*Machine Learning Based Peanut Maturity Classification from Hyperspectral Image*

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***Abstract-* The maturity of the seed is key information to ensure quality of the crops and better economic returns. But the assessment of the maturity of the peanut requires exocarp removal which suffers from observer’s color assessment skill and experience. Moreover, it requires a great amount of time for a large number of peanut and often ends up in a blasting peanut pod. In order to find an optimal solution, researchers tried to apply digital image processing method. Although this method does not cause pod blasting and does not require personal inspection, the method demands exocarp removal. Recently, a research group has shown why traditional RGB image fails to classify peanut maturity and they have introduced a hyper-spectral unmixing based classifier to solve the problem. In this project, I have worked the same problem with logistic regression, random forest and support vector machine to compare their performance with the previous classifier.**

Keywords ***– Machine Learning, Hyperspectral image, Peanut Maturity***

1. INTRODUCTION

Peanut ([*Arachis*](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/arachis) hypogaea)  is consumed all over the work due to its nutrition value and deliciousness. To be specific, peanut is source of protein, fat, carbohydrates, vitamin, and minerals and it prevents cardiovascular disease, cancer, diabetics, and obesity [1]. Therefore, peanut is a vastly cultivated crop in the United States. In 2021, the total production of peanut was around 6.63 billion pounds from 1.63 million acres of land in US [2]. To maximize the peanut production, maturity level of the peanut pod is one of the most important things to know. If the pod is immature while harvesting, it will not provide optimum seed quality, grade, and flavor. On the contrary, over-mature peanut pod can break the pegs where pods are attached [AZ,3].

Visual inspection has been a popular method among agricultural community for maturity classification for a long time. The most recognized method for peanut maturity level classification is MPB (Maturity Profile Board) which maps the color of the mesocarp to the five different maturity categories and the shades within the color into different subcategories [2]. But this method needs exocarp removal and it often causes pod blasting. Since, immature pods are

fragile compared to mature pods, most immature pod blows apart. Focusing on not destroying too many immature pods consumes a considerable amount of time. Moreover, color categorization using MPB requires human visual inspection, which is very subjective to human visual condition, lighting condition, observer skill in discriminating color that leads to the possibility of large error. This is very time consuming when one has to classify large number of pods. Authors in [6] also introduced a mesocarp color and pod size based nearest neighbor classifier for pod maturity classification which requires pod blasting but free from visual inspection. Thereby, recent advancement of vision technology has inspired researchers to automate the peanut maturity assessment which can speed up the process with optimum accuracy.

The idea of non-destructive peanut maturity classification is initiated by authors of [5], who have shown a positive correlation between tannin and maturity level. Interestingly, hyperspectral reflectance also varies with different chemical composition. Therefore, HSI image can be used as a peanut pod tannin distinguisher and hence their maturity level. Using all the information, authors in [4] established a linear unmixing model and fully constrained least square algorithm to classify mature and immature pods. They have made the classification based on the multispectral reflectance of the pericarp which does not require exocarp removal. They have also shown that visible part of the spectrum is indistinguishable for mature and immature pod.

But linear hyperspectral unmixing is a computationally costly process where spectrum of every pixel needs to participate. However, when all pixels of mature and immature peanut are averaged, the resulting average spectrum shows clear distinction between mature and immature peanut [AZ]. Moreover, average spectral feature based peanut maturity classification with a few key wavelength features can leverage a lot of computational time. Earlier, standard machine learning algorithm (SVM and random forest) has shown promising result for pod maturity classification of snap bean based on spectral and biophysical features [Am].

Therefore, the scope of this paper is to explore traditional machine learning (logistic regression, support vector machine and random forest) classifier to classify peanut pod maturity by selecting few key features and demonstrate the tradeoff between the number features and performance of the model. In this work, multiple peanuts have been identified and classified simultaneously which speed up the process for identifying optimum matured peanut pod. It is shown in this paper that it is feasible to automate the optimum matured peanut identification task by intelligent feature selection and classification.

