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Modelling the Spread of Corona Virus

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Abstract

The Corona virus has in a very short span wreaked havoc on a global scale. While efforts are on to develop a vaccine against the virus, the best course of action till then is to practice good hygiene and social distancing. In this work, we discuss some quantitative models for the spread of such viruses. These models imply that 'social distancing', i.e. a spatial separation of one to two metres between individuals could curtail the rate of spread by increasing the time scale for propagation. We also model the growth, flattening and decay of the curve and these models match with those observed in various regions (countries).

Keywords:

1. Introduction

In a few weeks, one deadly Corona virus has devastated and shackled all aspects of human activity (all over our planet). This includes trillion and billion dollar businesses, the vast global commercial air and ground transport systems, tourism and hospitality industries, cancellation of major sporting events like the Tokyo Olympics, Wimbledon and other tennis tournaments, various football competitions, etc. Also students and younger people are adversely affected by closure of educational institutions. More than a million have been infected worldwide and tens of thousands of

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deaths mostly in industrialised countries affecting global trade and manufacturing.

The SARS and Bird flu virus epidemics were nowhere on this scale. The vulnerability of mankind was also evident during the December 26, 2004 tsunami, when over two hundred thousand people died in the coastal areas from Indonesia, Sri Lanka and the East African shores. All again in a few days. We also have annually, cyclones, tornadoes, and hurricanes devastating various localised areas all over the globe. But the devastation has globally been nowhere near that now due to the Corona virus.

Several times in human history pestilences, pandemics, and plagues have taken heavy tolls, many times almost wiping out civilizations. The Black Dearth wiped out perhaps half of Europe's population in the 14th century. The plague of Athens in the third century BCE, killed hundred thousand or more when the many years of wars between Athens and Sparta were going on. The Roman civilization after 185 CE, became destabilised with several recorded plagues and diseases. A more recent example, a century ago, was the Spanish flu which killed reportedly more than 30 million worldwide (more casualties than WW I), over a period of a few years (Rosenwald, 2020). On smaller scales, we have had earlier in this millennium, the SARS, MERS, etc. Several plagues occurred in Indian townships in the late 19th and early 20th centuries and more recently in 1994, in Surat. The great plague and Great Fire of London of 1666, are well documented. So mankind has survived over millennia, attacks of vicious viruses disrupting thriving civilisations and cultures.

2. Modelling the virus spread

Micron size droplets, containing viruses from cough, sneeze, etc. from individuals presumably cause spread of the virus. Consider the random root mean square (rms) displacement of the drop, due to Brownian motion, as it passes through air (molecules). The Langevin equation, or also the Einstein-Smoluchowski formula (after removal of transients) gives (Dill and Bromberg, 2003) the displacement as:

$$\langle r^2 \rangle^{1/2} = \frac{k_B T}{\pi a \eta} t \tag{1}$$

where $\langle r^2 \rangle^{1/2}$ is averaged rms displacement in x, y, z directions, t is the time, T is the ambient temperature, a is the radius of droplet, η is the dynamic viscosity of air.

In general Einstein-Smoluchowski formula gives:

$$r = (2Dt)^{1/2}, \text{ where } D = \frac{k_B T}{\pi a \eta} \tag{2}$$

Typically, $T = 300K, \eta = 10^{-4}$ poise. So for $t = 10^2 s,$

$\langle r^2 \rangle^{1/2} = 0.1cm - 1cm$. So time taken to travel a distance D is:

$$t = \frac{D^2}{\langle r^2 \rangle^{1/2} v} \tag{3}$$

The velocity of the droplet can be estimated from Stokes law:

$$6\pi\eta a v = \frac{4}{3}\pi a^3 \rho g \tag{4}$$

This gives $v \approx 10cm/s$. Thus, for 1m distance we have, $t \approx \frac{10^4}{10.10} \approx 10^2 s$. For $D = 10cm$; $t \approx 1s$. So virus could spread in seconds if people are in proximity. Two meter distance requires several minutes, hence safer.

