

Modified Support Vector Machine and Animal Migration based Citrus Disease Recognition for Precision Farming

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Abstract

Citrus disease prediction plays the biggest role in the agricultural farm environment where differentiation of citrus disease from the black spots, scrub on fruits are more challenging. In the study that has been done up to now, this result is accomplished by presenting the multi-class SVM based citrus disease prediction system. However existing work tends to have followed issues: In top hat filter, with the presence of non-ground objects finding variation will be more difficult. Weighted segmentation requires more computational complexity. Hybridized feature selection cannot ensure the accurate selection outcome where features that satisfies all these parameters cannot be selected well. Multi class support vector machine is utilized to perform classification which requires supervised labels for ensuring the accurate classification rate. This problem is addressed in the study work that has been presented by the implementation of the approach known as Modified Support Vector Machine based Citrus Disease Recognition Framework (MSVM-CDRF). In the proposed work pre-processing is done using Improved Top Hat Filter. Here gradient is utilized to find the intensity elevation change between neighbouring pixels. Feature weighted fuzzy clustering method is introduced to ensure the accurate segmentation outcome. Here multi objective optimization methodology is presented to provide for the best function choices. To guarantee the best feature selection based on PCA score, entropy, and skewness-based covariance vector, an animal migrating method is used. A revised Support Vector Machine built on deep learning is developed to forecast citrus diseases. The MATLAB simulation environment is used for the whole study of the research project, and it has been shown that the suggested technique produces better outcomes than the current solution.

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1.INTRODUCTION

The pathogen *Xanthomonas citri* is responsible for the bacterial illness known as citrus canker [1]. Circular lesions, or scabs, are produced by this widespread citrus tree disease on citrus fruit, leaves, and twigs. More immature Citrus Canker lesions become brown, whereas younger lesions appear yellow [2]. Citrus canker can be transferred via pruning tools, ladders, cars, and garments [3]. Citrus canker causes tree deterioration, early fruit loss, and defective fruit [4]. Prophylactic Liquid Copper Fungicide sprays [5], are available to guard citrus plants against canker

infection. To avoid spreading the dangerous Citrus Canker disease, trees that are previously afflicted must be evacuated and killed. [6].

With the help of modern technology, human civilization is now capable of producing enough food to satisfy the needs of almost 7 billion people [7]. However, a number of causes continue to pose a danger to food safety, such temperature changes, a loss in pollination, crop diseases, and others. [8]. Plant diseases threaten global food safety and small producers their livelihoods depend on harvesting [9]. More than 80% of agricultural output in the growing countries is produced by smallholder farmers, and reports of yield losses of more than 50% due to pests and illnesses are frequent [10]. Moreover, smallholder farmers are especially susceptible to interruptions pathogens in the food supplies are to blame since the majority of hungry people (50%) reside in these families [11].

Many initiatives have been created to avoid crop loss from diseases. Integrated pest management (IPM) strategies have progressively been used to augment traditional methods of insecticide administration during the last ten years [12]. Whatever the technique, early, precise disease identification is crucial for efficient disease treatments. Historically, institutions like local plant nurseries or agricultural extension agencies have assisted disease detection. More recently, these initiatives have also been helped by the availability of online resources for illness detection, using the surge in Internet use throughout the world [13]. More importantly, taking advantage of the historically unparalleled worldwide use of smartphone technologies, mobile phone-based tools have evolved.

This study project's main goal is to furnish a technique for detecting illness in citrus fruit leaves, so that agricultural farm production can be controlled effectively. This research work attempt to perform the effective citrus disease prediction by adapting the machine learning techniques. This research work also attempts to accurately differentiate non disease fruits among the diseased fruits.

The following list outlines how the study was organised ultimately: This section provides a thorough overview to the citrus illness and its repercussions. The different associated research methods that aim to study the citrus disease are covered in depth in section 2. The suggested research approach is thoroughly discussed in section 3 along with pertinent examples and data. On the basis of practical analysis, simulated assessment of the research project is provided in section 4. In the last part, the research's general result is provided depending on the results of the simulations.

