



UNIVERSITÀ DEGLI STUDI DI TORINO

LABORATORY ON ADVANCED MODELING  
TECHNIQUES: MULTI-AGENT SYSTEMS

---

A Xylella diffusion MAS model

*Professors:*

Prof. Marco MAGGIORA

Dott. Marco DESTEFANIS

*Students:*

Elisa FASANELLI

Nicolò GOZZI

Sarah PERRONE

A.A. 2017-2018

---



# Contents

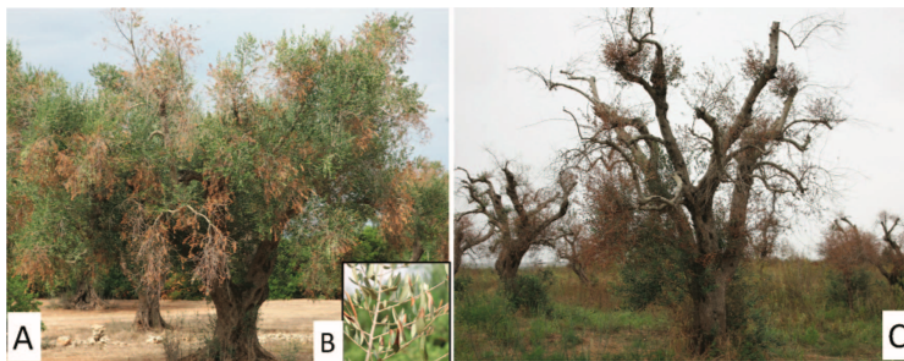
<b>Introduction</b>	<b>3</b>
<b>1 Model</b>	<b>5</b>
1.1 Province . . . . .	5
1.2 Xylella . . . . .	5
1.3 Olive . . . . .	7
1.4 Infection . . . . .	8
1.5 Movement . . . . .	10
1.6 Cut . . . . .	12
<b>2 Simulation</b>	<b>13</b>
<b>3 Results</b>	<b>15</b>
3.1 Epidemic Spreading . . . . .	15
3.2 Network Analysis . . . . .	18
<b>A Table of contents</b>	<b>23</b>
A.1 Additional contents . . . . .	29
<b>Bibliography</b>	<b>32</b>

# Introduction

*Xylella Fastidiosa* is a Gram-negative bacterium belonging to *Xylella* genus, that colonizes the xylem vessels of its host. It is known worldwide to be the responsible for the spreading of a plant disease with large impact on the economy of the countries where outbreaks take place. The impacts of the disease and their consequences led to the study of *Xylella Fastidiosa*'s genome and the publication of the complete sequence. It was the first genome of a plant pathogen to be completely published. In Europe it is a quarantine bacterium since 1992 [1], but the presence of this species was not confirmed until 2008, when olive groves in the Apulia region in South Italy, have started to be affected by the so called *Olive Quick Decline Syndrome* (QODS). Before the outbreak in Italy, *Xylella* was related to the Pierce's disease of grapevine in North America, the Citrus Variegated Chlorosis in Brazil and also Leaf Scorch in the south of United States. Furthermore, the bacterium has a wide range of host plants, some of which are asymptomatic.

One of the most reliable theory about the introduction of *Xylella* in Italy is that the bacterium was imported during commercial exchanges of infected and likely asymptomatic exotic plants. This and the presence of a suitable vector for the bacterium in Italy had led to one of the most dramatic plant diseases ever registered in Europe.

The biological studies so far, have shown that the vector responsible for the transmission of the bacterium is the Meadow Spittlebug (*Philaenus spumarius*), a cosmopolitan insect which takes its nourishment from the lymph of a wide range of plant species including olive trees. This insect, in its adult stage, is capable of hosting and spreading the *Xylella* during the feeding process. In particular, for what concerns the QODS, the introduction of the *Xylella Fastidiosa* in the lymphatic system of the olive trees causes occlusion of the vessels and water stress, both leading to disease's symptoms, such as leaf scorch, dieback of twigs and branches (see Figure 1).



**Fig. 1:** QODS symptoms in olive trees in South Apulia.

After ten years from the first detection of the bacterium in the south-western Apulia, the reasons why *Xylella* causes disease remain unknown, the list of vectors along with possible hosts is not complete and the human contribution in the spreading process is hard to determine. This fragmentary knowledge makes extremely difficult to develop an efficient cure against the proliferation of *Xylella* bacterium or against its vectors, so the strategies developed so far have as purpose to contain the disease by isolating the infected areas.

In this scenario, in 2013 the Italian authority defined two different areas: the infected area and the buffer zone. For each of them, the authority provided some phytosanitary rules for farm-owners and ordered the eradication of infected olive trees. Furthermore, this protocol introduced new and fastened pruning procedures that significantly affected the production of olive oil - Apulia provides the 40% of Italian oil production - and had a remarkable impact on the agricultural economy of the region.

In this work we used a Multi Agent System approach to replicate the spreading of the disease, by modeling the infection process that takes place when an infected insect feeds itself from an olive tree, and the cutting procedures that should turn the olive grove into an adverse environment for spittlebugs to live in.

In the next section we will explain our model framework and its structure: in particular we will focus on the agents and their most important behaviors. Then, there will be a section about the simulation building and settings where we will discuss the assumptions and approximations adopted. The last section of this report will be dedicated to the results of simulations.

# Chapter 1

## Model

We considered three species of agents: `province`, `olive` and `xylella`. In this section we describe agents' variables and behaviors as well as the rules that govern the interactions between agents.

### 1.1 Province

The `province` agent is designed to represent different provinces of Apulia. In our work, we considered only the southern part of the region, since it is the most infected by the *Xylella* bacterium. Then, we considered three `province` agents, representing the province of Brindisi, Lecce and Taranto. In particular, the `province` agent has been introduced mainly for technical reasons: it does not take part in the epidemic process, but it is the bound within swarms move and interact. It has the following variables:

- `rgb color`: the color of the agent in the experiment interface (gray by default);
- `string name`: the name of the Apulia province that the agent represents;
- `matrix<float> wind_direction_frequency`: a matrix of real numbers whose rows represent the frequency of wind directions in different seasons in that specific province (see Section 1.5).

### 1.2 Xylella

The `xylella` agent represents a swarm of *Philaenus Spumarius*, the species of insects that is considered as the main vector of the *Xylella* bacterium. It has the following variables:

- **rgb color**: the color of the agent in the experiment interface;
- **float radius**: the radius of the swarm. It is initialized at the beginning of the simulation and it remains fixed;
- **float perc\_infected**: percentage of infected insects in the swarm. Initially, if the agent is not infected, it is set at zero. When an interaction with an infected **olive** occurs, it is opportunely updated;
- **float perc\_sane**: percentage of sane insects in the swarm. It is updated whenever the percentage of infected changes;
- **float area**: the area covered by the swarm. Since we model the swarm as a circle it can be simply calculated given the radius;
- **geometry geom**: the geometry object (a circle) representing the swarm;
- **province current\_province**: the **province** agent in which it is currently located the swarm;
- **float density**: the density of insects (number per  $m^2$ ) in the swarm expressed as a percentage (with respect of the maximum value). It varies linearly with months with a maximum of 1.0 in June and a minimum of 0.3 in December. This approach is supported by empirical data [5].

The **xylella** agent has the following reflexes:

- **move**: it handles the movement of the swarm. In particular it is influenced by:
  1. **distance covered**: it is sampled at every cycle from a uniform distribution whose maximum value is the maximum distance that an agent can cover in one day;
  2. **heading**: we sample the heading of the movement from the wind direction distribution of the current season specified in the variable **wind\_direction\_frequency** of the agent **current\_province** of the swarm.
- **infects**: it handles the process of infection of olive groves. It triggers whenever the swarm overlaps an **olive** agent. In that case the infection evolves in two steps:
  1. it is evaluated a percentage of success of the process;

2. if the previous step succeeds is calculated the new fraction of infected of the `olive` agent (see Section 1.4).
- `update_density`: density changes every month and when it becomes higher it means that there are more insects that are born than ones that die. New offsprings are sane, so we have to update the percentage of sane in the swarm. We do this in the following way for `xylella` agent  $X$ :

$$X_{\%sane} = \frac{(X_{\%sane} + \eta - 1)}{\eta} \quad (1.1)$$

Where:

$$\eta = \frac{Density(t)}{Density(t-1)}. \quad (1.2)$$

Of course, also the variable `perc_infected` is opportunely updated.

