Stimator: A Method in Agriculture CPS Framework to Estimate Severity of Plant Diseases using Graph Neural Network

Kiran K. Kethineni*, Saraju P. Mohanty* and Elias Kougianos†
*Department of Computer Science and Engineering, University of North Texas, USA
†Department of Electrical Engineering, University of North Texas, USA
Email: kirankumar.kethineni@unt.edu, saraju.mohanty@unt.edu, elias.kougianos@unt.edu

***Abstract*—Plant diseases are a major factor affecting agriculture yield by accounting for approximately 20% of the total produce and pose a constant threat to global food security. Accordingly, many solutions have been proposed to detect the presence of disease and estimate severity using AI and ML. These techniques estimate the severity as the proportion of area that was affected by the disease. Instead, this article estimates the severity of disease as the harmonic mean of the percentage of area affected by the disease and the percentage of area the disease has spread to. It represents the data of diseased locations in farmland as a graph and performs estimation with the help of GNN. These insights can help a disease management A-CPS to automate its downstream tasks like resource allocation and targeted spraying to control the disease efficiently. The proposed method has been validated by training a GNN on images of apple leaves in which diseased parts have been identified and annotated. When presented with a new image, the trained model produced results resembling human visual estimation.**

***Keywords*—Smart Agriculture; Artificial Intelligence (AI); Agriculture Cyber-Physical System (A-CPS); Internet-of-Agro-Things (IoAT); Graphs; Message Passing; Graph Neural Network (GNN); Neural Network; Machine Learning (ML).**

I. Introduction

The global population has been rising rapidly and is expected to reach 9.7 billion by 2050. On the contrary, factors like global warming, climatic changes, and pathogens are contributing to the reduction in agricultural produce causing a global threat to food security [1]. Plant diseases are a major factor affecting agriculture claiming about 20% of the produce. Plant diseases can be caused by fungi, bacteria and be transmitted in various ways like wind, water, insects, direct contact, and indirect contact due to humans. Chances of a plant getting affected by a disease are controlled by environmental factors like temperatures, sunlight, soil conditions, humidity, and pathogens [2]. To ensure food safety and security to the world, there must be an efficient disease management system to handle diseases in plants. Integrating Various adaptive methods like using disease-resistant variants, crop rotation, climate, and epidemic forecast with disease management systems helps in preventing diseases and protecting the crop yield [3].

However, due to climate changes and genetic mutations, new kinds of diseases infest even after implementing preventive methods. In such cases, a plant disease detection mechanism is necessary. There have been various biological methods to detect diseases in plants [4] which are invasive and needed expertise. Hence, various noninvasive imaging techniques [5] were developed recently with the help of Artificial Intelligence (AI) to automate disease detection and estimation. As the usage of excessive amounts of pesticides to protect the crop from disease has negative effects on the health of the plants, farmers, and also environment [6], the severity of the disease has to be efficiently quantified. It aids in using the right amount of pesticide, efficiently allocating resources, and handling the disease. The proposed "Stimator" is a method to effectively estimate the severity of plant diseases in an Agriculture Cyber-Physical System (A-CPS) assigned with disease management as in Figure 1. Stimator accepts information on diseased locations from Internet-of-Agro-Things (IoAT) sensors, drones and spatially analyses them using Graph Neural Network (GNN) to estimate the severity.

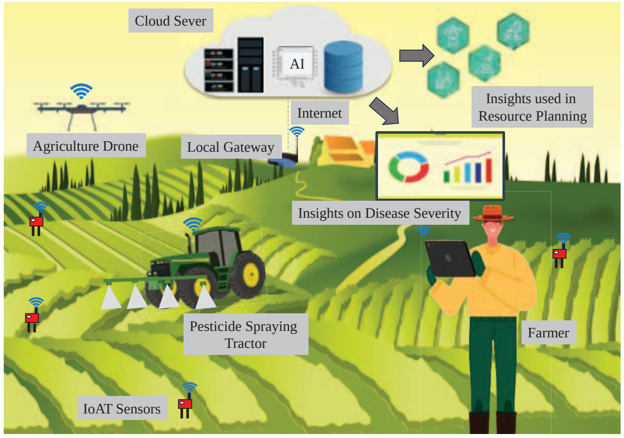

Figure 1: Overview of a disease management A-CPS.

