

# Determination and qualitative analysis of a continuous epidemic model

Giuseppe Franco, Federica Gottardo and Pietro Scuttari  
Math en Jeans - Liceo scientifico "R. Bruni", Padua (Italy)

## Abstract

The problem we faced consists in analyzing the spreading of a disease in a population. This illness had a given probability of spreading from person to person, a given probability of killing an infected person and a given probability that an infected person has to recover. Is it better to vaccinate the population or to isolate it in isolated groups? Firstly we tried to solve this problem utilizing the tree graphs and calculating a formula that would give us the number of the dead. The tree graph method did not lead to a general formula so we changed method and started to work out a formula by calculating how the number of healthy people, the number of the ill, the number of those who healed up and the number of the dead change: firstly in discrete time frame then, by calculating the derivatives, in continuous time obtaining a system of differential equations similar to the Kermack-McKendrick Model [1]. After a qualitative analysis of the system, confirmed by a computer simulation (with Python), we were able to answer the question in the case there is only one ill at the beginning.

## 1 Introduction

We have a population  $N$  individuals in which the disease is spreading with a certain probability of spreading from person to person,  $p_A$ , a certain probability that an infected has to die,  $p_M$ , and a certain probability that an infected has to heal,  $p_G$ .

We then divided the population in 4 groups:

- the ones that were not yet infected at the time  $i$ :  $S_i$
- the ill individuals at the time  $i$ :  $A_i$
- the dead at the time  $i$ :  $M_i$

- the healed individual at the time  $i$ :  $G_i$  that cannot be infected anymore.

It is worth noting that the sum of the probability that one has to die and the probability that one has to heal is equal to 1, because an ill can only die or heal and this makes the two probabilities complementary for the conditioned probability.

## 2 Hypothesis

We made some hypothesis to simplify the problem: we started by ensuring that the population stayed constant:

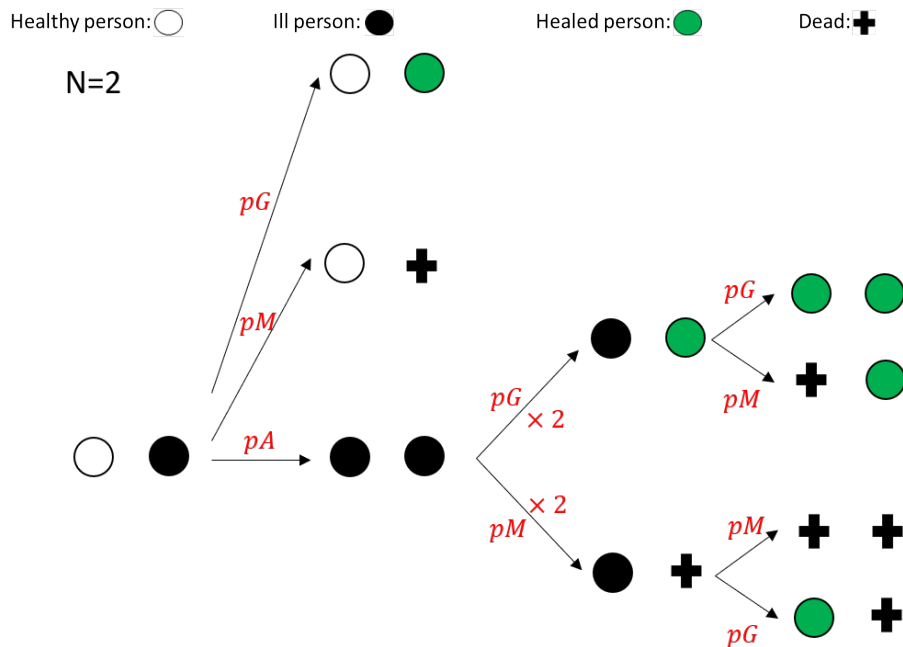
- the population is isolated
- there are no new born
- there are no dead for reasons other than the illness
- the dead ( $M_i$ ) are still part of the population ( $N$ )

We then laid some ground rules to determine how the disease spread:

- there is no incubation period
- the illness can only spread from direct contact between a healthy individual  $S_i$  and an ill one  $A_i$
- every individual has the same probability of meeting any other member of the population
- the vaccine has 100% effectiveness
- there is only one ill at the beginning

## 3 First approach: Tree graphs

Firstly we started with the method of tree graph. At the beginning we considered a population of two individuals and one of which is ill. So we considered  $S_0 = 1$  and  $M_0 = 0$ . We chose also that in every step only one individual can change his state.



