

SEMANTIC SEGMENTATION OF DISEASES IN MUSHROOMS USING ENHANCED RANDOM FOREST

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Abstract. Mushrooms are a rich source of antioxidants and nutritional values. Edible mushrooms, however, are susceptible to various diseases such as dry bubble, wet bubble, cobweb, bacterial blotches, and mites. Farmers face significant production losses due to these diseases affecting mushrooms. The manual detection of these diseases relies on expertise, knowledge of diseases, and human effort. Therefore, there is a need for computer-aided methods, which serve as optimal substitutes for detecting and segmenting diseases. In this paper, we propose a semantic segmentation approach based on the Random Forest machine learning technique for the detection and segmentation of mushroom diseases. Our focus lies in extracting a combination of different features, including Gabor, Bouda, Kayyali, Gaussian, Canny edge, Roberts, Sobel, Scharr, Prewitt, Median, and Variance. We employ constant mean-variance thresholding and the Pearson correlation coefficient to extract significant features, aiming to enhance computational speed and reduce complexity in training the Random Forest classifier. Our results indicate that semantic segmentation based on Random Forest outperforms other methods such as Support Vector Machine (SVM), Naïve Bayes, K-means, and Region of Interest in terms of accuracy. Additionally, it exhibits superior precision, recall, and F1 score compared to SVM. It is worth noting that deep learning-based semantic segmentation methods were not considered due to the limited availability of diseased mushroom images.

Key words: mushroom diseases, semantic segmentation, computer aided, Machine Learning, significant feature extraction, Random Forest classifier.

1. Introduction

To enhance mushroom yields, farmers frequently invest in controlled environment cultivation rooms. Despite these earnest endeavours, the persistence of diseases in substrates and mushrooms remains a challenge [1,2]. Even with precautionary measures in place, a lack of knowledge, crop management skills, and occasional human errors can contribute to the onset of diseases affecting both mushrooms and their substrate bags. Among the most prevalent mushroom diseases are cobweb, wet bubble, bacterial blotches, dry bubble, and mites. These diseases not only affect individual mushrooms but also have the potential to spread from one mushroom to another. Over time, they can proliferate throughout the cultivation bag, extending to other bags in the room, resulting in significant losses for the farmer. Timely detection and proactive measures are paramount for mitigating the impact of these diseases. The manual identification of mushroom diseases poses a formidable challenge, necessitating a profound expertise in disease recognition

and the capacity to implement effective corrective actions. Farmers frequently find themselves compelled to seek guidance from scientific experts, and any oversight in this process can result in significant losses. Moreover, the early-stage detection of diseases with the naked eye proves to be a daunting task, underscoring the imperative for computer-aided detection methods. Traditional methods for identifying diseases in mushrooms often depend on non-computer-aided techniques that utilize chemical and biological approaches in scientific laboratories. Nevertheless, these methodologies are often time-consuming. In response to this challenge, we introduce an innovative computer-aided methodology that harnesses the power of machine learning, particularly an Enhanced Random Forest technique. Our proposed method integrates an optimized selection of features to reduce complexity and elevate overall effectiveness in implementation.

The subsequent sections of this article are structured as follows: Section 2 presents a comprehensive literature review that encompasses mushroom diseases, various disease detection methods, and the application of machine learning techniques in disease segmentation. In Section 3, the design methodology is detailed, incorporating established segmentation methods such as K-Means clustering, Region of Interest extraction, Colour Threshold, Support Vector Machine (SVM), and the proposed Enhanced Random Forest method, with a specific focus on parameter optimization techniques. Section 4 provides a presentation of results and a discussion on mushroom disease segmentation, covering both existing standard methods and the newly proposed approach, followed by a comparative analysis. Finally, the conclusions of the work are summarized in Section 5.

2. Related work and motivation

The literature review outlines various methods and approaches employed in the detection and segmentation of mushroom diseases, emphasizing both manual and computer-aided techniques and also outlines some of the different disease detection methods. The proposed research aims to address the existing gap in automated mushroom disease segmentation by introducing a semantic segmentation method based on Enhanced Random Forest. This method is compared against established state-of-the-art techniques such as SVM, Naïve Bayes, K-means, ROI, and Colour Threshold methods. The review begins by discussing manual segmentation methods involving chemical and biological processes, such as Biological Material-RNA [3] analysis and Isolation of dsRNA [4] coupled with electron microscopy. These methods are noted for their time-consuming nature. Computer-aided methods, as outlined in [5] and [6], leverage techniques like Naïve Bayes, Sequential Minimal Optimization, and Ripple Down Rules (RIDOR) for classifying 16 images of diseased mushrooms. Human intervention is required in the conversion of these images to a suitable file format for classification. Additionally, an automated pixel-to-pixel image processing-based software, proposed by [7] and [8], is designed to inspect white button mushroom crops and detect signs of illness and pests.