2. RELATED WORK

Badnakhe et al [14] For the purpose of obtaining citrus Cab and LAI values, the suggested PROSAIL model has been performed. The real field data was used to verify these values. Models for predicting diseases based on soils and climate have been created and tested using MLR and SVR. Additionally, research on the impact of the Gummosis infection on plant characteristics was conducted using a novel statistical prediction model based on biophysical variables (LAI and Cab).

Barcelos et al [15] After choosing a protein using the BLASTp algorithm and aligning it with ClustalOmega, a PMI model was produced using the protein homologous modelling technique and developed using the MODELLER software. Using the WhatIf, ProCheck, Errat, Prove, and

Verify-3D softwares, the model was examined and verified. The verification and assessment experiments for the *Xanthomonas* PMI model demonstrated its dependability.

Perondi et al [16] created a web-based solution to help Florida citrus producers manage PFD risk by making spray choices. This tool was created using information technologies including computer languages, databases, and queries. The system gathers meteorological information from the Florida Automated Weather Network (FAWN) and weather sensors set up by the AgroClimate research team. It then utilises this information to run a PFD disease model and calculate the likelihood of an infection-friendly condition.

Chavarro-Mesa et al [17] a dataset was utilised, picture dereferencing using QGIS software was used, and six departments in the northern region of Colombia were removed. For illness surveillance and predicting the occurrence of HLB, initial Random Forest and K-Nearest Neighbours (KNN) machine learning models were utilised.

Lee et al [18] Using a random forest model for a danger evaluation of forests taking into account climatic and landscape data, researchers assessed the CFP's occurrence patterns and forecasted its possible occurrence locations in South Korea. We used a Geographic Information System to extract seven environmental characteristics and the percentage of various land cover types at each site of the CFP in South Korea using digital maps after collecting the data from literature and official documents.

Bibi et al [19] Introducing insect predictions systems may be used to use insecticides correctly only when necessary to minimise their negative effects on the environment and financial costs. The link between several predictors (abiotic and biotic) factors and the rate of insect infection on citrus trees was investigated using Pearson's correlation analysis. To forecast Asian citrus psyllid population dynamics, several statistical methods, including multiple linear regression, random forest repressor, and deep neural network, were evaluated. A deep neural network-based projection system exhibited the lowest root mean squared error rates when predicting egg, nymph, and adult populations when compared to other extrapolation methodologies. This was the case throughout all three life stages.

Jeffress et al [20] created an annotated draught assemblies of 26.01 Mb in size, 10,080 expected gene models, and poor (0.37%) coverage of transposons as a result of the entire genome sequencing effort for *E. fawcettii*. Only a tiny percentage of the assembly had indications of AT-rich regions, which may have boosted flexibility in some genomic areas.

Hasan et al [21] created an automated method that uses convolutional neural networks to classify photos of citrus fruit. Orange (*Citrus Sinensis*) and Kinnow are two separate citrus fruits that we classified (*Citrus Reticulate*). The photos of Orange and Kinnow were first gathered and prepared. Second, picture separation and border recognition were used to separate the fruit images from their backdrop.

Jin et al [22] There is a potential that miRNAs that are expressed play significant roles in the tolerance for iron deficit that citrus plants display. It is possible that the microRNAs that mediate Fe-deficiency tolerance in citrus plants are related to increased stress tolerance, which is caused by decreased expression of miR172; regulation of S homeostasis, which is caused by decreased

expression of miR395; effect of plant growth, which is caused by increased expression of miR319 and miR477; regulation of Cu metabolism, as well as activation of Cu/Zn dismutase action, which.

Dananjayan et al [23] In order to identify citrus leaf diseases using our CCL'20 datasets, we found the CNN-based detectors most suitable for agricultural engineering, such as Center Net, YOLOv4, Faster-RCNN, Detectors, Cascade-RCNN, Fovea box, and Deformable Detr, developed and improved.

Pathania et al [24] in 2018 and 2019 introduced the membership function value (MFV) technique. At the Punjab Agricultural University's Regional Research Station Abohar in Ludhiana, India, 60 days of salt stress were applied to rootstock seedlings that were approximately one and a half years old. In 2018 and 2019, the mean MFV for several rootstocks varied from 0.263 to 0.591, with an average of 0.469 0.087 and from 0.288 to 0.639, with an average of 0.460 0.085.

