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A METHOD FOR DETECTING THE FRESHNESS OF LAMB BASED ON NEAR-INFRARED SPECTROSCOPY DATA

Ruiqin MA[1], Xinxing LI[1], Norina POPOVICI[2], Gabriela VARIA[3], Carmen Georgeta NICOLAE[4], Liliana Mihaela MOGA[5]

[1]China Agricultural University, Beijing, 100083, P.R. China
[2]"Ovidius" University of Constanta, 1 University Alley, 900001, Constanta, Romania
[3]National University of Political Studies and Public Administration, 30A Expozitiei Blvd, District 1, 012104, Bucharest, Romania
[4]University of Agronomic Sciences and Veterinary Medicine of Bucharest, 59 Marasti Blvd, District 1, 011464, Bucharest, Romania
[5]"Dunarea de Jos" University of Galati, 47 Domneasca Street, 800008, Galati, Romania

Corresponding author email: liliana.moga@gmail.com

Abstract

Mutton is an important part of the national diet, and its quality and safety are directly related to people's health. Therefore, accurate non-destructive testing of mutton freshness can effectively improve the level of food safety and ensure public health. In this paper, fresh lake mutton was taken as the research object, starting from the quality change mechanism of mutton, and the near-infrared spectrum data of fresh mutton was collected by using near-infrared spectrometer. In order to improve the computational efficiency and model performance, a principal component analysis model was established to integrate the NIR spectral data and extract the most important nine principal component features. Then, five near-infrared spectral classification models including logistic regression, SVM, SGD, decision tree and random forest were established to predict volatile basic nitrogen (TVB-N) to detect the freshness of mutton. The freshness prediction of decision tree model and random forest model has high overall prediction accuracy, which is more than 95%. The recognition rates of "Level 1" and "Level 2" samples in the decision tree model are 94.44% and 96.78%, respectively. The recognition rates of the random forest model for the "Level 1" and "Level 2" samples of the prediction set are 100% and 96.88%, respectively. Compared with the decision tree model, the random forest model improves the recognition rate of "Level 1" and "Level 2" by 5.56% and 0.1% respectively. The random forest model shows excellent prediction performance as the best classification model, with an accuracy of 97.96%. In this study, the potential of using NIR spectroscopy and machine learning models to predict TVB-N to assess the freshness of lamb was demonstrated. The theoretical basis of the freshness analysis method of other meat product quality is proved.

Key words*: freshness detection, machine learning, mutton sheep, near infrared spectroscopy, principal component analysis.*

INTRODUCTION

Mutton is one of the main sources of meat for most people and is loved by the public for its unique taste and nutritional health benefits. Fresh lamb has high nutritional value (Zhang et al., 2022), while less fresh lamb has low nutritional value and may have a large number of bacteria multiplying in it, resulting in off-flavors and mold (Wen et al., 2022a; Xu et al., 2022), and consumption of unfresh lamb has adverse effects on health. In recent years, people have started to pay more attention to the safety and quality of meat products (Sun et al., 2021). Therefore, to ensure the taste and safety of lamb meat, it is very important for the mutton industry and the meat industry as a whole to have stable and reliable freshness testing of mutton (Jing-jing et al., 2019; Kari et al., 2021) during transportation and storage.

Mutton of different freshness has a similar appearance and is difficult to distinguish with the naked eye. Therefore, various analytical methods have been used to test the freshness of mutton. The traditional method of mutton freshness evaluation relies mainly on human senses, such as touch and smell. But there are many shortcomings, for example, sensory evaluation is easily influenced by the human factor and psychological state of the evaluator. Physical and chemical testing methods (Fathi et al., 2022; Wen et al., 2022b) have many

