

Research Paper:

Grape *Pseudocercospora* Leaf Specked Area Estimation Using Hybrid Genetic Algorithm and Recurrent Neural Network

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[Received April 10, 2022; accepted July 5, 2022]

Grapes are prone to *Pseudocercospora vitis* fungus which causes *Isariopsis* leaf speck disease to the crop's leaves, flower, and most importantly the fruit. Typical manual inspection of vineyard farmers is normally ineffective, destructive, and laborious. To address this, the use of integrated computer vision, machine learning, and computational intelligence techniques were realized to sort out healthy grape leaf image from a fungus-specked leaf image and to estimate the specked area percentage (SAP). A dataset made up of 343 normally healthy and 200 fungus-specked grape leaf images were initially pre-processed and segmented via graph cut prior to feature extraction and selection. Significant features were identified using classification tree (CTree). A multigene genetic programming tool called GPTIPsv2 was utilized to generate the fitness function needed for the optimization process done via genetic algorithm (GA). An optimal hidden neuron counts of 110, 50, and 10 were selected for a three-layered GA-optimized recurrent neural network (GA-RNN). Linear discriminant analysis (LDA) topped other disease recognition models with an accuracy of 99.99%. The developed GA-RNN model outperformed Gaussian process regression (GPR), regression tree (RTree), regression support vector machine (RSVM), and linear regression (RLinear) in performing leaf specked area estimation with an R^2 value of 0.822. The developed CTree-LDA₂-GA-RNN₂ hybrid model has been proven to be the most viable model for this task.

Keywords: computational intelligence, computer vision, grape leaf disease, *Pseudocercospora* fungus

1. Introduction

Agricultural products, especially fruit-bearing trees, are susceptible to disease caused by variants of fungus which can reduce quantity and quality of yield. The recognition of fungal infection and the amount of damage caused to plants can help farmers in preventing fungal spread and potential yield loss [1]. However, delayed detection of plant pathogens can cause wide-spread fungal infection that can inhibit plant growth and thereby decreasing quality and economic value [2].

Vitis vinifera (grapevine) is a species that bears grape berry fruits which are a good source of flavonoids, an antioxidant that is important for lowering blood cholesterol levels, relaxing blood vessels, and promoting overall blood circulation [3]. Sadly, fungus-infected grapevines tend to lose its grape produce quality and, it can also influence the taste of wine made from it [4]. This is due to delayed grapevine fungal infection that are diagnosed on a late basis. Also, inspection and health monitoring of these fruits are still done by manual observation which tends to be ineffective depending on the observer's bias, expertise, and observation skills.

With the emerging application of computer vision and machine learning (ML), these inaccuracies and late diagnosis can be prevented by automatically recognizing these pathogens and quantifying their damages to plants [5]. A previous study detected the presence of disease in tomato leaves using convolutional neural network (CNN) [6]. A collective study was done to investigate common disease detection process for cotton leaves [7]. Reviews of various image processing techniques were also done for automating the detection of leaf pest and disease and, it was evident that indeed, speed and accuracy are two main factors in detecting leaf diseases to promote agricultural



productivity [8–11]. A further study used a region-based convolutional neural network (R-CNN) to detect apple leaf diseases [12]. Gravitational search algorithm optimized recurrent neural network (GSA-RNN) was used to examine nitrate levels of a lettuce using images [13]. Root images were utilized to examine seed germination rate [14]. Lettuce biomarkers were used to investigate lettuce growth stage using genetic programming (GP), genetic algorithm (GA), and ML algorithms [15–18].

In this study, ML algorithms such as classification tree (CTree), support vector machine (SVM), k -nearest neighbors (k NN), and linear discriminant analysis (LDA), were used to differentiate a healthy grape leaf from a fungus-infected leaf for specked area percentage (SAP) assessment to quantify the amount of the damage of the leaf with respect to its entire leaf area with the use of ML algorithms such as Gaussian process regression (GPR), regression tree (RTree), regression SVM (RSVM), linear regression (RLinear), and a newly developed model, that put together the use of recurrent neural network (RNN) and GA. Images were enhanced using contrast adjustment. Then color-texture-morphology based feature extraction and selection was done. The grape leaf specked area was estimated based on popular regression models and the developed hybrid algorithm. This proposed technique is non-destructive and innovative in detecting and quantifying grape fungus-infected leaves. This study contributes to: (1) application of computer vision and interleaved computational intelligence in the field of phytopathology and (2) development of a non-destructive complementing tool for farmers in detecting the presence of fungal infection.