3. CITRUS DISEASE PREDICTION SYSTEM

In the suggested work, pre-processing is done using Improved Top Hat Filter. Here gradient is utilized to find the intensity elevation change between neighbouring pixels. Feature weighted fuzzy clustering method is introduced to ensure the accurate segmentation outcome. Here, a multi-objective optimization framework is provided for the best feature selection. The goal of the animal migration method is to guarantee the best feature selection based on PCA score, entropy, and skewness-based covariance vector. For the purpose of predicting citrus illness, modified SVMs are presented.

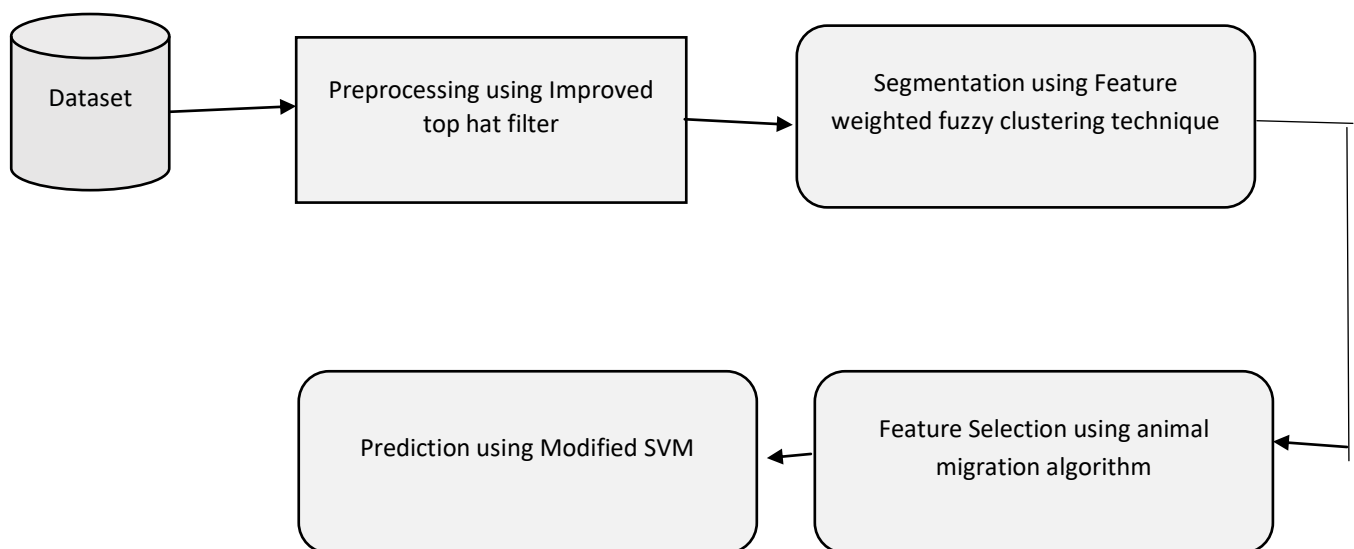


Figure 1. Processing flow of proposed research work

The diseased citrus fruit images were captured by using camera and kept as dataset. The dataset is shown in the following figure 2.



Figure 2. Dataset

3.1. PREPROCESSING

Non ground objects are primarily detected in three-dimensional lidar point clouds by the different height discontinuity of point clouds brought on by objects. The strength of the height difference between two adjacent places is measured by the gradient. The direction of elevation changes has no effect on the morphological gradients found with symmetrical SEs. Morphological gradients are useful for lidar sites with uneven distributions due to this property. There are numerous ways that mathematical morphology may be used to represent gradients numerically. The suggested filter employs internal gradient and external gradient, two different types of morphological gradients. The basic SE B (3 3 square) is used to represent the internal gradient of a location under consideration:

$$\rho^- B = f - \varepsilon B$$

The declining extent of point height in the neighbourhood is represented by internal slopes. The neighborhood's increasing extension of point elevation is represented by external gradients +, which are computed as

$$\rho^+ B = \delta B - f$$

To remove non ground items of various sizes using a top-hat filter, the employed windows' sizes must be adjusted. To prevent the absence of rough terrains while employing huge windows, the elevation differential criterion for top hats has to be high.

