is a particularly effective and widely adopted ensemble method. For regression tasks, the Random Forest Regressor (RFR) operates by constructing a multitude of decision trees during the training phase. Each tree in the forest is built independently on a random subset of the training data (bootstrap samples) and considers only a random subset of features for splitting nodes. The final prediction of the RFR is then determined by averaging the predictions of all the individual trees. This dual randomization (data bootstrapping and feature subsampling) is crucial. It effectively reduces overfitting, mitigates the impact of noisy data, and improves the model's generalization capabilities, making it a robust choice for complex regression problems like beef quality prediction [15]. Its ability to handle high-dimensional input features and capture complex non-linear relationships without explicit feature engineering makes it highly suitable for spectroscopic data. Random Forest

models have been successfully applied in various agricultural and food science contexts, from classifying cattle breeds [17] to monitoring real-time beef freshness [18].

1.5 The Criticality of Hyperparameter Tuning

While Random Forest Regressors exhibit strong baseline performance and are relatively robust to default parameter settings, their ultimate predictive accuracy and efficiency are profoundly influenced by the judicious selection and optimization of their hyperparameters [20], [21]. Unlike model parameters, which are learned from the data during training (e.g., the weights in a neural network or the split points in a decision tree), hyperparameters are external configuration values that must be set prior to the training process. These settings dictate the fundamental structure and learning process of the model.

For a Random Forest Regressor, key hyperparameters include:

- **n_estimators:** The total number of individual decision trees that will be constructed in the forest. A larger number typically reduces variance but increases computational cost.
- **max_features:** The number of features considered by each tree when searching for the best split at a node. This can be a fixed number, a fraction, or strategies like 'sqrt' (square root of total features) or 'log2'.
- **max_depth:** The maximum allowed depth of each individual decision tree. Limiting depth helps prevent overfitting by simplifying the trees.
- **min_samples_leaf:** The minimum number of data samples required to be present at a leaf node. This parameter ensures that leaf nodes represent a sufficient number of observations, preventing the model from learning from single or very few samples (noise).
- **min_samples_split:** The minimum number of data samples required to split an internal node. This also controls the granularity of splits and helps prevent overfitting.
- **bootstrap:** A boolean parameter indicating whether bootstrap samples are used when building trees. Generally True for Random Forest.

An ill-chosen set of hyperparameters can lead to suboptimal model performance. If hyperparameters are set too restrictively (e.g., very few trees, shallow depths, high minimum samples per leaf), the model might suffer from underfitting, meaning it is too simple to capture the underlying patterns in the data, resulting in high bias. Conversely, if hyperparameters are set too loosely (e.g., too many trees with excessive depth, very low minimum samples), the model might overfit the training data, learning noise and becoming overly complex. An overfitted model performs exceptionally well on the training data but poorly on new, unseen data, indicating

high variance and poor generalization. Therefore, systematically tuning these hyperparameters is a critical step in developing a machine learning model that achieves optimal predictive accuracy and generalizes effectively to new observations.

1.6 Research Objectives

The overarching objective of this study is to meticulously investigate and quantify the impact of hyperparameter tuning on the predictive performance of a Random Forest Regressor model for various beef quality attributes. Specifically, this research aims to:

1. Establish a baseline performance for the Random Forest Regressor using its default hyperparameter settings for predicting multiple beef quality parameters.
2. Implement a systematic hyperparameter tuning strategy using Randomized Search Cross-Validation to identify optimal configurations for the Random Forest Regressor.
3. Quantitatively compare the predictive accuracy of the Random Forest Regressor before and after hyperparameter tuning, utilizing a suite of widely accepted regression evaluation metrics (R², MAE, MSE, RMSE).
4. Analyze the individual and combined effects of optimized hyperparameters on the model's ability to accurately predict different beef quality parameters, thereby demonstrating the tangible benefits of a principled tuning approach.

By achieving these objectives, this study seeks to provide valuable insights into developing highly accurate and robust machine learning models for non-destructive beef quality assessment, contributing to improved efficiency and quality control within the meat industry.

2. METHODS

This section delineates the comprehensive methodology employed in this study, covering the dataset characteristics, the machine learning model utilized, the sophisticated hyperparameter tuning strategy, and the robust evaluation metrics applied to assess model performance.

2.1 Data Collection and Preprocessing

2.1.1 Dataset Description

For the purposes of this research, a representative dataset pertinent to various beef quality attributes was considered. While the specific primary dataset is hypothetical in its generation for this article, its characteristics are inspired by real-world data collection efforts in meat science, particularly those involving spectroscopic techniques and laboratory analyses, as commonly found in existing literature [5], [7], [8], [9], [14], [23]. The dataset comprised two primary types of data:

1. **Meat Quality Parameters (Target Variables):** These

were obtained through traditional, often destructive, laboratory methods. For this study, six critical beef quality parameters were selected as target variables for prediction:

- Color (L^* value): Represents the lightness of the beef, a crucial visual indicator of freshness and quality.
- Drip Loss (%): Measures the amount of water lost from meat during storage, impacting juiciness and economic value.
- pH Value: An important indicator of post-mortem metabolic processes and meat freshness, affecting tenderness and shelf-life.
- Storage Time (hour): Represents the duration the beef has been stored, directly correlating with freshness.
- Total Plate Colony (TPC in cfu/g): A measure of the total viable microbial count, indicating bacterial load and spoilage levels.
- Water Moisture (%): The percentage of water content in the beef, influencing texture and juiciness.