The rest of the paper is organized into the following sections: The problem statement of this paper and the proposed solution are presented in Section II, which is followed by a discussion of related prior research in Section III. Graph Classification is introduced to readers in Section IV to help them easily understand the method proposed in Section V. Experimental results are detailed in Section VI while Section VII concludes the paper.

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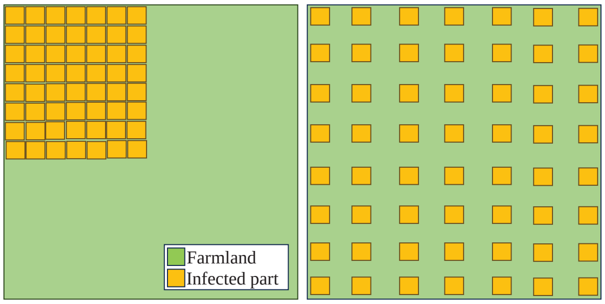
II. Novel Contributions of the Current Paper

A. The Problem Statement

To understand the severity better and to plan on the resource allocation in disease management, estimating the severity of the disease is critical. So, there have been multiple works in recent times to quantify the severity of a disease detected. However, they do not take the spatial spread into consideration. They estimate severity as the percentage of area that has been damaged by the disease. Consider a scenario where a number of disease instances are confined to one corner of the farmland and another scenario where the same number of instances are spread across the farmland as shown in Figure 2.



(a) Disease confined to a corner. (b) Disease spread throughout farmland.

Figure 2: Disease propagation scenarios.

Existing methods produce the same severity measure for both scenarios since the proportion of area damaged is the same. But, in the second scenario as the disease instances are spread across the entire farmland, the severity of the disease is higher, and it needs more resources to handle the disease when compared to another scenario. Hence, the estimation of severity of a disease must be computed by also considering the spatial spread of the disease in the farm.

B. Proposed Solution of the Current Paper

For the purpose of considering spatial spread of the disease across the farmland, the proposed "Stimator" performs spatial analysis to compute the percentage of area the disease has spread to and the percentage of area damaged by the disease using machine learning. Arithmetic mean of both the metrics computed will be misleading in cases where a few diseased locations are spread throughout the farm. On the other hand, harmonic mean reduces the influence of a single extreme number and produces a high mean only if both values are high. Owing to this, the harmonic mean of percentage of damaged area and percentage of area the disease has spread is considered as a severity measure for plant disease. The relation between the proposed severity measure and computed metrics has been visually presented in Figure 3.

C. Novelty and Significance of the Proposed Solution

The following reasons demonstrate novelty of the proposed Stimator.

1) Stimator considers the area affected by disease and its spatial spread to effectively estimate is severity.
2) The Proposed method represents data of the diseased locations as a graph to capture their spatial relationship.
3) It introduces a GNN based method to measure the percentage of the area the disease has spread to for estimating the severity.
4) The severity measure proposed is robust and is not affected by single extreme values.

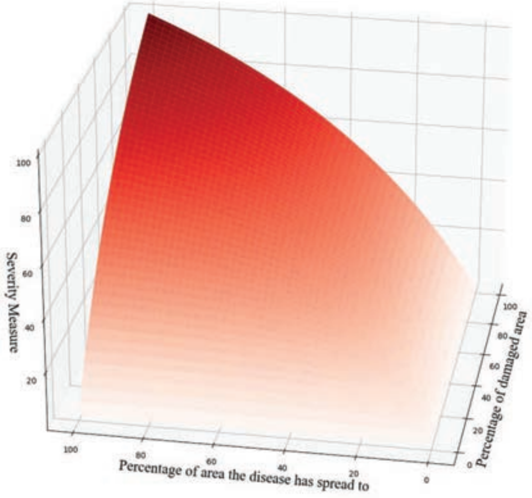


Figure 3: Proposed severity measure.

