A multigrid approximation to the expansion of *Xylella Fastidiosa* in almond trees

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Abstract: - Xylella fastidiosa (X.F.) is a plant pathogen that is transmitted exclusively by sap insects that feed on xylem fluid. This paper presents a theoretical grid-model to approach the expansion of this bacterium in almond trees orchards. The model is based on a multigrid approximation defined by both the environmental characteristics that have an impact on the status of the trees and the time which depicts their evolution. The trees can be healthy (S), exposed (E), infected (I) or dead (D). The dynamics of each grid is defined by a set of update rules which determine the value of the cells in a particular neighbourhood. The preliminary results of this work allow us to provide a relationship between the environmental characteristics and the status of the trees as time passes. This is useful to guide the decision making on the eradication policies.

Key-Words: - Xylella Fastidiosa, disease expansion, mathematical modelling, grid-model, neighbourhood, update rules

1 Introduction

Xylella fastidiosa (X.F.) is a plant pathogen that is transmitted exclusively by sap insects that feed on xylem fluid [1]. The most common transmitter vector for X.F. found in the Mediterranean countries is *Philaeus Spumarius*. The vectors move by jumping and making short flights, although they can also move passively if they enter a vehicle [2-4]. Nowadays there is no cure for this disease. The irruption of X.F. in Europe has turned on all the alarms. Italy, France and Spain are the most affected countries. The European eradication protocol is severe: if an isolated outbreak is identified, plants must be destroyed in 100 meters around and monitor 10 kilometers, although this distance has been reduced to 5 km away. If the infection is more widespread containment zones are implemented. Finally, the Organization for the Protection of European and Mediterranean Plants (OPEM) provides for strict controls and sampling to prevent infection [5, 6]. In Spain, as a result of the detection of the outbreaks in three regions of the province of Alicante, mobilizations of farmers and beekeepers have been organized, social and neighborhood movements have been born that, collectively, demonstrate against the European protocol that they believe excessive and little efficient since it is based on the preventive eradication of healthy trees for which it cannot be sufficiently accredited, with the current knowledge, that they will be infected in a certain time. In addition, the eradication is not being carried out completely due to the complicated orography of the most affected regions of Alicante. The protocol is then distorted because trees that are not cared in barren lands that are difficult to access are not cut, although they are very likely to be infected and, on the contrary, healthy trees on cultivated land with easy access are cut, since in the radius of 100 meters. The more than 35,000 almond trees that are calculated to be uprooted - one in four - will reduce the harvest by 140,000 kilos, which means losses close to one million euros. The technical difficulty of accessing all the trees together with the increasing opposition of a sector of the population that does not cooperate with the territorial authorities that coordinate and execute the European protocol can jeopardize the effectiveness of the eradication and, consequently, the satisfactory resolution of the problem.

Mathematical-computational modeling is a very valuable tool for decision making and the proper management of the protocols used to limit the damages caused by an epidemic. The most common model used in the expansion of contagious diseases follows the Susceptible-Infected-Recovered (SIR) model, by Kermack and McKendrick (1927), or some of its variants, such as Susceptible-Infected-Susceptible (SIS), Susceptible-Exposed-Infected-Recovered (SEIR) [7, 12]. Generally, these models are solved analitycally or numerically by systems of ordinary differential equations (ODE). However, this type of modeling has some shortcomings such as not taking into account the local interactions between the individuals that make up the population. In addition, differential equations assume that individuals are homogeneously distributed and all are connected to each other, therefore, it is difficult to access the individual dynamics of each of the elements of the system. These difficulties could be overcome by discrete models (based on agents or cellular automata) [13-16]. In this sense, modeling the state of the trees in an environment characterized by the distance between trees, the slope, the structure of the plots within a territory, isolated or not, would define usable guidelines for the design of actions tailored to specific scenarios, more acceptable to the owners of plots that right now harbor doubts and create obstacles. Our paper is divided in four sections. Following the introduction, Section 2 presents our Susceptible-Exposed-Infected-Dead (SEID) model, which is based on a variant of the well-known SIR model. Our frame uses a grid of size NxN. Each cell in the grid represents a tree. The contagion process will be modelled by means of a concrete connection pattern defined by both a particular neighbourhood which fixes the connection between trees through the vector flight, and a local rule which sets whether the contact vector/tree is infective or not. Then, we define the multigrid approach which pursues a complete characterization of a scenario. This approach incorporates a column of grids, one per environmental characteristic, and deals with the evolution of these grids as time passes. Section 3 discusses how the obtained results can help in decision making related to eradication measures. Finally Section 4 presents concluding remarks and future work.

2 Our Susceptible-Exposed-Infected-Dead (SEID) epidemic model

As mentioned in Section 1, generic epidemic models are very useful to deal with the dynamics of infectious diseases propagation. In this section, we present our SEID epidemic model to analyse the propagation of X.F. through the vector *'Philaeus Spumarius'*. This model divides the population of trees in four groups: S stands for susceptible trees, E for exposed trees, I for infected and D for dead.

2.1 Update rules

$$\begin{aligned} R:\{0,1\}\times\{0,1\} &\to \{0,1\} \\ (x,y) &\to R(x,y)=a_i \end{aligned} \tag{1}$$

Without loss of generality we can set $R(0, 0) = a_3$, $R(1, 0) = a_2$, $R(0, 1) = a_1$ and $R(1, 1) = a_0$

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We can define $2^4 = 16$ different local rules.

If $M = a_3\, a_2\, a_1\, a_0$, M is the four bits representation of an entire $m \in [0, 2^4-1] \subset N$.