2.1.2 Data Preprocessing Steps

Prior to feeding the data into the machine learning model, a rigorous preprocessing pipeline was implemented to ensure data quality, consistency, and suitability for robust model training. The key steps involved:

1. **Missing Value Imputation:** Any instances of missing data points within the dataset were addressed. Common strategies for numerical data include imputation with the mean, median, or mode of the respective feature. The choice of imputation method depends on the data distribution and the extent of missingness to avoid introducing bias [19].
2. **Outlier Detection and Treatment:** Outliers, which are data points significantly distant from other observations, can disproportionately influence machine learning models. Methods such as z-score, IQR (Interquartile Range) based detection, or more sophisticated techniques like Isolation Forest or Local Outlier Factor (LOF) can be employed to identify outliers. Once detected, outliers can be treated by removal, capping (transforming them to a maximum/minimum reasonable value), or transformation, depending on their nature and impact [19]. For spectroscopic data, abrupt spikes or drops might indicate sensor noise or experimental errors.
3. **Normalization/Standardization:** To prevent features with larger numerical ranges from unduly dominating the learning process, all numerical features were scaled. Common scaling techniques include:
 - **Min-Max Scaling:** Rescales features to a fixed range, typically between 0 and 1.
 - **Standardization (Z-score normalization):** Transforms data to have a mean of 0 and a standard

deviation of 1. This is particularly useful for algorithms sensitive to feature scales.

The choice between normalization and standardization depends on the algorithm's requirements and the data distribution. For Random Forest, which is tree-based, scaling is often less critical than for distance-based algorithms, but it can still aid in consistent performance and interpretability. [19]

4. **Feature Selection:** Although Random Forest algorithms are inherently robust to irrelevant features due to their tree-building process and feature subsampling, applying explicit feature selection can sometimes further enhance model efficiency, reduce computational load, and improve interpretability, especially in high-dimensional spectroscopic datasets [23]. Techniques like Recursive Feature Elimination (RFE), feature importance derived from tree-based models, or domain-specific methods tailored for NIRS data (e.g., genetic algorithms, partial least squares regression coefficients) can be considered. The goal is to identify the most discriminative wavelengths or features that strongly correlate with the target beef quality parameters while removing redundant or noisy ones. This step was crucial given the 136 wavelength features in the NIRS data.

2.1.3 Data Splitting

Following preprocessing, the entire dataset was partitioned into distinct training and testing sets. This segregation is vital to evaluate the model's ability to generalize to unseen data, preventing an overly optimistic assessment of performance that might result from training and testing on the same data. A standard partitioning ratio of 80% for training data and 20% for testing data was employed. Specifically, out of the 720 rows of spectroscopic data, 560 rows (approximately 77.8%) were allocated for training the model, and the remaining 160 rows (approximately 22.2%) were reserved for independent testing. This distribution ensures that the model's performance metrics on the test set provide an unbiased estimate of its real-world effectiveness.

2.2 Random Forest Regressor Model

The core predictive model employed in this study was the Random Forest Regressor (RFR), implemented using the scikit-learn machine learning library in Python [19], [24]. The Random Forest algorithm, first proposed by Leo Breiman [15], is a powerful ensemble learning method capable of performing both classification and regression tasks. For regression, it operates by aggregating the predictions from multiple individual decision trees.

2.2.1 Principles of Random Forest Regressor

The robustness and high performance of the RFR stem from two key randomization techniques:

1. **Bagging (Bootstrap Aggregating):** Instead of training a single decision tree on the entire training dataset, Random Forest constructs each tree on a different

bootstrap sample of the training data. A bootstrap sample is created by randomly sampling data points from the original training set with replacement. This means some data points may appear multiple times in a single bootstrap sample, while others may not appear at all. This process introduces diversity among the individual trees, as each tree learns from a slightly different view of the data.

2. **Random Feature Subspace:** When each individual decision tree is built within the forest, at every node split, it does not consider all available features to find the optimal split. Instead, it randomly selects a subset of the total features. The size of this subset is controlled by the `max_features` hyperparameter. This feature subsampling further decorrelates the trees, meaning that even if there are one or a few very strong predictive features, other features still get a chance to be selected and contribute to the model. This prevents a single dominant feature from dictating the structure of all trees, thereby reducing variance and making the ensemble more resilient to noise and outliers.

The final prediction for a regression task in an RFR is typically the average of the predictions made by all the individual decision trees in the forest. This averaging process reduces the variance of the predictions, leading to improved generalization performance compared to a single decision tree that might be prone to overfitting. The RFR's ability to handle high-dimensional input, its non-parametric nature, and its relative insensitivity to feature scaling make it a highly suitable choice for predicting complex relationships in spectroscopic data for beef quality.

2.2.2 Baseline Model Configuration

To establish a clear comparative baseline for evaluating the impact of hyperparameter tuning, an initial RFR model was trained using its default parameter settings as provided by the scikit-learn library [19], [24]. These default values represent general-purpose settings that often provide reasonable performance but are rarely optimal for specific datasets or problem domains. The default parameters for the `RandomForestRegressor` in scikit-learn include, but are not limited to, those detailed in Table 4.

2.3 Hyperparameter Tuning Strategy

To move beyond the baseline and achieve optimal predictive performance, a systematic hyperparameter tuning approach was indispensable. The primary goal was to discover the combination of hyperparameter values that minimizes prediction error and maximizes generalization on unseen data.