1. METHODOLOGY
2. Data Preprocessing

All the data preprocessing steps are shown in figure-1 as a part of the methodology. Spectral Python library (SPy) [7] has been used to read hyperspectral image data. Since each image file contains 15 images total, firstly, the peanut pixels have been segmented from the background. After segmentation, calibration panel and non-uniform background have been removed by cropping the segmentation mask beyond calibration panels’ location. Then, all the pixels in the image have been identified and labeled according to which peanut they belong to. Lastly, peanut spectrum has been calculated by averaging the spectrum of all pixels of a peanut and used for maturity classification.

Diagram

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Fig. 1 Training and Testing Procedures

1. *Image segmentation*

First of all, reflectance values of Red, Green and Blue wavelength from HSI image were merged together to form an RGB image for segmentation purpose (figure 2-a). For red, green and blue channel, 450 nm, 550 nm and 650 nm wavelength were considered respectively. Ostu thresholding has shown good peanut segmentation performance for all of the images. An example of ostu thresholded image is shown in figure-2 (b) where peanut pixels are labeled as white and backgrounds are labeled as black. In the segmentation mask, some peanut’s region has been labeled as background. Implementation of the morphological dilation operation with kernel size (12,4) has shown improvement in filtering those false background pixels in peanut region but it enlarges the peanut mask at the edges (figure-2c). Segmentation mask found after all of those mentioned operation has been used for the peanut indentification and feature matrix creation.

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(a)

A picture containing text

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(b) (c)

Fig. 2 Peanut RGB image(a), Ostu Thresholded Image (b) and (b) Morphologically filtered image of TUFRunner 511 replication 2

1. *Indentify each peanut from the image:*

The identification of each peanut in the segmentation mask is a tricky task. The pixel position (row and column of that pixel) of a peanut is far away from other peanuts. Therefore, peanut position is given as an input to the k-means clustering was algorithm to group peanut pixels based on the distance between the pixel position. Figure-3 is showing the masks of all identified peanut by k-means clustering. The convention of reading peanut number is given in the caption. From figure-3, it is clear that kmeans algorithm does not label all the peanut squentially. In figure-3, first peanut in the 3rd row has been labeled as 3. This issue has been handled by re-ordering the label of all the peanut pixel considering each peanuts position. Here, peanuts at the top row has been numbered as 1-5 (left to right), second row 6-10, 3rd row 11-15. The process is semi-automated since it requires manually inputing the number of peanuts but still it can help to speed up the mature peanut sorting process which has not been introduced by [AZ].

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Fig.*3*: *Each* TUFRunner 511 replication 2 *identified; Reading convention: Identified 1-5 are shown as red symbol in the center, 6-10 as green, 11-15 blue; in all color group (such as in red 1-5) are divided as square, X, circle, upward triangle, downward triangle sequentially. For an example, first one in the bottom row is red circle, so it is in 1-5 range since red and 3 since circle.*

1. *Create Feature Matrix for classification*

Section 2 only returns position of each peanut in the image. For spectral feature creation, average reflectange at all the pixel positions of a peanut at certain wavelength is calculated first and the average reflectance for all the wavelengths gives the spectrum of that peanut. Then, every spectrum is normalized by the sum of all reflectance value which ensures equal total reflectance. Figure-4a shows the spectrum for 2016 and 2017 data for mature and immature peanut. Figure 4-b shows the spectrum for mature and mature peanut for Georgia-OG replication 3 which resembles the spectrum found by [AZ].

*B. Create a Dataframe:*

Then, a dataframe has been created where Features are the spectrum of each peanut witheach peanut’s label. The final dataframe is of shape (number peanuts, number of wavelength).

*C. Classifier selection , Classification and Analysis:*

Lastly, a suitable classifier is chosen for maturity classification and hyperparameters are tuned to find out best model. Detailed analysis of classifier selection and performance of the classifier will be discussed in the Section IV.

*D. Evaluation Metrics:*

The performance of all the models is compared with [AZ] using the same evaluation metric used in [AZ]. The evaluation metrics were – confusion matrix, accuracy, precision, recall, specificity, and balanced accuracy.

1. DATASET

The dataset used by [AZ] were collected from the field experiment of the North Florida Research and Education Centre. In 2016 and 2017, total five and seven cultivators, were used respectively for experiment. The name of the cultivators used in 2016 are TUFRunner 511, FloRun 157, Georgia-06G and TUFRunner 257, FloRun 331. In 2017, two more cultivars named UF 08036 and FloRun 107 were added to the exiting 5 cultivars. Each cultivar had 3 replications and every replication had 15 samples. Therefore, 225 (5×3×15) and 315 (7×3×15) peanut samples were collected from 2016 and 2017 respectively. The details about sample collection will be found in [AZ].