For diagnosing mushroom diseases, [9] and [10] have developed a rule-based expert

system. This system necessitates text-based responses from farmers as inputs to detect diseases. While these methods utilize computer-aided techniques, it is important to emphasize that human intervention is still required to detect diseased mushrooms in a given image. The various image segmentation approaches [11] in general are threshold, edge and region based applied for disease segmentation in different fields like agriculture or medical diagnosis. In [12] the region growing method is used to segment disease spots on leaf and eliminate background by interactively selecting growing seeds in the ACCF map. Then morphological operation is used on the region growing method results.

In the identification of diseases in Arecanut, a two-step procedure is employed, incorporating K-Means clustering and the Otsu approach, as outlined in [13]. The colour-based K-Means clustering method is applied during pre-processing to effectively isolate Arecanut from the background. Subsequently, the Otsu thresholding method is employed to transform RGB images into monochrome images, facilitating the detection of diseases. The diseased area of the Arecanut is then accurately determined using the connected components method.

In addition to conventional state-of-the-art methods, numerous machine learning approaches have been proposed for disease classification in plants and fruits. For instance, in the segmentation and classification of plant leaf diseased areas, image thresholding, K-Means clustering, and Neural networks are utilized [14]. In the case of apple fruits, the identification of infected areas involves employing a Global threshold for segmentation. Further classification of the infected areas on apple fruits is accomplished using a Machine Learning Technique, specifically the multi-class Support Vector Machine (SVM) [15].

The random forest, as introduced in [17], operates on an ensemble of trees, each dependent on the values of a random vector. This vector is sampled independently, yet uniformly, across all trees within the forest. This strategic approach embodies a diversified learning mechanism, cultivating robustness against noise and enhancing adaptability in predictive modelling. T. K. Ho, in [18], proposed tree-based classifiers to arbitrarily increase capacity, thereby improving accuracy for both training and testing data. The approach involves developing multiple trees in randomly selected subspaces, particularly effective for handwritten digits.

Achieving accurate and effective semantic segmentation poses a challenge due to the necessity of classifying each pixel, a computationally demanding task. In addressing this challenge, [19] presents a random forest-based semantic segmentation algorithm that achieves precise and effective pixel-wise classification of body poses. The Random Forest (RF) approach [20] for pixel-level segmentation in images contributes in three significant ways. First, it demonstrates the applicability of Nearest Neighbour Matching and Texton Class Histograms to the Random Forest structure. Second, it underscores the importance of discriminative learning and geographic context for Random Forest, emphasizing how the architecture can enhance classifier performance. Lastly, segmentation performance is elevated by utilizing Random Forest to integrate multiple features, including colour,

textons, HOG features, and filter banks. A Flexible Random Forest model [21] has been developed to address a diverse and extensive range of video and image tasks, presenting a discussion that combines both theoretical insights and practical implementations.

In addition to employing machine learning techniques for segmenting diseases across various fields, deep learning methods are also utilized in disease segmentation. Several convolutional neural network-based techniques presented in [22] aim to enhance the accuracy of semantic segmentation. Deep learning approaches excel over other methods, partially due to their ability to learn intricate representations, coupled with hierarchical structures and non-linear activations. Notable deep learning-based semantic segmentation models such as DeepLab, CCNet, SegNet, ICNet, and RefineNet [23,24,25,26,27,28] have been developed for segmenting images of various types, including high-resolution and real-time image segmentation.

From the existing literature, it follows evidently that there is limited research on mushroom disease segmentation, and the current studies in this domain require human intervention rather than an automated approach. In response to this gap, a semantic segmentation method is proposed based on Enhanced Random Forest (ERF) for mushroom disease segmentation. This method is compared against standard state-of-the-art techniques such as SVM, Naïve Bayes, K-means, ROI, and colour threshold methods. Due to the scarcity of diseased mushroom images from diverse sources, deep learning-based semantic segmentation methods like DeepLab, SigNet, ICNet, etc., were not considered in the comparative analysis.