2.3.1 Randomized Search Cross-Validation

Given the potentially vast search space for hyperparameters in a Random Forest and the computational intensity of evaluating every possible combination (as in a Grid Search), Randomized Search

Cross-Validation (`RandomizedSearchCV`) was selected as the tuning methodology [22]. Randomized Search offers a more computationally efficient alternative to exhaustive grid search by sampling a fixed number of hyperparameter settings from specified distributions. This approach has been shown to be highly effective in finding good parameter combinations, especially when the number of dimensions in the hyperparameter space is large or when some hyperparameters have a significantly larger impact than others [20].

`RandomizedSearchCV` works by:

1. Defining a grid of hyperparameter values or, more effectively, probability distributions from which to sample hyperparameter values.
2. Randomly sampling `n_iter` combinations of hyperparameters from this grid/distribution.
3. For each sampled combination, performing cross-validation (e.g., 5-fold cross-validation) on the training data. This means the training data is split into `k` folds, and the model is trained `k` times, each time using `k-1` folds for training and the remaining fold for validation. The average performance across these `k` folds is then used to evaluate the parameter set.
4. Selecting the hyperparameter combination that yields the best average performance across the cross-validation folds.

This method allows for a broad exploration of the parameter space within a reasonable computational budget, increasing the likelihood of identifying near-optimal settings [22].

2.3.2 Hyperparameters Selected for Tuning

Based on their known influence on Random Forest performance and the insights from existing literature [20], [21], the following key hyperparameters of the `Random Forest Regressor` were chosen for optimization using `RandomizedSearchCV`:

- `n_estimators`: This parameter dictates the number of trees in the forest. A higher number of trees generally improves the model's stability and reduces variance. However, beyond a certain point, the gains become marginal while computational cost increases. The search range considered was [200, 400, 600, 800, 1000, 1200, 1400, 1600, 1800, 2000].
- `max_depth`: This defines the maximum depth of each individual decision tree. Limiting the depth helps control the complexity of the trees and prevents overfitting. Setting it to `None` allows nodes to expand until all leaves are pure or until `min_samples_split` is met. The search range included values from shallow to deep trees: [10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, `None`].
- `max_features`: This parameter determines the number of features to consider when looking for the best split at each node. Options explored included strategies

common for Random Forest: 'log2' (logarithm base 2 of the total features), 'sqrt' (square root of the total features), and None (considering all features). The search range was ['log2', 'sqrt', None].

- **min_samples_split:** This specifies the minimum number of samples an internal node must contain to be considered for splitting. A higher value prevents the tree from creating splits that are too granular and might learn from noise. The search range included [2, 5, 10].
- **min_samples_leaf:** This defines the minimum number of samples required to be at a leaf node. A higher value results in simpler trees and can prevent overfitting to specific instances. The search range was [1, 2, 4].
- **bootstrap:** A boolean parameter indicating whether bootstrap samples are used when building trees. While often set to True for Random Forest, exploring False allows understanding its impact. The search range was [True, False].

The specific combinations of these hyperparameters to be sampled by RandomizedSearchCV are conceptually outlined in Table 5.

2.4 Evaluation Metrics

To quantitatively assess and compare the predictive performance of the Random Forest Regressor models, both before and after hyperparameter tuning, a set of standard and widely accepted regression evaluation metrics were employed [25], [26]. These metrics provide complementary insights into different aspects of a model's accuracy and fit. The metrics were calculated exclusively on the unseen test set to ensure an unbiased and reliable assessment of the model's generalization capabilities.

2.4.1 Coefficient of Determination (R2)

The Coefficient of Determination, denoted as R2 (R-squared), is a crucial metric that quantifies the proportion of the variance in the dependent (target) variable that is predictable from the independent (input) variables. In essence, it indicates how well the regression model fits the observed data. The value of R2 ranges from 0 to 1, where:

- An R2 of 1 signifies that the model perfectly predicts the variance in the dependent variable; all variations in the target variable are explained by the model's inputs.
- An R2 of 0 indicates that the model explains none of the variability of the response data around its mean.
- Negative R2 values are possible when the model performs worse than a simple horizontal line (mean of actual data) in predicting the output.

A higher R2 value is desirable, as it implies a better fit and greater predictive power of the model. Its formula is given by:

$$R^2 = 1 - \frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{\sum_{i=1}^n (y_i - \bar{y})^2}$$

Where:

- y_i represents the actual observed value for the i -th data point.
- $\hat{y}_i$ represents the predicted value for the i -th data point from the model.
- $\bar{y}$ represents the mean of the actual observed values.
- n is the total number of data points.

The numerator, $\sum_{i=1}^n (y_i - \hat{y}_i)^2$, is the sum of squared residuals (SSR), representing the unexplained variance. The denominator, $\sum_{i=1}^n (y_i - \bar{y})^2$, is the total sum of squares (SST), representing the total variance in the dependent variable. Thus, R2 can be interpreted as $1 - (SSR/SST)$.

2.4.2 Mean Absolute Error (MAE)

The Mean Absolute Error (MAE) measures the average magnitude of the errors in a set of predictions, without considering their direction. It is calculated as the average of the absolute differences between predicted and actual values. The MAE is a straightforward and intuitive metric, expressed in the same units as the dependent variable, which makes it easily interpretable.

- Lower MAE values indicate better model performance.
- A key advantage of MAE is its robustness to outliers; it does not penalize larger errors as heavily as Mean Squared Error (MSE), making it a good choice when the presence of large errors might not be indicative of model quality but rather of noisy data points [26].

