A Literature Review on Cellular Automata Frameworks for Fruit Disease Modeling

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***Abstract*—This paper addresses the limitations of static disease detection by introducing a dynamic modeling approach using Cellular Automata (CA). While current methods like convolutional neural networks (CNNs) are proficient at classifying existing diseases, they do not capture the spatio-temporal progression of an infection. This work presents a CA framework to simulate how diseases spread across a fruit's surface over time. The model represents the fruit surface as a 2D grid where each cell can exist in one of four states: Healthy, Infected, Symptomatic, or Necrotic. The system evolves based on simple, local rules governing the probabilistic spread of infection and deterministic transitions between disease stages. The paper discusses the model's core components and demonstrates its ability to generate realistic lesion morphologies, from irregular spots to classic "target" rings. This framework serves a dual purpose: forecasting the future severity of an observed lesion and generating vast synthetic datasets for training more robust static classifiers. Overall, this CA approach promises to shift the paradigm from reactive detection to proactive, predictive crop management.**

***Index Terms*—Cellular Automata, Fruit Disease, Predictive Modeling, Spatio-Temporal Dynamics, Precision Agriculture, Simulation Introduction (Heading 1)**

I. INTRODUCTION

Cellular Automata (CA) provide an effective computational framework for modelling complex systems through simple local interaction rules. Wolfram established the fundamental concepts of cellular automata and demonstrated how simple rules applied to discrete cells can generate complex patterns and behaviours [1]. This concept makes CA suitable for representing dynamic processes such as disease spread, where the state of one region can influence neighbouring regions over time.

The application of deep learning has significantly improved plant disease identification through image-based analysis. Mohanty et al. demonstrated the effectiveness of deep learning techniques, particularly Convolutional Neural Networks (CNNs), for detecting and classifying plant diseases from images [2]. However, such image-based methods primarily provide a static representation of disease symptoms and have limited capability to predict how the disease will progress or spread over time.

Durrett and Levin highlighted the importance of discrete and spatial modelling in understanding biological and ecological systems [3]. Their work demonstrates that spatial interactions between neighbouring regions play an important role in modelling dynamic biological processes. This concept is particularly relevant to disease progression, where infection can spread from affected regions to nearby healthy areas.

Cellular Automata have also been applied to model biological growth processes. Kier and Cheng developed a Cellular Automata-based model for simulating tumor growth, demonstrating the ability of CA to represent the spatial development of biological phenomena through cell-level interactions [4]. This approach provides a foundation for applying similar computational models to simulate the growth and development of disease lesions on fruit surfaces.

Deep learning has also been used for identifying plant diseases based on individual lesions and spots. Barbedo demonstrated the potential of deep learning for recognizing plant disease symptoms from localized regions [5]. While such techniques are effective for disease identification, the proposed work focuses on extending the analysis toward disease progression by modelling how lesions may expand and change over time using Cellular Automata.

Shuman and Ristaino explored the use of a Cellular Automata model to simulate the spread of

Phytophthora infestans in potato fields, demonstrating the potential of CA for modelling spatial plant disease propagation [6]. Inspired by these studies, the proposed work develops a Cellular Automata-based framework to simulate disease spread across a fruit surface. The model aims to predict future lesion size and severity from early-stage observations, supporting timely intervention, proactive disease management, and precision agriculture.

II. LITERATURE REVIEW

Wolfram [1] presented a fundamental study on the statistical mechanics of Cellular Automata (CA), explaining how simple local rules and interactions between discrete cells can produce complex global patterns. This work established the theoretical foundation of Cellular Automata and demonstrated their potential for modeling dynamic systems. The concepts presented in this study are relevant to modeling disease progression, where changes in infected cells can influence neighboring healthy cells over time.

Mohanty et al. [2] investigated the use of deep learning for image-based plant disease detection. Their study demonstrated the effectiveness of Convolutional Neural Networks (CNNs) in identifying and classifying plant diseases from leaf images. Although deep learning provides accurate disease recognition, the approach mainly focuses on detecting the existing symptoms and does not explicitly model the future spatial progression of disease lesions.

