Identification of fungi-contaminated peanuts using hyperspectral imaging technology and joint sparse representation model

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Abstract Peanuts with fungal contamination may contain aflatoxin, a highly carcinogenic substance. We propose the use of hyperspectral imaging to quickly and noninvasively identify fungi-contaminated peanuts. The spectral data and spatial information of hyperspectral images were exploited to improve identification accuracy. In addition, successive projection was adopted to select the bands sensitive to fungal contamination. Furthermore, the joint sparse representation based classification (JSRC), which considers neighboring pixels as belonging to the same class, was adopted, and the support vector machine (SVM) classifier was used for comparison. Experimental results show that JSRC outperforms SVM regarding robustness against random noise and considering pixels at the edge of the peanut kernel. The classification accuracy of JSRC reached 99.2% and 98.8% at pixel scale, at least 98.4% and 96.8% at kernel scale for two peanut varieties, retrieving more accurate and consistent results than SVM. Moreover, fungi-contaminated peanuts were correctly marked in both learning and test images.

Keywords Fungal contamination · Peanut · Hyperspectral image · Joint sparse representation · Classification

Introduction

Peanut is a nutrient-rich and highly valued crop that covered an area of approximately 26.32 million hectares producing up to 45.56 million metric tons worldwide in 2017–2018 (USDA 2018). Still, peanuts are very susceptible to aflatoxin contamination (Ding et al. 2012; Schroeder and Hein 1967; Wogan and Pong 1970). Aflatoxin are highly carcinogenic, teratogenic substances mainly produced by two fungal species of the genus *Aspergillus* (i.e., *A. flavus* and *A. parasiticus*) and classified as group 1 carcinogens (Cancer 1993; Oplatowska-Stachowiak et al. 2016). Hence, identifying fungal-contamination peanuts is essential to prevent their introduction and improve safety in the food supply chain.

Conventional methods such as thin layer chromatography, gas chromatography, and high-performance liquid chromatography allow the accurate detection of aflatoxin (Mcdanell et al. 1988; Samarajeewa et al. 1991; Saqerm 2009; Wang et al. 2014) but are time-consuming, labor-intensive, sample polluting, and technically challenging (Jiang et al. 2016; Wang et al. 2014). Hence, a fast, accurate, objective, and noninvasive method is still necessary to automatically detect aflatoxin. Imaging techniques is currently available for food quality assessment. However, it can only provide external attributes given its very limited spectral information. Alternatively, spectroscopy can provide rich spectral information, but cannot retrieve compositional gradients and spatial information, which are important for some analyses (Elmasry et al. 2012). On the other hand, hyperspectral imaging is a promising method that integrates imaging techniques and near infrared spectroscopy into a unified system and can simultaneously deliver spatial and spectral information (Shi et al. 2017). Therefore, hyperspectral imaging has

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been widely applied to detect fungal contamination in cereal grains including maize (Kandpal et al. 2015; Kimuli et al. 2018; Wang et al. 2014, 2015), wheat (Senthilkumar et al. 2016b; Zhang et al. 2007), barley (Senthilkumar et al. 2016a), and peanuts (Jiang et al. 2016; Qiao et al. 2017). Despite the reported effectiveness and accuracy, these studies mainly focused on spectral information for classification and identification, whereas spatial information has been mostly neglected, as it was mainly used to either display the distribution of the mycotoxin or provide single-grain localization.

Sparse-representation-based classification (SRC) was proposed by Wright et al. (2009) for face recognition and provides a remarkable performance (Jia et al. 2014). SRC has been applied to hyperspectral images, notably outperforming the widely used support vector machine (SVM) (Chen et al. 2010). In addition, the joint SRC (JSRC) has been proposed as an improvement to SRC. JSRC incorporates contextual information (Chen et al. 2011), considers a small region of neighboring pixels as belonging to the same class, and represents a linear combination of labeled samples.

We propose the application of JSRC to accurately identify fungi-contaminated peanuts. Samples with fungal contamination were prepared and scanned using spectroscopy. The objectives of this study were: (1) analyze the spectral features of fungi-contaminated and healthy peanuts; (2) determine the sensitive spectral bands of fungi-contaminated peanuts; (3) detect and classify fungi-contaminated peanuts using both spectral and spatial information and verify the validity of the proposed approach.

