

# Complex Networks

## Project

Pest control in agriculture via Intercropping



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## Introduction

This project is based on the paper “Mathematical modeling for sustainable aphid control in agriculture via intercropping” from Alfonso Allen-Perkins and Ernesto Estrada.

<https://arxiv.org/pdf/1903.05043.pdf>

An aphid is a particularly important class of insect pest, which is one of the most important transmitters of plant viruses, being reported to transmit about 50% of insect-borne plant viruses (approximately 275 virus species).

Crops are affected by aphids, and different intercropping arrangements may improve significantly pest management in agricultural fields.

For this work, a Susceptible - Infected - Recovered/Removed (SIR) epidemic model is used taking into account the movement of aphids transmitting a virus in an agricultural field, as well as the spatial distribution of plants in the field (intercrop arrangements).

## SIR model

At the beginning of the epidemic, the number of Susceptible individuals decreases as the number of Infected individuals increases. Gradually the number of Recovered/Removed individuals increases. In this particular model, after the epidemic is over, not all of the individuals have been infected and recovered as, sometimes, some susceptible individuals remain uninfected (susceptible).

## Aphid mobility

The movements considered for this work include displacements to neighbouring plants or distant plants inside the same field. The separations between plants are topological, which means, that the separation between two plants are measured in terms of steps.

In a Complex Network each plant is a node, and the separation between two nodes  $i$  and  $j$ , is the shortest path length between the two nodes.

There is the parameter  $s$  for the insect mobility. When the aphid has poor mobility,  $s \rightarrow \infty$ , and when the aphid has large mobility  $s \rightarrow 0$ . So that the hop from an infected plant to a susceptible one separated by  $d$  steps is given by  $d^{-s}$ , as shown in Figure 1.

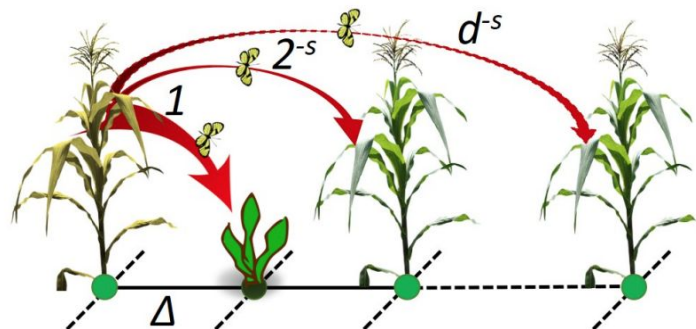


Figure 1: Inter-plants movements of an aphid.

With this, the Mellin d-path transformation is defined as follows, and will be used in the Markovian formulation of the epidemiological model:

$$\tilde{A}(i, j) = \begin{cases} d_{ij}^{-s} & \text{if } i \neq j \\ 0 & \text{if } i = j. \end{cases}$$

## Markovian formulation of the epidemiological model

The Markovian dynamics is valid for any epidemic prevalence. The following are the definitions of some of the terms used:

- $s_i(t)$ : probability that a node  $i$  is Susceptible at time  $t$ .
- $p_i(t)$ : probability that a node  $i$  is Infected at time  $t$ .
- $q_i(t)$ : probability that a node  $i$  is Recovered/Removed at time  $t$ .
- $q_i(t - \tau)$ : infection probability. For the purpose of this work,  $\tau = 0$ . Probability that, when a node  $i$  is healthy at time  $t$ , becomes infected at time  $t+1$ .

In the SIR model, the Markovian equations reads as shown in Figure 2:

$$q_i(t - \tau) = 1 - \prod_{j=1}^N \left[ 1 - \beta \tilde{A}_{ij} p_j(t - \tau) \right]$$

$$p_i(t + 1) = p_i(t)(1 - \mu) + (1 - p_i(t) - q_i(t))q_i(t - \tau)$$

$$q_i(t + 1) = q_i(t) + \mu p_i(t) ,$$

Figure 2: Markovian equations for SIR model.

## Intercrop arrangements

Among the different intercrop arrangements shown in Figure 3, Rows and Random have been used in this work to simulate the evolution of the system.