All hyperspectral images were taken using pushbroom line-scan hyperspectral imaging system. Then, all images were denoised using 4th order Savitzky eGolay filter. The size of the image was 1376×1000 for all 467 spectral channels in 400nm-1000nm range with 1.4 nm spectral resolution. The provided dataset has two files for each 15 peanuts - one header file with an extension hdr and one data file with an extension hyp. Reflectance values were quantized by 32 bit and therefore, the image contains very high-resolution reflectance value.

Chart, histogram

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1. RESULTS

The result section two subsection – 1) Results when 2016 dataset was used for training and the model was tested on 2017 dataset and 2) Results when 2017 dataset was used for training and vice versa. For each result section, 3 models are developed for two different feature selection techniques.

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1. Training on 2016 dataset and testing on 2017 dataset

Feature selection has been a key factor for hyperspectral image classification. Proper feature selection can reduce the computational complexity by a large margin. For hyperspectral images, some wavelengths show a strong contrast between the classes, and sometimes, only a few wavelengths hold enough information for good classification. In this work, two methods have been adopted for feature selection - taking N features having the largest difference between mature and immature class and ANVOA F-test [ref].

1. **Logistic Regression**

All logistic regression models’ class weights are balanced by multiplying the loss function by the proportion of mature and immature classes present in the dataset. The hyperparameter of the best logistic regression model is given in the appendix and the best model in the stushar7.github. Hyperparameter tuning is done by creating a hyperparameter grid in scikit learn and selecting the best model by 10-fold cross-validation. The result of the best logistic regression model has been compared with the result found in [AZ] in table 1. The model shows competitive classification performance for training and testing with 10 principal components extracted from 48 key wavelengths. Comparing this logistic regression model with [AZ], the overall accuracy for training and testing was 0.884 (199/225) vs 0.924 (208/225) and 0.946 (298/315) vs 0.952 (300/315) respectively. This shows that the model fails to classify 26 peanuts maturity in the 2016 dataset (9 less compared to [AZ]) and 17 peanuts maturity in the 2017 dataset (2 less compared to [AZ]). In 2016, the model fails to classify 2/56, 10/66, 9/32, and 5/71 black, brown, yellow, and orange peanut respectively (total of 26) which leads to 96.4%, 84.8%, 71.9%, and 93% classification accuracy respectively. When the classification performance is compared with the [AZ] paper, the model misclassifies +1 black peanut, +5 brown peanuts, equal yellow peanuts, and +3 orange peanuts. While in 2017, the model misclassifies equal black peanut, +6 brown peanut but -2 yellow peanut, -2 orange peanut and therefore, the model has equal, -5.8%, +4.6%, and +2.4% accuracy for all the different colored peanut. Total misclassified peanuts are also evident from the confusion matrix in figure 6. This shows that 14 immature peanuts are treated as mature and 12 mature peanuts as immature. Moreover, the model can classify 89/103 immature peanuts and 110/122 mature peanuts giving -2.9% recall, +4.9% specificity, -4% balanced accuracy. Since in the predicted immature peanuts (89 immature correctly predicted as immature and 12 mature incorrectly predicted as immature) 12/101 are wrong, the precision is 0.881. Similarly, for 2017 dataset, the model provides -3.9% precision, +3.2% recall, -3.2% specificity, equal balanced accuracy since 125/128 immature peanuts and 173/187 mature peanuts are correctly identified.

While considering accuracy among different species of 2016 data, the model shows better performance in predicting maturity in Georgia-06G (97.8% Vs 95.6%), equivalent for FloRun 157 (91.11%) and competitive performance for the other except TUFRunner 297 (75.6% vs 88.9%). For 2017 cultivars, the model shows better performance for Georgia-06G, TUFRunner 297, FloRunn 331 and FloRun 107 (97.8% vs 95.6%, 100% vs 95.6%, 95.6% vs 93.3% and 95.6% vs 93.3% respectively). Only in UF08036, +4 peanut are misclassified.