2. Materials and Methods

The model development framework of this study is presented in **Fig. 1**. The healthy and fungus-infected leaf images were initialized for image pre-processing to make the segmentation process easier and, to make the identification more accurate. Image segmentation was done to extract the entire leaf area and leaf specked area of the diseased leaf to assess its SAP. Then, feature extraction was done to extract significant leaf features. Various ML models have been used to estimate the infection percentage. An RNN was optimized using GA to improve performance ratings. MATLAB R2020b computational software was used to implement the vision-inspired processing, model development, optimization, classification, and prediction tasks.

2.1. Grape Leaf Dataset Information

Acquired image dataset with 1 : 1 aspect ratio has a resolution of 256-by-256 pixels per image. Healthy leaves have a total number of 343 images while the *Isariopsis*-leaf-spot-infected leaves are 200 images, for a total of 543 images utilized in this study. Dataset employed is extracted on [19].

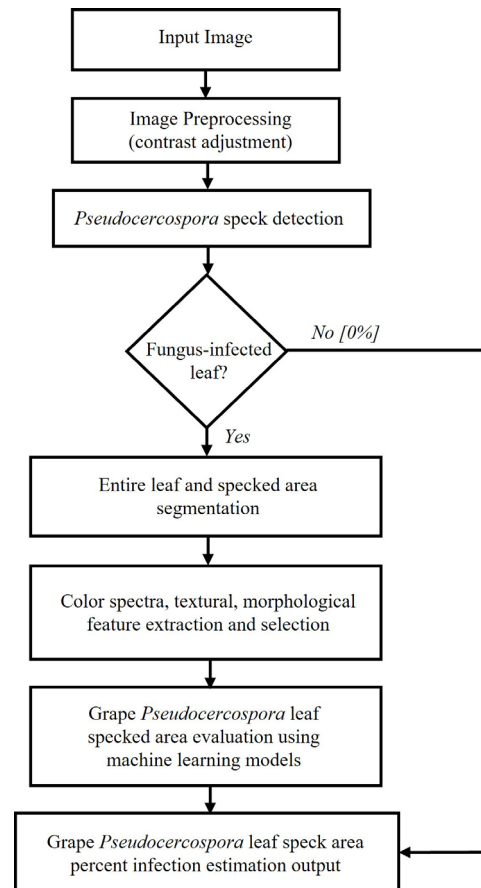


Fig. 1. Model development framework for grape leaf specked leaf classification and infected area estimation using ML models.

2.2. Image Pre-Processing (Contrast Adjustment)

The raw grape leaf images (healthy and leaf-speck infected) were pre-processed to make the image segmentation process easier by adjusting the image contrast using histogram stretching and equalization. The ImageJ built-in command in MATLAB was used to saturate the top 1% and bottom 1% of all pixel values with settings that can be adjusted from 0 to 1 for low-in, high-in, and low-out, high-out values. This command stretches the image histogram color map that ranges from 0 to 255. Healthy and speck-infected leaves were subjected to the following contrast settings: (0.2, 0.9), (0, 1), (0.1, 0.8), and (0, 1). Different values were assigned to improve the image quality, foreground-to-background distinction, and color properties. Additionally, to equalize the bin distribution, the histeq command was used for histogram equalization. The built-in command employs 64 bins by default. This will enable a much easier segmentation of the region of interests (ROIs) (entire-leaf area and speck-infected area). To pre-process all 543 images, image batch processing was done via MATLAB. The two categories of leaf, with different contrast setting need, were processed in two separate batches using a loop function. The pre-processing procedure can be visualized in **Fig. 2** for the fungus-infected leaf.

