Article

An epidemic grid model to address the spread of Covid-19:

A comparison between Spain, Italy and UK.

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Abstract: This paper presents a discrete compartmental Susceptible-Exposed-Infected-Recovered/Dead (SEIR/D) model to address the expansion of Covid-19 pandemic. When time passes, the status of the cells is determined by binary rules that update following both a neighbourhood and a delay pattern. The model assumes the environmental parameters have a crucial impact on the expansion of the disease so a grid is assigned to each parameter to model the single effect caused by this parameter. The expansion is then the weighted sum of all the grids. This proposal shows how the grid architecture, along with an update rule and a neighbourhood pattern is a valuable tool to model the pandemic expansion. This model has already been analyzed in previous works and compared with the corresponding continuous models solved by ordinary differential equations (ODE), coming to find the homologous parameters between both approaches. Thus, it has been possible to prove that the combination neighborhood-update rule is responsible for the rate of expansion and recovering/death of the illness. The delays (between Susceptible and Asymptomatic, Asymptomatic and Infected, Infected and Recovered/Dead) may have a crucial impact on both the peak of Infected and the Recovery/Death rate. This theoretical model has been successfully tested in the case of the dissemination of information through mobile social networks and in the case of plant pests.

Keywords: Covid-19; computational modelling; space time framework; multigrid implementation; update binary rules; Von Neumann and Moore neighbourhoods.

1. Introduction

Since December 2019, the world is facing the most serious pandemic since the Spanish flu of 1918. World Health Organization (WHO) declared the pandemic on March 11, 2020. The outbreak has caused near 79.000.000 infections and more tan 1.700.000 deaths as of the time of this publication. In response to this threat, all governments have ordered different degrees of containment measures, such as school and workplace closures, travel ban and quarantines, and have launched actions including social distancing, mandatory mask wearing, hand higiene and viral or antibody test realizations as well as contact tracing using cell phone tracking.

Many researchers have dedicated their efforts to cope with the dynamics of the spread of the disease, that is, they have provided insight into the underlying mechanisms of the virus propagation in order to guide the planning of the public health policies to ensure success in the fight against COVID-19.

Our work aims to study the spread of the virus. Our approach is based on the compartmental model paradigm and we use a grid model to cope with the different particularities of this process. The parameters that can have an impact on the evolution of the disease are highlighted and a grid is assigned to each of them. An update rule implements the changes of the number of people in each of the compartments.

Following the introduction, Section 2 analyzes the related works in which researchers approach Covid-19 using compartmental models. Section 3 is entirely devoted to present the method we use. Section 4 provides a first insight in the data of confirmed cases and deaths in three european countries, Spain, Italy and United Kingdom. Section 5 discusses an application of a 2-grid model and explains how it must be interpreted. Finally, Section 6 presents concluding remarks and some future research lines.

