

Agent-based Simulation Model applied to social behaviours determining pandemic dynamics - Part 2 (27 April 2020)

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Introduction

We have created a model based on artificial agents that describes some aspects of the diffusion dynamics of COVID-19, especially aspects related to the link between social behaviour and contagion dynamics. Starting from the first part of this article [1], published on April 2, we investigated how we can link a particular socio-cultural attitude to some effects on the lethality of the epidemic. As a starting data, we show the effect that the epidemic had in terms of difference between the number of deaths in the first quarter of 2019 and the first quarter of 2020, in 1,698 Italian municipalities [2]. Once we have established how the incidence of the virus was very irregular, we assume that one of the causes may be some social behaviour, through the simulation model described in the previous publication [1], which has been appropriately revised.

The pandemic in Italy

Coronavirus infection has spread in Italy with evident anomalies in the distribution of infected people in the country. We have data that show this evidence, starting from the different number of people who died in 2019 and 2020, in the different regions of Italy (sample of 1868 municipalities, Figure 1)

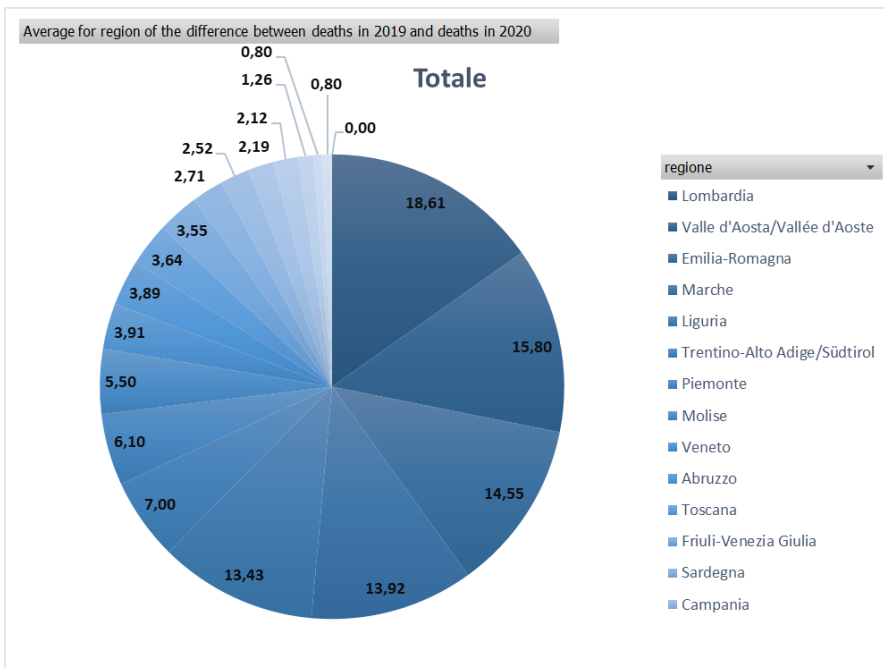


Figure 1 Average, for each municipality, of the difference in deceased persons (for whatever reason and in all age groups), divided by region. It should be noted that Lombardy had an increase of just over 18 deaths on average per municipality, compared to 0.8 in Umbria, for example.

In order to have a truly comparable picture on a geographical basis, we can divide this difference by the number of inhabitants of each municipality, thus obtaining a measure proportional to the number of people exposed, the **incidence** (Figure 2).

