Introduction

We model the propagation of the pandemic from a probabilistic standpoint. To do so, we first introduce random variables. Then, the individuals will be categorized as healthy, infected, or dead (such as in the SIR model or other compartmental models).

Let's introduce :

$$
\begin{cases}
N \in N : & \text{Total population at instant } t_0 \\
n \in N : & \text{Mesh step} \\
\Delta_t > 0 : & \text{Time step} \\
t_n = n\Delta_t & \\
S_n : & \text{number of individuals that can be infected at } t_n \\
I_n : & \text{number of infected individuals at } t_n \\
M_n : & \text{number of dead people at } t_n
\end{cases}
$$

1. Time partition hypothesis :

By taking a low Δ_t value, we can estimate that there is at most **one changing state** by time interval.
This morning, at 10 A.M, there are 4152 confirmed cases (Friday, April 10th, 2020). Hence, we can reasonably think that $\Delta_t \simeq 10s$ is a great approximation.

Therefore, each transition will concern one individual :

$$
\forall j \notin \{i-1, i, i+1\}, \ \forall k, \ \forall \ell, \ P((I,M)_{n+1} = (j,k) \mid (I,M)_n = (i,\ell)) = 0
$$
$$
\forall k \notin \{l, \ell+1\}, \ \forall i, \ \forall j, \ P((I,M)_{n+1} = (j,k) \mid (I,M)_n = (i,\ell)) = 0
$$

2. "Non-existence of zombies"

Let's add other conditions. We consider that any individual can't become infected and die at the exact same time. Hence, $P((I,M)_{n+1} = (i+1, \ell+1) \mid (I,M)_n = (i,\ell)) = 0$.

In the same way, if an infected individual dies, the number of infected individuals has to decrease : $P((I,M)_{n+1} = (i, \ell+1) \mid (I,M)_n = (i,\ell)) = 0$.

3. Infection

Let us assume that the virus spread with a speed β. A new case of infection can be traduced by $(I_n = i, M_n = \ell) \rightarrow (I_{n+1} = i+1, M_{n+1} = \ell)$, which implies:

$$P((I,M)_{n+1} = (i+1, \ell) \mid (I,M)_n = (i, \ell)) = b_i = \frac{\beta i(N - \ell - i)}{N - \ell}\Delta_t$$

One can become infected if there is contact with another infected individual. By taking into account the already dead persons, we obtain the number of healthy people: $N - \ell - i$, hence the previous formula.

4. Healing (or death) of an individual

In this model, we suppose that someone healthy/healed is not a threat to the others. We introduce a death rate α and a cure rate γ and we obtain :

$$P((I,M)_{n+1} = (i-1, \ell+1) \mid (I,M)_n = (i, \ell)) = d_{i,m} = \alpha i \Delta_t$$
$$P((I,M)_{n+1} = (i-1, \ell) \mid (I,M)_n = (i, \ell)) = d_{i,s} = \gamma i \Delta_t$$

We will use this notation below : $d_i = d_{i,m} + d_{i,s}$.

5. Stagnation

Our last condition is implied by the two previous ones :

$P((I,M)_{n+1} = (i, \ell) \mid (I,M)_n = (i, \ell)) = 1 - b_i - d_i$. This correspond to the scenario where there is no new infected.

6. Partial conclusion

By summing up all our conditions, we obtain the following conditional probability :

$$P((I,M)_{n+1} = (j,k) \mid (I,M)_n = (i,\ell)) = \begin{cases} b_i \\ \text{if } (j,k) = (i+1,\ell) \\ d_{i,m} \\ \text{if } (j,k) = (i-1,\ell+1) \\ d_{i,s} \\ \text{if } (j,k) = (i-1,\ell) \\ 1 - (b_i + d_i) \\ \text{if } (j,k) = (i,\ell) \\ 0 \\ \text{else} \end{cases}$$

7. Remark

In addition to choosing Δ_t small enough, we have to verify that $\max\limits_{1 \leq i \leq N}(b_i + d_i) \leq 1$ in order to ensure that our probabilities are positives.

Infectiousness analysis

1. $\mathcal{R}_0$

Intuitively, we can introduce $\mathcal{R}_0 = \frac{\beta}{\alpha+\gamma}$, characteristic of the basic reproduction rate.