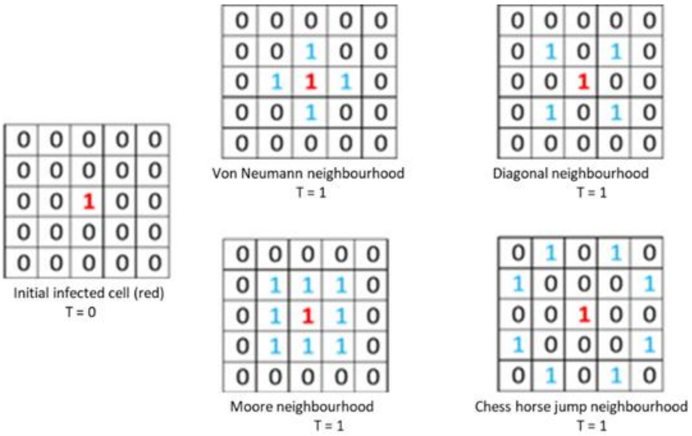
2. Materials and Methods

2.1. Related work

As follows, we review some publications in which researchers approach Covid-19 using compartmental models. Reference [1] presents a summary of the Susceptible-Infected-Recovered (SIR) model and its variants SEIR (with Exposed E compartment) and Susceptible- Unquanrantined infected- Quarantined infected- Confirmed infected (SUQC) models, in order to highlight the relationship between the health measures to curb the pandemic and the mathematics behind them. Although this work has no real research impact, it is very useful as a link between computer scientists and physicians. In [2] the authors analyse the SIR and SEIR models with the complementary Quarantine, Lockdown and Vaccine compartments. They also simulate the SIR model to explore the dynamics of coronavirus in Ghana based on available data up until 9th April 2020. Reference [3] divides the population into the following states: susceptible subjects (S), have close contacts (C, those exposed to infected subjects/pathogen but not necessarily infected), latent (E, infected and infectious but asymptomatic), infected (I; and symptomatic), recovered (V), and dead (D). This four-compartment model is applied to evaluate the epidemiological data and hospital burden in Italy, the UK, and the US. The control measures are identified as the key drivers for the observed epidemiological data through sensitivity analyses and provide a framework for major pandemics in the future. In [4], the authors introduct random sampling scheme that enables a stochastic extension of the SIR model to provide the ability to quantify uncertainty in both estimation and prediction, in connection to sampling variability. This added uncertainty is very useful because the model not only generates an average estimation or prediction, it also presents the best and worst possible scenarios. This is critical for policies that enable more robust and secure management of epidemics. In reference [5] the authors generalise the simple 3-compartment SIR model to the SLIAR model, by considering L (latency) and A (asymptomatic) compartments. This provides a reasonable approximation to the details of progression of the pandemia with a minimal number of parameters. The novelty is the further incorporation of Erlang distributions of the time of sojourn in some of the important compartments. In [6] the model is then described by a dynamical system enclosing a closed population with Susceptible (S), confirmed Infected (I), Asymptomatic (A), Quarantined (Q), Recovered (R) and Died (D), people. The authors conclude that the value of the peak, and thus the impact on the health care system, depends critically on the proportion of cases that are asymptomatic. In Spain, many research teams also present different approaches. At the R. Margaleff Institute of Research (University of Alicante), Dr. C. Bordehore leads a multidisciplinary research team which studies the spread of Covid-19. He follows an open SEIR model which can include different realistic scenarios to provide an estimate of the impact of each parameter on the spread. The model is currently in an update phase that aims to define R0 with more accuracy [7]. MUNQU (Modelling Uncertainty Quantification group) at the Politechnic University of Valencia has presented an epidemic model in order to provide a daily prediction of the expansion of Covid-19 which is available at https://covid19.webs.upv.es/. The model bases on SIR paradigm, with 9 compartments: Susceptible- Quarentine- Latent - Infected- Hospitalized- ICU (intensive care unit)- Hospitalized post ICU-Recovered-Dead. The system is solved by a set of differental ordinary equations (ODE) [8]. All these references highlight compartmental models are suitable for approaching the expansion of infectious diseases

2.2. Method

The generic model we use here for Covid-19 considers the spread of a disease depends on many environmental, sectorial or even cultural characteristics, in addition to the virus and patients ones, and the weighted impact of all them builds the realistic scenarios of the spread. Our model bases on a time space framework that follows a typical epidemic paradigm (SIR, SEIR,…). The basic framework is implemented by a grid in which an "infected" cell (value = 1) spreads the disease to its susceptible neighbors (value = 0). Different types of neighborhood are proposed (Von Neumann, Moore, Diagonal and chess horse jump), along with a local binary update rule, which defines the result of the interaction between neighbors in terms of contagion. Figure 1 shows the initial infected cell at T = 0 and the spread of the disease at T = 1 for different neighbourhood types.



Initial infected cell (red)
T = 0

0	0	0	0	0
0	0	0	0	0
0	0	1	0	0
0	0	0	0	0
0	0	0	0	0

Von Neumann neighbourhood
T = 1

0	0	0	0	0
0	0	1	0	0
0	1	1	1	0
0	0	1	0	0
0	0	0	0	0

Diagonal neighbourhood
T = 1

0	0	0	0	0
0	1	0	1	0
0	0	1	0	0
0	1	0	1	0
0	0	0	0	0

Moore neighbourhood
T = 1

0	0	0	0	0
0	1	1	1	0
0	1	1	1	0
0	1	1	1	0
0	0	0	0	0

Chess horse jump neighbourhood
T = 1

0	1	0	1	0
1	0	0	0	1
0	0	1	0	0
1	0	0	0	1
0	1	0	1	0

Figure 1. The grid implementation for four different neighbourhood types

This discrete model has been analyzed and compared with the continuous models solved by ordinary differential equations (ODE), coming to find the homologous parameters between both approaches. Thus, it has been possible to characterize the rates of expansion and recovery, the duration of the disease, the threshold values and the equilibrium values of the populations in each compartment and for each combination neighborhood/update rule [9-11].