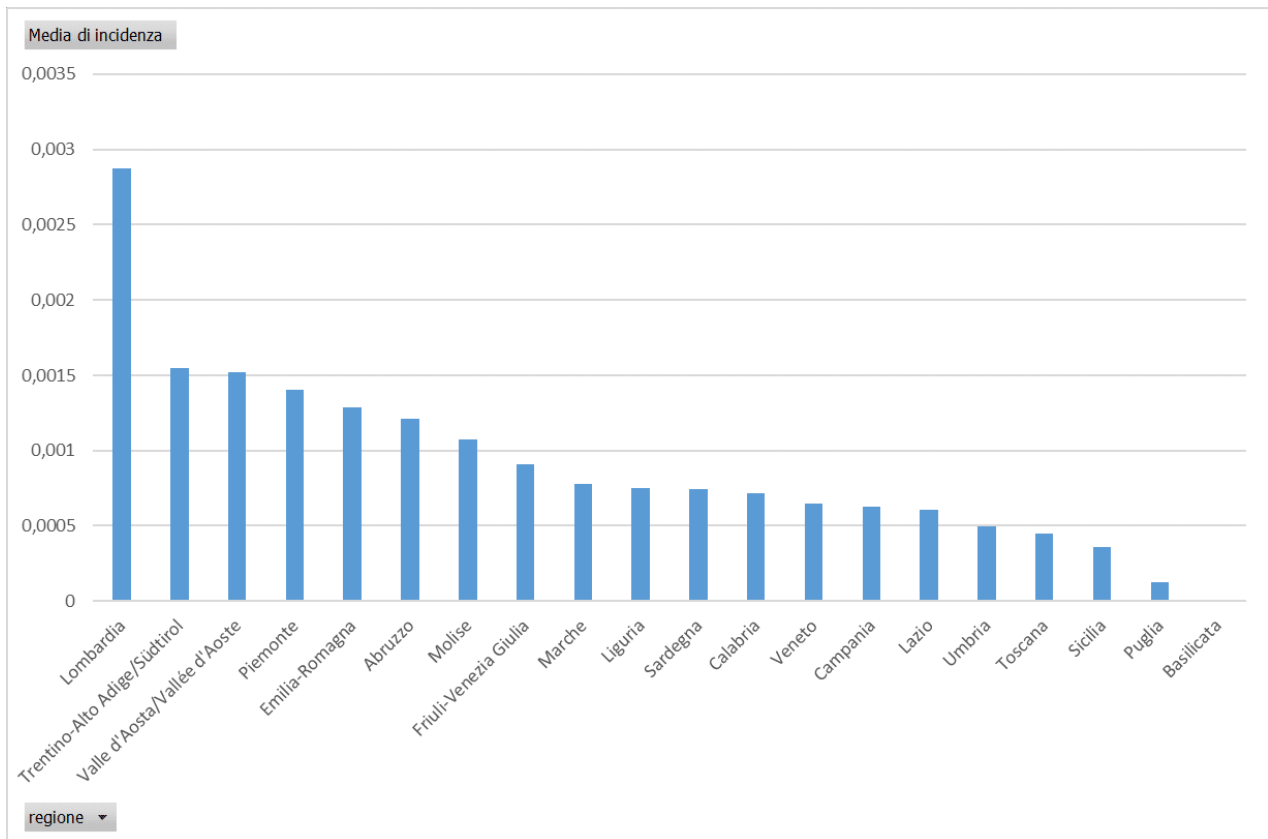


Figure 2 Incidence of the epidemic region by region. The incidence is the difference in the number of people killed divided by the number of inhabitants of each municipality. You can see that there is a significant difference between Lombardy and the rest of Italy and, in general, there is a higher incidence in northern Italy.

The incidence measured in Lombardy has an equally non-uniform distribution, assessed municipality by municipality and summarized by Province (Figure 3).