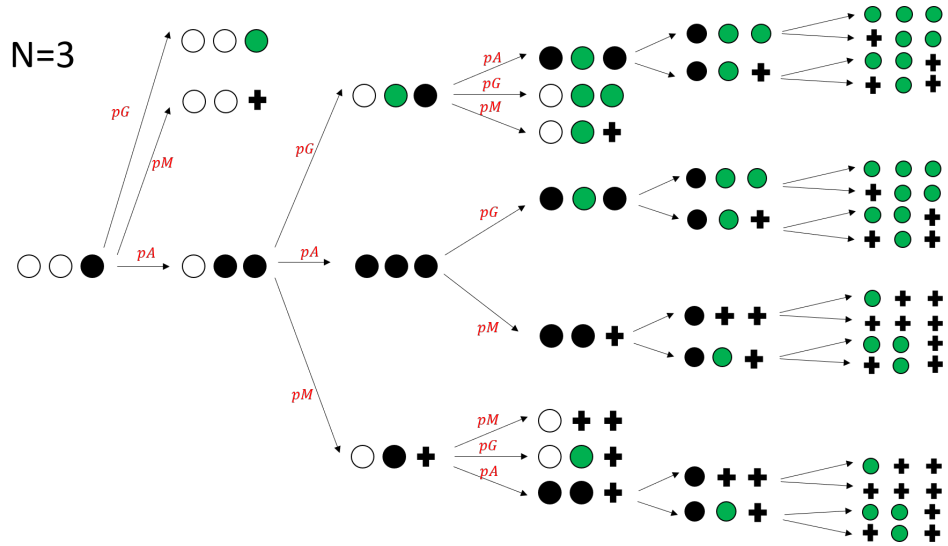
Thanks to the graph we observed all the possibilities which the illness has to spread: the ill can heal with a probability  $p_G$ , but he could also die with the probability  $p_M$ , and finally there is also the probability that the ill infect the other individual with the probability  $p_A$ .

If more than one individual is in the same state the probability of the change happening, is multiplied by the number of individuals.

So for example one of the two individuals that are ill, can heal or die. these two probabilities are multiplied for two because the change could happen to both.

We proceeded with this logic till there are no more ill people, so the population is made up of only healed or dead individuals.

Then we applied the same method with a population of three people in this way the chances of spreading grew a lot (we tried to describes the spreading of the pandemic also when there are four and five people in our problem).



Our idea was in the end for every population to count the dead individuals. For each population we found out the number of the dead and we saw that the dead people depend on the number of the previous deaths. This suggested us that the formulas could be a sequence:

$$\begin{aligned}
 M_1 &= p_M \\
 M_2 &= 2 \cdot p_M^2 \cdot p_A \\
 M_3 &= 20 \cdot p_M^3 \cdot p_A^2 \\
 M_4 &= 444 \cdot p_M^4 \cdot p_A^3 \\
 M_5 &= 16944 \cdot p_M^5 \cdot p_A^4 \\
 &\dots \\
 M_n &= (???) \cdot p_M^n \cdot p_A^{n-1}
 \end{aligned}$$

The coefficient of the literal part is recursive, but the number coefficient seems not to be recursive. We tried to find out a some sort of recursion but we didnt find anything. The purpose of that method is to find a general sequence so we could know the number of dead, healed and also healthy people in a population.

## 4 Finding a new formula

Since the tree graph method did not lead to any recursion, we started from the beginning trying to calculate a new formula with a deterministic approach.

We started by calculating the number of encounters between a healthy and an ill individual ( $S_n \cdot A_n$ ).