disadvantages, such as time-consuming, require professional testing technicians, and difficult to apply in the market. One of the commonly used indicators is total volatile base nitrogen (TVB-N) which refers to animal foods that produce ammonia and alkaline nitrogenous substances such as amines (Koxmak et al., 2019) due to the decomposition of proteins during spoilage by enzymes and bacteria. These substances are volatile, and the higher their content, the more amino acids are destroyed, especially methionine and tyrosine, so the nutritional value is greatly affected. Therefore, the content of total volatile salt nitrogen can be used to determine the freshness of animal food. The detection of TVB-N content is an effective method to evaluate the freshness of mutton, but its chemical determination process is complex and has the disadvantages of being destructive and costly (Li et al., 2019; He et al., 2022). Therefore, an accurate and efficient method for rapid non-destructive testing of mutton freshness is required. In the process of meat spoilage, due to changes in organic components such as proteins, the group multiplicity of related compounds also changes, and a fixed region of the NIR spectrum will appear corresponding to the absorption band, so that the degree of meat spoilage can be reflected by measuring changes in the NIR absorption band. Therefore, we can use the NIR spectroscopy method to detect the degree of meat deterioration. NIR spectroscopy is a simple and fast detection method that does not require tedious processing of the product (Jiang et al., 2021; Arias et al., 2022). The spectral data can be imported into a trained model to quickly obtain the degree of product spoilage, greatly reducing the detection cycle. Common classifiers such as logistic regression, Bayesian classification, random forests, and support vector machines, have been combined with spectral detection techniques to analyse target parameters and expand their applications.

In this study, mutton is used as the main object of study. NIR spectroscopy is used to predict the freshness of mutton. Principal component analysis was used for spectroscopic data feature selection to eliminate abnormal samples. Finally, comparing multiple classification prediction models, a classification model based on the random forest algorithm was constructed to investigate the feasibility of using NIR spectroscopic imaging to assess the freshness of mutton

MATERIALS AND METHODS

Data

Hu sheep is used as the main object of this study. Hu sheep is a unique sheep breed in China, mainly produced in Jiaxing, Zhejiang Province and Taihu Lake area. It has excellent traits such as fast growth, good lactation performance, ideal meat production performance after improvement, and resistance to high temperature and humidity.

Mutton samples were divided into four batches of three groups each. Different batches were stored at different temperatures (0°C, x4°C, 4°C, 8°C, and 20°C) for ten days and the NIR spectra, and TVB-N of the lamb were collected daily. All experimental protocols were approved by the Animal Ethics and Use Committee of China Agricultural University.

- ***Data Acquisition***
  - *Acquisition of NIR spectral data*

NIR absorption spectra are usually caused by the vibration and rotation of molecules, the atoms of the chemical bonds or functional groups of the substances to be measured are in a state of constant vibration or rotation. The absorption frequencies of different chemical bonds or functional groups are different, and they are finally expressed in the infrared spectrum as specific characteristic bands, so that the functional groups and chemical bonds contained in the molecules can be obtained from the near-infrared spectrum. During the spoilage process of mutton, due to the change of organic components such as proteins, the group multiplication frequency of the relevant compounds also changed, so that the near-infrared spectrum will appear in a fixed region corresponding to the absorption band so that the change of the near-infrared absorption band can be measured to reflect the degree of spoilage of mutton.

The NIR spectra were collected with a SpectreStar XT2600 NIR spectrometer from UNITY, USA. This NIR spectrometer has a resolution of 1 nm and a scan range of 680-2600 nm. Each sample was collected three times consecutively to obtain three NIR

spectra, and the three spectra were averaged to obtain the NIR spectral data of the samples.

- *TVB-N measurement*

The method for the detection of TVB-N was based on 95/149/EC, using a FOSS 8400 automatic Kjeldahl nitrogen determination instrument. The steps were as follows:

The lamb sample was weighed 10.00 g, stirred and packed into a 50 ml centrifuge tube, then fixed to 40 ml with 0.6 mol/L perchloric acid solution and centrifuged for 10 min at 4000 rpm in a centrifuge to obtain the supernatant. 20 ml of supernatant was separated and added to the digestion tube of the Kjeldahl apparatus. The filtrate was mixed with 40% NaOH solution and distilled in the digestion tube, and the distilled ammonia was introduced into the titration cylinder to react with the standard acid. A 4% boric acid solution was used as the absorbent solution to absorb the distilled ammonia, and the ammonia in the absorbent solution was titrated using a standard acid, which in this study was a 0.1 mol/L hydrochloric acid solution. A color mixture indicator was added to the boric acid solution, and the color indicator was prepared by dissolving 0.1 g of methyl red and 0.1 g of bromocresol green in 95% C_2H_5OH. The color in the titration cylinder does not change after the reaction reaches the endpoint.