Let R_m denote a particular rule. As an example, if we consider m = 7, we have M = 0111, so the values for R_7 are a_3=0; a_2 =1; a_1=1 and a_0=1 so, for this case, R_7 (0, 0) = 0, R_7 (1, 0) = 1, R_7 (0, 1) = 1 and R_7(1, 1) = 1.

Both the local rule and the particular neighbourhood define the dynamics of any infectious disease expansion in populations represented by a grid. When an infected cell (value = 1) contacts with susceptible neighbour cells (value = 0), these cells become infected and can infect other neighbour cells, R_7 (1, 0) = 1. Different particular situations can be modelled by means of different rules R_m.

We can define 2^4 =16 different local rules depending on the values of the sequence a_3 a_2 a_1 a_0.

Let R_m denote a particular rule, m $\in$ [0, 2^4-1]. The binary representation of m is: m = a_3 a_2 a_1 a_0.

In order to model the dynamics of SEID, we assume:

R(1, 0) = a_2 = 1, the infective insect infects a healthy tree. (“1” = infected and “0” = healthy).

R(1, 1) = a_0 = 1, the infective insect has no effect on an infected tree.

R(0, 1) = a_1 = 1, the healthy insect that feeds on an infected tree has no effect on the infected tree but it becomes infective and increases the population of infective insects.

R(0, 0) = a_3 = 0, the healthy insect that feeds on a healthy tree has no effect on the healthy tree.

So, the suitable local rule for this case is R_7.

We also use colours to discern between Susceptible and Exposed:

Cells (trees): yellow for Susceptible, grey for Exposed

Number (generation): red for Infected tree and black for Dead.

2.2 Neighbourhood

The neighbourhood points out the cells that will update by means of the local rule when an infected cell appears. In a N x N grid, we define L-neighbourhood which consists on moving two squares horizontally then one square vertically, or moving one square horizontally then two squares vertically. This neighbourhood is different from well-known Von Neumann (4-neighbours) or Moore (8-neighbours) that contact by the four sides or the four sides and the four vertex, respectively, see Fig.1. In the ANNEX. The fastest propagation is carried out by L-neighbourhood and the slowest is for Von Neumann neighbourhood, see previous work [13-16].

Table 1. A qualitative estimation of the impact of some environmental characteristics on the delays

Delays **Environmental characteristics**	Δ_{SE}	Δ_{EI}	Δ_{ID}
1- Distance between the trees	Low (I)	Low (I)	Low (I)
2- Gaps between lands + direction of the wind	High (III)	High (III)	Low (I)
3- Isolation of the plots	Average (II)	High (III)	Low (I)
4- Varietal susceptibility of the tree	High (III)	High (III)	Average (II)
5- Care level of the trees	Average (II)	Average (II)	Average (II)
6- Temperature	High (III)	High (III)	Average (III)

The application of an update rule on the grid consists of starting in an infected tree (centre) and following the expansion from the centre to the neighbours at the rate of one step per generation (generation = generic unit to measure the delays). The delays between Susceptible and Exposed (Δ_{SE}), Exposed and Infected (Δ_{EI}) and Infected and Dead (Δ_{ID}) are variable parameters depending on the environment characteristics such as the climate, the distance between trees, the gaps between lands, the isolation of the plots and whether the plot is cultivated or abandoned. In Table 1 we represent a qualitative estimation of the impact of the environmental characteristics on the delays Δ_{SE}, Δ_{EI} and Δ_{ID}.

Temperature has a high impact on proliferation of XF population. It is rare between -1.1 and 1.7 ºC. It is occasional between 1.7 and 4.2 ºC and severe for temperatures higher than 4.2 ºC. Nevertheless, for high temperatures proliferation is rare again as for very low temperatures. Mediterranean Basin is then suitable for the propagation of XF. The care the trees receive from the farmers makes them relatively resistant to infection. The varietal susceptibility is a good issue to avoid trees infection and to decrease deaths if infection occurs. Sloping terrain can be an inconvenience for the propagation of XF, except in the case of a wind that blows in favor and helps the insect reach the tree. The distance between the trees does not represent a crucial variable since this distance does not have an extended range of variation. When considering the delays, we observe Δ_{SE} has a strong dependence on varietal susceptibility and temperature. For Δ_{EI} the strong dependence is not only on varietal susceptibility and temperature but also on isolation of plots and direction of the wind. Finally, for Δ_{ID} the dependences are always low, since an infected tree will end up dying with an almost total probability regardless of any environmental characteristic. Only the varietal susceptibility together with the care level and temperature can cause a greater dependence. The estimation of the values of the delays can be set in Table 2, as follows:

Table 2. Estimation of the values of the delays (in generations) in the case of small, medium and high impact characteristics

Delays **Impact**	Δ_{SE}	Δ_{EI}	Δ_{ID}
high	0, 1, 2	1, 2, 3	1, 2, 3
medium	0, 1	1, 2	1, 2
small	0	1	1

In our framework, the delays corresponding to low impact characteristics are only assigned a value. When we consider medium impact, we assume two possible values, and finally for high impact we assume three values. More, the values are not the same for the different delays. As an example, Δ_{SE} can achieve the value 0 because the Susceptible immediately become Exposed, when an infected tree appears. The range of possible values could increase in a more fine-grained description.

2.3 The multi-grid approach

The multigrid approach pursues a complete characterization of a scenario. We consider a column of grids (one for each environmental characteristic, see Table 1). Each grid has its own neighbourhood, its own values for the delays and its own update rule. The entire scenario ***S*** is the result of processing all the grids in each column as time passes. Let's have

$$\boldsymbol{S} = \begin{pmatrix} G10 & \cdots & G1k \\ \vdots & \ddots & \vdots \\ Gq0 & \cdots & Gqk \end{pmatrix} = (\, \boldsymbol{S_0}\, \boldsymbol{S_1} \ldots\ldots \boldsymbol{S_k})$$

where the rows model q different superposed characteristics, and the columns stand for the temporal evolution of these processes (k + 1 generations).