Durrett and Levin [3] studied the importance of discrete and spatial modeling in biological systems. Their work highlighted how spatial interactions and discrete structures can be used to understand complex biological processes. These concepts are significant for fruit disease modeling, as infection can spread from an infected region to neighboring healthy regions based on spatial relationships.

Kier and Cheng [4] developed a Cellular Automata model for simulating tumor growth. Their study demonstrated how cell-level interactions and transition rules can be used to represent the growth and development of biological structures. This work provides a useful foundation for applying Cellular Automata to simulate the expansion of disease lesions on fruit surfaces.

Barbedo [5] explored plant disease identification from individual lesions and spots using deep learning techniques. The study showed that deep learning methods can effectively analyze localized disease symptoms and improve disease identification. However, the focus remains primarily on recognizing existing lesions rather than predicting their future growth and progression, creating an opportunity for dynamic disease modeling.

Shuman and Ristaino [6] investigated a Cellular Automaton model for simulating the spread of Phytophthora infestans in a potato field. Their work demonstrated the potential of Cellular Automata for representing the spatial propagation of plant diseases. Inspired by these studies, the proposed research focuses on using Cellular Automata to model disease spread across fruit surfaces and predict the future size and severity of lesions based on their early-stage development.

Overall, deep learning is effective for static disease identification, while Cellular Automata are suitable for modeling disease spread and progression. However, limited research focuses on predicting fruit disease progression using early-stage observations. Therefore, this study proposes a Cellular Automata-based model for simulating and predicting dynamic fruit disease progression.

III. SYSTEM DESIGN

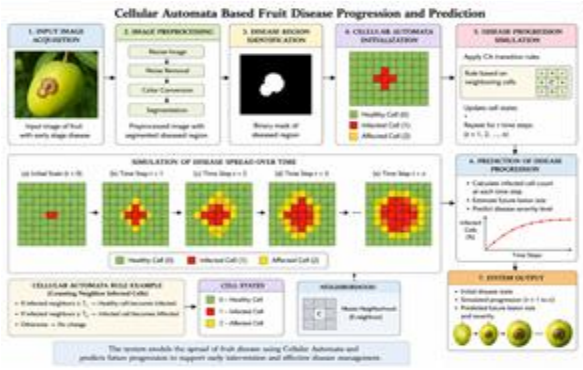

Figure 1: System Architecture for Fruit Disease Progression and Prediction Using Cellular Automata

To implement the methodology shown in the diagram for your Cellular Automata-Based Fruit Disease Progression and Prediction project, you can follow these
steps:

1. Input Image Acquisition:

Objective: Collect fruit images containing early-stage disease symptoms to provide the initial input for disease progression analysis.

- Capture fruit images using a camera or obtain them from a suitable dataset.
- Select images showing visible early-stage disease infections.
- Use the identified initial disease region as the starting point for the prediction process.

2. Image Preprocessing:

Objective: Prepare the input fruit images for accurate disease region analysis.

- Resize the images to a standard size and remove unwanted noise.
- Apply color conversion to obtain a suitable representation for disease analysis.
- Perform image segmentation to separate the diseased region from the healthy fruit surface.

3. Disease Region Identification:

Objective: Identify and isolate the initial infected region from the pre-processed fruit image.

- Analyse the segmented image to detect the initial disease region.
- Generate a binary mask to distinguish infected and healthy regions.
- Use the identified disease region to initialize the Cellular Automata grid.

4. Cellular Automata Initialization:

Objective: Represent the fruit surface as a Cellular Automata grid for disease progression simulation.

- Convert the fruit surface into a two-dimensional grid of interacting cells.
- Assign cell states as 0 (Healthy), 1 (Infected), and 2 (Affected).
- Map the initially detected infected region onto the corresponding cells of the grid.

5. Disease Progression Simulation:

Objective: Simulate the spatial spread of disease using Cellular Automata transition rules.