### 1.3 Olive

The `olive` agent represents a real olive grove. Each agent is designed as a circle whose centroid and radius have been extracted from a shapefile [2] containing geographical information of agricultural areas. So, thanks to these detailed data, we know the exact position and the area covered by each olive grove in Apulia. The `olive` agent has the following variable:

- `float area`: the area covered by the olive grove;
- `rgb color`: the color of the olive grove;
- `float radius`: the radius of the grove. It simply calculated starting from the area and considering the grove as a circle;
- `geometry geom`: the geometry object (a circle) representing the grove;
- `float perc_infected`: percentage of infected insects in the grove. Initially it is set at zero. When an interaction with an infected `xylella` occurs, it is opportunely updated;
- `float perc_sane`: percentage of sane olive trees in the grove. It is updated whenever the percentage of infected changes;
- `bool checked`: it records if the agent has been already checked during the checking period;



- **float prob\_checking**: the probability of being checked during the checking period.

The **olive** agent has the following reflexes:

- **infects**: it handles the process of infection of swarms that pass over the grove. It is symmetric to the **infects** reflex of the **xylella** agent;
- **check\_date**: it handles the process of cutting down of infected groves. It triggers only after 2013, since massive controls have officially started after that year. In particular, during the days of April, October and December each **olive** agent is controlled with the probability **prob\_checking** (see Section 1.6).

## 1.4 Infection

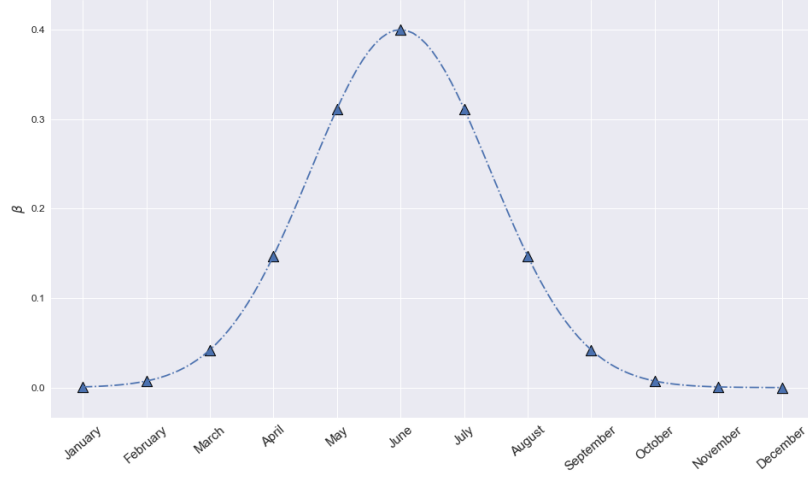
The aim of this work is to develop a model which is capable of reproducing effects the most like to those caused by the *Xylella* bacterium in southern provinces of Apulia. Thus, the process of infection is the most important for the model. We modeled infection as a one-to-one relationship, since **xylella** agents can infect **olive** agents as well as the opposite. In both cases, the process is triggered whenever an infected individual A overlaps an individual B of the other species: in other words, when exists an intersection I not null between the them. Then, it is calculated the probability of infection P as follows:

$$P = \beta \cdot A_{density} \cdot A_{infected} \cdot \left( \frac{A_{area}}{I_{area}} \right) \quad (1.3)$$

Where:

- $\beta \in [0, 1]$  is a number that represents the “infective power” of the bacterium. Since swarms feed on olive trees in the summer months when host grasses dry-out [3], this parameter varies from a minimum in December to a maximum in June (see Figure 1.1);
- $A_{density}$  is the density of A and it is considered only when a **xylella** infects an **olive**; otherwise, if an infected **olive** tries to infect a **xylella**, can be considered equal to 1;
- $A_{infected}$  is the percentage (between 0 and 1) of infected in individual A;
- $A_{area}$  is the covered by individual A;

- $I_{area}$  is the intersection area between individual A and individual B.



**Fig. 1.1:** Evolution of  $\beta$  throughout the year.

Basically, we followed a “mean field” approach, supposing a uniform distribution of infected inside the agent  $A$ . From this point of view,  $P$  is the probability of having a contact with an infected multiplied by the infective power factor. Thus, considering constant this factor, the infection is eased when individual  $A$  overlaps bigger portions of  $B$  or individual  $A$  is more infected (or even when the density of  $A$  is higher, in the case of a `xylella` infecting an `olive`). After the evaluation of this probability, the new percentage of infected for individual  $B$  is calculated as follows:

$$B_{\%infected} = B_{\%infected} + B_{\%sane} \cdot \left( \frac{I_{area}}{B_{area}} \right) \quad (1.4)$$

Where:

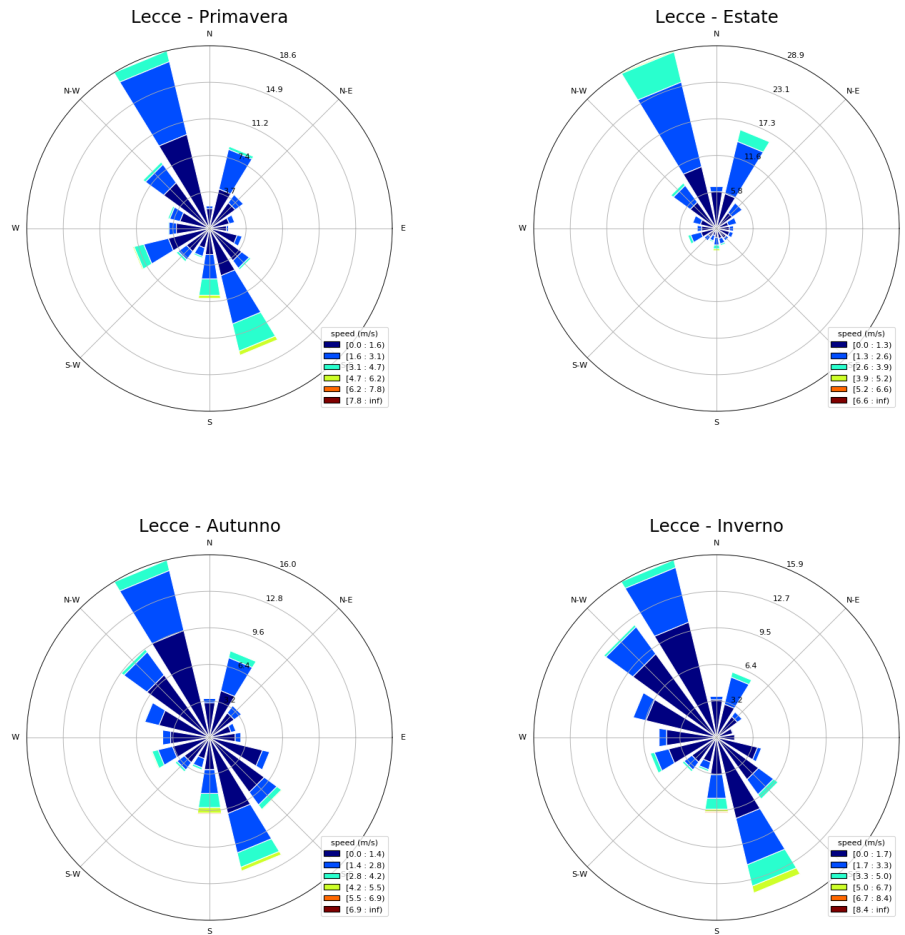
- $B_{\%infected}$  is the percentage of infected in individual  $B$  (before the update);
- $B_{\%sane}$  is the percentage of sane in individual  $B$  (before the update);
- $I_{area}$  is the area of the intersection between individual  $A$  and  $B$ ;
- $B_{area}$  is the area of individual  $B$ .

Again, this expression reflects a mean field approach, considering uniform the distribution of sane in individual  $B$ .

## 1.5 Movement

Empirically, swarms' movement is significantly influenced by wind. To reproduce this aspect, we analyzed real data [4] concerning the direction of wind in southern regions of Apulia from 2010 to 2018. What we derived through this analysis are the probability distributions of directions of wind in different provinces.

Since we observed small variations between results in different years, we decided to pool all data together distinguishing only by season. Thus, the results are four probability distributions - one for each season - for each province. In Figure 1.2 is summarized one of those distributions in a wind rose, a common tool used for visualization of this kind of data.



**Fig. 1.2:** Windrose statistic

In practice, at every step, the heading of the movement of each swarm is sampled from the probability distribution of directions related to the current province of the swarm and season.

