Color Classifier for Symptomatic Soybean Seeds Using Image Processing

Irfan S. Ahmad, Research Associate, John F. Reid, Professor, Marvin R. Paulsen, Professor, Department of Agricultural Engineering, and James B. Sinclair, Professor, Department of Crop Sciences, University of Illinois at Urbana-Champaign, Urbana 61801

ABSTRACT

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Symptoms associated with fungal damage, viral diseases, and immature soybean (*Glycine max*) seeds were characterized using image processing techniques. A Red, Green, Blue (RGB) color feature-based multivariate decision model discriminated between asymptomatic and symptomatic seeds for inspection and grading. The color analysis showed distinct color differences between the asymptomatic and symptomatic seeds. A model comprising six color features including averages, minimums, and variances for RGB pixel values was developed for describing the seed symptoms. The color analysis showed that color alone did not adequately describe some of the differences among symptoms. Overall classification accuracy of 88% was achieved using a linear discriminant function with unequal priors for asymptomatic and symptomatic seeds with highest probability of occurrence. Individual classification accuracies were asymptomatic 97%, *Alternaria* spp. 30%, *Cercospora* spp. 83%, *Fusarium* spp. 62%, green immature seeds 91%, *Phomopsis* spp. 45%, soybean mosaic potyvirus (black) 81%, and soybean mosaic potyvirus (brown) 87%. The classifier performance was independent of the year the seed was sampled. The study was successful in developing a color classifier and a knowledge domain based on color for future development of intelligent automated grain grading systems.

Additional keywords: feature space, grain quality, machine vision

The midwestern United States is a major marketer of soybean (*Glycine max* (L.) Merr.) seeds. The grading of soybean seeds is an important task in determining product quality, price, and marketability. At present, grading is conducted manually, and oil and protein contents are not routinely identified. Grading standards of the Grain Inspection Packers Stockyards Agency-Federal Grain Inspection Service (GIPSA-FGIS) of the United States Department of Agriculture (USDA) report a damage factor that includes damage due to fungal activity but does not distinguish between severely damaged and superficially damaged soybean seeds. Soybean seed diseases can cause significant losses in productivity and marketability. For example, during the years 1970, 1972-77, and 1984-87, *Phomopsis* spp. seed decay caused more than 2% loss for Illinois growers (17). At this threshold, grain buyers discount the price paid for soybeans, and loss to the disease has a direct economic effect.

Manual grading is a tedious task and requires good visual skills. Inspectors base their judgment on experience and intuition; hence, a logical explanation is not always forthcoming. Training and experience involve an inherently complex mental process that has to be transformed into a logical decision. Fuzzy inference techniques have potential to model the logical relationships (3). Furthermore, a method such as machine vision sensing for automating the grading process could bring increased speed and objectivity and provides an opportunity for improvements in marketing.

Some of the features used to describe the visual characteristics of the seed include color, morphology, and texture. Asymptomatic seeds are almost round, compact, and have a smooth seed coat and beige color. Color of the hilum is dependent on the cultivar. The size and shape of the seed may depend on the location of the seed in the pod. Green immature seed varies in color from whitish green to dark green and is a result of immaturity due to frost.

Morphological properties of diseased soybean seeds often are changed in a characteristic manner (18). Seed affected by *Alternaria* spp. are small, shriveled, with light to dark brown lesions covering parts of the seeds. *Cercospora* spp. seed damage is variable in size and color, ranging from

light to dark brown, purple, or gray. Seed coats typically become pink to red due to infection by *Fusarium* spp. The North Central Regional Committee report showed production losses due to *Cercospora* spp. to be 25.25 metric tons and for *Fusarium* spp. to be 50.53 metric tons (8). Seeds severely affected by *Phomopsis* spp. are shriveled and elongated, and seed coats are cracked and chalky (17). Oil and flour extracted from *Phomopsis*-infected seed can be unmarketable (16). Yellow-seeded cultivars infected with soybean mosaic potyvirus produce seeds that are mottled brown or black, depending on the hilum color, with a smooth coat (13). The mottling usually appears as a "bleeding" of the hilum pigment over the seed coat.

