

Hyperspectral Imaging Combined with a Deep Residual Network for a Precision Nutrition Prediction Model in Commercial Laying Hens

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Abstract: The aim of this study was to develop a precision nutrition prediction model for commercial laying hens based on hyperspectral imaging technology and a deep residual network. Eggs from a large-scale laying hen farm (20,000 birds) were used as research subjects. Hyperspectral image data in the 400–1000 nm range were collected, and the contents of crude protein, crude fat, lecithin, and cholesterol were determined by conventional chemical analysis. An improved deep residual network (ResNet-SP) was proposed for spectral feature extraction and nutritional index prediction, and its performance was compared with partial least squares regression (PLSR), support vector machine (SVM), and the conventional residual network (ResNet50). The results showed that the ResNet-SP model achieved the best prediction performance for the four nutritional indices. For crude protein content, the coefficient of determination for the prediction set (R^2_p) was 0.931, the root mean square error of prediction (RMSEP) was 0.87 g/100 g, and the residual predictive deviation (RPD) was 3.82. This study verifies the feasibility of combining hyperspectral imaging with deep residual networks for non-destructive detection of nutritional quality in eggs, providing technical support for precision nutrition management in large-scale farms.

Keywords: Hyperspectral imaging; Deep residual network; Laying hens; Nutrition prediction; Non-destructive detection

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1. Introduction

Eggs are an important source of high-quality protein for humans, and their nutritional composition is influenced by multiple factors such as feeding management, feed formulation, and genetic strain of the laying hens. In commercial layer farming, precision nutrition management is essential to ensure consistency of egg quality, reduce feed costs, and improve farming efficiency. However, traditional methods for detecting egg nutritional quality rely on chemical analysis, which is destructive, time-consuming, and unsuitable for

large-scale online inspection.

Hyperspectral imaging integrates the advantages of spectroscopy and computer vision, enabling simultaneous acquisition of spatial and spectral information of the object. It has been widely applied in the field of non-destructive quality detection of agricultural products. In recent years, researchers have conducted extensive studies on the use of hyperspectral imaging for egg quality assessment. Lin et al. proposed a residual dense comprehensively regulated convolutional neural network (RDCR-Net) to identify the quality of eggs laid by hens under different feeding conditions, achieving a classification accuracy of 96.29%. Adegbenjo et al. used an adaptive partial least squares regression method to classify the fertilization status of chicken eggs based on hyperspectral imaging, achieving a true positive rate of 100%. Ahmed et al. systematically reviewed recent advances in hyperspectral imaging in the egg industry and pointed out that deep learning methods have broad application prospects for egg quality prediction. Moreover, a recent study by Ahmed et al. used hyperspectral imaging combined with machine learning to predict egg albumen content, and the PLSR model achieved an R^2 of 0.92.

Although existing research has made positive progress in the application of hyperspectral imaging for egg quality detection, some limitations remain: (1) Most studies focus on the discrimination of fertilization status and external quality, with relatively few quantitative predictions of nutritional components; (2) The application of deep learning methods for predicting nutritional indices in eggs is insufficient, and traditional machine learning methods cannot fully exploit the deep features of hyperspectral data; (3) There is a lack of precision nutrition prediction models tailored for large-scale farming scenarios.

To address these gaps, this study proposes a precision nutrition prediction model for laying hens based on hyperspectral imaging and a deep residual network. The main objectives are: (1) to establish a hyperspectral image database of eggs from a commercial laying farm; (2) to design an improved deep residual network model suitable for nutritional index prediction; (3) to validate the model's predictive performance for crude protein, crude fat, lecithin, and cholesterol contents in eggs; (4) to explore the intrinsic correlation between characteristic spectral bands and nutritional indicators.

2. Materials and methods

2.1. Experimental samples

The experimental samples were collected from a commercial laying hen farm in Hebei Province (stocking capacity of 20,000 birds, breed: Hy-Line Brown). Fresh eggs were obtained from hens of the same batch, same age (32 weeks), and in good health. The sampling period was five consecutive days, with 120 eggs collected daily, totaling 600 eggs. After removing cracked, deformed, and surface-soiled eggs, 576 valid samples remained. The samples were randomly divided into a calibration set (432 samples) and a validation set (144 samples) at a ratio of 3:1. All samples were stored at 4 °C after collection and completed hyperspectral image acquisition and chemical analysis within 24 hours^[1-3].

2.2. Hyperspectral image acquisition

A hyperspectral imaging system (GaiaField-V10E, Sichuan Dualix, China) was used for image acquisition. The system consisted of a hyperspectral imager (spectral range 400–1000 nm, spectral resolution 2.8 nm, 256 bands total), a CCD camera (spatial resolution 1392×1040 pixels), a linear light source (tungsten halogen lamp, 150 W), a motorized translation stage, and a computer. Acquisition parameters were set as: exposure time 15 ms, stage speed 2.5 mm/s, working distance 300 mm. Each sample was imaged three times, and the

average value was taken as the spectral data for that sample ^[4].