In order to speed up deployment, the rows and columns of an indexing grid are subjected to the topping filtration from left to right and then from bottom to top. Each row and column are originally covered with top hats, and the brims extend from the top hat's border along each row and column. The brim extends until it reaches the point when one of the three conditions—(a) the point's original and opened heights do not differ by more than a predefined threshold; (b) the point has an extraordinary internal gradient; or (c) the point is connected to another top hat—is satisfied. If the brim meets requirement (a) above, it is considered to be the ground; otherwise, if it meets condition (b) above, it is considered to be a no ground item (c). The covered continuous points of a considered brim on a row or column are thus determined to be no ground points if they satisfy the following criteria:

$$\text{Object}_{\text{brim}} = \{\text{Point}(i) \mid dh_i > Th_{\text{brim}(i)} \wedge \text{Dist}(0) = 0 \wedge (\rho^-(n) > Th_{\text{brim}(n)} \vee \text{Dist}(n) = 0)\}$$

where $i \in [1, 2, \dots, n]$, dh_i is the distinction among the initial and opened heights of the i th lidar point obtained through top-hat transition, $Th_{\text{brim}(i)}$ is the height differential threshold of the i th point, $\text{Dist}(0)$ is the distance among the initial point and the top hat obtained through thresholding, and (n) is the internal gradient of the ending point. The number of grid cells is used to measure the distance $\text{Dist}(i)$ in order to make the calculation simpler:

$$Th_{\text{brim}(i)} = a \times \text{Dist}(i)$$

when a is a variable that determines how much of an elevation variation in the landscape relief around things is acceptable. For the database used to conduct this research, this coefficient is set to 1.

To make the aforementioned process clearer, the index grid's pseudo code for a row is as follows:

Step 1 Look through a string of consecutive grid cells that make up a top hat.

Step 2 /* the left part of the crown projects outwards */

for grid Cell = startCell-1 $\rightarrow$ 0

for every point $\in$ grid Cell

if $(dh(\text{point}) > Th_{\text{brim}(\text{point})})$

Mark the brim-related point.

if $(dh(\text{point}) \leq Th_{\text{brim}(\text{point})})$

all brim locations should be marked as surface;

an extended end for the brim.

if $(\rho^-(\text{point}) > Th_{\text{brim}(\text{point})})$ OR point $\in$ another top hat)

Label every brim step as having no area;

end for brim extending.

end

end

Step 3 /* the right side of the brim stretches outwards */

for gridCell = endCell+1 $\rightarrow$ gridWidth-1

for every point $\in$ grid Cell

if ($dh(\text{point}) > Th_{\text{brim}(\text{point})}$)

mark the brim-related point.

if ($dh(\text{point}) \leq Th_{\text{brim}(\text{point})}$)

all brim points should be marked as surface;

an extended end for the brim.

if ($\rho - (\text{point}) > Th_{\text{brim}(\text{point})}$ OR point $\in$ a nother top hat)

identify the brim at every position with "no ground";

an extended end for the brim.

end

end

Step 4 If you need to think of any additional top hats, go back to step 1.;

if not, stop.

begin Cell and end here Grid is the grid cell now being approached by the expansion of the brim, and The index grid's starting and stopping grid cells that correlate to a high hat across a row are called cell. The term "width" refers to the number of grid cells in each row, "point" signifies the lidar points included inside gridCell, " $dh(\text{point})$ " represents the differential between the elevation of a pointer when it is closed and when it is released, and " $Th_{\text{brim}(\text{point})}$ " designates the threshold. The technique is carried out similarly along the columns once the brim filtration has been carried out along the rows as described before.

The original and preprocessed image is shown in the following figures 3 and 4.



Figure 3 Original Image



Figure 4. Preprocessed Image

3.2. IMAGE SEGMENTATION USING FEATURE WEIGHTED FUZZY CLUSTERING METHOD

Let the sample to set $D = \{X_j\}$ $j=1 \dots N$, with $X_j = (x_{j1}, x_{j2}, \dots, x_{jd}) \in \mathcal{R}^d$, where N denotes the sampling set's total amount of items, and D denotes the characteristic space's dimensions. The FCM clustering algorithm minimises the subsequent goal purpose:

$$J(U, V; D) = \sum_{i=1}^c \sum_{j=1}^N \mu_{ij}^m \left[d_{ij}^{(w)} \right]^2$$

