

# **Fuzzy Rule based identification system of Apple Disease Identification**

Project Report submitted in partial fulfillment of the requirement  
for the degree of

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in

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under the Supervision of

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## Certificate

This is to certify that project report entitled “**Fuzzy Rule based identification system of Apple Disease Identification**”, submitted by Abhinav Kriti Gupta in partial fulfillment for the award of degree of Master of Technology in Computer Science & Engineering to Jaypee University of Information Technology, Waknaghat, Solan has been made under my supervision.

This report has not been submitted partially or fully to any other University or Institute for the award of this or any other degree or diploma.

**Date:** July 4, 2021



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Abhinav Kriti Gupta

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### **List of Abbreviations**

1. SSD: Single Shot Multibox Detector
2. LMD: Laser micro dissection
3. RRD: Rose replant disease
4. Dia : diameter
5. CCM: COlor co-occurrence method
6. PPV
7. VIS
8. NIR
9. DAS-ELISA
- 10.
11. PVP : PolyVinyl-Pyrrolidone
12. GCH: GLobal colour Histogram
13. CCV: Color Coherence Vector
14. CF : Cauliflower-like appearance

## Abstract

Timely and effective detection of apple diseases is crucial for ensuring the healthy development of the apple industry. *Alternaria* leaf blotch and rust are two common types of apple leaf diseases that severely affect apple yield. In general, these diseases are inspected by experienced experts one by one. This is a time-consuming task with unstable precision. Therefore, a low-cost, stable, high precision apple leaf diseases identification method, which is achieved by employing MobileNet model. Firstly, comparing with general deep learning model, it is a low-cost model because it can be easily deployed on mobile devices. Secondly, instead of experienced experts, everyone can finish the apple leaf diseases inspection stably by the help of our algorithm. Thirdly, the precision of MobileNet is nearly the same with existing complicated deep learning models. Finally, in order to demonstrated the effectiveness of our proposed method, several experiments have been carried out for apple leaf diseases identification. We have compared the efficiency and precision with the famous CNN models: i.e. ResNet152 and InceptionV3. The existing research uses complex image preprocessing and cannot guarantee high recognition rates for apple leaf diseases. It proposes an accurate identifying approach for apple leaf diseases based on deep convolutional neural networks.

Mosaic, Rust, Brown spot and *Alternaria* leaf spot are the four common types of apple leaf diseases. Early diagnosis and accurate identification of apple leaf diseases can control the spread of infection and ensure the healthy development of the apple industry. It includes generating sufficient pathological images and designing a novel architecture of a deep convolutional neural network based on AlexNet to detect apple leaf diseases. Using a dataset of 13,689 images of diseased apple leaves, the proposed deep convolutional neural network model is trained to identify the four common apple leaf diseases. Under the hold-out test set, the experimental results show that the proposed disease identification approach based on the convolutional neural network achieves an overall accuracy of 97.62%, the model parameters are reduced by 51,206,928 compared with those in the standard AlexNet model, and the accuracy of the proposed model with generated pathological images obtains an improvement of 10.83%. This research indicates that the proposed deep learning model provides a better solution in disease control for apple leaf diseases with high accuracy and a faster convergence rate, and that the image generation technique proposed in this paper can enhance the robustness of the convolutional neural network model.



\*\*\*\*\*

# CHAPTER 1 INTRODUCTION

## 1.1. Introduction

From the report of National Institute of Food and Agriculture, United States of America, worldwide due to pests and different types of crop disease 40-50% of all crop yields are affected and thus lost. In India, 15-25% of useful crop production is destroyed. When the demand and consumption are on critical rise thus a durable and critical time sustainable production that is free from menace is must required. This will help in boosting GDP of nations and providing free trade tariff between multinational companies. During the initial stages, identification of the disease in plant is very crucial for moving to sustainable agriculture as it can play a major and key role in preventing crop. Surely enabling the boost of quality as well as quantity of agricultural produces. There are 2 approaches to identification of plant disease. Firstly an expertise person in agriculture who can manually monitor the plant or Secondly building an expert system than can automate the process of Plant Disease identification from Human Learning. Apple trees are small to medium sized trees with height ranging from 5-10 m with several branches being divided from a central trunk. Its leaf can varies upto 13 cm in length to 7 cm in width

## 1.2 About apple cultivation:

Apple is a very significant crop, in terms of productivity worldwide India stands at fifth position in productivity. In India J&K tops the list of productivity with 64.5 % production followed by Himachal Pradesh 30.1 % and thirdly Utrkhand.

### Propagation :

Apple grows best in higher latitudes and in tropics, cold minter with mild growing season is requires in order to break its dormancy. At these temperate zones in spring the flower developed and during rainy season the fruit ripe. In order to make it essentially evergreen and flowering the leaves stay on trees longer and throughout the year sporadically fruiting will happen unless across the entire tree if a uniform cycle is managed to enforce to create a wide tree through shoots of bending. Budding is the propagation of apples's standard method. In order to prevention of the increasing dormancy of the buds plant seedlings are budded from stock of root as when planting an orchard or nursery of apple its highly advisable. For encouraging new shoot growth Budded trees must be pruned in the first year. For making sustainable the heavy crop loads careful management is required for apple trees in this tropics. Defoliation of the trees, pruning its tips and bending shoots are included in it. To promoting growth until the fruit's first production

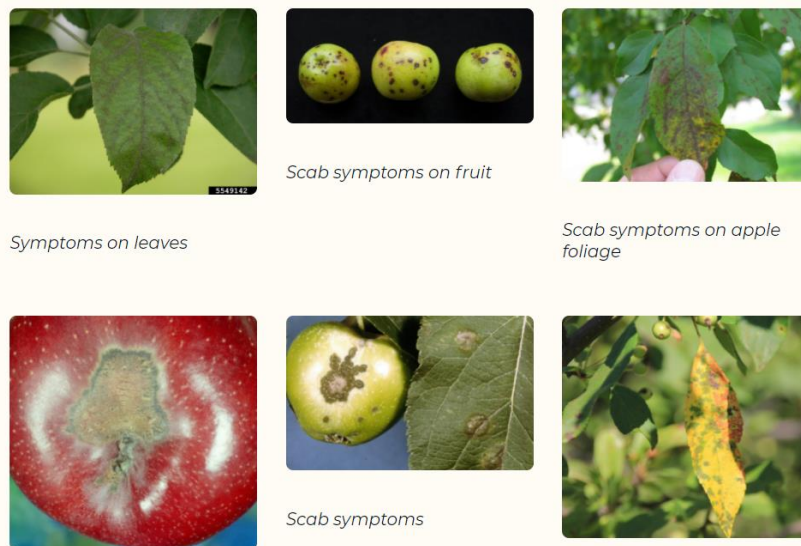
flowers are generally removed which generally takes place after 2 years. Through mound layering and grafting propagation of apple trees can be done possible. Joining of lower part one plant(root stock) with another upper (scion) part of another plant is involved in Grafting. During the dormant season grafting is usually done and must be done on stock wood and dormant scion.

Mound layering is done usually to propagate clonal root stocks of apple. Around shoots that have been cut back soil is mounded thereby stimulating the growth at the base of these shoots of roots. The plants are cut back during the spring season above the ground length is kept around 2.5 cm (1 inch) .Gradually formation of new shoots takes place and to mounds more soil and bark are added around the plants. Throughout the growing season continuation of this cycle can take place(occur) until further growth of the new shoots to exposition mother stool beds are kept to left till occurrence and hilling's another cycle has begin.

### 1.3 Management of Apple diseases:

#### 1.3.1CATEGORY : FUNGAL

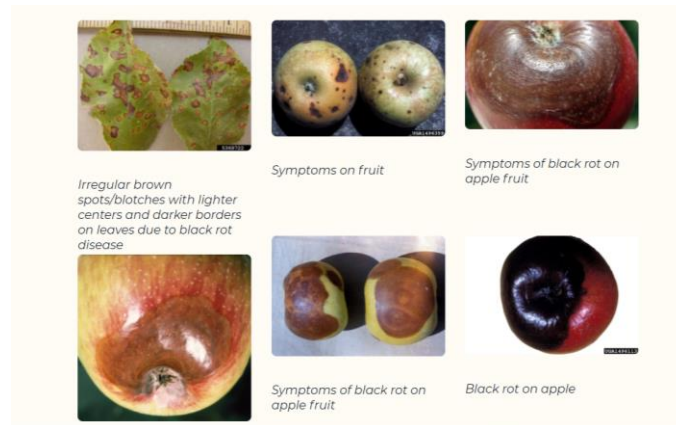
##### 1.3.1.1 Aple Scab *Venturia Inaequalis* Cooke:



**Fig 1: Scab in Apple**

Removal of all diseased leaves dropped from tree in the fall composting in order to prevention of any disease surviving in debris. Application of zinc and fertilizer grade urea in the fall may be necessary to speed leaf drop, to fallen leaves lime must be added.in the areas where leaves remain wet for more than 9 hours of fungicides application may be necessary in areas .Fungicides like copper scabs and Bordeaux mixtures should be applied as soon as leaf tips emerge if there's chance of wet period

### 1.3.1.2 Black Rot *Botryosphaeria obtusa*:



**Fig 2: Black rot in apple**

**1.3.1.2.1 Symptoms :** Puttle flecks or circular lesions which are brown in the center and purple at margin red flecks purple lesions and brown black rings on fruits

**1.3.1.2.2. Comments:** Spores can overwinter in twigs or fruit remaining on the tree and spread during rainfall.

**1.3.1.2.3 Management:** Dead wood removal, mummified fruit and cankers from trees for reducing spread of disease burn any pruning that have been made from the tree, disease can be controlled by applying fungicides from silver up to harvest.

### 1.3.1.3 Cedar apple rust *Gymnosporangium juniperi-virginianae* :



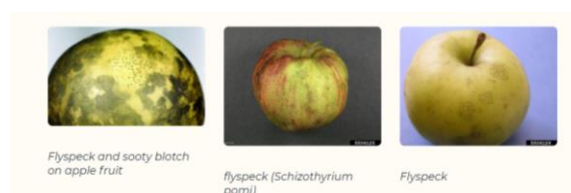
**Fig 3: Cedar apple rust**

**1.3.1.3.1 Symptoms :** On top side of leaves Bright yellow or orange colour surrounded by a red band and small black spots in the center, cup like structure called aecia are form on the leaf undersides by mid summer, in tubular structure these become covered from which spores are released.

**1.3.1.3.2 Comments:** To completion of lifecycle of fungus two hosts are required. On eastern red cedar galls are formed by wind spores in close planting apple.

**1.3.1.3.3 Management:** Remove nearby red cedar where possible plant resistant varieties. For plantation of proximity to red cedar of growing susceptible varieties , fungicide program is to be followed.

### 1.3.1.4 Fly Speck: *Zygraphiala jamaicensis*



**Fig 4: Fly speck**

**1.3.1.4.1 Symptoms:** Like dots shiny black fungal appearance of bodies takes place in irregular to circular patterns on fruit surface.

**1.3.1.4.2 Cause:** Fungus

**1.3.1.4.3 Comments:** Frequent rainfall and above Average summer temperatures are usually followed through outbreaks.

**1.3.1.4.4 Management:** To open canopy prune trees and drying of fruit surface is to be promoted; as a preventative measure fungicides may be applied.

### 1.3.1.5 Powdery mildew (*Podosphaera leucotricha*)



**Fig 5: Powdery mildew in apple**

**1.3.1.5.1 Symptoms:** On the underside of leaves, white velvety patches, whereas on the top side chlorotic color spots on the leaves.

**1.3.1.5.2 Cause :** Fungus

**1.3.1.5.3 Comments :** Spread by wind and in buds fungal spores overwinter

**1.3.1.5.4 Management:** Infected shoots are to be pruned out while dormant in early stage of spring, build up to be reduced at pink bud stage by apple sprays. Application of lime and sulfur is the organic treatments.

### 1.3.1.6 Sooty blotch and fly Speck:



*Sooty blotch and flyspeck on apple fruit*

**Fig 6: Sooty blotch and fly speck**

**1.3.1.6.1 Symptoms:** On surface of fruits with an indefinite margin of sooty blotches. Entire fruit may be covered by coalesce of blotches. Irregular to circular pattern of dots are appeared on fruiting bodies of shiny black fungal fruiting.

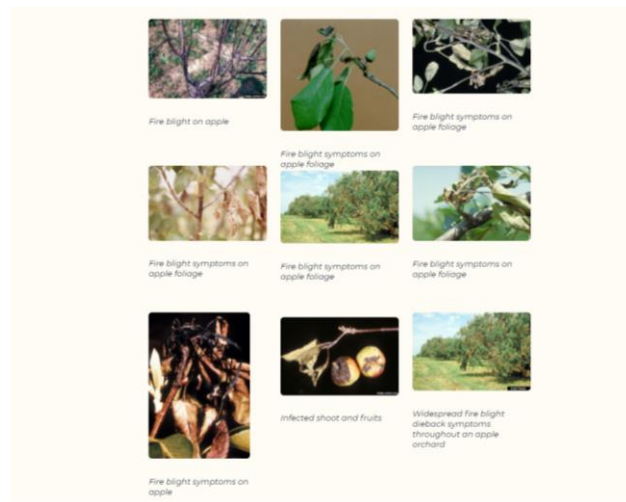
**1.3.1.6.2 Cause:** Fungi

**1.3.1.6.3 Comments:** During days of high rainfall and humidity, infection occurs mainly.

**1.3.1.6.4 Management:** In places of good sunlight and proper air circulation trees is to be planted; trees are to be pruned at open center blemishes superficial and can be washed off.

## 1.3.2 CATEGORY: BACTERIAL

### 1.3.2.1 Fire Blight (*Erwinia amylovora*)



**Fig 7: Fire Blight**

**1.3.2.1.1 Symptoms:** Plants appearance like that of getting scorched by fire on infected areas watery exudate might be present.

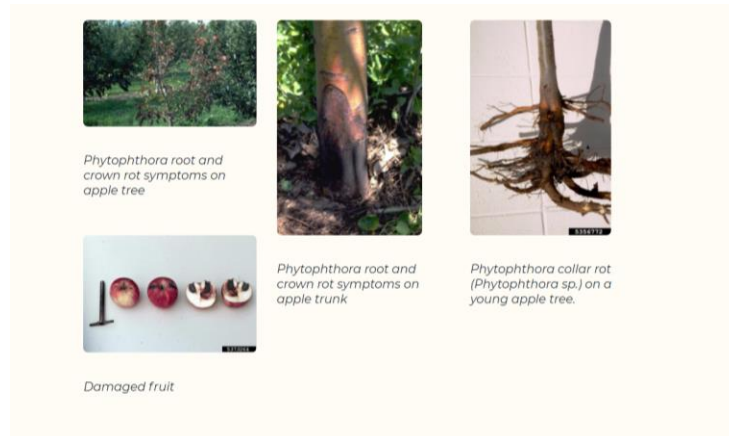
**1.3.2.1.2 Cause:** Bacterium

**1.3.2.1.3 Comments:** In cankers or bark, bacterium over winters; spread by rain splash and pollinating insects

**1.3.2.1.4 Management:** Cutting out the diseased wood, Bordeaux mixture treatment or approved materials of copper for organic production. Application of copper or streptomycin to blossoms might be necessary for the prevention of spread.

### 1.3.3 CATEGORY: Oomycete

#### 1.3.3.1 Phytophthora crown and root rot (*Phytophthora spp*)



**Fig 8: Phytophthora crown and root rot**

**1.3.3.1.1 Symptoms:** Although leaves are attached to the tree but have wilting in them, reduction of growth at soil level presence of cankers ; early senescence; dark discoloration of bark that is slimy when wet.

**1.3.3.1.2 Cause:** Fungus

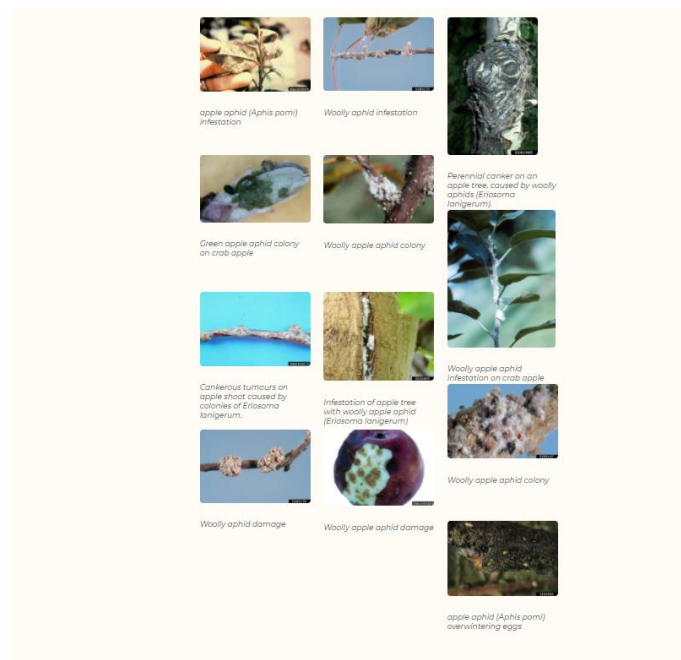
**1.3.3.1.3 Comments :** Poorly draining soil encourages Infection

**1.3.3.1.4 Management:** Proper water management practices help in prevention of emergence of disease; not allowing accumulate of water to soil increases chance to reduce it's possibility of happening .



### 1.3.4 CATEGORY: Insects/ Pests

#### 1.3.4.1 Aphids( Green apple aphid, Woolly apple aphid) *Aphis pomi*, *Eriosoma lanigerum*



**Fig 8: Aphids**

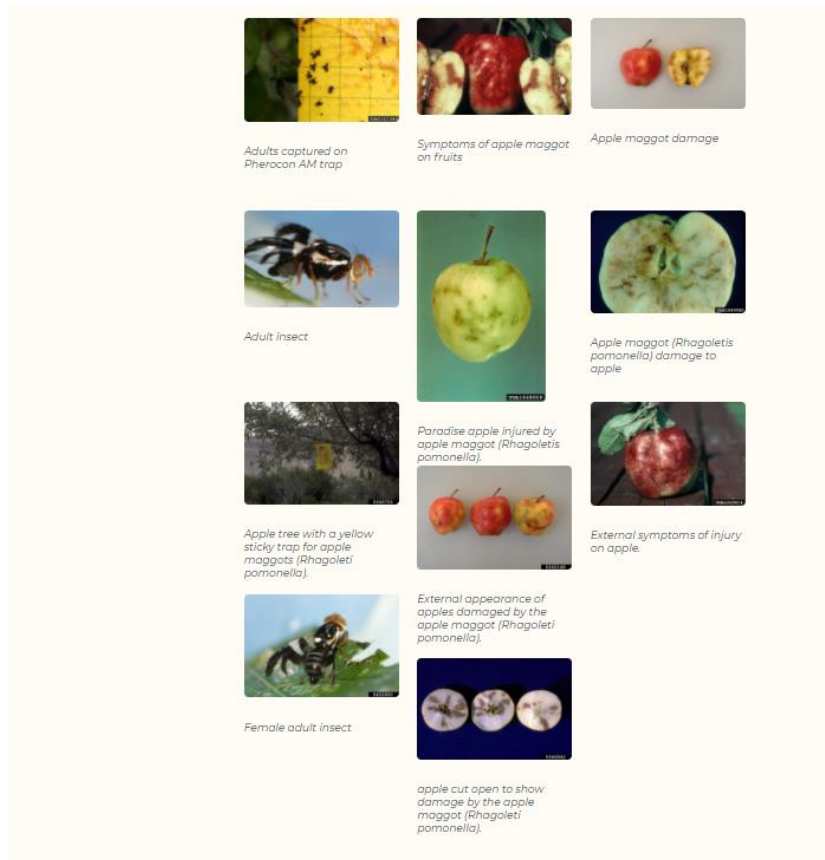
**1.3.4.1.1 Symptoms:** On underside of leaves presence of small soft bodied insects or on stem of plants. Usually color is yellow or green. In masses of wool-like white material woolly apple aphids are covered; green apple aphids changes to yellow-green with darker green spots as they mature and else are dark green when they hatch . Leaves may be caused to yellow and or distortion when if aphid infestation is heavy

**1.3.4.1.2 Cause :** Insects

**1.3.4.1.3 Comments:** The presence of cornicles (Tubular structures) is a distinguishing feature that is included that project backwards from the body of the aphid; When disturbed will generally not move very quickly.

