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Predicting Cattle Meat Types through Machine Learning Models Trained on Rapid Evaporative Ionization Mass Spectrometry (REIMS) Data

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Abstract

Currently, the meat industry faces several problems, one of them being consumer fraud, which has arised the need to guarantee to the consumer that the product offered for sale is what it says on the label. This leads to the main objective of this study, which was to use data obtained by Rapid Evaporative Ionization Mass Spectrometry (REIMS) analysis for the training of 12 predictive models in three different dimensional reduction methods in order to train these models for the quick and accurate identification of the bovine breed from which the meat is obtained. Steaks from the *Loggisimus dorsi* muscle in the USDA classification as "Prime" from the Angus breed and the Wagyu breed were used. Each method's five best predictive models were selected for analysis and discussion. The best dimensional reduction method was Feature Selection (FS), which showed accuracies ranging from 73.6 to 91.8% in the different predictive models, being the best predictive model SVM Poly, which obtained the highest percentages in the performance metrics in the three dimensional reduction methods. Thus, demonstrating the effectiveness of using REIMS data for predicting the bovine breed from which the *Longissimus dorsi* steaks derive.

Keywords: Dimensional reduction, Feature selection (FS), predictive model, prime, Wagyu.

Resumen

Actualmente, en la industria carnica se enfrentan a diversos problemas, uno de ellos es el fraude al consumidor, por lo que ha surgido la necesidad de poder garantizar al consumidor que el producto puesto en venta es realmente lo que marca en su etiqueta. Lo que conlleva al objetivo principal de este estudio, que fue utilizar datos obtenidos mediante el análisis de Espectrometría de Masas de Ionización Evaporativa Rápida (*REIMS, por sus siglas en inglés),* para el entrenamiento de 12 modelos predictivos, en tres distintos métodos de reducción dimensional, con el fin de poder entrenar estos modelos para la identificación rápida y precisa de la raza bovina que proviene la carne, en este caso en específico se utilizaron cortes del musculo *Loggisimus dorsi* en la clasificación del USDA, como ”Prime”, provenientes de la raza Angus y cortes provenientes de la raza Wagyu. Seleccionando así los cinco mejores modelos predictivos de cada uno de los métodos, para su análisis y discusión. Obteniendo que el mejor método de reducción dimensional fue el de Feature Selection (FS), el cual mostró tener precisiones desde 73.6 hasta 91.8% en los distintos modelos predictivos. Siendo el mejor modelo predictivo SVM Poly, el cual obtuvo los mayores porcentajes en las métricas de rendimiento en los tres métodos de reducción dimensional. Demostrando así la efectividad del uso de datos de REIMS para predicción de la raza bovina a la cual pertenecen los cortes.

Palabras clave: Feature selection (FS), modelos predictivos, prime, reducción dimensional, Wagyu.

Introduction

USDA has different meat grades based on various factors, including quality and yield grade. Categorized by the difference in marbling (content of intramuscular fat), maturity, and the amount of usable meat obtained from a carcass, respectively.

In the same way, depending on cattle type, there can be differences in the marbling of meat. In agreement with different studies, Black Angus cattle have relatively high marbling compared to other continental breeds, the prime grade with high marbling only accounts for a small fraction of Angus carcasses, so there is large room for improvement (Boykin et al., 2017; Liu et al., 2021; Moore et al., 2012). Moreover, Japanese Black cattle, also called Wagyu, which is a genetic resource, was exported to the USA in the 1990s and is now being used to produce Wagyu beef in several countries (Kawaguchi et al., 2018). Wagyu cattle is characterized by the extraordinary capacity for intramuscular adipose tissue accumulation, which improves the texture, juiciness, and tenderness of Wagyu beef (Yamada et al., 2020).

In their study, Radunz et al., 2009 indicated that steaks from Angus and Wagyu had similar ($P > 0.50$) tenderness at aging times of 72 h and 14 d. However, even though there are differences in marbling, it is difficult for consumers to differentiate between the two steaks. For this reason, the industry is looking for ways to identify each of these and avoid fraud.

Meat adulteration is a more common problem than one might think, leading to consumers´ distrust in the food industry. In this context, REIMS can be classified as a rapid screening method which could be employed as a front-line testing method to ensure the quality and authenticity of meat products (Kosek et al., 2019).

