

THE APPLICATION OF COMPUTER IMAGE ANALYSIS BASED ON TEXTURAL FEATURES FOR THE IDENTIFICATION OF BARLEY KERNELS INFECTED WITH FUNGI OF THE GENUS *FUSARIUM*¹

Ewa Ropelewska

Department of Systems Engineering, Faculty of Engineering,
University of Warmia and Mazury in Olsztyn, Poland

Corresponding author: e-mail: ewa.ropelewska@uwm.edu.pl

ARTICLE INFO

Article history:

Received: June 2018

Received in the revised form:

July 2018

Accepted: August 2018

Key words:

barley kernels;

fungal infection;

textures;

discriminative classifiers

ABSTRACT

The aim of this study was to develop discrimination models based on textural features for the identification of barley kernels infected with fungi of the genus *Fusarium* and healthy kernels. Infected barley kernels with altered shape and discoloration and healthy barley kernels were scanned. Textures were computed using MaZda software. The kernels were classified as infected and healthy with the use of the WEKA application. In the case of RGB, Lab and XYZ color models, the classification accuracies based on 10 selected textures with the highest discriminative power ranged from 95 to 100%. The lowest result (95%) was noted in XYZ color model and Multi Class Classifier for the textures selected using the Ranker method and the OneR attribute evaluator. Selected classifiers were characterized by 100% accuracy in the case of all color models and selection methods. The highest number of 100% results was obtained for the Lab color model with Naive Bayes, LDA, IBk, Multi Class Classifier and J48 classifiers in the Best First selection method with the CFS subset evaluator.

Introduction

Fungal infections occur on the outer surface of kernels and spread to the inside, causing changes in color, shape and chemical properties (Symons et al., 2002; Arabi et al., 2012; Jin et al., 2014). Grain infections caused by fungi of the genus *Fusarium* (FHB) can compromise the quantity and quality of yields (Suproniene et al., 2016) and lead to economic losses (Hossain and Goto, 2015). Grain processing conditions, such as high humidity and high temperature, promote fungal growth and development (Jin et al., 2018). Grain infected with fungi of the genus *Fusarium* can also contain mycotoxins (Karlsson et al., 2017) which pose a threat to human and animal health (Barbedo et al., 2017; Legrand et al., 2017). The consumption of foods and feeds contaminated with mycotoxins can have serious health

¹ This study was supported by grants Nos 16.620.014-300 and 16.610.001-300 from the University of Warmia and Mazury in Olsztyn and grant No. PBS3/A8/38/2015 from the National Centre for Research and Development

consequences, which is why *Fusarium*-infected grains should be detected before processing (Barbedo et al., 2015). Menesatti et al. (2009) and Jirsa and Polišenska (2011) discriminated infected and healthy cereal kernels based on the results of digital image analysis. However, these authors relied mainly on analyses of kernel shape and color. The aim of most research studies investigating the textural features of barley kernels in digital image analysis is to discriminate barley varieties or to identify the grain of crops grown in different locations. Paliwal et al. (2003) identified cereal grain from different geographic regions with the use of models based on textural features from the grey level co-occurrence matrix (GLCM) and the grey level run-length matrix (GLRM). The classification accuracy of barley grain exceeded 80%. Choudhary et al. (2008) discriminated grain from different locations based on its textural properties. The classification accuracy of malting barley kernels was estimated at 90%. Zapotoczny (2012) identified spring barley varieties based on digital image analysis of textural features in channels Y (brightness), S (saturation), V (red chrominance) and U (blue chrominance). Classification accuracy was high, reaching up to 100% in selected cases. These results indicate that image analyses based on textural features are a highly effective method of discriminating barley varieties and barley kernels originating from different regions. The applicability of digital image analysis for discriminating healthy kernels from kernels infected with fungi was evaluated in the present study. The aim of this study was to develop discrimination models based on textural features for the identification of barley kernels infected with fungi of the genus *Fusarium* and healthy kernels.

Materials and Methods

Materials

The experimental material comprised 5 kg samples of spring barley grain obtained from farms in northern Poland. Kernels with visible signs of infection with fungi of the genus *Fusarium*, including altered shape and discoloration, were manually selected from bulk samples. Infected and healthy barley kernels were subjected to digital image analysis.