**1.3.4.1.4 Management:** Infestation can be pruned out in providing control if to a few leaves or shoots. Aphid population is just limited . Before plantation checking for aphids transplants. Use of tolerant varieties if available . Aphids can be deterred from fording on plants through reflective mulches like silver colored plastic. Sturdy plants can be sprayed with strong effect of jets only to remove or knock off aphids from leaves. Only in the case of high infection are the use of insecticides is generally required to treat aphids. Infestation of medium and low types are generally tolerated by plants. usually the best method of control is the application of insecticidal soaps or oils like canola oil and neem. Always checking the labels of products prior to use of specific usage guidelines is usually recommended for it.

### 1.3.4.2 Apple Maggot *Rhagoletis pomonella*:



**Fig 9: Apple Maggot *Rhagoletis pomonella***

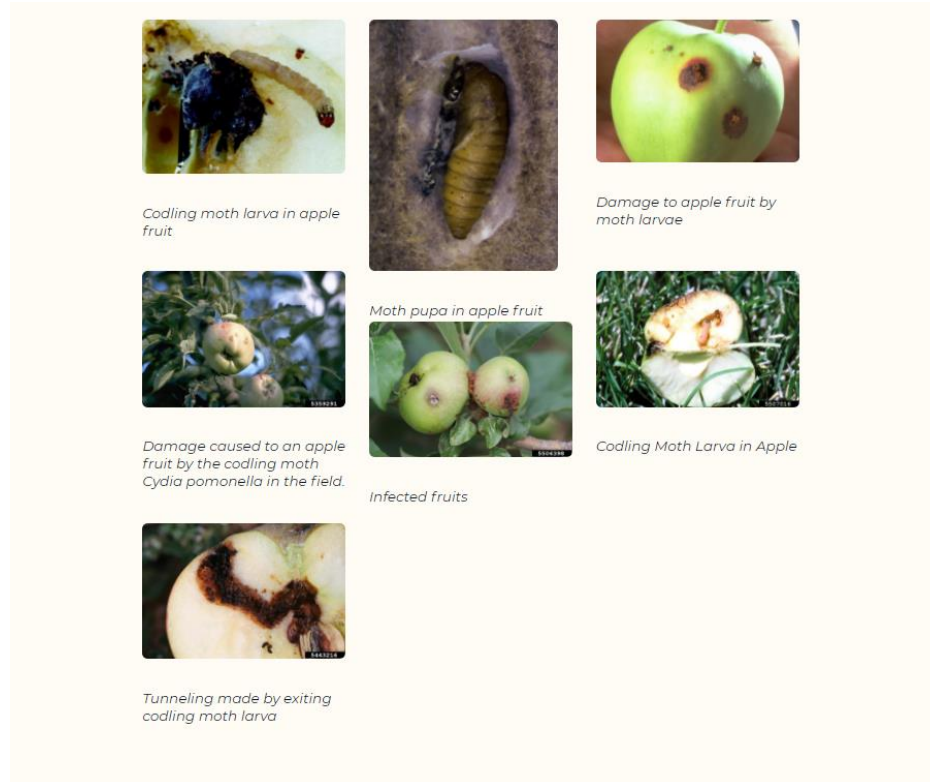
**1.3.4.2.1 Symptoms:** Misshapen, pitted and sunken areas on the surface of fruit, browning and rotting of apple skin.

**1.3.4.2.2 Cause:** Insect

**1.3.4.2.3 Comments:** Surface damage caused by female laying her eggs to fruit, by burrowing and feeding larvae damage it's flesh.

**1.3.4.2.4 Management:** Wrapping polythene bags around fruit to prevent birds from laying eggs by tying or stapling. Cutting corners from bag in order to ensure proper supply of air inside to fruit. Spraying fruit using insecticide prior to eggs being laid.

### 1.3.4.3 Codling moth (*Cydia pomonella*)



**Fig 10: Codling moth (*Cydia pomonella*)**

**1.3.4.3.1 Symptoms:** Holes and button in fruit; that may be blocked using crumbly brown frass (insect excrement) . Extending to the core of fruit might exist wounds that are deep burrows or may be shallow even. Length extending upto 1.3 cm (0.5 inch) long of larvae's that are pink with a brown head

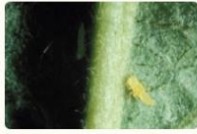
**1.3.4.3.2 Cause:** Insect

**1.3.4.3.3 Comments:** Insect usually undergoes 2-4 generations per year.

**1.3.4.3.4 Management:** For opening out tree's canopy proper pruning methods can help to it by ensuring treatments penetrate interior of the tree and reach larvae.Help towards removal of reservoirs of insects is done by removal of any wild hosts or trees that might be present in an abandoned orchards. Application of Entrust and kaolin clay are included as organically acceptable control methods. To reduce insect population before larva leaves the fruit infected fruit can be manually removed by small scale growers and home gardeners.

**1.3.4.4 Leafhoppers(White apple leafhopper, Rose leafhopper) *Typhlocyba pomaria* , *Edwardsiana rosae*:**

*Eumarosiana rosae*



White apple leafhopper nymph on underside of leaf



Characteristic white stippling on crab apple leaf caused by leafhoppers



White apple leafhopper adult



white apple leafhopper nymphal skin

### **Fig 11: Leafhoppers**

**1.3.4.4.1 Symptoms:** White stoppling on foliage. Presence of black specks on fruits. Possibility of reduction in fruit size. Because of insect's excretion of honeydew presence of sticky exudate on leaves and fruit.

**1.3.4.4.2 Cause:** Insect

**1.3.4.4.3 Comments:** Damage resembles to that of spider mites (more noticeable). Highest number of insects is usually reached close to or after harvest.

**1.3.4.4.4 Management:** Monitoring the tree for the presence of nymphs. Use of sprays of proper insecticides is most significant for it's control.

**1.3.4.5 Leafrollers (Omnivorous leafroller, Redbanded leafroller, etc) *Platynota stultana*, *Argyrotaenia velutinana*:**



Redbanded leafroller on apple leaf

### **Fig 12: Leafrollers**

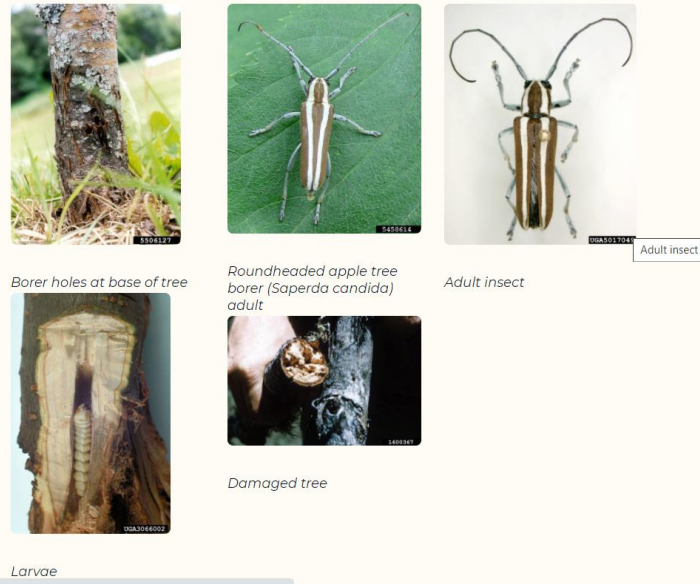
**1.3.4.5.1 Symptoms:** With silk webbing leaves of plant are tied and rolled together. Defoliation of plant. Presence of silk webbing on fruits. Larvae wriggle vigorously when disturbed and may drop on a silken thread from the plant.

**1.3.4.5.2 Cause:** Insect

**1.3.4.5.3 Comments:** Adult insect being moth that can fly over several miles for finding suitable hosts.

**1.3.4.5.4 Management:** For signs of infestation monitor plants; As weeds can act as hosts for leafrollers remove them from plant bases. *Bacillus thuringiensis* or entrust SC on organically grown plants may be applied to control insects on them. Apply sprays carefully so that inside rolled leaves treatment reaches.

**1.3.4.6 Roundheaded apple tree borer *Saperda candida***



**Fig 13: Roundheaded apple tree borer *Saperda candida***

**1.3.4.6.1 Symptoms:** At the base of tree presence of bore holes that are covered by pigtail shaped frass or darkened areas in the bark due to flow of sap. By 1 or 2 larvae infestation the young may kill. The older trees show drying and break off near the base.

**1.3.4.6.2 Cause:** Insect

**1.3.4.6.3 Comments:** In US and Canada the insect is quite common. Apple, pear, quince mountain-ash, serviceberry and hawthorn are the host range of this insect

**1.3.4.6.4 Management :** To avoid insect attack use of truck wraps. Removing and killing of larvae from the tunnel if possible. Suitable insecticide application.

### 1.3.4.7 Stinkbugs



*Adult red shouldered stink bug*

#### **Fig 14: Stinkbugs**

**1.3.4.7.1 Symptoms:** Dark colored pinpricks on fruit surface with white, pithy area underneath, stink bugs often carry pathogens with depressed dimples in their mouthparts that can cause secondary infections and decay of fruit. Adult insect is green or brown in color and is shield shaped may have yellow, pink or red markings. Eggs on the leaves are laid in cluster and are drum shaped. Larvae resembles the adults but are smaller. Visibility may be of insect frass on the fruit is small, brown tear dropped shaped deposits.

**1.3.4.7.2 Cause:** Insect

**1.3.4.7.3 Comments:** Under leaves Adult insects overwinter, on certain weeds like thistle(Russian) or mustard blackberries are present on .

**1.3.4.7.4 Management:** Practicing good weed management throughout the year by removal of weeds around the crop that may act as overwintering locations for stink bugs. The use of insecticidal soaps are included in the organically accepted control methods , kaolin clay and also prevention of natural enemies.

### **1.3.5 CATEGORY: MITES**

#### **1.3.5.1 Spider Mites *Tetranychus urticae***



*Characteristic stippled leaf  
caused by spider mites*

**Fig 15 Spider Mites**

**1.3.5.1.1 Symptom :** Yellow stripping of leaves that may appear bronzed. Leaves covered by webbing on the underside of leaves or on the web tiny mites may be visible as moving dots. Best viewed from using a hand lens. Usually not spotted until there are visible symptoms on the plant. Leaves may turn yellow and may drop from plant.

**1.3.5.1.2 Cause:** Arachnid

**1.3.5.1.3 Comments:** During dust conditions spider mites may drive. Water- stressed plants are more susceptible to attack

**1.3.5.1.4 Management:** Spraying plants with a strong jet of water in the home garden can help in reducing spider mites population from building up. Apply insecticidal soap to plants as mites become more problematic. Certain chemical insecticide might even by killing off natural enzyme increase mites population and thus hence promoting mite regeneration .

The first method being very time-consuming and cumbersome can also lead to human error after a lot data has been identified.



## **1.4. Research work (Literature) related to Apple disease :**

### **1.4.1 Based on Convolution neural Networks:**

In [ 2] the authors from Jaypee Institute of information and technology(JIIT) viz. Saraansh Baranwal, Siddhant Khandelwal and Anuja Arora present a novel method to detect Apple leaf detection using Convolution Neural Network of Deep Learning where the authors base layer length of the model is 4 and they have achieved an accuracy of 97.3% in case of Apple Scab. In terms of deep convolution neural networks [ ] this paper presents the view that complex image processing tactics could be employed but this is unable in generating high resolution rates apple leaf disease identification. They stated that their research is better than rest of traditional methods as their CNN based model that is developed achieved an accuracy of 97.62% that was considerably good thereof

Again in terms of Convolution Neural Networks Real-Time detection of Apple Leaf Diseases using deep learning approach was studied where firstly the apple leaf dataset was constructed via data augmentation & images annotation techniques uses deep-CNN is proposed by introducing the Google Net Inception structure & Rainbow Concatenation

### **1.4.2 Based on Patterns**

Authors in [ 3] have proposed a complex local binary pattern model for classification and detection of Apple Fruit disease .They have taken 3 classes into consideration : Apple Scab, Apple rot & apple blotch ,particularly they have used several layer of classification algorithms of which the final step uses is a Support Vector Machine (Multi- class) . A new paper on LSTM-Long Short Term Memory[idahon ] was explored that have created a real time database consisting of images of branches, fruits & leaves thus the system becomes easily employable for real-time applications in computing..

### **1.4.3 Biological Based Approaches:**

A paper [ ] studied ARD's i.e. Apple Replant Diseases in which for all experiments the apple's susceptible rootstock M26 was key in being useful towards early detection and being an indicator of ARD (Apple Replant Disease). In terms of cost if low cost is taken into consideration

This paper [mobile] on genetic algorithm based disease identification from feature selection method of correlation based approach deals with firstly for the input color image of stratus RGB a color transformation structure was designed and hence this RGB model was converted into HIS Hue, Saturation and Intensity, YUV and gray models. After this the Background was removed based upon threshold specific value and then segmentation of disease spot of image was performed in RGA region growing algorithm

#### **1.4.4 Other related works:**

A MOBINET [13] based identification for leaf of apple's classification followed by 2 models i.e ROSNETSS2 & Inception v3 were given, they stated that identification if occurred within a few seconds and that with a greater precision is required. Papers related to Plum were also studied in which Plum Pox plays a critical role, In the paper [] the researchers authors presented the view that 2 hyperspectral remote sensing techniques Firstly Spectral Reflectance & Chlorophyll fluorescence at early stage without visible symptoms on the leaves. In [] the authors proposed a development of an APP that will take the picture of leaf and hence identify the relevant or related plant infection. This study was done towards the identification in Phillipines.

### **1.5 Research Work related to Plum**

The paper [21 ] uses the extracts of Kakadu plum fruit for inhibiting extracts of rheumatoid arthritis (bacterial triggers) and thus for the components of stilbene tannin it's identification. The methanolic extract which was the most potent extract was analyzed by HPLC-QTOF mass spectroscopy with screening performed against 3 compound databases.

#### **1.5.1 Plum Pox Virus :**

The paper [] presented the remote sensing techniques applications for the folia horticulture of the identification of Plum' Trees biotic stress caused due to Plum Pox Virus. In which two hyperspectral remote sensing techniques viz chlorophyll florescence and spectral reflectance were used for the identification of sharka disease -biotic stress.

Another paper [19] presented the views of this identification in England. Corkscrew twisting in leaves and the chlorotic vein banding were caused by peach seedlings Graft transmission. They concluded that the virus emerged in Europe causing the transfer to subsequently parts of England via plum root-stocks. This paper was very helpful in this studies.

The paper [20] studied the potential role in sharks epidemics of alomnds for the major type of plum-pox potyvirus along with the survey for natural infections in the country of France. They stated that the development of efficient tools for characterization of the Plum Poty Virus-PPV has led to reassess the susceptibility (potential) of the specie to Sharh disease.

The paper [23] from the authors from Spain and France capital was useful in the identification of the virus 's Implicated Determinants in specific interactions over various *Prunus spp.* The 2 infection clones of PPV isolates pGPPV (D group) and pGPPVPS (M group) were studied under woody hosts where this was found that these two clones differed in their ability to infect plum and peach cultivars in systemic & local infection from nill.

This paper [22] has studied a negative effect on infection of virus of CI – Interacting protein from chloroplast by the identification of Plum pox virus. They stated that this protein was found to interact with the photosystem I PSI-K protein; from *Nicotiana benthamiana* the product of the gene psak. Their results shows and depicts that higher level of PPV accumulation in the plum plant can be achieved by downregulation of psak gene

### **1.5.2 Linear Regression Model :**

In the paper [18] the authors studied linear regression model for the variations in plum fruit size over diseased plant. They referred that the disease can interrupted plant's growth along with fruit growth, production growth and hence also the economic development. Thus the coauthors and authors presented a linear regression model for knowing the condition of plum fruit six based on plum's growth , length and width.

### **1.5.3 Convolution Neural Networks :**

The paper [2six] considered detection under True Field Conditions of Plum plants using CNN. They stated that widespread use of mobile devices for computing along with the advantages of artificial intelligence are taking key role in helping farmers towards pant disease treatment following it's detection. Through they have optimized the inception V3 model using parameter quantization that is to be deployed on resource optimized constraint devices.

### **1.5.4 Effect of 5 virus infection on *Prunus domestica* L. 3 varieties :**

This paper is one of the most significant one as it studied the effects on 3 varieties of Plum over a field trial period of duration of 10 years for the effects of 5 different virus inocula although it dates back to 1969. It was found that the yield of all 3 variety were decreased by Prune dwarf. The tree health declined progressively after symptoms initially appeared after 5 years from necrotic incompatibility between rootstock & scion

### **1.5.5 Hepatitis C virus entry :**

Hepatitis C virus has become an increasingly major cause of chronic liver disease which basically require plantation of liver for curing. The identification of inhibitors entry point must be known in order to screen the fruits with effects of hepatitis protective. It's identification is crucial for liver transplant recipients. They reported the identification of rutin, flavonoid i.e isolated from *Prunus Domestica* as a new HCV entry inhibitor.

## **1.6 Other Significant Research Papers**

### **1.6.1 Scab detection in Potato :**

In this paper the authors and co-authors proposed to increase the productivity need and stated the need of hour to identify potato disease by using image processing methodologies. I Enhancements is provided to the captured images from different potato fields then the disease spot or target region is captured by image segmentation carried over them. Finally based upon the histogram approach the target region's phase of the disease is detected.

### **1.6.2 Characteristic of Enzyme Immunosorbent for Plant Virus detection: [JV034...]**

In purified preparations also in unclarified extracts of herbaceous hosts and of crop plant that infected the analysis for morphologically different virus it's highly sensitive detection is enabled. Of the hydrolysed substrate the color intensity were photometrically measured for virus concentrations. Because of the speed, specificity and the scope provided for standardization favour is for serological techniques for possibility for virus detection <https://meet.google.com/dmr-obpg-urd>

**1.6.3 Pyrosequencing Technology evaluation for clinically relevant non-dematiaceous yeasts and related species identification:** Here from the yeasts of clinically non-dematiaceous species 133 isolates were identified by pyro sequencing which included 29 clinically isolates , 7 UAMH strains 97 ACTT strains-forty two type strains. Both the cycle sequencing and Pyrosequencing technology had identical results for the for 90.1% of all of the tested strains. From the species layout level by Pyrosequencing it's feasible to identify the most candida isolates in the given.