Since the environmental characteristics contribute to cause a global result on each cell (tree), we can compute the status of the trees by calculating the average of the values of the same cell (tree) in all the grids of the same column. To have a numerical estimate, we assume the following values:

S = 0; E = 0.5; I = 0.8; D = 1.

Let's have $\boldsymbol{S_i}$ $(0 \le i \le k)$, the scenario at the i^{th} generation, the mean value of a cell is:

$$c_{v,w} \quad \frac{\sum_{j=1}^{j=q} c_{vj\ wj}}{q} \qquad \text{Eq (1)}$$

$0 \le v \le N$ and $0 \le w \le N$

A final state is assigned to cell $c_{v,w}$ according to its value:

$$\begin{array}{lll} 0 \le c_{v,w} < 0.5 & \text{for S} & \\ 0.5 \le c_{v,w} < 0.8 & \text{for E} & \text{Eq. (2)} \\ 0.8 \le c_{v,w} < 1 & \text{for I} & \\ c_{v,w} = 1 & \text{for D} & \end{array}$$

So, the whole evolution of S, E, I and D can be represented for a particular scenario ***S***. As an example, we consider the environmental characteristics nº 5 and 6, for a grid of size 10 x 10 = 100 trees and we represent the evolution of *S*, taking only into account these two environmental characteristic. We assume the connection pattern is (R_7,"L"). See Fig.2a-b-c in the ANNEX.

The rest of the environmental characteristics should be represented in the same way. Then, the whole representation is carried out by means of the average of all the measures for S, E I and D. This allows having a numerical estimate of each cell (tree)

3 Discussion

As shown in Fig. 3a-b the evolutions are quite different for different the environmental characteristics, such as temperature and level of care of the trees that have been modelled. The overall evolution is not represented since it is the same as that of the level of care for dead trees. The same happens in the case of infected trees. We observe that the number of dead trees would be about 80% at generation nº 5 due to the mild temperature that favors a strong infection process, but a high level of care provides a valuable protection to the trees that would finally die (80%) at generation nº 12. The same occurs for infected trees: the high level care of the trees delays the infection of 3 generations. Although this model only provides few conclusions, these seem to be going in the right direction. Following this guide, it seems to be reasonable to cut the trees around the infected tree, but only when they are in the Exposed status. So, when the epidemic is fast, it is not easy to have time to eradicate it, and the protection effect is not assured,

so under these conditions, eradication could be useless.
Despite these encouraging results, a deeper study is needed to cope with all the parameters of the model in order to avoid too optimistic forecasts.

4 Conclusion

This work presents a preliminary approach to the expansion of XF in the almond trees in the orchards of the province of Alicante (Spain). This case is different from the well-known case of olive trees in southern Italy that is why our model incorporates six environmental characteristics, such as the distance between the trees, the orography (gaps between lands which are modulated by the direction of the wind in what refers to the vector flight), the isolation of the plots, the varietal susceptibility of the tree, the care level of the trees and the temperature. These characteristics are assigned a value according to their importance in a determined scenario. A grid-based model implements the environmental characteristics and applies an update rule to predict the evolution of the neighbour trees that exhibit four different status: healthy, exposed, infected and dead. Our results seem to go in the correct direction despite only two of six characteristics have been taken into account. The model must be improved. As future work we plan to develop a systematic experimentation with all the characteristics, and consider other types of calculation for the status of the trees instead of calculating the average of the values. Finally, we plan to compare our results with the official data in order to propose alternative measures to the current ones.

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ANNEX

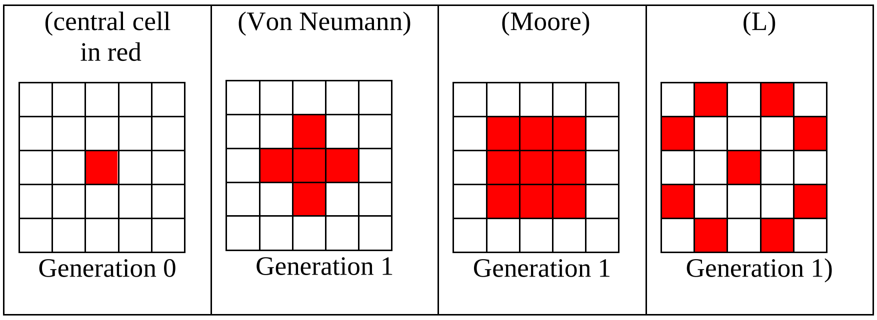
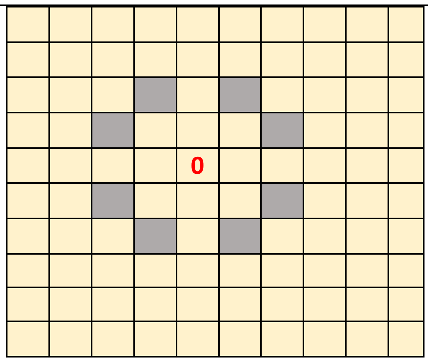


Fig. 1. The propagation in three types of connectivity: Von Neumann, Moore and L neighbourhoods, represented in a 5x5 grid.

- Grid nº 6: Temperature.

Mild temperature favours the propagation of Xylella, so $\Delta_{SE} = 0$, $\Delta_{EI} = 1$, $\Delta_{ID} = 1$. The three delays are assigned the minimal values because the infective process is fast.