When ANOVA feature selection is used, 60 wavelength feature provides better performance with just 5 principal components. Compared to strong feature selection, training and testing accuracy, precision, specificity, and balanced accuracy have been improved but not the recall. This means that the model created with ANOVA features predicts mature peanut better than immature peanut when compared to the model created previously, has a better quality of immature peanut prediction, and overall gives a well-balanced accuracy of both classes of peanuts. The confusion matrix shows that among 122 mature peanuts of 2016, it misclassifies only 6 peanuts compared to 6 and 12 for a strong feature and [AZ], and among 180 immature peanuts, it misclassifies 7 peanuts compared to 14 and 8. Therefore, the model is equivalent to [AZ] while predicting 2016 mature peanuts and better for 2017 mature peanuts. From recall, the model is not as good while predicting immature peanuts as predicting mature peanuts. The reason is the failure of predicting yellow peanuts as immature (56.3% vs 71.9%). For other colors, the model is overall better or competitive. For different species, the model is better for Georgia-06G and TUFRunner 297, equivalent for FloRun 157, and competitive for other species except TUFRunner 511. Again, all the results are shown in Table-1. Since the dataset has a more mature peanut than an immature peanut, it learns the feature of a mature peanut better than immature peanuts.

1. **SVM**

Among 103 immature peanuts of 2016, 84 and 85 peanuts are detected as immature by the strong features selected (SVMS) and ANOVA feature selected model (SVMA) compared to 92 detected by the HSI model. For SVMS, 14 yellow peanuts and 4 orange peanuts are predicted as mature. Whereas for SVMA, -1 yellow misprediction and +2 orange misprediction occur. Therefore, both SVM model has lower recall with slightly better precision. Moreover, SVMS and SVMA has slightly better specificity since only 10 and 6 mature peanuts are misclassified among 122 peanuts of 2016 compared to 6 of AZ. SVMS misclassified 4 more brown peanuts compared to SVMS and AZ. The model does an equivalent job for Flo Run 157 and a better job for Georgia-06G but moderate jobs for others. The scenario is the same for 2017 dataset, among 128 immature peanuts 25 and 24 are mispredicted compared to only 7 in HSI but for matured peanut only 6 and 1 are mis predicted as immature (just 1 and 6 brown peanuts are predicted as immature). Misprediction in yellow (16 & 14 respectively) and Orange (9 & 10) lead to even lower recall than logistic regression model but having a competitive precision. On the contrary, those models have high specificity (SVMA has even higher specificity than AZ) and slightly worse balanced accuracy than logistic regression model. For different species of 2016, FloRun 157 and Georgia-06G shows better performance for SVMS and FloRun 157, Georgia-06G and TUF Runner 297 shows better performance for SVMA. Other specifies shows competitive performance whereas TUFRunner 511 shows worst performance. For 2017 species, TUF Runner 511 & Flo Run 157 shows better performance SMVS whereas for SVMA, Georgia-06G and FloRun 331 has better performance. The worst performance is for UF 08036 for SVMS and SVMA.

1. **Random Forest**

Among the immature peanut of 2016 dataset, RFS and RFA misclassifies 11 and 5 peanut specifically compared to 11 misclassified case for AZ which explains good recall rate by those models. For RFS, 7 yellow and 4 orange peanuts are misclassified whereas for RFA only 5 yellow peanuts are misclassified compared to 9 & 2 misclassified case for AZ. Among mature peanuts, 4 brown peanuts are misclassified by compared to 5 brown peanuts and 1 black peanut are misclassified by AZ. For RFA, 8 mature peanuts are misclassified where 1 & 7 black and brown peanuts respectively. Therefore, RFS has higher specificity than AZ and RFA has competitive specificity. Because of good mature and immature peanut classification rate, RFS has good precision. Moreover, both model has better training accuracy and balanced accuracy than AZ.

For Testing dataset, among 128 immature peanuts, both model mis predict 10 and 11 cases respectively compared to 7 cases for AZ. For RFS 10 misprediction comes from 4 yellow peanuts and 6 orange peanuts whereas 3 & 2 misprediction of AZ. For RFA case, 8 yellow peanuts and 3 orange peanuts are misclassified. Among mature peanuts, 11 and 13 brown peanuts are misclassified by both models compared to 8 by AZ. All black peanuts are correctly classified.