For modeling reasons, we discretized possible directions in 16 cones of  $22.5^\circ$  of amplitude each. However, we observed that this approach alone ended up in all the swarms moving massively towards the most probable direction, causing high concentration of agents near the outer bounds of **province** agents, and low concentration inside. To prevent this, we introduced the possibility for the swarm to relocate randomly in any point of the map with 1% of probability. Through this approach we try also to include the possibility for the infection to travel between distant groves under the action of external factors, such as unintentional human vehicle movement.

## 1.6 Cut

The third key process of the simulation is cutting down part of the infected olive trees.

As stated in [10], the main weapon used against the spreading of *Xylella* in Apulia is the eradication of olive trees in seriously infected zones and an aggressive pruning in neighboring zones. According to available documents, this has started officially in 2013 when the “European Food Safety Authority (EFSA) published a statement on *Xylella* spreading and possible risk reduction options [1].

So far, there is scarcity of data related to the efficiency of the procedures carried out. Furthermore, since the activities of the inhabitants of the region significantly depend on olive trees, the European Commission’s decision to eradicate infected trees caused controversial reactions among landowners leading to a discrepancy between existing legislation and actual implementation. Thus, to reproduce these aspects, we implemented the global reflex `checking_date` that, starting from 2013, controls each `olive` agent during the three checking periods (April, October and December) and opportunely cut part of the infected trees. Furthermore, to take in account landowners’ non-compliance with legislation we associate each `olive` agent with a random probability of being subject to monitoring activities during checking periods. The `cut` action depends also on the province where `olive` agents are located. In particular, we wanted to replicate the increased rigidity of the phytosanitary rules imposed in the province of Lecce, the most infected zone in southern Apulia. For example an `olive` agent, namely *O*, will update its percentage of infected during checking period as follows:

$$O_{\%infected} = O_{\%infected} - O_{\%infected} \cdot r \quad (1.5)$$

Where:

- $O_{\%infected}$  represents the individual infection percentage;
- $r$  is a random variable sampled from  $U(0, 1)$  if it is located in the province of Lecce and from  $U(0, 0.5)$  if it is located in another province.

Since we are cutting down part of the trees we must update also the total area covered by the grove:

$$O_{area} = (1 - \alpha) \cdot O_{area} \quad (1.6)$$

where:

$$\alpha = 1 - (O_{\%sane} + O_{\%infected}) \quad (1.7)$$

## Chapter 2

# Simulation

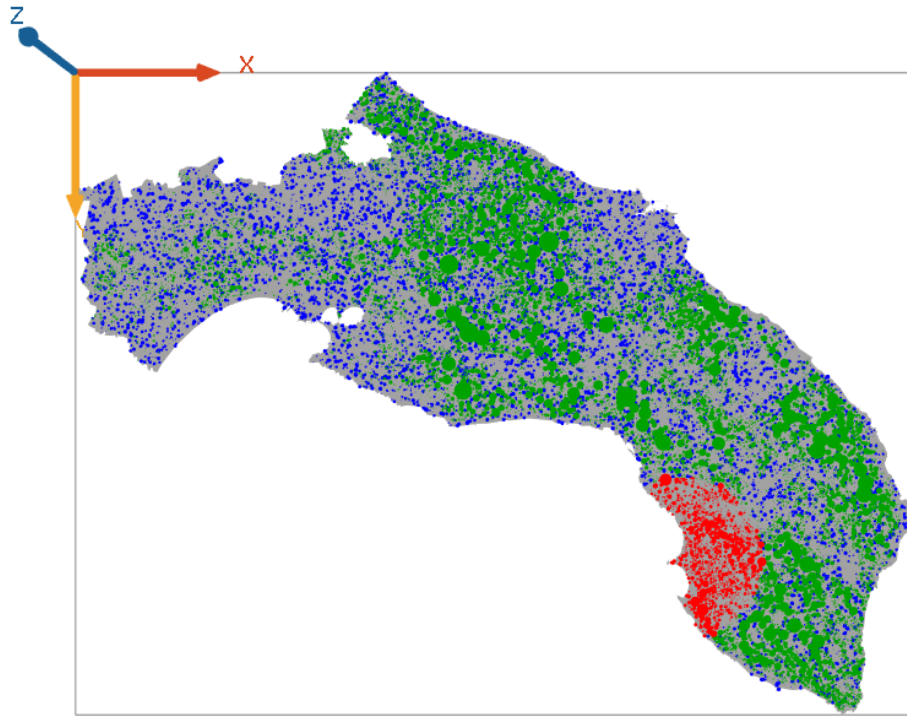
The simulation is governed by some parameters that must be given as input. Since these parameters significantly influence results we tried to derive them from empirical data to reproduce situations the most similar to the real world.

One of these parameters is the number of swarms. Available data suggest that meadow spittlebug feeds from a wide variety of plants species growing in Apulia and that, in general, its density - measured on agrarian area - can vary from 35 insects per  $m^2$  during the birth period, to a minimum of 10 insects per  $m^2$  registered during winter when insects die due to old age or due to lowering temperatures [5]. It is also known that offsprings are born without the bacterium in their system and become carrier only in the adult stage of their life cycle, when they feed on infected plants [9]. Starting from this, since agrarian area corresponds roughly to the 60% of the total Apulia area, we decided to group up insects in swarms so that their total area will be similar to the total agrarian area. This approach leads us to consider around 10,000 `xylella` agents.

Furthermore, to model the variation of insects' density, we assigned a density variable to the `xylella` agent. The monthly update of this variable represents both the birth and death of insects during the year.

The simulation is also significantly influenced by the distance covered daily by each swarm. From statistics reported in reference [6] we see that the maximum distance that can be covered by a single swarm is 100 meters. Then, we decided to distribute uniformly the distances covered between 0 and this maximum value. As suggested in reference [7], the epidemic spreading may have started in 2008. Because of this, we start the simulation in 01/01/2010 with a small fraction of agents already infected, and we let it run up to the end of 2014. However, as stated in the official resolution [10], we start the processes of checking and cutting down only in 2013.

Further studies [8], also shown that the epicenter of the epidemic spreading may be in a zone centered in Gallipoli with a radius of 15 kilometers. Then we start the epidemic process by infecting `xylella` and `olive` agents inside this zone.



**Fig. 2.1:** Display of the simulation: green circles represent sane `olive` agents, blue ones `xylella` agents and red ones both infected `olive` and `xylella` agents. At the beginning, all infected are located in a 15 km radius zone centered in Gallipoli.

## Chapter 3

# Results

In this section we present the results of simulations. All the data that we are going to represent are average values based on about 100 simulations. When necessary we report also their standard deviation to give an idea of the variability of results in different runs of the model.

We followed a double approach: on one hand, we look qualitatively at data, highlighting the effects of behaviors that we previously discussed; on the other hand, we carry out a more specific study using the tools of network analysis.

### 3.1 Epidemic Spreading

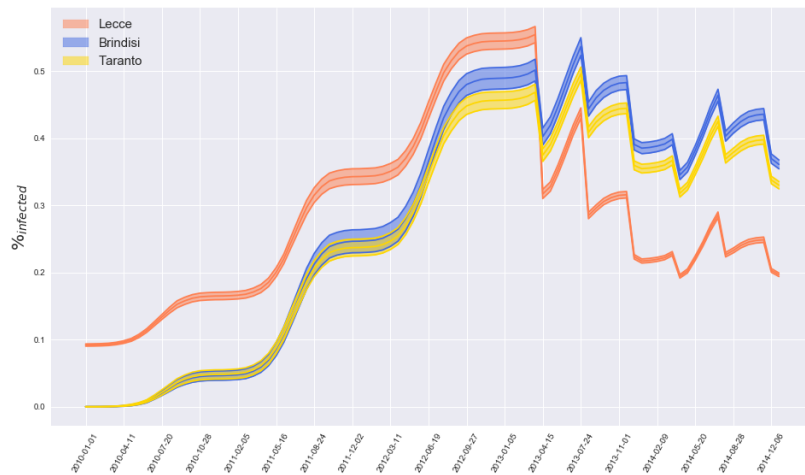
In this section we present the impact of the epidemic spreading between agents and we discuss whether we can consider our model “robust” enough.

In Figures 3.1 and 3.2 is represented the average percentage of infected among `olive` and `xylella` agents; in order to make easier the visualisation of critical aspects and the different results obtained with respect to different agents’ location, we plotted these percentages separately by province. In the plots the three solid lines represent the mean value calculated over all simulation and the shadowed bands represent the deviation from the reference value. The evolution of this percentage is quite similar for the two species. This is not trivial if one thinks that only `xylella` agents have the skills of moving. From the figure we can clearly see also periods during which the percentage of infected in swarms lowers because of a positive balance between births of non infected insects and deaths (in other words when the density grows).