where $U = (\mu_{ij})_{c \times N}$ is a fuzzy partitioning matrix, and the component X_j corresponds to the j th group. Its component ij represents the participation of the j th samples, $V = (V_1, V_2, \dots, V_c)^T = (v_{iq})_{c \times d}$ is the C group centres make up the centre matrix, $m > 1$ is the factor of the fuzziness, and $\|\cdot\|$ the Riemann average. It must be emphasised that the limitations must be satisfied by the participation μ_{ij} . $\mu_{ij} \in [0, 1]$ and $\sum_{i=1}^c \mu_{ij} = 1$ $C \ i=1$. Furthermore, $d_{ij}(w) = \|\text{diag}(w)(X_j - V_i)\|$ with $w = (w_1, w_2, \dots, w_d)$ is a feature-weight vector, and the components of the feature-weight vector w that meet the condition $\sum w_q = 1$ $d \ q=1$. Then, we arrive to the subsequent updating equations.

$$\mu_{ij} = \frac{1}{\sum_{k=1}^c \left(\frac{\left[d_{ij}^{(w)} \right]}{\left[d_{kj}^{(w)} \right]} \right)^{\frac{1}{m-1}}}$$

In this work, in order to, initialize feature-weight vector, the term variance is used. The easiest way to evaluate a concept's multivariate term variation suggests that characteristics with higher variation value include more important data.

Algorithm. Feature-Weighted Fuzzy C-Means

Input Dataset

Finished fuzzy segmentation matrix:

Final center matrix:

Final feature-weight vector:

Begin algorithm

Configure the fuzzy partitioning matrix, the fuzzing coefficient m , and the group count C .

Use normalised Product Variation to start the function vectors:

while

Refresh the group of centres

Determine the ranges.

Refresh the fuzzified division matrix.:

The function vector's components should be updated:

End while

End algorithm

The segmeneted image is shown in the following figure 5.

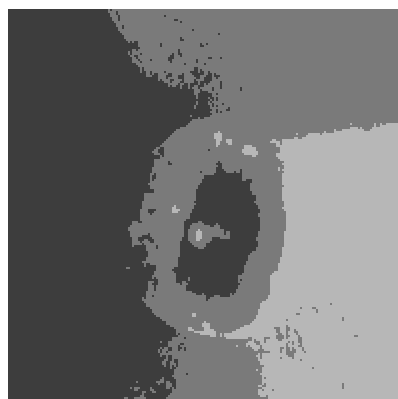


Figure 5. Segmented Image

3.3. FEATURE EXTRACTION

In the discipline of computer vision and pattern detection, feature extraction is essential for representing an image. Numerous industries, including robotics, agricultural, medical, and video monitoring, use feature extraction. The primary concern in this part is accurate categorization of

diseased areas via effective feature extraction and selections. A codebook is created by extracting three sorts of features—texture, colour, and geometric—to tackle this challenge.

3.4. OPTIMAL FEATURE SELECTION USING ANIMAL MIGRATION ALGORITHM

In animal migration algorithm, to arrive at a satisfying conclusion, the algorithm employs the immigration operation and the populations update method. In order to replicate animal migrating, the suggested algorithm employed a novel movement procedure that included the leader animal (individuals with the greatest fitness value) creating a new living space, and animals migrating from their existing positions into this new living area. By applying improved AMO (IAMO) method, which aims to increase AMO's searching capability on addressing high-dimensional issues, optimal additional server choice is assured.

Three enhancements are included in the suggested IAMO:

- (1) Implementing a collaborative training strategy;
- (2) Using a sophisticated search technique;
- (3) Creating a system for birth and death.

These three enhancements, as opposed to straightforward populations update and migrating, will help the algorithm become more intelligent and effective.

Behavioural Interaction in Studying: The research found that when animals live in clusters, they engage in social behaviour. It is said that people learn knowledge that is then digested via social contact to address intellectual issues, and that a solitary person cannot address such issues. Individuals' social interactions with one another may be seen as a learning process. In the meanwhile, sharing knowledge with others is a crucial way for people to learn from one another.

The Exact Searching Technique: Animal movement in a randomized situation is unpredictable. It is common knowledge that the natural world is full with uncertainty. Consequently, it might be said that animals often move at random.