3. Methodology and methods

3.1. Existing standard methods of segmentation

Image processing is a multidisciplinary field encompassing the manipulation, analysis, and interpretation of visual information extracted from considered images. Within this domain, diverse approaches are employed to extract insightful information and enhance image quality for various applications. Noteworthy methods in digital image processing include K-Means clustering, Region of Interest (ROI) extraction, the colour threshold method, and the application of Naïve Bayes, as well as SVM classification techniques, which are subject to comparative analysis. These techniques find application across various domains such as computer vision, remote sensing, medical imaging, and the detection of diseases in agricultural crops.

3.2. Random Forest-based semantic segmentation

In the proposed approach for segmenting mushroom diseases, we employ Random Forest-based semantic segmentation. Throughout this segmentation process, the initial pre-processing of image data is conducted to enhance both its quality and relevance. Following this, feature estimation procedures are implemented to capture pertinent image

attributes. Subsequently, significant features are extracted to facilitate the discrimination of key regions. To attain the final segmentation results, a pixel-wise Random Forest classifier is applied.

3.2.1. Data set

Firstly, the collection process involves gathering images of both diseased and healthy mushrooms for training purposes. Ground truth images are subsequently generated with the input of experts, who provide valuable insights into the distinctive characteristics of mushroom diseases. Subsequently, the images undergo a pre-processing stage before feature extraction. Each image considered for training is represented by the notation $I_{p \times q}$, where 'p' and 'q' denote the row and column of the matrix 'I.' In this matrix, every element, designated as I_i , corresponds to a pixel with an intensity value.

3.2.2. Image pre-processing

The original images are in the RGB colour model, but they have been converted to a single grayscale representation using the green channel for ease of processing. This conversion is advantageous due to the contrast property, which is particularly beneficial over the red (R) and blue (B) channels. The green channel response exhibits a lower contrast, while the blue channel demonstrates a less dynamic range.

3.2.3. Feature estimation

The preprocessing of training images involves the consideration of both diseased and non-diseased classes for feature estimation, aiming to accurately segment the diseased portions. Various features are computed from the training images, including Canny and Sobel edge detectors, as well as Roberts, Scharr, Prewitt, Bouda, and Kayyali edge detectors, which are derived from the Sobel operator. Additionally, Gaussian features with σ values of 3 and 7, Median with a size of 3, and Gabor filters with a kernel size of 9×9 and variations in orientation (ϕ), scaling (σ), and wavelength (γ) are employed. These features, each assigned corresponding weights, play a pivotal role in node splitting and classification decision within the random forest framework. The computation of features involves the mathematical operation of convolution between the input image and the filter, as expressed as follows

$$Y(i, j) = \sum_{k=1}^m \sum_{l=1}^n I(i+k-1, j+l-1)K(k, l), \quad (1)$$

where $i = \{1, 2, \dots, M - m + 1\}$ and $j = \{1, 2, \dots, N - n + 1\}$, $M \times N$ is the size of input image, m, n is the size of the filter (kernel). The kernel or filter coefficient of Roberts, 3×3 Sobel, 3×3 Prewitt, 3×3 Kayyali [29], Bouda [30] are as follows

$$\begin{aligned}
K_{\text{Roberts}} &= \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix}, \quad K_{\text{Sobel}} = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix}, \quad K_{\text{Prewitt}} = \begin{bmatrix} -1 & 0 & 1 \\ -1 & 0 & 1 \\ -1 & 0 & 1 \end{bmatrix}, \\
K_{\text{Kayali}} &= \begin{bmatrix} -1 & 0 & 1 \\ -1 & 0 & 1 \\ -1 & 0 & 1 \end{bmatrix}, \quad K_{\text{Bouda}} = \begin{bmatrix} \sqrt{2} & 0 & -\sqrt{2} \\ 2\sqrt{2} & 0 & -2\sqrt{2} \\ \sqrt{2} & 0 & -\sqrt{2} \end{bmatrix}, \quad K_{\text{Schar}} = \begin{bmatrix} -3 & 0 & 3 \\ -10 & 0 & 10 \\ -3 & 0 & 3 \end{bmatrix}.
\end{aligned}$$