- Define transition rules based on the condition of neighbouring cells.
- Analyze each cell using a Moore neighbourhood consisting of eight surrounding cells.
- Update the cell states iteratively based on the number of infected neighbouring cells.

6. Disease Spread Analysis:

Objective: Analyze the dynamic progression of disease across the fruit surface over multiple time steps.

- Start the simulation from the initial disease state ($t = 0$).
- Repeat the Cellular Automata process for subsequent time steps.
- Observe the expansion of infected and affected regions over time.

7. Disease Progression Prediction:

Objective: Predict the future size and severity of the disease based on the simulated progression.

- Calculate the number of infected and affected cells at each time step.
- Estimate the future lesion size and potential disease spread.
- Determine the disease severity and represent the progression using graphs or visualizations.

8. Final Output:

Objective: Provide visual and predictive information about the future development of fruit disease.

- Display the initial disease condition and simulated disease progression.
- Present the predicted future lesion size and estimated disease severity.
- Provide predictive insights to support early intervention and proactive disease management.

IV. METHODOLOGY

The methodology revolves around the design and implementation of a Cellular Automata model. The framework is defined by a grid, a set of states, a neighborhood, and a set of transition rules. The process begins with the conceptualization of the fruit surface as a 2D grid. Each cell in this grid can be in one of four states, as detailed in Table 1.

No.	State Name	Description	Visual
1.	Healthy (H)	Healthy fruit tissue with no visible disease infection.	Green
2.	Infected (I)	Initially infected tissue where the disease is developing and can spread to neighboring cells.	Red
3.	Affected (A)	Tissue surrounding the infected region that is influenced by or at risk of disease progression.	Yellow
4.	Diseased/Severe (D)	Advanced disease region with significant lesion development and increased disease severity.	Dark Red/Brown

Table 1. State description of cell grid

The model is initialized by setting one or more cells to the 'Infected' state. The simulation then proceeds in discrete time steps, following the logic outlined in the flowchart in Fig. 1. At each step, the state of every cell is updated simultaneously based on a set of rules and the state of its eight immediate neighbors (the Moore neighborhood).

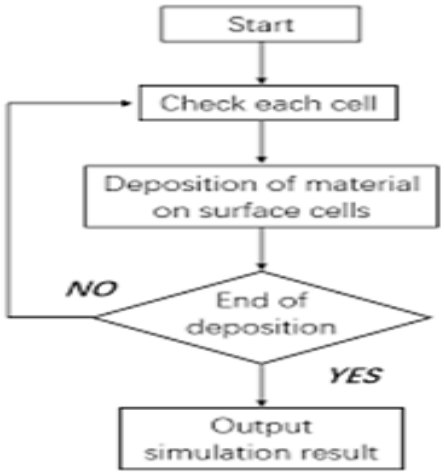

Fig. 1. Flowchart of Cellular Automata

The core rules are:
1) A healthy cell can become infected with a certain probability if it is next to an infectious cell.
2) An infected cell will become symptomatic after a fixed time period (the latency period).
3) A symptomatic cell will become necrotic after another fixed time period. The simulation's output is a sequence of images representing the grid's state over time.

The implementation of the CA model follows five key steps:

1. Define Grid and States: Initialize a 2D NumPy array for the fruit surface and assign numerical values to the four states (e.g., 0=Healthy, 1=Infected, 2=Symptomatic, 3=Necrotic).
2. Initialize the Simulation: Set the entire grid to the 'Healthy' state and "infect" one or more cells at the center by changing their state.
3. Create the Simulation Loop: Iterate for a defined number of time steps. In each step, for every cell, check its neighbors and apply the transition rules to determine its next state, updating a copy of the grid. After all cells are evaluated, the main grid is updated.
4. Visualization: At specified intervals, use a library like Matplotlib to create and store an image of the grid, using different colors for each state to visualize lesion growth.
5. Analysis and Prediction: Analyze the final grid state to measure properties like lesion area, and

use the generated sequence of images as a forecast of the disease's progression.