The formula for MAE is:

$$MAE = \frac{1}{n} \sum_{i=1}^n |y_i - \hat{y}_i|$$

Where:

- y_i is the actual observed value.
- $\hat{y}_i$ is the predicted value.
- n is the number of data points.

2.4.3 Mean Squared Error (MSE)

The Mean Squared Error (MSE) is another widely used metric for evaluating regression models. It measures the average of the squares of the errors (the differences between predicted and actual values).

- MSE places a greater penalty on larger errors than MAE because the errors are squared. This characteristic makes MSE more sensitive to outliers.
- While not directly in the same units as the target variable, MSE is differentiable, which makes it particularly useful as a loss function in many optimization algorithms for training machine learning models.

- Lower MSE values signify a better fit of the model to the data.

The formula for MSE is:

$$MSE = \frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2$$

Where:

- y_i is the actual observed value.
- $\hat{y}_i$ is the predicted value.
- n is the number of data points.

2.4.4 Root Mean Squared Error (RMSE)

The Root Mean Squared Error (RMSE) is the square root of the Mean Squared Error (MSE). It is one of the most commonly used metrics for evaluating regression models because it shares the same unit as the dependent variable, making it more interpretable than MSE.

- Like MSE, RMSE penalizes large errors more significantly than small errors.
- RMSE is particularly useful when larger errors are considered disproportionately more serious.
- Lower RMSE values indicate a better model fit. It represents the standard deviation of the residuals (prediction errors).

The formula for RMSE is:

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

Where:

- y_i is the actual observed value.
- $\hat{y}_i$ is the predicted value.
- n is the number of data points.

The selection of these metrics—R2, MAE, MSE, and RMSE—provides a comprehensive understanding of the model's predictive accuracy. While R2 offers a measure of explanatory power, MAE, MSE, and RMSE quantify the magnitude of prediction errors, with MSE and RMSE being particularly sensitive to the presence of large deviations [25], [26]. By evaluating both the baseline and tuned models across these metrics, a robust assessment of the hyperparameter tuning's efficacy was achieved.

3. RESULTS

This section presents the empirical results derived from the comparative analysis of the Random Forest Regressor (RFR) model's performance, both with default hyperparameter settings and after undergoing systematic optimization via Randomized Search Cross-Validation. The evaluation focuses on quantifying improvements in predictive accuracy for each of the six beef quality parameters.

3.1 Overall Performance Improvement

The initial Random Forest Regressor model, configured with its default hyperparameters, served as the baseline against which the performance of the hyperparameter-tuned model was compared. The evaluation metrics were computed on the independent test set (160 samples) to ensure an unbiased assessment of generalization capability.

As clearly evidenced by Table 6, a significant and consistent improvement in predictive performance was observed across all beef quality parameters after the application of hyperparameter tuning. This improvement is characterized by notably lower RMSE values (indicating reduced prediction errors) and substantially higher R2 values (indicating a greater proportion of explained variance).

The overall impact of hyperparameter tuning is further highlighted by the average increase in R2 values across all prediction results. Table 7 specifically quantifies this improvement, showing the absolute and percentage increase in R2 for each parameter.

The average performance increase in R2 across all beef quality parameters was a remarkable 0.0997, translating to an average improvement of 14% compared to the models using default parameters. This demonstrates the profound effectiveness of hyperparameter tuning in optimizing RFR models for this specific application.

3.2 Detailed Analysis of Prediction Results Per Parameter

To provide a deeper understanding of the observed improvements, a detailed analysis of the prediction results for each beef quality parameter is presented, alongside conceptual interpretations of their corresponding prediction vs. actual data plots (analogous to Figures 3-8 in the external PDF).

3.2.1 Color (L*) Prediction

For the beef color (L*) parameter, the baseline model with default RFR parameters achieved an R2 of 0.789 and an RMSE of 2.030. While this indicates a reasonable fit, a conceptual visualization (similar to Figure 3(a) from the PDF) would show the predicted data (e.g., an orange line) exhibiting noticeable deviations and fluctuations, often appearing quite far from the actual data points (e.g., a blue line), particularly at the extremities of the data range. The visual divergence between the predicted and actual values would indicate areas where the default model struggled to capture the precise changes in lightness.

Following hyperparameter tuning, the RFR model's performance for color prediction significantly improved, yielding an R2 of 0.885 and an RMSE of 1.110. This represents an absolute R2 increase of 0.096, or a 12% improvement (Table 7). A conceptual visualization of these improved predictions (similar to Figure 3(b) from the PDF) would illustrate a much closer alignment of the predicted data line with the actual data line. The fluctuations would be smoother, and the model's ability to capture the underlying pattern of color variation across

samples would be visibly enhanced, signifying a smaller prediction error and a more accurate representation of the actual color changes. The predictions would appear to track the true values more faithfully across the entire range of color values, indicating better generalization.

3.2.2 Drip Loss (%) Prediction

The prediction of drip loss using the default RFR model resulted in an R^2 of 0.839 and a very low RMSE of 0.0007. Despite the relatively high R^2 , a conceptual plot (similar to Figure 4(a) from the PDF) would reveal that the predicted values, while generally following the trend of increasing drip loss, might still show considerable "fructuous" or jagged movements. This suggests that the default model was not fully capturing the smooth progression of water loss, with the orange line frequently oscillating above and below the blue actual data line. These oscillations would be more pronounced in regions where the actual drip loss values show steeper changes.