The Gaussian filter kernel of size $(2k + 1) \times (2k + 1)$ convolved with input image is given by

$$K_{ij} = \frac{1}{2\pi\sigma^2} e^{-\frac{(i-(k+1))^2 + j-(k+1))^2}{(2\sigma^2)}} \quad 1 \leq i, j \leq 2k + 1. \quad (2)$$

Canny edge filter works with derivatives in direction of the edge textures on Gaussian filtered output [31]. Gabor filter function [31] is represented by the product of Gaussian function and exponential function given as

$$g_{\theta, \gamma, \lambda, \phi, \sigma}(x, y) = \exp\left[\frac{-(x^2 + \gamma^2 y^2)}{(2\sigma^2)}\right] \exp\left[\frac{i2\pi x}{\lambda\sigma + \phi}\right], \quad (3)$$

where θ gives rotation of Gabor envelope, λ Regulates the width of the Gabor function strips, γ regulates the Gabor filter height, σ regulates the Gabor filter overall size, ϕ is phase offset of sinusoid and is equal to zero in the considered case.

3.2.4. Significant features extraction

The features assessed in Section 3.2.3 lack significance. Extracting significant features proves beneficial in alleviating the computational burden during both training and testing phases, leading to time savings. To achieve this, we advocate for feature extraction through constant mean-variance thresholding. This approach helps eliminate features with low variance and zero-valued variables. Additionally, employing the Pearson correlation coefficient aids in identifying highly correlated features, which may result in feature duplication. By avoiding such redundancies, we aim to enhance computational efficiency.

Constant mean-variance thresholding

A non-constant feature extraction method employs mean-variance thresholding. This technique aids in discerning features that are either constant, approximately constant, or zero-valued. Such features lack significance in determining the pixel's class within a given image.

Let V represent a variable (one of the features among the total set of features). It becomes a significant feature if it satisfies the following condition

$$\begin{aligned}
&\text{if } v_i \leq (m - 2\sigma^2) \quad v_i \text{ is not significant} \\
&\text{otherwise} \quad v_i \text{ is significant,}
\end{aligned} \quad (4)$$

where v_i is feature considered at that instant, m is mean and σ^2 is variance of the feature set, respectively.

Pearson correlation coefficient

The Pearson correlation coefficient is a widely utilized statistical measure that gauges the strength of the relationship between two variables. This measure is particularly prevalent in the context of linear regression analysis. When employed for feature reduction purposes, the Pearson correlation coefficient (5), denoted as p_r , is calculated for two features, f_1 and f_2 .

$$p_r = \frac{N(\sum f_1 * f_2) - (\sum f_1)(\sum f_2)}{\sqrt{[N \sum f_1^2 - (\sum f_1)^2][N \sum f_2^2 - (\sum f_2)^2]}} \quad (5)$$

where f_1 is first feature set and f_2 is adjacent feature set under consideration. N is number of elements in the feature set. Higher the p_r value between f_1 and f_2 , higher the correlation, and it indicates duplication of these features, which is not effective for training.

3.2.5. Random Forest pixel-wise classifier

It constitutes an ensemble of decision trees, trained through the bagging method, typically with the maximum number of samples set to the size of the training set. This algorithm yields greater tree diversity, introducing a higher bias for lower variance and consequently leading to a superior model. In a Random Forest, during the splitting process at each node, a random subset of features is considered to grow the tree, searching for the best feature among this random subset. Moreover, it is possible to enhance the randomness of trees by also employing random thresholds for each feature, instead of searching for the best possible threshold as done in a traditional decision tree.

Let the dataset be denoted as $D = \{f_1, f_2, \dots, f_n\}$, where each point represents a feature. We randomly select a subset of features (pixels) from this dataset, with the pixels, in turn, corresponding to the class labels originally present in the dataset. A feature is represented by f_i [32] and is given by

$$f_i(p, P, V) = \sum_{i=1}^n w_i P_{(p+u_i/V_p, h)} \quad (6)$$

where p is a pixel under consideration, P is the input image, w is weight, V is depth map, h is channel index of P , u is offset parameter vector.