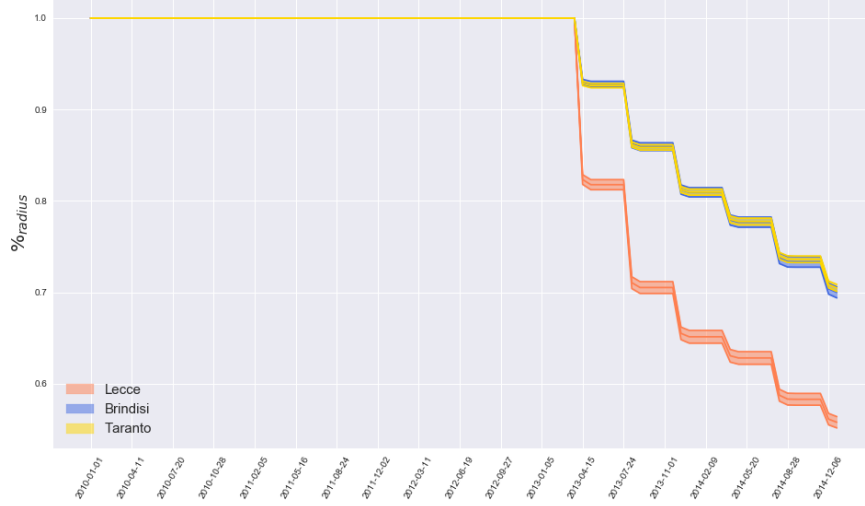


**Fig. 3.1:** Evolution of average percentage of infected *xylella* agents in the three provinces.



**Fig. 3.2:** Evolution of average percentage of infected *olive* agents in the three provinces.

On the other hand, the percentage of infected in groves has rush movement during checking periods, when infected trees are cut down. This process can also be seen looking at the evolution in time of the average radius of an grove in Figure 3.3.



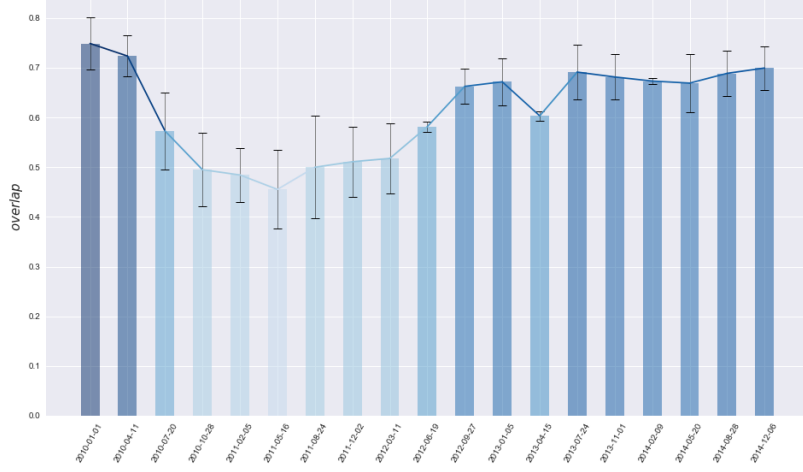
**Fig. 3.3:** Evolution of mean radius in different provinces normalized to initial value

Figures 3.2 and 3.3 represent the evolution of the most significant aspects of *olive*: the evolution of both percentage of infected agents and mean radius. Before the first cutting period, the percentage of infection is about 57% in Lecce province while its value in the other provinces is lower. As we may expect, Lecce is the province which is most affected by cut processes, where the mean radius of olive groves at the end of the simulation is almost the half of the initial one.

A robust model is one whose realizations are similar between them. In our case, a realization is identified by paths followed by the spreading of the bacterium. Thus, what we would like to be similar enough between different runs is the percentage of infected in different groves. First, we introduce the vector  $\vec{i}(t)$ , whose component  $i_j(t)$  is the percentage of infected in *olive* agent  $j$  at time  $t$ . Then, to quantify the similarity between two different realizations we use a version of the *Hellinger affinity* defined as:

$$\text{sim}(\vec{\delta}^I, \vec{\delta}^{II}) = \frac{\sum_j \sqrt{\delta_j^I \delta_j^{II}}}{\max(\sum_j \delta_j^I, \sum_j \delta_j^{II})} \quad (3.1)$$

Then, if two outbreaks are identical,  $\text{sim}(\vec{\delta}^I, \vec{\delta}^{II})$  will be equal to 1, otherwise it will be strictly lower. In Figure 3.4 we can see the evolution of  $\text{sim}(\vec{\delta}^I, \vec{\delta}^{II})$  in time.



**Fig. 3.4:** Evolution of similarity between different outbreaks in time.

In early cycles the overlap it is quite high. This is reasonable since olive groves are infected in a small region at the beginning of the simulation. Then, the overlap lowers significantly: this means that, initially, paths followed by the spreading are quite heterogeneous. On the other hand, already from June 2012 it returns to values around 70%, since, after a transient period, privileged epidemic pathways tend to emerge.

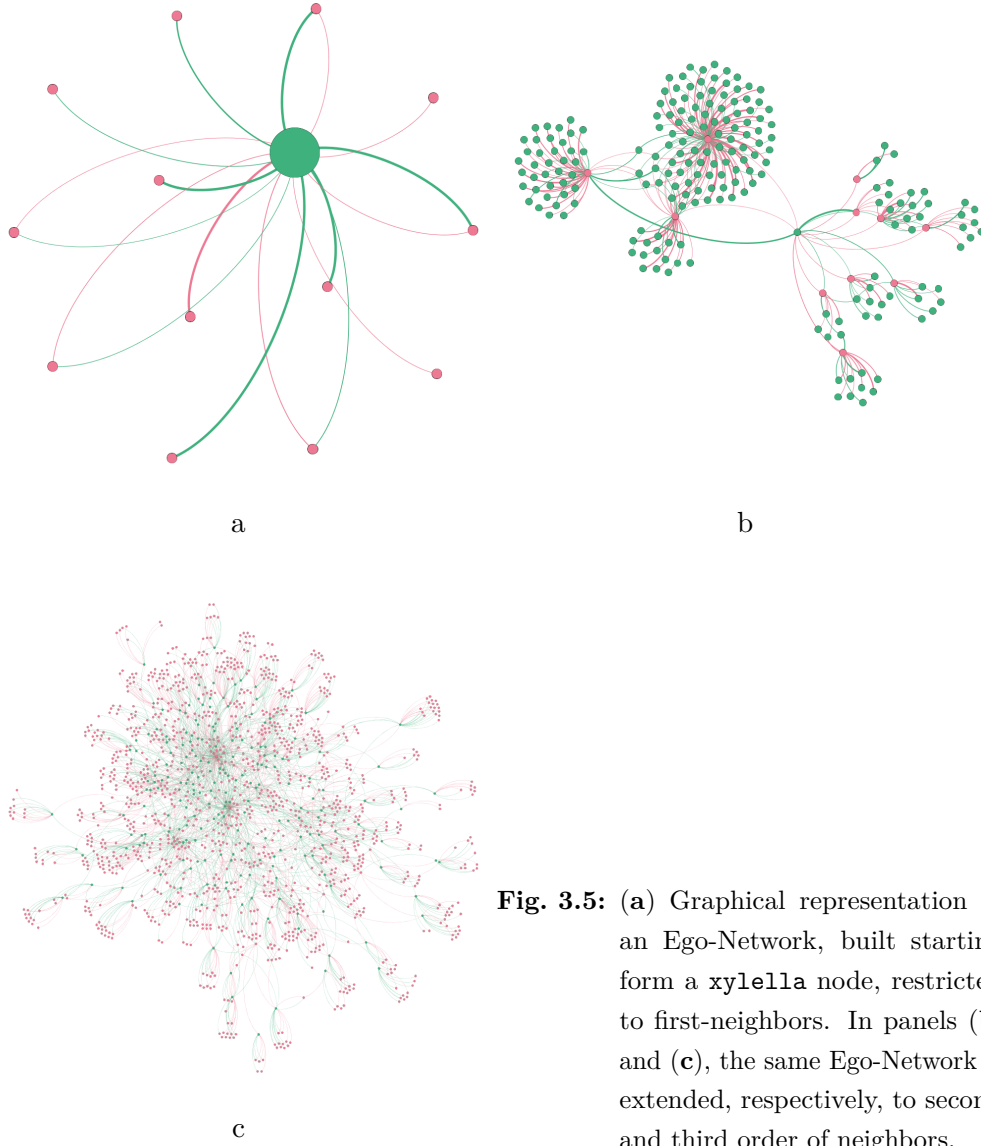
## 3.2 Network Analysis

In this section we analyse results from a network theory perspective. During last years this approach has gained a great success in science of complexity for the surprising simplicity of how it allows to inspect the underlying structure of complex systems.