The Birth-and-death Mechanism: Birth and death are ubiquitous occurrences for living creatures in nature. This suggested IAMO method simulates the birth-and-death process to leap from the localized optimum answer. The efficiency value of the newly generated person determines whether it will survive or be eliminated. The birth-and-death rule states that a new person survives if it is superior than the weakest member of the community.

Algorithm 1 contains the IAMO algorithm's pseudocode.

Algorithm 1: The pseudocode of IAMO

Input: N is the population size, and maxIter is the amount of competence assessments.

Output: The most beneficial remedy and fitness worth

```
1 Start each person 's location at randomized;
2 G=0;
3 while G<maxIter do
4 G=G+1;
5 for i=1; i≤N; i++ do
6 Upgrade the person 's status  $x_i$ ;
7 If  $x_i$  is surpassed by the new position, then
8  $x_i \leftarrow$  new position;
9 end
10 end
11 for i=1; i≤N; i++ do
12 forj=1; j≤D; j++ do
13 Choose  $r_1$  and  $r_2$  at randomized, where  $r_1, r_2 \in [1, N]$  and  $r_1 \neq r_2 \neq i$ 
14 if rand>pa then
15 the j-th component should be updated  $x_i$ 
16 else
17 Update the j-th dimension of  $x_i$ 
18 end
19 end
20 If  $x_i$  is exceeded by the current role, then
21  $x_i \leftarrow$  new position;
22 end
23 end
```

24 Activate the birth-and-death operation;

25 Note the optimal solutions x_{best} and the optimal fitting number fitting. (x_{best})

26 end

27 return x_{best} , fit (x_{best})

3.5. CITRUS DISEASE PREDICTION USING MODIFIED ARTIFICIAL NEURAL NETWORK

Finally based on weight assigned and network parameters observed. The suggested work implements Support Vector Machine, a machine learning approach that will learn the assault characteristics in the best possible way, for weight allocation. In each given dataset, the supervisory method support vector machine (SVM) is employed for prediction purposes. We employ SVM, which is the best separation the dual types of information's feature space to forecast Intrusion Detection System (IDS) characteristics. SVM models are utilised to get good predictive outcomes.

Formula

Training dataset (D)

$$D = \quad (1)$$

X and Y are input parameters, while D is the training database.

$$i=1 \text{ to } N \quad (2)$$

different parameters

We may apply the formula bellow to decrease error reduction.

$$(3)$$

Estimating function

$$F(x) = \quad (4)$$

SVM Algorithm Procedure

Given node information $D = (x_1, y_1), \dots, (x_n, y_n)$, C // x and y –labelled samples and C-class

Initialize vector $v=0$, $b=0$; class) // v-vector and b-bias

Learn the concept and train a basic SVM.

Each time do is used, x_i is a vector of characteristics characterising sample i.

Classify using $f()$

If $f() < 1$ // prediction class label

Find for known data // for new features

Add to known data

Utilize (3) to reduce the error function, and use (4) to estimate (4)

Retrain if the forecast was incorrect.

Repeat

End

Label characteristics as normal or abnormal.

The prediction outcome is shown in the following figure 6.