Differences in symptoms among pathogen-damaged soybean seeds may be distinguished based on color. Other distinguishing features with potential include morphology and texture (1). Color image analysis is based on a set of values represented in several models to identify color variations. These representations may use Red, Green, Blue (RGB), which can be transformed to: hue, saturation, intensity (HSI); hue, saturation, value (HSV); cyan, magenta, yellow (CMY); red, green, blue (rgb) chromaticity coordinates; and y-axis, in-phase, quadrature (YIQ) used in broadcast television. For accurate color specification, three qualitatively different parameters must be measured. Sometimes features can be segmented by transforming RGB coordinates to another coordinate space (15). As an example, chromaticity values mask out the effects of intensity changes (2).

Earlier machine vision studies used various gray-level and color representations for grain quality evaluation with varying success (5,10,14,19). Some of these studies included both corn and soybean seeds; therefore, direct comparative analysis was not appropriate. Chromaticity coordinates were used in an earlier study on symptomatic soybean seeds, but they did not include black discoloration due to soybean mosaic potyvirus (5). Quantification of color using machine vision systems requires careful consideration of all these factors to provide meaningful measurements (2).

The objective of this study was to identify features using color analysis, which

Corresponding author: Irfan S. Ahmad
E-mail: i-ahmad1@uiuc.edu

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best described symptomatic soybean seeds, and develop a color classifier for discriminating between asymptomatic and symptomatic seeds, and their types.

MATERIALS AND METHODS

A 90 MHz Pentium computer with a Comet image processing board (Matrox Electronic Systems, Ltd., Dorval, Quebec) was used to collect images from a Sony Model XC-711 CCD RGB 768(H) × 493(V) color camera (Sony Semiconductor Company of America, San Jose, CA). The charged coupled device (CCD) camera had three primary color filters (RGB) in a striped filter configuration on a single chip to achieve high-fidelity color reproduction. The camera had an RGB signal output in addition to a composite video signal output. Gain control was set to 2.0 (0 db position) and γ correction to 1.0 ("on" position). The camera was fitted with an Invaritar lens P/N 59 LGA 450 (Melles Griot, Inc., Auburn, MA) that had a large diameter and low distortion. For preliminary testing and evaluation of techniques and procedures, a script-based language native to Matrox Inspector was used.

A cylindrical light chamber internally coated with a flat white enamel paint was used to provide diffuse front lighting to the soybean seed samples (4). Two 75W quartz halogen lamps were set at 9.0 VDC supplied by a regulated DC power source. The two lamps were angled 45° upward in opposing directions toward the chamber walls 20 cm from the center of the chamber at either side.

We analyzed 645 seeds comprising asymptomatic seeds and six types of seed surface symptoms from crop years 1989 through 1994. The damage types were green immature seeds (*gis*) or symptoms caused by *Cercospora kikuchii* (purple seed stain) (*cer*), *Alternaria alternata* (*alt*), *Fusarium* spp. (*fus*), and *Phomopsis* spp. (*pho*) (18). An additional category representing brown (*smvbr*) symptoms of soybean mosaic potyvirus (*smv*) for color and texture analysis was used and treated separately from black symptoms associated with the same virus (*smvbk*). The damage types were classified into fungal damage, viral infection, and seed immaturity, according to GIPSA-FGIS standards (9), by the Department of Crop Sciences and the Illinois Farm Bureau Crop Services Division technicians (Table 1).

Color analysis of the seeds was based on an RGB histogram of pixel values tested. RGB representation is important in digital image processing due to its wide use in digital imaging hardware, such as color cameras and monitors. An International Commission on Illumination (CIE: Commission Internationale de l'Eclairage) designated specific wavelengths to the primary colors: Red 700 nm, Green 546.1 nm, and Blue 435.8 nm (6).

The color calibration was carried out using spherical red, green, blue, black, gray, and white disks from Labsphere (Labsphere, Inc., Sutton, NH). Each disk was placed in the lighting chamber, and RGB values were recorded for each disk at three different locations. The average of

the three locations was used as a benchmark and saved in an ASCII file for future data runs. For each data run, values were compared and identical lighting conditions were ensured. At the start of each data run, the system was switched on for at least 15 min before data collection to ensure stabilization of the system.

An algorithm was developed to compute average pixel values for each of the RGB components separately for each seed sample. Color features of seeds were extracted interactively using a custom-developed analysis program. This algorithm was developed using Microsoft C Compiler (Microsoft Corporation, Redmond, WA) and the Matrox Image Series color board. On-board functions were used from the Matrox imaging library.