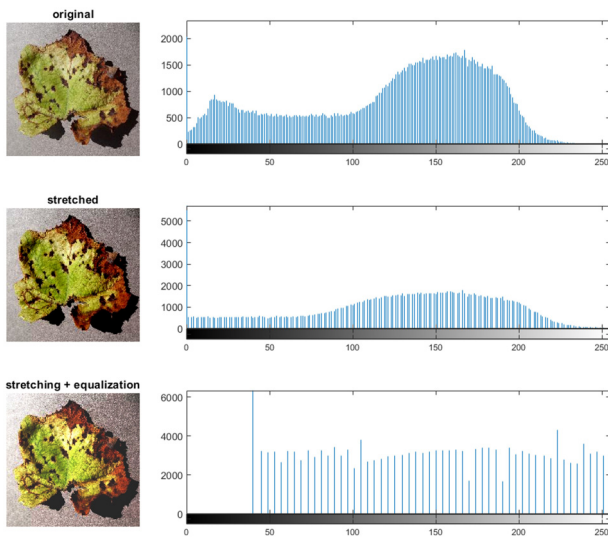


Fig. 2. Image histogram stretching and equalization of fungus-speckled leaf for better segmentation output.

2.3. Image Segmentation of Entire Leaf Area and Specked Area

Segmentation is the process of eliminating the background image pixels, retaining only the ROI that is subjected to the analysis. After the leaf health analysis has been done, healthy and fungus-speckled leaves were segmented using graphcut segmentation via lazysnapping. This is done by manually identifying the foreground pixels and background pixels of the image (Figs. 3(B) and (F)). A masked image was obtained during this step and was subsequently utilized in the color feature extraction (Figs. 3(C) and (G)). The settings that generated the segmented images is exported for multiple image batch processing. Figs. 3(D) and (H) show the binarized masked image which will be used for texture and morphological area feature extraction. Binarized representation of the image pixels means that a black pixel is considered a zero value while a white pixel has a value of 1. It will also be used as the ground truth of the specked-area estimation.

2.4. Color, Texture, and Morphological Feature Extraction and Dimensional Reduction

For the development of the detection and computational model, color (R, G, B, H, S, V, L, a*, b*, Y, Cb, and Cr), texture (correlation, contrast, energy, entropy, and homogeneity), and morphological (leaf vegetative pixel area) were used for a total of 18 features. The extracted morphological area is used as the basis for the fungus-infected area (A_{speck}) and entire leaf area ($A_{entire\ leaf}$). The SAP can be computed using the formula in Eq. (1).

$$SAP = \frac{A_{speck}}{A_{entire\ leaf}} \times 100. \dots \dots \dots (1)$$

A total of 18 features were extracted from these images. However, only significant features were considered for the

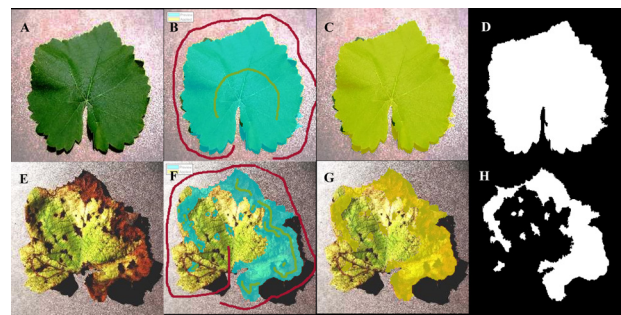


Fig. 3. Image segmentation via graphcut lazysnapping: (A) pre-processed healthy leaf image, (B) lazysnapping for healthy leaf, (C) masked RGB image for healthy leaf, (D) binary masked image of healthy leaf, (E) pre-processed fungus-speckled leaf image, (F) lazysnapping for fungus-speckled leaf, (G) masked RGB image for fungus-infected leaf, and (H) binary masked image of fungus-speckled leaf.

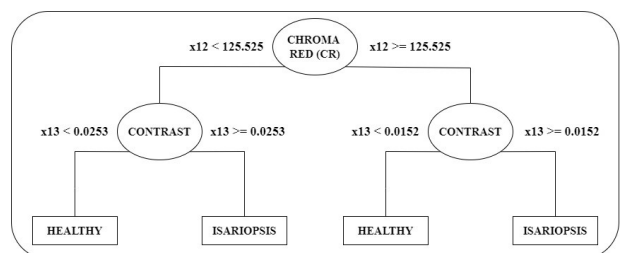


Fig. 4. Feature tree classifier with two features being selected: Cr (12th feature) and contrast (13th feature).