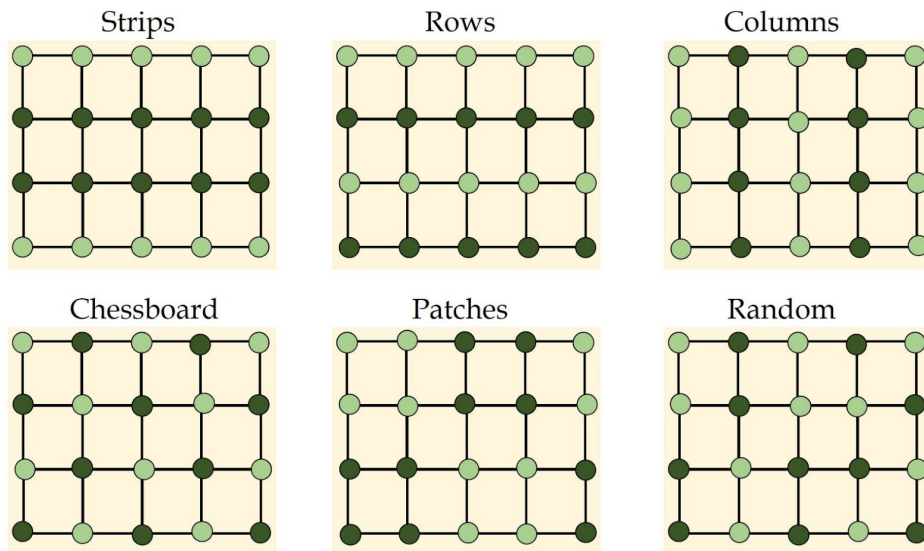


Figure 3: Different organizations of intercrops between two species.

Light green nodes represent the main crop and the dark green nodes represent the secondary crop, which is considered to be not susceptible to the disease spreading on the field, so its plants can not become infected ( $p_i = 0$  for every plant  $i$  that belongs to the secondary crop).

## Experiments

The rectangular plots have been shown - both theoretically and experimentally - to delay more the propagation of epidemics than square plots with the same area and density of plants.

For this work, every plot consists of 20 rows and 50 columns. To make the computation a little bit more efficient, the adjacency matrix has been previously computed for 20 rows and 50 columns and loaded to the program.

As can be seen in Figure 3:

- Rows arrangement: Rows of the main and secondary crops are alternated one-by-one.
- Random arrangement: Plants of the secondary crop are randomly inserted among those of the main crop.

There is always the same number of plants for the main crop than for the secondary one.

### Initialization of the Network

When the network is created, for each of the different arrangements:

- All the nodes of the main crop are set to Susceptible, except for one that is set to Infected and will be the one that starts the spread of the disease. For all of them, the initial probability of infection is set to 0.2.
- All the nodes of the secondary crop are set to Recovered/Removed with initial probability of infection 0. Notice that, as half of the nodes of the Networks are R, the simulations will not start with R value at 0 value.

The initial probability of becoming recovered/removed is set to 0.0 for all the nodes of the Network.

### Monte Carlo Simulation

We are interested in the calculation of  $R$ , the average fraction of Recovered/Removed nodes in the Network, for different values of  $\beta$  (infection probability of a Susceptible individual when it is contacted by an Infected one), from 0.00 to 1.00 (51 values; increases of 0.02).

Every simulation is done over many time steps. The average of  $R$  when the system has reached the stationary state is computed, and the Simulation is repeated many times to average over initial conditions and temporal evolutions.

The final value of  $R$  is an average (over repetitions) of averages (over time steps).

This simulation is done over different  $s$  (insect mobility) and  $\mu$  (spontaneous recovery probability) values.