Many seeds had two or more different region types including symptomatic and asymptomatic. RGB histograms were collected on regions of each seed and used to evaluate seed color and sensitivity and response of the sensor to color variations. Histograms were extracted from three different regions: background, asymptomatic areas, and symptomatic areas. Asymptomatic seeds had only asymptomatic regions. Seeds with symptoms associated with *cer* and *smv* had three regions, while *alt* and *fus* had two. Green immature seeds and *pho* had variations unique to their surface characteristics, which may have taken the form of two or more symptomatic regions of varying intensity and surface texture. For each damage type, overlapping regional information was recorded due to the masking of local variations in color when the image was treated at a global level.

Images of soybeans seeds were captured and processed by carrying out multilevel thresholding to remove the background. Initially, the object (seed) was segmented from the dark background, then if symptomatic, the asymptomatic and symptomatic areas were identified using RGB values. Varying regions of interest (*roi*) were evaluated: the whole seed, 63 by 63, 30 by 30, and 15 by 15 pixels. For each seed, a 30 by 30 pixel *roi* was identified from the symptomatic region and RGB

Table 1. Soybean seed samples analyzed across years and the quantity of training and test samples

Seed type (symptoms)	Years	Seeds (no.)	Training sample	Test sample
Asymptomatic	1989-94	135	60	60
<i>Cercospora</i> spp.	1989-93	100	41	41
Green immature	1989-94	100	44	44
Soybean mosaic potyvirus (black)	1989-94	100	42	42
<i>Alternaria</i> spp.	1991	60	21	21
<i>Fusarium</i> spp.	1991	60	23	23
<i>Phomopsis</i> spp.	1991	61	23	23
Soybean mosaic potyvirus (brown)	1991-94	30	14	14
Total		645	268	268

Table 2. Red, Green, and Blue color feature values based on 15 by 15 pixel region of interest

Feature ^b	Seed types ^a							
	<i>asy</i>	<i>cer</i>	<i>gis</i>	<i>smvbk</i>	<i>alt</i>	<i>fus</i>	<i>pho</i>	<i>smvbr</i>
<i>ravg</i>	187	124	161	77	146	155	156	149
<i>gavg</i>	146	90	135	55	109	119	123	103
<i>bavg</i>	103	71	89	40	72	82	89	65
<i>rmin</i>	136	48	76	30	91	96	59	87
<i>gmin</i>	96	38	65	24	62	65	46	50
<i>bmin</i>	64	32	40	18	32	44	30	34
<i>rvar</i>	10.9	83.2	15.1	238.2	48.4	24.9	89.9	76.3
<i>gvar</i>	11.0	77.8	12.1	139.7	53.7	26.0	89.2	92.4
<i>bvar</i>	14.9	37.5	12.1	57.0	42.1	21.4	78.3	82.7

^a *asy* = asymptomatic, *cer* = *Cercospora* spp., *gis* = green immature seed, *smvbk* = soybean mosaic potyvirus (black), *alt* = *Alternaria* spp., *fus* = *Fusarium* spp., *pho* = *Phomopsis* spp., *smvbr* = soybean mosaic potyvirus (brown).

^b *r* = Red, *g* = Green, *b* = Blue; *avg* = average on a scale of 0 to 255; *min* = minimum; *var* = variance values.

values were analyzed. It was observed that almost identical information was achieved with varying *roi*; therefore, to reduce the computation time, the *roi* was reduced to 15 by 15 pixels.

To investigate the marginal distributions, *VTFIT* was used for fitting probability distribution functions to sample data and to aid in visual and formal interpretation of the goodness-of-fit (7). Several variables were found to be skewed and needed transformations.

The initial RGB data set was reduced using Pearson correlation coefficients. From each of the two highly correlated

features, one was selected for further evaluation (11). The final data set comprised averages (*avg*), minimums (*min*), and variances (*var*) for each of the RGB components. Features involving maximums, medians, and standard deviations were dropped from further evaluation, as they were highly correlated with averages and variances. The reduced data set then was evaluated using stepwise discriminant analysis for classification of seed types. The entry criteria were set to $F = 3.84$ and 2.71 for entry and removal, respectively. The summary table obtained gave the significance of each discriminant function (if

$P < 0.05$, the function was considered to discriminate significantly among groups). To achieve a reduction in the problem to a lower dimension, functions that were not significant were discarded. The goal of the analysis was to determine which RGB features provided the best model for highest classification accuracy.