A more complex and realistic expansion can be carried out by means of a multigrid implementation, that is, a set of grids in a vertical stack, where each grid depicts the impact of a single characteristic (parameter) Gi on the spread of the disease, as shown in Figure 2, where a SEID model is implemented. This approach needs a previous knowledge of the crucial parameters of the spread in order to fix both the number of grids and the suitable neighbourhood for each grid.

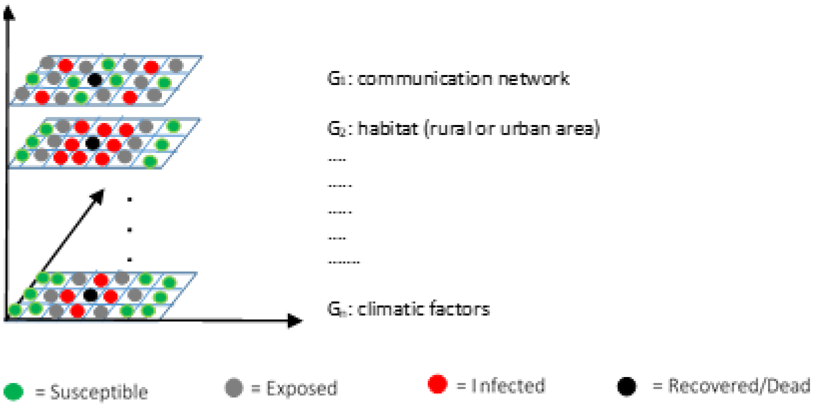


Figure 2. The multigrid implementation

The resulting global evolution is obtained by the sum of the values of the same cell in all the grids belonging to a same column, and for any time, as indicated by Eq (1) and Eq (2) in Figure 3.

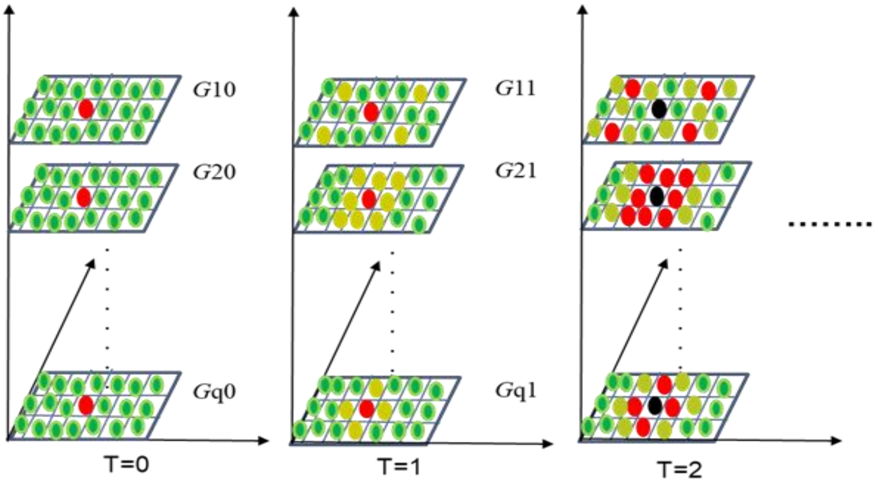


Figure 3. The time evolution of the spread of the pandemic

The calculation of the values of the cells is carried out as follows:

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

This is the mean value of the same cell in a column.

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

$0 \leq c_{v,w} < 0{,}5$ for S

$0{,}5 \leq c_{v,w} < 0{,}8$ for E

$0{,}8 \leq c_{v,w} < 0{,}9$ for I Eq (2)

$0{,}9 \leq c_{v,w} < 1$ for R

$c_{v,w} = 1$ for D

This theoretical model has been successfully tested in similar situations that occur in the spread of plant pests [12,13] or the dissemination of information through mobile social networks [14-16]. The advantages of this discrete model are the ability to include both behavioral variability at the cell level (by modifying the neighborhood and/or the update rule) and modularity (by modifying the number of grids) which allows to deal with realistic scenarios. In the case of Covid-19 we estimate the impact on the spread of the disease of environmental parameters (climatic factors, habitat, communication network), cultural practices, and personal health state (age, previous pathologies) [17].