The operating conditions of the apparatus were set as follows: the amount of boric acid solution added was 30 mL, the amount of NaOH solution added was 10 ml, the delay mode was 5 S, and the steam distillation running time was 5 min. Finally, the TVB-N content was calculated according to the volume of the consumed standard acid solution. The formula for calculating TVB-N was:

$$x = \frac{(V_1 - V_2) \times c \times 14}{m \times (V/V_0)} \qquad (1)$$

where: x is the content of TVB-N (mg/100 g); V_1 is the volume of hydrochloric acid required for the sample titration (mL); V_2 is the volume of hydrochloric acid required for the blank titration (mL); c is the standard concentration of hydrochloric acid (mol/L); m is the weight of the minced mutton sample; V is the volume of filtrate (V = 10 mL); V_0 is the total volume of the sample liquid.

- ***Data preprocessing***

As high dimensional data can lead to problems such as increased computational complexity, learning difficulties and data sparsity. In this study, principal component analysis is used for feature selection of collected data to improve computational efficiency, remove redundant information, enhance visualization and interpretability, and avoid problems such as dimensionality catastrophe. Principal component analysis is a commonly used statistical method and dimensionality reduction technique. It expresses the most important information in the data by transforming the original data into a new set of variables through linear transformation. Its goal is to find an orthogonal transformation that maps the original data from a high-dimensional space to a low-dimensional space so that the projected data has the maximum variance while retaining as much information as possible. This means that PCA tries to find the most dominant patterns in the data and represent the data with fewer variables.

In PCA, we first need to normalize the raw data to eliminate scale differences between different features. Next, we compute the covariance matrix of the data, which reflects the correlation between individual features in the data. The eigenvectors of the covariance matrix are the principal components of the data, and the corresponding eigenvalues of these eigenvectors represent the variance of the data on each principal component. The eigenvalue decomposition of the covariance matrix is performed to obtain the eigenvalues and the corresponding eigenvectors. Based on the magnitude of the eigenvalues, the eigenvectors corresponding to the top k eigenvalues are selected as principal components. Project the original data onto the selected principal components to obtain the dimensionality reduced data. Usually, we select the eigenvectors corresponding to the first k largest eigenvalues as the principal components of the data. Those principal components are sorted according to the magnitude of the eigenvalues and represent the most important structural information in the data. By selecting fewer principal components, we realize the dimensionality reduction of the data, reduce the number of features, and retain as much information as possible from the original data.

Methods

- ***Principal component analysis***

Principal component analysis (PCA) is a method for analyzing the internal relationship between large samples and multivariate data. Using the idea of dimension reduction, this method converts many linearly dependent indexes into a few linearly independent comprehensive indexes by vector transformation, so as to cut off the related interference, point out the dominant component, and make more accurate estimation.

Before applying PCA, we need to preprocess the data to make sure it has zero mean. This can be done by subtracting the mean of each feature. The preprocessed data helps to calculate the covariance matrix accurately.

The core of PCA is to calculate the covariance matrix of the data. The covariance matrix describes the correlation between the features of the data. For a dataset of n samples with m features, the dimension of the covariance matrix is m × m. The elements of the covariance matrix represent the covariance between the different features.

By performing eigenvalue decomposition on the covariance matrix, the eigenvalues and corresponding eigenvectors can be obtained. The eigenvalues represent the variance of the data in the direction of the eigenvector. The eigenvectors represent the main directions of the data in the new coordinate system.

After that, the principal components are selected. The method of selecting the principal components is based on the ranking of the eigenvalues. The corresponding eigenvectors with larger eigenvalues represent the largest variance contained in the data. Usually, we select the top k eigenvectors with large eigenvalues as principal components.

Dimensionality reduction can be achieved by mapping the data into the new space formed by the principal components. Data projection is performed by dot multiplication of the original data with the selected principal components. The projected data has a lower dimension but still retains the information of the original data as much as possible.

Using PCA can reduce the data dimension and remove redundant information. In addition, the main features of the data are extracted to reduce the cost of data storage and calculation, and to facilitate subsequent data analysis and visualization.

The disadvantage of PCA algorithm is that it is sensitive to outliers, which may have a large impact on the calculation of principal components.