Image analysis

Digital images of barley kernels were obtained using the Epson Perfection 4490 Photo flatbed scanner (UK) and the SilverFast Ai Studio Epson v6.6.1r6 scanning application (LaserSoft Imaging, Inc., USA). 150 infected kernels and 150 healthy kernels were scanned individually at a resolution of 500 x 700 pixels, 1200 dpi, and saved in TIFF format. The acquired images were analyzed with the use of MaZda software (Łódź University of Technology, Institute of Electronics, Poland) (Szczypiński et al., 2009). The images were converted to color channels R, G, B, Y, U, V, H, S, I, L, a, b, X, Y, Z. Textures based on the run-length matrix, co-occurrence matrix, Haar wavelet transform, autoregressive model, gradient and the histogram were computed.

Statistical analysis

Statistical analysis was carried out with the use of the WEKA 3.9 application (Machine Learning Group, University of Waikato) (Bouckaert et al., 2016). First, the attributes (textures) with the highest discriminative power were selected using the following selection methods and the appropriate attribute evaluators: (i) Ranker with the OneR attribute evalua-

tor, (ii) Ranker with the InfoGain attribute evaluator, (iii) Best First with the CFS (correlation-based feature selection algorithm) subset evaluator. Ten features from each color channel (R, G, B, Y, U, V, H, S, I, L, a, b, X, Y, Z) and each color model (RGB, YUV, HSI, Lab, XYZ) were chosen for each attribute selection method and the discriminant analysis was carried out for each variant. The attribute selection mode was 10-fold cross-validation. Then, infected and healthy kernels were classified with the use of selected Bayes (Naive Bayes), Functions (LDA), Lazy (IBk), Meta (Multi Class Classifier), Rules (JRip) and Decision trees (J48) classifiers by 10-fold cross-validation. The accuracies of analyzes were compared. The criterion for the selection of classifiers and evaluation of analysis was the highest classification accuracy. The results for RGB, Lab and XYZ color models were included in this paper, because the accuracies of classification based on textures selected from these models were the highest.

Results and Discussion

Images of infected and healthy barley kernels are presented in Figure 1. Kernels infected with fungi of the genus *Fusarium* (Fig. 1 A-D) were characterized by altered shape and pink or orange discoloration. Discoloration was not observed on the surface of healthy kernels (Fig. 1 E-H).



Figure 1. Images of barley kernels: A, B, C, D – infected kernels, E, F, G, H – healthy kernels

Ten surface textures of barley kernels selected from color models RGB, Lab and XYZ in the Ranker selection method with the OneR attribute evaluator, in the Ranker method with the InfoGain Attribute Evaluator, and in the Best First method with the CFS subset evaluator are presented in Table 1. Six attributes in the RGB model, 5 attributes in the Lab model, and 7 attributes in the XYZ model were repeated in Ranker selection methods with the OneR attribute evaluator and the InfoGain attribute evaluator. In the Best First selection method with the CFS subset evaluator, only one texture from Lab model was repeated with the texture selected for Ranker selection methods with the InfoGain attribute evaluator.

Table 1.

The textural parameters of infected and healthy barley kernels selected from color models RGB, Lab and XYZ