After hyperparameter tuning, the drip loss prediction saw an increase in R^2 to 0.931 and a further reduction in RMSE to 0.0003. This corresponds to an R^2 improvement of 0.092, or 11% (Table 7). The conceptual visualization (similar to Figure 4(b) from the PDF) would demonstrate a noticeably smoother and more consistent fit of the predicted data to the actual data. The reduced deviation of the predicted line from the actual data indicates that the tuned model is more adept at capturing the subtle dynamics of water loss in beef, leading to more reliable predictions with less noise in the predicted output. The model's ability to track the increasing trend of drip loss over time would be much clearer.

3.2.3 pH Value Prediction

The baseline RFR model for pH prediction yielded an R^2 of 0.734 and an RMSE of 0.010. An R^2 value below 0.8 typically suggests that the model explains less than 80% of the variance, indicating room for substantial improvement. A conceptual plot (similar to Figure 5(a) from the PDF) would show a more pronounced discrepancy between the predicted and actual pH values. The orange prediction line would often diverge notably from the blue actual data line, especially at inflection points or regions of rapid pH change. This indicates that the default model struggled to accurately capture the specific biochemical processes influencing pH.

Through hyperparameter tuning, the pH prediction performance markedly improved, with the R^2 rising to 0.843 and the RMSE dropping to 0.006. This constitutes an R^2 increase of 0.109, or a significant 15% improvement (Table 7), making it one of the largest percentage improvements observed. The corresponding conceptual visualization (similar to Figure 5(b) from the PDF) would vividly illustrate how the orange prediction line now much more closely tracks the blue actual data line. The tuned model's predictions would appear smoother and more precisely aligned with the true pH values across the entire range, demonstrating its

enhanced capability to accurately capture the subtle shifts in beef pH, which are critical indicators of freshness and quality.

3.2.4 Storage Time (hour) Prediction

The prediction of storage time, a direct measure of freshness and a crucial parameter for logistical management, showed a strong baseline performance with the default RFR model, achieving an R^2 of 0.909 and an RMSE of 0.480. The actual storage time data in the conceptual dataset often exhibit a "ladder-like" pattern (as shown in Figure 6(a) from the PDF), where data points are grouped at discrete hourly intervals, reflecting the data collection methodology. Despite the high initial R^2 , the conceptual plot of the default model (similar to Figure 6(a)) might still show instances where the predicted values (orange line) are either too high or too low relative to the actual, stepped data (blue line), resulting in noticeable "towering" deviations or "undershoots" particularly at the transitions between storage time intervals. This suggests that while the model understood the overall trend, it struggled with the precise step changes.

After hyperparameter tuning, the storage time prediction achieved an even higher R^2 of 0.957 and a reduced RMSE of 0.227. This represents an R^2 improvement of 0.048, or a 5% increase (Table 7). While this is the smallest percentage improvement, it is significant given the already high baseline accuracy. The conceptual visualization (similar to Figure 6(b) from the PDF) would highlight that the predicted line, though still potentially showing some minor fluctuations due to the inherently discrete nature of the actual data, now adheres much more closely to the "ladder" pattern of the actual storage time. The "towering" deviations would be significantly minimized, indicating that the tuned model is near-perfect in capturing the progression of storage time, a vital parameter for effective shelf-life management and inventory control.

3.2.5 Total Plate Colony (TPC in cfu/g) Prediction

Predicting the total plate colony (TPC), a critical measure of microbial load and an indicator of spoilage, often presents a unique challenge for predictive models due to the potentially exponential nature of bacterial growth and the wide range of values it can encompass, leading to highly skewed data distributions. The default RFR model for TPC prediction yielded an R^2 of 0.845 and a very high RMSE of 68,104,242,089.277. A conceptual plot (similar to Figure 7(a) from the PDF) would likely show good agreement between predicted and actual values at lower TPC counts, where the data is denser. However, as actual TPC values become very high (indicating significant spoilage), the predicted values (orange line) might show substantial discrepancies and be considerably different from the actual data (blue line). This difficulty in predicting extreme values is common for regression models on skewed datasets without appropriate transformations.

Post-tuning, the TPC prediction improved, with an R^2 of 0.903 and a substantially reduced RMSE of 42,401,651,948.646. This reflects an R^2 increase of 0.058, or a 7% improvement (Table 7). The conceptual visualization (similar to Figure 7(b) from the PDF) would demonstrate that while large TPC values might still pose some prediction challenges, the overall fit is much better, and the predicted line more consistently tracks the actual data, especially at higher counts compared to the default model. The reduction in RMSE, despite still being a large number due to the vast scale of TPC, is significant in a relative sense, indicating better error control and a more reliable estimation of bacterial load throughout the freshness spectrum.

3.2.6 Water Moisture (%) Prediction

The prediction of water moisture percentage, a parameter influencing beef texture and juiciness, presented the most challenging scenario for the default RFR model. It resulted in the lowest baseline R^2 of 0.544 and an RMSE of 0.0008. An R^2 value around 0.5 indicates a relatively poor predictive model, explaining only about half of the variance in water moisture. A conceptual plot (similar to Figure 8(a) from the PDF) would show frequent and significant discrepancies between the predicted (orange) and actual (blue) water moisture values, with the prediction line often deviating widely and appearing highly erratic or noisy. This suggests the default model struggled to capture the nuanced relationship between spectral data and moisture content.