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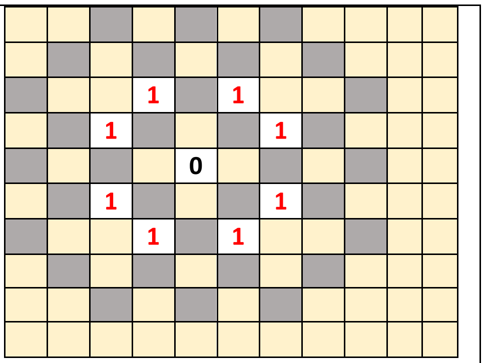
Generation 0
1 Infected tree (centre), 8 exposed trees, 91 susceptible trees



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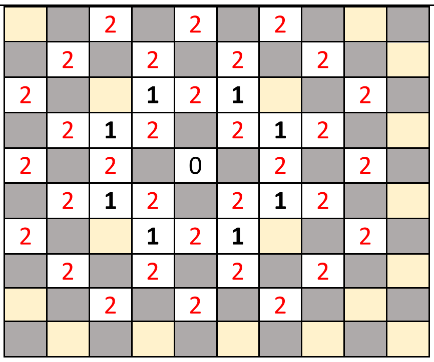
Generation 1
1 dead tree, 8 new infected, 32 exposed, 59 susceptible trees



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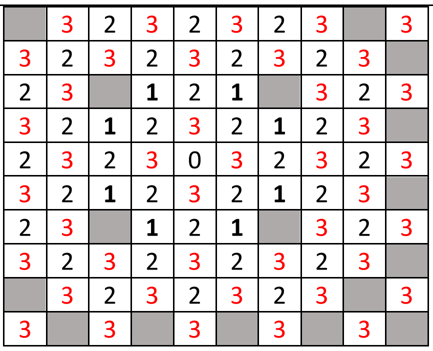
Generation 2
9 dead, 32 new infected, 42 exposed and 17 susceptible



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3	2	**1**	2	3	2	**1**	2	3	▨
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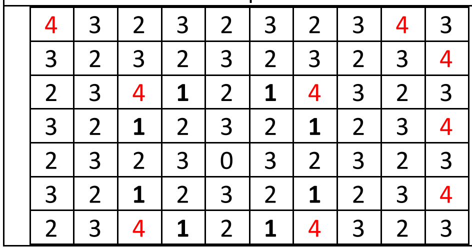
Generation 3
41 dead, 42 new infected, 17 exposed



4	3	2	3	2	3	2	3	4	3
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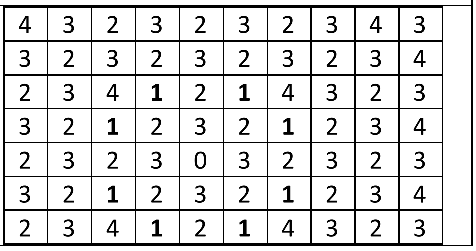
2	3	4	**1**	2	**1**	4	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3



4	3	2	3	2	3	2	3	4	3
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2	3	4	**1**	2	**1**	4	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3

