Multi-agent Simulation to Predict Global Behavior of Population Based on Elementary Local Markovian model*

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Abstract—New technologies based robotics and data analysis are starting to be used for the treatment of disease in horticulture field. Such autonomous systems evolving in dynamic environment need automatic operation and control based on dynamic scheduling. To do so, it is necessary to predict the behaviour of this environment to better control these autonomous systems. This paper aims to define the behaviour of plants infection by mildew disease in greenhouses in order to optimise the robotized treatment, which should be fully autonomous. We propose a Markovian approach to model individual plants behaviour and their interactions to predict the dynamics of mildew disease in greenhouses. A multi-agent based simulation is implemented to validate the model. Simulation results have shown the efficiency of the proposed approach to reproduce the behaviour .

Index Terms—Stochastic behaviour, Markov chain, Simulation, Multi-agent-system, UV-C treatment

I. INTRODUCTION

The last decade has known a huge revolution in the use of robotics and 4.0 technologies in different economic sectors. The new technologies brought by this fourth industrial revolution, called Industry 4.0, are affecting the agricultural sector as much as the industry [1]. The previous industrial revolutions began at the end of the 18th century and the beginning of the 19th century, with the invention of steam engines. The second industrial era was born thanks to the massive use of machines. These machines made it possible to pass from artisanal production in workshops to mass production in factories, like the automobile factories in the 19th century. Then, the development of electronic cards and computer technologies in the 20th century allowed the automation of industrial production and revolutionized the industry for a third time. Today, the development of digital technologies allows the possibility to connect all objects and devices, such as computers, robotic tools, products, etc. This connectivity, reinforced by Internet of Things (IoT), makes easier the control of physical world from a virtual world. Moreover, the availability of affordable computational devices (computer with acceptable computational capacity) gives the possibility to use distributed supervision systems and to allow more decision capacity to smart devices.

Associated with the fourth industrial revolution, Agriculture 4.0 needs all the technologies used in Industry 4.0. [2] Similarly to other agriculture sub-sectors, the horticulture is using more and more robotics, sensors, simulation and optimisation in its daily operations. In Agriculture 4.0 era, connected farms or greenhouses are equipped with supervisors based on Internet of Things technologies. The supervisor is able to collect data about the state of the plants through sensors in the greenhouses or drones in open-field farms. After collecting the data and extracting the information it contains, the supervisor decides whether to harvest the plants or treat them [3]. In [4], harvesting is ensured by harvesting robots, which can be customized regarding the type of plants and can work in group. For the treatment of plants against diseases, chemicals are generally sprayed manually or using spraying robots [5]. Recently, a new technology is being developed to replace chemicals by ultraviolet (UV) radiation. Especially, the UV Type C has demonstrated its efficiency in the eradication of plant disease such as mildew [6]. The manual deployment of this new technology cannot be possible due to the numerous and real risks such as burns or cancer. Robots equipped with UV-lamps are suitable for this kind of operations [3]. These robots have to move next to plant with turned on UV-lamps and to make some decisions related to the selection of row to treat, charging cycle planing and speed. These set of automatic decisions are based on the mildew level for each plant or zone in the greenhouse.

The main issue when dealing with plant's diseases is come from their stochastic apparition and evolution process. The

main parameters that influence the behavior of disease (like mildew in greenhouses) are humidity, temperature and airing [7]. In order to treat them automatically with robots, it is necessary to predict the behavior of the disease. Ignoring the behavior of the disease represents a high risk to treat plants with inadequate dozes. Therefore, the use of sensors to measure the disease levels on plants is inevitable. However, as sensors might need a certain time to make sampling, measurement, and calculation, it will not be possible to get instantaneous measurements of the level of mildew in the complete greenhouse. That is why, it is necessary to predict the evolution of the disease to ensure a good treatment with the robots.

The evolution behavior of mildew in a greenhouse can be modeled using the logistic function with three parameters used in [8]. The use of this function allows to reproduce the same expected global disease behaviour for all the plants in the greenhouse. However, it is not possible to predict the behaviour of an individual plant and the assumption that each plant follow the same logistic function (with different parameters) is not realistic. In fact, the disease behaviour of each plant is stochastic and modeled as a discrete function based on human observations. In addition, it is known that the evolution of disease is not the same for each plant, and it has not a uniform distribution on different zones in the greenhouse.