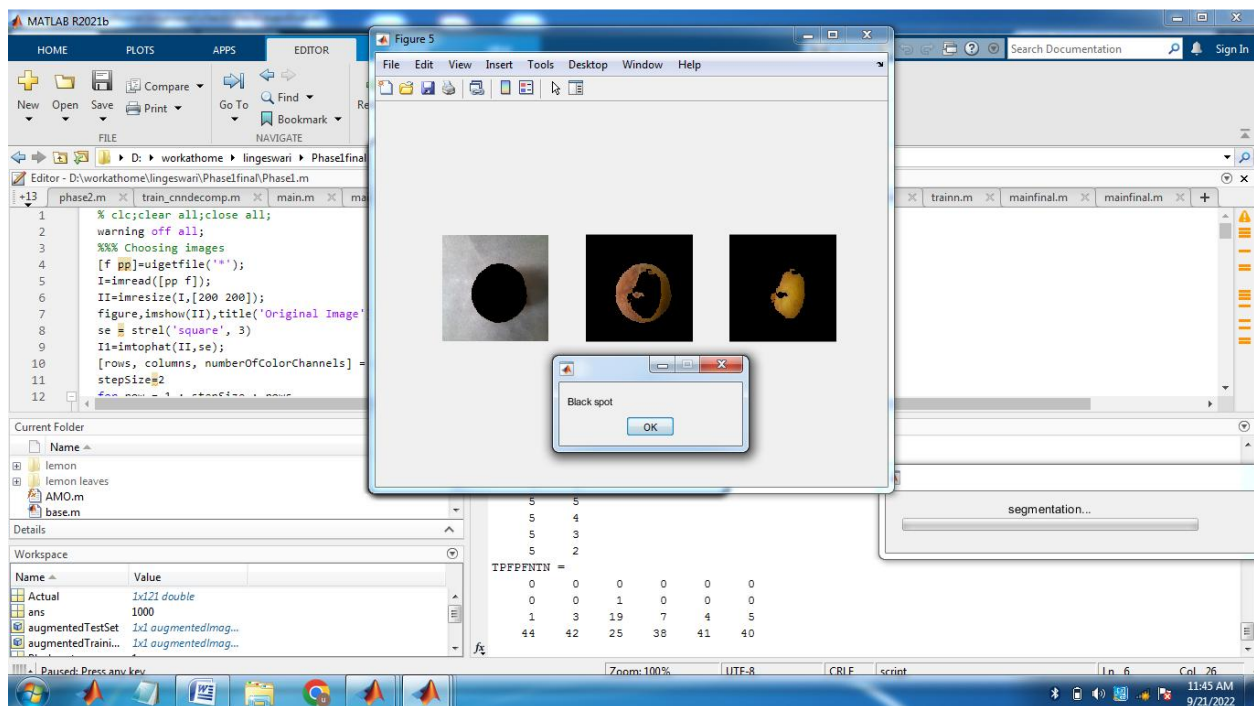


Figure 6. Prediction Outcome

4. SIMULATION RESULTS

This section evaluates the suggested research methodology numerically in terms of various success metrics to examine the efficiency improvement of the suggested and existing study methodologies. The suggested research technique is put into practise using the Matlab simulation environment. Accuracy, Precision, Recall, and F-Measure are indicated as the performance metrics taken into account in this study. The suggested technique, MSVM-CDRF (Modified Support Vector

Machine based Citrus Disease Recognition Framework), is compared to the current methods. Dual-class SVM (MC-SVM).

ACCURACY: It is described as the accuracy with which medicine names in tweets are identified. There are fewer false positives now. The suggested system's reliability ought to be superior to existing systems like MSVM-CDRF. The true positive, false positive, true negative, and false negative values of the drug predictions system are used to determine the reliability rating. The reliability is determined in a manner similar to this:

PRECISION: It is the percentage of meaningful results from searches.

RECALL: The percentage of the total number of pertinent occurrences that was successfully recovered is known as recalls.

F-MEASURE: The weighted harmonic mean of the test's specificity and recall is what is known as the F measure (also known as the F1 score or F score), which serves as a gauge of how accurate a test.

The below table 1 lists the results for the efficiency measures.

Table 1. Performance metric values

	MC-SVM	MSVM-CDRF
Accuracy	93.3333	97.7778
Precision	93.3333	96.3333
Recall	92.1333	95.1333
F- Measure	92.7296	95.7296
FDR	6.6667	2.2222
TPR	0.9333	0.9778
FNR	0.0667	0.0222

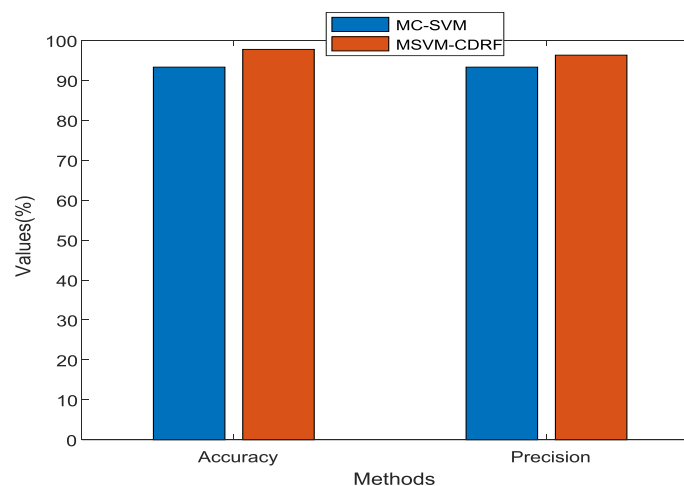


Figure 7. Accuracy and precision comparison

Figure 7 provides a comparative study of the suggested approach with the currently used method, MSVM-CDRF. This analysis demonstrates that the suggested method outperforms the current method. Compared to MC-SVM, the proposed MSVM-CDRF has a 3% higher accuracy. Compared to the current MC-SVM, the accuracy has risen by 3%.