1. Training on 2016 dataset and testing on 2017 dataset
2. **SVM**

Among 128 immature peanuts of 2017, 84 and 85 peanuts are detected as immature by the strong features selected (SVMS) and ANOVA feature selected model (SVMA) compared to 92 detected by the HSI model.

For SVMS, 14 yellow peanuts and 4 orange peanuts are predicted as mature. Whereas for SVMA, -1 yellow misprediction and +2 orange misprediction occur. Therefore, both SVM model has lower recall with slightly better precision. Moreover, SVMS and SVMA has slightly better specificity since only 10 and 6 mature peanuts are misclassified among 122 peanuts of 2016 compared to 6 of AZ. SVMS misclassified 4 more brown peanuts compared to SVMS and AZ. The model does an equivalent job for Flo Run 157 and a better job for Georgia-06G but moderate jobs for others. The scenario is the same for 2017 dataset, among 128 immature peanuts 25 and 24 are mispredicted compared to only 7 in HSI but for matured peanut only 6 and 1 are mis predicted as immature (just 1 and 6 brown peanuts are predicted as immature). Misprediction in yellow (16 & 14 respectively) and Orange (9 & 10) lead to even lower recall than logistic regression model but having a competitive precision. On the contrary, those models have high specificity (SVMA has even higher specificity than AZ) and slightly worse balanced accuracy than logistic regression model. For different species of 2016, FloRun 157 and Georgia-06G shows better performance for SVMS and FloRun 157, Georgia-06G and TUF Runner 297 shows better performance for SVMA. Other specifies shows competitive performance whereas TUFRunner 511 shows worst performance. For 2017 species, TUF Runner 511 & Flo Run 157 shows better performance SMVS whereas for SVMA, Georgia-06G and FloRun 331 has better performance. The worst performance is for UF 08036 for SVMS and SVMA.

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| Metric | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Accuracy | 0.924 | 0.952 | 0.884 | 0.946 | 0.871 | 0.902 | 0.933 | 0.933 |
| Precision | 0.939 | 0.938 | 0.881 | 0.899 | 0.894 | 0.945 | 0.958 | 0.915 |
| Recall | 0.893 | 0.945 | 0.864 | 0.977 | 0.816 | 0.805 | 0.893 | 0.922 |
| Specificity | 0.951 | 0.957 | 0.902 | 0.925 | 0.918 | 0.968 | 0.967 | 0.941 |
| Balanced Accuracy | 0.922 | 0.951 | 0.882 | 0.951 | 0.867 | 0.886 | 0.930 | 0.931 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| TUFRunner 511 | 91.1% | 93.3% | 84.4% | 93.3% | 77.8% | 93.3% | 86.7% | 97.8% |
| FloRun 157 | 91.1% | 97.8% | 91.1% | 95.6% | 91.1% | 91.1% | 93.3% | 97.8% |
| Georgia-06G | 95.6% | 95.6% | 97.8% | 97.8% | 97.8% | 93.3% | 97.8% | 95.6% |
| TUFRunner 297 | 88.9% | 95.6% | 75.6% | 100% | 82.2% | 88.9% | 93.3% | 95.6% |
| FloRun 331 | 97.8% | 93.3% | 93.3% | 95.6% | 86.7% | 86.7% | 95.6% | 93.3% |
| UF 08036 |  | 97.6% |  | 84.4% |  | 82.2% |  | 84.4% |
| FloRun 107 |  | 93.3% |  | 95.6% |  | 95.6% |  | 88.9% |

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| Color | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Black | 98.2% | 100% | 96.4% | 100% | 98.2% | 100% | 100% | 100% |
| Brown | 92.4% | 92.3% | 84.8% | 86.5% | 86.4% | 94.2% | 93.9% | 89.4% |
| Yellow | 71.9% | 88.6% | 71.9% | 93.2% | 59.4% | 63.6% | 78.1% | 90.9% |
| Orange | 97.2% | 97.6% | 93% | 100% | 91.5% | 89.3% | 94.4% | 92.9% |