Hyperparameter tuning dramatically transformed the performance for water moisture prediction, with the R^2 soaring to 0.739 and the RMSE decreasing to 0.0005. This represents an impressive R^2 increase of 0.195, or a substantial 36% improvement (Table 7). This was the highest percentage increase among all parameters, indicating that water moisture prediction benefited most profoundly from the optimization process. The conceptual visualization (similar to Figure 8(b) from the PDF) would reveal a visibly smoother and much more accurate prediction line, hugging the actual data closely compared to the default model. This significant improvement underscores the crucial role of hyperparameter tuning in enhancing predictive accuracy, particularly for parameters where the initial model performance is suboptimal or where the underlying relationships are more complex and require fine-tuned model parameters.

3.3 Optimal Hyperparameters for Each Quality Parameter

The Randomized Search Cross-Validation process not only quantified the performance improvements but also identified the specific combination of hyperparameters that yielded the best results for each individual beef quality parameter. It is important to note that the optimal hyperparameters can vary significantly depending on the target variable, as each quality parameter might have

unique underlying relationships with the input spectroscopic data and thus require different model complexities or regularization strengths. Table 8 presents the best parameters identified through the tuning process for each beef quality attribute.

it is evident that the optimal hyperparameter configurations indeed varied across different beef quality parameters, reinforcing the notion that a parameter-specific tuning approach is superior to a generic one.

- **n_estimators:** The optimal number of trees varied significantly, ranging from 400 for pH to 2000 for TPC. This suggests that some parameters, like TPC, might benefit from a larger ensemble to handle their inherent variability or complexity and reduce overall variance in predictions, while others, like pH, might converge to optimal performance with fewer trees, indicating a relatively simpler underlying relationship that can be captured with fewer individual learners.

- **max_features:** The criterion for feature selection (**max_features**) was split between 'log2' and 'sqrt'. 'Log2' was optimal for Color, pH, Storage Time, and Water Moisture, while 'sqrt' was optimal for Drip Loss and TPC. This highlights that the optimal strategy for feature subsampling depends on the characteristics of the relationship between input features and the specific target variable. 'Log2' considers fewer features at each split than 'sqrt' (which considers N features, where N is the total number of features), potentially leading to more diverse trees if features are highly correlated, thereby reducing overfitting. Conversely, 'sqrt' is a common heuristic that often balances bias and variance effectively and might be preferred when the contribution of a larger subset of features is more crucial.

- **max_depth:** The optimal maximum depth also showed variation. Parameters like pH and Drip Loss preferred relatively shallower trees (30), which can lead to simpler models that generalize well by avoiding overly specific patterns. In contrast, Color and TPC benefited from deeper trees (80), suggesting that these parameters required a more complex decision boundary to capture intricate patterns within the data. For Storage Time, None (allowing nodes to expand until all leaves are pure or **min_samples_split** is met) was found to be optimal. This indicates that full tree complexity was beneficial for this parameter, which already had a high baseline R^2 , and further depth helped refine its predictions for the stepwise data.

- **min_samples_split:** For most parameters (Color, Drip Loss, pH, TPC, Water Moisture), the optimal **min_samples_split** was 2, which is the default in scikit-learn. This suggests that for these parameters, allowing splits with as few as two samples was beneficial for capturing the nuances of the data. However, for Storage Time, a slightly higher value of 5 was optimal. This indicates that for Storage Time, requiring a few more samples to initiate a split helped to refine the tree

structure and perhaps smooth out predictions around the discrete storage time intervals.

- **min_samples_leaf:** Interestingly, for all beef quality parameters, the optimal `min_samples_leaf` was found to be 1. This implies that allowing leaf nodes to contain as few as one sample, coupled with other regularization constraints like `max_depth` and `min_samples_split`, did not lead to overfitting in this specific context and helped capture the most granular patterns in the data. This observation is consistent with the external PDF, which noted that `min_samples_leaf` did not show significant differentiation in the hyperparameter selection process.

- **bootstrap:** Similarly, for all parameters, `False` was identified as the optimal setting for bootstrap. This is a somewhat unusual finding for Random Forest, where `True` is the default and typically expected for ensemble diversity through bagging (sampling with replacement). A `bootstrap=False` setting implies that each tree is built on the entire dataset without resampling. If this is truly the optimal setting consistently across all parameters, it might suggest that for this particular dataset and problem, the inherent variability introduced by bootstrap sampling was detrimental to predictive performance, or that the other regularization parameters (`max_features`, `max_depth`, `min_samples_split`, `min_samples_leaf`) were sufficient to prevent overfitting even without bootstrapping. The external PDF also mentioned bootstrap not affecting the selection process, which supports this finding and warrants further investigation into the specific data characteristics.

These specific optimal parameters underscore that a "one-size-fits-all" approach to hyperparameter settings is generally not optimal. Tailoring the tuning process to individual prediction targets can yield superior results, as different quality attributes may have distinct underlying data patterns and noise characteristics that respond differently to varying model complexities and regularization strategies.

4. DISCUSSION

The empirical findings of this study provide compelling evidence for the critical role of hyperparameter tuning in significantly enhancing the predictive accuracy and robustness of Random Forest Regressor models applied to beef quality assessment. The consistent and substantial improvements observed across all evaluated metrics (R2, MAE, MSE, RMSE) for every beef quality parameter, subsequent to the application of Randomized Search Cross-Validation, strongly validate the necessity of optimizing these model configuration parameters for real-world deployment.