This work aims to define a stochastic model of the behaviour of plants regarding mildew disease and uses simulation its validation. The proposed approach is based on the adoption of a Markovian model based behaviour for each individual plant. This model is calibrated and tested using multi-agent simulation to ensure estimate the global behaviour of the greenhouse.

The rest of this article is structured as follows. Section II describes the behaviour of the mildew disease. Section III details the proposed modeling approach to end with a Markovian transition matrices, defined at plants level, allowing to reproduce a predefined behavior of mildew disease at greenhouse level. Finally, the conclusion and future work are discussed in section IV.

II. DISEASE BEHAVIOR

The evolution of the level of mildew infection directly influences the UV-C dose to be applied, ie the duration of the treatment. To adjust the doses of UV-C treatment, the robot changes its speed according to the level of infection of the plant. When the infection level is high, the robot treats the plant at low speed. The plant therefore receives a sufficient dose of UV-C radiation. In addition, the robot's energy consumption is proportional to the treatment dose applied. As the UV-C lamps make up the largest part of the robot's power consumption, when the robot moves slowly with lamps on, they consume more power even when the motor consumption is low.

The reproduction of the disease behavior in the simulator is the most important point in the UV-Robot environment. In order to study the stochastic process of the evolution of mildew in greenhouses, the simulation of its behavior must be close to reality. We succeeded in simulating the behavior of mildew in two steps. At a first step, we used a three-parameter logistics function [9] which allowed us to obtain uniform probabilities for all plants. In this work, we seek to model mildew behavior in a greenhouse based on a Markovian process [10] for each plant. To render the disease levels of each plant as the states of a Markov chain, different Markovian transition matrices should be defined for all plants to simulate the evolution of their states (disease levels) and therefore the state of the whole greenhouse.

In order to properly calibrate our solving algorithms in our system, mildew behavior needs to be simulated to bring it closer to reality. We used data from [11], which represents the evolution of the level of mildew over time in tomato greenhouses in Spain. Figure 1 shows the mildew behavior curves as a percentage of diseased leaf area over days. The disease levels are represented with percentage in this graph, but we are going to use disease levels which are defined by the partners of the UV-robot project. We have six disease levels in all (0, 3, 6, 12, 20, and 30).
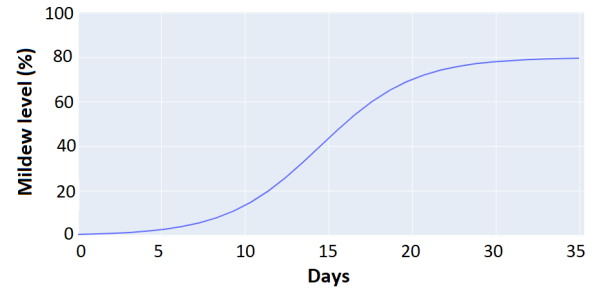

Fig. 1. Mildew behavior in greenhouse [11]

The function which estimates this curve is a logistic function with three parameters. It looks like the sigmoid but it is not symmetric in $x = 0$. The sigmoïd function is a logistic function with three parameters which are equal to 1 ($a = b = c = 1$). The equation 1 shows the estimation function $\hat{f}(t)$, it only remains to define the parameters a, b and c.

$$\hat{f}(t) = \frac{c}{1 + be^{-at}} \qquad (1)$$

The parameters of $\hat{f}(t)$ are:
- The numerator c is the limit of the function at infinity (the curve peaks under a horizontal asymptote).
- The function is symmetric with respect to its inflection point of abscissa $\frac{ln(b)}{a}$ and ordinate $\frac{c}{2}$.
- c is the maximum disease level, in figure 1 the maximum is 80%. The highest level in our simulator is 30, so 80% of 30 is 24.
- Then $c = 24$

To calculate a and b it suffices to take a point in the curve of the graph of the figure 1. We take the point $(20, 72)$ which indicates a level of disease of 72% after 20 days, 72% represents in our case the level 21.6, so we need the point $(20, 21.6)$ to construct the equation 2. And the point of inflection of abscissa which equals 15 to construct the equation 3. Then we solve the two equations 2 and 3.

$$\frac{c}{1 + be^{-20a}} = 21.6 \tag{2}$$

$$\frac{ln(b)}{a} = 15 \tag{3}$$

After solving the equations 2 and 3, we find $a = 0.44$, $b = 735$ and $c = 24$. So $\hat{f}(t)$ is given by the equation 4.

$$\hat{f}(t) = \frac{24}{1 + 735e^{-0.44t}} \tag{4}$$

By using the function $\hat{f}(t)$ we manage to reproduce the same real disease behavior, on the other hand the probability of disease progression is the same for all the plants in the greenhouse. But in reality each plant has its own behavior, and according to the horticulturalists the plants in the edges of the greenhouse have a faster disease course compared to the plants in the center. to have a disease behavior close to reality it is necessary to model the behavior of each plant. The solution we propose for this step is to find a Markovian transition matrix for each plant. By calibrating the Markovian matrices with several simulation tests.