- ***Support Vector Machine***

Support vector machines (SVM) are a set of supervised machine learning methods which is widely used for classification tasks. The hinge loss function is used in support vector machines to compute the empirical risk and add a regularization term to the solution system to optimize the structural risk, which is a classifier with sparsity and robustness.

Based on hyperplane, define the decision function of binary classification:

$$\text{sgn}(\omega^T x + b) = +1, \text{ if } \omega^T x + b \geq 0 \quad (2)$$

$$\text{sgn}(\omega^T x + b) = -1, \text{ if } \omega^T x + b \quad (3)$$

Distance r of feature point x to hyperplane:

$$r = \frac{|\omega^T x + b|}{\|\omega\|} \quad (4)$$

where $\|\omega\|=\sqrt{\omega^T \omega}$.

The mathematical representation of the SVM problem of finding the optimal classification hyperplane is:

$$\max_{(\omega, b)} \frac{2}{\|\omega\|} \quad (5)$$

$$\text{s.t. } y_i(\omega^T x_i + b) \geq 1 \quad (6)$$

- ***Stochastic gradient descent***

Stochastic gradient descent (SGD) is a simple yet very efficient approach to fit linear models. It is a simple yet very efficient approach to fitting linear classifiers and regressors under convex loss functions such as (linear) Support Vector Machines and Logistic Regression. Besides, batch gradient descent uses the entire training set for each learning. The exact same set of samples is used each time, so these calculations are redundant. To overcome the drawbacks of batch gradient descent, the stochastic gradient descent algorithm is used. This way only one sample is randomly selected to participate in the computation each time the coefficients are updated. It can reduce the number of iterations and save computation time, but also prevent memory overflow and

reduce the computation overhead. Therefore, this study uses stochastic gradient descent.
The objective function has the form of a sum:

$$Q(\omega) = \frac{1}{n}\sum_{i=1}^{n} Q_i(\omega) \quad (7)$$

When used to minimize the above function, the standard gradient descent method would perform the following iterations:

$$\omega := \omega - \eta \nabla Q(\omega) = \omega - \frac{\eta}{n}\sum_{i=1}^{n} \nabla Q_i(\omega) \quad (8)$$

where η is a step size.

- ***Decision Tree***

Decision tree is a classification algorithm based on a tree structure to make decisions. It learns a model from a given training data set and uses the model to classify new samples by judging the attributes of the samples (one or more) sequentially from top to bottom to the leaf nodes of the decision tree.
The decision tree can show the process and results of classifycation very intuitively and is more efficient in classifying new samples.
It is a method that uses probabilistic analysis to intuitively determine the feasibility of various situations based on their known probability of occurrence.
The most classical decision tree algorithms are ID3, C4.5, CART. ID3 algorithm can handle classification of discrete attribute samples, C4.5 and CART algorithms can handle more complex classification problems. The concept of entropy is used in the spanning tree algorithms of ID3, C4.5 and C5.0.
There are three bases for the division of decision trees (Table 1).

Table 1. Decision Tree Segmentation Diagram

Name	Branching method	Features
ID3	Information Gain	ID3 can only form decision trees for datasets with discrete attributes. The disadvantage of information gain is that it tends to select attributes with more values and in some cases such attributes may not provide much valuable information.
C4.5	Information Gain Rate	The optimization solves the problem that the ID3 branching process always prefers to bias the attributes with more selection values. The resulting classification rules are easy to understand and have a high accuracy rate. However, the process of constructing the tree requires several sequential scans and sorting of the dataset, leading to inefficiency of the algorithm.
CART	Gini values and Gini index	Can perform classification and regression, can handle discrete attributes as well as continuous attributes.