Bootstrap data sets $D_i | i = 1, 2, \dots, B$ are generated from the data set D , by randomly selecting the significant features discussed in Section 3.2.4, where repeating is allowed. Each randomly chosen Bootstrap set D_i helps in constructing Decision Tree T_i . Root node of the Tree can be any one of the features in D_i . At each decision tree nodes splitting

S_j is done and the best split is chosen as that which has the highest information gain:

$$S_j = S_j^L \cup S_j^R, \quad (7)$$

where S_j^L is left split, S_j^R is right split. Information gain in terms of entropy for the node split is given by (8), where entropy at the node is given by (9):

$$I_j = H(s_j) - \sum_{i \in (L,R)} \frac{S_j^i}{s_j} H(S_j^i), \quad (8)$$

$$H(s) = \sum_i^C -P_i(s) \log_2 P_i(s), \quad (9)$$

where S_j is target population before the split, $H(s)$ is entropy of s , $H(S_j^i)$ is entropy of S_j^i , S_j^i are data points falling into right or left subtree based on $i \in (L, R)$. P_i is the probability of a class i in the data s . The conditional probability from each tree T_i for a data point p being a class c considered at each node is given by

$$PT_i(c/p, P, V) < Q \quad \text{or} \quad PT_i(c/p, P, V) > Q, \quad (10)$$

where Q is the threshold. Then, the majority voting out of the total decision trees is considered to decide the p being class c .

Algorithmic steps

Mushroom images, both diseased and non-diseased, are initially divided into training and test sets. Subsequently, mask images are generated for the training dataset. The algorithmic flow can be outlined in the following steps:

Step 1: Consider mushroom images

Step 2: Image Preprocessing – Convert the image from RGB to grayscale and resize it to a standard size of 128×128 .

Step 3: Feature Extraction – Extract features such as Gabor features, original image pixels, Canny edge, Roberts, Sobel, Scharr, Prewitt, Bouda, Kayyali, Gaussian ($\sigma = 3$ and $\sigma = 7$), Median ($\sigma = 3$), and variance with a size of 3 from the mushroom images.

Step 4: Extract significant features using a constant mean-variance threshold and Pearson correlation for training.

Step 5: Image Pre-processing for Labelled Mask Images – Convert the images to grayscale and resize them to a standard size of 128×128 .

Step 6: Split the Data into Train and Test sets – The data is split with a train size of 70% and a test size of 30%. The random state parameter is set to 20.

Step 7: Build a Random Forest (RF) Classifier model. The RF model is trained using significant features, and 20 estimators are employed, representing twenty decision trees with a depth of 10.

Step 8: Test the model by predicting on the test data, and calculate the accuracy.

4. Results and discussions on mushroom disease segmentation

The proposed method has been employed on a dataset comprising mushroom diseases to effectively segment diseases from input mushroom images. Non-diseased images, along with diseases such as Dry Bubble, Wet Bubble, Cobweb, Bacterial Blotch, and mites on mushroom images, were selected for experimentation using the Random Forest semantic segmentation algorithm. The proposed approach, founded on a random forest classifier combined with a robust feature extraction process, outperforms the SVM classifier, Naïve Bayes, and other methods, including the K-Means clustering method, Region of Interest, and Colour Threshold method.

Approximately 250 mushroom images, encompassing both diseased and non-diseased instances, were gathered from diverse organizations and a popular website (i.e., from [33,34,35]). These images were subsequently divided into training (70%) and test (30%) datasets. Ground truth images were generated for the training set to characterize the diseases present in mushrooms and distinguish the background parts of the images.

Features from the Gabor filter are extracted from the mushroom image using a kernel size of 9×9 . The parameters for extraction include theta values ranging from 0 to 45 degrees, γ values of 0.05 and 0.5, σ with values of 1 and 3 and λ values of 0, 45, 90, and 135. In addition to Gabor features, other features extracted include original image pixels, and edges by Canny, Roberts, Sobel, Scharr, Prewitt, Bouda, and Kayyali (extracted from the Sobel operator), Gaussian with $\sigma = 3$ and 7, median and variance in the windows of size 3×3 .

The total number of features amounts to 43, with 32 originating from the Gabor filter and the remaining 11 from other filters. Since some of these features are not significant, a process involving Pearson correlation and a constant mean-variance threshold is applied to extract meaningful features. This process eliminates constant and highly correlated features, thereby enhancing the performance of the Random Forest semantic segmentation results. Additionally, it contributes to the reduction of computation time and complexity.

The Random Forest semantic segmentation model is constructed using 20 decision trees with a depth of 10. The results of the Random Forest simulation on the mushroom diseased image dataset are compared with the Naïve Bayes method, basic standard methods such as Region of Interest, Colour Threshold method, unsupervised K-means clustering algorithm, and other supervised machine learning techniques. Support Vector Machine with a Radial Basis Function kernel is employed in the comparison process.