Attribute selection		
Ranker+OneRAttributeEval	Ranker+InfoGainAttributeEval	Best First+CfsSubsetEval
Selected attributes		
RGB		
RS4RZGLEvNonU	GSGArea	RSGArea
GS4RHGLEvNonU	GS4RVGLEvNonU	RTGabH4
GS4RVRLNonUni	GS4RZRLNonUni	RTGabH5
GS4RVGLEvNonU	GS4RZGLEvNonU	GHVariance
BS4RHGLEvNonU	BS4RVRLNonUni	GHPerc50
BS4RZRLNonUni	BS4RZRLNonUni	GSGSkewnes
BS4RZGLEvNonU	BS4RZGLEvNonU	GTGabH5
BS4RNRLNonUni	BS4RNRLNonUni	BHPerc01
BS4RNGLevNonU	BS4RNGLevNonU	BS5SV1Entropy
BAArea	BAArea	BTGabZ2
Lab		
LS4RHGLEvNonU	LSGArea	LSGArea
LS4RZGLEvNonU	LS4RNGLevNonU	LS5SV1Entropy
aSGArea	LS4RVGLEvNonU	aSGSkewness
aS4RVRLNonUni	LAArea	aS5SH1Entropy
aS4RVGLEvNonU	aS4RVGLEvNonU	aS4RVShrtREmp
aS4RZRLNonUni	aS4RZRLNonUni	bHPerc10
aS4RZGLEvNonU	aS4RZGLEvNonU	bHPerc99
aS4RNGLevNonU	aS4RNGLevNonU	bSGSkewness
aAArea	aAArea	bS5SH1AngScMom
bS4RHRLNonUni	bSGArea	bS5SV1DifEntrp
XYZ		
XS4RVRLNonUni	XS4RZGLEvNonU	XHSkewness
XS4RVGLEvNonU	XS4RNGLevNonU	XSGArea
XS4RZGLEvNonU	YS4RNGLevNonU	XS5SH1SumEntrp
YS4RNGLevNonU	ZS4RHGLEvNonU	XS5SV1SumOfSqs
YAArea	ZS4RVRLNonUni	XS5SV1Entropy
ZS4RVGLEvNonU	ZS4RVGLEvNonU	XS5SH3AngScMom
ZS4RZGLEvNonU	ZS4RZGLEvNonU	YHSkewness
ZS4RNRLNonUni	ZS4RNRLNonUni	ZHPerc01
ZS4RNGLevNonU	ZS4RNGLevNonU	ZATeta3
ZAArea	ZAArea	ZTGabV4

The classification accuracies of infected and healthy barley kernels based on 10 selected textures with the highest discriminative power from color models RGB, Lab, XYZ in the Ranker selection method with the OneR attribute evaluator, in the Ranker method with the InfoGain attribute evaluator, and in the Best First selection method with the CFS subset evaluator are presented in Table 2. Selected classifiers were characterized by 100% accuracy in all color models and selection methods. The highest classification accuracies (%) were noted for textures selected with the use of the Best First method with the CFS subset evaluator. Classification accuracy ranged from 98% (color model: RGB, classifier: JRip; color model: Lab, classifier: JRip and color model: XYZ, classifier: JRip) to 100% (color model: RGB (two results of 100%), classifiers: LDA, Multi Class Classifier; color model: Lab (five results of 100%), classifiers: Naive Bayes, LDA, IBk, Multi Class Classifier, J48 and color model: XYZ (two results of 100%), classifiers: Naive Bayes, LDA).

Table 2.

The classification accuracy of infected and healthy barley kernels based on textural features from color models RGB, Lab and XYZ

Color model	Classifier	Attribute selection		
		Ranker+OneR AttributeEval	Ranker+InfoGain AttributeEval	Best First+CfsSubsetEval
Classification accuracy (%)				
RGB	bayes.Naive Bayes	100	100	99
	functions.LDA	96	96	100
	lazy.IBk	100	100	99
	meta.Multi Class Classifier	96	97	100
	rules.JRip	99	99	98
	trees.J48	99	99	99
	Lab	bayes.Naive Bayes	100	100
functions.LDA		96	99	100
lazy.IBk		100	100	100
meta.Multi Class Classifier		98	100	100
rules.JRip		100	100	98
trees.J48		99	99	100
XYZ		bayes.Naive Bayes	100	100
	functions.LDA	96	96	100
	lazy.IBk	100	100	99
	meta.Multi Class Classifier	95	98	99
	rules.JRip	99	100	98
	trees.J48	99	99	99

Classification accuracy ranged from 95% to 100% in the Ranker selection method with the OneR attribute evaluator. Classification accuracy was lowest (95%) for color model XYZ and the Multi Class Classifier. The lowest accuracy of RGB and Lab models was 96%. In this selection method, Naive Bayes, IBk and JRip classifiers had 100% accuracy in the Lab color model (three results of 100%). In color models RGB (two results of 100%) and XYZ (two results of 100%), classification accuracy reached 100% when Naive Bayes and IBk classifiers were used.

In the Ranker selection method with the InfoGain attribute evaluator, classification accuracies ranged from 96% (color models: RGB and XYZ, classifier: LDA) to 100% (color model: RGB (two results of 100%), classifiers: Naive Bayes, IBk; color model: Lab (four results of 100%), classifiers: Naive Bayes, IBk, Multi Class Classifier, JRip; color model: XYZ (three results of 100%), classifiers: Naive Bayes, IBk, JRip). The highest accuracy (99-100%) in this selection method was noted in the Lab color model.