### **1.6.4 Using the techniques of mass spectrometry intact microorganisms rapid identification :[claydon]**

With the increasing and emerging fast need for accurate identification of bacteria's as Antibiotic – resistant strains as keep to emerge is required. It's possible for the analysis of single colony of bacteria enabling the mixed cultures screening. Specter is provided from automated analysis as since the simple is the preparation of sample that too takes within minutes. Of the microorganism the unique mass spectral fingerprint is provided by the procedure.

### **1.6.5 Detection of Plant disease (terrestrial) plant based on Android:**

As android and smartphone industry is very large it's the base of this paper published by the authors of who have described the project on the territories of Phillipines and have used Deep Neural Networks for the image processing task. Considering the fact that large number of images were used the identification of diseaseat certain accuracy and

rate could be made possible by application of training the results using special sophisticated classifiers.

#### **1.6.6 Using a time-saving direct transfer protocol**

It's of paramount importance the correct identification of pathogens for the treatment of invasive infection patients. Various Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) systems have been compared in studies with focus on identification rates for various pathogens. Another aspect that is important for laboratories of microbiology routine but has not been systematically assessed is daily routine performance

#### **1.6.7 Virus detection by ELISA:**

ELISA or Enzyme – Linked Immunosorbent Assay concept is very fruitful, for detection of 2 morphologically different plant viruses the use of antibodies that are enzyme – linked is studied and described. The assay were prepared using the microplate method [Voller 1974 to be downloaded].

The virus studied under this category were Plum-Pox virus (PPV) and Arabis Mosaic Virus (AMV). AMV particle size is nearly 30 nm while PPV's is 750 x 20 nm.

#### **1.6.8 Mass spectroscopy for reliable and fast identification of Isolates in Clinical Yeasts:**

In this paper also like 3.6 MALDI-TOF MS i.e Matrix assisted laser desorption ionization-time of flight mass spectroscopy is evaluated of isolates in clinical yeasts for rapid routine identification. A total of 267 recent isolates of candid and a net of 18 type collection strains have been identified by MALDI-TOF MS. 92.5% was the clinically achieved value of isolates in terms of accurate species identified by MSALDI-TOF MS that was achieved for 247 of them starting with cells from single colonies.

#### **1.6.9 Identification of clinically relevant non-dematiaceous yeasts through evaluation of Pyrosequencing Technology :**

133 isolates of non-dematiaceous yeast that were clinically relevant were identified using Pyrosequencing. These identified strains included 7 UAMH strains, 97 ATCC strains (42 type strain) and 29 clinical isolates. These isolates were further grouped and these groups that are classified are as follows: Candida (18 species), Cryptococcus(7) , Trichosporon (10) , Malassezia (3) , Blastoschizomyces (1), Geotrichum (1), Kodamaea(1), Rhodotorula (2).Using pyrosequencing technology AHVITS were obtained. *Amplicons of a Hyper-Variable ITS region*

#### **1.6.10 Plant disease identification by fine-tuning of deep learning models;s comparative study on work in China :**

This paper focused on identification of plant disease by image based disease classification by deep convolution neural network that had fine tuning and evaluation of state of the art deep learning architecture. The data is taken from plant village of 38 different classes that included healthy as well as diseased images of leaves of a total of 14 plants. In this paper, researchers evaluated their benefit of achieving a testing accuracy of 99.75 % to beating the rest of the architectures as dense nets have the tendency of improving consistently w.r.t epochs

### **1.6.11 SiNC based medical radiographs efficient retrieval:**

Saliency-injected neural codes-SiNC is the term described in this paper . They proposed an efficient way of representing medical images. This is achieved by incorporating visual saliency and also deep features obtained by a finely tuned CNN-Convolution neural Network. Efficient ways to represent radiographs features are most appropriately identified from the comprehensive study of different CNN layers from where neural codes aka. Neuronal activation features are taken into consideration. SiNC are thus obtained from taking from entire image the neural codes only.

## **CHAPTER 2: LITERATURE REVIEW**

### **A) APPLE RELATED LITERATURE ;**

- 2.1 REAL TIME DETECTION OF APPLE LEAF DISEASES USING DEEP LEARNING APPROACH BASED ON IMPROVED CONVOLUTION NEURAL NETWORKS:
- 2.2 BASED APPLE DISEASE IDENTIFICATION
- 2.3 MOLECULAR IDENTIFICATION OF NECTRIACEAE IN INFECTIONS OF APPLE REPLANT DISEASE AFFECTED ROOTS COLLECTED BY UNI-CORE PUNCHING OR LASER MICRODISSECTION
- 2.4 IDENTIFICATION OF APPLE LEAF DISEASES BASED ON DEEP CONVOLUTION NEURAL NETWORKS
- 2.5 REAL TIME DETECTION OF APPLE LEAF DISEASE USING DEEP LEARNING APPROACH BASED ON IMPROVED CONVOLUTION NEURAL NETWORK
- 2.6 MULTI MODEL LSTM BASED CONVOLUTION NEURAL NETWORKS FOR DETECTION OF APPLE DISEASES AND PESTS
- 2.7 TOWARDS IMPROVEMENT OF MARKER ASSISTED SELECTION OF APPLE SCAB RESISTANT CULTIVARS
- 2.8 DETECTION AND CLASSIFICATION OF APPLE FRUIT DISEASES USING COMPLEX LOCAL BINARY PATTERNS:
- 2.9 DEEP LEARNING CONVOLUTION NEURAL NETWORK FOR APPLE LEAVES DISEASE DETECTION
- 2.10 APPLE LEAF DISEASE IDENTIFICATION USING GENETIC ALGORITHM AND CORRELATION BASED FEATURE SELECTION METHOD
- 2.11 Bitter Rot of Apple
- 2.12 IDENTIFICATION AND CHARACTERIZATION OF COLLETOTRICHUM SPECIES CAUSING APPLE BITTER ROT IN NEW YORK AND DESCRIPTION OF *C. NOVEBORACENSE* SP. NOV.

## **2.1 REALTIME DETECTION OF APPLE LEAF DISEASES USING DEEP LEARNING APPROACH BASED ON IMPROVED CONVOLUTION NEURAL NETWORKS:**

Real-Time detection of Apple Leaf Diseases using deep learning approach was studied where firstly the apple leaf disease [ALDD] dataset was constructed via data augmentation & images annotation techniques from complex images and composed laboratory images under real field condition. From this a new model that is useful for leaf disease detection in apple is proposed that uses deep-CNN by introducing the Inception structure of GoogleNet & Rainbow Concatenation. A deep convolution neural network is employed for the real time detection of apple leaf-diseases. The proposed deep learning based approach can automatically identify the discriminative features of the diseased apple images & detect the 5 common types of apple leaf diseases with high accuracy. The data set is collected not only in laboratory but also in real field conditions. This paper has its advantages like that it uses latest deep learning approach that is basically functioning on improved convolution neural networks in performing apple leaf disease real-time detection. The proposed model's generalization capability is guaranteed importantly by the built ALDD. The robustness of CNN is enhanced by the dataset is collection of diseased apple images not only in laboratory rather also in real field conditions, this collection is done both for complex and uniform background. Via its through data augmentation technology it's the fact that is compromised the images of diseased apple leaf are insufficient and thus overfitting is prevented for the CNN-model during its training process, thus natural diseased apple images are processed. Based on SSD a novel model for the real-time detection of apple leaf disease is proposed. Modification is done in VGGNet to obtain the new basic pre-network namely VGG-INCEP (VGGNet combined with module of Inception) by the introduction of GoogLeNet Inception module for improving the extraction performance of disease spots (multiscale). Then the integration in R-SSD of Rainbow Concatenation method is done. Simultaneous utilization of Pooling and deconvolution is done for integrating feature pyramid's context and fuse features at the back of SSD via that larger small diseased object detection of performance can be realized. Automatically the deep-learning based approach that is proposed can identify the diseased apple images discriminative features. Thus detecting 5 common types with high accuracy of apple leaf disease

The paper hence uses methods that overcome the following drawbacks.

The paper discussed issues in real-time detection of disease in apple leaf and the difficulties there forth like on the leaf, multiple disease can occur, secondly the leaf disease spot may vary among even the same disease despite the fact that alternation can be possible amongst other, thirdly many spots are small in apple leaf disease. Lastly environmental factors like soil, glow, shadow on sample may interfere in leaf disease detection of apple.

Thus the proposed model not only detects various disease within the same leaf but also same disease of varying sizes in the same image of diseased leaf. Further more the proposed approach can handle the images of diseased apple that were captured under real field conditions in an environment of apple field



## **2.2 MULTI MODEL LSTM BASED CONVOLUTION NEURAL NETWORK FOR DETECTION OF APPLE DISEASES AND PESTS**

During the past 15 years a vast studies on the topic of detection of pests and plant diseases based upon computer vision and image processing has gained importance for the detection of pests and plant diseases. In this study they have captured images of plant's leaves, branches and fruits as real time and from cameras. Thus in real time studies this system application can be easily employed. Through the literature survey done in this paper the coauthors have stated that via ensemble learning deep feature concatenation is quite efficient thus they also in their paper have used deep feature extraction via ensemble learning. Precisely the use of individual and hybrid models are proposed for the detection of plant diseases and pests as a problem of classification. Based on LSTM network along with the deep features obtained from pre-trained deep learning models like DenseNet201, GoogleNet and AlexNet are the proposed models based upon. By using the input of the LSTM layer deep features from the fully connected layer are put into evaluation for their performance in the individual model. Upon Multi-Model LSTM based pre-trained Convolution Neural Network (MLP-CNN) as a voting classifier on an ensemble majority the hybrid model is based. In order to determine the best choice of the training parameters of the LSTM layer the use of automatic schema is in addition. The ensemble hybrid model that was proposed, data consisting of apple disease from Turkey and also pest images has been evaluated for it. The experimental results showed that the proposed hybrid model provides better performance that pre-trained without a preprocessing stage deep learning models. The main contributions of this paper are as follows:

Usefulness of LSTM based MLP-CNN as an majority voting classifier ensemble in order to solve plant disease and pest classification problems.

In areas like 1D signal, text, speech and phoneme LSTM is generally used for classification and recognition process .

This study performs experiments using real-time images obtained from different conditions like illumination . background variations and object size.

Thus the hybrid proposed ensemble model is usable in real-time applications.

Compared to pre-trained deep architectures the experimental results showed that the performance is better of proposed ensemble hybrid model. In the detection of plant disease and pests important role is played by deep features from the pre trained deep models , it also suggests that LSTM based models is an effective network with these deep models that can be used.

## **2.3 DEEP LEARNING CONVOLUTION NEURAL NETWORK FOR APPLE LEAF DISEASE DETECTION [ baranwal ]**

To automate the detection and identification task of the apple disease serious and extensive research is required. The first step lying of detection and identification of the type of disease. Leaves are easiest to observe as they are abundant, occupy and occupy most part of the tree. Thus a model is Implemented that recognizes the exact disease that has infected the crop. For automation of the same task CNN based model is trained in order to distinguish between the input infected leaf and input healthy leaf images with the disease class being identified as well. Use of Deep Learning CNN with tuned hyper-parameters for achieving better results on accuracy is the summed up solution to this problem while keeping the computational requirements and error rate low. For implementing the model

the focus is on the popular architecture GoogLeNet that is designed for Dataset of ImageNet in the context of Large Scale Visual Recognition Challenge. The said experimentation is applied for the specific disease detection of the 3 commonly found apple diseases viz. Apple Scab, Apple Black Rot and Apple Cedar Apple rust. The primary goal of this research work was to build a network that could classify whether the plant is healthy or diseased, if the diseased being so then further the type of disease is to be determined as well. The dataset used comprised of 4 prominent classes: three being diseased and last being of healthy plant leaves. They had 1526 samples of diseased leaves while 1000 samples of healthy leaf images. The implementation of augmentation of data is made possible using Python 3 Keras library. Initially into the variable "train\_images" the dataset is loaded onto and input images are downsized to 60 x 60. Further more each image is normalized into Z distribution is division by standard deviation after subtraction from Mean. In a random manner the rearrangement is done on the dataset of these images and by selecting set of first 500 images the validation set is prepared while the remaining randomly arranged images are used to train this deep learning Convolution Neural Network model. By simple transformation of rotation, width shift horizontal and vertical flips and height shifts new images are produced using the data generator function in Keras. These scaling are done to further enhance the size and potential of the dataset in tackling every possible situation making absolute use of the limited dataset. Hence using the image generator function of the Keras library the problem of having less number of images in this dataset is dealt with. The anaconda package manager is used in importing all the dependencies while Keras library is used that works on top of Tensor flow. Implementation is as follows: Firstly Loading in the ratio of 80:20 of the training-testing dataset and saving them in numpy arrays. The normalization of these training and testing images is done using Z transforms that involves the division of SD by the difference computed from Mean. Secondly, Loading the saved numpy arrays of training and testing images as they had relatively less number of images so performing various operations on existing dataset that produces new images.

The CNN Model built is similar in working to that of standard LeNet architecture. The model is trained with various parameters after building the model. Thus the achieved accuracy in this deep learning Convolution Neural Network is 98.42% with worst case accuracy achieved in case of "Apple Scab".

## 2.4 DETECTION AND CLASSIFICATION OF APPLE FRUIT DISEASES USING COMPLEX LOCAL BINARY PATTERNS:

Precise image segmentation is required for the problem of classification of fruit disease, else the features of infected region was dominated by features of non infected region. Here k-Means clustering based image segmentation approach was preferred and used in detecting the region of interest that was the infected part of the region only. Once segmentation is done the features from the segmented region of apple image is extracted. Finally on a Multi-class SVM Classifier training and classification are performed. Thus the basic procedure of the proposed approach were i) Data set Preparation ii) Image Segmentation iii) Feature extraction iv) Training and Testing by a Classifier. In the K-Means clustering technique that is used for the image segmentation performs the partition of Images into 4 clusters where 1 cluster are containing the majority of the diseases part of the image. As the algorithm was developed by J. MacQueen in 1967 that classifies the objects -pixels in our problem into classes of k-number of types based upon a set of features. By minimizing the distances of sum of squares between corresponding cluster and the data objects the classification is carried out. The sum of squared distances that is used for k-means clustering is called Euclidean distance in this experiment. For causing the reduced processing time for the segmentation of image. They have used L\*a\*b\* color space since this color component in the L\*a\*b\* color space is stored in two channels i.e. a\* and b\* component and the input images were partitioned into 4 components in this experiment. It's found out that 3 to 4 clusters were suitable for yielding good experimental result(from the empirical observations). They have used some state of the art texture features and color features to validate the accuracy and efficiency. This include (the features that are included i.e. used for the disease classification problem of apple fruit ) Color coherence vector, Complete Local Binary pattern, Global color Histogram, Local Binary Pattern. Global Color Histogram(GCH) was one of the most simplest approach that was used to encode the information present in an image. It's a set of ordered values that for each distinct color representing the probability of a pixel of being of that color. For reducing the scaling bias and reducing the number of distinct colors Uniform normalization and quantization is used. CVC is an approach to compare images based on color coherence vectors as they define color coherence as the degree of extent to which image pixels of that color are members of a large region including homogeneous color. "Coherent regions" is the reference used to define these regions. To some sizable contiguous regions coherent pixels are belonging to incoherent pixels . In order to computing CCVs, to eliminate small variations between neighboring pixels the method blurs and the image's color space is discretized. Then the connected components was found in the image in order to classify the pixels either incoherent or coherent in a given color bucket. After the classification of image pixels is done, the CCV computes 2 color histograms 1 for incoherent pixels and the other for coherent ones' pixels. In LBP in the input image given a pixel it's computed by comparing it with it's neighbors  $LBP(N, R) = \sum_{n=0}^{n-1} s(v_n - v_c) 2^n$ ,  $s(x) = \begin{cases} 1, & x \geq 0 \\ 0, & x < 0 \end{cases}$

It's  $v_c$ : Value of the central pixel

$v_n$ : value of it's neighbours

R: radius of the neighborhood

N: total number of neighbours

CLBP: In LBP only neighboring differences are taken so CLBP consider all sign (S), magnitude(M) of local difference as well as original center gray level value(C)

## **2.5 MOBINET BASED APPLE DISEASE IDENTIFICATION**

The algorithm to identify apple disease must have the following 3 characteristics :Firstly it should be stable i.e. the ability to identify the similar apple leaf diseases should be present in the method. Secondly : It should be low cost i.e. the method should be a simple one to implement or be used in mobile devices. Lastly The efficiency and precision of the app should be to identify the disease within one second that too with high precision. The paper stated that the current existing approaches did'nt followed the satisfaction of these 3 issues for the disease identification of apple leaf. Thus they divided existing approach into 2 classifications Firstly: Inspection by experienced experts Lastly by using deep learning methods inspection. The later can't be directly used in mobinet devices as they are complex to be used directly in mobile devices in identification of apple leaf diseases. In this paper the researchers and coauthors built a mobile based model for the identification of apple leaf diseases based on MobiNet. This is the mobile version of CNN model whose precision is nearly the same as with the general CNN model although it has high efficiency for identification of apple leaf diseases. To obtain all kinds of leaves having different leaf diseases in apple the coauthors have invited agriculture experts from Chinese Academy of Agricultural Sciences, Chine for letting the disease identification as STABLE as possible. For demonstrating the effectiveness of the proposed model they have mainly used 2 kinds of apple diseases viz. Apple rust and Alternaria Leaf Blotch. Also in order to achieve goal of LOW COST ISSUE for identification of leaf disease in apple the MobiNet model is employed. Lastly in order to achieving this final goal of HIGH Precision the mobinet model is optimized accordingly with the features of diseases of apple leaf. After trying other models also the coauthors concluded that the MobiNet based approach leads to the best choice of results as an overall balance in precision and efficiency is achieved using this for identification of leaf disease in apple. In order to achieving higher accuracy the trend of general development of CNNs has been making more complicated and make deeper networks. However, in terms of size and speed the complex networks of model structure cannot be made more efficient of the network.

## **2.6 MOLECULAR IDENTIFCATION OF NECTRIACEAE IN INFECTIONS OF APPLE REPLANT DISEASE AFECTED ROOTS COLLECTED BY HARRIS UNI-CORE PUNCHING OR LASER MICRODISSECTION:**

In apple nurseries and orchards the plants growth and fruit yield is negatively as well as affected by the replant disease of apple. Like necrosis and blackening this early symptoms are described in the roots of fine ARD-affected apple as shown by detailed microscopic analysis. Also these symptoms have been often colocalized with fungal infection sites in tissues of cortex. The repeated intercellular fungal structures observation with a CF in their previously microscopic analysis of apple fine roots led to this motivation of the study. In plant genotypes like 'M26' and 'Bittenfelder' that are susceptible they could be already detected after 2 weeks of growth in soil affected with ARD. In contrast to other studies they found that strong evidence for Nectriaceae fungi being major cause of rapidly affecting young root tissue of the tested susceptible genotypes. They developed special fungal structures by the spread in the tissues in diseased roots segments with contribution to blackening and necrosis by the fungi. In a detailed study(histological) on the roots of *Rosa corymbifera*, it was confirmed that a close co-occurrence of necroses,

Nectriaceae and blackening was similarly formed for also rose replant disease. Here in the core objective was in collecting these fungal structures from the cells of the affected cortex for an immediate identification by molecular tools. Nectriaceae accounted for 37.7% of these ARD associated endophytes of fungal root as a large proportion occurrence of disease from more than 150 endophytic fungal isolates from affected roots of ARD that were obtained by microbiological approaches and the identification of their pure cultures were determined. A lot of time was required in this classical cultural-dependent approach but was proven to be indispensable for later inoculation tests and also contributed especially to ARD's unravel biotic causes of it. Of cryo-sections the paper established the protocols for two sampling methods applied for fixed fine or fresh roots namely Laser micro dissection (LMD) and Harris Uni-Core punching and tailored them to apple root tissue's structural properties. These methods helps in identifying the possibilities of fungi harvested from selected tiny root sections down to selected cells.