4.1 Significance of Performance Improvements

The baseline performance of the RFR model with default parameters, while generally acceptable, was demonstrably suboptimal across several key beef quality

indicators, particularly for pH and water moisture. The average R2 improvement of 14% and the considerable reductions in MAE, MSE, and RMSE metrics signify that the tuned models are not merely marginally better but represent a fundamental shift towards more accurate and reliable predictions. For instance, the 36% improvement in R2 for water moisture prediction demonstrates how targeted tuning can transform a moderately performing model into a highly effective one, unlocking significant predictive power that would otherwise remain untapped. This resonates with the established understanding in machine learning that while default settings provide a starting point, meticulous optimization is often the key to maximizing a model's potential [20], [21]. In the context of the beef industry, where quality assurance directly impacts consumer trust, market value, and waste reduction, even incremental improvements in predictive accuracy translate into substantial economic and operational benefits. More accurate predictions mean better grading, more effective shelf-life management, and reduced financial losses due to spoilage or quality inconsistencies.

4.2 Interpretation of Optimal Hyperparameter Settings

The varied optimal hyperparameter settings identified for each beef quality parameter (Table 8) offer valuable insights into the underlying data characteristics and the nuances of predicting each attribute.

- **n_estimators:** The observation that TPC required the highest number of trees (2000), while pH was optimized with significantly fewer (400), is particularly insightful. TPC data, often highly skewed and exhibiting exponential growth, presents a more complex regression challenge due to its wide range and potential for high variability. A larger ensemble can better capture this complexity and reduce variance associated with individual tree predictions on such data. Conversely, the more stable nature of pH values might allow for a smaller ensemble to achieve optimal performance, demonstrating computational efficiency when appropriate.

- **max_features:** The preference for 'log2' over 'sqrt' for parameters like Color, pH, Storage Time, and Water Moisture implies that restricting the number of features considered at each split to a smaller subset (logarithm base 2 of total features) facilitated greater diversity among the individual trees. This could be particularly beneficial if many spectroscopic features are highly correlated, and limiting their consideration at each split helps prevent individual trees from becoming too similar. For Drip Loss and TPC, 'sqrt' was preferred, suggesting that a slightly broader subset of features was more effective in capturing their predictive signals. This variation highlights the importance of exploring different feature sampling strategies based on the specific target variable and the nature of the input features.

- **max_depth:** The differing optimal `max_depth` values (e.g., 30 for pH and Drip Loss, 80 for Color and TPC,

and None for Storage Time) reflect the varied levels of complexity required to model each attribute. Shallower trees (smaller `max_depth`) serve as a strong regularization technique, reducing the risk of overfitting by creating simpler decision boundaries. This is beneficial for attributes where the relationship is relatively straightforward. Conversely, deeper trees (larger `max_depth` or None) allow the model to learn more intricate and hierarchical patterns, which seems necessary for complex attributes like TPC or those with stepwise changes like Storage Time. The optimal `max_depth=None` for storage time indicates that the RFR could benefit from growing trees to their fullest extent, allowing the model to capture the precise thresholds and plateaus inherent in the data's ladder-like structure.

- `min_samples_split` and `min_samples_leaf`: The consistent optimal `min_samples_leaf=1` across all parameters is noteworthy. This suggests that, in combination with the other optimized hyperparameters (especially `max_depth` and `max_features`), allowing single-sample leaf nodes did not lead to overfitting but rather enabled the trees to capture fine-grained patterns without memorizing noise. Similarly, `min_samples_split=2` for most parameters indicates that minimal splitting requirements were generally optimal. The slight deviation for Storage Time (`min_samples_split=5`) might imply that for this specific parameter, requiring slightly more samples before a split improved the robustness of the decision points. The consistent optimal values for these parameters, as also implicitly noted in the original PDF, suggest their influence might be more consistent or less sensitive to specific target variables within this context compared to `n_estimators` or `max_features`.

The finding that `bootstrap=False` was consistently optimal is particularly interesting and deviates from the common intuition for Random Forest, where bootstrapping (`bootstrap=True`) is fundamental to generating diverse trees and reducing variance [15]. When `bootstrap=False`, each tree is trained on the entire training dataset without replacement. If this consistently leads to better performance, it might indicate a specific characteristic of the dataset itself—perhaps the dataset is relatively small, or the inherent noise is low, such that introducing further randomness via bootstrapping is counterproductive. Alternatively, the regularization provided by `max_features` and `max_depth` might be sufficient to prevent overfitting, even with trees trained on the full dataset, implying that ensemble diversity is sufficiently achieved through feature subsampling alone. This warrants further investigation in future studies, potentially involving larger datasets or analyzing the impact of bootstrap in isolation.

4.3 Practical Implications and Industrial Relevance

The successful application of hyperparameter-tuned Random Forest Regressors for beef quality prediction holds significant practical implications for the meat

processing industry.

- **Enhanced Quality Control:** More accurate prediction models enable precise, real-time assessment of beef quality attributes on processing lines. This can facilitate immediate sorting and grading of meat, ensuring that products meet specific quality standards before reaching the consumer.

- **Reduced Waste and Economic Benefits:** By accurately predicting shelf-life indicators like storage time and TPC, the industry can optimize inventory management, reduce spoilage, and minimize economic losses associated with degraded products. Furthermore, predicting attributes like drip loss and color can help in reducing product downgrade and maintaining visual appeal, which is crucial for marketability.

- **Improved Consumer Satisfaction:** Consistent high-quality beef leads to greater consumer trust and satisfaction, fostering brand loyalty and driving demand. Non-destructive methods make it feasible to assess every cut of meat, rather than just a sample, leading to more uniform quality.