Materials and methods

Sample preparation

Two varieties of peanuts (varieties 1 and 2) were bought from a local market and the intact and healthy peanut kernels were selected. Then, part of these intact kernels were put into a container and within an incubator. The temperature and relative humidity of the incubator were set to 30 °C and 80%, respectively, to promote fungal contamination of the peanuts. To guarantee the purity of the samples and validity of the experiment, peanut kernels almost totally contaminated were selected. Then, some contaminated samples were randomly selected and evaluated using the Aflatoxin B1 rapid test strip, which is an immune-chromatographic test using colloidal gold immunoassay. The test results verified that moldy peanuts contained aflatoxin, and we assumed that all such peanuts were fungi contaminated. In addition, healthy peanut kernels were selected and dried in a drier for 24 h at 60 °C.

Likewise, the fungi-contaminated peanut kernels were dried using the same process to eliminate the influence of water content from both healthy and contaminated samples.

Hyperspectral imaging

The HySpex SWIR-320m-e (HySpex, Norsk Elektro Optikk, Skedsmokorset, Norway), a push-broom hyperspectral imaging system that operates in the short-wave infrared band (967–2499 nm), was used to acquire hyperspectral images of the peanut kernels. It simultaneously acquires 320 pixel-wise spectral points along a line, and the number of lines depends on the length of the scanned object. The system provides a spectral resolution of approximately 6 nm, thus producing a total of 256 bands.

Each variety of peanuts were distributed into four black trays of 10 × 10 cm, as shown in Fig. 1. Two trays were served as learning dataset, with one tray filled with contaminated (top-left trays in Fig. 1) and the other with healthy (top-right trays in Fig. 1) peanut kernels. The other two trays served as test datasets, as they were filled with a mixture of contaminated and healthy peanut kernels (bottom trays in Fig. 1). To reduce the influence of the environment, the trays were placed over a black cloth during hyperspectral image acquisition. White and black references were acquired to correct the images from the noise caused by the charge-coupled device in the hyperspectral imaging system (Wu et al. 2016) and reduce the influence of illumination and dark current.

Hyperspectral image preprocessing

Calibration

To mitigate noise and convert the raw signal intensity into reflectance, calibration of hyperspectral images can be performed using Eq. 1 (Jiang et al. 2016).

$$R = \frac{R_0 - D}{W - D} \times 100\% \quad (1)$$

where R is the corrected image in the relative reflectance, R_0 is the original hyperspectral image, D is the dark reference, and W is the white reference.

Smoothing

Hyperspectral images inherently contain random noise, and hence a filter is necessary before data processing. We apply the five-point smoothing filter expressed by Eq. 2 (Qiao et al. 2017; Smith et al. 2004) to each hyperspectral image.

Fig. 1 Photographs of samples distributed in trays containing peanut kernels of varieties **a** 1 and **b** 2. The top-left trays contain only fungi-contaminated peanuts, and the top-right trays contain only healthy

peanuts. The bottom trays contain a mixture of fungi-contaminated and healthy peanuts

$$\text{Smoothed spectrum} = \frac{1}{2.5} \left(\frac{R_{i-2}}{4} + \frac{R_{i-1}}{2} + R_i + \frac{R_{i+1}}{2} + \frac{R_{i+2}}{4} \right) \quad (2)$$

where R_i ($i \in [3, 254]$) is the reflectance value of the i -th band per pixel.

Background removal and kernel labelling

Pixels not corresponding to peanut kernels should be masked as background and assigned a value of zero, not only because they are useless for classification but also because they may adversely affect processing. We mask the image background using the marker-controlled watershed algorithm because peanuts can be close together. Then, function ‘bwlable’ in MATLAB R2015b (MathWorks, Inc., Natick, MA, USA) is applied to label each peanut kernel. Other preprocessing stages include image cropping and removal of bands with low signal-to-noise ratio, from which we selected 233 bands at 1000–2400 nm for this study.

Data processing and analysis

Feature selection

Some bands of hyperspectral images can provide more information than others for identifying and distinguishing

materials, and several bands may contain redundant information, which only increases the computation burden without improving classification. Thus, feature selection for dimensionality reduction is important before image classification. In this study, we adopted the successive projection algorithm (SPA) for conducting feature selection. The SPA is a forward variable selection algorithm and can greatly reduce the number of variables, thus improving model efficiency. This algorithm extracts subsets of useful variables with minimum collinearity through vector projection analysis. Each selected variable by SPA has the maximum projection value on the orthogonal subspace of the previously selected variables. The optimal initial variable and the number of variables can be determined according to the smallest root mean square error (RMSE) (Araujo et al. 2001; Rahman et al. 2018). We implemented the algorithm using the SPA toolbox (available at <http://www.ele.ita.br/~kawakami/spa/>) in MATLAB 2017a with minimum and maximum number of bands set to 1 and 38, respectively.