2.3. The expansion of Covid19 in three european countries

In order to model the expansion of Covid19 by means of multigrid implementation, we must have a first insight in the data of confirmed cases and deaths. We pay attention to the pandemic in three european countries, Spain, Italy and United Kingdom in order to find similarities and differences that may point to the parameters that cause them. These parameters may be crucial for the multigrid implementation. To this day, we have the following data provided by the WHO Coronavirus Disease (COVID-19) Dashboard [18]. See Table 1

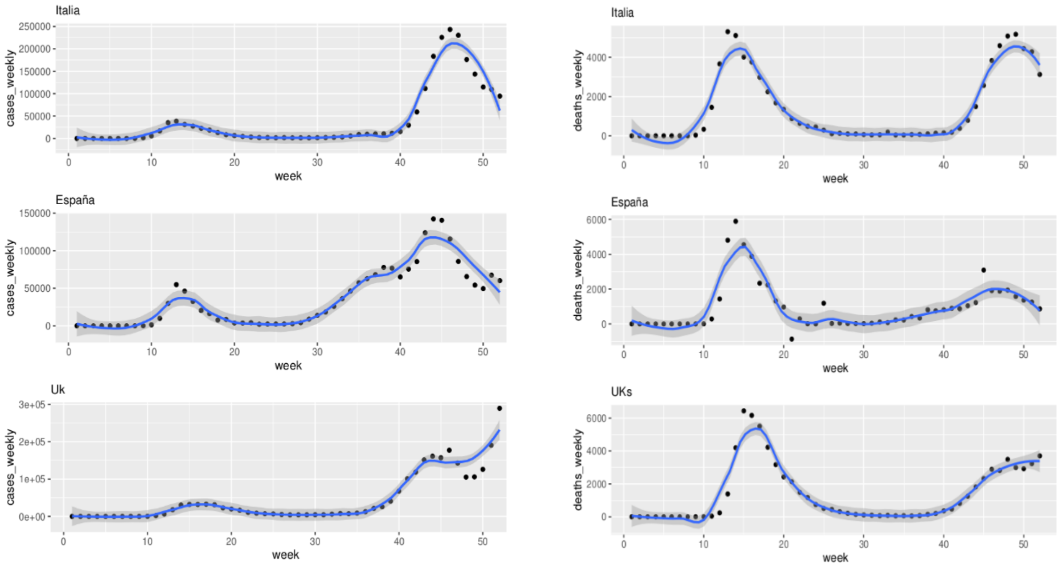
	Italy	Spain	U.K
population	60,360,000	46,940,000	66,650,000
confirmed cases	2,067,487 (34‰)	1,893,502 (40 ‰)	2,382,869 (35 ‰)
deaths	73,029 (1,2 ‰)	50,442 (1,1 ‰)	71,567 (1,1 ‰)

Table 1. Confirmed cases and deaths in Italy, Spain and U.K.

The situation is roughly equivalent in the three countries. We also analyze the evolution of the situation by weeks, in what refers to the confirmed cases and deaths. As follows, Figure 4 presents the number of cases and death from january 2020 to 28th december 2020 (52 weeks) in Italy, Spain and U.K. Data are collected from Covid-19 data sets of European Union [19,20].

In Figure 4a the patterns of Italy and U.K. are quite similar until week 40 (Italy and U.K have about 60 M. inhabitants). The cases start from week 10 and reach the first peak (50,000 cases) at week 12. Then, they decrease and remain equal to 0 until week 40. Then the evolution is different. Italy has a new steep peak (230,000) at week 48 and then dicreases, while in U.K. the number of cases increase slowly. Spain (46 M inhabitants) follows a different pattern. The first peak is also about 50,000 cases at week 12 and then, at week 30, we observe a slow but continued increase that achieves the maximum (120,000 cases) at week 42.

In Figure 4b for the deaths, we observe that Italy and U.K. have again the same behaviour until week 40. The number of weekly deaths starts from week 10 and reaches the first peak (about 4,500-5,000) at weeks 15-17, respectively. Then the number of deaths quickly falls to 0 and stays that way until the 40th week. After week 40, the number of deaths increases again and seems to achieve the second peak (about 4500 for Italy at week 48 and 3000 for U.K. with the same delay. For Spain, the evolution is quite the same as Italy and U.K. for the first 30 weeks, but nest, we observe a slow but continued increase that achieves the maximum (2,000 cases) at week 42.



a) b)

Figure 4. The pandemics data in Italy, Spain and U.K.