Pseudocercospora fungus detection model and speck infection computational model. To select the important features, a decision tree will be used to perform an iterative binary splitting. This is a type of recursive calculation by continuously splitting the data into small portions. It will eliminate irrelevant features that only consumes computational power. Based on the tree classifier generated in MATLAB (Fig. 4), the selection process concluded that the 12th feature (Cr) and 13th feature were significant.

2.5. Grape *Pseudocercospora* Leaf Specked Image Recognition Using Machine Learning Models

For the leaf specked image recognition task, the classification ML algorithms such as SVM, naïve Bayes (NB), kNN, and LDA were implemented. SVM had the following optimization parameters: box constraint (795.38), kernel (1.9335), bias (-242.13), and solver (sequential minimal optimization). kNN had the following optimization parameters: (7 numneighbors; Euclidean distance). Hyperparameter tuning for SVM, kNN, and LDA were done using Bayesian optimization. The image dataset was divided into three subsets: training data (56%), validation data (24%), and testing data (20%). This data partitioning method implemented are recognized as stratified sampling in statistics, whereby a population or data are subdivided into smaller subgroups. It minimizes the errors for classifying the fungus infected leaf from a healthy one.

To assess the performance of each ML models in recognizing a fungus-infected leaf, accuracy and inference time were considered as the main evaluation metrics. Additionally, the following ML model metrics were added to further justifications in identifying the most suitable algorithm to consider in this study: Matthew correlation coefficient (MCC), precision, recall, fall-out, and hamming loss.

2.6. Genetic Programming for Fitness Function Derivation

Artificial neural network (ANN) is a powerful bioinspired computational model primarily derived from a brain neuron. This model primarily mimics how a human being decides. Usually, it is composed of three main constituents: input layer, hidden layer, and output layer. Among these constituents, the neuron count of the hidden layer plays a vital role in making intelligent decisions. Therefore, an acceptable number of hidden neurons must be specified to maximize the network's computational power. Defining the right number of hidden neurons also influences its ability to provide a minimized-error prediction output which is measured in terms of a parameter called mean squared error (MSE). A value of zero is a good indication that an ANN model is performing well. For this study, a three-layered RNN was utilized. RNN is a type of neural network that can process an on-going input data while being lenient in accepting a previously processed input data in sequential manner. Thirty-eight predefined hidden neuron combinations together with its corresponding MSE output values were arranged into a dataset to initiate the creation of a fitness function using GP. This dataset will also be subjected to stratified sampling with three subsets: 56% of data for training, 24% of data for validation, and 20% of data for testing.

GP is a type of computational evolutionary algorithm that integrates the use of RTree and GA to solve a problem. This combination is recognized as multiple-gene symbolic regression (MGSR) technique. The three-layered-hidden-neuron-combination dataset previously mentioned has been utilized as input to produce the most desirable fitness function. A GP tool called GPTIPSv2, which is incorporated with MATLAB compatibility, was chosen for this study. The run parameters used were population size (20), maximum generations (50), training instances (20), tournament size (50), probability of pareto (0.2), maximum genes (10), and maximum total nodes (infinite).

2.7. Recurrent Neural Network Optimization Using Genetic Algorithm

GA, a type of metaheuristic algorithm based on Darwinism (a well-known theory that talks about biological evolution based on survival-of-the-fittest concept), is implemented in this study to optimize the RNN model by solving the fitness function derived to know the optimal three-layered-hidden-neuron combination necessary

to solve the derived fitness function. Optimoptions function in MATLAB was used to do task with the following settings: population size of 50, crossover of 1, constraint tolerance of $1e^{-6}$, elite count, ceil of $0.05 \times \text{population}$, migration factor of 1, migration interval of 10, nonlinear constraint algorithm, selection roulette, a zero-fitness limit, functional tolerance of $1e^{-6}$, 100 max generations, 50 max stall generations, and geometric weighted stall test.

2.8. Grape Leaf Specked Area Estimation Using Computationally Intelligent Models

The SAP of grape leaves were computationally assessed using GPR, RTree, RSVM, RLinear, and GA-optimized RNN (GA-RNN). GPR has the following optimization parameters: constant basis function ($2.27e^4$ beta; 8.6367 sigma), exponential kernel function (squared), exact fit and predict method, and random active set method. RTree has the following optimization parameter: minimum leaf size (1). RSVM employed the following optimization parameter: box constraint (0.0010027), kernel scale (0.063967), epsilon value (0.10514), bias (79.7085), and solver (sequential minimal optimization). The RNN model was developed using the MATLAB built-in command newelm. The following indicates the network training specifications: training algorithm (scaled conjugate gradient), parameter goal ($1e^{-7}$). The following transfer function assignments were utilized: "tansig," "purelin," and "log." The parameters used to evaluate the computational intelligence models used are as follows: root mean square error (RMSE), coefficient of determination (R^2), and mean absolute error (MAE). R^2 has an ideal value of 1. RMSE and MAE have ideal value of 0.