Our network is built during the simulation: when an agent  $A$  infects an agent  $B$  we add a link from  $A$  to  $B$ . This simple rule gives the network a few peculiar characteristics:

- it is a directed network, since links have a direction associated;
- it is a weighted network, since links have weights represented by the new percentage of infected;
- it is a dynamic network, since links are added gradually;

- it is a bipartite network, since there can only be a link between agents of different species.



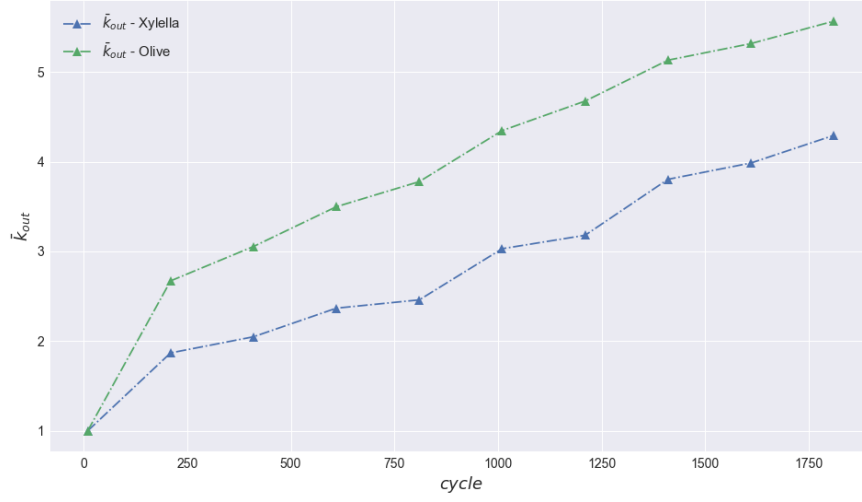
**Fig. 3.5:** (a) Graphical representation of an Ego-Network, built starting from a `xylella` node, restricted to first-neighbors. In panels (b) and (c), the same Ego-Network is extended, respectively, to second and third order of neighbors.

In the following table we report some characteristic network variables with respective values averaged over the whole simulation set.

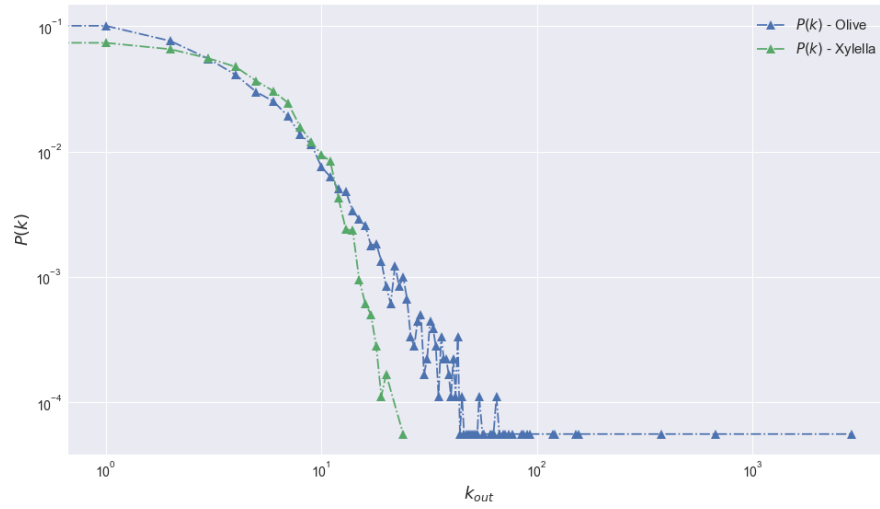
Variable	Mean value	Standard deviation
n. of nodes	17800	100
n. of link	71000	1500
mean degree	4	0.1
degree variance	450	70
max degree	2600	250

One of the most significant tools that can be used to understand how a network is structured is its degree distribution. Dealing with a directed network we must distinguish between in-degree, the number of links ingoing, and out-degree, the number of links outgoing of a node. Since the obtained network is bipartite, we decided to plot separately the out-degree distribution of `xylella` and `olive` nodes (see Fig. 3.7). These distributions show a typical scale free property and the maximum observable degree in the network reasonably grows in time. This means that the probability of having a node with a particularly high degree is non-negligible. These nodes are called “hubs” and are present in most of real networks. Their main effect is to reduce distances between two nodes in a network: in other words, having high connectivity vertices makes easier to find a “short” path. Thus, in an epidemic perspective, hubs play a crucial role in the spreading of the infection.

Surprisingly, at the end of the simulation period, `olive` nodes generally present higher out-degree than `xylella` nodes (see Fig. 3.6). This means that, after a transient period, the infection is mainly carried out by `olive` agents. This is supported by results presented in [7], where the authors, through a similar approach, conclude that the epidemic spreading is eased by the topology of the agricultural area.



**Fig. 3.6:** Average out-degree of olive and xylella nodes.



**Fig. 3.7:** Out-Degree distribution

From this perspective, a direct action on olive groves aimed to contain the infection seems extremely reasonable.

# Conclusions

The aim of this project was to model from an agent-based perspective the diffusion of *Xylella* in southern provinces of Apulia. Thanks to detailed information about agricultural areas and weather conditions, we managed in reproducing an environment the most similar to the real one. On the other hand, previous specific studies on the bacterium provided us with empirical data related to infective rate and its evolution throughout the year as well as information about the movement of main vectors.

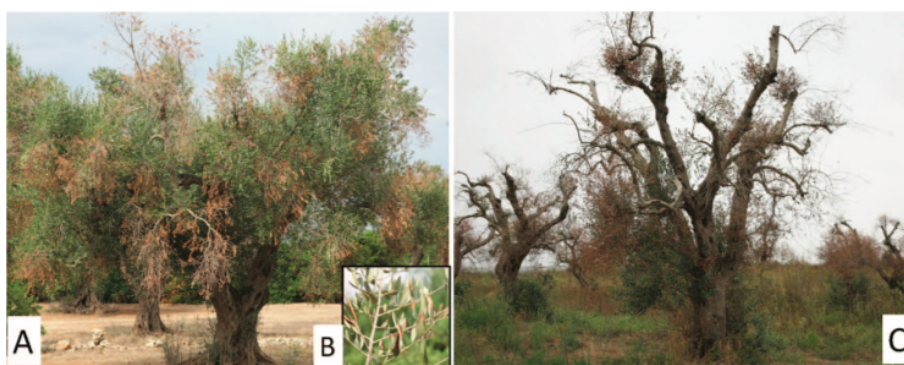
Results show how the simulation we built is robust and how multi-agent system approaches can play a crucial role in epidemic forecasting. We believe that similar tools can support authorities in confronting phytosanitary policies and in evaluating their possible consequences.

Furthermore, we have shown how additional modern modelling techniques like network analysis, can be used concurrently with the multi-agent system paradigm. This opens a new chapter in the epidemic spreading containment. Further studies, for example, may focus in trying to include information related to the network, like degree and betweenness centrality of olive groves, in the cut policies.

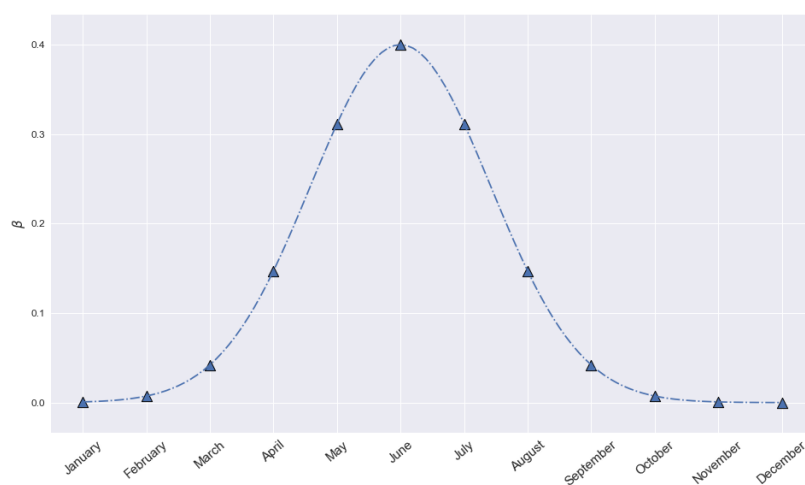
Another improvement to the model can be obtained through collection of data about the presence of other hosts for *Xylella* in Apulia region and on Italian agricultural area. In this way, the model could be more accurate and complete and the simulation can be extended to the province of Bari at first. We know that despite the extreme cutting procedures the epidemic is far away from be stopped or at least contained. In fact, in the early months of 2018 *Xylella* has been detected in Spain, France and Corsica. In this scenario becomes necessary to combine high quality data with scientific knowledge in order to develop complex and efficient strategies capable of predict and thus defeat the disease.