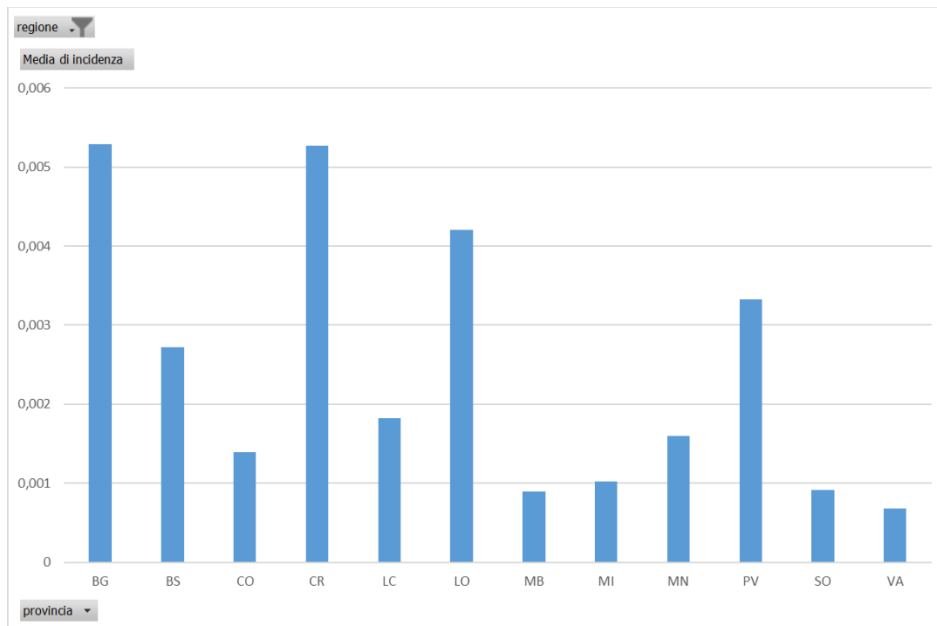


Figure 3 Incidence in Lombardy Province

Goals to achieve

Our aim is to determine why we have seen such a rapid and extensive spread of the virus in Lombardy compared to other regions [3]. In particular, we believe that there are essentially behavioural and social structure reasons. To do this, we will use an ABM model[1], described below, which will be applied to the different territorial realities. We used probabilities derived from the study of Covid19 diffusion and from socio-demographic considerations [2].

Description of our model

We took into account a population of 1,500 agents divided by age group, gender and belonging to three distinct social groups: "social family group", "social work group" and "social leisure group". The distribution was normalized by drawing on ISTAT data [2] The groups are dynamically populated at each simulation according to composition parameters. In the family group, families are simulated according to age groups and number of members: of course, families composed of a single agent are also simulated, thus covering the social cases of single elderly people and single people. In the work group, we find the workers of individual companies according to the specification that increasing the number of agents within the work group, the number of operators decreases, so we go towards a model of small and medium enterprise. Similarly, in the leisure group, as the number of leisure groups increases, the number of participants decreases (at the limit, if the leisure group increases considerably, we are assuming that each agent performs activities independently, i.e. everyone goes for a jog; on the contrary, if the number of leisure groups decreases, it means that a large number of agents go to the gym). The simulation takes place within the 24 hours of the day in which the social interactions of agents and groups of agents are simulated for a total of 1200 hours equal to 50 days.

Therefore, we have described how the disease is spread through social interactions using the data available to date [3] assigning, for each agent according to the status it is in (infected, sick,

deceased or healed) the group to which it belongs (or no group), the age group and at a precise time, the probability that it will change status according to the predetermined sequence used in the SIR model [4]. The model was developed using R: the data input files are in csv format while the population composition parameters are entered in the code.

Simulation diagram

The model is based on matrices that describe the probabilities of passing from one state to another: the matrices describe (1) the probability that an agent i has to change the state of an agent j , modifying its state, (2) the probability that an agent i has to pass in one of the following states: Sick, Healed, Deceased.

For example, table (a) describes the probabilities of transit from Susceptible to Infected status for an individual j belonging to the same working group as agent i ,

randomly chosen in the population. Tables (b) and (c) respectively: the probabilities of passing from the infected state to the sick, healed, deceased states for the various age groups; the probabilities of changing the state of an agent, ignoring the groups to which it belongs.