III. Related Prior Works

In recent times many automation solutions have been developed in smart agriculture using AI and ML. Likewise, there have been various works using ML to detect and estimate the severity of diseases and damages due to climate in agriculture for effective treatment of plants. Since detection of disease / damage is out of the scope of the current paper, this section presents methods proposed to estimate the severity by various researchers in recent times. In the article [7], authors divided the area of interest into small squares to estimate the severity as the number of squares that show damage out of the total number of squares. Authors of [8] estimated severity as the percentage of area that has been damaged by the disease. Similarly, in article [9] area occupied by lesion due to disease is computed and the percentage of area it occupied is considered as severity measure. In sugarcane plants, the leaf disease severity was estimated as the percentage of area of the diseased spots in [10]. A two-stage image processing was performed in [11] to segment diseased areas and estimate severity as the percentage of area occupied by the segments.

All the above methods do not consider the spatial spread of the disease to estimate severity. Whereas the proposed "Stimator" considers the proportion of area affected and the proportion of area where the disease has spread to effectively estimate the severity of the disease. A summary of the above discussed methods has been presented in Table I.

Table I: A brief summary of relevant literature.

Research	Factors considered	Remark
Mitra et al. [7]	Proportion of area damaged by climate	Does not consider spatial spread
Parikh et al. [8]	Percentage of area affected by disease	Does not consider spatial spread
Jamadar et al. [9]	Area occupied by lesion due to disease	Does not consider spatial spread
Ratnasari et al. [10]	Area covered by spots due to diseased	Does not consider spatial spread
Divyanth et al. [11]	Percentage of area occupied by diseased segments	Does not consider spatial spread
Stimator	**Percentage of area affected by disease and its spatial spread**	**Considers spatial spread for effective estimation**

IV. Introduction to Graph Classification

A. *Introduction to Graph Neural Networks*

A graph G can be defined as a data structure used to represent entities and relationships between them. In a graph, each entity is represented as a node and the relation between a node pair is represented by an edge connecting them [12]. Hence, a graph $G = (V, E)$ consists of set of nodes/vertices $V = \{v_1, v_2, v_3, \ldots, v_n\}$ and edges: $E = \{(v_i, v_j), (v_j, v_k), \ldots\}$. The edges between the nodes can be weighted or unweighted. Any node v that is connected to node u by an edge is considered as a neighbor and all neighbors of a node u constitute neighborhood $N(u)$ as represented by Figure 4.

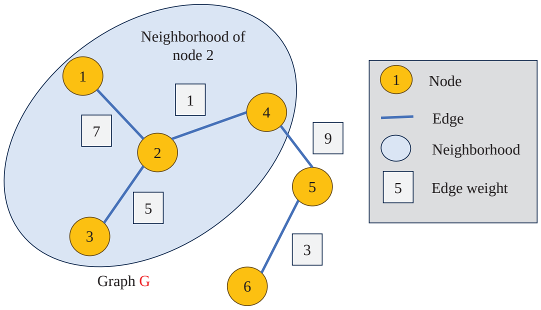


Figure 4: Example of a Graph.

Apart from capturing relations between entities, features of the entities can also be captured as node feature vector h_u for every node u to assist downstream tasks like classification and prediction. Traditional machine learning methods assume data to be tabular data, each data point is considered as an individual data point. They cannot work on graph structures or consider the relationship between nodes. A new machine learning model named "Graph Neural Network" (GNN) was developed by authors of [13] to work with graph data. GNNs make use of an information diffusion mechanism called message passing to enable nodes to learn about their neighbors and their relationships. In message passing, every node u in the graph passes its feature vector $h_u^{(k)}$ to all its neighbors so that information diffuses across the neighborhood and every neighbor node $v \in N(u)$ learns about the node u. Upon receiving information from neighbor nodes, each node updates its feature vector to $h_u^{(k+1)}$ to reflect its relationship with neighbors. This process is repeated multiple times till information diffuses across the graph and all the nodes reach a state of equilibrium. In consequence, every node captures its relationship with its neighbors and other nodes in the graph. These updated features can now be fed to traditional machine learning models/neural networks to classify the node or generate a new feature representation for the node as shown in Figure 5. Thus, message passing in the graph learns complex patterns and relations making GNN more expressive [14].