V. ALGORITHM

The proposed framework utilizes a Cellular Automata (CA) algorithm to model the spatio-temporal spread of fruit diseases on the surface of a fruit. The fruit surface is represented as a two-dimensional grid of cells, where each cell corresponds to a small region of the fruit. Every cell can exist in one of four possible states: Healthy (H), Infected (I), Symptomatic (S), and Necrotic (N). The disease propagates through local interactions among neighbouring cells using the Moore Neighbourhood, which consists of eight adjacent cells.

Initially, all cells are assigned the Healthy state except one or more infected seed cells. During each simulation step, every cell simultaneously updates its state according to predefined transition rules. A healthy cell becomes infected if at least one neighbouring cell is infectious and the infection probability condition is satisfied. Infected cells remain latent for a predefined latency period before becoming symptomatic. After the lesion development period, symptomatic cells become necrotic, indicating dead tissue. The simulation continues for a specified number of iterations, generating realistic disease progression patterns that closely resemble natural lesion growth.

Mathematical Equations

Let the fruit surface be represented as an M × N grid:

$G = \{C_{ij}\},\ 1 \le i \le M,\ 1 \le j \le N$

where each cell C_{ij} can occupy one of four states:

$S(C_{ij}) \in \{H, I, S, N\}$

where

- H = Healthy
- I = Infected
- S = Symptomatic
- N = Necrotic

Infection Rule

A healthy cell becomes infected if at least one neigh boring cell is infectious.

$P_{infection} = 1 - (1 - p)^k$

where

- p= Infection probability
- k= Number of infected neigh boring cells

Transition condition:

$H \to I$

if

$Random(0, 1) < P_{infection}$

Latency Transition

After the latency period T_L,

$I \to S$

if

$t_I \ge T_L$

where

- t_I= Time spent in infected state

Lesion Development

After lesion duration T_S,

$S \to N$

if

$t_S \ge T_S$

where

- t_S= Time spent in symptomatic state

Moore Neighborhood

The neighboring cells are defined as

$N(i, j) = \{(i, +xj + y), | xy \in \{-, 1, 01\}(x, y) \ne (0, 0)\}$

which considers all eight surrounding cells.

VI. EXPERIMENTAL RESULTS

The Cellular Automata (CA) model was implemented and a series of simulations were conducted to validate its behaviour and demonstrate its predictive capabilities. The results demonstrate the model's ability to generate diverse, realistic lesion morphologies and function as a forecasting tool.

The primary validation of the model is its ability to generate morphologically complex patterns from simple rules, as shown in Fig. 2. This figure displays a time-series sequence from a simulation using moderate parameters (P_inf = 0.5, T_latent = 5, T_lesion = 15). The simulation begins with a single infected cell and evolves over 90-time steps. The output clearly shows the emergence of a "target lesion" with a necrotic core (black), surrounded by a ring of symptomatic tissue (brown), an outer latent infection front (yellow), and healthy tissue (green). This emergent behaviour, creating concentric rings, is highly characteristic of real-world diseases like anthracnose and provides strong qualitative validation for the model's underlying rules.

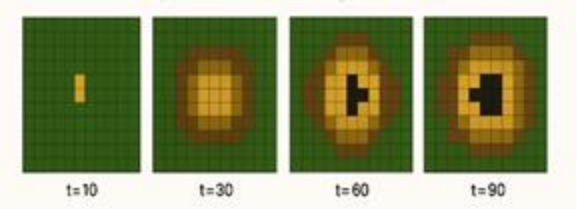

Fig. 2. Simulation of a Target Lesion: A sequence of four images showing the CA grid at t=10, t=30, t=60, and t=90. The simulation uses moderate parameters, resulting in the emergence of a classic "target lesion".

To analyze the model's sensitivity to its parameters, the infection probability (P_inf) was varied, with the results displayed in Fig. 3. The figure compares the lesion morphology after 50-time steps for a low P_inf (e.g., 0.15) and a high P_inf (e.g., 0.85). A low probability results in slow, stochastic growth with a highly irregular and fragmented boundary, which could simulate a less virulent pathogen. Conversely, a high probability leads to rapid, uniform growth, forming a near-perfect circular lesion analogous to an aggressive blight. This demonstrates that the model can be tuned to represent a wide spectrum of disease characteristics.