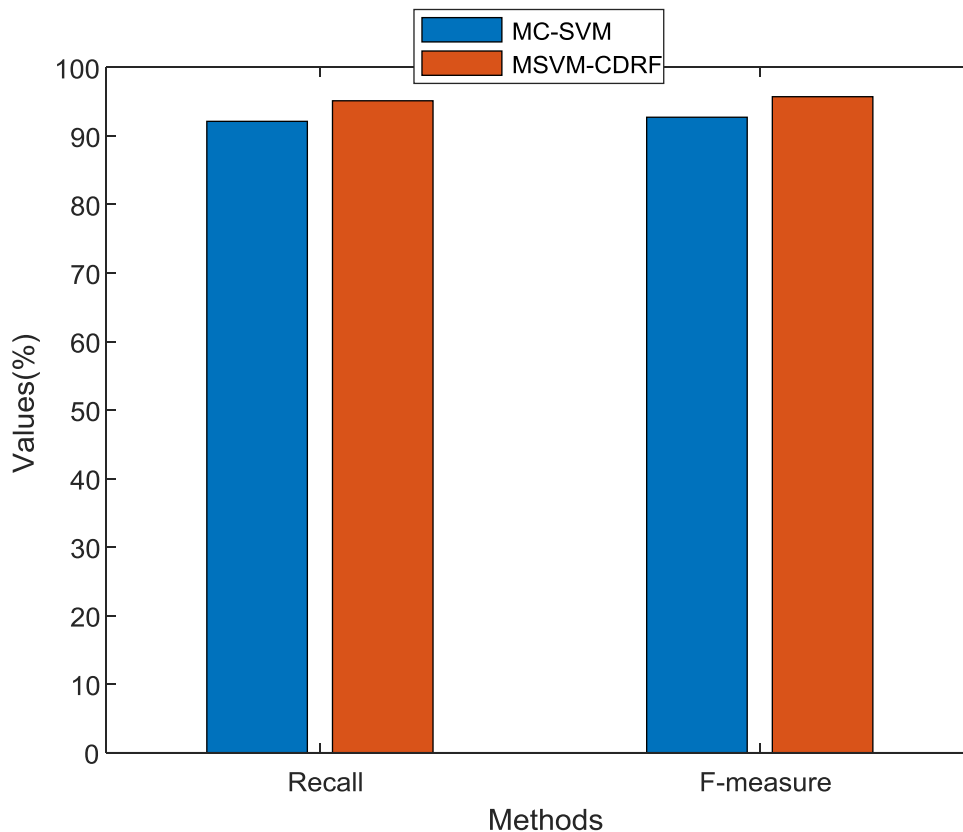


Figure 8. Recall and F-Measure comparison

Figure 8 provides a comparative study of the suggested approach and the current method, MC-SVM. This analysis demonstrates that the suggested method outperforms the current method. Compared to MC-SVM, the proposed MSVM-CDRF exhibits a 6% higher recall. F-Measure rose by 13% compared to MC-SVM.

5. CONCLUSION

In the proposed work pre-processing is done using Improved Top Hat Filter. Here gradient is utilized to find the intensity elevation change between neighbouring pixels. Feature weighted fuzzy clustering method is introduced to ensure the accurate segmentation outcome. Here, a multi-objective optimisation approach is shown for the best feature selection. To guarantee the best feature selection based on PCA score, entropy, and skewness-based correlation vector, an animal migrating method is used. A modified Support Vector Machine built on deep learning is developed to forecast citrus diseases. The MATLAB simulated environment is used for the whole study of the research project, and it has been shown that the suggested technique produces better outcomes than the current solution.

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