Most of the individual features had significantly different variances for each symptomatic group. In such cases, quadratic discriminant functions, which are based on the separate covariance matrices for the groups instead of the pooled one, were used. Quadratic analysis does not

Seed type	Original RGB image	Multi-threshold	63 by 63 region of interest (<i>roi</i>) and thresholded symptomatic region	Comments
<i>asy</i> =asymptomatic <i>cer</i> = <i>Cercospora</i> spp. <i>gis</i> =green immature seed <i>smvbk</i> = soybean mosaic potyvirus (black) <i>alt</i> = <i>Alternaria</i> spp. <i>fus</i> = <i>Fusarium</i> spp. <i>pho</i> = <i>Phomopsis</i> spp. <i>smvbr</i> = soybean mosaic potyvirus (brown).				
<i>asy</i>				-The yellow spot indicates reflection from seed surface and is identified as asymptomatic region. Orange indicates an asymptomatic region, which covers almost the entire seed.
<i>cer</i>				-Orange indicates an asymptomatic region. -Dark area is used for seed analysis to represent seed color.
<i>gis</i>				-Orange indicates an asymptomatic region. -The light area is used for seed analysis to represent seed color.
<i>smvbk</i>				-Orange and yellow indicate asymptomatic region. -The dark area is considered symptomatic and was analyzed for seed color.
<i>alt</i>				-Orange indicates an asymptomatic region, which was minimal in this case. -Dark area was considered symptomatic and was analyzed for seed color.
<i>fus</i>				-Orange indicates an asymptomatic region. -The light area was considered symptomatic and was analyzed for seed color.
<i>pho</i>				-Orange indicates an asymptomatic region. The asymptomatic area is minimal. -Dark area was considered symptomatic and was analyzed for seed color.
<i>smvbr</i>				-Orange indicates an asymptomatic region. -Dark area was considered symptomatic and was analyzed for seed color.
Note: True and pseudo-colors may not be truly depicted due to reproduction. Images and <i>roi</i> not to actual size.				

Fig. 1. Visual representation of multi-thresholding operation to separate symptomatic regions from asymptomatic regions of seeds. Asymptomatic region of the seed is shown in orange.

perform very well for large sample sizes. However, the linear discriminant function worked well if the within-group covariance matrix was the same for each group (11). Marks and Dunn (12) showed that a linear function was satisfactory in cases where covariance matrices were not too different. Due to large sample sizes and differences between covariance matrices, both linear and quadratic discriminant analyses were performed. It was observed that most of the time, the quadratic analysis gave a more accurate classification, but not significantly better than the discriminant analysis. Due to their simplicity and ease of interpretation, linear functions were used with the understanding that optimality would be hard to achieve since there were instances when assumptions were violated.

The data were not from a random sample and did not represent the entire soybean seed population. For this reason, outside estimates of the frequency of occurrence of the diseases were used as prior probabilities of classification. Discriminant analysis was performed using equal prior and unequal (estimated) probabilities. For the aforementioned reasons, the second classification did not fit this particular data set as well; but in an application involving random samples, the second one was expected to be more accurate than the one with equal priors. Therefore, in this paper, clas-

sification based on unequal priors is reported. The accuracy was dependent on the accuracy and reliability of the priors, so the results obtained have to be viewed in that context.

RESULTS AND DISCUSSION

The individual RGB color features for 645 seeds were averaged for each seed category (Table 2). These measurements were based on 15 by 15 pixel regions of interest and were reflective of asymptomatic and symptomatic regions. Asymptomatic seeds had the highest average R, G, and B values due to the beige appearance of the seed. The intense black of *smvbk* tended to lower the average RGB values toward 0. The largest RGB variation was found for *smvbk*, followed by *cer* and *pho*, but for asymptomatic and *gis* the variances were low. It was observed that *rmin* (minimum of Red component) was unique for each of the seed types (Table 2).

Multilevel thresholding was conducted to separate the background and object and the asymptomatic from symptomatic region on the seed. Original RGB images with the thresholding process for each category are shown (Fig. 1). The multi-threshold column shows the asymptomatic and symptomatic regions of the seed, with pixel values below 45 set to 0 to represent background, and above 160 set to 255 to

represent the asymptomatic region. The pixel values 46 to 159 represented symptomatic regions of the seeds. For asymptomatic seeds, pseudo-orange color represented the asymptomatic region, with yellow considered as part of the asymptomatic region. The difference in appearance was the reflective surface of the seed. For *cer* and *smv*, the asymptomatic region was a continuous area, with a distinct symptomatic region. In the case of materially damaged seeds, the asymptomatic regions varied in size and shape and were discontinuous, surrounded by symptomatic regions. This nonuniformity among materially damaged seeds made the distinction based on color more difficult compared with seeds of other colors.