The calculation formulas for the three characteristics used to classify decision trees are as follows:

- *Information gain*:

$$Ent(D) = -\sum_{k=1}^{n} p_k \log_2^{p_k} \quad (9)$$

Assume that the proportion of the Kth class of samples in the current sample set D is $p_k = 1, 2, \ldots, |y|$, $p_k = \frac{C^k}{D}$ is the number of samples of class K.If a is used to partition the sample set D, V branch nodes are generated, where the Vth branch node contains all samples in D that take value on attribute a^v, denoted as D^v.

$$Gain(D,a) = Ent(D) - Ent(D|a) =$$

$$= Ent(D) - \sum_{v=1}^{V} \frac{D^v}{D} - Ent(D^v) \quad (10)$$

- *Information gain rate*:

$$Gain_{ratio(D,a)} = \frac{Gain(D,a)}{IV(a)} \quad (11)$$

- *Gini value and Gini index*:

$$Gini(D) = \sum_{k=1}^{|y|} \sum_{k' \neq k} p_k p_{k'} = 1 - \sum_{k=1}^{y} p_k^2 \quad (12)$$

$$Gini_{index(D,a)} = \sum_{v=1}^{V} \frac{D^v}{D} Gini(D^v) \quad (13)$$

The advantage of decision trees is that they are relatively small in computation and easily translated into classification rules. By simply following the root of the tree all the way down to the leaves, the splitting conditions along the way are able to uniquely determine a predicate for classification. In addition, it is highly accurate. The accuracy of the mined classification rules is high and easy to understand, and the decision tree can clearly

show which fields are more important. Decision trees are non-parametric learning and do not require setting parameters.

- ***Random Forest***

Random Forest is a machine learning method based on bagging, which is widely used for classification and regression tasks. Its base learner is fixed as a decision tree, and multiple trees make up the forest. The "randomness" lies in the randomness of the selection of the division attributes. The random forest adds sample perturbation by means of put-back sampling when training the base learner. It also introduces an attribute perturbation. In the training process of the base decision tree, when selecting the division attributes, Random Forest first randomly selects a subset containing K attributes from the set of candidate attributes, and then selects the optimal division attributes from this subset. Since each tree selects some samples and some features, overfitting is avoided to some extent. In addition, each tree randomly selects samples and randomly selects features, which makes a good noise immunity and stable performance.

RESULTS AND DISCUSSIONS

Feature wavelength pre-processing

Considering the amount of data obtained for the waveforms is quite large. Each characteristic wavelength in the sample data reflects the key information of the spectrum in different degrees, and there is a certain correlation between the individual indicators, so that in theory the statistical information obtained by the model study will overlap to a considerable extent. In order to effectively achieve classification and improve the efficiency of model calculations, it is necessary to transform the raw data to obtain the features that best reflect the nature of the classification. The study chooses to use the principal component analysis method to reduce the dimensionality of the full-band near-infrared spectral data and combine multiple wavelength indicators into some independent principal component indicators (Table 2). A few representative variables with low mutual correlation coefficients are extracted from numerous variables and indicators by certain methods.

In the total variance explained graph, the total variance explained reflects the contribution rate and cumulative contribution rate of each principal component, the third column indicates the contribution rate and the fourth column indicates the cumulative contribution rate.

Through the Table 2, principal component and eigenvalue analysis table and Figure 1, it is easy to find that the first principal component has the largest contribution of 83.97%, while the second principal component only accounts for 11.93%.

Table 2. Principal Components and Eigenvalue Analysis

Component number	Percentage of variance	Cumulative
PCA1	83.968%	83.968%
PCA2	11.930%	95.898%
PCA3	2.087%	97.985%
PCA4	0.518%	98.503%
PCA5	0.453%	98.956%
PCA6	0.417%	99.373%
PCA7	0.189%	99.562%
PCA8	0.094%	99.656%
PCA9	0.079%	99.735%

The combined contribution of the first three principal components is already close to the overall 97.99%. These three principal components concentrate 97% of the information of 1920 original variables. And the component matrix (factor loading matrix) reflects the correlation of the extracted 9 principal components with the original variables.

Therefore, in this study, it chooses to combine the 1920 indicators responding to the original data into 9 composite indicators as the input of the lamb freshness prediction model by principal component analysis. It effectively reduces the training speed of the model algorithm and speeds up the model construction.

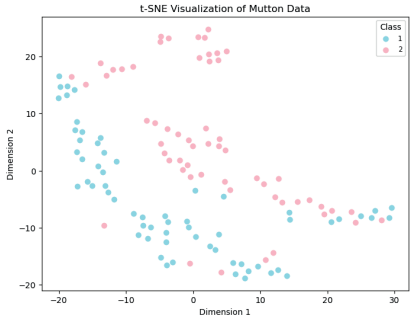

Figure 1. Cumulative Contribution Graph

In a correlation heat map, darker colors represent stronger correlations and lighter colors represent weaker correlations (Figure 2). Therefore, the strength of the correlation between the variables can be visualized by the color shades.