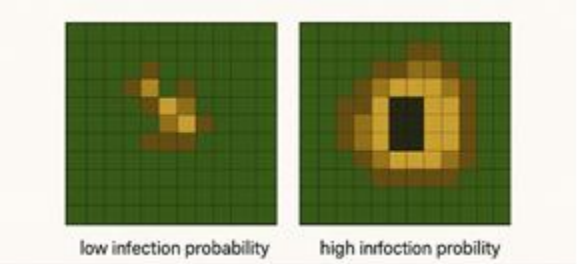

Fig. 3. Effect of Infection Probability on Lesion Shape: A panel of two images, both at t=50. Left: A simulation with low infection probability. Right: A simulation with high infection probability.

The framework's ultimate utility lies in its predictive capability, as illustrated in Fig. 4 and Fig. 5. Here, the model is used to forecast the development of an infection. Fig. 4 depicts the initial state of a small, observed lesion on a fruit, which is used to initialize the CA model. Fig. 5 shows the output of the CA simulation after being run forward for 50-time steps. The model predicts significant growth in the lesion's area and the development of a necrotic core. This provides a visual and quantifiable forecast that can inform a grower's decisions, moving beyond simple detection to proactive management.

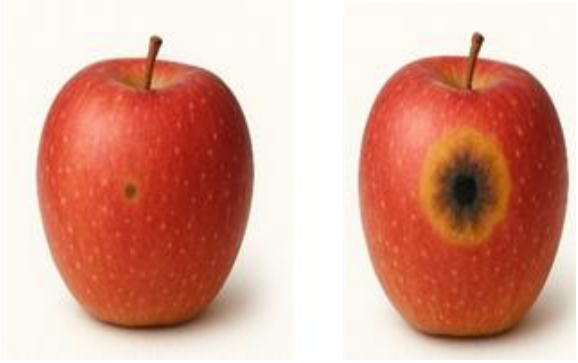

Fig 4 Initial State of Lesion Fig 5 Predictive Forecast

VII. CONCLUSION

This research presents a Cellular Automata (CA)-based framework for modelling and predicting the dynamic progression of fruit Fig. 4. diseases through spatio-temporal simulation. Unlike conventional deep learning approaches that focus primarily on static disease classification, the proposed model captures how infections evolve over time by representing the fruit surface as a two-dimensional grid of interacting cells. The implementation of local transition rules enables the simulation of realistic lesion growth patterns, including infection spread, symptom development, and tissue necrosis.

The experimental results demonstrate that the Cellular Automata model effectively generates realistic disease propagation under varying infection probabilities and disease parameters. The framework not only provides visual predictions of disease progression but also estimates lesion growth and disease severity, enabling timely intervention and improved crop management. Furthermore, the model can generate synthetic disease progression datasets that may support the training and validation of future artificial intelligence and deep learning models. Overall, the proposed approach offers a computationally efficient, scalable, and predictive solution for precision agriculture and intelligent plant disease management.

VIII. FUTURE SCOPE

The proposed framework can be further enhanced by integrating real-time image acquisition systems, Internet of Things (IoT) sensors, and deep learning

techniques to develop a comprehensive smart agriculture platform. Future work may involve combining Cellular Automata with Convolutional Neural Networks (CNNs) or Vision Transformers (ViTs) to achieve both accurate disease detection and reliable disease progression forecasting.

The model can also be extended to support multiple fruit varieties and different plant diseases by incorporating environmental factors such as temperature, humidity, rainfall, and soil moisture into the simulation. Additionally, deploying the system as a cloud-based or mobile application would allow farmers to monitor disease development remotely and receive early warning alerts. These advancements would improve decision-making, reduce crop losses, minimize pesticide usage, and contribute to sustainable and precision farming practices.

IX. ACKNOWLEDGMENT

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