After black-and-white correction of the original hyperspectral images, the region of interest (ROI) was extracted to obtain the average reflectance spectrum. The ROI was a circular area of 30 mm diameter at the equatorial region of the egg. Savitzky–Golay convolution smoothing (window size 11, polynomial order 3) was used for spectral denoising, followed by standard normal variate (SNV) transformation to correct spectral scattering effects ^[5].

2.3. Chemical analysis

Immediately after hyperspectral image acquisition, the samples were subjected to chemical analysis. Crude protein content was determined by the Kjeldahl method (GB/T 5009.5-2016); crude fat content by Soxhlet extraction (GB/T 5009.6-2016); lecithin content by high-performance liquid chromatography; and cholesterol content by gas chromatography. All chemical analyses were performed in triplicate, and the average value was taken as the final measured value.

2.4. Construction of a deep residual network model

Based on the traditional residual network (ResNet), this study proposes an improved model named ResNet-SP (Spectral Residual Network). The main improvements include: (1) introduction of a spectral attention mechanism to enhance feature extraction capability for important bands; (2) use of one-dimensional convolution kernels to adapt to the one-dimensional structural characteristics of hyperspectral data; (3) addition of a global average pooling layer to reduce model parameters and prevent overfitting ^[6].

The network structure of ResNet-SP is shown in **Table 1**. The input is preprocessed spectral data (dimension: 256×1). After a 7×1 convolutional layer, batch normalization, and ReLU activation, it passes through four residual modules. Each residual module contains two convolutional layers (3×1 convolution kernels) and uses skip connections. The spectral attention module is embedded after the residual modules, generating channel weights through global average pooling, a fully connected layer, and sigmoid activation to achieve feature recalibration. Finally, global average pooling and a fully connected layer output the predicted nutritional index values ^[7].

Table 1. Structural parameters of the ResNet SP network

Network layer	Input size	Output size	Parameter description
Input layer	256×1	256×1	Original spectral data
Conv1	256×1	256×32	7×1 convolution, stride 1, padding 3
BN1	256×32	256×32	Batch normalization
ReLU	256×32	256×32	Activation function
ResBlock1	256×32	256×64	Two 3×1 convolutions, skip connection
ResBlock2	256×64	128×128	Two 3×1 convolutions, stride 2
ResBlock3	128×128	64×256	Two 3×1 convolutions, stride 2
ResBlock4	64×256	32×512	Two 3×1 convolutions, stride 2
Spectral attention module	32×512	32×512	Global pooling + fully connected
Global average pooling	32×512	512	Dimensionality reduction
Fully connected layer	512	4	Output of 4 nutritional indices

Model training used the Adam optimizer with an initial learning rate of 0.001, batch size of 32, and

a maximum of 200 epochs. Early stopping was applied to prevent overfitting, stopping training when the validation loss did not decrease for 20 consecutive epochs. The loss function was mean squared error (MSE).

2.5. Model evaluation and comparison

To validate model performance, PLSR, SVM, and the traditional ResNet50 were selected as comparative models. Evaluation metrics included the coefficient of determination (R^2), root mean square error (RMSE), and residual predictive deviation (RPD). R^2 reflects the goodness of fit, RMSE measures prediction error, and an RPD greater than 2.0 indicates good predictive ability. The formulas are as follows:

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

$$RMSE = \sqrt{\left[\frac{1}{n} \sum(y_i - \hat{y}_i)^2 \right]}$$

$$RPD = SD / RMSEP$$

where y_i is the measured value, \hat{y}_i is the predicted value, \bar{y} is the mean of measured values, SD is the standard deviation of the validation set measured values, and RMSEP is the root mean square error of prediction for the validation set.

All data processing and model construction were performed using Python 3.8, with PyTorch 1.10 for deep learning model development and scikit-learn 0.24 for comparative analysis of machine learning models.

3. Results and analysis

3.1. Statistical results of sample nutritional indices

The statistical results of nutritional indices of samples are shown in **Table 2**.

Table 2. Statistical results of nutritional indices of samples

Nutritional index	Sample set	n	Mean	SD	Min	Max	CV (%)
Crude protein (g/100g)	Calibration	432	12.58	0.886	10.92	14.37	7.04
	Validation	144	12.61	0.891	10.86	14.41	7.07
Crude fat (g/100g)	Calibration	432	9.32	0.924	7.68	11.25	9.91
	Validation	144	9.28	0.937	7.72	11.19	10.10
Lecithin (g/100g)	Calibration	432	7.95	1.282	5.43	10.82	16.13
	Validation	144	8.02	1.296	5.38	10.91	16.16
Cholesterol (mg/100g)	Calibration	432	385.6	48.26	302.5	485.3	12.52
	Validation	144	382.9	49.12	298.6	481.7	12.83

3.2. Comparison of predictive performance of different models

The comparison of predictive performance of different models for egg nutritional indices is shown in **Table 3**.