4.1. Subjective analysis

The experiment produced a series of images, showcasing both the original input images and the resulting images, as illustrated in Figure 1. The first row denotes the disease names, the second row displays the original images of diseased mushrooms, and the

Tab. 1. Summary on number of diseases segmented correctly by various segmentation methods.

| Segmentation method | Cobweb Diseases (total 65) | Dry bubble Diseases (total 70) | Wet bubble Diseases (total 41) | Mites Diseases (total 24) | Bacterial blotch Diseases (total 50) |
|------------------------|----------------------------|--------------------------------|--------------------------------|---------------------------|--------------------------------------|
| Enhanced Random Forest | 64 | 69 | 40 | 22 | 49 |
| SVM | 59 | 69 | 39 | 21 | 43 |
| Naïve Bayes | 58 | 68 | 38 | 22 | 45 |
| K-means | 61 | 64 | 36 | 22 | 47 |
| Region of Interest | 58 | 68 | 35 | 22 | 47 |
| Colour Threshold | 59 | 65 | 36 | 22 | 43 |

third row exhibits the resultant images generated by the proposed Enhanced Random Forest. Following suit, the fourth row presents Naïve Bayes' resultant images, the fifth row displays SVM's resultant images, the sixth row exhibits K-means' resultant images, and the seventh row illustrates the ROI resultant images. Additionally, the seventh row showcases resultant images corresponding to the Colour Threshold method [16], all aligned with the respective diseased images are shown in the 8th row.

Upon subjective analysis, it is discerned that the Enhanced Random Forest excels in accurately segmenting disease areas for cobweb, dry bubble, wet bubble, and bacterial blotch diseases, outperforming Naïve Bayes, SVM, K-means, ROI, and Colour Threshold techniques. However, it exhibits suboptimal performance in some mite images, occasionally extracting background elements alongside the diseased portions.

4.2. Objective analysis

To evaluate the performance of the proposed Enhanced Random Forest, a comparative analysis was conducted with several other methods, including Naïve Bayes, Support Vector Machine, K-means, ROI, and colour threshold. The dataset used for this assessment comprised 250 images depicting various mushroom diseases. Table 1 presents the statistics for the number of correctly segmented mushroom disease images out of the total 250, categorized as cobweb (65), dry bubbles (70), wet bubbles (41), mites (24), and bacterial blotches (50). The graphs illustrating the segmentation results obtained by different methods across various mushroom disease categories are shown in Figure 2.

Table 2 shows accuracies derived from statistics from Table 1, calculated as

$$ACC = N_{iC}/N_i, \quad (11)$$

where ACC – accuracy, N_{iC} – number of images correctly identified, and N_i – total number of images. Notably, the Enhanced Random Forest outperforms Naïve Bayes,

| Mushroom disease | Cobweb | Dry bubble | Wet bubble | Mites | Bacterial blotch |
|--|--------|------------|------------|-------|------------------|
| Original image | a1 | a2 | a3 | a4 | a5 |
| Enhanced RF based disease segmented | b1 | b2 | b3 | b4 | b5 |
| Naïve Bayes based disease segmented | c1 | c2 | c3 | c4 | c5 |
| SVM based disease segmented | d1 | d2 | d3 | d4 | d5 |
| K-means based disease segmented | e1 | e2 | e3 | e4 | e5 |
| ROI based disease segmented | f1 | f2 | f3 | f4 | f5 |
| Colour Threshold based disease segmented | g1 | g2 | g3 | g4 | g5 |

Fig. 1. Comparative results of Enhanced RF (ERF), Naïve Bayes, SVM, K-Means, ROI, Colour Threshold methods for different diseases. 1st row: a1-a5 – sample original input images; 2nd row: b1-b5 – ERF methods results; 3rd row: c1-c5 – RF methods results; 4th row: d1-d5 – SVM method results; 5th row: e1-e5 – K-Means method results; 6th ro: f1-f5 – ROI method results; and 7th row: g1-g5 – Colour Threshold method results for the corresponding input diseased images a1-a5.