The rigorous observation of the three examples leads to some conclusions. The patterns are roughly the same except for delays and overall cases and deaths counts. So, climatic factors, cultural factors (mediterranean countries customs), territorial organization (Spain is a decentralized state compared to Italy and U.K. so different health policies can be applied) do not seem to have a strong impact on the disease expansion. On the contrary, communication network, habitat (rural or urban), age and previous pathologies seem to be crucial.

3. Results

In this section we present a 2-grid model for the spread of the disease. The grids are G1: communication network, G2: habitat. Age and/or previous pathologies are not important in the spread, but in the deaths. We do not consider them in our current application.

We set:

- Neighbourhoods

G1: Chess horse jump neighbourhood (speedy spread, strong impact)

G2: Chess horse jump nighbourhood (speedy spread, strong impact)

- Delays:

Δ_{SE} (between Susceptible and Exposed)

Δ_{EI} (between Exposed and Infected)

$\Delta_{IR/D}$ (between Infected and Recovered or Dead)

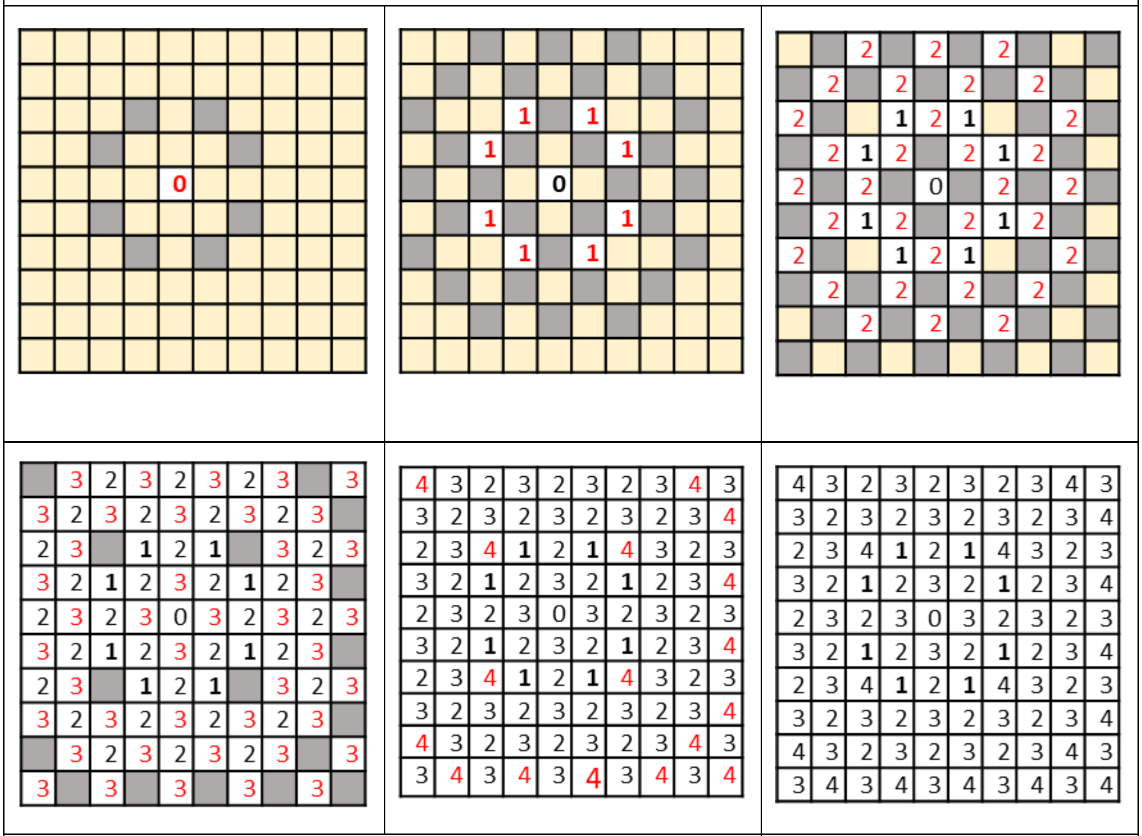
The delays can modulate the speed of the spread.