From the above graph, it can be concluded that the elements on the diagonal line are all 1, which is because each variable always has the strongest correlation with itself.

The correlation values between the PCA features (PCA1 to PCA9) are distributed between -0.32 and 0.69.

The correlation between PCA2 and PCA7 is -0.014957, which indicates that they are hardly correlated with each other; while the correlation between PCA2 and PCA8 is 0.036816, which is also a weak positive correlation.

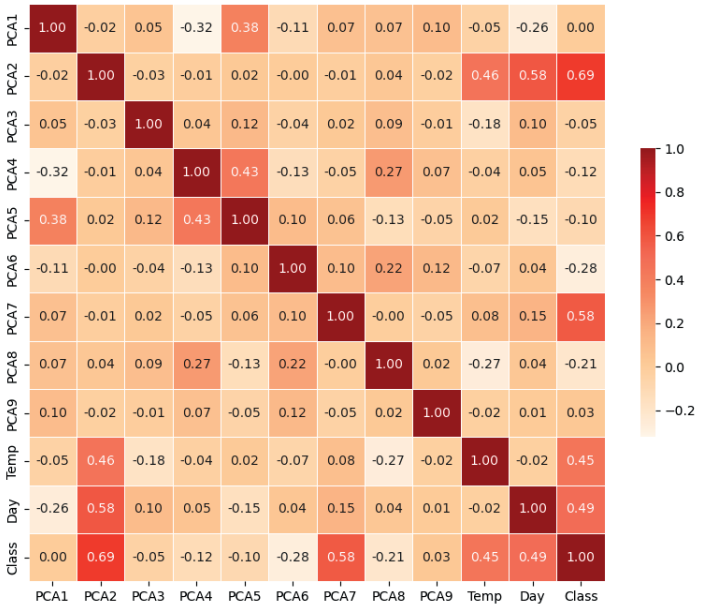

Figure 2. Correlation Heatmap

The correlations between PCA features are both positive and negative, but most of the values are close to 0, indicating that these PCA features are relatively independent from each other. Temp (temperature), on the other hand, has the strongest correlation with PCA2 at 0.457087, showing a positive correlation. This can be obtained that temperature has a strong correlation with the variable or pattern represented by PCA2.Day (number of days) has a stronger correlation with PCA2 and PCA7 at 0.584592 and 0.148191 respectively. This indicates that the number of days is correlated with the variables represented by these two PCA features. The correlation between Temp (temperature) and Day (number of days) is -0.022127 indicating that they are hardly correlated with each other. Class has a strong correlation with all the other variables, especially with PCA2, PCA7 and temperature.

Freshness prediction model implementation

The NIR spectral data of mutton is visualized as shown in Figure 3.