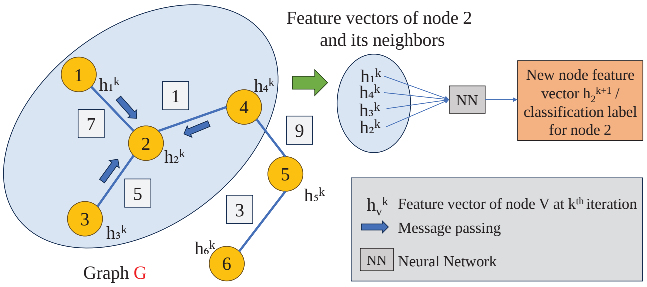

Feature vectors of node 2 and its neighbors
1
2
3
4
5
6
h_1^k
h_2^k
h_3^k
h_4^k
h_5^k
h_6^k
1
7
5
9
3
h_1^k
h_4^k
h_3^k
h_2^k
NN
New node feature vector h_2^{k+1} / classification label for node 2
Graph G
h_v^k Feature vector of node V at kth iteration
Message passing
NN Neural Network

Figure 5: Illustration of Graph Neural Network.

B. *Graph Classification using Graph Neural Networks*

Graph classification refers to assigning a label to a graph depending on its node features using machine learning [15]. Passing raw/actual features of nodes through the classification model can't capture the structure of the graph and will miss-classify the graph. So, message passing is performed throughout the graph to learn neighbor relations and graph structure. These updated node features h_u when fed to the classification model as depicted by Figure 6 will help in effectively classifying the graph.

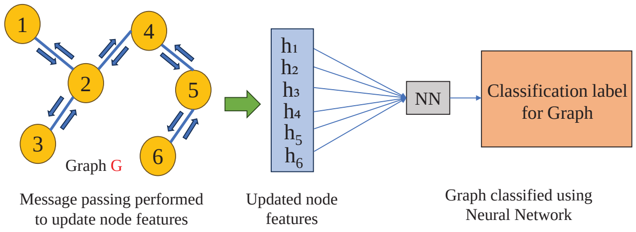

1
2
3
4
5
6
Graph G
h_1
h_2
h_3
h_4
h_5
h_6
NN
Classification label for Graph
Message passing performed to update node features
Updated node features
Graph classified using Neural Network

Figure 6: Illustration of Graph Classification using GNN.

In agriculture, disease propagation from one plant to another depends on environmental conditions and plants nearby. To efficiently model the disease spread or derive insights from them, spatial analysis must be performed considering the impact of neighboring plants. If a graph can be generated by representing plants as nodes where conditions of plants, and environment are node features and an edge between neighbor plants represents their proximity, exploring such a graph by GNN can analyze the neighbors of each plant and perform spatial analysis. This paper presents a method to perform spatial analysis and classify the graph generated using GNN to compute the spatial spread of the disease.

V. Proposed Method

A Graph Neural Network method to estimate the severity of a disease as the harmonic mean of the percentage of area affected by the disease and the percentage of area the disease has spread to is detailed in this section. Since detecting the presence of a disease is not in the scope of the current article, the proposed method starts with loading data of the identified diseased locations in the farmland. Flow chart of the proposed method is explained in Figure 7. The workflow of Stimator has different sub-processes which are described below.