## Appendix A

### Table of contents

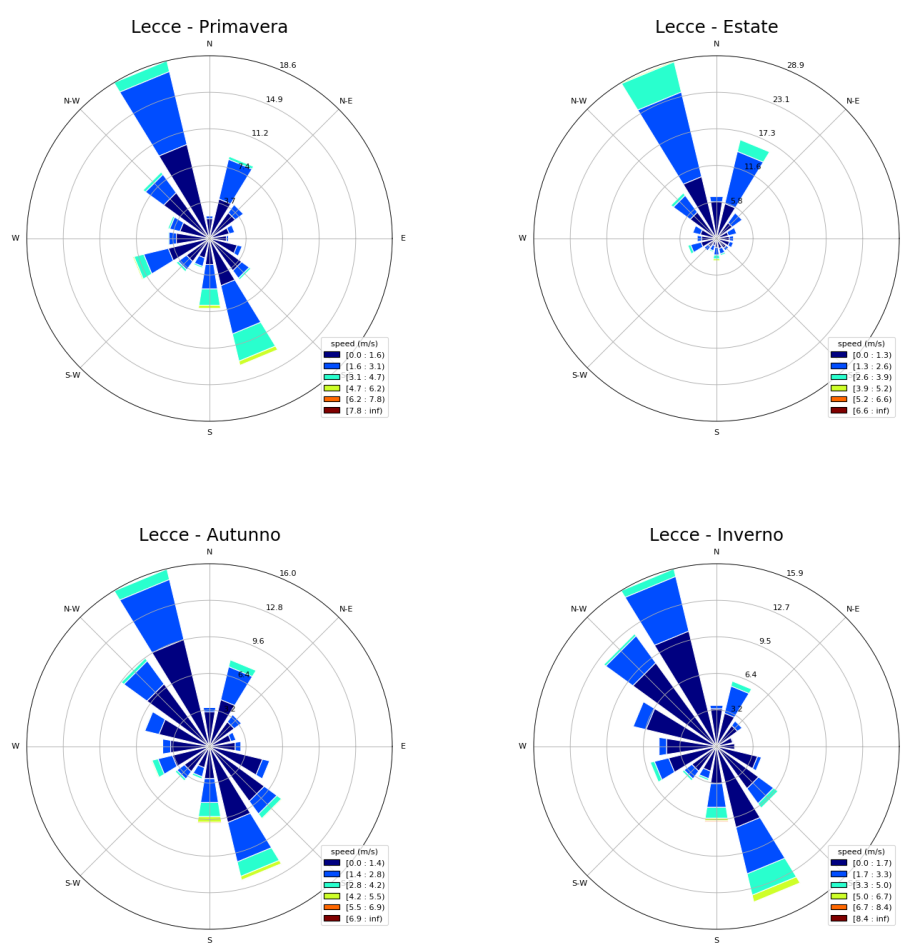


**Fig. A.1:** QODS symptoms in olive trees in South Apulia.

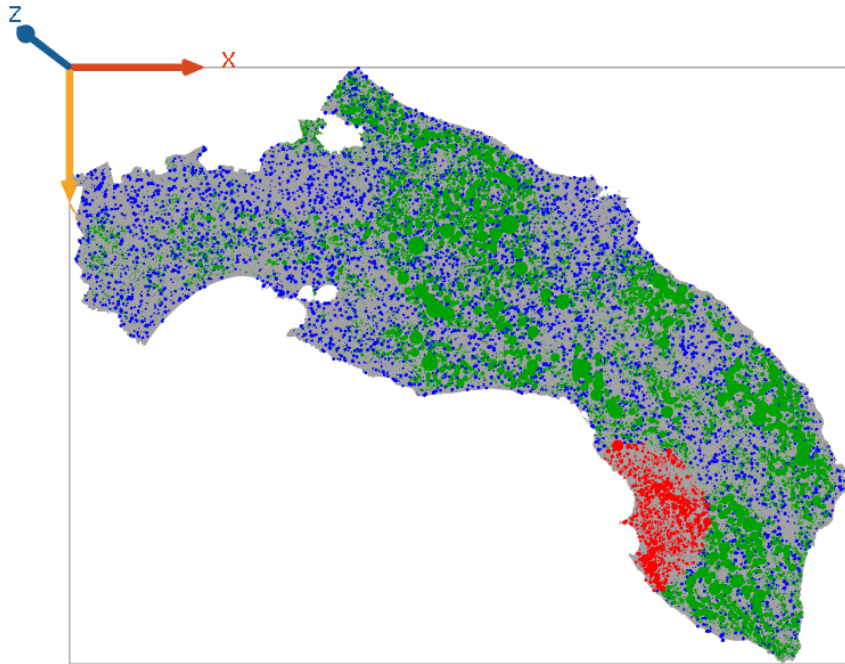


**Fig. A.2:** Evolution of  $\beta$  throughout the year.

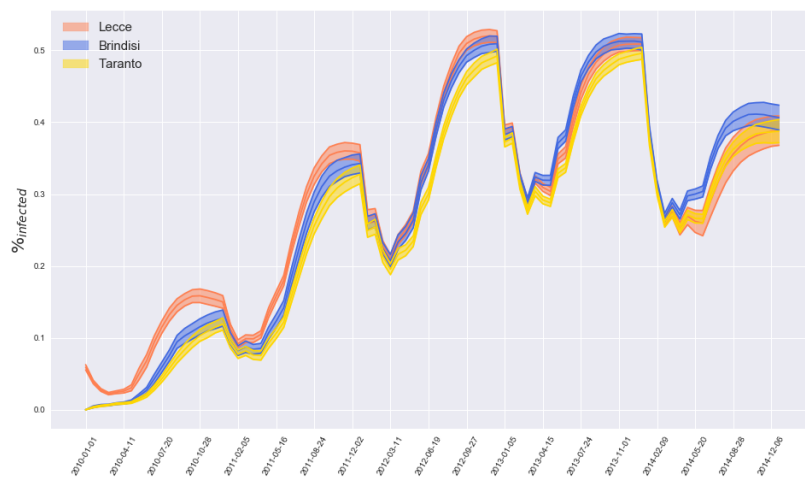




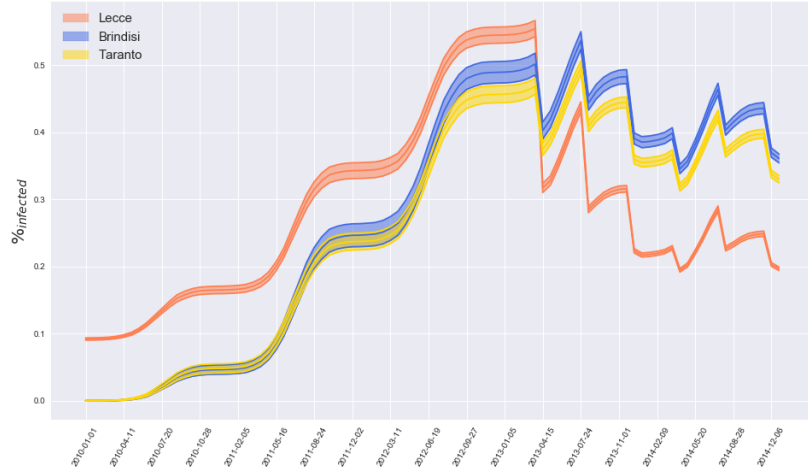
**Fig. A.3:** Windrose statistic in Lecce province



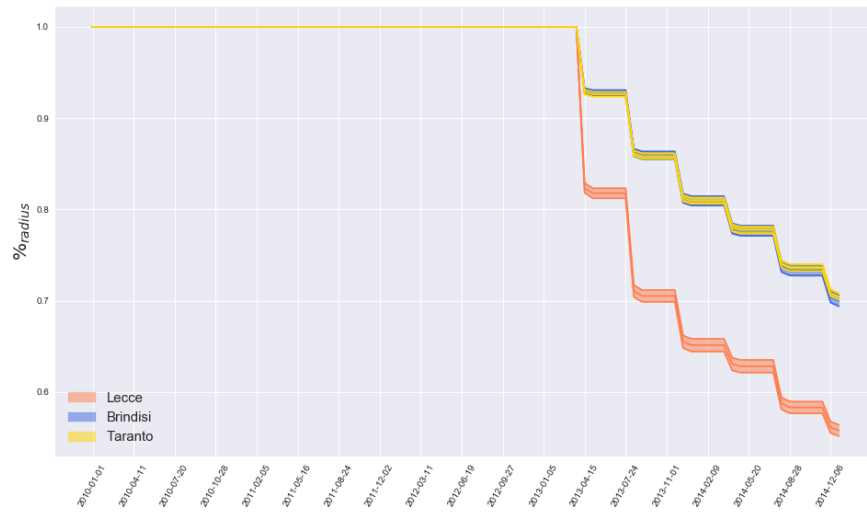
**Fig. A.4:** Display of the simulation: green circles represent sane olive agents, blue ones xylella agents and red ones both infected olive and xylella agents. At the beginning, all infected are located in a 15 km radius zone centered in Gallipoli.