We divided it by the number of total encounters, equal to the binomial coefficient  $\binom{N}{2}$ .

So multiplying this result by the probability of the disease spreading, we obtain the probability that a healthy individual meeting an ill gets infected. We then multiplied the result by the population  $N$  and so we obtain the number of the new ill  $2S_n \cdot A_n / (N - 1) \cdot p_A$ .

After this we calculated the number of new deaths  $A_n \cdot p_A$  and the number of new healed  $A_n \cdot p_G$ .

Using these results we were able to create a system that describes the evolution of the illness from the time  $n$  to the time  $n + 1$ :

$$\begin{cases} S_{n+1} - S_n = -2p_A S_n \cdot A_n / (N - 1) \\ A_{n+1} - A_n = (2p_A S_n / (N - 1) - 1) A_n \\ M_{n+1} - M_n = p_M \cdot A_n \\ G_{n+1} - G_n = p_G \cdot A_n \end{cases}$$

To generalize this system, that shows the situation in the discrete times, we moved to a continuous time. We did this by multiplying the formulas by an real increment  $h$  (the new time interval is  $[t, t + h]$ ):

$$\begin{cases} S(t + h) - S(t) = -2p_A S(t) \cdot A(t) / (N - 1) \cdot h \\ A(t + h) - A(t) = (2p_A S(t) / (N - 1) - 1) A(t) \cdot h \\ M(t + h) - M(t) = p_M \cdot A(t) \cdot h \\ G(t + h) - G(t) = p_G \cdot A(t) \cdot h \end{cases}$$

Dividing by  $h$  we obtain the incremental ratio and calculate the derivative of our formulas by imposing the limit for  $h$  to 0:

$$\begin{cases} S'(t) = -2p_A S(t) \cdot A(t) / (N - 1) \\ A'(t) = (2p_A S(t) / (N - 1) - 1) A(t) \\ M'(t) = p_M \cdot A(t) \\ G'(t) = p_G \cdot A(t) \end{cases}$$

So we obtained a system of differential equations but was very difficult solve it, so we studied it in a different way. We found a confirmation of our work in in the SIR model by Kermack-McKendrick (see [1] or [2]).

## 5 Qualitative analysis

Since we were not able to solve the system we tried to analyze the formulas with a qualitative analysis. The idea is to look for an invariant by working on relationships between the derived functions. We started by calculating the ratio of  $A'/S'$ , by substituting  $\beta$  in the formula

$$\beta = \frac{N-1}{2p_A},$$

we are able to find a differential equation.

$$\begin{aligned}\frac{A'}{S'} &= \left( \frac{2p_A \cdot S(t)}{N-1} - 1 \right) \frac{N-1}{-2p_A \cdot S(t)} \\ &= -1 + \frac{N-1}{2p_A \cdot S(t)} \\ &= -1 + \frac{\beta}{S(t)},\end{aligned}$$

then

$$A' = S' \left( \frac{\beta}{S(t)} - 1 \right).$$

We then calculated the sign of the derivative of the ill function and we found a point where the derivative is equal to zero, which it should result in a local maximum, in  $S(t) = \beta$ :

$$A' = 0 \Rightarrow S(t) = \beta.$$

We solved the equation by calculating the derivative

$$A(t) = -S(t) + \beta \ln \left( \frac{S(t)}{S(0)} \right) + N,$$

and then substituted  $S(t)$  with the value found to find where in the graph this maximum should be:

$$A(t) = N - \beta \left( 1 - \ln \left( \frac{\beta}{S(0)} \right) \right).$$

The other analysis we made is finding where the number of healthy stabilized, that is the derivative is equal to zero. Remembering that

$$S'(t) = -2 \frac{S(t) \cdot A(t)}{N-1} p_A,$$

this happens when the ill are reduced to zero:

$$S'(t) = 0 \rightarrow A(t) = 0.$$

We also found a maximum limit to the number of ill possible but only in discret case: from

$$S_{n+1} = S_n \left( 1 - \frac{2 \cdot A_n}{N-1} p_A \right)$$

we can deduce that

$$S_{n+1} \geq 0 \Rightarrow A_n \leq \frac{N-1}{2 \cdot p_A}, \forall n \in \mathbb{N}.$$