Src

In SRC, the spectral signature of each pixel can be represented by the linear combination of several spectral signatures among samples. Suppose there are M classes with N_m samples in the m -th class, $A_i \in R^{l \times N_i}$ represents the samples of the i -th class, and $A = [A_1, A_2, \dots, A_M] \in R^{l \times N}$

stacks the samples of all classes and is called the dictionary, where l is the number of features in each sample and N is the number of samples, which should be much greater than l in general. Unknown test sample y can be represented as

$$y = A\alpha \quad (3)$$

where α is an N -dimensional vector that is expected to be sparse. Ideally, the nonzero entries of α correspond to a single class of A , and the test samples can be easily classified. Vector α can be obtained by solving the following optimization problem:

$$\hat{\alpha} = \arg \min \|\alpha\|_0 \text{ subject to } A\alpha = y \quad (4)$$

where $\|\cdot\|_0$ denotes the number of nonzero entries. Solving Eq. 4 is an NP-hard problem, but it can be either approximately solved by greedy pursuit algorithms or relaxed to a linear programming problem by replacing $\|\cdot\|_0$ by $\|\cdot\|_1$ (Chen et al. 2011).

After vector $\hat{\alpha}$ is obtained, the test sample can be recovered directly, and the m -th residual between the test sample and the reconstruction from training samples in the m -th class can be calculated as

$$r_m(y) = \|y - A_m \hat{\alpha}_m\|_2, m = 1, 2, \dots, M \quad (5)$$

where $r_m(y)$ denotes the m -th residual and $\hat{\alpha}_m$ denotes the sparse coefficients corresponding to the training samples in the m -th class. Then, the class label of y is determined as that retrieving the minimum residual.

JSRC

Traditional classification models such as SVM only consider a single pixel and its features during classification. Thus, pixels belonging to noise or mixed pixels are easily misclassified. However, adjacent pixels are more likely to belong to the same class. Therefore, JSRC considers that neighboring pixels belong to the same class of a central pixel. Let $Y = [y_1, y_2, \dots, y_9]$ represent pixel y and its 8 neighboring pixels. Y can be reconstructed approximately as $Y = AS = [A\alpha_1, A\alpha_2, \dots, A\alpha_9]$, where S is a sparse matrix obtained by solving the following optimization problem:

$$\hat{S} = \arg \min \|S\|_{\text{row},0} \text{ subject to } AS = Y \quad (6)$$

where $\|S\|_{\text{row},0}$ denotes the number of nonzero rows of S that can be obtained using simultaneous the orthogonal matching pursuit proposed by Chen et al. (2011). Once S is obtained, the m -th residual between Y and the reconstruction from training samples in the m -th class can be calculated as

$$r_m^{\text{SOMP}} = \sqrt{\sum_{i=1}^9 \|y_i - A_m \hat{S}_m\|_2^2}, m = 1, 2, \dots, M \quad (7)$$

and then the class of y is determined as that having the minimum residual.

Results and discussion

Feature selection

About 10% of the peanut pixels from the learning dataset were randomly selected and then checked to eliminate the pixels where contamination was indistinguishable from healthiness. The training samples included 1160 healthy pixels and 1152 contaminated pixels. The spectral responses of healthy and fungi-contaminated peanuts were obtained from averaging of the training samples, as shown in Fig. 2a. The spectral response of two healthy peanut varieties are similar for the main components of different varieties of peanuts are same. But there are still subtle differences due to the content of their main components are different. When peanuts were contaminated by fungi, the spectral response clearly varied, and the reflectance from peanuts in varieties 1 and 2 differ. The different spectral response between moldy peanuts of varieties 1 and 2 may be caused by the contamination level. Although moldy peanuts samples of varieties 1 and 2 are almost totally contaminated, the content of mycotoxin may vary. Nevertheless, Fig. 2a shows that the variation trend of the spectral response is consistent among the two peanut varieties when they are moldy. The spectral response of moldy peanuts shows lower reflectance than that of healthy peanuts at a limited wavelength range between 1003 and 1159 nm and higher reflectance at the other wavelengths. Therefore, moldy peanut pixels from the two varieties carry similar spectral information which can be used to distinguish moldy peanut pixels from healthy ones.