Based on the obtained results, it was found that in the case of each color model (RGB, Lab, XYZ), the accuracy reached 100% for selected classifiers. However, the highest number of 100% results (5) was observed for the Lab color model with Naive Bayes, LDA, IBk, Multi Class Classifier and J48 classifiers in the Best First selection method with the Cfs subset evaluator. In summary, the discrimination models based on textural features from color model Lab are the most appropriate for the identification of barley kernels infected with fungi of the genus *Fusarium* and healthy kernels.

The classification accuracies noted in this study are similar to those reported by Ropelewska and Zapotoczny (2018) in the classification of infected and healthy wheat kernels. In models containing textural features from the ventral and dorsal sides of kernels, Ropelewska and Zapotoczny (2018) observed classification accuracies in the range of 94-100% for images acquired with a flatbed scanner and 76-98% for hyperspectral images. Jirsa and Polišenska (2011) reported 85% accuracy in infected and healthy wheat kernels classified with the use of a model containing color descriptors. In a study by Menesatti et al. (2009), the classification accuracy of healthy wheat kernels and shriveled and chalky wheat kernels infected with *Fusarium graminearum* and *Fusarium culmorum* reached 56.9% and 68.4%, respectively. In own study, cereal kernels were classified with higher accuracy based on textural features, which indicates that digital image analysis effectively discriminates *Fusarium*-damaged kernels from healthy kernels. In future studies, digital image analysis based on the textural features of cereal kernels can be applied to determine the correlations between textural parameters and the amount of fungal DNA.

Conclusions

Digital image analysis based on the textural features of barley kernels effectively discriminated healthy kernels from kernels infected with fungi of the genus *Fusarium*. The developed discrimination models classified healthy and infected kernels with an accuracy of up to 100%. The highest number of 100% results was observed for the Lab color model. Therefore, the discrimination models based on textural features from color model Lab are the most appropriate for the identification of barley kernels infected with fungi of the genus *Fusarium* and healthy kernels. The results of this study can be used in future research to determine the correlations between textural properties and the amount of fungal DNA in

cereal kernels. The developed models can have practical applications as they support rapid, effective and low-cost identification of infected kernels and the determination of the severity of fungal infections.

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ZASTOSOWANIE KOMPUTEROWEJ ANALIZY OBRAZU OPARTEJ O CECHY TEKSTURALNE DO IDENTYFIKACJI ZIARNIAKÓW JĘCZMIENIA PORĄŻONYCH PRZEZ GRZYBY Z RODZAJU *FUSARIUM*

Streszczenie. Celem pracy było opracowanie modeli dyskryminacyjnych opartych o cechy teksturalne do identyfikacji ziarniaków jęczmienia porażonych przez grzyby z rodzaju *Fusarium* oraz ziarniaków zdrowych. Porażone ziarniak jęczmienia o zmienionym kształcie i z przebarwieniami oraz zdrowe ziarniak jęczmienia zostały zeskanowane. Tekstury zostały obliczone przy użyciu programu MaZda. Ziarniak były klasyfikowane jako porażone i zdrowe z wykorzystaniem oprogramowania WEKA. W przypadku modeli barwnych RGB, Lab i XYZ, dokładność klasyfikacji w oparciu o 10 wyselekcjonowanych tekstur o największej mocy dyskryminacyjnej zawierała się w przedziale od 95 do 100%. Najmniejszy wynik (95%) odnotowano dla modelu barwnego XYZ i Multi Class Classifier dla tekstur wyselekcjonowanych za pomocą metody Ranker i ewaluatora atrybutów OneR. Wybrane klasyfikatory charakteryzowały się dokładnością 100% w przypadku wszystkich modeli barwnych i metod selekcji. Najwięcej wyników 100% uzyskano dla modelu barwnego Lab dla klasyfikatorów: Naive Bayes, LDA, IBk, Multi Class Classifier i J48 dla metody selekcji Best First z ewaluatorem CFS.

Słowa kluczowe: ziarniak jęczmienia; infekcja grzybowa; tekstury; klasyfikatory dyskryminujące