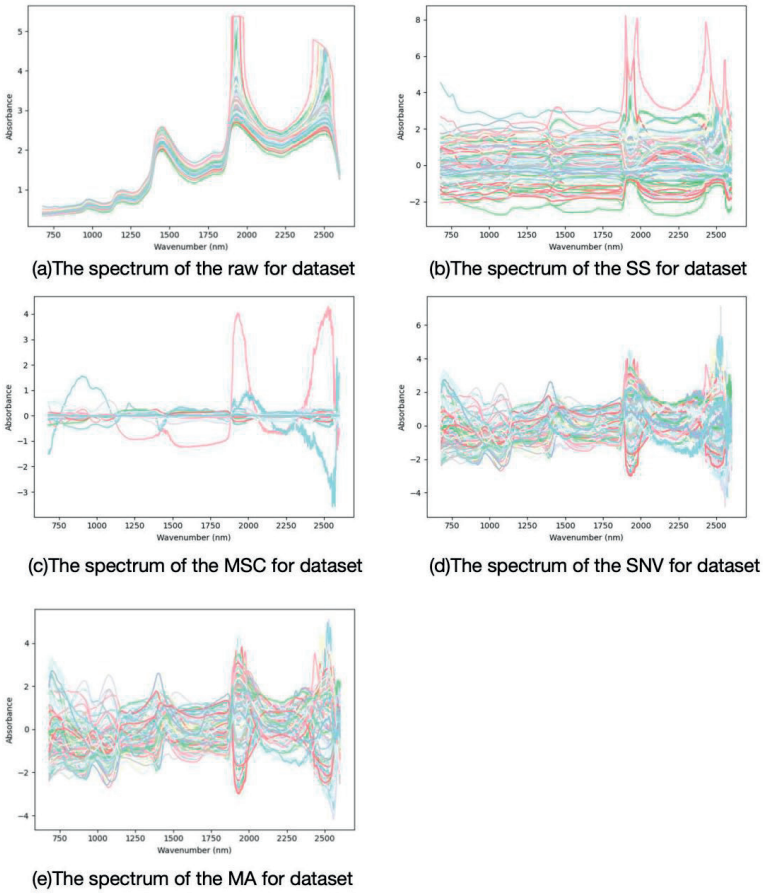

Figure 3. Near-infrared spectrogram

Subsequently, pre-processing such as standardization (Std), Standard Normal Variation (SNV), Moving Average Smoothing (MAS) and Multiple Scattering Correction (MSC) are implemented. The standardization eliminates the spectral intensity variations caused by instrumental, environmental and sample differences, improves data comparability and reduces analytical errors. SNV reduces the nonlinear and non-normal features in the data, enhances the applicability of statistical analysis of the data, and improves the model stability and prediction accuracy. MAS smoothes the spectral curves, reduces the influence of instrumental noise and environmental interference, and enhances the spectral signal-to-noise ratio. Considering the baseline offset and translation phenomena in the measurement, MSC effectively eliminates the scattering effect, enhances the correlation between the spectral absorption information and the sample composition, and further improves the data accuracy. Together, these preprocessing steps optimize the near-infrared spectral data of mutton and lay the foundation for subsequent accurate analysis.

- ***Model parameter input***

The input feature parameters of the model were the most important nine principal components extracted to after principal component analysis as well as the recorded temperature and number of days. The output level variable of the model is the freshness of the meat lamb against the predicted grade. The freshness of lamb was classified by referring to expert experience for different TVB-N. The freshness of meat sheep was classified into two classes corresponding to category labels 1 and 2. The spectral data were

outlier-processed and normalized to obtain 121 sets of valid data samples, where each set contained 11-dimensional feature parameters. Among them, 85 groups were in the training set and 36 groups in the test set.

- ***Model training***
  - *Logistic Regression Model Implementation*

The common parameters in the logistic regression model are random state. It is necessary to set this parameter when each training is the same, and set random state to 0 since the selected training set is the same. Max iter indicates the maximum number of training iterations. And tol (tolerance) denotes the criterion to stop training.

- *SVM Model Implementation*

There are two key parameters that can be set in the support vector machine algorithm model: the loss coefficient c of the model and the kernel function selection coefficient g. This section uses the third-party library scikit-learn to build the model, and uses the automatic parameter tuning method GridSearch to label multiple kernel functions including linear kernel functions, Gaussian kernel functions, polynomial kernel functions, and sigmoid kernel functions, and calls them in turn to find a most suitable model to deal with the problem of predicting the transport stress classification of meat sheep. The loss coefficients c is set to 0.001, 0.01, 0.1, 1, 10, and 100, and the optimal loss coefficients are selected by calling them sequentially.

- *SGD Model Implementation*

Two main parameters are set in the SGD model implementation. Toll parameter indicates the stopping criterion of the iteration. It has a default value of False and is set to 1e-4 in this study. Max iter represents the maximum number of passes in the epoch, and the default is 1000.

- *Decision Tree Model Implementation*

The main parameters of the decision tree are max depth, criterion and splitter. Max depth indicates the maximum depth of the tree, which is set to 5 to 30 in this study. criterion indicates the feature selection method. In this study, Gini and entropy are chosen. splitter indicates the feature division point selection method (best or random). Best is to find the optimal division point among all division points of the feature, and random is to find the locally optimal division point among some randomly selected division points.