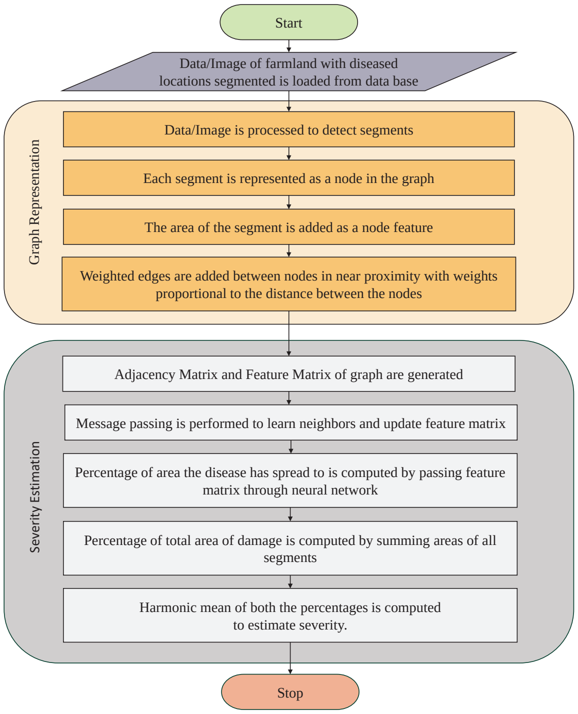

Start
Data/Image of farmland with diseased locations segmented is loaded from data base
Graph Representation
Data/Image is processed to detect segments
Each segment is represented as a node in the graph
The area of the segment is added as a node feature
Weighted edges are added between nodes in near proximity with weights proportional to the distance between the nodes
Severity Estimation
Adjacency Matrix and Feature Matrix of graph are generated
Message passing is performed to learn neighbors and update feature matrix
Percentage of area the disease has spread to is computed by passing feature matrix through neural network
Percentage of total area of damage is computed by summing areas of all segments
Harmonic mean of both the percentages is computed to estimate severity.
Stop

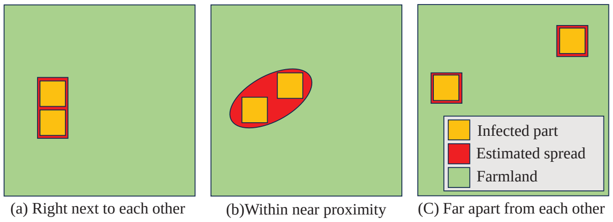
Figure 7: Flow chart of the proposed method.

A. Graph Representation

This sub-process is intended to represent the data of disease locations in the form of a graph. The loaded data/image is processed to identify all the locations labeled/segmented as diseased. Each of the identified locations is represented as a node constituting $V = \{v_1, v_2, v_3, \dots, v_n\}$ in the graph structure $G = (V, E)$. In semantic image segmentation, all the adjacent instances will be represented as a single instance and if the plantations are too close, multiple instances will be identified as one instance. To factor in these discrepancies, the area of each identified location is added as a node feature f_1 of corresponding node u. As a result, the feature representation h_u of node u can embed severity at the corresponding location into the graph. In agriculture, diseases are transmitted from one plant to another by factors like irrigation water, insects, and pathogens. The mobility of these agents restricts them from spreading the disease to a couple of meters. To be able to perform efficient image classification, the image must exhibit significant features that can be captured from a distance of a few meters. On this basis, a pair of diseased locations within 10% of width of the image are considered as neighbors. So, the Euclidean distance between all pairs of i^{th} and j^{th} nodes is computed, and if the distance is below 10% of the width of the image an edge (v_i, v_j, w) is added between the pair of nodes with (10% of image's width)/(distance between them) as edge weight. In addition, a self-edge (v_i, v_i) is added to every node with weight 1 to constitute $E = \{(v_i, v_j, w), (v_j, v_k, w'), \dots\}$ of $G = (V, E)$. The intuition behind adding edge weights proportional to the distance between nodes and adding a self-edge will be presented in the downstream processes. As a result of this process, the data/image has been represented as graph $G = (V, E)$ made up of nodes $V = \{v_1, v_2, v_3, \dots, v_n\}$, edges $E = \{(v_i, v_j, w), (v_j, v_k, w'), \dots\}$, features $F = \{f_1\}$, feature vectors $H = \{h_1, h_2, \dots\}$ similar to the one in Figure 5 while capturing spatial relation between neighbor diseased locations and severity at each instance.