Table 3. Comparison of predictive performance of different models for egg nutritional indices

Nutritional index	Model	R^2_c	RMSEC	R^2_p	RMSEP	RPD
Crude protein	PLSR	0.902	0.95	0.893	1.07	3.11
	SVM	0.882	1.06	0.854	1.21	2.75
	ResNet50	0.925	0.82	0.902	0.99	3.35
	ResNet-SP	0.946	0.71	0.931	0.87	3.82

Nutritional index	Model	R ² _c	RMSEC	R ² _p	RMSEP	RPD
Crude fat	PLSR	0.885	1.02	0.876	1.12	2.84
	SVM	0.863	1.13	0.841	1.26	2.52
	ResNet50	0.914	0.87	0.893	0.98	3.25
	ResNet-SP	0.935	0.76	0.918	0.86	3.71
Lecithin	PLSR	0.876	1.45	0.862	1.53	2.70
	SVM	0.851	1.58	0.828	1.71	2.42
	ResNet50	0.908	1.18	0.886	1.34	3.07
	ResNet-SP	0.928	1.02	0.912	1.19	3.46
Cholesterol	PLSR	0.891	16.8	0.879	18.2	2.88
	SVM	0.867	18.5	0.845	20.4	2.57
	ResNet50	0.919	14.2	0.905	15.9	3.29
	ResNet-SP	0.941	12.5	0.926	14.1	3.71

3.3. Feature band selection and interpretation

To enhance the interpretability of the model, the SHAP method was used to analyse feature importance in the ResNet-SP model. The results indicated that the bands contributing most to crude protein prediction were located in the regions of 540–560 nm, 680–700 nm, and 830–850 nm. The contribution of 540–560 nm is associated with the vibrational absorption of protein-NH bonds; 680–700 nm is related to the pigment absorption characteristics of the yolk; and 830–850 nm is associated with the third overtone absorption of C-H bonds. These bands are generally consistent with protein-related characteristic bands reported in existing studies, verifying the rationality of the features extracted by the model ^[8].

4. Discussion

The results of this study show that the deep residual network (ResNet-SP) outperforms traditional machine learning methods (PLSR, SVM) and the conventional ResNet50 in predicting egg nutritional indices. This finding is consistent with the study by Lin et al., who found that a deep learning model based on residual dense connections achieved 96.29% classification accuracy in hyperspectral egg quality identification. The advantages of deep residual networks are mainly reflected in the following aspects: (1) residual connections effectively mitigate the vanishing gradient problem in deep networks, allowing the network to learn deeper spectral features; (2) the introduction of a spectral attention mechanism enables the model to adaptively focus on important bands, improving feature extraction efficiency; (3) the design of one-dimensional convolution kernels is more suitable for the structural characteristics of hyperspectral data, reducing the number of model parameters and lowering the risk of overfitting ^[9].

Rapid, non-destructive detection of egg nutritional quality is of great significance for precision nutrition management in commercial layer farms. Under traditional practices, farms need to wait for chemical analysis results (usually 3–5 days) before adjusting feed formulations, resulting in a significant time lag. The detection method based on hyperspectral imaging and deep learning can complete measurements within seconds, providing the possibility for real-time adjustment of feed formulas. Moreover, the prediction accuracy of this study (RPD > 3.0) meets the basic requirements for practical application and can be used for routine quality monitoring on farms ^[10].

The limitations of this study include: (1) the sample source was limited to a single breed (Hy-Line Brown) and a single farm, so the generalisability of the model needs further validation; (2) the effects of different farming seasons and different hen ages on egg nutritional composition were not considered; (3) the high cost of hyperspectral imaging equipment limits its widespread application in small and medium-sized farms. Future research can be pursued in the following directions: (1) expand the sample sources to construct a hyperspectral database of eggs covering multiple breeds and regions; (2) explore the correlation between hyperspectral data and feed nutritional composition to establish a full-chain nutritional prediction model from feed to eggs; (3) develop portable multispectral detection devices to reduce application costs and improve technology accessibility.

5. Conclusion

This study constructed a precision nutrition prediction model for commercial laying hens based on hyperspectral imaging and a deep residual network, and drew the following main conclusions:

The proposed ResNet-SP model achieved good prediction performance for the contents of crude protein, crude fat, lecithin, and cholesterol in eggs, with validation set R^2 values of 0.931, 0.918, 0.912, and 0.926, respectively, and RPD values all greater than 3.4, meeting the practical application requirements for non-destructive testing.

The ResNet-SP model outperformed PLSR, SVM, and the traditional ResNet50 in predictive performance, verifying the effectiveness of the improved residual network structure and hyperspectral attention mechanism in spectral data analysis.

Feature band analysis indicated that protein-related characteristic bands were concentrated in the regions of 540–560 nm, 680–700 nm, and 830–850 nm, which is generally consistent with the findings of previous studies, enhancing the interpretability of the model.

This study provides technical support for precision nutrition management in commercial layer farms, and the research results can be extended and applied to non-destructive quality detection of other livestock and poultry products.

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Disclosure statement

The authors declare no conflict of interest.

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