- Agent i is Infected
- The group connecting i with j is the Work Group
- The effect we can have on j with probability p is: j becomes infected
- Ages are divided into classes: 1 means up to 18 years old, 2 from 19 to 35 years old, 3 from 35 to 65 years old, 4 from 65 to 75 years old, 5 over 75 years old.

p	Età di j				
Età di i	1	2	3	4	5
1		0,0001	0,0001	0,0001	0,0001
2	0,0001	0,001	0,001	0,001	0,0001
3	0,0001	0,001	0,05	0,05	0,001
4	0,0001	0,001	0,05	0,001	0,0001
5	0,0001	0,0001	0,001	0,0001	0,0001

Table (a). Transition table, for each age class, for agent j , from Susceptible to Infected, meeting an Infected agent, within the Work Group

- Agent i is infected
- The group connecting i with j is the Work Group
- The effect we can have on j with probability p is: j becomes infected
- Ages are divided into classes: 1 means up to 18 years old, 2 from 19 to 35 years old, 3 from 35 to 65 years old, 4 from 65 to 75 years old, 5 over 75 years old.

	p	
Età di i	Guarito	Deceduto
1	0,95	0,0001
2	0,85	0,0001
3	0,75	0,005
4	0,4	0,05
5	0,3	0,05

Table (b). Transition table, for agent i , to change its condition from sick to healed or deceased

- Agent i is infected
- There is no group connecting i with j
- The effect we can have on j with probability p is: j becomes infected

p	Qualsiasi età
Età di i	
1	0,005
2	0,005
3	0,005
4	0,001
5	0,001

Table (c). Transition table for agent j , from Susceptible to Infected, meeting an Infected agent

Results

We used an experimental model where they modified the probability of infecting agents in the same work group, in this way

Work

Basic condition. Work group

p	Età di j				
Età di i	1	2	3	4	5
1		0,0001	0,0001	0,0001	0,0001
2	0,0001	0,001	0,001	0,001	0,0001
3	0,0001	0,001	0,05	0,05	0,001
4	0,0001	0,001	0,05	0,001	0,0001
5	0,0001	0,0001	0,001	0,0001	0,0001

No Work condition. Work group

p	Età di j				
Età di i	1	2	3	4	5
1		0,0001	0,0001	0	0
2	0,0001	0,0001	0,001	0	0
3	0,0001	0,001	0,05	0	0
4	0	0	0	0	0
5	0	0	0	0	0

Leisure

Basic condition. Leisure group

p	Età di j				
Età di i	1	2	3	4	5
1	0,001	0,0001	0,001	0,001	0,0001
2	0,0001	0,01	0,05	0,001	0,001
3	0,001	0,05	0,05	0,05	0,001
4	0,001	0,001	0,05	0,001	0,001
5	0,0001	0,001	0,001	0,001	0,0001

No Leisure Condition. Leisure Group

p	Età di j				
Età di i	1	2	3	4	5
1	0,001	0,0001	0,001	0	0
2	0,0001	0,01	0,05	0	0
3	0,001	0,01	0,05	0	0
4	0	0	0	0	0
5	0	0	0	0	0

The simulation goes from the basic tables to the No Work, No Leisure tables continuously, transforming the cells shown in yellow from the initial values to zero. As these probabilities decrease, the simulator proportionally increases the probabilities on the same age classes that do not involve work and leisure.

The results are summarized in Figure 4 and Figure 5.