3. Results and Discussion

3.1. Grape Leaf Specked Image Recognition Results Based on Machine Learning Models

Based on the confusion matrix presented in **Fig. 5**, all models (SVM, NB, k NN, and LDA) were able to classify a healthy leaf from a speck-infected leaf with 100% accuracy (**Table 1**). However, there is a noticeable difference in terms of inference time. LDA is 61.09% faster than SVM, 47.03% faster than k NN, and 25.56% faster than NB. Note that these results are based on the testing phase of the algorithms since this study applied stratified sampling. Moreover, the reduction of features improved the ability of all four models to recognize the fungus-infected leaf more accurately while minimizing the use of computational resources.

3.2. Fitness Function Output Based on Genetic Programming

The model report given by GPTIPSv2 indicated the use of the following function set; times, minus, plus, sqrt, square, sin, cos, add3, mult3, log, cube, neg, and abs, to

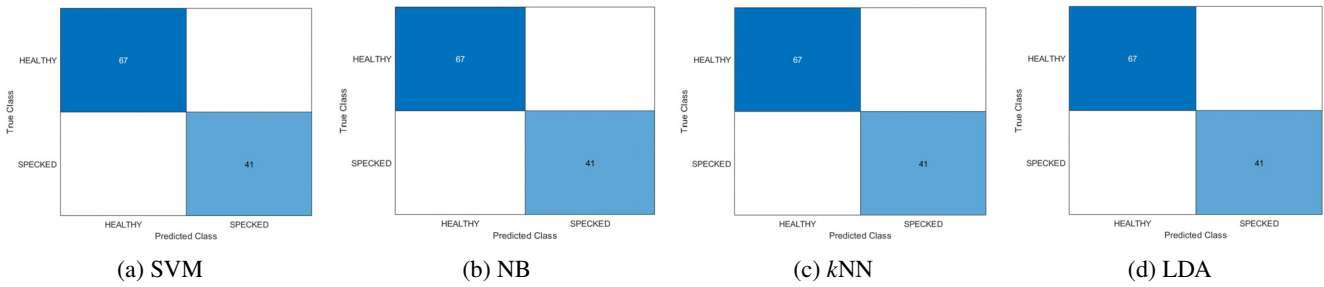


Fig. 5. Confusion matrix at the testing phase for the detection of grape *Pseudocercospora* leaf speck using two significant features.

Table 1. Evaluation summary for fungus-infected leaf classification using ML models.

Model	Training	Validation	Testing								
	Accuracy	Accuracy	Accuracy	Fallout	Precision	Specificity	Recall	F1-score	MCC	Hamming loss	Inference time [s]
SVM ₂	97.490	100.000	100.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	39.606
NB ₂	100.000	100.000	100.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	20.702
kNN ₂	96.030	98.020	100.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	29.091
LDA ₂	96.600	100.000	100.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	15.409

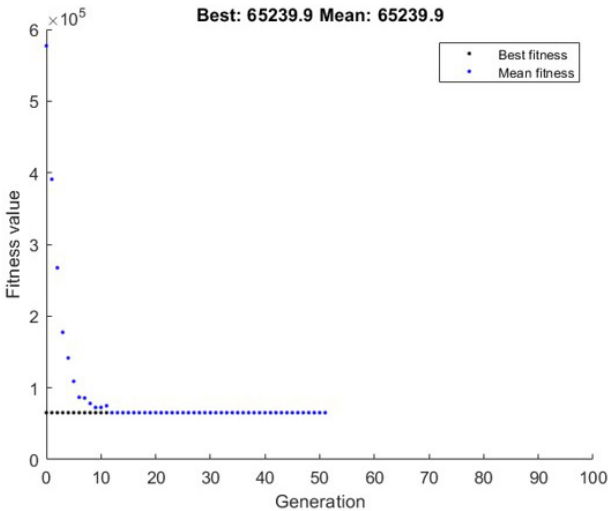


Fig. 6. Hidden neuron combination derivation by solving the generated fitness function with GA.