- *Random Forest Model Implementation*

The main parameters set in the random forest model are random state and n estimators. Random state is a random seed. When random state takes a certain value, a rule is determined to generate a fixed forest. N estimators indicates the number of trees in the forest. Any model has decision bounds, and after a certain upper limit of n estimators is reached, the accuracy of the random forest tends not to rise or starts to fluctuate. The larger the n estimators, the more computation and memory are required, and the longer the training time will be. This study is set to 100.

- *Model parameter design and training*

In order to test the accuracy of the trained model, 36 sets of data from the test set were used with optimal parameters to test the overall performance of the meat sheep freshness prediction model, respectively. The classification test results of the model will test the test set are shown in Table 3.

Table 3. Comparison table of classification accuracy

Algorithm	Class	Precision (%)	Recall (%)	F1-Score (%)	Total accuracy (%)
Logistic Regression	1	93.33	77.78	84.85	89.80
	2	88.24	96.77	92.31	
SVM	1	80.00	88.89	84.21	87.76
	2	93.10	87.10	90.00	
SGD	1	94.12	88.89	91.93	93.88
	2	93.75	96.77	95.24	
Decision Tree	1	94.44	94.44	94.44	95.92
	2	96.78	96.77	96.77	
Random Forest	1	100.00	94.44	97.14	97.96
	2	96.88	100.00	98.413	

Evaluation of classification results

In order to compare the prediction effect of five models such as logistic regression, SVM, SGD, decision tree, and random forest, the nine extracted principal components, temperature, and number of days were used as input variables, and lamb freshness categories were used as outputs to build a lamb freshness prediction model and validate the prediction effect of the model.

Among them, we found that the accuracy of freshness prediction of both logistic regression model and SVM model was less than 90%. Especially, the SVM model has an identification rate of 80.00% and 93.10% for the prediction set of "level 1" and "level 2" samples, and a recall rate of 88.89% and 87.10%, respectively, resulting in the total accuracy of 87.76%. In addition, Random Forest Model and Decision Tree Model have higher prediction accuracy for the prediction set "Level 1", and the highest accuracy for Random Forest Model is 100%; since the recall rate of Random Forest Model for the prediction set "Level 2" is as high as 100%. Random forest model has the highest prediction accuracy for prediction set "level 2", which is 96.88%.

The freshness prediction statistics of the decision tree model and the random forest model are shown in Table 2, and the total accuracy is high, above 95%. The recognition rate of the decision tree model for the prediction set of "level 1" and "level 2" samples is 94.44% and 96.78% respectively. The recognition rates of the random forest model for the prediction set of "level 1" and "level 2" samples are 100% and 96.88%, respectively. Compared with the decision tree model, the random forest model has improved the recognition rate of predicting "level 1" and "level 2" by 5.56% and 0.1%, respectively. The above study shows that the random forest model is more accurate and stable, and the misclassification is mainly concentrated in the adjacent freshness classes, which may be caused by the TVB-N values of the adjacent freshness samples being closer to each other, and the differences between the classes are smaller.

CONCLUSIONS

Among the methods for testing the freshness of meat products, the traditional methods mainly rely on human senses, such as touch and smell, and the errors of detection are large. Physical and chemical testing methods have many shortcomings such as time-consuming and requiring professional testing technicians, which are difficult to apply in the market. Therefore, the use of NIR spectral data for freshness classification has good application prospects. Mutton is a common meat product in the market which was used as the experimental subject of this study. In this study, a classification model of mutton freshness based on near-infrared spectroscopy was developed with lamb samples. The main conclusions drawn from this study are as follows.

The TVB-N of the samples was detected by Kjeldahl method. After collecting the NIR spectral data of the samples using the NIR spectrometer, the principal component analysis (PCA) was used for feature selection of the NIR spectral data. After selecting the most effective features, multiple models were applied for classification. After comparing the accuracy, precision, recall and F1 score of each model, the random forest model could classify the freshness of lamb more effectively with a total accuracy of 97.96%.

The method proposed in the study provides an easy, fast and effective way to assess the freshness of lamb, and the method should be applicable to other foods. Further research should increase the diversity of samples by obtaining samples from different regions, growth cycles, and species to improve the stability and applicability of this detection method. In addition, a detection system with integrated NIR spectral images should be designed to facilitate its wider application.

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