Tab. 2. Accuracy of ERF, RF and SVM classifier based semantic segmentation and other standard segmentation methods.

| Segmentation method | Accuracy |
|------------------------|----------|
| Enhanced Random Forest | 0.98 |
| SVM | 0.93 |
| Naïve Bayes | 0.92 |
| K-means | 0.92 |
| Region of Interest | 0.90 |
| Colour Threshold | 0.92 |

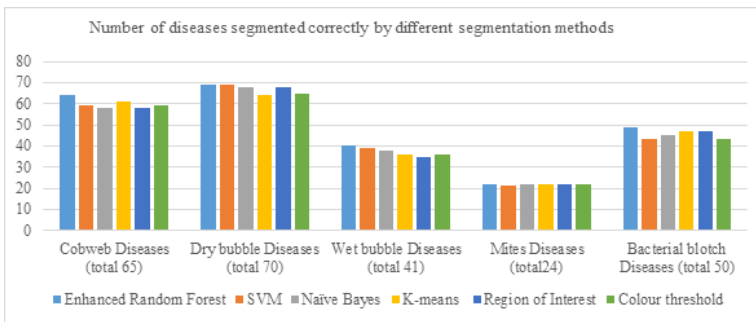


Fig. 2. Bar graph of number of diseases segmented correctly by different segmentation methods.

achieving the highest accuracy of 98%. This suggests that the Enhanced Random Forest, utilizing features selected through constant mean-variance thresholding and Pearson correlation coefficient, is more effective in mushroom disease segmentation tasks compared to SVM, widely-used supervised machine learning technique which achieved an accuracy of 93%. The second-highest accuracy of SVM indicates its correct classification of 93% pixels or regions in mushroom disease images. Naïve Bayes also a supervised machine learning technique used for disease segmentation, demonstrated an accuracy of 92.4%, performing well but slightly less accurately than SVM and the Enhanced Random Forest in segmenting mushroom diseases. K-means is an unsupervised machine learning clustering algorithm, achieved a respectable accuracy of 92% and almost equals Naïve Bayes, showcasing its effectiveness in a classification context, albeit slightly behind other machine learning techniques. Region of Interest (ROI), a conventional segmentation technique for identifying specific areas in an image, achieved an accuracy of 90%, indicating its lesser effectiveness compared to other methods in mushroom disease segmentation tasks. Colour Thresholding, a basic method relying on colour information for image object segmentation, attained an accuracy of 92%, aligning with K-means, Naïve Bayes and slightly below other machine learning methods.

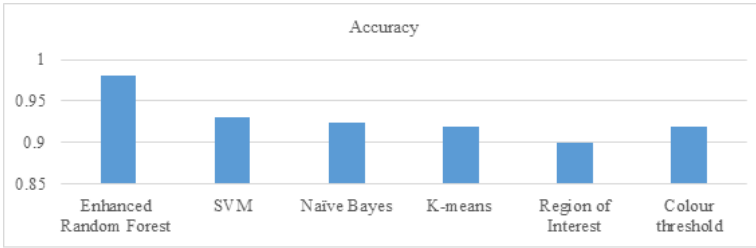


Fig. 3. Bar graph of accuracies attained by the tested methods.

The accuracy results of the proposed enhanced Random Forest and other standard segmentation methods are shown as a bar graph in Figure 3.

The metrics of precision, recall, and F1 score are taken into account, offering a comprehensive perspective on the effectiveness of the proposed semantic segmentation methods in identifying regions affected by mushroom diseases in a given image. Specifically, the metric of specificity evaluates the model’s capability to accurately predict non-disease regions. It’s worth noting that, in the context of semantic segmentation for disease detection, True Negatives (TN) are of lesser relevance, leading to the infrequent use of specificity as a metric in this particular domain.

$$PRE = TP / (TP + FP), \tag{12}$$

$$REC = TP / (TP + FN), \tag{13}$$

$$F1 = (2 * PRE * REC) / (PRE + REC), \tag{14}$$

where PRE – precision, REC – recall, F1 – F1 score.

Table 3 presents the confusion matrix, while Table 4 displays the performance metrics of pixel-based classifiers for ERF, SVM, and NB. Additionally, Figure 4 illustrates the corresponding bar graph. The objective analysis of ERF, SVM, and NB pixel-level classifiers employs performance metrics such as Precision, Recall, and F1 score, as outlined in equations (12), (13) and (14), respectively. These metrics are computed based on the False Positive (FP), False Negative (FN), True Positive (TP), and True Negative (TN) values derived from the confusion matrix. TP represents pixels correctly identified by the semantic segmentation model as part of the actual mushroom diseased area in a given image, while FP signifies pixels identified by the model as part of the disease region but not belonging to the actual diseased area. FN corresponds to pixels within the mushroom disease region that are incorrectly classified as not belonging to the disease by the semantic segmentation model, and TN represents pixels correctly identified as not belonging to the mushroom disease region when they actually do not belong. It is noteworthy that semantic segmentation models typically emphasize the identification of positive mushroom diseased regions more than the negative (healthy) regions, rendering True Positive less relevant in the context of semantic segmentation.