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| Metric | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Accuracy | 0.924 | 0.952 | 0.893 | 0.965 | 0.893 | 0.921 | 0.942 | 0.924 |
| Precision | 0.939 | 0.938 | 0.934 | 0.947 | 0.934 | 0.990 | 0.925 | 0.90 |
| Recall | 0.893 | 0.945 | 0.825 | 0.969 | 0.825 | 0.813 | 0.951 | 0.914 |
| Specificity | 0.951 | 0.957 | 0.951 | 0.963 | 0.951 | 0.995 | 0.934 | 0.930 |
| Balanced Accuracy | 0.922 | 0.951 | 0.888 | 0.966 | 0.888 | 0.904 | 0.943 | 0.922 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| TUFRunner 511 | 91.1% | 93.3% | 77.8% | 97.8% | 80% | 91.1% | 86.7% | 95.6% |
| FloRun 157 | 91.1% | 97.8% | 91.1% | 97.8% | 91.1% | 93.3% | 97.8% | 97.8% |
| Georgia-06G | 95.6% | 95.6% | 97.8% | 100% | 97.8% | 95.6% | 100% | 95.6% |
| TUFRunner 297 | 88.9% | 95.6% | 88.9% | 100% | 88.9% | 91.1% | 91.1% | 91.1% |
| FloRun 331 | 97.8% | 93.3% | 91.1% | 97.8% | 88.9% | 93.3% | 95.6% | 88.9% |
| UF 08036 |  | 97.6% |  | 86.7% |  | 88.9% |  | 86.7% |
| FloRun 107 |  | 93.3% |  | 95.6% |  | 91.1% |  | 91.1% |

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| Color | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Black | 98.2% | 100% | 98.2% | 100% | 98.2% | 98.8% | 98.2% | 100% |
| Brown | 92.4% | 92.3% | 92.4% | 93.3% | 92.4% | 93.3%(81.7%) | 89.4% | 87.5% |
| Yellow | 71.9% | 88.6% | 56.3% | 93.2% | 56.3% | 77.3%(75%) | 84.4% | 81.8% |
| Orange | 97.2% | 97.6% | 94.4% | 98.8% | 94.4% | 94%(91.7%) | 100% | 96.4% |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Metric | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Accuracy | 0.952 | 0.871 | 0.962 | 0.88 | 0.990 | 0.849 | 0.978 | 0.871 |
| Precision | 0.938 | 0.836 | 0.983 | 0.874 | 0.989 | 0.810 | 0.974 | 0.855 |
| Recall | 0.945 | 0.893 | 0.952 | 0.910 | 0.995 | 0.943 | 0.989 | 0.918 |
| Specificity | 0.957 | 0.853 | 0.977 | 0.845 | 0.984 | 0.738 | 0.961 | 0.816 |
| Balanced Accuracy | 0.951 | 0.873 | 0.964 | 0.877 | 0.990 | 0.840 | 0.975 | 0.867 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| TUFRunner 511 | 93.3% | 86.7% | 97.8% | 77.8% | 95.6% | 77.8% | 100% | 77.8% |
| FloRun 157 | 97.8% | 88.9% | 100% | 93.3% | 100% | 86.7% | 95.6% | 91.1% |
| Georgia-06G | 95.6% | 86.7% | 95.6% | 95.6% | 100% | 93.3% | 100% | 93.3% |
| TUFRunner 297 | 95.6% | 84.4% | 100% | 84.4% | 100% | 80% | 100% | 80% |
| FloRun 331 | 93.3% | 88.9% | 95.6% | 88.9% | 100% | 86.7% | 97.8% | 93.3% |
| UF 08036 | 97.8% |  | 86.7% |  | 97.8% |  | 93.3% |  |
| FloRun 107 | 93.3% |  | 97.8% |  | 100% |  | 97.8% |  |