III. MARKOVIAN TRANSITION MATRIX

The objective of using Markovian transition matrices is to have a unique behavior for each plant. This matrix must be define in a way that the global behavior of disease progression in the greenhouse is similar to the estimated function $\hat{f}(t)$ defined in section II. So we try to obtain the global mildew behavior (average of the levels of all the plants) from the local behavior (disease evolution for each plant). In Figure 2, it is possible to observe the diagram representing six states for six levels of disease (0, 3, 6, 12, 20, and 30) and the associated transition probabilities between them. Let $i \in [1, I]$ be the index of plants, (x_i, y_i) their x- and y-coordinates, and $P_{i,.,.}$ their transition matrices. Therefore, the Markovian transition matrix to build for each plant is an upper triangular matrix, as shows Eq. (5).

$$P_{i,.,.} = \begin{bmatrix} P_{i,1,1} & P_{i,1,2} & P_{i,1,3} & P_{i,1,4} & P_{i,1,5} & P_{i,1,6} \\ 0 & P_{i,2,2} & P_{i,2,3} & P_{i,2,4} & P_{i,2,5} & P_{i,2,6} \\ 0 & 0 & P_{i,3,3} & P_{i,3,4} & P_{i,3,5} & P_{i,3,6} \\ 0 & 0 & 0 & P_{i,4,4} & P_{i,4,5} & P_{i,4,6} \\ 0 & 0 & 0 & 0 & P_{i,5,5} & P_{i,5,6} \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \tag{5}$$

This means that the matrix is representing only the progression of the disease. In practice, the reduction of mildew level is ensured only by treatment (chemical or UV-C).
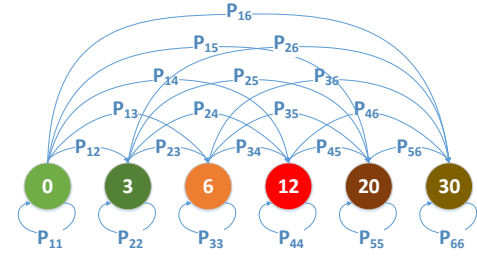

Fig. 2. The probabilities of transition on the levels of mildew

A. Global behavior simulation

Most of reference observation available in the literature concerns global behaviour of population of plants that compose a farm or a greenhouse. in order to calibrate and validate our Markov model of individual plant behaviour we have to find the link between its behaviour and its impact on the global behaviour of the farm. We propose to use multi agent simulation to reproduce this behaviour. A multi-agent base simulator is then developed using NetLogo software to represent the behaviour of greenhouse. The greenhouse is a part of global simulation of UV-C treatment already presented in other works such as [3] and [12]. Among the existing agents of the model, the agent class " `Plants` " is considered as a holon [13], which contains several sub-agent " `Plant` ". The contamination phenomena is supposed integrated in the transition matrix already proposed of each plant.

B. Transition matrix calibration

The construction of matrices is done during the initialization of the " `Plants` " agents, such that each one have its own matrix. For each matrix $P_{i,.,.}$ generated for a plant i, the simulator takes into account the distance of the plant from the center of the greenhouse $d_i = \sqrt{(x_i - x_0)^2 + (y_i - y_0)^2}$, where x_0 and y_0 are the x- and y-coordinates of the center of the greenhouse, respectively. Then, it generates a probability of disease progression proportional to the distance from the center. This value is calculated with the function $g(i) = 0.1 \times d_i + 0.5$. This linear function is chosen empirically with respect to its growth as the distance increases.