Rapid Evaporative Ionization Mass Spectrometry (REIMS) is a relatively new type of ambient mass spectrometry that has demonstrated applications in both human health and food science (Gredell et al., 2019). Initially designed for detecting tumor margins during cancer surgery, now according to studies carried out by Gatmaitan et al. (2021) and He et al. (2021) it has been successfully

used in meat science, since it performs analysis of intact samples and real-time evaluations. More specifically, the technique works by generating mass spectra of the lipids released from the cell wall across one or more mass ranges, generating a metabolic fingerprint (Graeve et al., 2023).

REIMS-based tissue analysis generally takes only a few seconds and can provide histological tissue identification with 90−98% correct classification performance (Balog 2013). Additionally, REIMS has been used to predict beef quality attributes such as carcass type, production background, breed type, and muscle tenderness. Balog et al., 2016; Robson et al., 2022 has shown REIMS itself to be capable of identifying several key features of beef cuts from a single rapid measurement, it has been demonstrated that the type of cut can be reliably determined with an accuracy greater than 98%, whilst the production system can be determined with an accuracy of around 85%, despite different breeds of cattle being used to develop the models, an approach taken to ensure the models were representative of commercial beef production.

To utilize molecular profiles generated by REIMS or any of the ambient ionization techniques as a means to classify samples, one must employ machine learning algorithms to generate a predictive model (Gredell et al., 2019). Machine learning (ML) is a subset of artificial intelligence consisting of learning from data. Training these algorithms allows the characterization of patterns in complex data, enabling them to identify and make predictions based on the provided information. ML has different types of algorithms and is differentiated by the mathematical approaches, for example, linear regression, support vector machines (SVM), network analysis, and decision tree learning, for each one expected variation in the predictions, and that one of them is typically better than the others. Recent advances in machine learning techniques have provided an opportunity to develop an objective and automated approach for meat quality assessment (Buddiga, 2023; Penning et al., 2020).

Therefore, this study aims to predict cattle meat types through machine learning models Trained on Rapid Evaporative Ionization Mass Spectrometry (REIMS) data. Secondly, preprocess and analyze the REIMS data of various cattle meat samples using three data reduction methods using

machine learning. Lastly, train machine learning models using the preprocessed REIMS data to predict cattle meat types (Angus and Wagyu) and evaluate the performance of the trained models through metrics such as accuracy, specificity, sensitivity, recall, and F1 score.

Materials and Methods

Estudy Location

The research and data analysis were carried on at Texas Tech University (TTU), Lubbock, United States of America. The REIMS (Rapid Evaporative Ionization Mass Spectrometry) was made at the TTU REIMS Laboratory in the Animal and Food Science (AFS) Building. The preparation of the cooked steaks was carried out at TTU Kitchen.

Materials

Longissimus dorsi muscle was the raw material used, collected from 2 carcass types [Prime (n=40) and Wagyu (n=80)] shown in Appendix A. The carcass-type specifications were verified by the company that provided them. For each *longissimus dorsi* muscle was fabricated into one 2 cm steak. Moreover, liquid nitrogen, compressed nitrogen, LeuEnk, sodium formate, Whirl pack bags, scalpels disposable #11, and cool box were acquired from AFS Laboratories of TTU. As well as a spatula, trays, knife, and strainer from the TTU Kitchen. In addition, the equipment used during the research is shown in Table 1.

Table 1

Equipment used

Equipment	Brand
Rapid Evaporative Ionization Mass Spectrometry (REIMS)	Waters, SYNAPT G2-Si MS
Electrosurgical pencil (iKnife)	Erbe Medical
Steam convection oven	Rational, SCC WE 61 E
Thermometer	Cooper-Atkins Corporation, AccuTuff 340
Electrosurgical system	Erbe Elektromedizin GmbH, VI0 50C
Electronic scale	Adam Equipment, AE CQT1501
Computer	ThinkVision

Sample Preparation

The individual steaks were frozen in a cold room (-20 °C) to preserve them before they were cooked for testing, 24 - 48 hours before the frozen steaks were thawed at 2 - 4 °C. The steaks were grouped into groups of four in relation to weight and size.

Steaks cooked in the combi-oven model SCC WE 61 E (Rational, Landerberg am Lech, Germany) at a peak internal temperature of 70 °C. They were monitored throughout the process using a built-in probe in the oven, placed in the center of a representative sample, the thinner steak, and double-checked with calibrated thermocouple thermometer (AccuTuff 340, model 34040, Cooper-Atkins Corporation, Middlefield, CT, USA) in each one. Once removed from the oven and placed in a plastic tray to sidestep over-cooking in the hot grilled, was recorded the final peak temperature for each steak using calibrated thermocouple thermometer (AccuTuff 340, model 34040, Cooper-Atkins Corporation, Middlefield, CT, USA).