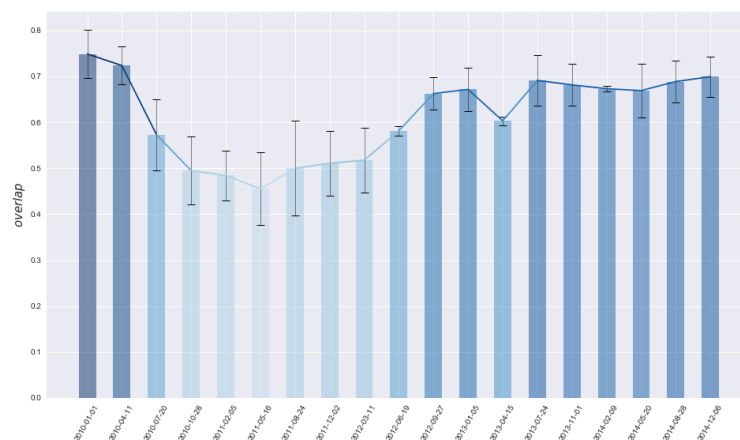
**Fig. A.5:** Evolution of average percentage of infected xylella agents in the three provinces.



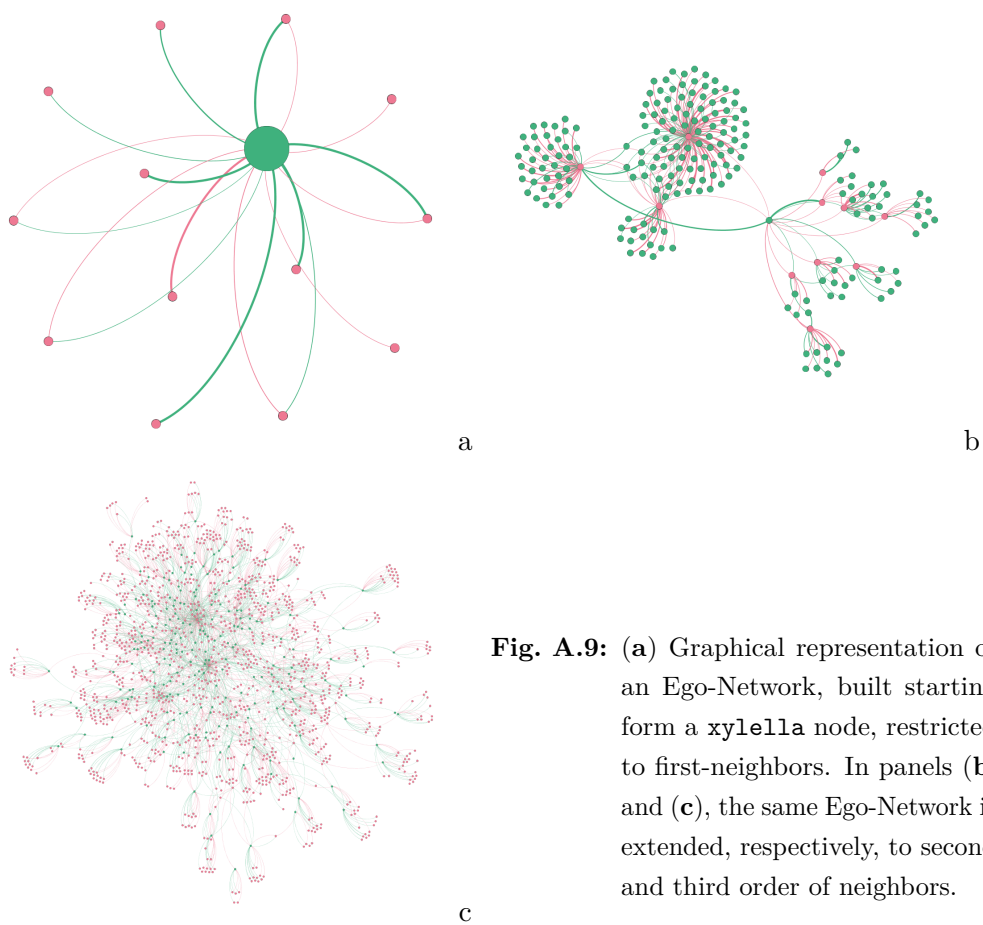
**Fig. A.6:** Evolution of average percentage of infected olive agents in the three provinces.



**Fig. A.7:** Evolution of mean radius in different provinces normalized to initial value



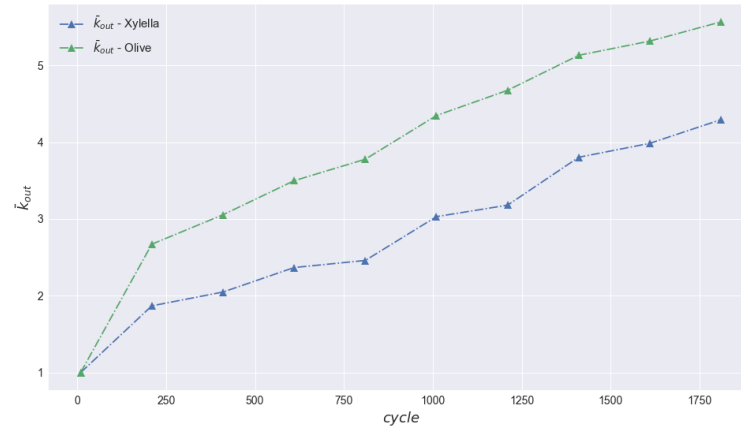
**Fig. A.8:** Evolution of similarity between different outbreaks in time.



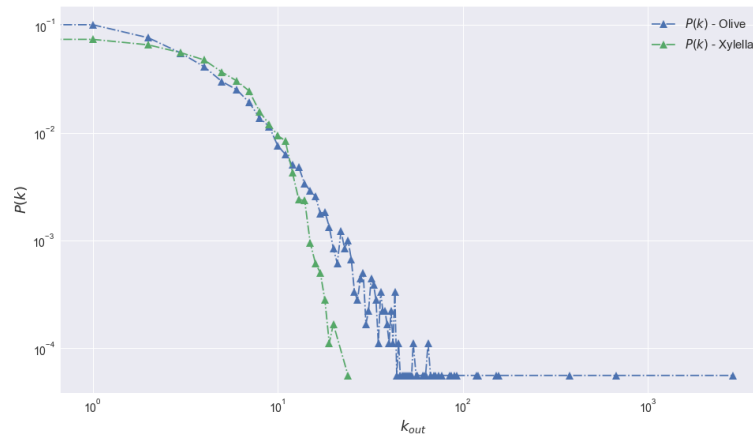
**Fig. A.9:** (a) Graphical representation of an Ego-Network, built starting from a *xylella* node, restricted to first-neighbors. In panels (b) and (c), the same Ego-Network is extended, respectively, to second and third order of neighbors.