## Results

For one single simulation the fraction of individuals Susceptible, Infected and Recovered/Removed every time step is shown in Figure 4:

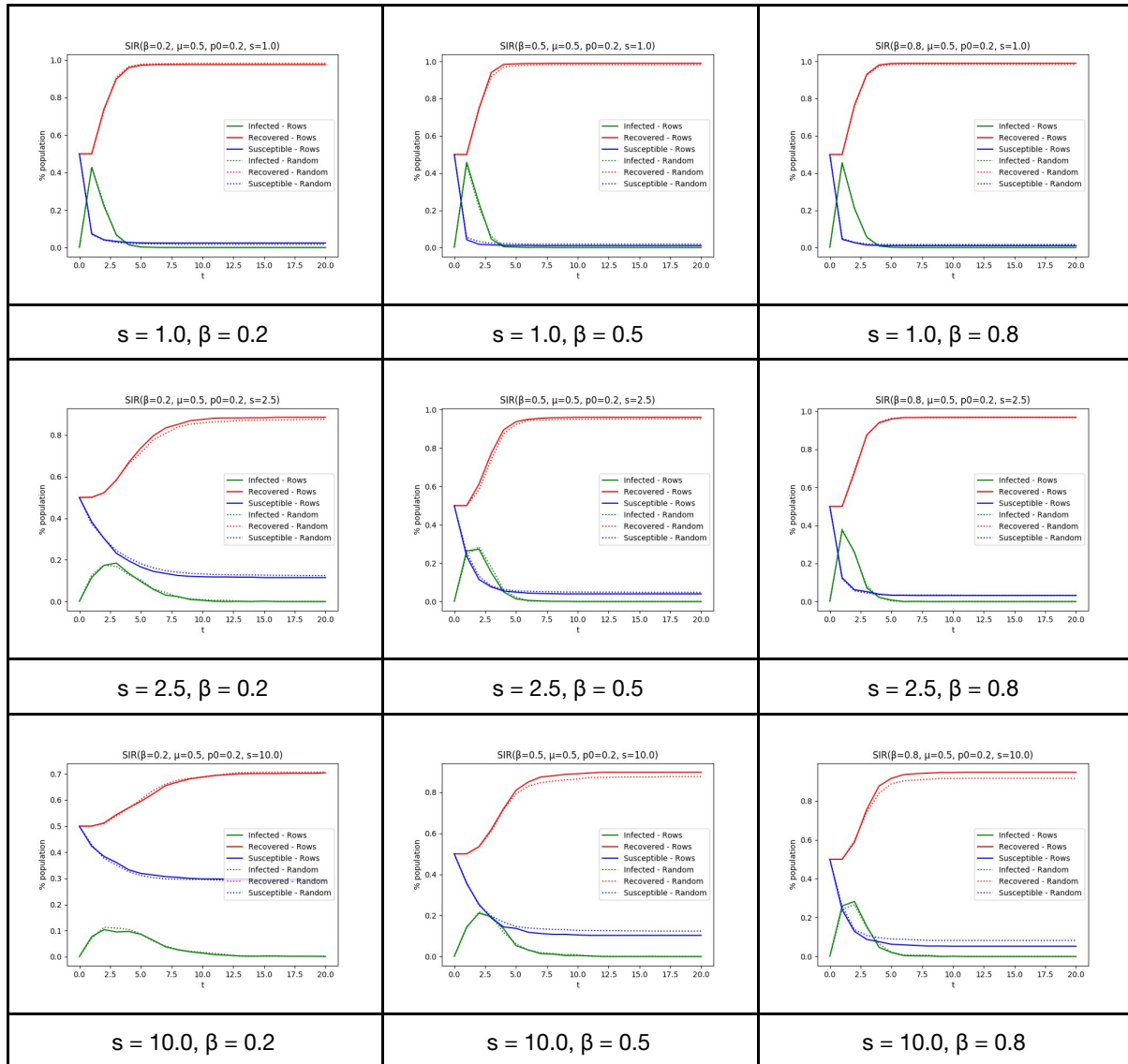


Figure 4: Evolution of the number of Susceptible, Infected and Recovered/Removed plants in a 20x50 plot for Rows and Random arrangements. The modeling is performed with different  $s$  and  $\beta$ , for a fixed  $\mu = 0.5$ .

As explained before, the initial fractions for  $S$  and  $R$  are 50%. At step 2 the infection has the higher value and, the higher the infection probability, the less steps lasts the infection and a higher number of individuals are infected (i.e. 30% for  $s = 10.0$  and  $\beta = 0.8$ ). Also less time it takes for the individuals to become Recovered/Removed.