For G1, we set: $\Delta_{SE} = 0$, $\Delta_{EI} = 1$, $\Delta_{IR/D} = 1$

For G2, We set: $\Delta_{SE} = 1$, $\Delta_{EI} = 2$, $\Delta_{IR/D} = 2$

We represent in Figures 5 and 6 the schedules of the contribution of parameters G1 and G2 to the spread of the disease. Yellow cells are susceptible. Exposed cells are grey. Infected cells are white and the number inside the cell means the generation number. This is a generic measure of the time (i.e. hours, days, weeks, depending on the case). Finally, black numbers in white cells mean the cell is recovered/dead). The delays are also measured in generations. The update rule is as follows:

G1: communication network



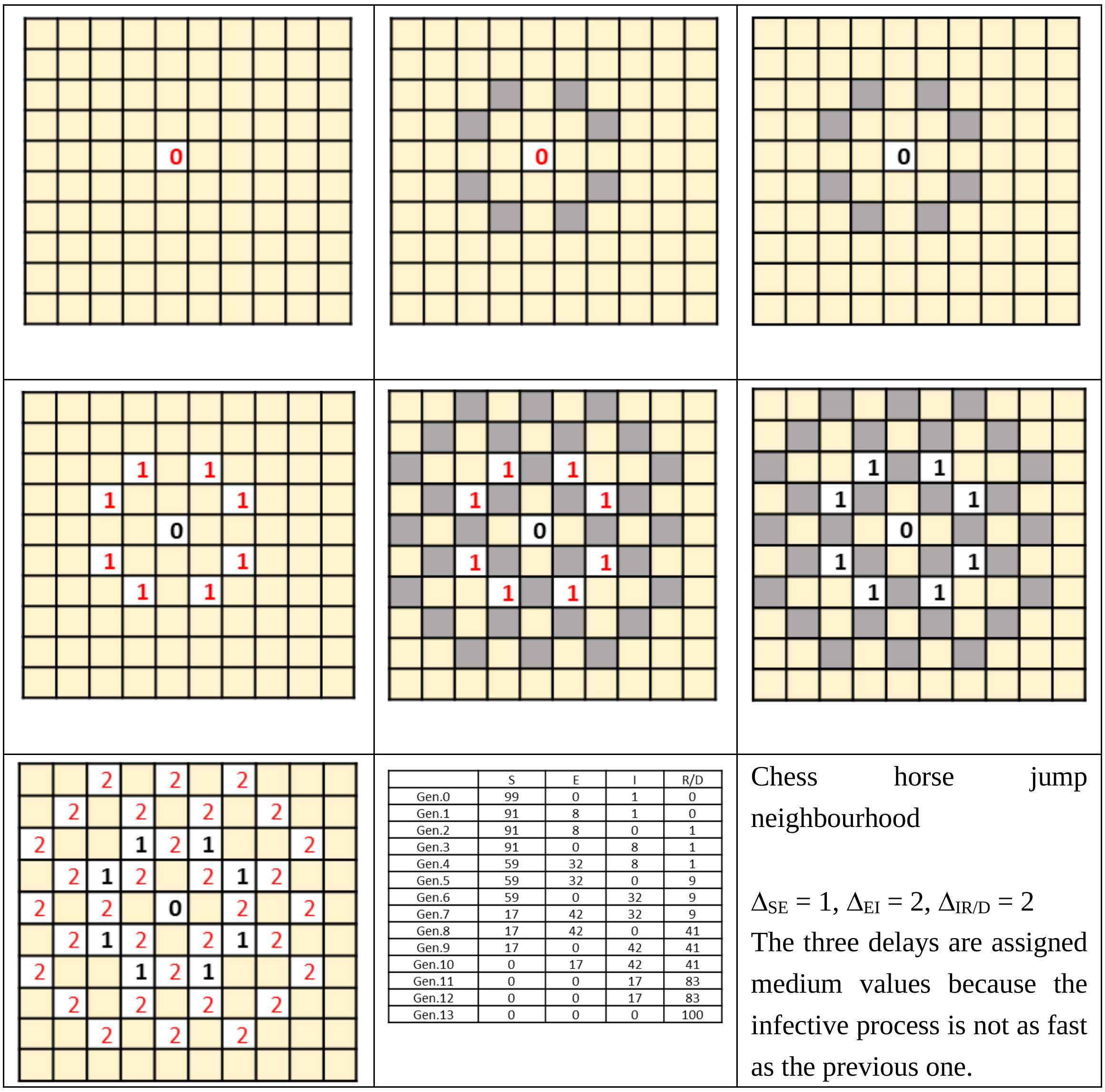
	S	E	I	R/D
Gen.0	91	8	1	0
Gen.1	59	32	8	1
Gen.2	17	42	32	9
Gen.3	0	17	42	41
Gen.4	0	0	16	84
Gen.5	0	0	0	100