3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
3	4	3	4	3	4	3	4	3	4

Generation 4
84 dead, 16 new infected

3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
3	4	3	4	3	4	3	4	3	4

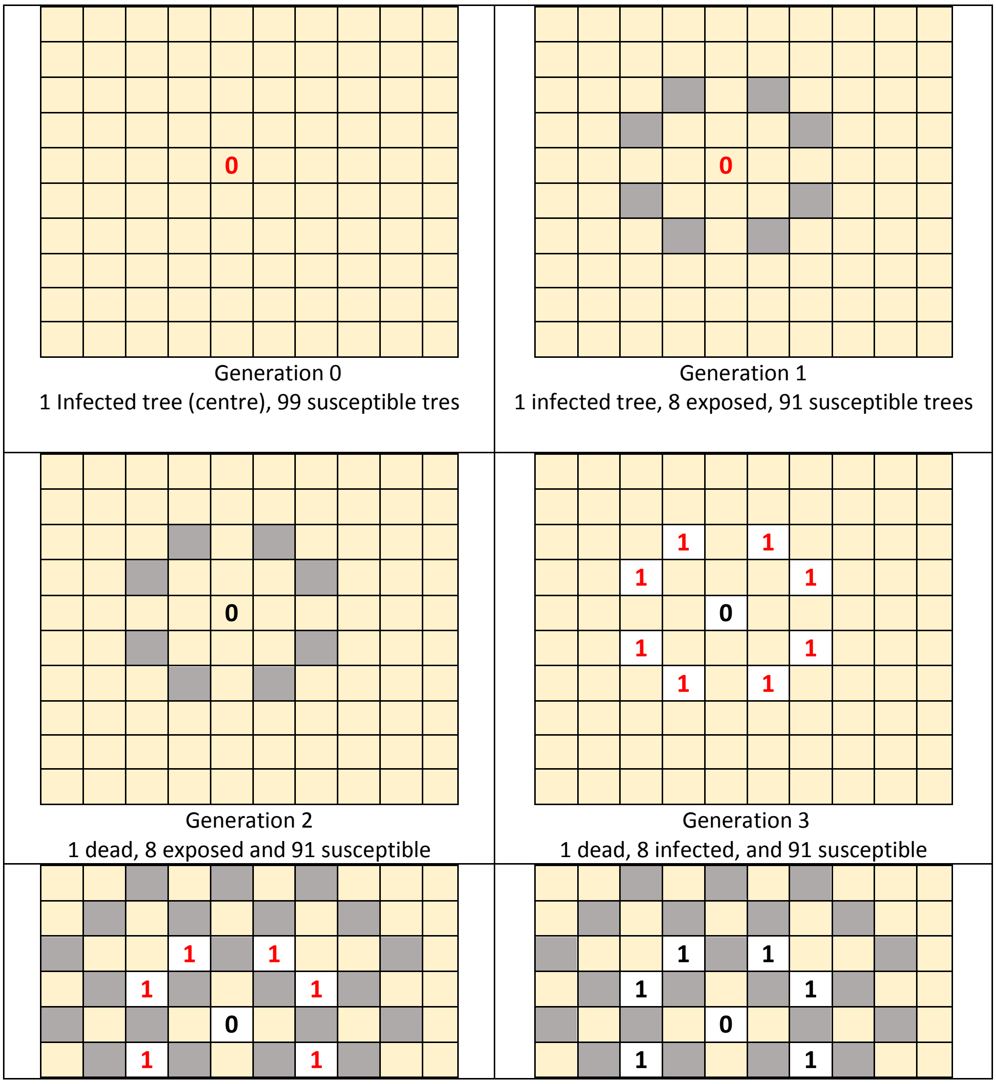
Generation 5
All dead

	S	E	I	D
Gen.0	91	8	1	0
Gen.1	59	32	8	1
Gen.2	17	42	32	9
Gen.3	0	17	42	41
Gen.4	0	0	16	84
Gen.5	0	0	0	100

Fig. 2a. The expansion process for environmental characteristic nº 6 (Temperature).
We assume (R_7, “L”) in a 10x10 grid.

- Grid nº 5: Care level of the trees.

We consider the case of a high level care plot. The values are $\Delta_{SE} = 1$, $\Delta_{EI} = 2$, $\Delta_{ID} = 2$, respectively (see Tables 1-2). We assume L-neighbourhood and R_7. We represent the schedule for $\Delta_{SE} = 1$, $\Delta_{EI} = 2$, $\Delta_{ID} = 2$.

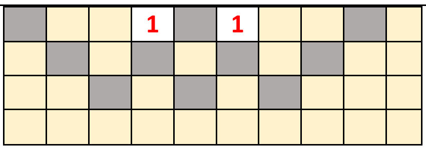


Generation 0
1 Infected tree (centre), 99 susceptible tres

Generation 1
1 infected tree, 8 exposed, 91 susceptible trees

Generation 2
1 dead, 8 exposed and 91 susceptible

Generation 3
1 dead, 8 infected, and 91 susceptible



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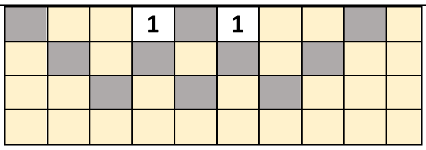
Generation 4
1 dead, 8 infected, 32 exposed, 59 susceptible



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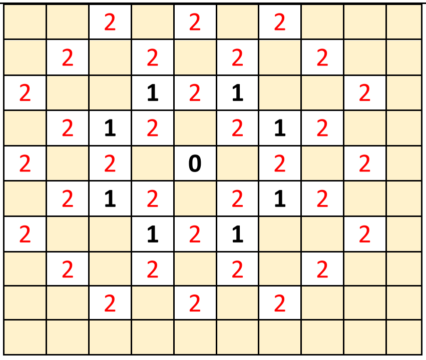
Generation 5
9 dead, 32 exposed, 59 susceptible



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	2		2		2		2		
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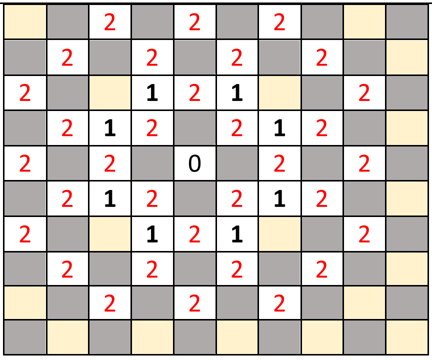
	2	**1**	2		2	**1**	2		
2		2		**0**		2		2	
	2	**1**	2		2	**1**	2		
2			**1**	2	**1**			2	
	2		2		2		2		
		2		2		2			

Generation 6
9 dead, 32 new infected, 59 susceptible



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▨	2	**1**	2	▨	2	**1**	2	▨	
2	▨	2	▨	0	▨	2	▨	2	▨
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2	▨		**1**	2	**1**		▨	2	▨
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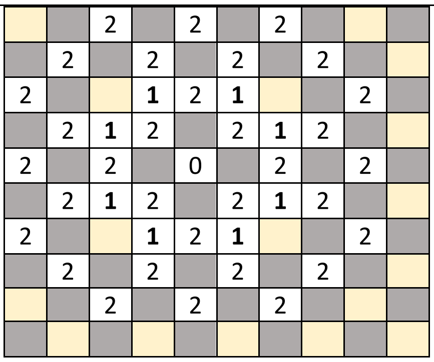
Generation 7
9 dead, 32 infected, 42 exposed and 17 susceptible



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2	▨	2	▨	0	▨	2	▨	2	▨
▨	2	**1**	2	▨	2	**1**	2	▨	
2	▨		**1**	2	**1**		▨	2	▨
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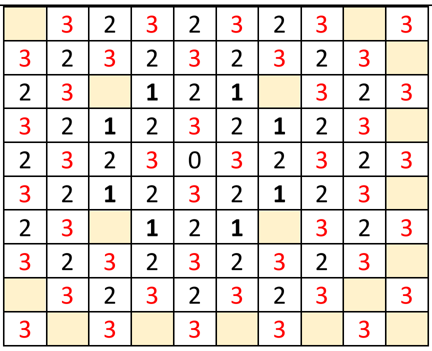
Generation 8
41 dead, 42 exposed and 17 susceptible