Several RGB features were visualized using 2- and 3-D color feature spaces. The surface characteristics of soybean seeds, such as color, varied depending on the causal agent. Seed samples exhibited symptoms of more than one pathogen, which is normal (18).

Figure 2 shows selected features for RG components for asymptomatic and seeds of other colors individually. Each seed category is represented by distinguishable clusters, but clusters overlap. The major overlap occurs between *cer* and *smvbk* due to their frequent similar color variations. Manual observations of both seed types showed instances of *cer* with dark purple stains and *smvbk* with light to dark black surface appearance. Green immature seed is more in proximity to *asy* due to the Green component.

Figures 3 and 4 show 2-D plots of R and G averages with distinct separation between asymptomatic and symptomatic seeds. Since the Blue component was not visualized to have distinctly separable information, it was not considered in these plots. *gis* approaches *asy* due to its light green color (Fig. 3). Higher R and G values contributed to the beige appearance of *asy*.

A 3-D representation of R, G, and B averages with distinct separation between asymptomatic and symptomatic seeds is shown (Fig. 5A). In this representation, 15

Fig. 2. Seeds of other colors in Red, Green, and Blue (RGB) feature space.

Fig. 3. Red and Green pixel value averages form three distinct clusters for *asy*, *cer*, and *gis*.

Fig. 4. Red and Green pixel value averages for *asy* and *smvbk* forming two distinct clusters.

by 15 *roi* was used only on the symptomatic region of the seed located next to the hilum. Figure 6B shows only seeds of other colors with overlapping *cer* and *smvbk* clusters. *Gis* had some overlap with *smvbr*.

Color classifier. Six discriminant functions with unequal priors were computed with six variables for each of the eight seed types. The first two discriminant functions were selected because they represented the largest ratio of between-groups to within-groups sum of squares. The developed expressions are given as:

$$D_{\text{color1}} = -3.41 - 0.12 \cdot \text{ravg} + 0.02 \cdot \text{rmin} + 0.24 \cdot \text{gavg} + 0.03 \cdot \text{gmin} - 0.16 \cdot \text{bavg} + 0.005 \cdot \text{bmin} \quad (1)$$

$$D_{\text{color2}} = -5.29 + 0.11 \cdot \text{ravg} + 0.09 \cdot \text{rmin} - 0.32 \cdot \text{gavg} + 0.01 \cdot \text{gmin} + 0.22 \cdot \text{bavg} - 0.08 \cdot \text{bmin} \quad (2)$$

The canonical correlation for a function is the square root of the between-groups to total sums of squares. The canonical discriminant functions were derived so that the pooled within-groups variance was 1. Function 1 accounted for 58.5% of the total between-groups variability, and function 2 accounted for 29.18% variability; and the variability reduced progressively to 0.05% for function 6 (Table 3).

A test of the null hypothesis, that the population means of all discriminant func-

tions in all groups are equal and zero, can be based on Wilks' λ . The significance level of the observed Wilks' λ was based on χ^2 transformation of the statistic (Table 3). Since observed $\alpha < 0.00005$, the null hypothesis that means of the functions are equal in the eight populations can be rejected. Table 3 shows the successive removal of the functions with associated statistics. The column labeled "After *fcn*" shows the number of the last function removed. The 0 indicates that no functions were removed, while a value of 5 indicates

that the first five functions were removed. In this case, Wilks' λ associated with function 5 after function 4 has been removed is 0.994. As this was the final remaining function, the Wilks' λ obtained is simply the univariate value. The significance levels associated with fourth and fifth functions were 0.021 and 0.504, respectively, showing that they did not contribute to group differences. Only the first two functions showed maximum variability; therefore, the four remaining functions (3 to 6) were not considered (Table 3).

Fig. 6. Linear discriminant functions with separable seed groups with distinct centroids. *asy*, *cer*, *gis*, *smvbk*, and *smvbr* are distinct from *alt*, *fus*, and *pho*.

o Asymptomatic + *Cercospora* spp.
x Green immature seed

A

+ *Cercospora* spp. x Green immature seed
* Soybean mosaic potyvirus (black) * (brown)

B

Fig. 5. 3-Dimensional cluster plots in Red, Green, and Blue (RGB) feature space for (A) asymptomatic, *Cercospora* spp., and green immature seed, and (B) *Cercospora* spp., green immature seed, soybean mosaic potyvirus (black), and soybean mosaic potyvirus (brown).