The transition matrix for each plant i is obtained after the following sequence of construction:
1) $P_{i,1,2} = g(i) \times \beta$
2) $P_{i,2,3} = P_{i,1,2} \times 3$
3) $P_{i,3,4} = P_{i,1,2} \times 6$
4) $P_{i,4,5} = P_{i,1,2} \times 12$
5) $P_{i,5,6} = P_{i,1,2} \times 20$
6) $P_{i,j,k} = \dfrac{P_{i,j,k-1}}{10 \times k} \quad \forall i \in [1,I] \quad \forall j \in [1,6] \quad \forall k \geq j+3$
7) $P_{i,j,j} = 1 - \displaystyle\sum_{\substack{k=1 \\ k \neq j}}^{5} P_{i,j,k} \quad \forall i \in [1,I] \quad \forall j \in [1,6]$

C. Test and validation

After the construction of the Markovian transition matrices we launched several simulations to calibrate β allowing to get

an estimated function $\hat{f}(t)$ as close as possible to observed function of mildew level evolution. The simulation results are shown in Figure 3. The best behavior is that of the pink curve, with $\beta = 5.5 \times 10^{-6}$. Eq. (6) shows an example of transition matrix generated for a plant situated at 40 meters from center of the greenhouse, with $\beta = 5.5 \times 10^{-6}$. Then, the calibrated transition matrix is used to simulate the behavior of mildew disease in a $2,000$ meter^2 surface green house, which is composed of $10,000$ plants arranged in 100 rows of 100 plants. The simulation starts with a healthy greenhouse (AVG mildew level=0) and is stopped after 30 days.

As observed in the greenhouses and confirmed by growers, the disease appears first in the corners of the greenhouse and in its border and start its propagation to the the other plants. Figure 4 represents the state of a greenhouse, assumed completely treated in the first day, after 2, 7, 9, 14, 16 and 23 days. It is possible to validate the model based on this observation because it behaves like the real observations. Unfortunately, it is not possible to verify these observation with real data, because every time growers are treating their greenhouse before reaching such high level of mildew.

$$\begin{bmatrix} 0.9999725 & 0.0000248 & 0.0000025 & 0.0000002 & 2.475e\text{-}08 & 2.475e\text{-}09 \\ 0. & 0.9999218 & 0.0000742 & 0.0000037 & 0.0000002 & 9.281e\text{-}09 \\ 0. & 0. & 0.9998464 & 0.0001485 & 0.0000049 & 0.0000002 \\ 0. & 0. & 0. & 0.9996956 & 0.000297 & 0.0000074 \\ 0. & 0. & 0. & 0. & 0.999505 & 0.000495 \\ 0. & 0. & 0. & 0. & 0. & 1. \end{bmatrix} \quad (6)$$
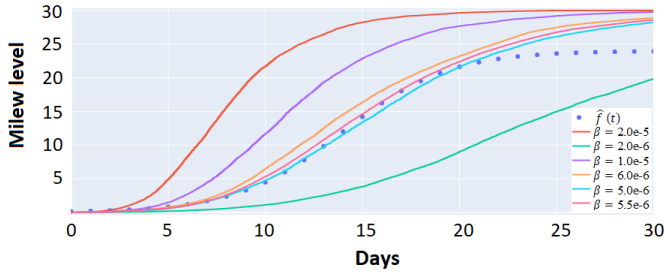