Were allowed to cool in the plastic trays a then cut into squares of approximately 9.5 x 9.5 cm. Using a strainer, were placed the samples in liquid nitrogen to freeze them, put the pieces in a 9.5 x 18 cm whirl pack bags, closed it, and preserved them in a freezer at -80 °C. As shown in Appendix B.

REIMS

Using 120 samples (80 Wagyu, 40 Prime), 16 - 24 h before doing the analysis, took out of the freezer the samples and put them in a cold room at refrigerator condition (2 - 4 °C). REIMS analysis of tissue specimens was performed by electrosurgical evaporation and online mass spectrometric analysis of the aerosol produced (Balog et al., 2016). Samples were analyzed using SYNAPT G2-Si MS. They come equipped with a monopolar handpiece electrosurgical pencil (iKnife) for burns/steam, connected to an electrosurgical generator providing power-controlled 50/60 Hz alternating current. The generator was used in “auto cut” mode at 50 W power setting. Under the samples was placed a rubber mat to facilitate the flow of electric current. During sampling, a continual flow (100 µL/min) of 1ng/mL leucine enkephalin (LeuEnk) was introduced directly to the REIMS source for an internal standard. For each sample, a minimum of three “burns”, in squares of approximately 9.5 x 9.5 cm, were performed in the center of the steak for approximately 1 s. Mass spectra were acquired in negative ion mode at a 0.5 m/z scan per second in a 50 – 1,500 m/z range. The calibration was

performed at the beginning of each day using a 0.5M sodium formate solution. All the steaks were analyzed in two days in a random order.

REIMS data pre-processing

Mass spectra data were imported to preprocessing in the Abstract Model builder (AMX) [Beta] version 1.0.1581.0 software (Waters Corporation, Budapest, Hungary). There was used for lock mass correction (leucine-enkephalin, 556.28 m/z standard) and background noise subtraction. Therefore, from the burns, select the highest peak for each sample. Raw data are binning at intervals of 0.5 m/z from 50 to 1,500 m/z, creating 2,900 m/z variables. For the potential effects of LeuEnk in the spectra, remove the bins. Finally, a single representative value was exported.

Dimension reduction and predictive models

The data reduction and predictive models were executed within the R statistical software (version 4.2.3, R Foundation, 2023), with a total of 2 classification categories: Angus in the quality grade of Prime, and Wagyu.

Once the data was pre-processed and reduced, cross-validations must be performed to determine the accuracy of ML models during the training data. X-fold cross-validation refers to the removal of a random (100/X) % of the total data set to use as a validation set. The remaining (100-(100/X)) % of the dataset is used as the training set which is used to create the models. This procedure is repeated X times, and the maximum accuracy is reported (Sarchet, 2022).

For this study, selected 80% randomly the data to train the models, and the 20% remaining set to test the prediction accuracy. Splitting of the data was performed separately for each model so that each classification category could be evenly distributed between training and testing sets (Gredell, 2018). Resulting in a distribution shown in Table 2. Based on this, eight samples were used for the prime category and sixteen for the Wagyu category for the testing.

Table 2

Datasets split in porcentage and amount.

Dataset	Training	Testing
% of dataset	80%	20%
Amount	96	24

The dimensionality reduction protocols were described by Gredell et al. (2019). Consequently, the preprocessed REIMS data created reduced data sets for feature selection (FS), principal component analysis (PCA), and principal component analysis feature selection (PCA-FS). The dimensionality reduction methods, the function, and the package in R software used are shown in Table 3.

Feature selection (FS) was preprocessed using a high correlative variable (>0.75), finding the high correlations between data points using the *findcorrelation()* function of the "caret" package values great than 0.75 were removed as they were considered highly correlated. FS is accomplished with the recursive feature elimination function in the caret package (Kuhn, 2023). The principal component analysis feature selection (PCA-FS) was also created using the recursive feature elimination (*rfe*) function on the created PCA dataset. To perform PCA, we use the PCA function from the FactoMineR package (Josse, 2017). Therefore, the recursive feature elimination (*rfe*) function parameter was validated with a five-fold cross-validation for the FS and PCA-FS methods.

Predictive modeling uses 12 machine learning techniques in conjunction with the three dimensionally reduced datasets, creating 12 models for each technic. The modeling techniques, the function, and the package in R software used are shown in Table 4. All models were trained using 10-fold cross-validation, and the top accuracy model (from each combination of data set and modeling technique) was selected as the final model (Sarchet, 2022).