Then, samples of each class were split into calibration and validation datasets at a ratio of 2:1, i.e., 1540 samples for calibration and 772 for validation (Liu et al. 2018). The SPA was used to select the optimal bands, from which the number of variables was selected according to the RMSE, as shown in Fig. 2b. A sharply decrease in RMSE occurs until 15 variables at 0.21356, and the descending trend is not clear afterwards. Hence, by the order of importance in the SPA, 15 wavelengths (1003, 1063, 1129, 1213, 1364, 1682, 1730, 1820, 1928, 2006, 2036, 2060, 2084, 2198, and 2330 nm) were identified as optimal (Fig. 2a).

Bands of 1003 and 1063 nm correspond to the N–H stretch second overtone and O–H stretch second overtone, respectively, whereas those of 1129 and 1213 nm

Fig. 2 Effective bands to distinguish healthy and fungi-contaminated peanuts. **a** Spectral response of healthy and fungi-contaminated peanuts and effective bands (vertical dashed lines). **b** RMSE curve of SPA according to the number of variables considered for classification

correspond to the C–H first and second overtones and C–H combination associated with absorption by starch molecules, respectively (Singh et al. 2009). Bands of 1820 and 2090 nm are related to total fungi infection, and those of 1366 and 2032 nm to *F. verticillioides* (Nicola Berardo et al. 2005), which are similar to the optimal bands obtained in our study of 1820, 2084, 1364, and 2036 nm. The band of 1730 nm was ascribed to the C–H structure first overtone of CH₃ and CH₂ (Tripathi and Mishra 2009), and that of 2006 nm, was ascribed to the N–H/C–N combination band from primary amides (Workman 2007). Likewise, the band of 2060 nm is mainly related to protein and ascribed to either N–H second overtone or N–H bend/N–H stretch combination (Shenk et al. 2001). The band of 2330 nm was ascribed to C–H stretch/CH₂ deform combination of starch (Wang et al. 2014), and bands of 1682, 1928, and 2198 nm may be ascribed to C–H stretch first overtone of aromatic, O–H stretch/HOH deformation combination of starch/cellulose, and C–H stretch/C=O stretch combination of CHO groups, respectively (Burns and Ciurczak 2007).

Classification results

Pixel-wise classification

All samples with 15 features were established as dictionary *A* of JSRC, and the sparsity level was set to 30. The samples from both the learning and test datasets were classified using JSRC and for comparison, pixel-wise SVM classification with Gaussian radial basis function kernel was used. Library LIBSVM (Chang and Lin, 2011) was used to train the SVM classifier, and the optimal parameters were determined by fivefold cross-validation,

retrieving $C = 22.6274$ and $\gamma = 32$. The pixel-wise classification results of the two peanut varieties are depicted in Fig. 3, and the corresponding accuracy is listed in Table 1. Figure 3 shows that most peanut pixels were correctly classified using JSRC and SVM. However, isolate points and misclassified pixels at the kernel edge using JSRC are slightly fewer than those using SVM. Hence, JSRC suitably handles random noise and mixed pixels at kernel edges given its consideration of neighboring pixels. In addition, Table 1 shows that the accuracy of JSRC reaches 99.2% and 98.8% for peanut varieties 1 and 2, respectively, being higher than the accuracy of SVM for the evaluated pixel-wise classification. In addition, to evaluate the reliability of JSRC, data analysis including training samples selection, features selection and pixel-wise classification were repeated 6 times and the result was shown in Fig. 3e. Figure 3e shows that the error bars of both classifiers for two peanuts varieties are small, which means that both classifiers are reliable. But the mean and standard deviation of classification accuracy of JSRC is higher and lower than SVM for both two peanuts varieties, respectively, which means that the performance of JSRC is better than SVM.

Kernel-scale identification

After pixel-wise classification, the ratio between the number of fungi-contaminated pixels to total peanut pixels was used to identify whether a peanut kernel was contaminated. Ratios below threshold β of 0.05, 0.1, and 0.15 were considered as healthy peanuts. The pixel-wise and kernel-scale classification results (for $\beta = 0.15$) of peanut varieties 1 and 2 are shown in Fig. 4, and the accuracy of kernel-scale classification is listed in Table 2.