Table 3. Analysis of discriminant functions for classification of soybean seed categories

<i>Fcn</i> ^a	Eigen value	Variance (%)	Canonical correlation	After <i>fcn</i>	Wilks λ	χ^2	df	σ
				0	0.014	1,105.8	42	0.0000
1	5.8923	58.50	0.924	1	0.097	603.9	30	0.0000
2	2.9391	29.18	0.863	2	0.386	247.4	20	0.0000
3	0.8845	8.78	0.685	3	0.727	82.7	12	0.0000
4	0.2985	2.96	0.479	4	0.944	14.8	6	0.0216
5	0.0531	0.53	0.224	5	0.994	1.3	2	0.5042
6	0.0053	0.05	0.224					

^a The six canonical discriminant functions (*fcn*) remaining in the analysis.

Table 4 shows individual matrices for classification accuracy for unequal priors for the test data set. Asymptomatic seed accuracy is 98%. The higher accuracy for the unequal priors can be attributed to a higher probability of occurrence of asymptomatic seed of 81.45% (1).

For *cer*, the highest misclassification of 7.1% occurred with *asy*, while some instances of misclassification are observed with asymptomatic, *smvbk*, *alt*, and *pho*. In the case of *gis*, a misclassification of 29.5% occurred with the asymptomatic category due to similar RGB variances (Table 2).

To assess the performance of the classifier without the inclusion of asymptomatic seeds, further evaluation was carried out based on the combined training and test data files (1). In the first stage, performance was evaluated by eliminating asymptomatic seeds, being the major source of misclassification from the data set. In the

second stage, asymptomatic and materially damaged seeds were removed. In the third stage, asymptomatic and seeds of other colors were removed from the original data set. In the final stage, performance was evaluated based on probability of occurrence of asymptomatic and symptomatic seeds. Classification accuracy increased when only symptomatic seeds were considered (Table 5), compared with when both asymptomatic and symptomatic were considered (Table 4).

The elimination of asymptomatic and materially damaged seeds resulted in an increase in classification accuracy (Table 6). The individual accuracy for *cer* was 94%, *gis* was 99%, *smvbk* was 89%, and *smvbr* was 97%. Similarly, among the materially damaged seeds, *alt* had 76% and *pho* 82% classification accuracy (Table 7). In the case of *fus*, the classifier performed poorly due to lower probability of occurrence and overlapping characteristics with

alt and *pho*. A higher individual and overall classification accuracy was achieved for seeds of other colors compared with materially damaged seeds (Tables 6 and 7). This was due to the large variations in color among seeds of other colors, compared with variation of materially damaged seeds, which showed no or subtle variations. Classifier performance based on the highest probability of occurrence is presented (Tables 8 and 9). Table 8 shows performance of over 58% for each of the seeds considered. The main misclassifications occurred for *pho*, with seeds being wrongly predicted as asymptomatic and *cer*. This did not seem to be the case when all seeds were considered, and there was no instance of *pho* being classified as *cer* (Table 4).

Table 9 shows classification accuracy for symptomatic seeds with highest probability of occurrence. The seeds included damage types from both seeds of other

Table 4. Individual classification accuracy for asymptomatic and symptomatic soybean seeds

Seed types ^a	Quantity	Predicted group membership % accuracy							
		<i>asy</i>	<i>cer</i>	<i>gis</i>	<i>smvbk</i>	<i>alt</i>	<i>fus</i>	<i>pho</i>	<i>smvbr</i>
<i>asy</i>	59	58	0	0	0	0	0	1	0
%		98.3	0	0	0	0	0	1.7	0
<i>cer</i>	42	3	35	0	1	1	0	2	0
%		7.1	83.3	0	2.4	2.4	0	4.8	0
<i>gis</i>	44	13	0	30	0	0	0	1	0
%		29.5	0	68.2	0	0	0	2.3	0
<i>smvbk</i>	42	0	1	0	34	5	0	2	0
%		0	2.4	0	81	11.9	0	4.8	0
<i>alt</i>	20	12	0	0	0	4	0	4	0
%		60	0	0	0	20	0	20	0
<i>fus</i>	24	18	0	0	0	2	0	4	0
%		75	0	0	0	8.3	0	16.7	0
<i>pho</i>	22	10	0	0	0	2	0	9	0
%		45.5	0	0	0	9.1	0	40.9	0
<i>smvbr</i>	15	1	0	0	0	3	0	1	10
%		6.7	0	0	0	20	0	6.7	66.7
Overall	268								67.16