$$\begin{aligned}
 \text{MSE} = & 2.05N_1 - 2.05N_3 + 41.8 \cos|N_2 - N_3|^{0.5} \\
 & + \sin(N_1 + N_2)^3 - 52.9 \cos N_1^{0.5} \\
 & + 50.1 \cos(N_1 - N_3)^9 \\
 & - 22.8 \sin(N_1^3 \cos(N_2) (N_1^2)^{0.5}) \\
 & + 34.5 \sin(8N_1^3)^{0.5} + 0.0863N_3^{0.5} \\
 & - 166|N_2|^{0.25} + 1.8N_3^{0.5} + 65.5 \dots \dots (2)
 \end{aligned}$$

3.3. Recurrent Neural Network Optimization Results

For the RNN model utilizing GA optimization, a three-layered-hidden-layer combination of 110, 50, and 9.7612 (rounded up to 110, 50, and 10) was given as the optimal number for N_1 , N_2 , and N_3 . The assessed output from the optimization process has the following additional outputs: 51 generations, 2450 function evaluations, and $6.5240e^4$ fitness value. The visual representation of the GA-RNN is shown in Fig. 7.

3.4. Grape Leaf Specked Area Estimation Using Computationally Intelligent Models

Based on Table 2, it can be noted that the GA-RNN₂ has the lowest MAE and RMSE for testing phase. It also has the highest R^2 value which is closer to 1. As seen in Fig. 8, the data points of GA-RNN₂ are mostly contained within the regression line at the lower left corner of the graph. It bested all other ML models used in this study. To compare in terms of R^2 value, GA-RNN₂ is 10.58% higher than RLinear₂, 34.91% higher than RSVM₂, 11.68% higher than RTree₂, and 18.24% higher than GPR₂, respectively, which indicates that GA-RNN₂ has significantly lesser prediction error. Among the developed models, Rlinear₂ performed the worst while

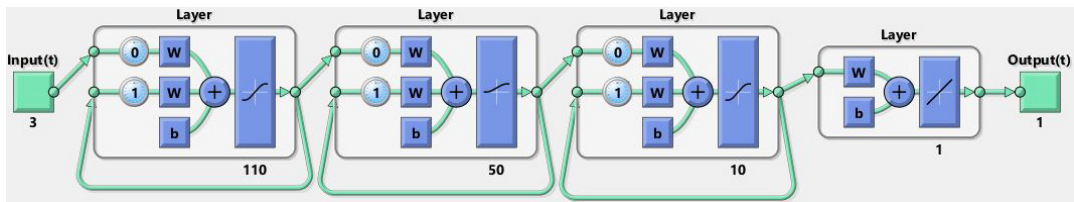


Fig. 7. RNN model (GA-RNN framework).

Table 2. Evaluation summary for estimating the grape leaf SAP using intelligent models.

Model	Training			Validation			Testing		
	RMSE	R^2	MAE	RMSE	R^2	MAE	RMSE	R^2	MAE
GPR ₂	18.491	0.588	10.177	11.772	0.784	20.663	15.757	0.672	15.208
RTree ₂	14.807	0.689	14.348	14.633	0.886	10.493	13.506	0.726	13.373
RSVM ₂	15.340	0.637	14.295	15.458	0.6970	20.893	11.065	0.730	11.192
RLinear ₂	13.371	0.601	12.849	12.583	0.741	12.755	16.329	0.535	16.396
GA-RNN ₂	9.361	0.729	8.922	10.551	0.877	10.410	10.245	0.822	10.153

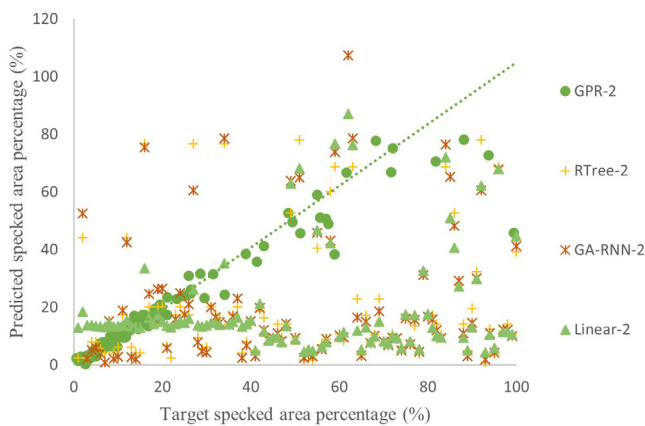


Fig. 8. Regression plot for grape specked area estimation using computational intelligence models.