Then

$$A(t) \leq \frac{N-1}{2 \cdot p_A}, \forall t \in [0, +\infty[.$$

## 6 Qualitative analysis with Python

We then used the equation that we found to write a computer program that would allow us to simulate the evolution of the illness, so we gave the values for the variables.

```

1 #Population
  N=1000
3 #Probability of getting ill
  P_a=0.7
5 #Probability of healing
  P_g=0.55
7 #Probability of dying
  P_m=1-P_g
9 #Number of ill at the start
  A=1
11 #Number of death at the start

```

```

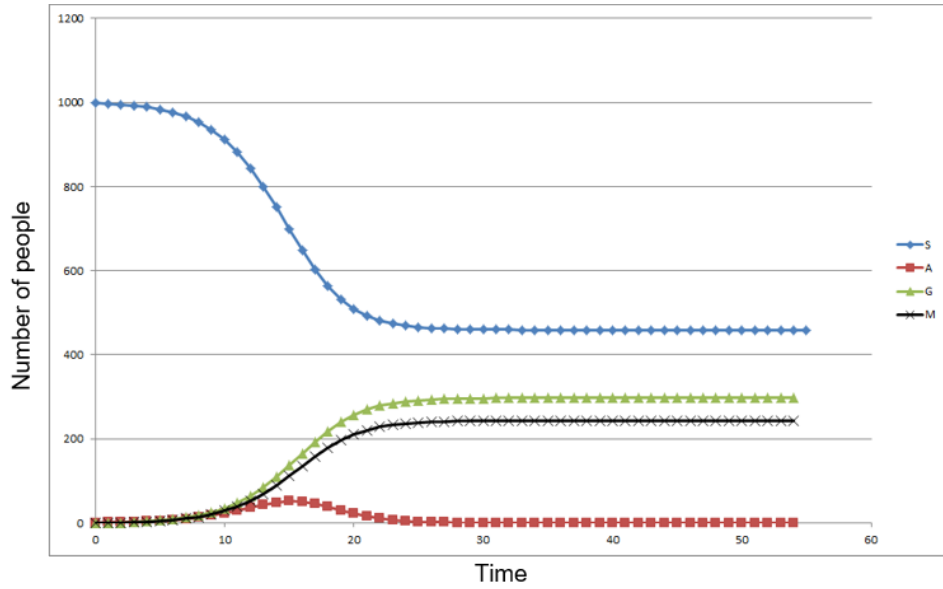
M=0
13 #Number of healed at the start
G=0
15 #Number of healthy at the start
S=N-A-M-G
17
19 t=0
21
23 while 1:
25     #calculating the healthy
27     t+=1
29     if S>0:
31         S1=S-(2*P_a*(S*A)/(N-1))
33     else:
35         S1=0
37
39     #calculating the ill
41     A1=(2*S*A*P_a/(N-1) - A*(P_g+P_m))+A
43
45     if A<=0.00001:
47         S=S1
49         A=A1
51         M=M1
53         G=G1
         break
         #calculating the dead
         M1=A*P_m +M
         if S<=0.00001 and A<=0.00001:
             break
         #calculating the healed
         G1=A*P_g +G
         if S<=0.00001 and A<=0.00001:
             break
         S=S1
         A=A1
         M=M1
         G=G1

