

# SIR Model with Leslie Matrices Approach and Why It does not Work

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**SIR Model** is a continuous model used in epidemiology to analyze the spread of infectious diseases. By separating the population into three groups **S**, **I**, and **R** (**S**usceptible, **I**nfectious, and **R**ecovered), and defining  $s$ ,  $i$ , and  $r$  as the proportions of the population in **S**, **I**, and **R** respectively, with  $s + i + r = 1$ , we can describe the rate of change over time for each group by the following equations:

$$\frac{ds}{dt} = -\beta si \tag{1}$$

$$\frac{di}{dt} = \beta si - \gamma i \tag{2}$$

$$\frac{dr}{dt} = \gamma i \tag{3}$$

where  $\beta$  is the average number of contacts per person per time unit, and  $\gamma$  is the inverse of the mean infectious period. In general, we solve these ordinary differential equations to study the rate of change over time. We also derive  $R_0 = \frac{\beta}{\gamma}$ , the basic reproduction number, which indicates whether an epidemic is occurring in the system.

**Leslie Matrix** is a discrete model used in population ecology to analyze population trends. It also separates the population into groups of interest. Let's consider three age groups (for example, less than 30, 30-60, and more than 60). Let  $n_1(t)$ ,  $n_2(t)$ , and  $n_3(t)$  represent the proportions of the population in each group at time  $t$  (with  $n_1(t) + n_2(t) + n_3(t) = 1$ ). We can write:

$$v(t) = \begin{pmatrix} n_1(t) \\ n_2(t) \\ n_3(t) \end{pmatrix}, v(t+1) = \begin{pmatrix} f_1 & f_2 & f_3 \\ s_1 & 0 & 0 \\ 0 & s_2 & 0 \end{pmatrix} v(t) = Lv(t) \quad (4)$$

where  $f_j$  is the fertility rate and  $s_j$  is the survival rate for each age group. The matrix  $L$  is called the Leslie matrix. By considering the eigenvalues of  $L$ , the dominant eigenvalue  $\lambda$  ( $|\lambda| \geq |\lambda_j|$ ) can indicate whether the population is increasing, decreasing, or remaining the same.

We have the idea that both models are dynamical systems that explain changes in population groups, so we should use the latter approach to solve the former problem.

We can construct a discrete version of the SIR model similarly to equation (4) as:

$$v(t+1) = \begin{pmatrix} s(t+1) \\ i(t+1) \\ r(t+1) \end{pmatrix} = \begin{pmatrix} s(t) - \beta s(t)i(t) \\ i(t) + \beta s(t)i(t) - \gamma i(t) \\ r(t) + \gamma i(t) \end{pmatrix} \quad (5)$$

We can observe that this is a nonlinear system of equations. Consequently, we cannot find a matrix  $L$  such that  $v(t+1) = Lv(t)$ , meaning we cannot determine a trivial eigenvalue. Additionally, we can see a fundamental difference between these two models: in the SIR model, the rate of number of people who become infected depends on both the susceptible and the infectious populations, making the system nonlinear.

$$s(t+1) = s(t) - \beta s(t)i(t) \quad (6)$$

$$i(t+1) = i(t) + \beta s(t)i(t) - \gamma i(t) \quad (7)$$

$$r(t+1) = r(t) + \gamma i(t) \quad (8)$$

Even if we cannot find an exact solution for this system of equations, with initial conditions, these equations are easier to implement through simulation.

## References

- [1] H. Bachmann (2024). Linear Algebra. [https://www.henrikbachmann.com/uploads/7/7/6/3/77634444/linear\\_algebra\\_v\\_20.pdf](https://www.henrikbachmann.com/uploads/7/7/6/3/77634444/linear_algebra_v_20.pdf), Online Accessed: 2024-07-21.

- [2] S. Richard (2024). Graph theory. <http://www.math.nagoya-u.ac.jp/~richard/teaching/s2024/Graph.pdf>, Online Accessed: 2024-07-21.