^a *asy* = asymptomatic, *cer* = *Cercospora* spp., *gis* = green immature seed, *smvbk* = soybean mosaic potyvirus (black), *alt* = *Alternaria* spp., *fus* = *Fusarium* spp., *pho* = *Phomopsis* spp., *smvbr* = soybean mosaic potyvirus (brown).

Table 5. Classification accuracy for symptomatic soybean seeds only

Seed types ^a	Quantity	Predicted group membership % accuracy						
		<i>cer</i>	<i>gis</i>	<i>smvbk</i>	<i>alt</i>	<i>fus</i>	<i>pho</i>	<i>smvbr</i>
<i>cer</i>	83	72	0	3	2	1	5	0
%		86.7						
<i>gis</i>	88	0	67	1	2	3	15	0
%			76.1					
<i>smvbk</i>	84	3	0	69	8	0	2	2
%				82.1				
<i>alt</i>	41	0	0	0	27	0	11	3
%					65.9			
<i>fus</i>	47	0	0	0	26	2	19	0
%						4.3		
<i>pho</i>	45	2	0	1	6	0	35	1
%							77.8	
<i>smvbr</i>	29	1	0	0	7	0	0	21
%								72.4
Overall	417							70.3

^a *cer* = *Cercospora* spp., *gis* = green immature seed, *smvbk* = soybean mosaic potyvirus (black), *alt* = *Alternaria* spp., *fus* = *Fusarium* spp., *pho* = *Phomopsis* spp., *smvbr* = soybean mosaic potyvirus (brown).

colors and materially damaged seeds. Most of the misclassification in both categories occurred with *smvbk* and *pho*, which showed a close resemblance when *cer* has a dark purple discoloration.

The occasional instances of asymptomatic seed being misclassified as *smvbk*, *smvbr*, *alt*, or *pho* can be attributed to dirty or cracked seed coats. *Cer* was likely to be misclassified due to its occasional dark purple appearance, leading to misclassification as *smvbk*, and to its occasional light pink appearance, resulting in misclassification as *fus*. The major misclassification occurred when *cer* and *gis* were misclassified as asymptomatic due to their close resemblance. *Cer* seeds had demonstrated regions on the seed coat unaffected by pink or purple staining (asymptomatic regions), while *gis* had variation in intensity levels that matched those of asymptomatic, resulting in high misclassification (Table 4). Similarly, *fus* was excessively misclassified as asymptomatic, *alt*, and *pho*.

The misclassifications of *alt* to *smvbr* were due to the similarity in brown color. *Alt* seeds also were misclassified as *fus* and *pho*. The tan color of *alt* was similar to that of some of the seeds infected by *fus* and *pho*. *Alt* was misclassified as *fus* more than as *pho*. This was attributed to the similarity of gray color between *alt* and *fus*.

Figure 6 shows the scatter plot for the first two canonical discriminant functions for linear discriminant analysis with unequal priors. Asymptomatic, *cer*, *gis*, *smvbk*, and *smvbr* formed distinct clusters compared with materially damaged seeds. The variability along the x-axis seems to show classification more toward asymptomatic, *cer*, *gis*, *alt*, and *fus*; whereas along the y-axis, distinct classification was observed for *cer*, *smvbk*, and *smvbr*. Therefore, the differences among the eight seed types were adequately described primarily by the first function and to a certain level by the second function.

Summary. Linear discriminant analysis with unequal priors was presented in this paper as it reflected the real probabilities of occurrences of asymptomatic and symptomatic seeds. The classification accuracy for symptomatic soybean seeds with highest probability of occurrence ranged from 83 to 93%. The classification accuracy for linear and quadratic functions ranged from 67 to 81% for test samples with all seed types included. Among the color features, minimum values of RGB contributed to higher classification accuracy in comparison with averages of each of the components. The possible explanation for this contribution was that the RGB averages may have masked the spatial variation. In the case of minimum values, each of the seed types had a minimum level, which was unique.