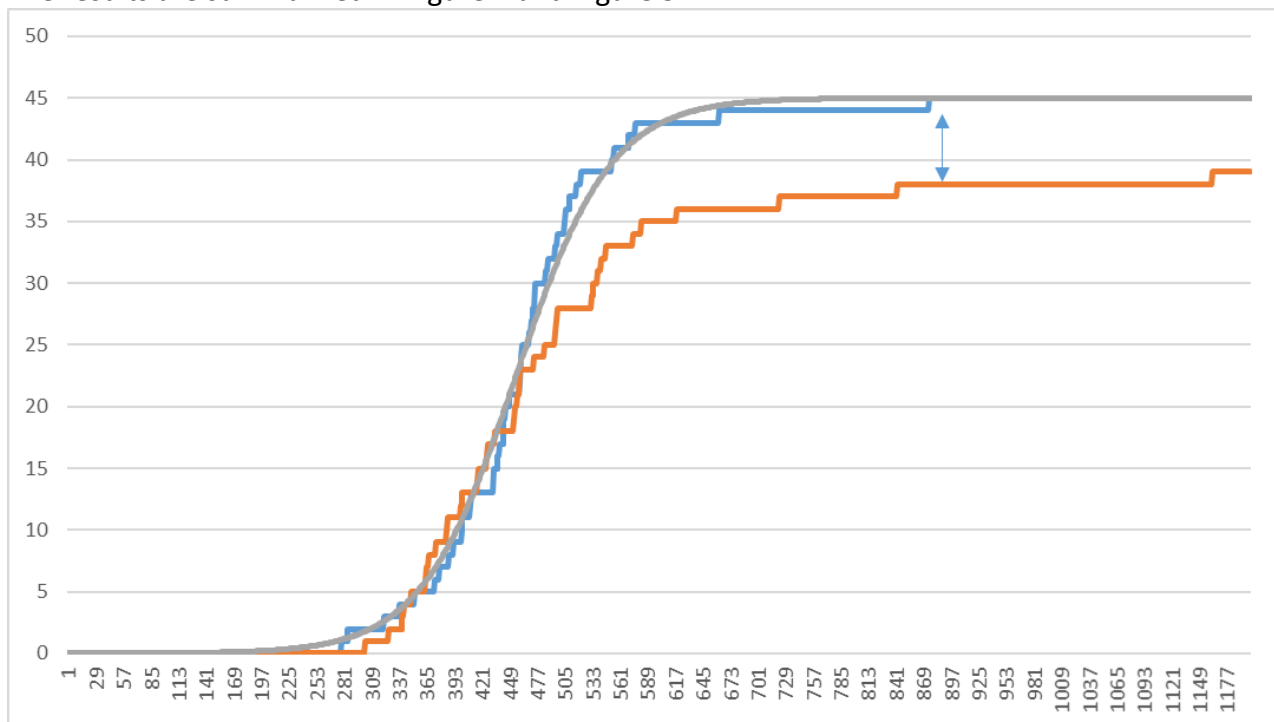


Figure 4 Number of deceased in the basic condition (blue) and in the condition with no probability of infection in work and leisure groups (orange). The grey curve represents the function that describes the trend in the number of deceased persons over time.

Figure 4 shows the effect of the decrease in the probability of infection in work and leisure groups for older people. We compared two socio-cultural situations: Basic (blue) for northern Italy, with higher probability of employment and maintenance in the productive fabric of elderly people, with the typical socio-cultural structure of northern regions, where elderly people continue to have relationships with each other during their leisure; No Work, No Leisure, (orange) with neither of these two active interactions. Using data from the Base curve we defined the function that describes the dynamics, which is a logistic curve (grey), as we expected. We performed a series of simulations, starting from the No Work, No Leisure condition and we calculated the distance

between the number of deaths at the end of the dynamics and the number of deaths expected by the logistic curve (blue arrow).

The results are very clear: as we move from the No Work, No Leisure to the Base condition, the number of deaths increases, thus showing that at least one of the factors that explain the different incidence of Covid19 in northern Italy compared to the rest of the country, is due to behaviours and socio-cultural structures typical of the north of the country.

It should be noted that the differences in terms of deaths derive from differences in the dynamics of very mild contagions (Figure 5): it is the type of virus itself, represented by the transition matrices, that explains the amplification of seemingly minimal differences.