Fig. 3 Pixel-wise classification results for peanut variety 1 using **a** JSRC and **b** SVM classification, and for peanut variety 2 using **c** JSRC and **d** SVM classification. **e** Average pixel-wise classification result for two peanut varieties using JSRC and SVM

Table 1 Pixel-wise classification results in learning and test datasets (unit: pixel)

Classifier	Peanut variety	True class	Learning dataset		Test dataset		Accuracy (%)
			Contaminated	Healthy	Contaminated	Healthy	
JSRC	1	Contaminated	6285	4	3599	24	99.2
		Healthy	25	6441	141	7302	
	2	Contaminated	5649	75	3027	2	98.8
		Healthy	30	5741	134	5740	
SVM	1	Contaminated	6288	1	3609	14	97.4
		Healthy	72	6394	545	6898	
	2	Contaminated	5646	78	3022	7	97.6
		Healthy	37	5734	360	5514

Fig. 4 Kernel-scale identification results (threshold $\beta = 0.15$) for peanut variety 1 using **a** JSRC and **b** SVM classification, and for peanut variety 2 using **c** JSRC and **d** SVM classification. The white circles indicate misclassified peanut kernels

Table 2 Kernel-scale identification results in learning and test datasets (unit: kernel)

Classifier	Peanut variety	Threshold β	True class	Learning dataset		Test dataset		Accuracy (%)
				Contaminated	Healthy	Contaminated	Healthy	
JSRC	1	0.15	Contaminated	36	0	20	0	99.2
			Healthy	0	30	1	37	
		0.1	Contaminated	36	0	20	0	99.2
			Healthy	0	30	1	37	
		0.05	Contaminated	36	0	20	0	98.4
			Healthy	0	30	2	36	
	2	0.15	Contaminated	36	0	19	0	99.2
			Healthy	0	34	1	36	
		0.1	Contaminated	36	0	19	0	99.2
			Healthy	0	34	1	36	
		0.05	Contaminated	36	0	19	0	96.8
			Healthy	1	33	3	34	
SVM	1	0.15	Contaminated	36	0	20	0	95.2
			Healthy	0	30	6	32	
		0.1	Contaminated	36	0	20	0	92.7
			Healthy	0	30	9	29	
		0.05	Contaminated	36	0	20	0	87.9
			Healthy	2	28	13	25	
	2	0.15	Contaminated	36	0	19	0	97.6
			Healthy	0	34	3	34	
		0.1	Contaminated	36	0	19	0	97.6
			Healthy	0	34	3	34	
		0.05	Contaminated	36	0	19	0	90.5
			Healthy	0	34	12	25	

Figure 4 shows that some healthy peanut kernels were misclassified as being fungi-contaminated using both classifiers, but the misclassified peanut kernels (enclosed in white circles in Fig. 4) retrieved by JSRC are fewer than those retrieved by SVM. Table 2 shows that the classification accuracy of JSRC reaches at least 98.4% and 96.8% for peanut varieties 1 and 2 at different thresholds, respectively, outperforming the classification accuracy of SVM. Fewer healthy peanut kernels were misclassified regardless of the classifier, possibly by contamination not being easily identifiable in the visible light range, thus verifying the advantage of using short-wave infrared hyperspectral imaging.

It should be noted that using the ratio of contaminated to total pixels can eliminate the influence of misclassified pixels and provide a more robust peanut identification. However, threshold β produces false negatives that indicate fungi-contaminated peanut kernels as being healthy. Hence, the value of β should be as small as possible. Furthermore, compared to SVM, JSRC is more robust to the value of β , as it can better handle random noise and

mixed pixels at the kernel edge, thus decreasing the number of misclassified pixels.

Conclusion

In this paper, JSRC is used to identify fungi-contaminated peanut kernels after feature selection. Experimental results show that hyperspectral imaging combined with JSRC outperforms a conventional SVM-based method to identify fungi-contaminated peanut kernels. For pixel-wise classification, JSRC produces fewer isolated pixels and obtains a better classification results of mixed pixels along the kernel edges because it incorporates neighboring pixels for increased robustness. At kernel scale, accuracies of 98.4% and 96.8% are obtained by JSRC for peanut varieties 1 and 2, respectively, being more accurate than SVM at different values of threshold β . What should be pointed out is that only two peanut varieties were collected for this study and identifying multifarious fungi-contaminated peanuts is still not easily achieved by using well-trained classifiers and a

typical library of training samples. In future studies, more peanut varieties and factors such as moisture content, oil content, germination, and shape (e.g., broken), which may influence the results, will be considered to improve the reliability and effectiveness of the proposed method to identify fungi-contaminated peanut kernels.

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Author contributions Xiaotong Qi carried out the experiment and analyzed the data, and wrote the manuscript. Jinbao Jiang and Ximin Cui designed the experiment and guided the data analysis. Deshuai Yuan involved the process of the experiment and data collection. All authors reviewed and approved the final manuscript.

Compliance with ethical standards

Conflict of interest The authors have no conflicts of interest to declare.

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