- **Efficiency and Cost-Effectiveness:** Compared to traditional laboratory methods, spectroscopic techniques coupled with optimized machine learning models are fast, non-invasive, and can be automated, significantly reducing labor costs and analytical turnaround times. The ability to reuse samples for further processing after assessment adds another layer of efficiency.

- **Data-Driven Decision Making:** The predictive models provide actionable insights, enabling producers and processors to make informed decisions regarding handling, storage, and distribution strategies. This moves the industry towards a more data-driven approach to quality management.

4.4 Limitations and Future Directions

While this study robustly demonstrates the benefits of hyperparameter tuning, it is important to acknowledge certain limitations and outline avenues for future research.

- **Dataset Specificity:** The specific optimal hyperparameters and the magnitude of performance improvement are inherently dependent on the characteristics of the dataset used. A different dataset, perhaps from a different beef cut, breed, feeding regimen, or acquired with different spectroscopic instruments or conditions, would likely necessitate re-tuning and might yield different optimal parameters. Future work should validate these findings on larger, more diverse, and multi-source datasets to ensure broader applicability.

- **Computational Cost:** Although Randomized Search Cross-Validation is more efficient than exhaustive Grid Search, hyperparameter tuning can still be computationally intensive, especially with very large datasets or extremely wide parameter search ranges. As

model complexity grows, alternative and more advanced optimization techniques, such as Bayesian Optimization or evolutionary algorithms, which intelligently navigate the search space, could be explored to find optimal hyperparameters more efficiently [20].

- **Scope of Hyperparameters:** This study focused on the most impactful hyperparameters for Random Forest Regressors. However, other parameters (e.g., `oob_score`, `ccp_alpha` for pruning) could also be considered in a more exhaustive tuning process, although their impact is often less pronounced than those explored. Future research could investigate the combined effect of a broader range of hyperparameters.

- **Data Preprocessing and Feature Engineering:** The quality of predictions is not solely dependent on the machine learning model and its hyperparameters, but also significantly on the quality of input data and feature representation. Future work could explore more advanced preprocessing methods tailored for NIRS data, such as various spectral transformation techniques (e.g., Savitzky-Golay smoothing, multiplicative scatter correction, standard normal variate) or advanced feature engineering strategies. The external PDF explicitly suggests combining hyperparameter tuning with several preprocessing methods, such as feature selection and NIRS data transformation [23]. This sequential application (e.g., feature selection, then data transformation, then hyperparameter tuning) is a promising avenue for further performance enhancement, as each step can contribute synergistically.

- **Alternative Machine Learning Models:** While Random Forest is a powerful and robust algorithm, exploring other ensemble methods (e.g., Gradient Boosting Machines like XGBoost, LightGBM, CatBoost) or deep learning architectures (e.g., Convolutional Neural Networks for spectral data [16]) could potentially yield even higher accuracies for beef quality prediction. A comparative study involving multiple tuned machine learning models would provide a more comprehensive understanding of the state-of-the-art in this field.

- **Real-World Deployment:** Transitioning these models from laboratory environments to industrial settings involves challenges such as sensor robustness, environmental variability, and computational resources for real-time inference. Future research should also focus on developing practical, embedded solutions for on-line beef quality assessment.

- **Multi-objective Optimization:** Instead of optimizing solely for prediction accuracy, future tuning could consider multi-objective optimization, balancing accuracy with model interpretability, computational efficiency, or even ethical considerations related to data usage and privacy.

In summary, while this research provides robust evidence for the benefits of hyperparameter tuning, it also opens several avenues for further exploration,

ultimately aiming to develop even more sophisticated and practically deployable solutions for beef quality assessment.

5. CONCLUSION

This comprehensive study has unequivocally demonstrated the substantial positive impact of systematic hyperparameter tuning on the predictive performance of Random Forest Regressor models for assessing multiple beef quality attributes. By diligently applying Randomized Search Cross-Validation, the models achieved a remarkable average increase of 14% in R^2 values and significant reductions in RMSE and MAE across all parameters, when compared to baseline models utilizing default settings. This highlights a critical insight: simply deploying an off-the-shelf Random Forest model is often insufficient. Instead, a dedicated and iterative effort in hyperparameter optimization is crucial to unlock the full predictive potential of the algorithm, ensuring that the model is optimally adapted to the specific characteristics of the beef quality dataset.

The research provided detailed insights into the nuanced optimal hyperparameter configurations for each individual beef quality parameter, underscoring that a "one-size-fits-all" approach is less effective. Factors such as the number of estimators, the feature subsampling strategy, and the maximum depth of individual trees were found to vary significantly, reflecting the diverse complexities inherent in predicting parameters like color, drip loss, pH, storage time, TPC, and water moisture. Notably, parameters like water moisture, which showed the lowest initial predictive accuracy, experienced the most dramatic improvements post-tuning (a 36% increase in R^2), emphasizing the transformative power of optimization in challenging prediction scenarios.

The findings of this study reinforce the importance of robust machine learning practices in the development of accurate, reliable, and non-destructive beef quality assessment systems. Such systems are pivotal for the modern meat industry, promising enhanced quality control, reduced waste, improved economic efficiency, and ultimately, greater consumer satisfaction. This research serves as a foundational step, advocating for continued exploration into advanced tuning methodologies and their synergistic combination with sophisticated data preprocessing techniques to further refine the next generation of predictive models for food quality and safety. The continuous pursuit of such precision will undoubtedly pave the way for more efficient, sustainable, and consumer-centric practices in the global beef supply chain.

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