B. Severity Quantification

The two things that represent how severe the disease infestation is in farmland are the proportion of area that has been damaged due to the disease and the proportion of farmland across which the disease has been spread/distributed. As the graph G generated in Section V-A embedded areas of each location as node feature, adding up all the node features gives us the area of the farmland damaged by disease, and its percentage can be computed by simple arithmetic. But the percentage of area the disease has spread to cannot be computed by simple arithmetic, it needs a method equivalent to how humans visually estimate it. Consider Figure 8 representing three different possibilities of how far any two diseased locations could be. The first possibility is two locations closer to each other and the third possibility is two locations far from each other and are not neighbors as defined in Section V-A. In both cases, a human computes the area where the disease has spread as the sum of each location. But in the case of the second possibility where the locations are a little far and are neighbors as defined in Section V-A humans consider a contour encircling both the locations as represented in red color as the area the disease has spread to. This implies that in the case of neighboring locations, the area between them also contributes to the area of the disease's spread and is proportional to the distance between them.



(a) Right next to each other (b)Within near proximity (C) Far apart from each other

Figure 8: Visual estimation of spread.

To account for the above mentioned relationship between neighbors and the area of contour encircling them, we set weights of edges in graph G (generated in Section V-A) to (10% of image's width)/(distance between them). Accordingly, the sum of the node feature h_u of node u and product of edge weight $W(uv)$, node feature vector h_v for every node v in the neighborhood $N(u)$ as described by Equation 1 provides as a relative measure to denote the spread of the disease:

$$\text{Spread at } u = \sum \left(h_u, \sum \left(\{h_v \times W(uv) : v \in N(u)\}\right)\right) \qquad (1)$$

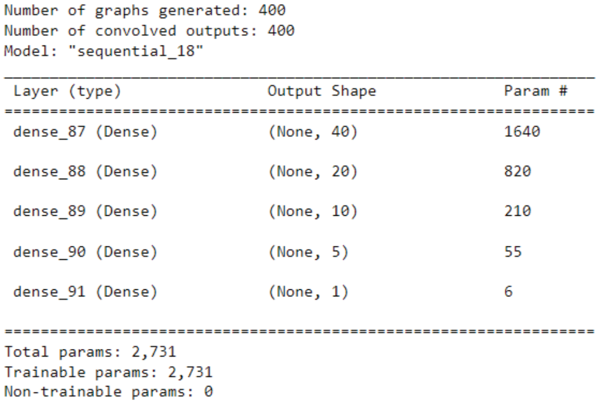
Upon careful analysis, Equation 1 can be rephrased as "To estimate the spread of the disease around node u, it has to get node feature h_v for every node v in the neighborhood $N(u)$ and perform an arithmetic on thus learned features", which is message passing described in Section IV-A and represented in Figure 5. Hence, performing one iteration of message passing throughout the graph as per Equation 1 updates features of all the nodes to a measure proportional to the spread of the disease around the node.

Adjacency matrix A of a graph G with m number of nodes is a square matrix of size $m \times m$ whose element $A[i][j]$ represents weight of the edge (v_i, v_i) between i^{th} and j^{th} nodes. Multiplying square matrix A of size $m \times m$ with a $m \times 1$ column matrix H $(A \times H)$ will result in a column matrix of size $m \times 1$ in which the i^{th} element represents the sum of products of node features and corresponding edge weights for all neighbors of i^{th} node. To estimate the spread around node i the obtained sum must be added to node feature node i. Instead, adding a self-edge to the node with weight 1 will set $A[i,i]$ to 1 and $A \times H$ adds the feature of node i to the sum and performs message passing as per Equation 1. This is the foundation for including a self to every node while building the graph in Section V-A.