## **2.7 IDENTIFICATION OF APPLE LEAF DISEASES BASED ON DEEP CONVOLUTION NEURAL NETWORKS**

Expensive cost and low efficiency is lead by trained experts for the visual inspection by and for scoring the plant disease severity. With digital cameras popularity, IT advances in agriculture has wide use of cultivation and management systems and have been practiced generally for improving the plant's production capacity of. However for the experts system, expression and extraction characteristics of pests and diseases are mainly depending upon expert experience that leads to low recognition rates and relative lack of standardization. Traditional machine learning methods like SVM, k-nearest neighbors and random forest diagnosis for the study of automated plant disease has been done by researchers in order to increasing the improvement of accuracy and rapidity of the diagnosis results, as the usefulness of the machine learning algorithms and it's popularity in CV has taken place. However since the classification features are selected and adopted based on the experience of humans, these approaches have contributed in increasing the recognition accuracy but still the recognition rate is not high enough and thus is vulnerable to artificial feature selection. The discriminative features for the classification of image that can be automatically discovered by the deep convolution neural network approach as that is an end-to end pipeline as an development in recent years, with advantage lying in the use of shared weights for reducing the improve performance and memory footprint and of the image the direct input into the model. As of this date the CNN has been rated and regarded as the one of the best classification approached for pattern recognition tasks. In agricultural information a new research hotspot has emerged following the break through of the CNN in image based recognition. It has inspired the used of CNN in identifying early disease images. Thus this CNN is widely studied and used in the field of crop disease recognition. Also these studies shows that CNN are widely studied and thus used in the fields of recognition of disease in crops. Moreover this studies have showed that CNN have not only helped in reducing the demand of image processing but also helped in improving the recognition accuracy. Although this approach of using those CNN faces two difficulties, Firstly apple pathological images , for training the model are not that sufficient, Lastly determination of the best structures of the network model is a more difficult task fundamentally. For all the stages of object recognition, research appropriate datasets are

required from training the CNN- based model till evaluation of the recognition algorithms'. In this research 4 common leaf disease of apple were chosen as the research objects those with lesions as more widespread than others these are cause of doing great harm to apple quality and quantity are it. A total of 1053 images were acquired that had typical disease symptoms consisting of 252 images of Mosaic(cause: *Papaya ringrot* virus), 319 images of Brown spot(cause: *Marssonina coronaria*), 300 images of Alternaria leaf spot( cause: *Alternaria f.sp mali*) and 182 images of Rust(cause: *Pucciniaceae gluerust*).

From the Baishui county, Shanxi Provanance, Chine and Qingyang county Gausu Province, Chine these two experimental stations were responsible in pionerring the supply of the captured apple leaf disease images. Startingly the lesions caused by the same disease show the certain commonality under similar natural conditions secondly the yellow lesion of Mosaic diffuses throughout the leaf that exist as different from the other lesions diseases. Lastly Brown spot is easy to detect, is different from others irregular green edge

## **2.8 IDENTIFICATION AND PATHOGENICITY ASSESMENT OF COLLETOTRICHUM ISOLATES CAUSING BITTER ROT OF APPLE FRUIT IN BELGIUM**

*Colletotrichum spp.* are stated to be one of the most important polyphagous fungal pathogens worldwide to cause anthracnose on vegetables, wheat fruit and ornamental plants. In Belgium *Colletotrichum spp.* become an increasing post-harvest problem in bitter rot of apple fruit caused by it. Studies done in Germany and Sweden showed a post-harvest loss of apple fruits of respectively 10% and 25 % respectively by *Colletotrichum acutatum*. Worldwide upto 50% of the apple production can be lost due to bitter rot. The post-harvest and pre-harvest diseases on apple can be caused by this pathogen *Colletotrichum*. Due to temperature causes in northern regions only post-harvest problems are noticed until now. Disease symptoms in diseased apple fruit of bitter rot start with the development of small dark brown spots expanding to light brown sunken lesions after or during storage. In the center of the lesion afterwards on the host, in acervuli concentricly conidia are formed. In European region the *C. florinae* and *C. godetiae* both belonging to the *C. acutatum* species complex are the main species contributing to this problem of bitter rot and symptoms on fruit of apple. In USA and Brazil, such as the more southern regions both the species of *C. gloeosporioides* and *C. acutatum* complexes are stated to be the causal agents. Thus in general both this *C. gloeosporioides* and *Colletotrichum acutatum* species complex have been associated with this problem of apple's bitter rot on it. With specific *Colletotrichum spp.* associated with the problem of bitter rot now a days in Belgium is unknown. Taxonomical naming and delineation of the different species belonging to the *Colletotrichum* genus has always been complex as well as difficult. Until 1957, the speciation was only based on the host from which this material was isolated therein. From then on, von Arx proposed, on morphological characteristics to base the species name , characteristics like colony color, shape of conidia and appressoria's size and shape and growth rate making a significant reduction from 750 to 11 species, as those characteristics were not reliable for species identification. *Colletotrichum species* were revised in 1980 combining morphological with pathological characteristics that resulted in a distinction between *C. acutatum* and *C. gloeosporioides*, afterwards these species were actually considered in being species complexes i.e. *C. acutatum, sensu lato* and *C. gloeosporioides sensu lato*, based upon morphological and molecular analysis and containing different

species that were new like *C. fioriniae* and *C. godetiae*. Now using morphological characterization pathogens are identified alongside molecular methods. Different regions of genes have been used molecularly and shows potential to make a clear distinction between several *Colletotrichum spp.*, including *C. acutatum* and *C. gloeosporioides* complexes along with DNA sequence analysis. By different hypothetical aspects this *Colletotrichum* problems increase in Europe can be explained, like use of more specific fungicides before harvest, cross infections of different plants, differences in fungicide's sensitivity or the climatic changes effects. One of the first important step is in identifying the true species that is present in the given orchard/ forest. In pathogenicity *Colletotrichum species* differ also and in their response to fungicides, making it necessary to study the sensitivity of this fungicide. Management in orchard can be optimized by doing this. No information is currently available about this very disease of causal agents in apple fruit with Bitter rot moreover this has been in a rise in Belgium. This method of pure cultures is described in having equal efficiency in producing pure isolates in less time.

## **2.9 IMAGE PATTERN CLASSIFICATION FOR PLANT DISEASE IDENTIFICATION USING LOCAL TRI-DIRECTIONAL FEATURES:**

To measure the affected area and the classification of the disease type computer vision is employed for performing efficient classification and detection by an automated computational system that is capable of it for plant diseases prove for agronomist worthy asset that tend in performing diagnosis via optical observation of infected leaves of plant's part. Computer programs are mainly consisted of computer vision based symptoms that takes input as images and automatically processed them for detection of disease. To perform and work efficiently and in order to match the level and methodology these systems are designed so as to match the level and methodology that is adopted by experts in agriculture industry and farmers. As compared to the human experts these systems need less information and high throughput for processing . Using genetic algorithms, image segmentation and artificial neural networks are used in order to realize classification and detection of plant disease to perform by computer-vision based systems . This paper presented a framework for computer-based system that consists of the combination of CBIR and SVM for the disease detection of tomato plant at an early stage. They proposed the use of local tri directional patterns LTriDP that performed for the feature extraction after pre processing from leaf image. Their proposed system for identification of plant disease takes plant leaf image as input and consists of two major proposed processing stages i.e. Feature classification and feature extraction. In first stage the input image is enhances and the local Tri-Directional Patterns are extracted. These features are the representation of individual leaf image and are used in classification stage. Classification

of the plant's disease is done by Support Vector Machine classifier. The feature extraction can be done by i) Local Binary Pattern: [32] first proposed the use of local binary patterns for texture classification. Due to its speed, of discriminant feature information efficient representation LBP is widely useful and used mostly in face recognition and detection, image classification and object tracking tasks. The LBP operators is defined as below:

$$LBP_{p,r} = \sum_{l=0}^{p-1} 2^l X_{S_l(I_l - I_c)} \quad S_l(x) = \begin{cases} 1, & x \geq 0 \\ 0, & \text{otherwise} \end{cases} \quad \text{where } I_l \text{ and } I_c \text{ are}$$

neighborhood and center pixel values respectively for p neighborhood and r radius.

**Local Tri-directional Pattern:** The pattern of Local Tri-directional (LTriDP) is extended variant of Local Binary Pattern feature descriptor. For image retrieval applications LTriDP is originally proposed for plant disease identification. LTriDP proves to be effective feature descriptor when combined with Support Vector machine classifier.

Its use is of the relationship that is based on various ways in the place of relationship in uniform with all adjacent pixels. Few neighboring pixels are in place with individual central pixels in a particular radius of the. fruit More relevant information is provided only by few neighboring pixels due to less distance from the center. Here a pattern is supposed to be formed by considering the eight neighborhood pixels. With central pixel each neighborhood pixel that is individual compared with two most nearby neighborhood pixels. Either vertical ones or horizontal ones are the pixels that are in neighboring and pixels that are two in quantity since both of these are closet to be deliberated neighboring pixel. With its two most adjacent pixels, the difference between each neighborhood pixel is determined and with central pixel.

## 2.10 APPLE LEAF DISEASE IDENTIFICATION USING GENETIC ALGORITHM AND CORRELATION BASED FEATURE SELECTION METHOD: [10.25165]

The First step to controlling the apple disease is to detect and identify the type of disease. The leaves of the apple trees are abundant and thus occupy the most part of the tree and are the easiest part in observing. To consider that the majority of the diseases in apple can be recognized through their diseases leaf symptoms their research interest lies in the apple leaves rather than the whole of apple tree. So far mostly the approach adopted in practice for the detection and identification is the observation through eye's by farmers or of expert in the field is the main approach. This leads to a drawback that it's inefficient, difficult and expensive. IT's a well known fact that the perception capability of the human eye cannot is unable in minor variations for discrimination in the infected part of leaf images. This is very tiny, the pattern change of color leaf caused by different disease on leaf. Confusing judgement standards of the diseases in apple might be resulted from symptoms description's of quantitative method and in the meantime, long time failures to adopt the accurate methods for the same, that might even lead to utilization(blind) of pesticides and serious pollution of agricultural products, soil and water. Feature extraction is a key task in CV technique with in the research of identifying and diagnosing of plant diseased leaf image dimensionality reduction along with feature extraction is a key task. Usually C,T etc. are different in disease ACT normal ones. Apple diseased leaf image collection. They chose powdery mildew, mosaic and rust as the testing diseases among over 100 common diseases of apple. Powdery mildew is a very common apple leaf disease, except for damaging apple, powdery mildew also damages begonia, binzi etc. In the apple orchard generally Mosaic is the kind of virus disease that occurs. Another kind of leaf



disease of apple is the apple rust that is another main threat to apple leaf stick, leaves, shoots and tender green fruits. In the recent years with the development of city and road planting as well as with the large number of distant transportation of planting trees rust becomes much more popular in some growing areas and the incidences of disease is increasing year by year. In order to avoid external negative influences of the experimental conditions during collection of the apple diseases leaf image so as to avoid the external influence factors of negative nature of the same experimental conditions like light intensity and viewing conditions as they designed a set of leaf images collection system that includes a luminous box, a CCD digital camera, a computer system that includes a software system for leaf image capturing. The system includes a plant image collector A and a leaf image processor B. CCD camera is with the S, bulbs that provides color light source, glass( put the leaf) and some other structure to push and pull the glass. For The image of plant leaf collection in A, B plays a role to control it.

The control function includes start, CCD camera focus adjustment, image denoising, plant recognition and image segmentation etc. Through a USB cable A and B are connected and the captured plant leaf images are stored in SD card in B. Amongst all of them, the CCD digital camera is used with close-up mode, auto white balance, flash off, and the same conditions to collect each leaf image various settings are fixed to generate. With a resolution of 2560x1920 the leaf images were collected and transformed into computer in the form of JPEG mode. With light blue background 90 diseased samples were taken.

#### 2.11 Bitter Rot of Apple :[ppfs]

On the outer surface of fruit the bitter rot lesions i.e. spots begin as small sunken, localized areas. As these lesions mature they remain circular and sunken moreover some spots may develop red halos. Over time, these lesions darken to brown and expand to develop a bulls eye pattern. During days of rainy weather periods, salmon or pink spores may appear in circular patterns. An internal rot is revealed in cross sections of fruit with a “V” shape i.e firm and brown. As it can take several days, the symptoms of bitter rot may not appear immediately after infections to it can take several months like two months in order to become visible. Symptoms begin to appear in early to mid-Summer as early as mid June in Kentucky and this disease often increases as fruit ripen and harvest approaches. Premature fall may be occurred in infected fruits or they may remain attached to trees as mummies (dried fruit). In storage after harvest symptoms may also develop. Fungal disease is the bitter rot that is caused by multiple species i.e. *Colletotrichum acutatum* *Colletotrichum gloeosporioides* sp. Complex 38 individual species are contained in each complex. Till date (as of publishing of this article) exactly 12 individual species of *Colletotrichum* have been identified as fruit rot pathogens in the south eastern U.S. In Kentucky, 6 individual species have resided in to cause apple bitter rot. Species identification is important because individual species exhibit differences in : Spore production, Infectivity and aggressiveness, Competition/fitness, Host preference, fungicide sensitivity and temperature preference. In fallen fruit bitter rot can overwinter, dried fruit that remains attached to the tree (mummies) and diseased or dead wood e.g fire blight cankers. It has been confirmed by research the presence of dormant enzymes in fruit in tissues of wide range of apple trees in the late winter and early spring (before plant growth resumes), particularly on fruit mummies and their pedicels as well as in fire blight-infected shoots. Fruiting structure is produced when weather warms (acervuli) on the surface of

tissue in plant. These structures absorb water and release infective spores (conidia) during wet conditions. Some species are pioneer in producing orange to salmon-colored mucilage that carries spores as it oozes from lesions. These spores may be blown or splashed onto susceptible tissues in plants that to within small distances and wind driven rain may move across an orchard the spores identified. As early as bloom, infections can occur also with infections additional to possible throughout the growing season and into harvest. Ongoing research has the topic that whether when the fungus breaks dormancy in spring and specific times of sporulation and infection of flowers and fruit. As with all fungal pathogens these fungi favor wet conditions and moderate temperatures. Thus during wet seasons this bitter rot disease is more severe. In dense orchards disease can also be more severe in locations where there is limited air circulation, high humidity and restricted sunlight. By the bitter rot causing fungus that is *Colletotrichum* fungi in addition to other fruits other plant species may become infected by it, this fungus as these plants may serve as reservoir hosts or alternative hosts. While alternative hosts may become infected and develop leaf spots or dieback the latter reservoir hosts can also act as catalyst in harvesting endophytic infections (harbor them) in that where no symptoms develop. It has been confirmed that the presence of *C. fioriniae* the most common *Colletotrichum* species on apple in Kentucky by research. In trees that are common on insects and weeds the presence of it is established as a matter of fact. It's unclear whether infections can move from alternative hosts to fruits this research is still ongoing in heading institutes. Fungicides are not curative.

## **2.12 IDENTIFICATION AND CHARACTERIZATION OF COLLETOTRICHUM SPECIES CAUSING APPLE BITTER ROT IN NEW YORK AND DESCRIPTION OF *C. NOVEBORACENSE* SP. NOV. : [10.1038]**

The diseases affecting yields and fruit quality. Fruit and plant of apple is vulnerable to a wide range of diseases. Bitter rot caused by *Colletotrichum spp.*, is one of the most important fungal diseases of apple causing remarkable economic losses under warm and wet weather conditions in the US and globally. From 14-25% is the range of apple fruit losses to bitter rot in New York as per reports and up to 100% in certain other orchards that to also up to 100% in North Carolina and are 30%. Amongst this nine major clades of the *C. gloeosporioides* species complex (CGSC), *Colletotrichum* and the *C. aetatum* species complex (CASC) are the two most common clades that cause bitter rot of apple. *C. godetiae*, *C. nymphaea* and *C. fioriniae* from CACS and *C. fructicola*, *C. aenigma*, *C. theobromicola* and *C. siamense* from CGSC are well known so far in causing bitter rot on apple at worldwide scale. Besides causing bitter rot species like *C. limeticola*, *C. melonis* and *C. paranaense* in CASC and *C. fructicola* in CGSC are suitable in causing Glomerella leaf spot (GLS) of apple. Although these 2 diseases are associated with the same fungal genus the differences in pathogenicity, morphology and cultural characteristics of species have been reported. Due to species-level variation in pathogenicity related characteristics the accurate identification of *Colletotrichum* species causing bitter rot is crucial due to it. Resistance breeding PROGRAMS IS Facilitated by the identification of causal agent(s) and the determination of the best control strategies for diseases in apple. On hosts, cultural and morphological description the identification of *Colletotrichum* was traditionally reliant on to the species level as well as comparison of nuclear rDNA internal transcribed spacer sequences. In cultural and morphological characteristics like the size and shape of conidia, pigmentation of *Colletotrichum* isolates and colony growth rate these variations are known to be caused by temperature and as growth medium these identification techniques are

limited in their effectiveness. In the CGSC to delimit species the ITS region known for fungi as the barcode locus is considered insufficient. While species delimitation of using ITS based phylogeny and morphology remains insufficient for resolution of *Colletotrichum* at the species level, In addressing challenges in the identification multi-locus phylogenetic analysis have been proven to be reliable of *Colletotrichum* species. Various species in the CGSC like glutamine synthetase (GS), calmodulin (CAL), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), chitin synthase (CHS-1),  $\beta$ -tubulin (Tub2), DNA Lyase (APN2), actin (ACT) and the intergenic region between DNA lyase and the mating type (Mat1-2) gene (ApMat) in addition to ITS, loci have been used in resolving various species. A prerequisite in successfully managing this disease in apple production regions is the accurate identification of *Colletotrichum* species causing bitter rot since different species of *Colletotrichum* respond differently to fungicides and vary in traits like enzyme activity and pathogenicity of species is of extreme complex importance for the future research on the control of bitter rot. The virulence capacity and pathogenicity is determined by the ability of *Colletotrichum* species in producing extracellular enzymes. In *Colletotrichum* species the variable levels of amylolytic polygalacturonase (PG), pectolytic, polymethylgalacturonase (PMG) and amylolytic activities with different plant diseases are detected in *Colletotrichum* species associated; with different diseases of plant disease in it.