(a) Day 2   (b) Day 7

(c) Day 9   (d) Day 14

(e) Day 16   (f) Day 23

0   3   6   12   20   30

Fig. 4. Behavior mildew in greenhouse

Fig. 3. Simulation of several mildew behaviors with different β

IV. CONCLUSION

This paper proposes a Markovian modeling based approach to characterise the behavior of plants in terms of mildew disease apparition and evolution within a greenhouse. The objective is to reproduce a sigmaoïd-shaped evolution of the overall disease level. The results of the simulations on the behavior of mildew are satisfactory. Markovian transition matrices will be initialized with $\beta = 5.5 \times 10^{-6}$. The study of behavior is an important issue that will enrich future work on the development of dynamic and accurate preventive or corrective treatment. Other perspective of this work concerns the consideration of the contamination phenomena based on the multi-agent paradigm. The rest of the work will be carried out on the scheduling of evolutionary tasks for scenarios for treating mildew in the greenhouse.
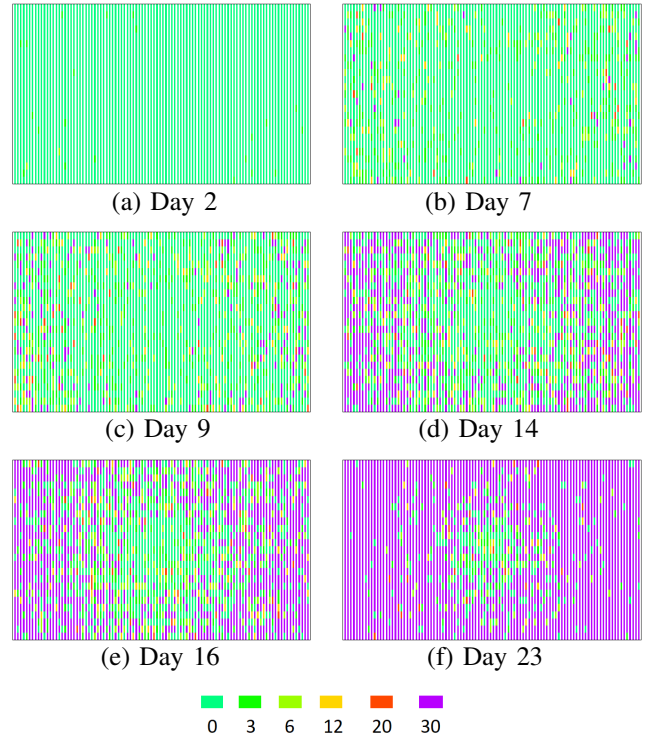
REFERENCES

[1] Z. Zhai, J. F. Martínez, V. Beltran, and N. L. Martínez, "Decision support systems for agriculture 4.0: Survey and challenges," *Computers and Electronics in Agriculture*, vol. 170, p. 105256, 2020.

[2] M. Sahnoun, Y. Xu, B. Belgacem, B. Imen, B. David, and A. Louis, "Fractal modeling of cyber physical production system using multi-agent systems," in *2019 International Conference on Applied Automation and Industrial Diagnostics (ICAAID)*, vol. 1, pp. 1–6, IEEE, 2019.

[3] M. Mazar, M. Sahnoun, B. Bettayeb, N. Klement, and A. Louis, "Simulation and optimization of robotic tasks for uv treatment of diseases in horticulture," *Operational Research*, pp. 1–27, 2020.

[4] B. Southall, T. Hague, J. A. Marchant, and B. F. Buxton, "An autonomous crop treatment robot: Part i. a kalman filter model for localization and crop/weed classification," *The international journal of robotics research*, vol. 21, no. 1, pp. 61–74, 2002.

[5] R. Oberti, M. Marchi, P. Tirelli, A. Calcante, M. Iriti, E. Tona, M. Hočevar, J. Baur, J. Pfaff, C. Schütz, *et al.*, "Selective spraying of grapevines for disease control using a modular agricultural robot," *Biosystems Engineering*, vol. 146, pp. 203–215, 2016.

[6] O. Peries, "Studies on strawberry mildew, caused by sphaerotheca macularis (wallr. ex fries) jaczewski," *Annals of Applied Biology*, vol. 50, no. 2, pp. 211–224, 1962.

[7] UCIPM, "Integrated pest management (ipm)." http://www.ipm.ucdavis.edu/MODELS/index.html., 2021. Accessed: 2021-05-02.

[8] M. Mazar, B. Bettayeb, N. Klement, M. Sahnoun, and A. Louis, "Dynamic scheduling of robotic mildew treatment by uv-c in horticulture," in *10th SOHOMA European Workshop on Service Oriented, Holonic and Multi-Agent Manufacturing Systems for Industry of the Future*, 2020.

[9] M. A. Magableh, *A theoretical and empirical analysis of the Wagner hypothesis of public expenditure growth*. PhD thesis, University of Western Sydney, 2006.

[10] J. G. Kemeny and J. L. Snell, *Markov chains*, vol. 6. Springer-Verlag, New York, 1976.

[11] S. D. White, *Implications of new sustainable greenhouse systems for pests, diseases and biological control: A modelling approach using Oidium neolycopersici and Tetranychus urticae*. PhD thesis, University of Warwick, 2012.

[12] M. Mazar, M. Sahnoun, B. Bettayeb, and N. Klement, "Optimization of robotized tasks for the uv-c treatment of diseases in horticulture," in *The 2018 International Conference of the African Federation of Operational Research Societies (AFROS 2018)*, 2018.

[13] G. Z. Rey, C. Pach, N. Aissani, A. Bekrar, T. Berger, and D. Trentesaux, "The control of myopic behavior in semi-heterarchical production systems: A holonic framework," *Engineering Applications of Artificial Intelligence*, vol. 26, no. 2, pp. 800–817, 2013.