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3	2	**1**	2	3	2	**1**	2	3	
2	3		**1**	2	**1**		3	2	3
3	2	3	2	3	2	3	2	3	
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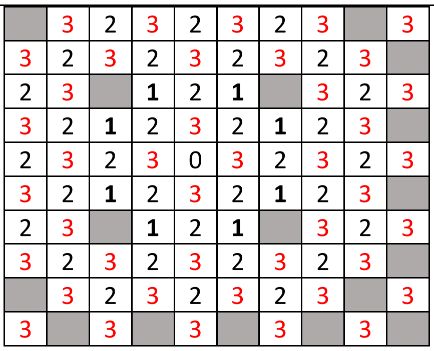
3		3		3		3		3	

Generation 9
41 dead, 42 new infected, 17 susceptible



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3	2	**1**	2	3	2	**1**	2	3	▨
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	▨
2	3	▨	**1**	2	**1**	▨	3	2	3
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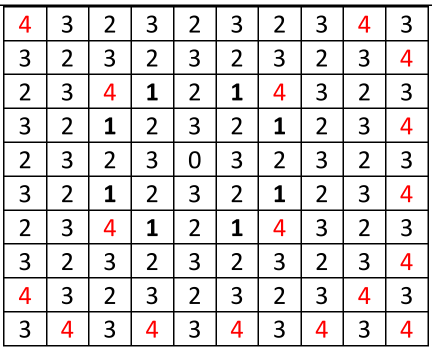
▨	3	2	3	2	3	2	3	▨	3
3	▨	3	▨	3	▨	3	▨	3	▨

Generation 10
41 dead, 42 infected, 17 exposed, 0 susceptible



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3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3
3	2	3	2	3	2	3	2	3	4
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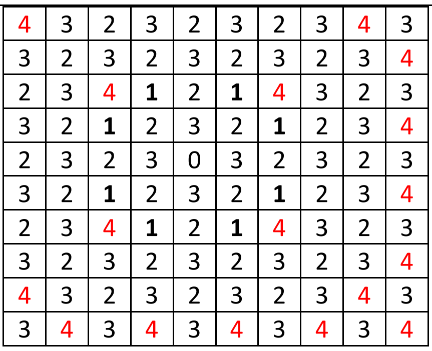
Generation 11
83 dead, 17 new infected, 0 exposed, 0 susceptible



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3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3
3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
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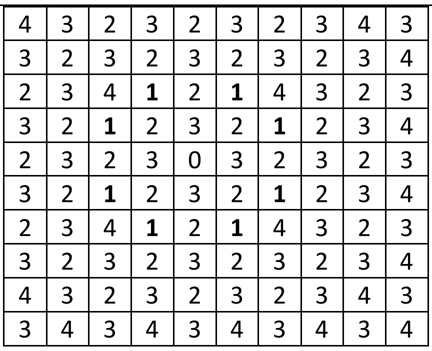
Generation 12
83 dead, 17 new infected, 0 exposed, 0 susceptible



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3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
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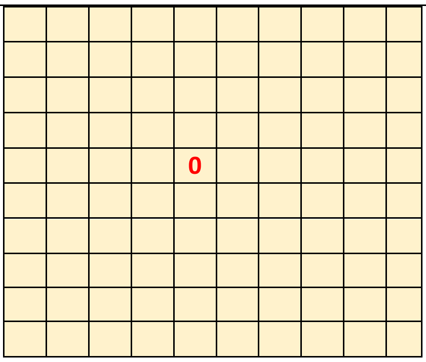
3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
3	4	3	4	3	4	3	4	3	4

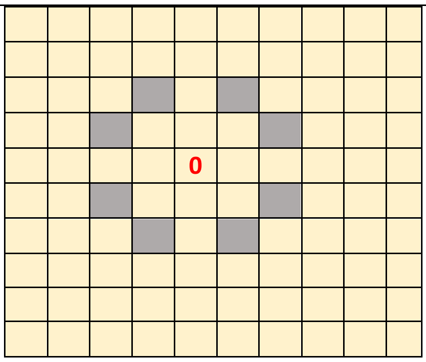
Generation 13
100 dead

	S	E	I	D
Gen.0	99	0	1	0
Gen.1	91	8	1	0
Gen.2	91	8	0	1
Gen.3	91	0	8	1
Gen.4	59	32	8	1
Gen.5	59	32	0	9
Gen.6	59	0	32	9
Gen.7	17	42	32	9
Gen.8	17	42	0	41
Gen.9	17	0	42	41
Gen.10	0	17	42	41
Gen.11	0	0	17	83
Gen.12	0	0	17	83
Gen.13	0	0	0	100

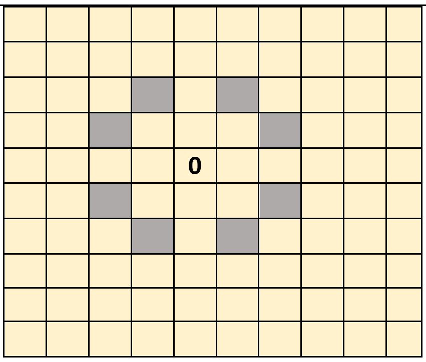
Fig. 2b. The expansion process for environmental characteristic nº 5 (Care level of the trees). We assume (R_7, “L”) in a 10x10 grid.