Table 3

Modeling technics classifications with their funtion and package in R statistical software.

Algorithm	Function in R	R Package
Dimensionality reduction methods		
Feature Selection	rfFunc, rfe	Caret
Principal component analysis	PCA	FactoMineR
Principal component analysis- Feature Selection	PCA, rfe	Caret, FactoMineR
Modeling methods		
Bagged classification tree (Tree bag)	treebag	ipred, plyr, e1071
Boosted logistic regression (LogitBoost)	LogitBoost	caTools
Extreme gradient boosting (XGboost)	xgbTree	xgboost, plyr
K-nearest neighbors (Knn)	knn	class
Lasso and elastic-net regularized generalized linear model (GLMnet)	glmnet	glmnet, Matrix
Penalized discriminant analysis (PDA)	pda	mda
Random forest (RF)	rf	randomForest
Recursive partitioning tree (Rpart)	rpart	rpart
Stochastic gradient boosting (GBM)	gbm	gbm, plyr
Support vector machine: linear kernel (SVM linear)	svmLinear	kernlab
Support vector machine: polynomial kernel (SVM poly)	svmPoly	kernlab
Support vector machine: radial kernel (SVM)	svmRadial	kernlab

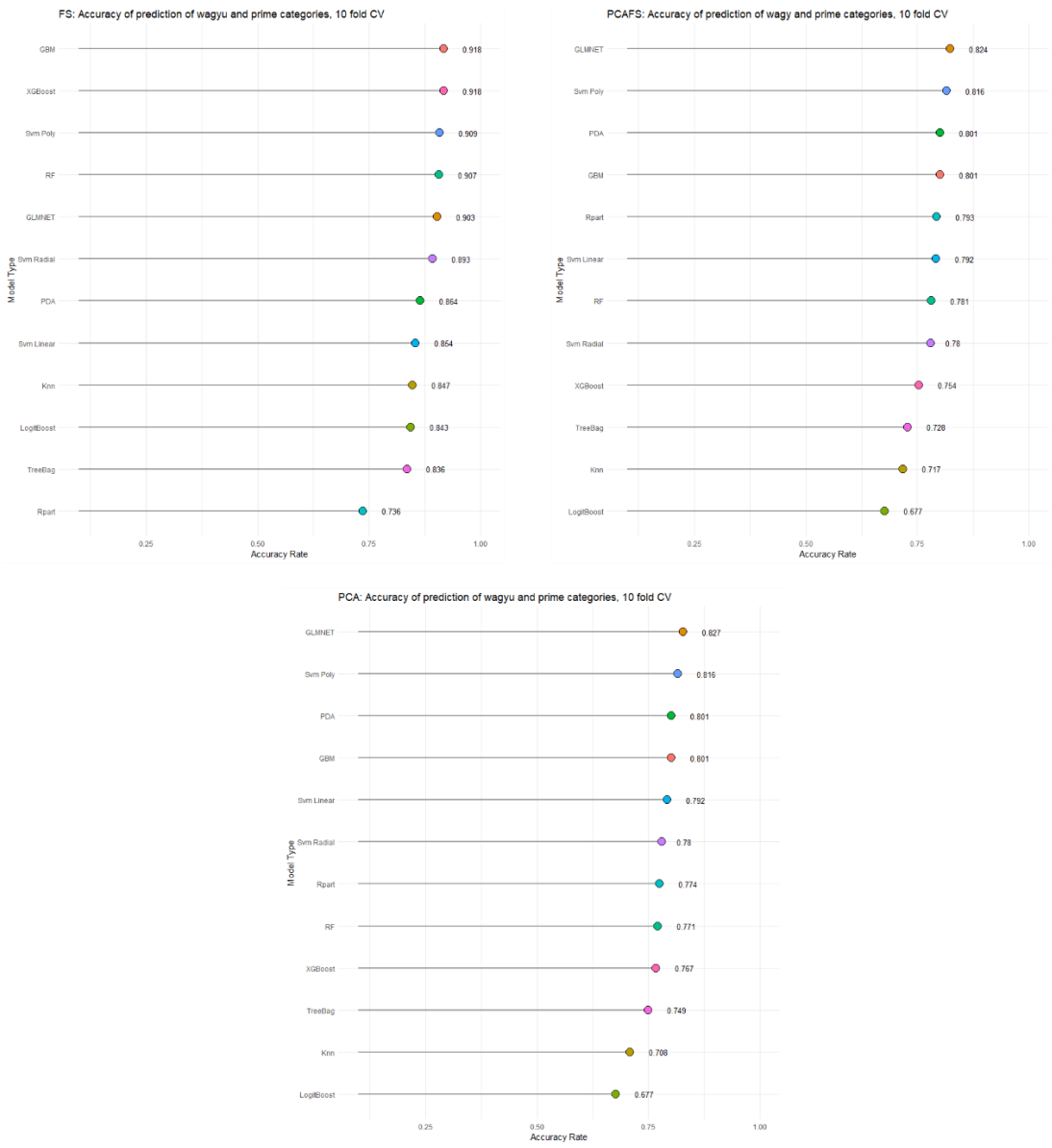
Results y Discussion

Figure 1 demonstrates the effectiveness application of the FS, PCA-FS, and PCA methods with 10-fold cross-validation in the different models for predicting cattle types. That resulted in an accuracy range of 0.736 (73.6%) to 0.918 (91.8%), 0.677 (67.7%) to 0.824 (82.4%), and 0.677 (67.7%) to 0.827 (82.7%), respectively. Gredell et al., 2019 mention that several machine learning algorithms evaluated their study predicted Angus breed type with greater than 80% accuracy, and successful prediction of Grass-fed, Wagyu, and Dark Cutter carcasses with considerable accuracy, which agrees with the data obtained in this study.

The notion of "best" is relative to the problem you are trying to solve, but typically means highest accuracy (Brownlee, 2014). Therefore, it can be said that the FS method was better compared to the others since it had a higher range of accuracy in its models. This is due to the fact that at the time of its prediction is primarily focused on removing non-informative or redundant predictors from the model (Kuhn & Johnson, 2013), which leads to a better selection of data, reducing the chance of making incorrect decisions, which means higher accuracy, and at the time of training the models, since there is less data, the training time is reduced. On the other hand, principal component analysis (PCA) is a technique used to reduce the dimensionality of a dataset while preserving maximum variation. It transforms the original variables into a new set of linearly uncorrelated variables called principal components (avcontentteam, 2016). This generates assumptions about normality and linearity of the variables, leading to the possibility of loss of information. Finally, PCA-FS is based on reducing the data into components, then performing FS on components to reduce redundancy in the data matrix (Nollet, 2020). This method, however, goes through a double selection of data, using the two methods described above, which may lead to leaving out some important components, thus reducing its level of accuracy. Consequently, the top five predictive models for each dimensional reduction method were selected for further analysis.

