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On the relevance of Reproduction number to Mathematical modeling

[1]A.G. Ibraheem and [2]A.Abdullahi
[1,2]Department of Mathematics and Statistics Federal Polytechnic, Ado-Ekiti
Ekiti state-Nigeria

Abstract: *We discuss basically the importance of reproduction number in Mathematical modeling as a summary measure of the transmission potential of an infectious disease.The basic reproduction number R_0 for a compartmental disease model is often calculated by the next generation matrix (NGM) approach. It provides significant insight into the transmission dynamics of a disease and can guide strategies to control its spread.*

I. Introduction

Epidemic models provide significant practical insights into the epidemiology of infectives diseases. Such concepts are widely used in the design and implementation of infection control programmes. Infact, epidemic theory has been instrumental in our understanding of the threshold phenomena that govern the spread of most infectious diseases.

A typical example is the discovery of Ross (1910) as cited by Farrington, C.P.(2001) that the number of mosquitoes per head of population must exceed a certain value for malaria to be become endemic. The effect of threshold cannot be underestimated in infectious diseases epidemiology. As an example, for infections directly transmitted from person to person, an infection can only take off and become endemic if the population of susceptible individual exceeds a certain critical value. This phenomena finds formal expression in the threshold theorems derived from deterministic and stochastic epidemic models. More importantly, some infections can be eradicated completely, as was in the case of small-pox and very soon with polio. Of the various threshold parameters arising in epidemic theory perhaps the most useful is the basic reproduction number, denoted by R_0.

One of the fundamental questions of mathematical epidemiology is to find threshold conditions
that determine whether an infectious disease will spread in a susceptible population when the disease is introduced into the population. The threshold conditions are characterized by the so called reproductive number, the reproductive ratio, basic reproductive value, basic reproductive rate, or contact number, commonly denoted by R0 in mathematical epidemiology.

The basic reproduction number R0 is arguably the most important quantity in infectious disease
epidemiology.

The concept of R_0, introduced by Ross as cited by James et al (1999) is defined in epidemiological modeling such that if $R_0 < 1$, the modeled disease dies out, and if
$R_0 > 1$, the disease spreads in the population. Also, Farrington et al (2001) defined reproduction number as the average number of secondary infections generated by a single typical infective individual in a totally susceptible population.

The basic reproduction number R_0 for a compartmental disease model is often calculated by the next generation matrix (NGM) approach. Since R_0 synthesizes important
elements of the infection transmission process, it identifies the most important factors in the
infection transmission cycle.

When the interactions within and between disease compartments are interpreted differently, the NGM approach may lead to different R_0expressions.Majid, B (2012).

Although the environment could play different roles in the disease transmission process, leading to different R_0 expressions, there is a unique type reproduction number when control strategies are applied to the host population. All R_0 expressions agree on the threshold value 1 and preserve their order of magnitude. The basic reproduction number, R_0, is considered as one of the most practical tools that mathematical thinking has brought to epidemic theory. Depending on the biological interpretations of the disease compartments, different R_0 expressions can be derived for a compartmental model.

1. **Model equation**(James, 1999)

$$\frac{dS}{dt} = \mu\left(S^{0} - S(t)\right) - \lambda(t)S(t)$$

$$\frac{dI}{dt} = \lambda(t)S(t) - (\mu + v)I(t)$$

$$\frac{dA}{dt} = vI(t) - \delta A(t)$$

where S, I, and A denote the individuals susceptible to infection, the infected individuals, and the AIDS cases, respectively; μS^{0} is the input flow into the susceptible group; μ the removal rate; vthe rate of contracting AIDS; δ the removal rate due to the death from AIDS or other reasons; and λ is the rate of infection given by

$$\lambda(t) = \frac{I(t)}{S(t) + I(t)} \text{ and}$$

$$R_{0} = \frac{r\beta}{\mu + v}$$

2.**An SEI model with two latent categories**(Diekmann, 2015)

$$\frac{dS}{dt} = \mu N - \beta\frac{SI}{N} - \mu S$$

$$\frac{dE_{1}}{dt} = p\beta\frac{SI}{N} - (v_{1} + \mu)E_{1}$$

$$\frac{dE_{2}}{dt} = (1 - p)\beta\frac{SI}{N} - (v_{2} + \mu)E_{2}$$

$$\frac{dI}{dt} = v_{1}E_{1} + v_{1}E_{2} - (\gamma + \mu)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

Linearised system gives

$$\frac{dE_{1}}{dt} = p\beta - (v_{1} + \mu)E_{1}$$

$$\frac{dE_{2}}{dt} = (1 - p)\beta - (v_{2} + \mu)E_{2}$$

$$\frac{dI}{dt} = v_{1}E_{1} + v_{1}E_{2} - (\gamma + \mu)I$$

The corresponding Jacobian matrices at the disease free equilibrium of the above system are

$$F = \begin{pmatrix} 0 & 0 & p\beta \\ 0 & 0 & (1 - p)\beta \\ 0 & 0 & 0 \end{pmatrix}$$

$$v = \begin{pmatrix} -(v_1 + \mu) & 0 & 0 \\ 0 & -(v_2 + \mu) & 0 \\ v_1 & v_2 & -(\gamma + \mu) \end{pmatrix}$$

$$v^{-1} = \begin{pmatrix} \frac{1}{v_1 + \mu} & 0 & 0 \\ 0 & \frac{1}{v_2 + \mu} & 0 \\ \frac{v_1}{(v_1 + \mu)(\gamma + \mu)} & \frac{v_2}{(v_2 + \mu)(\gamma + \mu)} & \frac{1}{\gamma + \mu} \end{pmatrix}$$