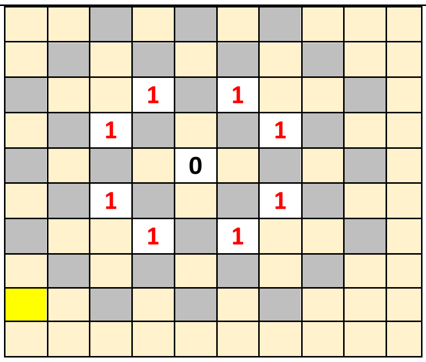
Generation 0



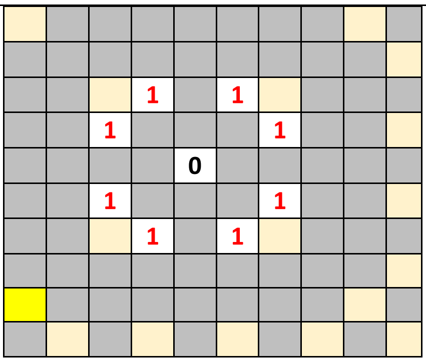
Generation 1



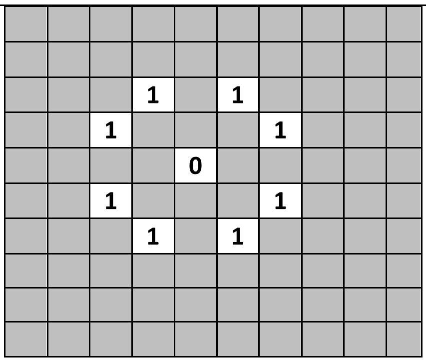
Generation 2



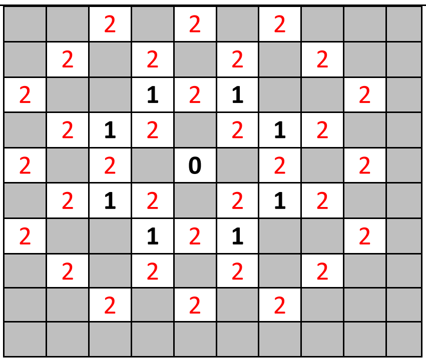
Generation 3



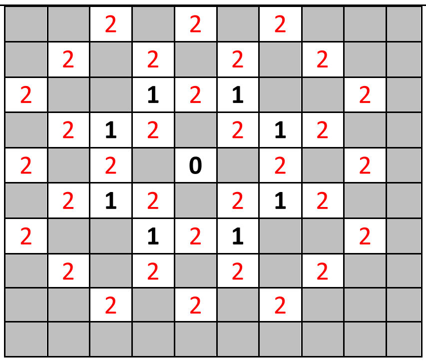
Generation 4



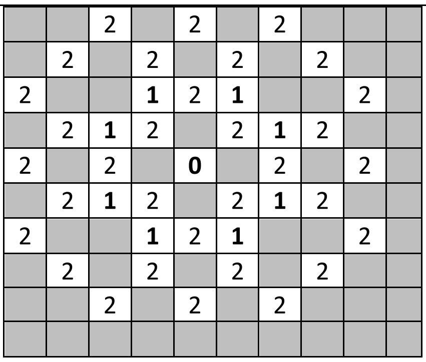
Generation 5



Generation 6

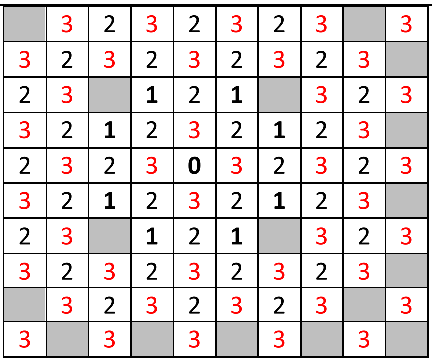


Generation 7



		2		2		2			
	2		2		2		2		
2			**1**	2	**1**			2	
	2	**1**	2		2	**1**	2		
2		2		**0**		2		2	
	2	**1**	2		2	**1**	2		
2			**1**	2	**1**			2	
	2		2		2		2		
		2		2		2			

Generation 8



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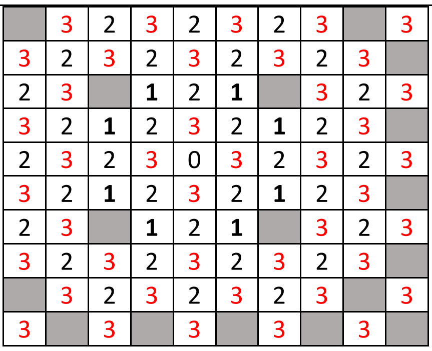
3	2	**1**	2	3	2	**1**	2	3	
2	3	2	3	**0**	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	
2	3		**1**	2	**1**		3	2	3
3	2	3	2	3	2	3	2	3	
	3	2	3	2	3	2	3		3
3		3		3		3		3	

Generation 9



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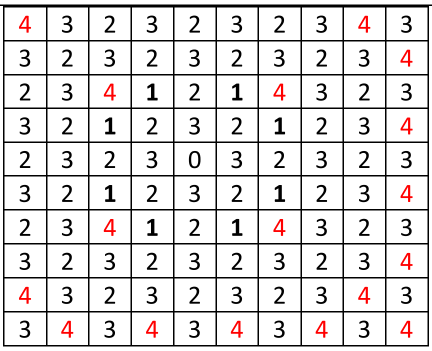
2	3		**1**	2	**1**		3	2	3
3	2	**1**	2	3	2	**1**	2	3	
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	
2	3		**1**	2	**1**		3	2	3
3	2	3	2	3	2	3	2	3	
	3	2	3	2	3	2	3		3
3		3		3		3		3	

Generation 10



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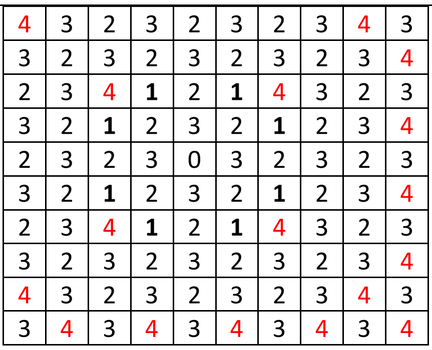
2	3	4	**1**	2	**1**	4	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3
3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
3	4	3	4	3	4	3	4	3	4