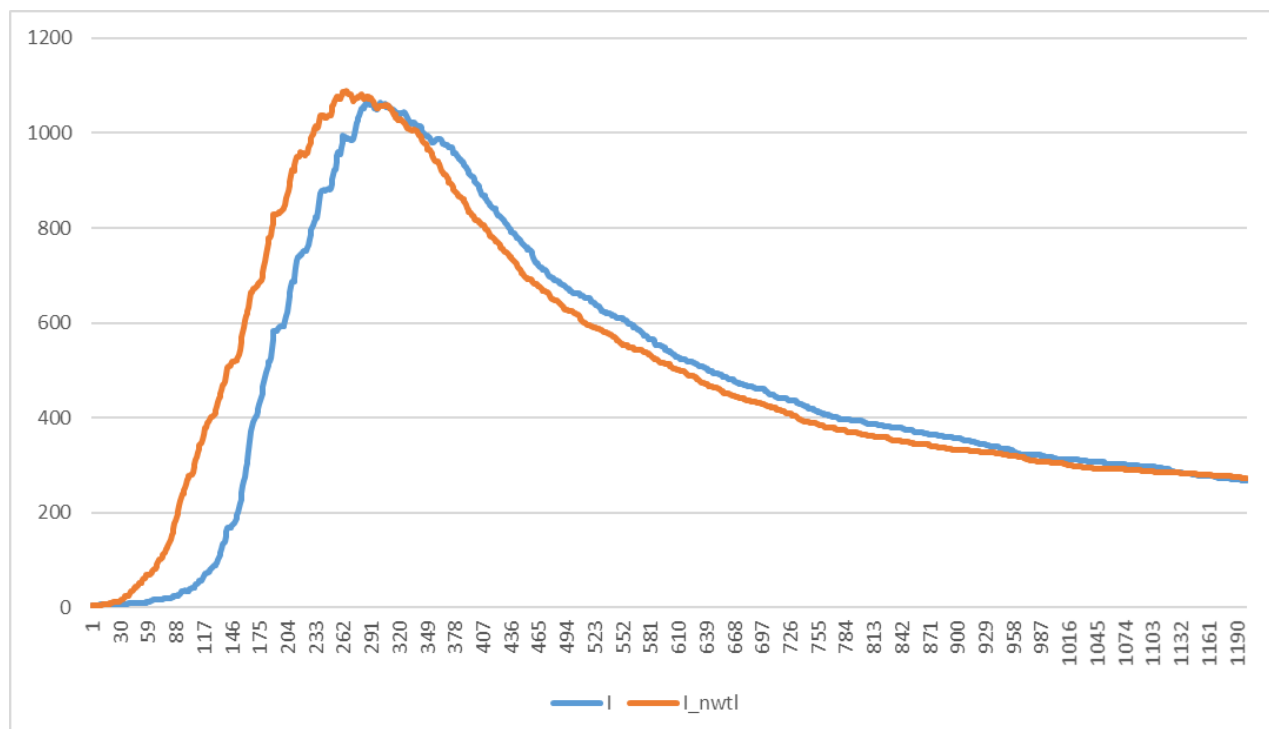


Figure 5 Dynamics of basic condition (blue) and no Work no Leisure (orange) infections

Next insights

The next work, in addition to looking for behavioral evidence, will describe the topological structure of the municipalities involved in the calculation of incidence, trying to cross-reference data related to the number and distance between municipalities, with information on the presence or absence of commuting, and on which directions.

The idea is still to look for evidence that leads to explanations of the difference between incidence referring to economic/social structures.

Bibliography

- [1]. UCM, Modello di Simulazione ad Agenti applicato ai comportamenti sociali determinanti la dinamica di pandemie (2 aprile 2020)
- [2] ISTAT istituto Nazionale di Statistica www.istat.it
- [3] Ministero della Salute www.salute.gov.it; Worldmeters.info <https://worldmeters.info>
- [4] Hethcote H (2000). "The Mathematics of Infectious Diseases". SIAM Review. 42 (4): 599–653. Bibcode:2000 SIAMR..42..599H. doi:10.1137/s0036144500371907