The basic reproduction number for the vertical transmission is calculated as the spectral radius of the next generation matrix

$$FV^{-1} = \begin{pmatrix} \frac{p\beta v_1}{(v_1 + \mu)(\gamma + \mu)} & \frac{p\beta v_2}{(v_2 + \mu)(\gamma + \mu)} & \frac{p\beta}{\gamma + \mu} \\ \frac{(1-p)\beta v_1}{(v_1 + \mu)(\gamma + \mu)} & \frac{(1-p)\beta v_2}{(v_2 + \mu)(\gamma + \mu)} & \frac{(1-p)\beta}{\gamma + \mu} \\ \end{pmatrix}$$

Therefore

$$R_0 = \left(\frac{pv_1}{v_1 + \mu} + \frac{(1-p)v_2}{v_2 + \mu} \right) \frac{\beta}{\gamma + \mu}$$

3. The model(Majid, 2012)

The model consists of the standard *SIRS* model where*S*, *I*,*R* denotes the number of susceptible, infectious, and recovered hosts, respectively. Susceptible individuals become infectious either by adequate contacts with infectious individuals or the contaminated environment. Infectious individuals contaminate the environment by shedding pathogen that is capable of growth and survival in the environment.

Hence, the set of ordinary differential equations (ODEs) representing the *SIRSP* model is given by

$$\frac{dS}{dt} = b - \beta SI - \delta SP + \alpha R - \mu S$$

$$\frac{dI}{dt} = \beta SI + \delta SP - (\mu + m + v)I$$

$$\frac{dR}{dt} = vI - (\alpha + m)R$$

$$\frac{dP}{dt} = \gamma I + gP(1 - cP) - rP$$

The corresponding Jacobian matrices at the disease free equilibrium of the above system are

$$J = \begin{pmatrix} \beta S_0 & (\mu + m + v) \\ \gamma & g - r \end{pmatrix} \quad F = \begin{pmatrix} \beta S_0 & \delta S_0 \\ 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} (\mu + m + v) & 0 \\ -\gamma & r - g \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \dfrac{\beta b}{m(\mu + m + v)} + \dfrac{\delta\gamma b}{m(\mu + m + v)(r - g)} & \dfrac{\delta b}{m(r - g)} \\ 0 & 0 \end{pmatrix}$$

$$R_0 = \frac{\beta b}{m(\mu + m + v)} + \frac{\delta\gamma b}{m(\mu + m + v)(r - g)}$$

Model with incomplete treatment and vaccination

$$\frac{dS}{dt} = quA - (\mu + p)S - \beta SI + \varepsilon V$$

$$\frac{dV}{dt} = (1 - q)\mu A + pS - \beta\sigma VI - (\mu + \varepsilon)V$$

$$\frac{dE}{dt} = \beta I(S + \sigma V) - (\mu + \gamma)E + (1 - k)\delta T$$

$$\frac{dI}{dt} = \gamma E - (\mu + \alpha_1 + \xi)I + k\delta T$$

$$\frac{dT}{dt} = \xi I - (\mu + \alpha_2 + \delta)T$$

$$f(x) = \begin{pmatrix} \beta I(S + \sigma V) \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \quad v(x) = \begin{pmatrix} (\mu + \gamma)E - (1 - k)\delta T \\ (\mu + \alpha_1 + \xi)I - \gamma E - k\delta T \\ (\mu + \alpha_2 + \delta\}T - \xi I \\ \beta SI + (\mu + p)S - q\mu A - \varepsilon V \\ \beta\sigma VI + (\mu + \varepsilon)V - (1 - q)\mu A - pS \end{pmatrix}$$

$$F = \begin{pmatrix} 0 & \beta(S_0 + \sigma V_0) & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad V = \begin{pmatrix} \mu + \gamma & 0 & -(1 - k)\delta \\ -\gamma & \mu + \alpha_1 + \xi & -k\delta \\ 0 & -\xi & \mu + \alpha_2 + \delta \end{pmatrix}$$

And

The model reproduction number is given by

$$R_0 = FV^{-1} = \frac{\beta\gamma(\mu + \alpha_2 + \delta)(S_0 + \sigma V_0)}{(\mu + \gamma)(\mu + \alpha_1 - \xi)(\mu + \alpha_2 + \delta) - \delta\xi\left[(1 - k)\gamma + (\mu + \gamma)k\right]}$$

II. Discussion

The reproductive number R0 is one of the most important concepts in epidemiological theory. It characterizes the threshold behavior such that if R0 < 1, the modeled disease will die out if a small number of infected individuals are introduced into a susceptible population, and if R0 >1, the disease will spread in the population. A good estimate of the reproductive number can provide significant insight into the transmission dynamics of the disease and can lead to effective strategies to control and eventually eradicate the disease. Such findings can be used to plan educational campaigns.

Formulas for R0 can also be used to establish effective vaccination programs . Effects of different vaccination programs on R0 are useful in setting the programs.

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