RSVM₂ is the second best among the four algorithms in estimating the grape specked area of a *Pseudocercospora* fungus. The developed models for classifying fungal infected grape leaf and non-destructively computing the SAP in this study provide a clear advantage from other previous models [12–15, 17, 18, 20] with respect to sensitivity and accuracy. Aside from examining the model’s compatibility of embedding to a mobile phone, the current study’s focus is on developing interleaved computational intelligence models.

4. Conclusion

Leaf disease detection and leaf SAP prediction were applied to evaluate the capability of a vision-based leaf health assessment model and disease percentage estimation based on healthy and fungus-infected grape leaf images. Images were pre-processed to perform histogram stretching and equalization for a much clearer detail of

the regions of interest such as the pure green leaf and the spotted regions of a *Pseudocercospora* infected grape leaf. The pre-processing of images also helped in a better foreground to background separation for an easier image segmentation process. These were performed simultaneously by using image batch processing. Image segmentation used a lazysnapping algorithm to select the specific pixels of interest which are subject for feature extraction and selection. The selection of important features was done using CTree. Grape leaf disease detection was performed using the developed SVM, NB, *k*NN, and LDA models. CTree selected leaf color (Cr) and textural (contrast) features as the most significant features in identifying a completely healthy leaf from a fungus-infected leaf. When spot infected leaves were identified, they were subjected to estimation of SAP. This defines the amount of infection on a leaf. ML models such GPR, RTree, RSVM, and RLinear were used for the SAP prediction. These models were compared with an GA-RNN model in three evaluation metrics: R^2 , MAE, and RSME. The use of the GP tool GPTIPsv2 in the generation of fitness function to be solved by the optimization algorithm helped in deriving the optimized version of RNN with 110-50-10 neuron combination for N_1 , N_2 , and N_3 . GA was effective in optimizing the generated function to select the right combination of hidden neurons. LDA outperformed every other classification algorithm used with 99.99% while being agile in terms of hyperparameter optimization with the shortest inference time of 15.409 seconds. GA-RNN₂ performed well against other models with an R^2 of 0.822, RMSE of 10.425, and MAE of 10.153. The developed hybrid algorithm CTree-LDA₂-GA-RNN₂ proved to be a seamless way of identifying a fungus-infected leaf from a healthy one and, performing a specked infection percentage to assess the percentage area of the whole leaf infected by the fungus. This hybrid model is a non-destructive and cost-effective approach in assessing fungus infection in leaves which enables farmers to perform a real-time phe-

notyping and, avoiding any incurred loss if these fungi are left unchecked. For further studies, it is recommended to explore the use of deep learning, CNNs, and other intelligent models to make a more robust and accurate model.

Acknowledgments

The authors are thankful for the full support given by the Engineering Research and Development for Technology under the Department of Science and Technology of the Philippines (DOST-ERDT), and the Intelligent Systems Laboratory and Smart Farm Research Team of De La Salle University, Manila, Philippines.

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Membership in Academic Societies:

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Brief Biographical History:

2012 Received B.Sc. degree in Electronics and Communications Engineering from University of the Philippines
2017 Received M.Sc. degree in Electronics and Communications Engineering from Mapua University
2021 Received Ph.D. degree in Electronics and Communications Engineering from DLSU
2021- Associate Professor, DLSU

Main Works:

- Artificial intelligence, evolutionary computing, computer vision, precision agriculture, and plant ecophysiology.

Membership in Academic Societies:

- Institute of Electrical and Electronics Engineers (IEEE)
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Brief Biographical History:

2009-2014 Production Quality Engineer, Cebu Mitsumi, Inc.
2014- Faculty, Cebu Technological University
2015-2017 Graduate Student, University of San Carlos
2019- Ph.D. Student, DLSU

Main Works:

• Towards tracking: investigation of genetic algorithm and LSTM as fish trajectory predictors in turbid water.