```

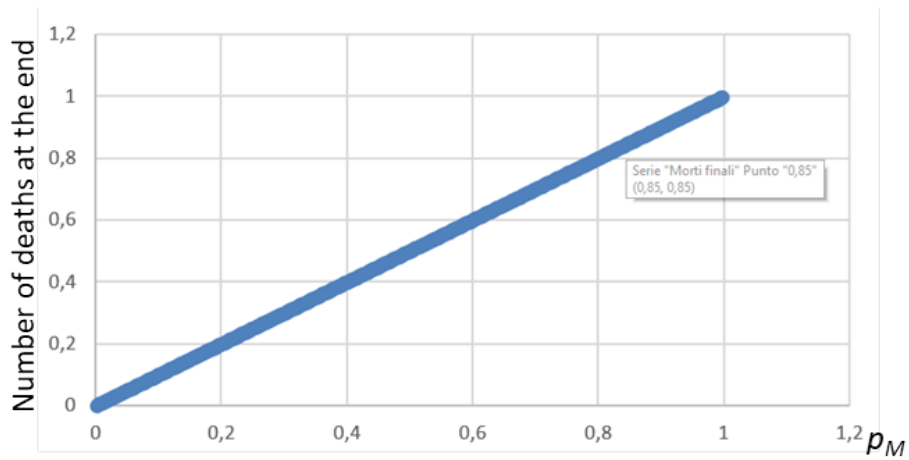
Evoluzione\_malattia.py



This let us plot this graph where there are both the local maximum and the threshold that we calculated earlier.



We then proceeded by changing the variables, firstly  $p_M$  and  $p_G$ , making sure to keep them complementary, then  $p_A$ , and plotting the resulting graphs. Thanks to the graph we can clearly determine that  $p_M$  and  $M$  are directly proportional.



## 7 Conclusion

To answer the final question, is it better to vaccinate the population or divide it in isolated groups? We asked ourselves how our formulas change considering the two cases? We determined that dividing the population is equal to only considering one division of the population, because there is only one ill at the beginning, and vaccinating the population is equal to having a part of the population healed from the beginning, so they can't be infected anymore. This means that for the formula of the isolations we substituted  $N$  for  $N/q$  (where  $q$  is the number of divisions):

$$(7.1) \quad A'(t) = \left( 2^{\frac{N/q - A(t) - G(t) - M(t)}{N/q - 1}} p_A - 1 \right) A(t);$$

instead, for the formula of the vaccination, we substituted  $S$  for  $S(t) - N \cdot (1 - 1/q)$  because we subtracted from the healthy individuals  $S(t)$  the population vaccinated and to make a sensible comparison we assumed that dividing the population in  $q$  groups would correspond to vaccinating  $1 - 1/q$  of the population  $N$ :

$$(7.2) \quad A'(t) = \left( 2^{\frac{N - A(t) - G(t) - M(t) - N(1 - 1/q)}{N - 1}} p_A - 1 \right) A(t).$$

We then compared the two formulas, that is we ask ourselves if the  $A'(t)$  in (7.1) is greater, equal or less than  $A'(t)$  in (7.2) for all  $t \in [0; +\infty[$ ; after some simple simplification we get that:

$$\frac{N/q - A(t) - G(t) - M(t)}{N/q - 1} > \frac{N - A(t) - G(t) - M(t) - N(1 - 1/q)}{N - 1}.$$

With further elementary simplifications we get that, for all  $t \in [0; +\infty[$ ,  $N > N/q$ .

Isolating the population always results in an higher number of ill individuals and, since we know that the number of ill people is directly proportional to the number of deaths, this also means a higher number of deaths. For this reason it is better to vaccinate the population.

### Remark

- Using the first approach, the tree graph, it is possible to calculate further elements (for example  $M_6$ ,  $M_7$ , ...) but this method would

became too complex, maybe with a specific computer program we would obtain a greater number of coefficients and so in this way we could determine a possible recursion and so a formula for any number of population  $N$ .

- We found this solution thanks to the hypothesis  $A_0 = 1$ . If we were to remove it the answer would depend on  $p_A$  and the calculation would be much more complex (see [3]).

## 8 Bibliografy

[1] W. Kermack and A. McKendrick, *A contribution to the mathematical theory of epidemics*, Proc. R. Soc. London A115, pp. 700-721, 1927.

[2] B. Cifra, L. Lamberti and S. Marone, <http://www1.mat.uniroma1.it/people/pensionati/lamberti/lauree/sir.pdf>, AA 2008/'09.

[3] J. M. Mahaffy, <https://jmahaffy.sdsu.edu/courses/f09/math636/lectures/epidemics/epidemics.pdf>, AA 2008/'09.