Generation 11



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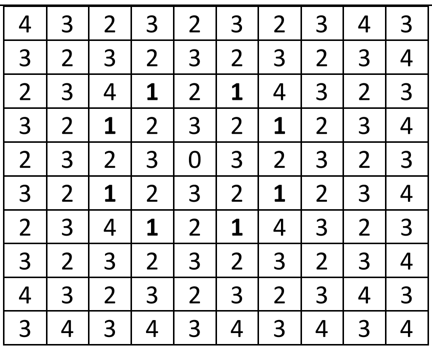
3	2	3	2	3	2	3	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3
3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
3	4	3	4	3	4	3	4	3	4

Generation 12



4	3	2	3	2	3	2	3	4	3
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2	3	4	**1**	2	**1**	4	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	2	3	0	3	2	3	2	3
3	2	**1**	2	3	2	**1**	2	3	4
2	3	4	**1**	2	**1**	4	3	2	3
3	2	3	2	3	2	3	2	3	4
4	3	2	3	2	3	2	3	4	3
3	4	3	4	3	4	3	4	3	4

Generation 13

	S	E	I	D
Gen.0	99	0	1	0
Gen.1	91	8	1	0
Gen.2	91	8	0	1
Gen.3	59	32	8	1
Gen.4	17	74	8	1
Gen.5	0	91	0	9
Gen.6	0	59	32	9
Gen.7	0	59	32	9
Gen.8	0	59	0	41
Gen.9	0	17	42	41
Gen.10	0	17	42	41
Gen.11	0	0	17	83
Gen.12	0	0	17	83
Gen.13	0	0	0	100

Fig. 2c. Representation of the ***S*** scenario, with only two environmental characteristics.
nº 5 (Care level of the trees) and nº 6 (Temperature)
We assume (R_7, "L") in a 10x10 grid.

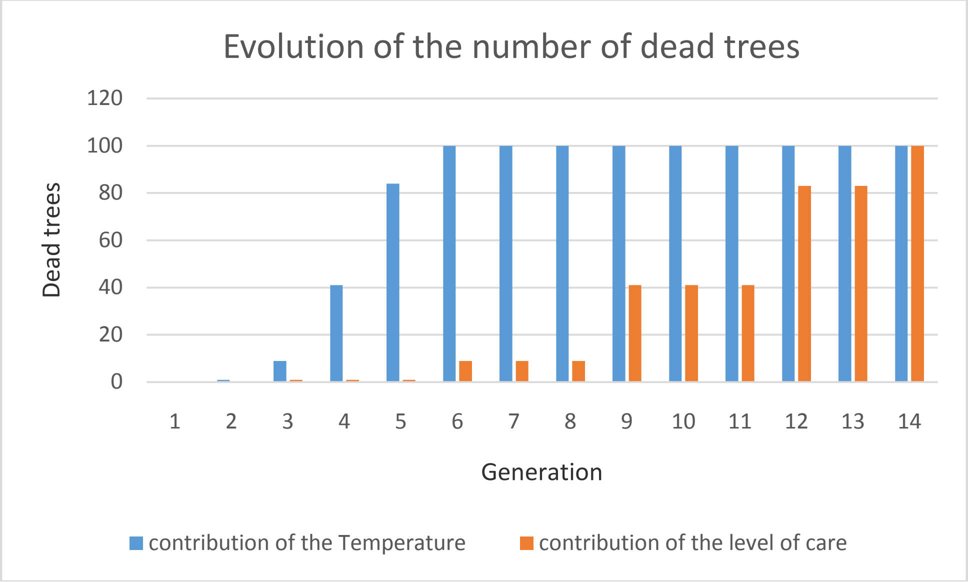

Fig.3a. Evolution of the number of dead trees vs. generation.

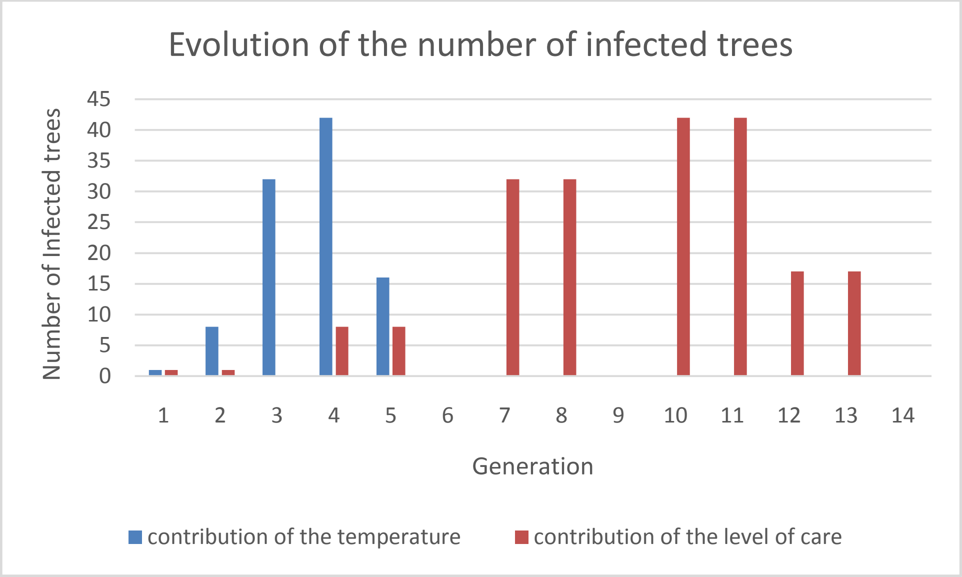

Fig.3b Evolution of the number of infected trees vs. generation.