## **B) PLUM RELATED LITERATURE :**

### **DISEASE DETECTION IN PLUM USING CONVOLUTION NEURAL NETWORK USING TRUE FIELD CONDITIONS:**

This paper involves the method of on-field monitoring and disease detection of plum fruit plants using a deep learning algorithm has been proposed to maintain plant health by minimized further infections. This will definitely enable farmers in detecting early disease in a plum fruit plant in a real-time environment using a smartphone. In this same regards under true field conditions a dataset of abnormal and normal images is collected locally. Nutrient deficiency, shot-hole (leaves) and (fruits) and brown-rot are the major diseases affecting plum fruit and leaves. In the collected dataset all of these diseases were covered. A fine-grained classification problem is the disease identification in plum fruit where in a healthy fruit is discriminated from an unhealthy one based on subtle differences in texture and color of the fruit. Due to visual similarities a healthy fully grown fruit can be confused with a fruit affected by a brown rot or a shot-hole to some degrees, for instance. Similarly a very challenging task is due to identical visual symptoms for the detection of nutrient deficiencies in leaves and shot-hole (leaf) in since these make their average detection very challenging. Using this dataset the co-authors have trained and evaluated multiple CNN in order in performing disease detection in image captures from mobile phones or smartphones. In order in training a robust detection model, parameters like scales, angles, direction and external environment that are related to the image are considered while developing the proposed symptoms. On mobile devices The trained model is then optimized for deployment by quantizing the network parameters till 16-bit floating point (FP16) from 32-bit floating point (FP32).

On a mid range device it can be run conveniently and the final optimized model yields considerable accuracy, eliminating the needs to access the cloud storage services. Careful design of the whole image analysis process was designed in order to address all of the

issues, to true field conditions keeping in view the fact that the images will be captured under the same where severe environmental lighting variations, unfavorable image capturing environment and sensory limitations of cheap smartphone cameras may make it very challenging for simple image processing techniques to analyze like a farmer may capture the image of the affected leaves/ fruit while standing at the ground of the top of the tree. This will lead to the process of capturing a lot of noise, and loss of details due to the small scale of the objects of interest and also possibly motion blur. For coping with this situation and similar the proposed method has been optimized to work efficiently in true field conditions. Details of each step are as follows:

**Preprocessing:** There is a very limited or no preprocessing step required in a typical end-to-end learning environment as in most cases the data available is highly feasible for input thus eliminating the need to preprocess.

**Data augmentation:** It's is very challenging for the variations in scale, orientation and position of the object in the images that make it's prediction for CNN. The network has to cope with all these variations in a robust manner. Data augmentation can be one of the most popular approaches that can be used.

**Geometric Transformation:** 13 additional images from this transformation alone were formed by the application of several geometric transformations like scaling, rotation and translation (image cropping at the center and four corners) .

**Contrast Adjustment:**  $g(x,y)=\{ a_1f(x,y), f(x,y)<r_1; \quad a_2(f(x,y)-r_1)+s_1, r_1>=f(x,y)<r_2; \\ a_3(f(x,y)-r_2)+s_2, f(x,y) >=r_2 \}$

### **KAKADU PLUM FRUIT EXTRACTS INHIBIT GROWTH OF THE BACTERIAL TRIGGERS OF RHEUMATOID ARTHRITIS: IDENTIFICATION OF STILBENE AND TANNIN COMPONENTS: [IMPORTANT]**

Autoimmune inflammatory disease is Rheumatoid Arthritis (RA) in this case it 's an autoimmune disease that may afflict genetically susceptible individuals. There are currently no cures for RA and to alleviate the symptoms the aim of current treatment strategies is (particularly swelling and pain) via the use of anti-inflammatory and analgesics agents, or/and to modify the disease process through the use of disease modifying anti-rheumatic drugs(DMARDs). As prolonged usage of these drugs can result in unwanted side effects and toxicity thus none of these treatments is ideal. For the treatment of RA there is a need to develop safer, more effective drugs for the treatment of RA that will not only alleviate the symptoms but may also prevent or cure the disease. For drug design an attractive target is the-Eradication of the cause of an inflammatory disease is as this would not only decrease/block the late phase inflammatory symptoms but would also decrease the immune response and subsequent tissue damage associated with auto-immune inflammatory disorders. The cause of RA have not yet been comprehensively understood BUT the generally accepted notion about these is that it's an autonomous disorder that by specific microbial infections is triggered in susceptible individuals (Genetically). As a trigger of rheumatoid arthritis *Proteus mirabilis* infections have been proposed as elevated serum level of *P. mirabilis* specific having frequently been reported in individuals surfacing from RA having specific cross-reactive antibodies. On joint possessing *P.mirabilis* cross-reactive antibodies antibodies of *P.mirabilis* have cytopathic effects from RA patients and sera from rabbits immunized with HLA-DR3 positive lymphocytes binded specifically to the proteus. In the *P/ mirabilis* haemolysins of the 'ESRRAL' and the 'EQ/KRRRAA' motif present in RA/HLA-susceptibility antigens homologies of the

amino acid sequence between them have been identified. Of type XI collagen-present in cartilage( joint ) and the IRRET motif present in *P. mirabilis* urease enzyme sequence homology between the 'LRREI' sequence of former further have been reported. *Proteus* spp. Growth has been known to have been inhibited by many antibiotics already and/or have bactericidal effects towards *proteus* spp. However super resistant bacterial strains development has resulted currently in antibiotic resistance leading to end many bacterial infections. For new antimicrobials the search is ongoing either by i) new agents synthesis and design or ii) re-searching the repertoire of natural resources for as yet unrecognized or poorly characterized antimicrobial agents. Anti *P. mirabilis* activities have been examined by recent studies of conventional antimicrobials like carbapenems and of complementary and alternative therapies including nano-metallic preparations and the traditional medicinal plants of south Africa. For the treatment of rheumatic conditions and inflammation a re-examination of functional foods is an effective prospect as the antiseptic qualities of medicinal plants have been long recognized and recorded. Also a revival of interest has been recently in herbal medications because of the perception that there exists a lower incidence of adverse reactions to plant preparations as compared to synthetic pharmaceuticals. The highest ascorbic acid levels have been reported in the fruits of this *Terminalia ferdinandiana* as compared to any plant of this world with levels reported to be having reached at 6% of any recorded wet weight. This is approximately 900 times the acid level in blueberries. Extremely high antioxidant content have been found in *Terminalia ferdinandiana* that is an Australian endemic plant.

#### **IDENTIFICATION OF A PLUM POX VIRUS CI-INTERACTING PROTEIN FROM CHLOROPLAST THAT HAS A NEGATIVE EFFECT IN VIRUS INFECTION:[MPMI]**

Plum pox virus causes sharka disease and is a polyvirus that is found in fruit trees of the *Prunus* genus and also has the ability in infecting different herbaceous hosts. The role of the CI Protein in both cell-to-cell movement and replication of virus also its relevance in at least one resistance gene's activity is suggesting that varying factors of hosts that may have interaction with the CI protein during the infection of virus. Between CI protein's helicase domain from TEV and the protein P58<sup>IPK</sup> an interaction has been reported but about the host proteins little is known about their interaction with the polyviral CI protein and its role in the infection of virus. To identify host proteins the yeast two-hybrid system previously has been used to identify which have interactions with polyviral proteins like HCPro, Nib or VPg. To screen a *Nicotiana benthamiana* cDNA library the used bait was of PPV CI protein by the two hybrid system in this study. CI-interacting protein was identified by the PSI-K subunit of photosystem 1 and its relevance of its interaction was studied through the analysis of the effect of interfering in PPV infection's of PSI-K expression. With different host factors movement and replication of the virus infection multiple interactions are expected to be involved in the CI proteins activities. Therefore to identify the yeast two-hybrid structure was used in the cDNA library for the plant CI-interacting proteins from *N. benthamiana*. To code for products of CI-interaction 2 clones were found in the first screening using pLex9-CI as bait while 10 clones were identified using pAS-CI plasmid AS bait that has also the two selected from the I-Screening. Also these 2 clones identified in both the screenings allowed in minimal medium the growth of yeast when more selective yeast strain PJ69/4a was used. For 31-amino-acid(aa) peptide one of the clone coded for; the sequence analysis showed that which corresponded to an

unknown protein. TO the photosystem I PSI-K protein for a 130-amino-acid peptide the second clone coded for; of several plants with 50% to 85% of identity levels, the clone also included 3' and 5' noncoding regions of 48 and 44 nucleotides (nt) respectively, and was named pACT-PSIK. Of cDNA ends (RACE) method a rapid amplification of was used ; inorder to obtain the psaK mRNA complete sequence. To the library clone the RACE product was identical to. By a nuclear gene (psaK) PSI-K is encoded by a and it's synthesis is done as a precursor in the cytoplasm and thus transported to the chloroplast where it's localized and processed in the non appressed region of the membranes of thylakoid. They analysed in more details the CI-PSI-K interaction in the 2 hybrid system using the PJ69/4a yeast strain. Positive interactions were detected with an N-terminal CI fragment of 409 aa (CI409) of PSI-K. The 7 conserved motifs of the RNA helicase are included in the CI409 fragment of it and has neem shown in the 2-hybrid system to self-interact. In CI-CI interaction that was also involved in; PSI-K did'nt including the CI 177 fragment interact with the other CI fragments. Positive interactions were not detected between PSO-K and any other PPV protein analyzed like CP(coat protein), P3/6k1 or Nib. The activation of  $\beta$ -galactosidase ( $\beta$ -gal) gene reporter was included in the interaction of these 2 hybrid proteins. The interaction strength was more accurately assessed through the resulting  $\beta$ -gal activities quantitative analysis. The levels were comparable with those detected in yeast of  $\beta$ -gal levels in yeast transformed in pAS-CI409 or pAS-CI and pACT-PSIK; transformed with control plasmids pTD1-1 and pVA3-1 indicates CI409-PSI-K and CI-PSI-K interacted with the high efficiency. Some yeasts transformed grew in the less restrictive conditions.

#### **IDENTIFICATION OF A FLAVONOID ISOLATED FROM PLUM (PRUNUS DOMESTICA) AS A POTENT INHIBITOR OF HEPATITIS C VIRUS ENTRY[S415]:**

The leading cause of chronic viral hepatitis is the Hepatitis C virus (HCV) and that is estimated to infect 160-million people globally. Liver cirrhosis, hepatocellular carcinoma and liver fibrosis are the results from leading persistent HCV infection. Unavailability of a preventive vaccine against HCV infection is there. For HCV infection the standard treatment includes the administration of pegylated interferon alpha in combination with ribavirin. However this therapy has limitation that includes low sustained virological response (SVR). In the last few years, efficiency and treatment options have improved with the advent of several classes of direct-acting antivirals(DAAs) that constitutes of protease inhibitors, NS5B and NS5A inhibitors. Although with the dramatically increased the SSR; the currently approved DAAs have done it's rates and revolutionized the treatment regimen they are associated with severe side effects and this therapy may not be able to abrogate the infection in a substantial number of cases. Due to high replication of HCV and it's high genetic heterogenicity there exists a high risk for the development of virus strains that are drug resistant. In the lesser resource countries this high cost of that are associated makes it inaccessible of the association with this treatment. Thus for the development of antivirals that are less expensive, well tolerated and mire readily available there exists an imperative need for the development of such new antivirals. The HCV lifecycle's replication step is targeted by most of the DAA's is a well known fact, recent studies depicts that the addition of entry inhibitors to the DAAs; on the antiviral treatment's efficiency, a synergic effect is exerted. Thus of the virus lifecycle different stages that are targeted by different combination of inhibitors; the stages including replication, entry and secretion/assembly

might be a better therapeutic strategy in order in reducing the escape of viral mutants risk. With end stage liver disease, chronic infection is associated that represents the major cause of liver transplantation. HCV infection is seen , in majority of the patients to occur in the grafted liver. By inhibiting viral entry the donor allograft reinfection can be prevented; into hepatocytes using entry inhibitors. In India the most prevalent genotype of HCV is 3a, thus this study was initiated using hepatitis C virus-like particles (HCV-LPs) that constituted of core E1-D2 derived from genotype 3a. using a HCV-LP based system This study was carried out since the VLPs(Virus like particles) ; of native viruses mimic their morphology and represented a well-established system for studies on entry and viral binding in it. For the cure of various diseases the traditional medicines have been used for decades. To possess antiviral activities phytochemicals extensive variety are demonstrated. For they antiviral effect from natural sources compounds have been reported against various infections like herpes simplex virus, hepatitis B, influenza virus and even hepatitis C Virus. Based on their hepatoprotective effect for this study of anti-HCV activities the fruits and vegetables were chosen. *Prunus domestica* (plum) exhibited the highest inhibitory activities of the several extracts examined. In hepatoma cells the binding and entry of HCV-LP were evaluated and the efficiency of rutin in binding and blocking of it and also the potential of rutin are assessed in the prevention of HCV JFH1 Japanese fulminant hepatitis I infection *ex vivo*. The hepatoprotective property of fruits and vegetables that are known to possess were selected, in order in investigating the cytotoxic effect of these extracts huh7 cells were treated with different concentration of cell viability and extracts was assessed by MTT [3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide] assay.

#### IDENTIFICATION OF PLUM POX VIRUS DETERMINANTS IMPLICATED IN SPECIFIC INTERACTIONS WITH DIFFERENT PRUNUS SPP.: [PHYTO]

Produced in vivo or in vitro the infectious transcripts from full-length cDNAs previously have been done for PPV isolates. From the PPV-D, PPV-R (Rankovic isolates), PPV-NAT group first were of/while the construction of a cDNA clone was very recently described of the PPV-PS isolates a relative of the PPV-M group from which transcripts of the infections can be made. From the parental full-length cDNA clones of PPV-PS(pGPPVPS) and PPV-R(pGPPV) chimeric viruses were constructed and the viability of all the transcripts were in *Nicotiana clevelandii* and *Pisum sativum*, allowing the first evaluation of symptom of PPV determinants on these herbaceous **genus** plants. The chimeric PPV and these parental were utilized, clones of these were to be investigated with viral sequences governing the pathogenesis of PPV on *Prunus* spp., its natural host in the framework of the understanding and the identification of the numerous factors determining the properties (epidemiological) of this virus. From full length cDNA clones of PPV-PS(pGPPVPS) and PPV-R(pGPPV) the infectious transcripts of these isolates were previously obtained. Currently sequence analysis and typing tools assigned to the PPV-D group the PPV-R isolates and the PPV-PS isolates to the PPV-M group. Progeny from up to 15 chimeric viruses and as well as from these 3 clones isolates whose construction was described by other researchers [Saenx et.al] has been used in this study. With progeny of infectious transcripts the initial analysis was performed of pGPPV and pGPPVPS and with a limited number of chimeric viruses in order to so as to identify the inoculation protocols and identify plant material appropriate for these sources of virus. In this study the juvenile seedlings that are commercially available that were obtained from distinct species of virus free-seeds of *Prunus* rootstock were used. They adopted a protocol of the inoculation

(mechanical) of the seedlings that allowed for the simultaneous work with the several viruses of chimeric and multiple seedlings (for each virus source a minimum of 10 seedlings per experiment). Amongst these nonclonal seedlings that were derived in order to the possible genetic heterogeneity limiting the effect of these assays were limited. From *Nicotiana benthamiana* plants inoculum sources were obtained from it in order to get inoculated with these infectious transcripts. At -80 °C storage was done and at 10 days postinoculation (dpi) the systematically infected leaves were mixed in order to use the similar lots of inoculum so as to perform for each experiment. By using double-antibody, sandwich enzyme-linked immunosorbent assay (DAS-ELISA) in these samples the virus concentration were evaluated. With Carborundum and inoculated mechanically the virus-free seedlings were dusted of the first leaves of the juvenile of it (approximately 20 days after sowing) and with the crude sap extracts of infected *Nicotiana benthamiana* leaves diluted 10-fold in a phosphate solution (by 0.03 M Na<sub>2</sub>HPO<sub>4</sub> consisting of 0.2% Sodium-diethyl dithiocarbamate). By the simultaneous inoculations of *Pisum sativum* and *Nicotiana benthamiana* the infectivity of the inoculum sources was determined by the simultaneous inoculations. According to French safety regulations the plants were confined to and in a temperature 18°C/25°C (night/day) were kept in a growth chamber under fluorescent lamps (10,000 lux) with a 16-h/day photoperiod. By using DAS-ELISA for PPV infections the plants were individually tested for, accordingly to the procedure first described by Adams and Clark in 1997 [7] and in the laboratory were optimized. At a 1:50 final dilution plants extracts were used at a in phosphate-buffered saline with Tween plus 2% (wt.vol) PVP 40k.

THE IDENTIFICATION OF PLUM POX (SHARKA) VIRUS IN ENGLAND: [CRPLY] in 2 young cv. Italian Plum prune trees Sharka virus (Plum pox) was identified. 'Corkscrew' twisting and chlorotic vein banding were caused by Graft transmission to peach seedlings of the leaves. *Nicotiana clevelandii* and *Chenopodium foetidum*; by sap inoculation these plants were infected by and the virus was transmitted to *N. clevelandii* from *N. clevelandii* by *Myzus persicae*. The indication that this virus was introduced from Europe to England has circumstantial evidences; in plum root stocks. When in the infected site all trees were tested, no further infection was found when diseased trees were destroyed. A disease previously located in England (plum-pseudo-pox), experiments with it have established that this disease isn't caused by plum pox virus. In mid-European countries like Yugoslavia, Czechoslovakia and Bulgaria the most important limiting factor is probably the plum pox in the commercial production of plums. This virus has the tendency in spreading to other healthy trees rapidly unlike affecting fruit trees by most other viruses. To the west of the German federal republic in the European countries until recently, this virus has not been reported from any part; to the latter part where it was diagnosed by Schunch (1962), Ellenberger and Posnette described a disease virus in England that caused similar in some respect fruit blemishes to plum pox and concluded that this virus that they called OOsV (Plum Pseudo-pox), was different from PPV (European plum pox). For this distinction their evidence was held that while PPV caused chlorotic blotches, lines and rings on plum leaves, the latter PPV didn't. By grafting Pozegaza when infected with the English virus, whereas cultivar develops fruit symptoms and severe leaf while got infected in Europe with PPV. In the leaves at East malling one young Italian prune tree [in 1965] developed a severe yellow mottle. In the collection of plum trees this tree was in a previously thought to be a virus-free viz. symptoms were pure virus-like but not like those



that had early been seen at East Malling. In phosphate buffer the leaves were macerated and to the young plants the sap used to isolate it of *Chenopodium amaranticolor*, *Cucumis sativus*, *Petunia hybrida*, *C. quinoa* and *Phaseolus vulgaris* cv. On any plants no symptoms were developed. By Prune d'Ente and Krikon (Plum cvs.) they were inoculated by using double budding and destroyed and removal from the plot was done to the affected Italian Prune tree. In 1966 the development of a diffuse mottle on the leaves was formed of the Prune d'Ente and Krikon trees that were inoculated from the Italian Prune trees and were inoculated with buds while the inoculated plants from symptomless Italian Prune plants that were done with from buds were found to be very remained healthy. From the site where the first tree had been removed in 1965, in 1966 a second Italian Prune tree adjacent to the later site developed mottled leaves on 1 branch while on the other branches the leaves were absolutely healthy. From the branch showing symptoms in a glasshouse by the inoculation by the bark grafts the young peach seedlings growing in them was seen and from 3 branches not showing symptoms From the buds close to the point of inoculation to encourage the growth of the peach shoots; the peach seedlings were pruned. After the three weeks of inoculation only the grafts containing peach seedlings with it from the branch with symptoms that developed the chlorotic vein banding on the leaves that had been twisted and deformed in a corkscrew fashion. Symptoms of these were identical with those that had been reported by Baumann (1964) and Nemeth (1963) who ascribed them to PPV. Removal and burning of all of them of inoculated trees and of the Italian prunes and all of the subsequent work was completely done in an aphid proof glasshouse.