Features updated by message passing serve as a measure proportional to the area the disease has spread to around each node but not the percentage of area the disease has spread to. By performing the above discussed method on a good number of images to generate updated feature matrices, a machine learning model can be trained against the labeled percentage of the area the disease has spread in each image. When a new image data is represented as a graph and its feature matrix is passed through the neural network of the machine learning model, it will classify the generated graph and assign the computed percentage of area the disease has spread to as its label. Now that the percentage of the area damaged by disease and the percentage of area the disease has spread to are computed, as per Section II-B severity of the disease is estimated as the harmonic mean of the two computed metrics. Thus, the proposed "Stimator" can effectively estimate severity of the disease considering its spatial spread using GNN.

VI. Experimental Verification

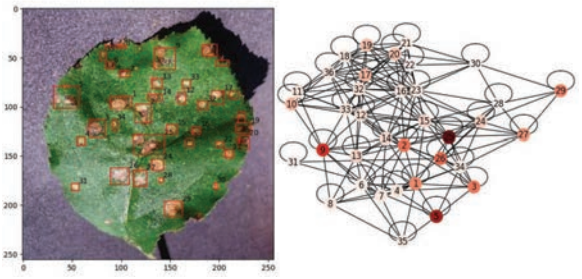
The GNN solution explained in Section V has been experimentally validated on a data set [16] from Kaggle which contains images of apple leaves with diseased parts of the leaf annotated. But in real-time, images of farmland will be used. The solution was developed in Python using NetworkX and Keras libraries for graph creation, manipulation, and machine learning tasks respectively. Initially, a shallow neural network presented in Figure 9 has been trained on 400 images for 200 epochs with a batch size of 50 to perform graph classification by accepting updated feature matrix of the generated graph G. The machine learning model developed accepts an array of size 40 as input and so, in cases where nodes in the graph were less than 40, 0s were appended to the feature matrix to increase its size to 40.



```
Number of graphs generated: 400
Number of convolved outputs: 400
Model: "sequential_18"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 dense_87 (Dense)            (None, 40)                1640

 dense_88 (Dense)            (None, 20)                820

 dense_89 (Dense)            (None, 10)                210

 dense_90 (Dense)            (None, 5)                 55

 dense_91 (Dense)            (None, 1)                 6

=================================================================
Total params: 2,731
Trainable params: 2,731
Non-trainable params: 0
```

Figure 9: Summary of the designed Neural Network.

The developed method was then presented with an image of a diseased leaf whose annotated image and graph representation are shown in Figure 10. Since the presented image had 36 identified disease locations, the generated graph had 36 nodes in it with color intensity proportional to its node features.



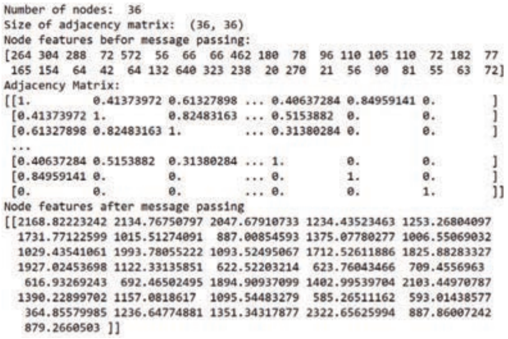
(a) Inputted image

(b) Graph representation of inputted image

Figure 10: Input image and its graph representation.

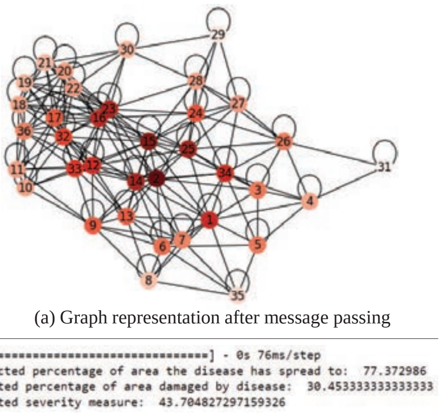
Figure 11 presents the fundamental information related to the input image before and after message passing. Since edge weight was (10% of image's width)/(distance between them) and only the ones within a distance less than 10% of image's width were considered as neighbors, elements of adjacency matrix were less than one and diagonal elements were 1 due to weight 1 on self-edges.