Tab. 3. Confusion matrix of Enhanced Random Forest – ERF, Naïve Bayes – NB, and Support Vector Machine – SVM.

| Classes | Correctly Segmented labels | | | Incorrectly Segmented labels | | |
|----------------|----------------------------|------|------|------------------------------|-----|-----|
| class | ERF | SVM | NB | ERF | SVM | NB |
| 1 (diseased) | 5246 | 5172 | 5031 | 98 | 178 | 312 |
| 2 (undiseased) | 1039 | 1042 | 1061 | 171 | 162 | 150 |

Tab. 4. Classifier performance metrics at pixels level: ERF – Enhanced Random Forest, NB – Naïve Bayes, SVM – Support Vector Machine methods.

| Class | Precision | | | Recall | | | F1-Score | | |
|----------------|-----------|------|------|--------|------|------|----------|------|------|
| class | ERF | SVM | NB | ERF | SVM | NB | ERF | SVM | NB |
| 1 (diseased) | 0.97 | 0.95 | 0.95 | 0.99 | 0.97 | 0.98 | 0.98 | 0.97 | 0.97 |
| 2 (undiseased) | 0.91 | 0.85 | 0.88 | 0.87 | 0.87 | 0.79 | 0.89 | 0.85 | 0.83 |

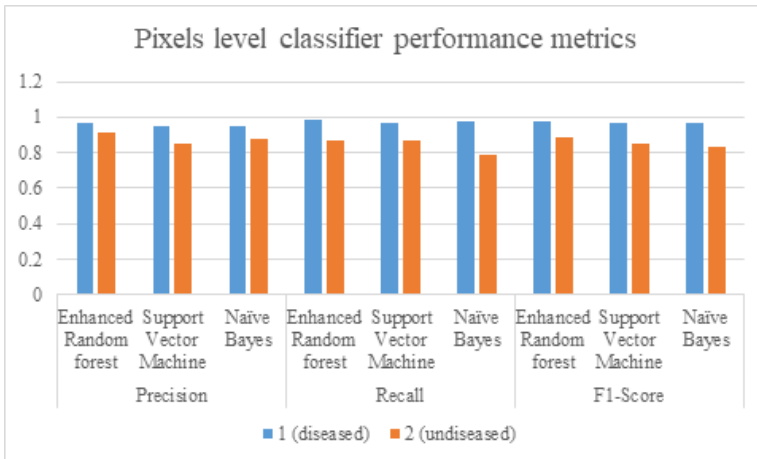


Fig. 4. Bar graph of pixels level classifier performance metrics of ERF – Enhanced Random Forest, NB – Naïve Bayes, SVM – Support Vector Machine.

5. Conclusion

In mushroom cultivation, the segmentation of mushroom diseases stands out as a crucial task, playing a pivotal role in estimating disease severity, suggesting necessary preventive actions, and mitigating potential losses for farmers. This work presents a novel approach to automatically perform semantic segmentation specifically for identifying various mushroom diseases, employing the Enhanced Random Forest method. Despite the existence of advanced deep learning methods for semantic segmentation in image object recognition, the decision to utilize machine learning methods in this context stems from the limited availability of data. This proposed method is further strengthened by the integration of substantial feature extraction, achieved through constant mean-variance thresholding and the Pearson correlation coefficient. The effectiveness of the proposed method is underscored by its impressive accuracy rate of 98 percent, outperforming Naïve Bayes, SVM, k-means, ROI, and colour threshold methods. A comprehensive comparative analysis, based on confusion matrices and performance metrics such as precision, recall, and F1-score values, further highlights the superiority of our approach over Naïve Bayes and SVM. These metrics serve as reliable indicators of the efficiency of our semantic segmentation approach in accurately identifying and delineating mushroom diseases in images. This study substantiates the efficacy of the Enhanced Random Forest approach as a valuable tool for managing and preventing mushroom diseases, emphasizing the importance of employing machine learning techniques in situations characterized by limited data availability.

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