**POTENTIAL ROLE OF ALMOND IN SHARKA EPIDEMICS: SUSCEPTIBILITY UNDER CONTROLLED CONDITIONS TO THE MAIN TYPES OF PLUM POX POTYVIRUS AND SURVEY FOR NATURAL INFECTIONS IN FRANCE: [DALLT]**

In cropping conditions the changes of almond and for the characterization and detection of the development of the efficient tools of PPV (plum pox potyvirus) have led the authors to reassess the potential susceptibility of it to sharks disease by this species and its role as the central reservoir to virus. To nine isolates the almond cv. Ai susceptibility of, amongst PPV population representative of the known population diversity, under controlled conditions was assessed. To almonds most of the isolated were able in infecting, by aphid or graft inoculation without any obvious sharks symptoms causing generalized stable infections. A potential source of virus were found to be constituted by these infected almonds for the aphid vectors in the case of M isoates mainly. In the foci of D and M strains of PPV in the south of France surveys were carried out of the natural infections of almonds to evaluate the presence of. The virus was not known to be ever detected and no typical symptoms were observed. To infection be allowed in almond trees in France the actual limited prevalence of PPV it can be assumed that this does not lead to a sufficiently high inoculum pressure to be allowed. Of the stone fruit trees this Sharka is one of the most serious diseases present throughout the Mediterranean region and its caused by PPV (Plum pox potyvirus) transmitted on grafting and aphids in a non-persistent manner. Rapid epidemics is included in PPV especially on plum, peach and apricot. On to other cultivated Prunus species on the incidence of the disease being cultivated on the incidence a very little information is available on Prunus species like cherry or the almond, in the sharka epidemics and on their potential role as virus reservoirs. With particular strains of PPV new reports have shown that this cherry can be infected the sweet and sour cherry but

earlier this cherry was long considered to be resistant. By several authors [ Susic,1965; Festic 1978] the description of the susceptibility of almond to Plum Pox Potyvirus was done under particular conditions of inoculation ( of young almond seedlings the known of the mechanical inoculation) And that to without specific tools for the strains characterization and detection. In desvignes more recently due to a Greek isolate a case of almond contamination was proved to be found. Previously precisely evaluated The occurrence of natural infections has never been however. In order to detect PPV in almond very little surveys have been carried out in France due to the low economic importance of this very crop. For almonds the improvement of Cropping conditions( with high potential yields the irrigated orchards farms) for and the development of efficient tools for the typing of PPV population and detection to assess the susceptibility of almonds have led the authors to assess to the main type of PPV and as potential reservoir of the virus it's role. In foci of PPV-D and PPV-M strains surveys were carried out at occurring in the south of France, the levels of infections (natural ) in order to evaluate. As much as possible of the known diversity of PPV populations with the aim of taking this into account9 isolates of PPV were used in this study. The isolates were selected according to their original host, the results of characterization tests and their geographical origin. The representative strains of these 2 groups of PPV-D and PPV-M present in France have distinct epidemiological properties. For it's molecular divergence the El A isolates were selected from Egypt for it's molecular divergence (3<sup>rd</sup> group). In peach GF305 all isolates were propagated in peach in an glasshouse that was insect-roof until it's use as it'san inoculum.

#### **FOLIA HORTICULTURAE APPLICATION OF REMOTE SENSING TECHNIQUES FOR THE IDENTIFICATION OF BIOTIC STRESS IN PLUM TREES CAUSED BY THE PLUM POX VIRUS: [2083]**

2 remote sensing techniques (hyperspectral) chlorophyll fluorescence and spectral reflectance, were used for the identification of sharka disease(biotic stress) in plum trees without visible symptoms on the leaves at an early stage. Cultivars that are wide spread in Bulgaria, ' Black Diamond' , 'Angelina' and 'Mirabelle' this research was mainly focused on them. By means of; the fluorescence and reflectance (hyperspectral) data were collected ; through a portable multichannel fibre-optics spectrometer in the near infrared range of spectral i.e. 400nm-1000 nm and the visible range of spectral i.e nm – nm. for assessing the significance of the difference b/w infected plum leaves and the spectral data of healthy(control) leaves Deterministic analyses and the statistical analyses were applied for. Broad implemented in virology in plants with complementary serological tests DAS\_ELISA, Comparative analysis were performed with. From the 2 remote sensing techniques the strong relationship that was found to have been established between the results from them and the serological analysis indicates that the applicability of hyperspectral reflectance and fluorescence techniques before the appearance of visible symptoms without damage and conducting for the health condition assessments of vegetation easily. In terms of agronomic effects and the importance of economically the Sharka (plum pox virus) of stone fruits is considered to be one of the most devastating diseases and in the world is among the most studied viral diseases. Around 1917 for the time this disease was first described for plums and for apricots in 1933 on Bulgaria Around the Mediterranean basin and the Middle East and the near ;to a large part of the European continent since then this virus has progressively spread since then. It has also been found in America (Canada, USA and Chile) and in the India, It's most injurious to Prunus

domestica (European plum) Across Bulgaria this virus. In cultivars of this crop that are sensitive to PPV the yields can be completely compromised to after the infection of trees. Over the long distances this PPV is spread through the infected propagative plant material introduction of ;in a non persistent manner followed by local dispersion by aphids . Very difficult is the disease control since the symptoms of sharka on the sensitivity of the host plant and the environmental conditions like temperature, age of the trees etc. are highly normally dependent. On leaves, petals, stones and fruits the symptoms of the sharks may appear on the surface. On leaves in spring they are particularly clear, and on chlorotic spots, vein clearing or yellowing, bands or rings, mild light green discoloration or even leaf deformation. On petals the flower symptoms can appear- discoloration of some peach varieties. In general, chlorotic spots or light pigmentation of yellow rings or line patterns are shown by infected fruits. Irregular or deformed in shape may be fruits become and develop small brown or necrotic areas. Internal browning of the flesh may be shown by the diseased fruits and with reduced quality. Prematurely drop in the diseases fruits from the tree in some case may be present. As compared to late cultivars to symptoms expression on fruits early cultivars are much more sensitive to in general. In many cases parts of the crown trees; depending on the source of the PPV infection and the way can remain with a low virus concentration or with remain uninfected. Leaves symptoms may not every year appear on separate leaves or may not appear the leaf symptoms for some varieties. Of virus Enzyme-linked immun- osorbent assay (ELISA) isthemostcommon serologicaltechnique for the routine diagnosis.

#### **AN ANALYSIS STUDY BASED ON LINEAR REGRESSION MODEL FORCHANGES OF FRUIT SIZE OVER PLUM DISEASE: [AN ANALYSIS]**

In plants and fruits there are different types of disease that occur due to changes of not only the climate, seasons and weather but also the temperature and other environmental factors like rainfall, humidity etc. The structure of also the crop, fruit and plants can be changes by the disease. The influence of disease on plants and fruits affects our agriculture sector and agriculture industry. Plant's growth can be interrupted by disease and also production growth, fruit growth and all over the world on economic growth and also makes an effect on economic growth of it. In various plants farmers can easily identify the various diseases and also in problem detecting these farmers have a lot of experience. For environmental factorial diseases the farmers can easily take actions or the care of it but sometimes it's not working. For good production of fruit's quality and their methods are more reliable in improving farmer's crop and the former, technologies can support farmers to make it happen. Different types of plum plant diseases are therefor in this study they have analyzed and then used the linear regression model for knowing the condition of plum fruit size using plum length, plum growth and of plum width. In most of the agriculture based countries more than 50%-60% of the people depends on farming. To select suitable Crops, vegetables and fruits these farmers have a different type of diversity. For quality produce and crops yields the plantation of these ways however is good and 60-100% reliable but nowadays around the world many kinds of diseases are presented and also that the factor that a disease can be able to change the function or the structure of a animal, human and plant due to the fact of climate, seasons and significance of environmental

conditions like temperature, rainfall, humidity etc along with weather conditions have changed. The disorder of structure or function in a word a disease is in a human, plant and animal. Around the world there are various enormously diseases present. The agricultural sectors like plant growth, production growth and economic growth the termination of plants disease affects not only the agriculture industry but also our these latter mentioned sectors. With technological support it's high time to improve farmer's method to make for our society huge production. From use of the linear regression model to analysis , analysis of plant disease this study deals to ; this deals to of plum fruits size using plum growth, plum width and plum length. An art of science is from also this plant disease diagnosis. LIKE BACTERIAL diseases, miscellaneous diseases, fungal diseases, nematodes, virus and virus-like diseases, phytoplasma, parasitic in plum plants mostly, different type's of diseases that have occurred are listed as latter. cherry leaf spot, Bacterial canker, bacterial spot, anthracnose, brown rot, black knot, crown gall, cystospore canker, plum leaf spot, peach leaf curl, powdery mildew, plum pox, peach scab, Rhizopus rot, prunus stem pitting and rusty spot are some of the common plum plant diseases. For environmental factors first at the coauthors and the authors have the ability in to identify which types of diseases occur in plant of plum and then using the model of linear regression model to analysis the plum data for plum fruit size using the physical factors such as the for size of fruit of plum like the growth in plum, the width of plum and the length of plum.

### **DECLINE AND OTHER EFFECTS OF FIVE VIRUS INFECTIONS ON THREE - VARIETIES OF PLUM (*PRUNUS DOMESTICA*): [ POSNETTE]**

On three varieties of plum (*Prunus domestica* L.) the effects of 5 different virus inocula were studied of 10 years duration in a field conditions. The line causing pattern of

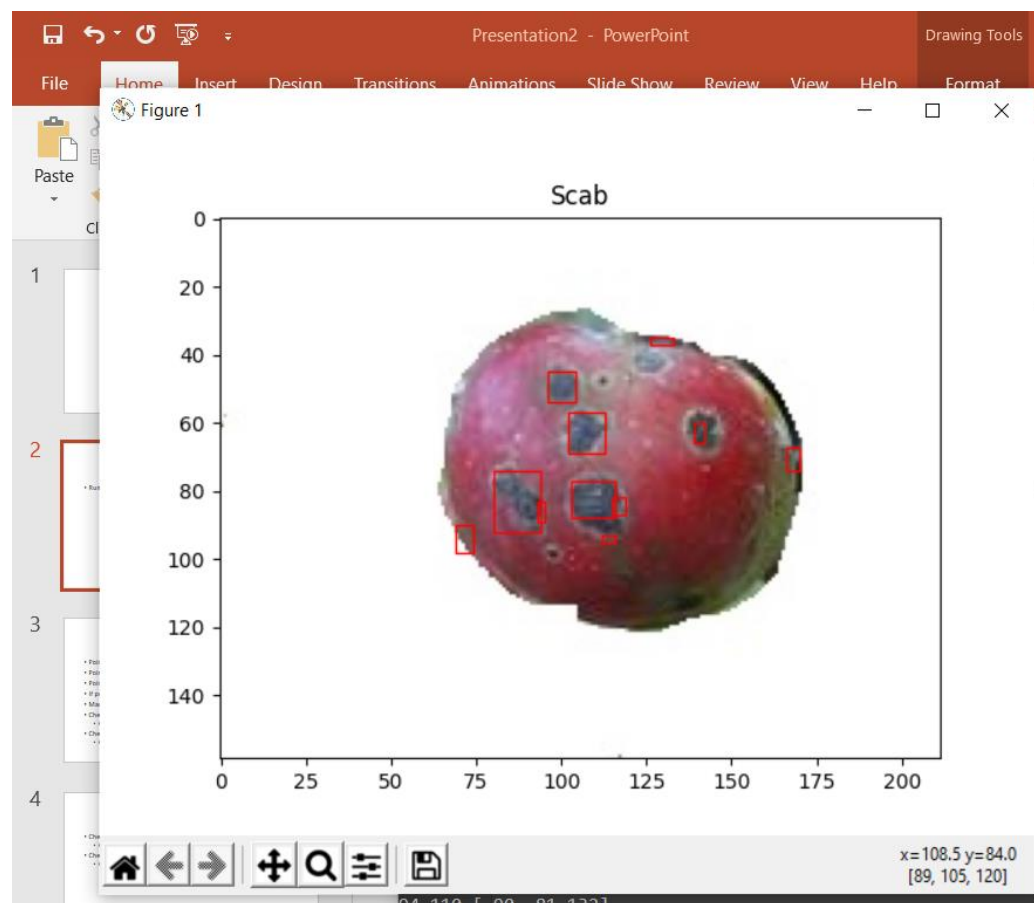
The viruses with prune dwarf, ringspot and bark split on the growth of Marjorie's Seedlings had no effect and on the Cambridge gage and also prune dwarf stuted oullins gage trees only that causing it. However to the fruit yield these viruses diminished on 1 or more varieties and the yield of all three have been seriously decreased by prune dwarf virus. By a strain of *Prunus* necrotic ringspot virus probably caused decline disease that are developed in Marjorie;s Seedling but not in other varieties. After 5 years the symptoms first appeared and then the trees declined progressively with necrotic 'incompatibility' between scion and rootstock. On the cropping and the growth of plum trees to study the effect of 5 different virus infections a trial was planted in 1957 that was continued for 10 years. In England because of for their commercial importance 4 varieties of *Prunus domestica* L. were chosen: Victoria, Cambridge Gage, Marjorie's Seedling and Oullins Golden Gage. On clonal Myrobalan B (*P. cerasifera* Ehrh.) the first 3 were grafted rootstocks and the last on *P. domestica* L. (Brompton) because mechanically weak have been seen in the Oullins/Myrobalan unions. By silverleaf disease (*Stereum purpureum* Pers.) the comparison of virus effects on Victoria were invalidated. The occurrence of a disease

was a feature of this disease that which has not been reported in Europe and that resembles a condition called decline, in New York State affecting Stanley prune trees .

# CHAPTER 3: PROPOSED METHOD

## Rule based Fuzzy System

In logic, fuzzy logic is a form of many-valued logic in which the truth value of variables may be any real number between 0 and 1 both inclusive. It is employed to handle the concept of partial truth, where the truth value may range between completely true and completely false. The present research work has been based using rule based system of if-else clauses in order to solve the problem of apple disease identification through image processing.

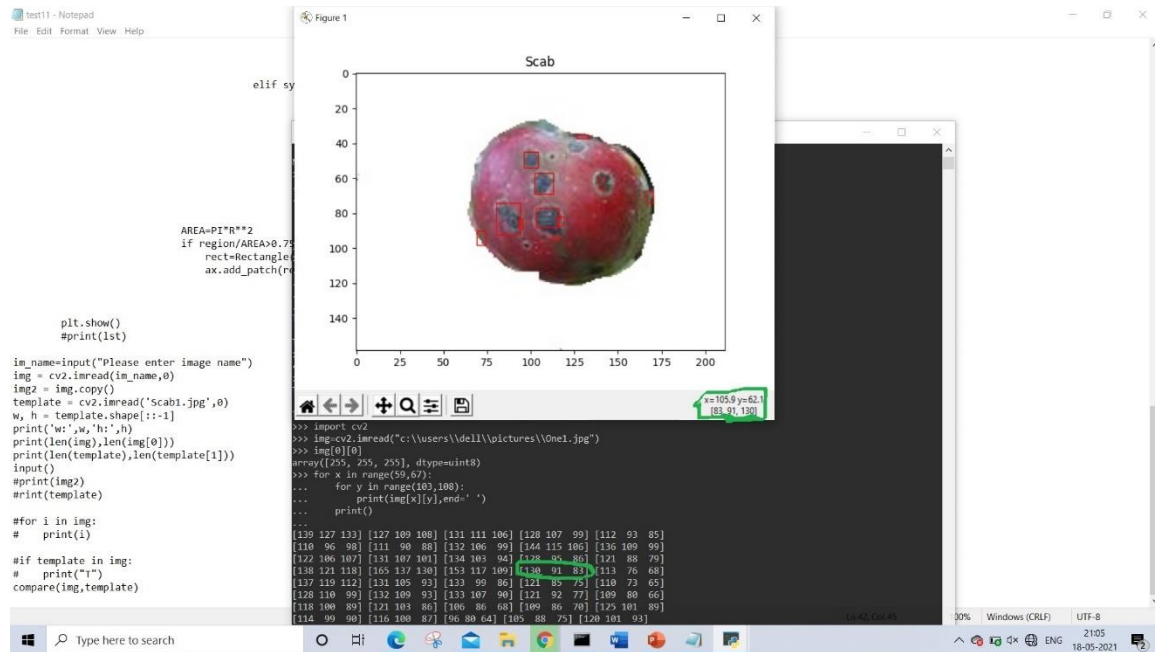


- 3.1 The methodology involves the following steps:**
  - 3.1.1 Selecting the points values of RGB color in picture**
  - 3.1.2 Creating the Min-Max values from identified points**
  - 3.1.3 Defining rules using if-else clause for the detection of disease**
  - 3.1.4 Counting number of points of each separate disease respectively**
  - 3.1.5 Finding the maximum value of the separate points scored by each disease.**
  - 3.1.6 Re-runng the program to find the disease coordinates.**

### 3.1.7 Marking the color pixels that come under this range

### 3.1.8 Plotting of the Picture

#### 3.1.1 Selecting the points values of RGB color in picture



This can be realized using any of 2 methods:

- i) Creating python script that traverse values :  
This is a given code that traverse the x-y coordinates value from the range of points that within lies the diseased segment of cumulative disease.

```
The code : 1. import cv2
2. img=cv2.imread("c:\users\del1\pictures\One1.jpg")
3. for x in range(59,67):
4.     for y in range (103,108):
5.         print(img[x][y],end=' ')
6.         print()
```

In line 1: the module cv2 is imported  
In line 2: it's imread() function is utilized to read file 'One1.jpg' with the path Specified

In line 3: the x is iterated from 59- > 67  
In line 4: the y is iterated from 103 till 107.  
In line 5: this value of RGB corresponding to [x,y] is printed without line space  
In line 6: "\n" is executed by calling just print() so that new X has

newline

This gives the iteration of [X,Y] values with n1-n0 rows and y1-y0 cols where

n1,n0 are values of x in range(n0,n1) and  
y1,y0 are values of y in range(y1,y0)

ii) Dragging mouse over pyplot image:

Image can be displayed by running the programs as it is without specific set of rules or garbage rule values and when this program displays it or another light weight program displays it using *matplotlib.pyplot* function then dragging over the region of disease plant, From here the n<sub>1</sub>,n<sub>0</sub> and y<sub>1</sub>,y<sub>0</sub> values as discussed earlier can be found out by choosing randomly or specifically the extreme corners of diseased dissection . By dragging we get the BGR values – reverse of RGB values in the bottom right corner highlighted by Green in the above image and then manually finding the min/max R, Min/ max G, min/ max B from this shown output is also but tedious.

As seen the table is drawn that gives value of RGB

x/y	130	R
62 (x)	91	G
106(y)	83	B

x/y	83	B
62.1	91	G
105.9	130	R

Thus from the two tables we can calculate that the both values are consistent.