Variable	Mean value	Standard deviation
n. of nodes	17800	100
n. of link	71000	1500
mean degree	4	0.1
degree variance	450	70
max degree	2600	250

**Table A.1:** Characteristic network variables.



**Fig. A.10:** Average out-degree of olive and xylella nodes.

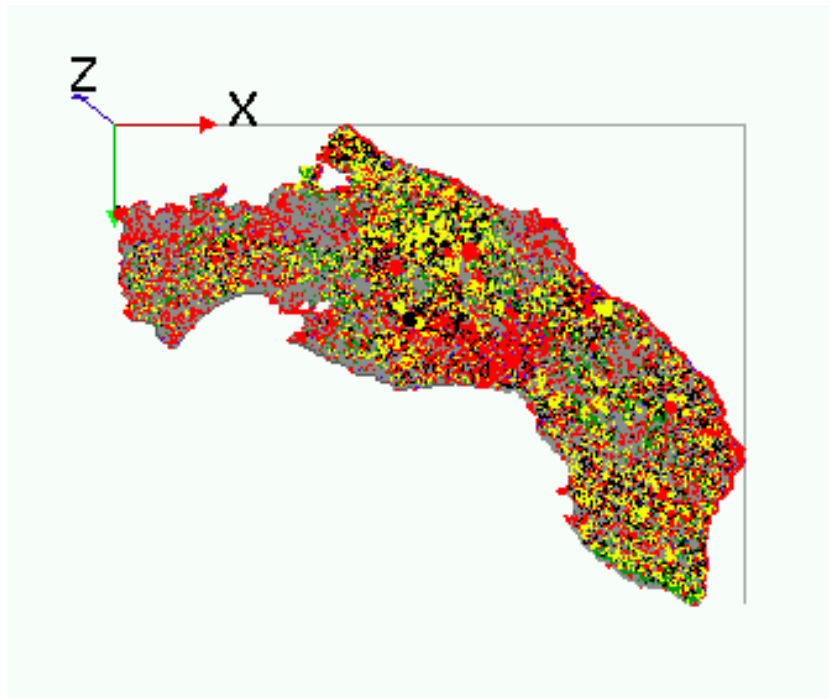


**Fig. A.11:** Out-Degree distribution

## A.1 Additional contents



**Fig. A.12:** Number of checked and cutted olive agents during simulation.



**Fig. A.13:** Display at the end of the simulation: green circles represent sane olive agents, blue ones xylella agents, red ones both infected olive and xylella agents. If an olive agent's infection percentage is between 30% and 60%, the agent is coloured in yellow; if this percentage is larger than 60%, the agent becomes black.

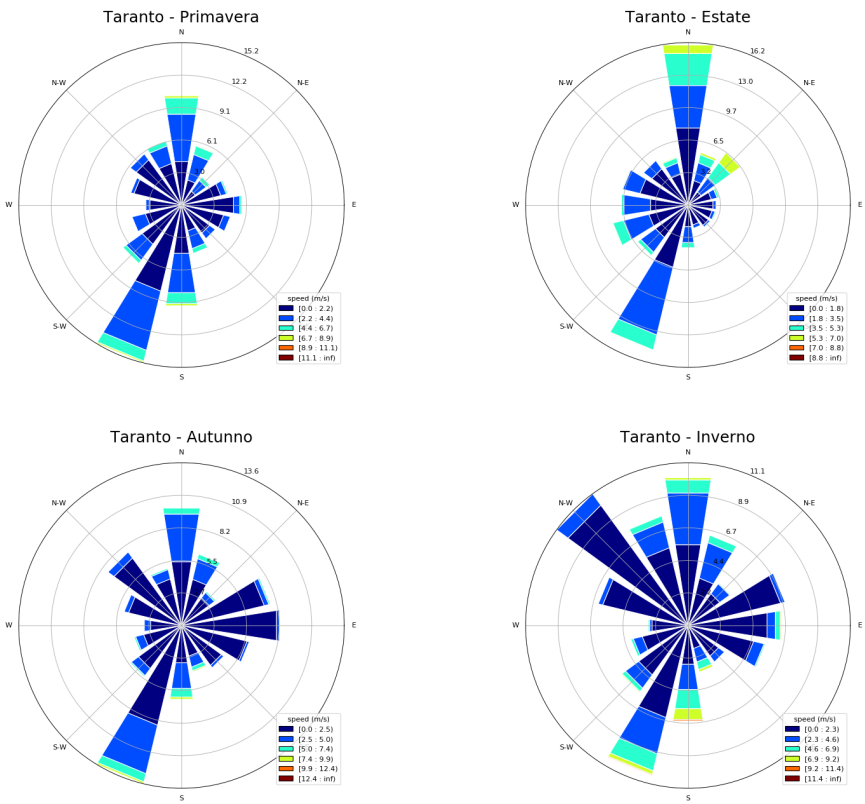


Fig. A.14: Windrose statistic in Taranto province

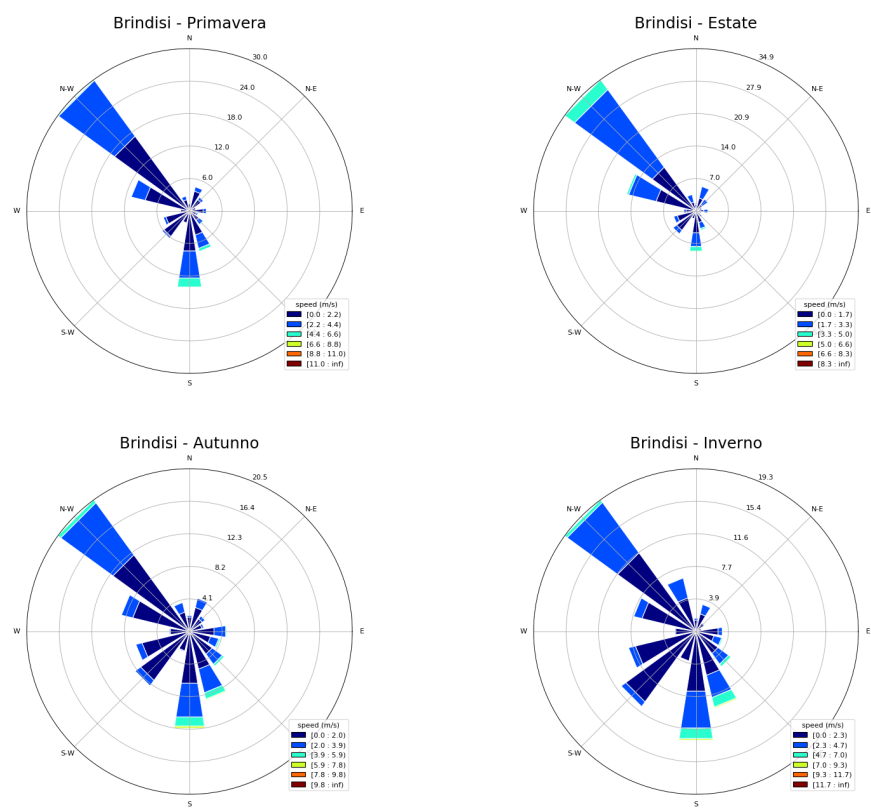


Fig. A.15: Windrose statistic in Brindisi province



# Bibliography

- [1] *Timeline of EU's actions against Xylella fastidiosa*, European Commission, Brussels, 17/12/2015.
- [2] *puglia.con - conoscenza condivisa per il governo del territorio*, URL: <http://www.sit.puglia.it/portal/portale>.
- [3] EFSA PLH Panel, *EFSA Panel on Plant Health* (2015).
- [4] Arpa Puglia, URL: <http://www.arpa.puglia.it/web/guest/serviziometeo>.
- [5] J. B. Whittaker, *Density Regulation in a Population of Philaenus spumarius (L.) (Homoptera: Cercopidae)*, Journal of Animal Ecology, 42, 1, 163-172 (1973).
- [6] S. S. Nilakhe; C. M. Buainain, *Observations on movement of spittlebug adults*, Pesquisa Agropecuária Brasileira, 23, 119-122 (1988).
- [7] G. Strona; c. J. Carstens; P. S. A. Back, *Network analysis reveals why Xylella fastidiosa will persist in Europe*, Scientific Reports, 7, 71 (2017).
- [8] M. Ciervo, *The olive quick decline syndrome (OQDS) diffusion in Apulia Region: an apparent contradiction according to the agricultural model*, Belgeo, 4 (2016).
- [9] M. Saponari; G. Loconsole; D. Cornara; R. K. Yokomi; A. De Stradis; D. Boscia; D. Bosco; G. P. Martelli; R. Krugner; F. Porcelli, *Infectivity and transmission of Xylella fastidiosa by Philaenus spumarius (Hemiptera: Aphrophoridae) in Apulia, Italy*, J Econ Entomol., 107, 4, 1316-9 (2014).
- [10] Delibera di Giunta della Regione Puglia n. 2023, *Misure di emergenza per la prevenzione, il controllo e l'eradicazione del batterio di quarantena X. fastidiosa associato al Complesso del disseccamento rapido dell'olivo* (29/10/2013).