Chess horse jump neighbourhood

$\Delta_{SE} = 0$, $\Delta_{EI} = 1$, $\Delta_{IR/D} = 1$
The three delays are assigned low values because the infective process is fast.

Figure 5. Schedule of the contribution of G1 to the spread of the disease

G2: habitat



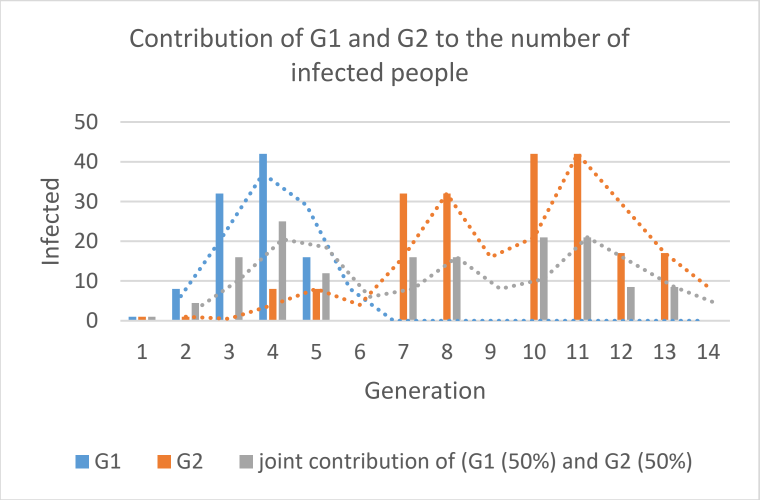
	S	E	I	R/D
Gen.0	99	0	1	0
Gen.1	91	8	1	0
Gen.2	91	8	0	1
Gen.3	91	0	8	1
Gen.4	59	32	8	1
Gen.5	59	32	0	9
Gen.6	59	0	32	9
Gen.7	17	42	32	9
Gen.8	17	42	0	41
Gen.9	17	0	42	41
Gen.10	0	17	42	41
Gen.11	0	0	17	83
Gen.12	0	0	17	83
Gen.13	0	0	0	100

Chess horse jump neighbourhood

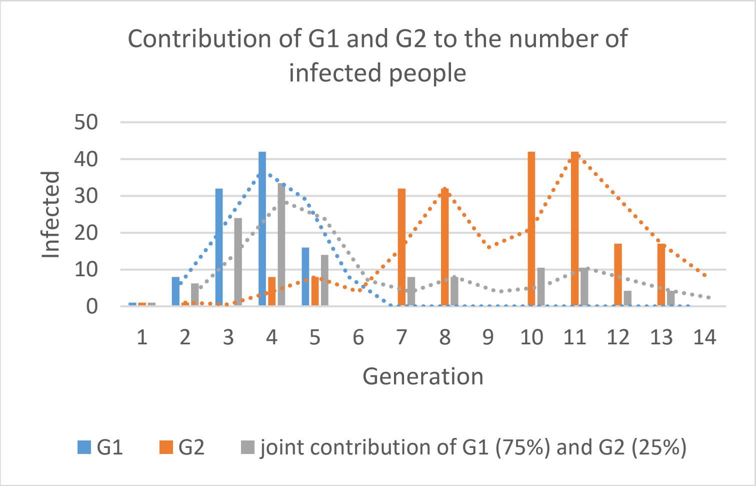
$\Delta_{SE} = 1$, $\Delta_{EI} = 2$, $\Delta_{IR/D} = 2$
The three delays are assigned medium values because the infective process is not as fast as the previous one.