	103	104	105	106	107
59	[133 127 133]	[127 109 108]	[131 111 106]	[128 107 99]	[112 93 85]
60	[110 96 98]	[111 90 88]	[132 106 99]	[144 115 106]	[136 109 99]
61	[122 106 107]	[131 107 101]	[134 103 94]	[128 95 86]	[121 88 79]
62	[138 121 118]	[165 137 130]	[153 117 109]	[130 91 83]	[113 76 68]
63	[137 119 112]	[131 105 93]	[133 99 86]	[121 85 75]	[110 73 65]
64	[128 110 99]	[132 109 93]	[133 107 90]	[121 92 77]	[109 80 66]
65	[118 100 89]	[121 103 86]	[106 86 68]	[109 86 70]	[125 101 89]
66	[114 99 90]	[116 100 87]	[96 80 64]	[105 88 75]	[120 101 93]



### 3.1.2 Creating the Min-Max values from identified points

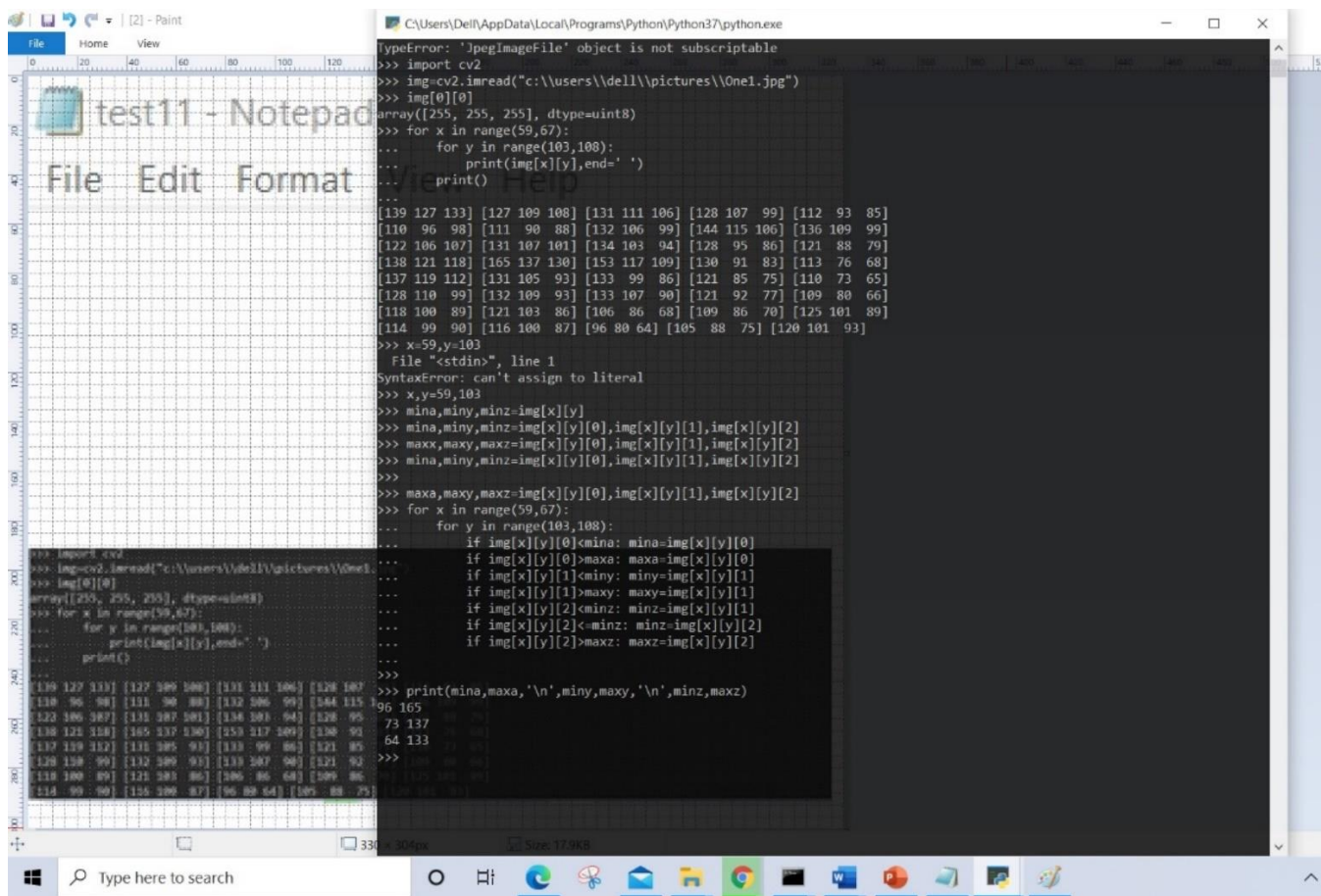
```
>>> import cv2
>>> img=cv2.imread("c:\\users\\dell\\pictures\\One1.jpg")
>>> img[0][0]
array([255, 255, 255], dtype=uint8)
>>> for x in range(59,67):
...     for y in range(103,108):
...         print(img[x][y],end=' ')
...     print()
...
[139 127 133] [127 109 108] [131 111 106] [128 107 99] [112 93 85]
[110 96 98] [111 90 88] [132 106 99] [144 115 106] [136 109 99]
[122 106 107] [131 107 101] [134 103 94] [128 95 86] [121 88 79]
[138 121 118] [165 137 130] [153 117 109] [130 91 83] [113 76 68]
[137 119 112] [131 105 93] [133 99 86] [121 85 75] [110 73 65]
[128 110 99] [132 109 93] [133 107 90] [121 92 77] [109 80 66]
[118 100 89] [121 103 86] [106 86 68] [109 86 70] [125 101 89]
[114 99 90] [116 100 87] [96 80 64] [105 88 75] [120 101 93]
```

	103	104	105	106	107
59	[133 127 133]	[127 109 108]	[131 111 106]	[128 107 99]	[112 93 85]
60	[110 96 98]	[111 90 88]	[132 106 99]	[144 115 106]	[136 109 99]
61	[122 106 107]	[131 107 101]	[134 103 94]	[128 95 86]	[121 88 79]
62	[138 121 118]	[165 137 130]	[153 117 109]	[130 91 83]	[113 76 68]
63	[137 119 112]	[131 105 93]	[133 99 86]	[121 85 75]	[110 73 65]
64	[128 110 99]	[132 109 93]	[133 107 90]	[121 92 77]	[109 80 66]
65	[118 100 89]	[121 103 86]	[106 86 68]	[109 86 70]	[125 101 89]
66	[114 99 90]	[116 100 87]	[96 80 64]	[105 88 75]	[120 101 93]

Here the minimum and maximum values correspondingly are as follows:

	Min	Max
R	96	165
G	79	137
B	64	133

	Min coordinate		Max coordinate	
	X	Y	X	Y
R	66	105	62	104
G	63	107	62	104
B	66	105	59	103



This is a screenshot of the same computation using python that was one of the lastly added feature here in this report. As can be verified manually and through the points of script that these lies in this tabular form as earlier got sample space.

	Min	Max
--	-----	-----

R	96	165
G	79	137
B	64	133

### 3.1.3 Defining rules using if-else clause for the detection of disease

Color	R		G		B	
	Min	Max	Min	Max	Min	Max
White rot	22	57	41	75	126	162
Bitter rot	16	79	37	78	23	73
Scab	76	131	75	115	62	120
Sooty Blotch	0	57	33	200	50	200
Black Rot	0	50	0	50	0	50

These are stored in the table with identity: *val*

```

68 print(scab, head, ex, toa)
69
70 ey=stack[head][1]
71 aa[ex][ey]=1
72 print(ly, ll, ex, ey, toa)
73 if ey==ly:
74     print('11') and img[ex][ey-1][0]<val[14][0][1] and img[ex][ey-1][0]<val[14][0][0]
75     if aa[ex][ey-1]==0 and img[ex][ey-1][0]<val[14][0][1] and img[ex][ey-1][0]<val[14][0][0] and img[ex][ey-1][1]<val[14][1][1] and img[ex][ey-1][1]<val[14][1][0]:
76         tap=[]
77         stack.append([ex, ey-1])
78         toa=toa-1
79         aa[ex][ey-1]=1
80         print('11')
81 if ex==ll:
82     print('21')
83     if aa[ex-1][ey]==0 and img[ex-1][ey][0]<val[14][0][1] and img[ex-1][ey][0]<val[14][0][0] and img[ex-1][ey][1]<val[14][1][1] and img[ex-1][ey][1]<val[14][1][0]:
84         tap=[]
85         stack.append([ex-1, ey])
86         toa=toa-1
87         aa[ex-1][ey]=1
88         print('21')
89
90 if ex==0:
91     print('3')
92     if aa[ex-1][ey]==0 and img[ex-1][ey][0]<val[14][0][1] and img[ex-1][ey][0]<val[14][0][0] and img[ex-1][ey][1]<val[14][1][1] and img[ex-1][ey][1]<val[14][1][0]:
93         tap=[]
94         stack.append([ex-1, ey])
95         toa=toa-1
96         aa[ex-1][ey]=1
97         print('31')
98
99 if ey==0:
100     print('4')
101     if aa[ex][ey-1]==0 and img[ex][ey-1][0]<val[14][0][1] and img[ex][ey-1][0]<val[14][0][0] and img[ex][ey-1][1]<val[14][1][1] and img[ex][ey-1][1]<val[14][1][0]:
102         tap=[]
103         stack.append([ex, ey-1])
104         toa=toa-1
105         aa[ex][ey-1]=1
106         print('41')
107
108 head=head-1
109 print(head)
110 print(stack[0][0])
111 invl_stack[0][0]
112 invl_stack[0][1]

```

# CHAPTER 4: RESULTS AND DISCUSSION

## 4.1 Counting number of points of each separate disease respectively

```
C:\Windows\System32\cmd.exe - python tt12_backup1.py
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
94 110 [ 90 81 132]
[41, 307, 356, 0, 106, 92]
[[0, 0], [0, 0], [0, 0], [0, 0], [0, 0], [0, 0]]
Scab
94 110 [ 90 81 132]
94 110 [ 90 81 132]4. Counting number of points of each separate disease respectively
2
```

The table with col No3 has been deleted in the above table while the other values corresponding are projected:

Disease	Value
<i>White rot</i>	41
<i>Bitter rot</i>	307
<i>Scab</i>	356
<i>Sooty Blotch</i>	106
<i>Black Rot</i>	92

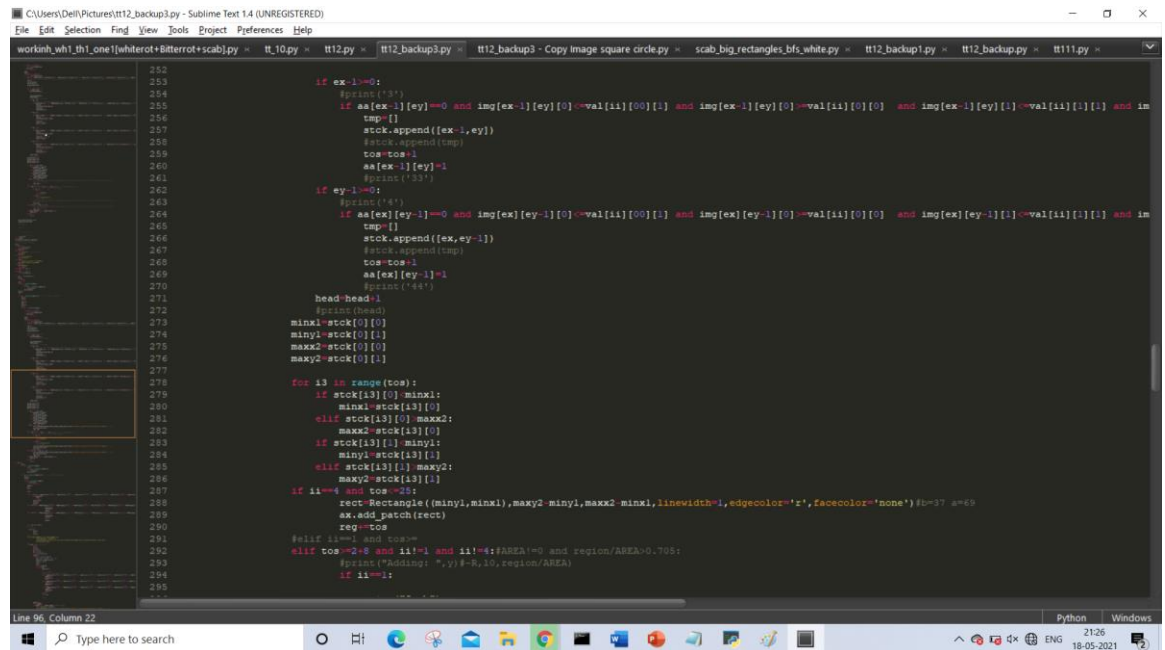


## 4.1.2 Re-running the program to find the disease coordinates.

```
C:\Users\Devi\Pictures\tt12_backup3.py - Sublime Text 14 (UNREGISTERED)
File Edit Selection Find View Tools Project Preferences Help
workinh_wht_1_one[whiterot+Biterror+scab].py - tt_10.py - tt12.py - tt12_backup3.py - tt12_backup3 - Copy image square circle.py - scab_big_rectangles_bfs_white.py - tt12_backup1.py - tt12_backup.py - tt111.py
202
203
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206
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208
209
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212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
Line 96, Column 22
Python Windows
Type here to search
2125
18-05-2021
```

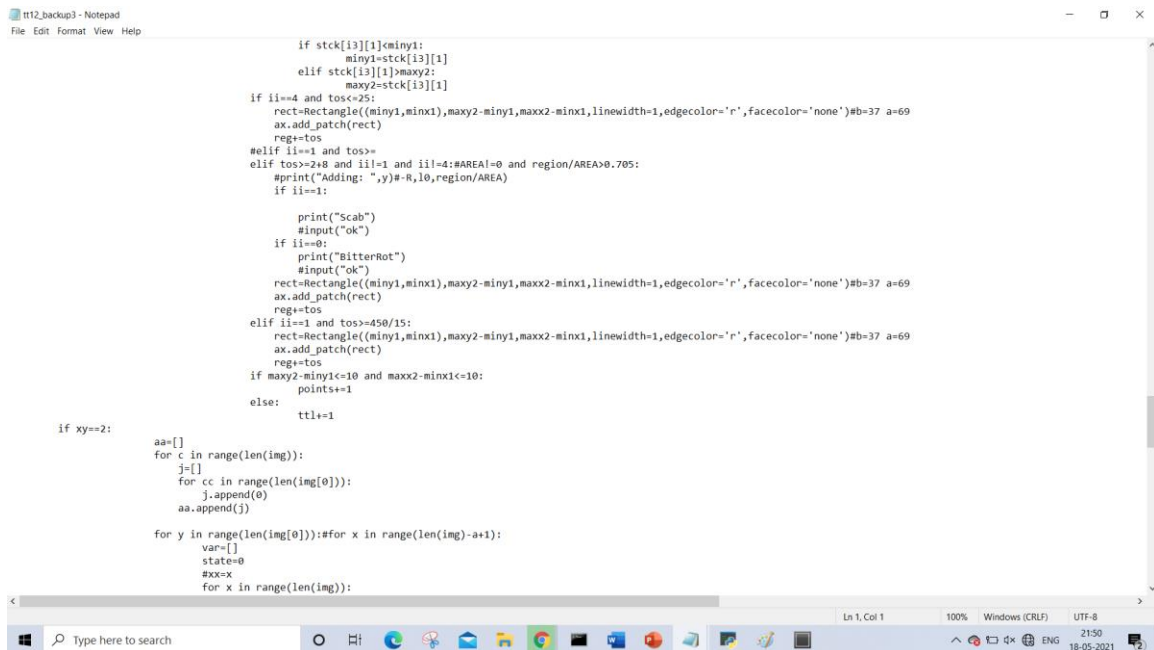
```
C:\Users\Devi\Pictures\tt12_backup3.py - Sublime Text 14 (UNREGISTERED)
File Edit Selection Find View Tools Project Preferences Help
workinh_wht_1_one[whiterot+Biterror+scab].py - tt_10.py - tt12.py - tt12_backup3.py - tt12_backup3 - Copy image square circle.py - scab_big_rectangles_bfs_white.py - tt12_backup1.py - tt12_backup.py - tt111.py
218
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220
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243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
Line 96, Column 22
Python Windows
Type here to search
2125
18-05-2021
```

Except scab which is run specially using methods that will be discussed later uses the re-run of same program



```
252
253
254     if ex-1==0:
255         #print("33")
256         if aa[ex-1][ey]==0 and img[ex-1][ey][0]<=val[i1][0][1] and img[ex-1][ey][0]<=val[i1][0][0] and img[ex-1][ey][1]<=val[i1][1][1] and im
257             tmp=[]
258             stck.append((ex-1,ey))
259             #stck.append(tmp)
260             tos=tos+1
261             aa[ex-1][ey]=1
262             #print("333")
263     if ey-1==0:
264         #print("44")
265         if aa[ex][ey-1]==0 and img[ex][ey-1][0]<=val[i1][0][1] and img[ex][ey-1][0]<=val[i1][0][0] and img[ex][ey-1][1]<=val[i1][1][1] and im
266             tmp=[]
267             stck.append((ex,ey-1))
268             #stck.append(tmp)
269             tos=tos+1
270             aa[ex][ey-1]=1
271             #print("444")
272     #print("head")
273     head=head+1
274     minx1=stck[0][0]
275     miny1=stck[0][1]
276     maxx2=stck[0][0]
277     maxy2=stck[0][1]
278     for i3 in range(tos):
279         if stck[i3][0]<minx1:
280             minx1=stck[i3][0]
281         elif stck[i3][0]>maxx2:
282             maxx2=stck[i3][0]
283         if stck[i3][1]<miny1:
284             miny1=stck[i3][1]
285         elif stck[i3][1]>maxy2:
286             maxy2=stck[i3][1]
287     if ii==4 and tos<=25:
288         rect=Rectangle((miny1,minx1),maxy2-miny1,maxx2-minx1,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
289         ax.add_patch(rect)
290         reg=tos
291     #elif ii==1 and tos==
292     #elif tos>=2*8 and i1=1 and i1=4:#AREA=0 and region/AREA>0.705:
293         #print("Adding: ",y)#R,10,region/AREA)
294         if ii==1:
295             print("Scab")
296             #input("ok")
297             if ii==0:
298                 print("BitterRot")
299                 #input("ok")
300                 rect=Rectangle((miny1,minx1),maxy2-miny1,maxx2-minx1,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
301                 ax.add_patch(rect)
302                 reg=tos
303             elif ii==1 and tos>=450/15:
304                 rect=Rectangle((miny1,minx1),maxy2-miny1,maxx2-minx1,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
305                 ax.add_patch(rect)
306                 reg=tos
307             if maxy2-miny1<=10 and maxx2-minx1<=10:
308                 points+=1
309             else:
310                 ttl+=1
311
312 if xy==2:
313     aa=[]
314     for c in range(len(img)):
315         j=[]
316         for cc in range(len(img[0])):
317             j.append(0)
318         aa.append(j)
319     for y in range(len(img[0])):#for x in range(len(img)-a+1):
320         var=[]
321         state=0
322         #xxx=x
323         for x in range(len(img)):
```