Figure 1

Accuracy of the 12 predictive models based on 10-fold cross-validation for each dimensional reduction method (FS, PCA-FS, PCA).



According to the data obtained in Figure 1 for the different models, the best ones predictive models' was obtained a highest accuracy were: gradient boosting machine (GBM), extreme gradient boosting (XGboost), support vector machine: polynomial kernel (SVM poly), random forest (RF),

generalized linear model with net elastic penalty (GLMnet), support vector machine: linear kernel (SVM linear), penalized discriminant analysis (PDA), recursive partitioning decision trees (Rpart).

Gradient Boosting Machine (GBM)

Gradient boosting refers to a class of ensemble machine learning algorithms that can be used for classification or regression predictive modeling problems. Ensembles are constructed from decision tree models. Trees are added one at a time to the ensemble and fit to correct the prediction errors made by prior models. This is a type of ensemble machine learning model referred to as boosting. Models are fit using any arbitrary differentiable loss function and gradient descent optimization algorithm (Brownlee, 2020). Therefore, this model referrers to as algorithm can automatically select relevant variables, fit accurate models, and identify and model parameter interactions (Zhang & Haghani, 2015).

Extreme Gradient Boosting (XGboost)

XGBoost model, defined as a new tree-based algorithm that has been increasing in popularity for data classification recently that has been proven to be a highly effective method for data classification (Parashar et al., 2020). This algorithm was designed for large datasets. The system´s success was also witnessed in KDDCup 2015, where XGBoost was used by every winning team in the top 10 (Chen & Guestrin, 2016).

Random Forest (RF)

RF is an iterative process where each step gives rise to a new description of the original data set. The two most similar features are replaced by a new one whose values are computed as the average of them (Del Coz et al., 2004). The RF algorithms can increase model performance compared to other classification tree methods by decorrelating the trees (Engelhardt et al., 2014).

Generalized Linear Model with Net Elastic Penalty (GLMnet)

Glmnet is a package that fits generalized linear and similar models via penalized maximum likelihood. The regularization path is computed for the lasso or elastic net penalty at a grid of values (on the log scale) for the regularization parameters. On the other hand, this model is sensitive to missing values; therefore, any sample with missing values is removed (Mahmoudian et al. 2021).