There was a minimal increase in accuracy when asymptomatic seeds were eliminated compared with all seed types;

whereas there was a significant increase in accuracy when seeds of other colors and materially damaged seeds were considered independently of each other and of as-

ymptomatic seeds. When seeds with the highest probability of occurrence were considered, classification accuracy ranged from 83 to 93%. The range of variations

Table 6. Classification accuracy for soybean seeds of other colors (*cer*, *gis*, *smvbk*, and *smvbr*)

Seed types ^a	Quantity	Predicted group membership % accuracy			
		<i>cer</i>	<i>gis</i>	<i>smvbk</i>	<i>smvbr</i>
<i>cer</i>	83	78	2	3	0
%		94			
<i>gis</i>	88	0	87	1	0
%			98.9		
<i>smvbk</i>	84	2	0	75	7
%				89.3	
<i>smvbr</i>	29	0	0	1	28
%					96.6
Overall	284				94.4

^a *cer* = *Cercospora* spp., *gis* = green immature seed, *smvbk* = soybean mosaic potyvirus (black), *smvbr* = soybean mosaic potyvirus (brown).

Table 7. Classification accuracy for materially damaged soybean seeds

Seed types ^a	Quantity	Predicted group membership unequal priors % accuracy			
		<i>alt</i>	<i>alt</i>	<i>fus</i>	<i>pho</i>
<i>alt</i>	41	30	31	0	10
%		73.2	75.6		
<i>fus</i>	47	8	23	0	24
%				0	
<i>pho</i>	45	9	8	0	37
%					82.2
Overall	133				51.1

^a *alt* = *Alternaria* spp., *fus* = *Fusarium* spp., *pho* = *Phomopsis* spp.

Table 8. Classification accuracy for asymptomatic and selected symptomatic soybean seeds with highest probability of occurrence

Seed types ^a	Quantity	Predicted group membership % accuracy		
		<i>asy</i>	<i>cer</i>	<i>pho</i>
<i>asy</i>	119	118	0	1
%		99.2		
<i>cer</i>	83	8	74	3
%			89.2	
<i>pho</i>	45	16	3	26
%				57.8
Overall	247			88.3

^a *asy* = asymptomatic, *cer* = *Cercospora* spp., *pho* = *Phomopsis* spp.

Table 9. Classification accuracy for selected symptomatic soybean seeds with highest probability of occurrence

Seed types ^a	Quantity	Predicted group membership unequal priors % accuracy			
		<i>cer</i>	<i>smvbk</i>	<i>alt</i>	<i>pho</i>
<i>cer</i>	83	74	3	1	5
%		89.2			
<i>smvbk</i>	84	3	70	8	3
%			83.3		
<i>alt</i>	41	0	0	30	11
%				73.2	
<i>pho</i>	45	1	2	7	35
%					77.8
Overall	253				82.6

^a *cer* = *Cercospora* spp., *gis* = green immature seed, *smvbk* = soybean mosaic potyvirus (black), *alt* = *Alternaria* spp., *fus* = *Fusarium* spp., *pho* = *Phomopsis* spp., *smvbr* = soybean mosaic potyvirus (brown).

exhibited within each seed type was expected due to the inclusion of a wide range of seeds comprising crop years 1989 to 1994. In earlier research, the performance of the classifier was improved by replacing seed samples that varied considerably and by treating samples for various years in isolation (5). This approach was not followed in the current research, as the range of variations actually facilitated the development of robust methods for characterization of seed surfaces.

Alt was the dominant source of misclassification, followed by *fus* and *pho*, due to its frequent occurrence compared with *fus*. Asymptomatic seed was the next highest among the categories with misclassification occurrences. Seeds of other colors contributed minimally to misclassification. Among seeds of other colors, *smvbr* was the main source of misclassification, followed by *smvbk* and *cer*. This was attributed to light color variations, which at times may be similar to *smvbk* and *cer*. Overall, it was observed that *alt* was one of the major sources of misclassification, while *gis* contributed minimally to misclassification for all seed types. The RGB intensity of surface symptoms on seeds varied with disease and within diseases. It was concluded that image processing facilitated the classification of asymptomatic and symptomatic soybean seeds and the development of a knowledge domain based on color information. The performance of the

classifier can potentially be enhanced by using a combination of color, morphological, and textural features. The inherent constraints in manual grading and the objectivity of machine vision justify further efforts to automate the grading process.

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