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| Color | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Black | 100% | 89.3% | 100% | 98.2% | 100% | 98.2% | 100% | 96.4% |
| Brown | 92.3% | 81.8% | 91.3% | 84.8% | 99% | 90.9% | 98.1% | 87.9 |
| Yellow | 88.6% | 71.8% | 93.2% | 65.6% | 95.5% | 46.9% | 93.2% | 59.4% |
| Orange | 97.6% | 97.2% | 100% | 93% | 100% | 85.9% | 97.6% | 91.5% |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Metric | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Accuracy | 0.952 | 0.871 | 0.971 | 0.884 | 0.930 | 0.876 | 0.965 | 0.853 |
| Precision | 0.938 | 0.836 | 0.973 | 0.863 | 0.899 | 0.862 | 0.954 | 0.894 |
| Recall | 0.945 | 0.893 | 0.979 | 0.934 | 0.995 | 0.918 | 0.989 | 0.828 |
| Specificity | 0.957 | 0.853 | 0.961 | 0.825 | 0.836 | 0.825 | 0.930 | 0.883 |
| Balanced Accuracy | 0.951 | 0.873 | 0.970 | 0.880 | 0.915 | 0.872 | 0.959 | 0.856 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| TUFRunner 511 | 93.3% | 86.7% | 97.8% | 77.8% | 91.1% | 77.8% | 93.3% | 77.8% |
| FloRun 157 | 97.8% | 88.9% | 97.8% | 91.1% | 95.6% | 91.1% | 97.8% | 91.1% |
| Georgia-06G | 95.6% | 86.7% | 100% | 97.8% | 97.8% | 97.8% | 100% | 97.8% |
| TUFRunner 297 | 95.6% | 84.4% | 100% | 86.7% | 93.3% | 82.2% | 100% | 64.4% |
| FloRun 331 | 93.3% | 88.9% | 95.6% | 88.9% | 93.3% | 88.9% | 95.6% | 95.6% |
| UF 08036 | 97.8% |  | 91.1% |  | 88.9% |  | 91.1% |  |
| FloRun 107 | 93.3% |  | 97.8% |  | 91.1% |  | 97.8% |  |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Color | Hyperspectral Unmixing [AZ] |  | Logistic Regression |  | Support Vector Machine |  | Random Forest |  |
|  | Train | Test | Train | Test | Train | Test | Train | Test |
| Black | 98.2% | 100% | 100% | 98.2% | 100% | 98.2% | 100% | 98.2% |
| Brown | 92.4% | 91.3% | 96.2% | 89.4% | 99% | 86.4% | 98.1% | 69.7% |
| Yellow | 71.9% | 88.6% | 90.9%( | 56.3% | 70.5% | 56.3% | 86.4% | 71.9% |
| Orange | 97.2% | 97.6% | 98.8% | 94.4% | 90.5% | 94.4% | 96.4% | 95.8% |

LR:

Among 128 immature peanuts of 2017, 3 and 5 peanuts are mis predicted by the strong features selected (LRS) and ANOVA feature selected model (LRA) compared to 7 mispredictions by the HSI model. For LRS,the misprediction comes from the 3 yellow peanuts, and for the LRA, the misprediction comes from 4 yellow peanuts and 1 orange peanuts whereas the HSI model gives 5 and 2 misprediction respectively. On the other hand, for 187 mature peanuts, 9 and 4 brown peanut is misclassified for LRS and LRA models whereas HSI gives the wrong prediction of 8 brown mature peanuts. Therefore, both LR model has a recall, precision, and specificity. Among all the species, only for FloRun 157 and TUFRunner 297 all maturity classes are detected for the strong feature selected model but provides above 90% accuracy for all species except UF08036.  Whereas the model trained by features selected ANOVA fails to detect maturity class except Georgia-06G and TUFRunner 297 but provides above 90% accuracy for all species. Moreover, the balanced accuracies are 0.964 and 0.970 for the LRS and LRA models respectively.

On the other hand, among 103 immature peanuts of 2016, 87 and 85 peanuts are classified accurately the strong features selected (LRS) and ANOVA feature selected model (LRA) compared to 92 detected by the HSI model. For the LRS model, 11 yellow peanuts and 5 orange peanuts are predicted as mature. Whereas for LRA, 14 yellow misprediction and 4 orange misprediction occur. For all 122 mature peanuts, 111 and 114 are classified correctly by the LRS and LRA model respectively compared to 104 by the HSI model. Therefore, both LR model has lower recall with slightly better precision. Moreover, LRSand LRA have slightly better specificity since only 11 and 8 mature peanuts are misclassified compared to 18 of HSI.  The misclassification comes from 1 black, 10 brown for the LRS case and 1 black, 7 brown for the LRA case. The LRS and LRA models predict correct classes for all the classes in more than 84.4% and 86.7% of the cases respectively except TUFRunner 511. In addition to that, the balanced accuracies are 0.877 and 0.880 for the LRS and LRA models respectively.