Figure 6. Schedule of the contribution of G2 to the spread of the disease

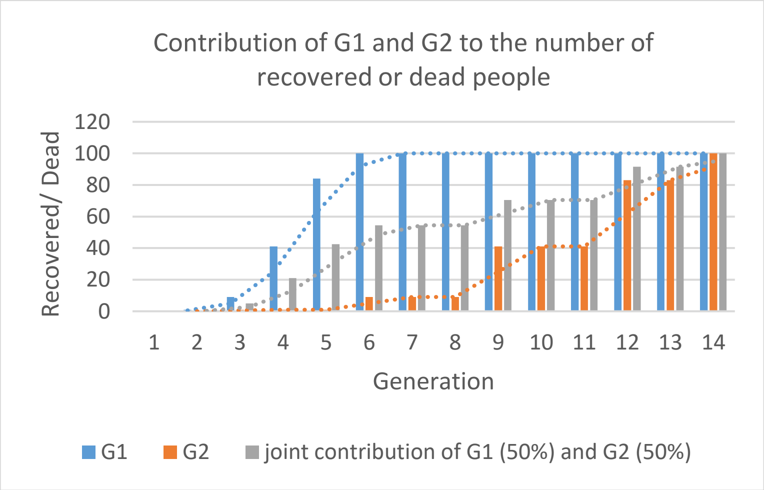
In Figure 7 we have plotted the results of the joint contribution of G1 and G2 to the spread of the pandemic. For this case we have used a simple weighting formula, not Eq(1) and Eq(2), because we are not interested in the particularisation of the cells behaviour, but in the overall result.



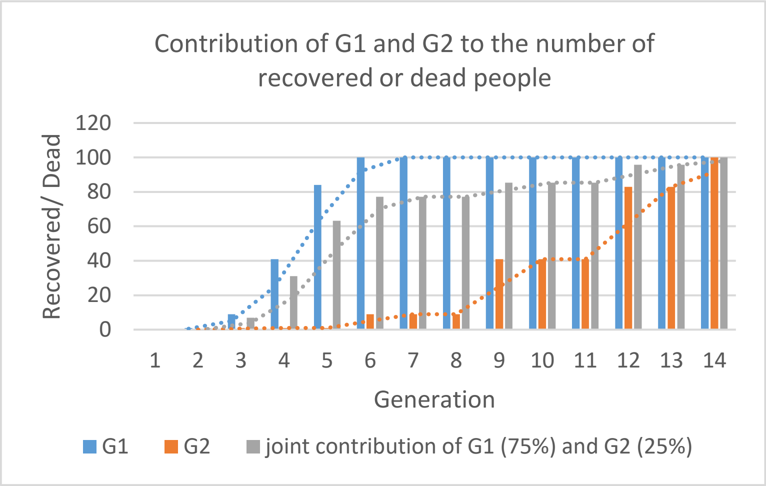
We observe that the G1 (communication network speeds up the number of infected people and causes the first peak. The second and third peaks are caused by G2 (habitat) more slowly (grey line).



The weighting of the contributions shows a modified evolution: the first peak is higher and the other peaks are lower and flattened.



We observe that G1 (communication network) speeds up the number of recovered/dead people. G2 can slow down the number of recovered /dead people.



The weighting of the contributions shows a modified evolution: If G1 is weighted 75%, we notice a stronger impact of G1 and people become recovered /dead earlier.

Figure 7. Joint contribution of G1 and G2 to the spread of the disease

We highlight the capabilities of multigrid model to adapt to any trend in the pandemic evolution, by using several grids. Each grid is governed by a neighbourhood and its impact is modificable by the delays.

5. Conclusions

The fight against Covid 19 has taught us a lot in a short time. In addition to the importance of knowing the virus and having treatment and vaccines, it is crucial to have a correct management of the pandemic because it has become clear that the main drawbacks of the outbreak management came from the pressure in the ICUs and the hospitals that were on the verge of collapse. The management of the pandemic with the modification of its parameters can be an alternative way to avoid the overflow of the sanitary structures. Forecasting is achieved if we are able to find the keys of the expansion in order to control it. In this sense, our model succeeds in pointing out some variables of the environment and discard some other that are not relevant for the spread. Furthermore, it is a simple and scalable model that can also be used to simulate other phenomena such as propagation of pests in plants or spread of computer viruses in computer networks. As future work, we plan to perform a more detailed study where the prameters can be broken down into other parameters, as an example, G2 may include a set of cases such as apartments in a building, nursing home, family home. G1 may include subway, bus, flights,…This will provide a better undestanding of the impact of environmental factors in the pandemic expansion.

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