The higher the mobility of the aphid, the higher fraction of infected individuals in the peak time (i.e. 40% for  $s = 2.5$  and  $\beta = 0.8$ , and 45% for  $s = 1.0$  and any  $\beta$ ) and the less time to become Recovered/Removed.



For the examples of  $\beta$  selected, almost no difference is found between the different arrangements of crops.

For the Monte Carlo simulation the fraction of Recovered/Removed for different infection probability ( $\beta$ ) is shown in Figure 5:

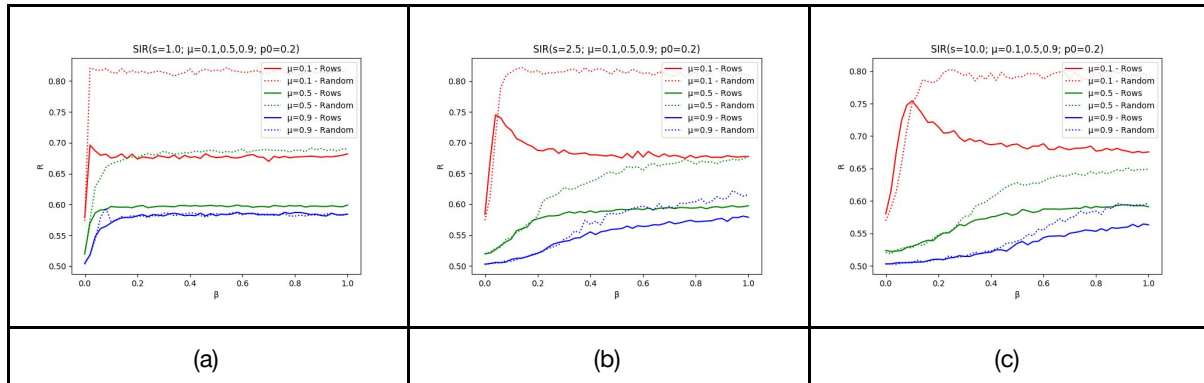


Figure 5: Relation of Recovered fraction of plants in a 20x50 plot, for Rows and Random arrangements and different  $\mu$ . The modeling is performed for (a)  $s = 1.0$ , (b)  $s = 2.5$  and (c)  $s = 10.0$

The plots show that the Random arrangement produces better Recovery/Remove results than the Rows arrangement for any of the combinations of mobility of the aphid ( $s$ ), spontaneous recovery ( $\mu$ ) and probability of infection ( $\beta$ ).

The lower the spontaneous recovery, the higher the recovery for any of the values of the infection probability, although for random arrangement that value is always increasing with infection probability, it's not the case for rows arrangement where the higher recovery fraction takes place for very low values of infection probability.

The higher the mobility of the aphid, the result for all the infection probabilities is the same; however, when the mobility is lower, a higher value of infection probability is needed to get higher fractions of recovery.

## Conclusions

Random arrangement seems to improve the recovery values for all of the combinations studied.

As experienced in personal garden projects, plots with different crops in a random arrangement (or, at least, not monocrop or in straight lines) helps auxiliar fauna to pollinize and prevent plant diseases as well as enrich the soil they are living in due to the nutrient interchange.

## Git Repository

In [https://github.com/ovalls/mai\\_cn](https://github.com/ovalls/mai_cn) you can find the code for this project (folder “project”) along with some other scripts, files and plots:

- `ComputeDistances.py`: script to compute the shortest path lengths between nodes of the Graph (20 rows x 50 columns).
- `distances_grill.csv`: CSV with the shortest path lengths between nodes of the Graph (20 rows x 50 columns).
- `SIRinTime.py`: script to generate the simulation to PLOT S,I,R fraction of population in time for ROWS/RANDOM arrangement.
- **`CN_Project_OlgaValls.py`**: Main program. Monte Carlo simulation to PLOT the Recovered fraction of nodes for each beta for ROWS/RANDOM arrangements.
- `PlotsExtra.py`: script to generate the plots for all simulations for each of the s values, from the project results.
- `Plots`: Folder with the different plots generated for this project.