Support Vector Machine: Linear Kernel (SVM Linear) and Polynomial Kernel (SVM Poly)

SVM utilizes different kernel functions such as the radial base function (RBF) or polynomial kernel and, when used for minimal training sets, has good classification performance (Sun et al., 2018). SVM linear is used for linear data, which means the dataset can be classified into two classifications, using a straight line, calling linearly separable data, and the Linear SVM classifier. Creating a better line or decision. The common functions are polynomial, linear, and radial.

Penalized Discriminant Analysis (PDA)

The PDA algorithm uses nonlinear spline basis functions and includes a penalty term that adds smoothness to the coefficients of the model to reduce the problem of multi-collinearity in the predictors. Therefore, this penalized algorithm typically performs well when there are many highly correlated variables (Gredell et al., 2019).

Recursive Partitioning Decision Trees (Rpart).

This machine learning algorithm was selected and used in the classification of research papers due to its shortest running time to classify the datasets (Benard Magara et al., 2018). In R, this package applies the tree-based model for regression and classification problems.

Performance Metrics

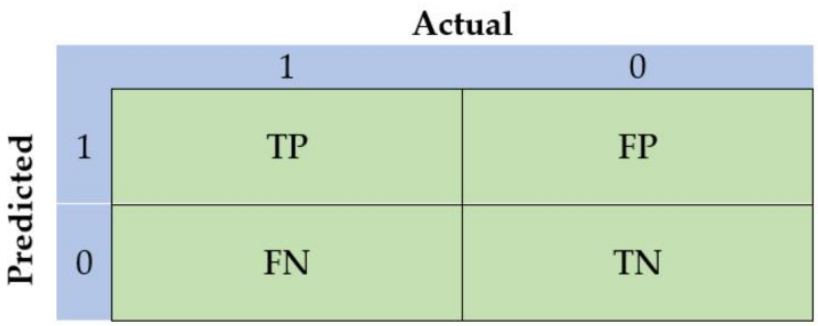
These metrics provide a standard measure to evaluate the algorithms. They influence several characteristics, like the algorithm's performance or weighting. For this reason, it is important the selection of the appropriate metrics.

The confusion matrix is one of the most relevant metrics for finding the correctness of a model. According to Benos et al., 2021 in a simplified case, the confusion matrix is a 2 × 2 table having two dimensions, namely "Actual" and "Predicted", while its dimensions have the outcome of the comparison between the predictions with the actual class label. Following this model represented in Figure 2, and considering the number of variables to be predicted, they were assigned a binary code of positive and negative, where the "prime" variable was assigned as positive and, therefore, "Wagyu" was assigned as negative, following the principle shown in Figure 2. Based on this, data were collected on the number of successes for each algorithm in the three methods of dimensional reduction (FS, PCA-FS, PCA) was described in appendix C, D, and E.

The values were assigned according to our categories, being 1 in the "prime" category and, consequently, 0 in the "Wagyu" category, where our model classifies as true positive (TP) the prime sample (1) that is classified as prime (1), true negative (TN) as the Wagyu sample (0) that was classified as Wagyu (0), false positive (FP) the Wagyu sample (0) that was classified as prime (1), and false negative (FN) the prime sample (1) that was classified as Wagyu (0).

Figure 2

Representative illustration of a simplified confusion matrix described by Benos et al., 2021



Other significant performance metrics are precision, sensitivity or recall, specificity, and F1 score. Where precision is defined as the ability of the model to identify positive instances correctly. The sensitivity or recall is defined as the model's ability to capture all positive instances. The specificity evaluates the performance of a predictive model or classifier in detecting the negative class or true negatives. The F1 score (also known as F-score or F-measure) is a combination of precision and recall in a single measure, which makes it especially useful when there is an imbalance between classes in the dataset. We used what Leila Ismail et al., 2021 proposed in the previous literature works for these metrics, as shown in Table 4. According to these metrics, calculations were performed for the five best algorithms in the three methods of dimensional reduction. These described below:

Table 4

Formulas used for measuring performance metrics

Name	Formula
Accuracy	(TP + TN)/ (TP + FP + FN + TN)
Recall	TP/ (TP + FN)
Precision	TP/ (TP + FP)
Specificity	TN/ (TN + FP)
F1 score	(2 × Recall × Precision)/ (Recall + Precision)

Feature Selection

Table 5 shows the different metrics for each of the algorithms for feature selection (FS) method. Based on the data obtained, all five algorithms showed a value of 87.5%, so it can be concluded that they were equally precise and sensitive in predicting prime grading. However, they were better at predicting Wagyu classification since three (SVM Poly, RF, GLMNET) obtained 100% specificity. Similarly, those mentioned above were the ones that brought a value of 93.3% in the F1 score, which means that these three models show a better balance between both categories, so they perform more correct classifications.