- If $\mathcal{R}_0 > 1$: it's a highly infectious virus.
- If $\mathcal{R}_0 < 1$: the pandemic will be stabilized almost surely.
- If $\mathcal{R}_0 = 1$: limit case scenario.

2. Will the pandemic end ?

One can try to estimate the end of the pandemic using $\mathcal{R}_0$ based on this model. The corresponding metric is : $T = \inf[n \geq 0 \mid I_n = 0]$.

This random variable (which is a stopping time) represents the first moment where the virus will no longer exist (the only one, considering the expression of b_i).

Let us look at the **average time** of extinction in function of the initial number of infected k : $\tau_{k,0}(\alpha, \beta, \gamma, \Delta_t) = E[T \mid (I, M)_0 = (k, 0)]$.

3. Expression of the average stopping time

Let's consider $1 \leq i \leq N$. By conditioning with respect to the first change of state, we have :

$$
\begin{aligned}
\tau_{i,\ell} &= E[T \mid (I, M)_0 = (k, \ell)] \\
&= P((I, M)_1 = (i + 1, \ell) \mid (I, M)_0 = (i, \ell)) E[T \mid (I, M)_1 = (i + 1, \ell), (I, M)_0 = (i, \ell)] \\
&\quad + P((I, M)_1 = (i - 1, \ell + 1) \mid (I, M)_0 = (i, \ell)) E[T \mid (I, M)_1 = (i - 1, \ell + 1), (I, M)_0 = (i, \ell)] \\
&\quad + P((I, M)_1 = (i - 1, \ell) \mid (I, M)_0 = (i, \ell)) E[T \mid (I, M)_1 = (i - 1, \ell), (I, M)_0 = (i, \ell)] \\
&\quad + P((I, M)_1 = (i, \ell) \mid (I, M)_0 = (i, \ell)) E[T \mid (I, M)_1 = (i, \ell), (I, M)_0 = (i, \ell)] \\
&= b_i(1 + \tau_{i+1,\ell}) + d_{i,m}(1 + \tau_{i-1,\ell+1}) + d_{i,s}(1 + \tau_{i-1,\ell}) + (1 - b_i - d_i)(1 + \tau_{i,\ell})
\end{aligned}
$$
$$
(b_i + d_i)\tau_{i,\ell} = b_i\tau_{i+1,\ell} + d_{i,m}\tau_{i-1,\ell+1} + d_{i,s}\tau_{i-1,\ell} + 1
$$

by using the **strong Markov property**.

We define $\tau = (\tau_{0,0}, \tau_{1,0}, \ldots, \tau_{N,0}, \tau_{0,1}, \ldots, \tau_{N,N})^T$. We thus have $\tau_k = \tau_{i,\ell}$ où $i \equiv k - 1 \mod (N + 1)$ and $\ell = \lfloor \frac{k}{N+1} \rfloor$.

We can rewrite the previous expressions as a linear system : $A.\tau = B$ with $B = (1, \ldots, 1)^T \in R^{(N+1)^2}$ and

$$
\begin{aligned}
A_{k,j} &= \sum_i \delta(i \equiv k - 1 \mod (N + 1))\delta(j = \lfloor \frac{k}{N+1} \rfloor)(b_i + d_i) \\
&\quad - \delta(i - 1 \equiv k - 1 \mod (N + 1))\delta(j = \lfloor \frac{k}{N+1} \rfloor)d_{i,s} \\
&\quad - \delta(i - 1 \equiv k - 1 \mod (N + 1))\delta(j + 1 = \lfloor \frac{k}{N+1} \rfloor)d_{i,m} \\
&\quad - \delta(i + 1 \equiv k - 1 \mod (N + 1))\delta(j = \lfloor \frac{k}{N+1} \rfloor)b_i
\end{aligned}
$$

so $\tau_{i,0}$ corresponds to the index $i + 1$ of $A^{-1}.B$.

4. Last remark

This model allows us to evaluate our Markov chains on concrete examples by fixing some initial conditions (initial population N_0, including i_0 infected individuals). This framework is particularly appropriate with small populations (state or county) and takes into account the intrinsically stochastic character of a pandemic.