Updated graph after message passing and severity estimated by graph classification is represented in Figure 12. The proposed model estimated severity as 43.7% though the percent of the damaged area is 30.4% by considering the spatial spread of the disease which was 77.3% of the leaf.



```
Number of nodes:  36
Size of adjacency matrix:  (36, 36)
Node features befor message passing:
[264 304 288  72 572  56  66  66 462 180  78  96 110 105 110  72 182  77
 165 154  64  42  64 132 640 323 238  20 270  21  56  90  81  55  63  72]
Adjacency Matrix:
[[1.         0.41373972 0.61327898 ... 0.40637284 0.84959141 0.        ]
 [0.41373972 1.         0.82483163 ... 0.5153882  0.         0.        ]
 [0.61327898 0.82483163 1.         ... 0.31380284 0.         0.        ]
 ...
 [0.40637284 0.5153882  0.31380284 ... 1.         0.         0.        ]
 [0.84959141 0.         0.         ... 0.         1.         0.        ]
 [0.         0.         0.         ... 0.         0.         1.        ]]
Node features after message passing
[[2168.82223242 2134.76750797 2047.67910733 1234.43523463 1253.26804097
  1731.77122599 1015.51274091  887.00854593 1375.07780277 1006.55069032
  1029.43541061 1993.78055222 1093.52495067 1712.52611886 1825.88283327
  1927.02453698 1122.33135851  622.52203214  623.76043466  709.4556963
   616.93269243  692.46502495 1894.90937099 1402.99539704 2103.44970787
  1390.22899702 1157.0818617  1095.54483279  585.26511162  593.01438577
   364.85579985 1236.64774881 1351.34317877 2322.65625994  887.86007242
   879.2660503 ]]
```

Figure 11: Information related to the graph generated.



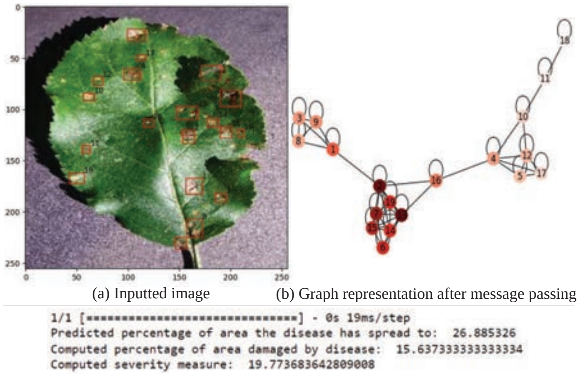
(a) Graph representation after message passing

```
1/1 [==============================] - 0s 76ms/step
Predicted percentage of area the disease has spread to:  77.372986
Computed percentage of area damaged by disease:  30.453333333333333
Computed severity measure:  43.704827297159326
```

(b) Estimated severity

Figure 12: Updated graph and estimated severity.

When a less affected image as in Figure 13 was presented to the method, the computed metrics were 26.8%, 15.6% and estimated severity was 19.7%. These outputs of the developed model which are similar to estimates by human vision explain the accuracy of it in estimating the severity of the disease.



(a) Inputted image (b) Graph representation after message passing

```
1/1 [==============================] - 0s 19ms/step
Predicted percentage of area the disease has spread to:  26.885326
Computed percentage of area damaged by disease:  15.637333333333334
Computed severity measure:  19.773683642809008
```

(c) Estimated severity

Figure 13: Inputted image, its graph and estimated severity.

VII. Conclusion

This article presented a novel method to efficiently estimate the severity of disease in farmland considering the spatial spread of the disease for better resource planning. It can perform spatial analysis on existing conditions but cannot predict the further spread of the disease. However, incorporating various environmental conditions as node features in the novel graph representation presented can be instrumental in developing an epidemiology model [17] to predict the future spread of disease. Also, efficient routes can be designed for pesticide sprayers as in article [18] using the graph generated. Development of an A-CPS with the help of IoAT solutions that can efficiently predict areas that can be affected subsequently and propose efficient routes for sprayers to effectively manage the disease can be sought for future research.

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