SVM:

Among 128 immature peanuts of 2017, 2 and 21 peanuts are mispredicted by the strong features selected (SVMS) and ANOVA feature selected model (SVMA) compared to 7 mispredictions by the HSI model. For SVMS, the misprediction comes from the 2 yellow peanuts, and for the SVMA, the misprediction comes from 13 yellow peanuts and 8 orange peanuts whereas the HSI model gives 5 and 2 misprediction respectively. On the other hand, for 187 mature peanuts, 1 brown peanut is misclassified for both models whereas HSI gives the wrong prediction of 8 brown mature peanuts. Therefore, both SVM model has a recall, precision, and specificity. Among all the species, only TUFRunner 511 and UF 08036 has some misprediction (95.6% & 97.8% accuracy) for the strong feature selected model. But the model trained by features selected ANOVA fails to detect maturity class in all species but provides 90% accuracy for all except UF08036. Moreover, the balanced accuracies are 0.990 and 0.915 for the SVMA and SVMS models respectively.

On the other hand, among 103 immature peanuts of 2016, 76 and 85 peanuts are classified accurately the strong features selected (SVMS) and ANOVA feature selected model (SVMA) compared to 92 detected by the HSI model. For the SVMS model, 17 yellow peanuts and 10 orange peanuts are predicted as mature. Whereas for SVMA, -3 yellow misprediction and +2 orange misprediction occur. For all 122 mature peanuts, 115 and 112 are classified correctly by the SVMS and SVMA model respectively compared to 104 by the HSI model. Therefore, both SVM model has lower recall with slightly better precision. Moreover, SVMS and SVMA have slightly better specificity since only 7 and 10 mature peanuts are misclassified compared to 18 of HSI. The misclassification comes from 1 black, 6 brown for the SVMS case and 1 black, 9 brown for the SVMA case. The SVMS and SVMA models predict correct classes for all the classes in more than 80% and 82% of the cases respectively except TUFRunner 511. In addition to that, the balanced accuracies are 0.84 and 0.872 for the SVMA and SVMS models respectively.

RF:

Among 128 immature peanuts of 2017, 5 and 9 peanuts are mispredicted by the strong features selected (RFS) and ANOVA feature selected model (RFA) compared to 7 mispredictions by the HSI model. For RFS, the misprediction comes from the 3 yellow peanuts and 2 orange peanuts, and for the RFA, the misprediction comes from 6 yellow peanuts and 3 orange peanuts whereas the HSI model gives 5 and 2 misprediction respectively. On the other hand, for 187 mature peanuts, 2 brown peanuts are misclassified for both models whereas HSI gives the wrong prediction of 8 brown mature peanuts. Both the models have better recall and precision. Although RFS has better specificity, but the RFA model has slightly less specificity compared to HSI. Among all the species, only TUFRunner 511 and UF 08036 has some misprediction (95.6% & 97.8% accuracy) for the strong feature selected model. RFS and RFA have the worst-case prediction accuracy of 93.3% and 91.1% and provide better results for 5 species. The accuracy and balanced accuracy are found better for both the models compared to the HSI model.

On the other hand, among 103 immature peanuts of 2016, 84 and 91 peanuts are classified accurately the strong features selected (RFS) and ANOVA feature selected model (RFA) compared to 92 detected by the HSI model. For the RFS model, 13 yellow peanuts and 6 orange peanuts are predicted as mature. Whereas for RFA, -4 yellow misprediction and -3 orange misprediction occur. For all 122 mature peanuts, 112 and 101 are classified correctly by the RFS and RFA model respectively compared to 104 by the HSI model. Therefore, the RFS model has lower recall with slightly better precision whereas the RFA model has better recall and precision. Moreover, RFS has better specificity since only 10 mature peanuts are misclassified but RFA misclassifies 21 mature peanuts leading to lower specificity. The misclassification comes from 2 black, 8 brown for the RFS case and 1 black, 20 brown for the RFA case. The RFS and RFA models predict correct classes for more than 91% cases for all species except TUFRunner 511 and TUFRunner 297. The accuracy and balanced accuracy are found competitive for both the models compared to the HSI model.