Table 5

Measuring performance metrics for each feature selection (FS) method algorithm

	GBM	XGBoost	SVM Poly	RF	GLMNET
Sensitivity	87.5%	87.5%	87.5%	87.5%	87.5%
Specificity	93.8%	93.8%	100.0%	100.0%	100.0%
Precision	87.5%	87.5%	100.0%	100.0%	100.0%
Recall	87.5%	87.5%	87.5%	87.5%	87.5%
F1 Score	87.5%	87.5%	93.3%	93.3%	93.3%

Principal component analysis-feature selection (PCA-FS)

Table 6 shows the different metrics for each of the principal component analysis-feature selection (PCA-FS) Method algorithms. This table shows that the SVM Poly algorithm had the highest values in all the performance metrics, having a specificity of 81.3%, the highest value represented in the whole table. As for the F1 score, it also said that it was the one that presented the best classification of the categories, obtaining a value of 53.3%. On the other hand, it also observed that the Rpart was the lowest value, having a value of 15.4% in its F1 score, which means that it had a low precision and sensitivity during prediction of the sensitivity categories, being the highest value represented in the whole table.

Table 6

Measuring performance metrics for each principal component analysis- feature selection (PCA-FS) method algorithm

	GLMNET	SVM Poly	PDA	GBM	Rpart
Sensitivity	37.5%	50.0%	37.5%	37.5%	12.5%
Specificity	75.0%	81.3%	75.0%	68.8%	75.0%
Precision	42.9%	57.1%	42.9%	37.5%	20.0%
Recall	37.5%	50.0%	37.5%	37.5%	12.5%
F1 Score	40.0%	53.3%	40.0%	37.5%	15.4%

Principal component analysis (PCA)

Table 7 shows the different metrics for each Principal component (PCA) method algorithm. In this method was obtained the exact values are shown in Table 6. The only difference is that the Rpart

algorithm was substituted by the SVM linear algorithm in this model. However, SVM Poly still has the highest percentage in each metric.

Table 7

Measuring performance metrics for each principal component analysis (PCA) method algorithm

	GLMNET	SVM Poly	PDA	GBM	SVM Linear
Sensitivity	37.5%	50.0%	37.5%	37.5%	50.0%
Specificity	75.0%	81.3%	75.0%	68.8%	62.5%
Precision	42.9%	57.1%	42.9%	37.5%	40.0%
Recall	37.5%	50.0%	37.5%	37.5%	50.0%
F1 Score	40.0%	53.3%	40.0%	37.5%	44.4%

The data obtained in the tables described above indicate that the best algorithm was the SVM Poly since, in the three methods of dimensional reduction, it obtained the best percentages in the measuring performance metrics. Similar results were obtained by when using REIMS data to train a model for classification of meat tenderness SVM yielded the highest predictive accuracy (90.8% based on 100-fold cross validation) (Ross et al., 2021). This coincides with the data obtained in this experiment since a prime steak differs from a Wagyu steak because of its tenderness, which indicates that this model has the expected replicability. The SVM Poly best fits the data because the algorithm creates an optimal line or decision boundary that can dimensionally space into categories, placing the new data set into the correct category in the future. Vasconcelos et al., 2023 mentioned that selecting the appropriate kernel function depends on the quantitative data, and it requires optimization techniques for the best model selection. They used the first kernel linear function, which gave poor prediction results, therefore, non-linear ones were used. Results similar to those obtained in this study are reflected in Table 7, where SVM Poly obtained better results compared to SVM linear.

The GLMNET algorithm, in the FS method obtained one of the best values, but the following ones had different numbers of correct predictions. This is because each of the models generates its selection of data that it considers correct; as explained above, this model, since it is a fusion of the other two dimensionally reduction methods, tends to leave out much more data, which is reflected in

the measuring performance metrics values obtained. However, this model indicates that the dimensional reduction method will affect the prediction of the algorithms because leaves out more relevant data for the correct selection.