Membership in Academic Societies:

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1990 Received B.S. degree in Electronics and Communications Engineering from DLSU
1990- Faculty Member, Electronics and Communications Engineering, DLSU
1993 Received M.Sc. degree in Electronics and Communications Engineering from DLSU
1996 Received Ph.D. degree in Electronics and Engineering from DLSU

Main Works:

• Computer vision, machine learning, deep learning, robotics, and signal processing.

Membership in Academic Societies:

• Institute of Electrical and Electronics Engineers (IEEE)
• IEEE Computational Intelligence Society
• IEEE Philippines Section
• IEEE Computational Intelligence Society Philippines Chapter
• IEEE Robotics and Automation Society



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Brief Biographical History:

2008 Received B.Sc. degree in Electronics and Communications Engineering from Polytechnic University of the Philippines
2012 Received M.Sc. degree in Electronics and Communications Engineering from DLSU
2012- Full-Time Faculty Member, DLSU
2014 Received Ph.D. degree in Electronics and Engineering from DLSU

Main Works:

• Artificial intelligence, robotics, vision systems, swarm robotics, and multi agent systems.

Membership in Academic Societies:

• Institute of Electrical and Electronics Engineers (IEEE)
• IEEE Computational Intelligence Society
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Brief Biographical History:

2000 Received B.Sc. degree in Electronics and Communications Engineering from University of Santo Tomas
2001- Full-Time Faculty Member, University of Santo Tomas
2008 Received M.Sc. degree in Electronics and Communications Engineering from DLSU
2014 Received Ph.D. degree in Electronics and Engineering from DLSU
2017- Associate Professor, Department of Manufacturing Engineering and Management, DLSU

Main Works:

• Control systems, computational intelligence, and fuzzy logic.

Membership in Academic Societies:

• Institute of Electrical and Electronics Engineers (IEEE)
• IEEE Computational Intelligence Society
• IEEE Philippines Section
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Brief Biographical History:

1996 Received Ph.D. degree from Loughborough University
1997 Exchange Scientist, Japan Society for the Promotion of Science, Tokyo Institute of Technology
1998-1999 Director, Engineering Graduate School, DLSU
2003-2004 Director, School of Engineering, DLSU
2003- General Chair of Humanoid, Nanotechnology, Information Technology, Communication and Control, Environment, and Management (HNICEM)

Main Works:

- "Fuzzy Logic—Controls, Concepts, Theories and Applications," IntechOpen, 2012.
- "Fuzzy Logic—Algorithms, Techniques, and Implementations," IntechOpen, 2012.

Membership in Academic Societies:

- Institute of Electrical and Electronics Engineers (IEEE) Computational Intelligence Society, Philippines, Founder and Chair
- IEEE Region 10, Executive Member
- The Mechatronics and Robotics Society of the Philippines (MRSP), Founder and President
- IEEE, Senior Member
- HNICEM, General Chair



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Brief Biographical History:

2017 Received B.Sc. degree from Bataan Peninsula State University
2020- M.Sc. Student, DLSU

Main Works:

- Development of sustainable cultivation technologies and optimization techniques for controlled-environment agricultural systems using applied computational intelligence.

Membership in Academic Societies:

- Institute of Electrical and Electronics Engineers (IEEE)



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Brief Biographical History:

2018 Received B.Sc. degree from University of Perpetual Help System JONELTA
2020- M.Sc. Student, DLSU

Main Works:

- Lettuce cropping system optimization and non-invasive methodologies for lettuce phenotypic surveillance via computer vision and computational intelligence integration.

Membership in Academic Societies:

- Institute of Electrical and Electronics Engineers (IEEE)



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2012 Received B.Sc. degree in Biology from UNINA
2015 Received M.Sc. degree in Biology from UNINA
2019 Received Ph.D. degree in Agricultural and Food Sciences from UNINA

Main Works:

- Plant-environment interaction, controlled environment agriculture for life support systems in space, and plant ecology and conservation.

Membership in Academic Societies:

- Italian Botanical Society
- American Society for Horticultural Science (ASHS)
- Association of Applied Biologists (AAB)
- International Astronautical Federation (IAF)
- International Society of Photosynthesis Research (ISPR)