#### 4.1.3 Marking the color pixels that come under this range



```
if stck[i3][1]<miny1:
    miny1=stck[i3][1]
elif stck[i3][1]>maxy2:
    maxy2=stck[i3][1]
if ii==4 and tos<=25:
    rect=Rectangle((miny1,minx1),maxy2-miny1,maxx2-minx1,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
    ax.add_patch(rect)
    reg=tos
#elif ii==1 and tos=
elif tos>=2*8 and i1=1 and i1=4:#AREA=0 and region/AREA>0.705:
    #print("Adding: ",y)#R,10,region/AREA)
    if ii==1:
        print("Scab")
        #input("ok")
        if ii==0:
            print("BitterRot")
            #input("ok")
            rect=Rectangle((miny1,minx1),maxy2-miny1,maxx2-minx1,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
            ax.add_patch(rect)
            reg=tos
        elif ii==1 and tos>=450/15:
            rect=Rectangle((miny1,minx1),maxy2-miny1,maxx2-minx1,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
            ax.add_patch(rect)
            reg=tos
        if maxy2-miny1<=10 and maxx2-minx1<=10:
            points+=1
        else:
            ttl+=1

if xy==2:
    aa=[]
    for c in range(len(img)):
        j=[]
        for cc in range(len(img[0])):
            j.append(0)
        aa.append(j)
    for y in range(len(img[0])):#for x in range(len(img)-a+1):
        var=[]
        state=0
        #xxx=x
        for x in range(len(img)):
```

The same program that is run and disease spots are marked by calculating  $n_0, n_1$  and  $y_0, y_1$  like coordinates these are the extremes of the rectangle to be drawn.

```

tt12_backup3 - Notepad
File Edit Format View Help

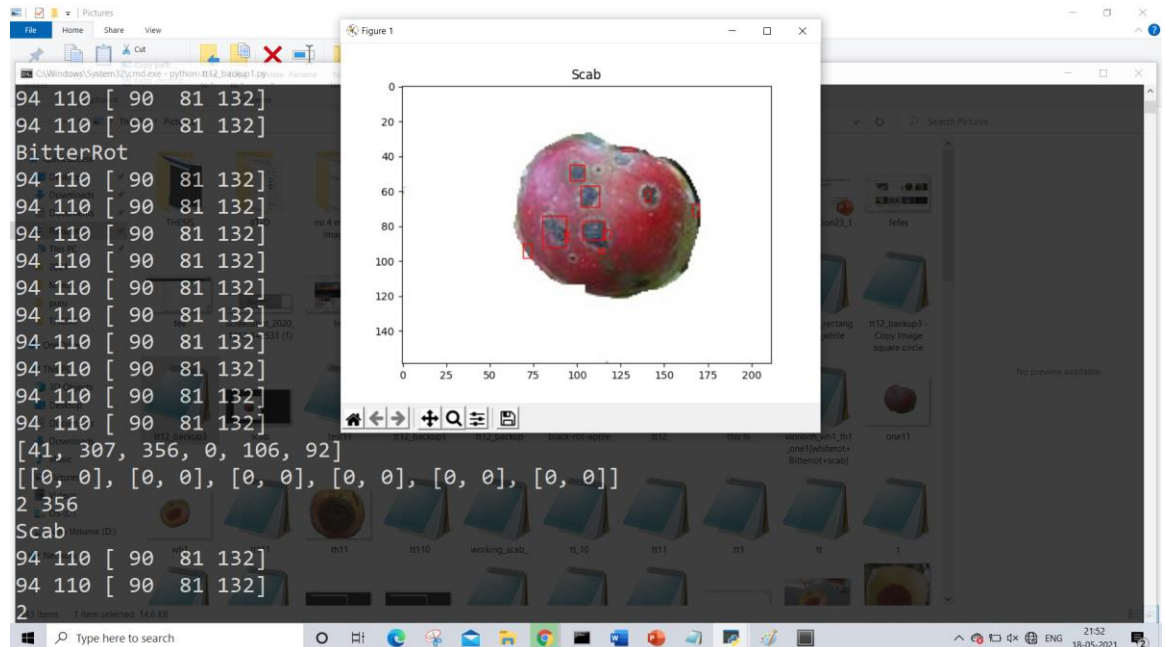
print(10,11,0,R,C)
region=0
for i in range(10,11+1):
    X=int((R**2-(i-C)**2)**0.5)
    X3=min(len(img[0]),y+x)
    X1=max(0,y-X)
    z=X1
    syt=0
    print(X,X1,X3)
    while z<X3:
        aa[i][z]=1
        #elif syt==2:
        #[[81-5,131],[75,115],[72-10,120]
        while img[i][z][0]<=190 and img[i][z][0]>=137 and img[i][z][1]<=176 and img[i][z][1]>=112 and img[i][z][2]<=183 and img[i][z][2]>=
            region+=1
            aa[i][z]=1
            z=z+1
        while img[i][z][0]<=131 and img[i][z][0]>=76 and img[i][z][1]<=115 and img[i][z][1]>=75 and img[i][z][2]<=120 and img[i][z][2]>=
            region+=1
            aa[i][z]=1
            z=z+1
        while img[i][z][0]<=190 and img[i][z][0]>=137 and img[i][z][1]<=176 and img[i][z][1]>=112 and img[i][z][2]<=183 and img[i][z][2]>=
            region+=1
            aa[i][z]=1
            z=z+1
        z=z+1
        print(z)
    #z=X3

AREA=PI*R**2
print(AREA)
if AREA!=0 and region/AREA>0.505 and R>=5:
    print("Adding: ",y-R,10)
    rect=Rectangle((y-int((xx-x)/2),x),xx-x,xx-x,linewidth=1,edgecolor='r',facecolor='none')#b=37 a=69
    ax.add_patch(rect)

xxy.append([points,tt1])
regions.append(reg)
input(ii)
plt.title(ch)

```

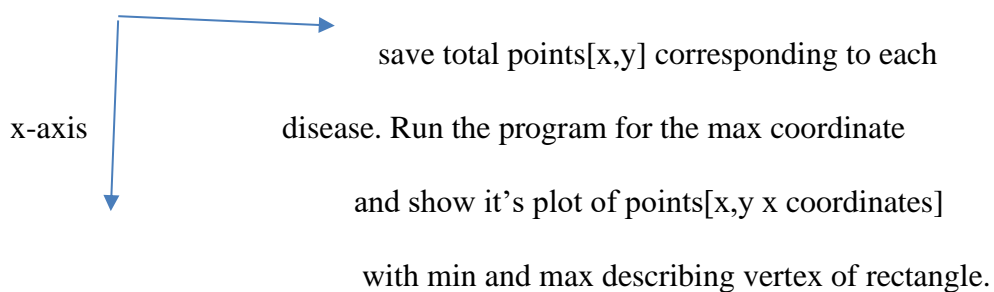
#### 4.1.4 Plotting of the Picture



Once the coordinates have been marked this is plotted using `pyplot` function of `matplotlib`



## 4.2 METHODOLOGY :

- Point 0: mark disease pixel range and iterate it.
  - Point 1: move y from 1 to max\_length[y:coordinate]
  - Point 2: move x from 1 to max\_length[x:coordinate]
  - If point[x][y] falls in range of disease:
    - Mark done[x][y]=True
    - Check if right pixel point[x][y+1] fall in range:
      - Place in queue ; mark done[x][y+1]=True
    - Check if DOWN pixel point[x+1][y] fall in range:
      - Place in queue ; mark done[x + 1][y]=True
  - Check if UP pixel point[x-1][y] fall in range:
    - Place in queue ; mark done[x - 1][y]=True
  - Check if LEFT pixel point[x][y-1] fall in range:
    - Place in queue ; mark done[x][y-1]=True
  - [0,0] y-axis
- 
- save total points[x,y] corresponding to each disease. Run the program for the max coordinate and show it's plot of points[x,y x coordinates] with min and max describing vertex of rectangle.

## 4.3 ALTERNATIVE APPROACH:

**Step I :** first move left to right and then from top towards bottom.

**Step II:** if this pixel has color in the range move towards downwards till the point the pixel fall in this range.

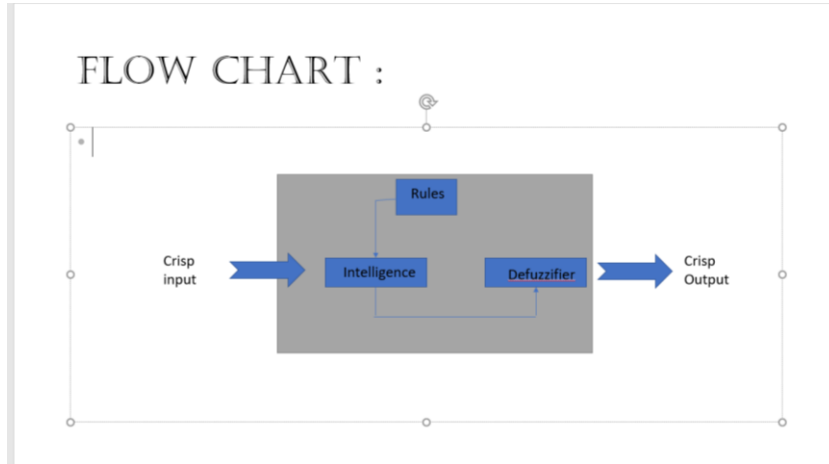
**Step III:** The radius is the length from top to bottom.

**Step IV:** Traverse again from top to bottom with LEFT-RIGTH forming a circle with points from  $X = \text{int}((R^{**2} - (i - C)^{**2})^{**0.5})$  where i is the x-coordinate And C the center x-coordinate of the circle.

**Step V:**  $X3 = \text{min}(\text{len}(\text{img}[0]), y + X)$   $X1 = \text{max}(0, y - X)$  These are the right and left values

If the  $R \geq 5$  and fraction of matched color  $\geq 0.505$  then this is identified as disease

## 4.4 FLOW CHART



## CHAPTER 5 : DISCUSSIONS

In [7] leaf disease identification of apple based on MobiNet methodology is proposed. They stated that the burden of getting task done by experts can be greatly reduced by this method for leaf disease detection in apple as stable identification results can be offered by it. Since it's a low cost method as in mobile devices it can be easily deployed. Further a good balance between precision and efficiency is given to be made and that is achieved through several deep learning models comparison . They stated that collecting more datasets is it's extension for improvement in identification process. Although they have planned to collection of 2,000,000 images of leaf diseases of all apple as training dataset that will help in effectively develop a deep learning model for identification of apple leaf disease

In [9] a model for novel deep convolution deep neural network was proposed for apple leaf disease accurate identification in which the discriminative features can be automatically discovered of leaf disease and also end-to-end learning pipeline enablement that to with high accuracy. A total of 13689 images were generated for providing adequate apple pathological images by image processing technologies like light disturbance, PCA jittering etc. They have obtained an accuracy of 97.62% in recognition.

In [1] a novel approach was introduced v.z MLP-CNNs i.e. Mutli-model LSTM based Pre-trained Convolution Neural Network a majority voting classifier for plant disease and pests detection. For deep feature extraction initially various CNN Models were initially employed and then SVM and LSTM classifiers were used for the classification of features. In concatenated form and individual the outputs of the CNN Models were used in order to the performance evaluation of the deep models. The concatenated model proved in producing better results in comparison to the individual models by the results evaluation showed. Also the results achieved by LSTM were better than SVM classifiers . The highest accuracy score of 99.2% has been obtained through MLP-CNN and LSTM Classifier

In [3] solution based on image processing techniques is proposed and evaluated for the classification and detection of apple fruit disease. Their approach comprises of mainly 3 steps, very first being segmentation of image using technique of K-Means clustering . In the second step it involves where features are extracted and the last step involves the classification and training that are performed on a Multiclass Support Vector Machine [SVM].Although the experimental results were 93% accuracy in identification of apple disease but this paper considered only 3 disease viz Apple Scab, Apple Rot and Apple Blotch.

In [2] the focus the disease detection in trees in apple is via it's leaves images. Here a deep learning based approach i/e a convolution neural network is used for disease detection .

Once a path is specified and after system runs the code it will be capable in predicting disease class of the tree of apple is suffering from.

In [10.] studies revealed that amongst a RGA, SVM and GA-CFS the best results were showcased by GA-CFS, the features extracted for image recognition of disease in apple were of the following: color features texture features and shape features

In [7] they stated that the symptoms identification of plant disease through machine vision systems during the daily struggle of farmers can support them against plant disease outbreaks. Here digital images were used of crop plants that showcased particular disease visual symptoms. These were identified by diseases regions and with the help of algorithm were segmented. Once from each segmented region features were extracted they were then used as an input to the classifier. As for the best classification model the features were to be classified they used the cross-validation to identify these about the target. Same amount of information was not supposed to be given by all the features. Primarily two folded were the results of the images. Firstly for some types of images useful discriminator can be the measurements of texture. Secondly visual symptoms in plant diseases can be identified by using ML systems and in remote locations this can have for crop producers or farmers have a particular application.

In [6] they stated that during the struggle against disease outbreak farmers are supported by means of image processing systems for the symptoms of plant disease detections. They used images of plant leaves that of particular diseases visual symptoms. Their proposed framework is capable of useful features extraction from images and performing of disease type classification. During experimentation the maximum achieved accuracy is 94%. One of the drawback of this system is that their's proposed system only utilized texture features.

In [8] they analyzed citrus disease in Florida as Citrus is one of the important constituent of Florida's agri-economy with an accuracy of identification of 95% by considering Hue, Saturation and Intensity [HSI] color features in combination with classification algorithms that were statistically driven. These accuracy was achieved by using CCM textural features with leaf sample discriminant analysis when using saturation and hue texture features for all classes. Four different classes of citrus leaves viz scab, normal, greasy spot and melanose were used for this study. The SAS discriminant analysis achieved efficiency of above 81% using intensity features on all data models and above 95.8% while utilizing saturation and hue features alone. An image texture feature dataset that utilized a reduced saturation and hue feature set (odel IB and IF) arrived as the best data model achieving an accuracy of 96%.

In [10] the study followed the utilization of RGA, SVM and GA-CFS for achieving image recognition of apple diseases based upon the extracted color, textural features and shape features from the diseased leaf images and also their features combined. Experimental results proved that the selection of useful features can be used by GA-CFS for achieving identification and classification of the leaf diseases in apple based on image processing of disease and pattern recognition. With the proposed methods of the paper by acquisition of leaf disease of apple combined with plant protection expert system with selection and

feature extraction, mosaic, powdery mildew and rust specifically could be more accurately identified. The method extends to other leaf diseases in apple.

PLUM: In [26] they studied the disease detection performance of fine-tuned and newly trained CNN on a dataset that was challenging as it was collected in true field conditions. For increasing the number of images data augmentation was performed so that robust models could be trained on the dataset to be made more challenging. The images were mostly captured from ground while dealing with the images of plum trees resulting in scale differences. Therefore authors proposed to study both methodologies: firstly of plain CNN and secondly of those architectures where in an integrated manner (inception network) multi-scale processing is performed. The result they got was that the inception network yielded superior performance even in the presence of background clutter. Lastly in order to enable efficient inference on devices that are resource constrained the Inception v3 model they quantized from FP32 precision to FP6 gaining 2 times speedup and two times less memory requirement.

In [17] 2 remote sensing techniques applied revealed differences that are statistically significant between healthy plum leaves spectral data and those infected by PPV in the NIR and VIS spectral ranges. From the results of 2 remote sensing techniques and DAS-ELLISA tests the comparative analysis performed on these revealed correlation between the extent of changes of the emitted and reflected radiation from plum leaves and the degree of the viral infection. In the two hyperspectral techniques, chlorophyll fluorescence and leaf reflectance the strong relationship between these findings indicates their effectiveness and applicability for preliminary screening for biotic stress in fruit trees (latent virus infection) and their importance for protection in plant practices.

In [18] This paper showed different types of environmental factorial disease in the plum plant. They stated that to get higher production of crop/plant the farmers must be aware of the disease type and its effects. In this paper the authors have identified and studied various types of disease in plum plants and also checked the growth in plum, plum width and length of plum. They concluded also that if the disease affected not the levels of plum growth like width of the plant/length then this type of disease won't affect in the plum plant or fruit either. They also found that environmental factors do not really alter the plum fruit size to that effect (huge extent).

## GENERAL

In [11] they explored the study of Neural Network with Deep Learning Algorithm that had the capability in detecting diseases of terrestrial plant with accuracy based F1 score testing method and under the evaluation of experts in the field of botany and agriculture implementation of the algorithm. Through the use of dataset that was served by publicly gathered images in creating of the training model in detection of terrestrial plant diseases. The results showed that the developed application had an efficiency of 80% accuracy rate thus supporting the usability, efficiency, reliability, accuracy, portability performance and functionality of the application. This paper showed that android had an edge in detection of the common terrestrial plant diseases in the Philippines. This application can be used as

a tool applied to prevent and raise awareness on common diseases found in terrestrial plants.

IN [37] the study was comparison of performance of two common MALDI-TOF mS Systems VitekMS and Biotyper for the identification of yeasts isolated from clinically relevant materials using a time saving direct transfer protocol. Both MALDI-TOF MS systems were able to correctly identify 96.2% of isolates. For VitekMS only misidentification were recorded (5 cases). However at the genus level (minor error) all misidentified isolates were correct and reported from the same species complex or reported as members of closely related species. For all these isolates high confidence score was reported that indicated that the VitekMS db might include some strains of mis identified references. Similar reference problems were reported for the earlier versions of SARAMIS and Biotyper DB. Thus for the clinical laboratories working ewith VitekMS they therefore recommended to report *C. parapsilosis* as *C. parapsilosis* complex , *S. capitata* as *Saprochaete sp.* and *C. guillirtmondii* as *C. guillieromdii*

In [33] the major concern for optimal patient management is the correct and fast identification of fungal pathogens from clinical specimens and from environment of patients especially in outbreak situations and too the implementation of disease control effective measures. High resolution based DNA molecular techniques like 26S rRNA or internal transcribed spacer DNA sequencing (6,29,36) and real time PCr assays (35) are expensive and time consuming. For the pathogenic Candida strains the accurate identification is proved to be by MALDI-TOF MS as rapid and reliable procedure with minimal time required for the interpretation of the results

In [35] fresh potato images were used for testing proposed algorithm, Firstly they got the Original potato and another diseased potato then the gray scale values for each potato were calculated and finally using K-Means clustering the segmentation of each image was done. The background of image was removed and from each histogram they get the pick values and define the detection of disease. In it there is more scope for reducing the various errors that will be occurred during the simulation that can be minimized as greater the number of input is provided accordingly.

In [36] the task involves the fine-tuning and evaluation of state of the art deep convolution neural network for classification of image based plant disease is performed. The architectures evaluated include VGG 16, Inception V4 , ResNet with 50,101 and 152 layers and Dense nets with 121 layers. From the experiments it was revealed that the Dense Nets have a tendency to yield increment in accuracy (coherent) with rising number of epochs with null or zero manifestations of overfitting and performance deterioration. In fact the computing time and number of parameters in Dense Nets is significantly less

## **CHAPTER 6**

### **FUTURE WORKS AND CONCLUSION**

The present method provided a method for the detection of only 1 type of disease at a time in the given apple fruit. It's proposed that there will be methodology for providing the detection of more than 1 type of disease simultaneously in a fruit of apple might be scab and bitter rot going together or other but the form is that more than two or equal disease can be identified in this future work or scope in future. Also it's proposed that the Cloud storage and platform for SAAS software as a service will be useful in making prediction so that online the identification can be done and the farmer or concerned person would not be required to have the software piece as such but can locally from any place with working internet connection can get the required results online.

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