Gredell et al., 2019 demonstrate that integrating machine learning with REIMS data can predict beef quality attributes with considerable accuracy, including quality grade, production background, breed type, and muscle tenderness. Additionally, Balog et al., 2016 and Ross et al., 2021 found that REIMS could also differentiate between beef from different breeds of cattle, including Wagyu beef, and venison with 100% accuracy at the species level and 97% accuracy at the breed level. The present study provides evidence of the effectiveness of using REIMS for cattle type classification based on the data obtained through various dimensional reduction methods and predictive model algorithms. The results showed accuracies of up to 91.8%, indicating the potential applicability of this approach in the industry. By offering a rapid response to classification needs, REIMS has the potential to reduce costs and enhance efficiency in the production chain. These findings underscore the practical value of implementing REIMS as a valuable tool in cattle type classification.

Conclusions

The successful prediction of cattle types was achieved using machine learning models trained with REIMS data, using three data reduction methods and machine learning techniques. Models that, when trained in machine learning with the preprocessed REIMS data, obtained accurate predictions of cattle types.

The performance of the trained models was evaluated using metrics such as accuracy, specificity, sensitivity, recall, and F1 score, providing an accurate assessment of the predictive ability of the models. Furthermore, it demonstrates the algorithms' effectiveness in classifying cattle types from REIMS data.

The results of this study have practical applications for the industry, as they show the potential use of REIMS and machine learning to classify beef types efficiently and accurately.

Recommendations

Explore additional dimensional reduction methods to improve accuracy further and expand the methods available for cattle type identification.

Conduct research using REIMS data, with the difference of using raw steaks, and compare the results.

Conduct further complementary studies to complete the existing research, as currently, limited information is available. Expanding the knowledge through which a more complete understanding of the capabilities and limitations of REIMS in cattle type classification can be obtained.

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Annexes

Annex *A*

Samples of Longissimus dorsi muscle using for the project.

Annex B

Samples of the steaks already cooked and cut, the freezing process of the steaks in liquid nitrogen, and the packaged samples ready to take to the freezer


WHIRL-PAK
WHIRL-PAK
WHIRL-

Annex C

Prediction values for each of the variables in the FS model, for the five best algorithms, with their respective Sensitivity, and Specificity

GBM					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	7	1	8	0.8750	0.9375
Wagyu	1	15	16		
Total correctly predicted			22		

XGBoost					
	Reference				
Prediction	Prime	Wagyu	Total	Sensitivity	Specificity
Prime	7	1	8	0.875	0.9375
Wagyu	1	15	16		
Total correctly predicted			22		

SVM Poly					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	7	0	7	0.8750	1.0000
Wagyu	1	16	17		
Total correctly predicted			23		

RF					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	7	0	7	0.8750	1.0000
Wagyu	1	16	17		
Total correctly predicted			23		

GLMNET					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	7	0	7	0.8750	1.0000
Wagyu	1	16	17		
Total correctly predicted			23		

Annex D

Prediction values for each of the variables in the PCA-FS model, for the five best algorithms, with their respective Specificity, and Sensitivity.

GLMNET					
	Reference				
Prediction	Prime	Wagyu	Total	Sensitivity	Specificity
Prime	3	4	7	0.3750	0.7500
Wagyu	5	12	17		
Total correctly predicted			15		

SVM Poly					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	4	3	7	0.5000	0.8125
Wagyu	4	13	17		
Total correctly predicted			17		

PDA					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	3	4	7	0.3750	0.7500
Wagyu	5	12	17		
Total correctly predicted			15		

GBM					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	3	5	8	0.3750	0.6875
Wagyu	5	11	16		
Total correctly predicted			14		

Rpart					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	1	4	5	0.1250	0.7500
Wagyu	7	12	19		
Total correctly predicted			13		

Annex E

Prediction values for each of the variables in the PCA model, for the five best algorithms, with their respective Specificity, and Sensitivity.

PDA					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	3	4	7	0.3750	0.7500
Wagyu	5	12	17		
Total correctly predicted			15		

GBM					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	3	5	8	0.3750	0.6875
Wagyu	5	11	16		
Total correctly predicted			14		

SVM Poly					
	Reference		Total	Sensitivity	Specificity
Prediction	Prime	Wagyu			
Prime	4	3	7	0.5000	0.8125
Wagyu	4	13	17		
Total correctly predicted			17		

GLMNET					
	Reference				
Prediction	Prime	Wagyu	Total	Sensitivity	Specificity
Prime	3	4	7	0.3750	0.7500
Wagyu	5	12	17		
Total correctly predicted			15		

Svm Linear					
	Reference			Sensitivity	Specificity
Prediction	Prime	Wagyu	Total		
Prime	4	6	10	0.5000	0.6250
Wagyu	4	10	14		
Total correctly predicted			14		