3. Critical social distancing

We can estimate the rate of increase in virus density, n. Suppose it is captured after $N = D^2/\lambda^2$ encounters, where D is the separation distance, the average velocity of virus droplets = v, mean free path given as $\lambda \approx 0.1 - 1cm$ similar to $\langle r^2 \rangle^{1/2}$ estimated above. For $D \approx 10cm,$ this gives $N \approx 10^2 - 10^3$. Each infected cell say releases β viruses, $\beta > 1$ can be 1 – 10, or more. In a volume W for time dt we have $\frac{nWv(\beta-1)}{\lambda N}$ as net increase per unit time due to encounters.

Number striking (or escaping) from region is, $nv\frac{4\pi R^2}{4}dt$, i.e. striking surface surrounding volume. So the rate of increase of virus density can be written as (assuming a spherical volume):

$$\frac{dn}{dt} = nW\left[\frac{\beta-1}{\lambda N} - \frac{4\pi R^2}{4\frac{4}{3}\pi R^3}\right] \tag{5}$$

So the critical distance, to avoid increase of density of propagating virus is $\left({dn}/{dt} = 0\right)$.

$R > \frac{\lambda N}{\beta - 1}\frac{4}{3} > 1.5m$

(6)

(for typical values assumed)

So social distancing should be at least 2 metres, to avoid rate of increase. Just in terms of β and λ, we have a relation:

$$D > \frac{4}{3}\lambda(\alpha - 1) \quad (7)$$

$\alpha \approx 10^3, \lambda \approx 0.1cm$. This gives $D \approx 1.5m$.

Formulae can be averaged over different sizes, path lengths, and number of viruses released. In any case, general result is, the larger the social distancing the less probable the spreads. So it makes sense that the estimated critical distancing for typical parameters is $\approx 2m$.

Here we had assumed that the rate of increase in virus density is uniform. But there could be areas (regions) where the increase is more. Thus in volumes W_1, W_2, etc. we have the rate of increase as, n_1, n_2, etc. for H regions, $\sum_{i=1}^{H} \frac{n_i W_i v(\beta_i - 1)}{\lambda_i N_i}$, the velocity of propagation, v, remains constant. For hotspots, $\beta \gg 1$. These would propagate away from the region over a combined surface area, $A = 4\pi R^2$. So the modified equation is:

$$\frac{dn}{dt} = \sum_{i=1}^{H} \frac{n_i W_i v(\beta_i - 1)}{\lambda_i N_i} - \sum_{i=1}^{H} n_i \pi R^2 dt \quad (8)$$

$\frac{dn}{dt} = 0$ would now give the critical distance. To simplify, we can take average values of λ, N, β, etc. It is evident that 'hotspots' would necessitate larger social distancing as well as larger distances between containment zones.

4. Possible model for the curve

For a single species growth, rate of increase of the virus population is proportional to the number p, present at any time,

i.e. $\frac{dp}{dt} = \alpha p$ (9)

α is a constant. This gives $p = p_0 e^{\alpha t}$ (10)

Here $p = p_0$ is the initial number, i.e. at $t = t_0$.

I.e. the exponential growth, holds in the initial phases of the virus propagation. The model for the exponential growth can be written as: $p = p_0 e^{\alpha t}$. If the number of infected cases doubles, say, every 3 days, $p/p_0 = 3, t = 3 \Rightarrow 3 = e^{3\alpha}$, and hence we have: $\alpha = \frac{1}{3} log_e 3$. If there is a steady decline in the number of infected cases, α can be estimated. Right now there are not many countries showing a steady decline. For a doubling time of 3 days, the growth constant, $\lambda = \frac{0.693}{3}$. Then the time taken to increase the infection by 100 times is:

$$t = \frac{2.303}{\lambda} log_{10} 100 \approx 10 \text{ days} \tag{11}$$

This is for example observed in the Indian city of Mumbai, with over 2500 cases reported in ten days.

The inhibiting phase, caused by constraining factors (like social distancing, growth of antibodies within cells, environmental effect, etc.) can be considered proportional to βp (β is a constant) which in turn is already proportional to αp. So we have a factor, γp^2 (where $\gamma = \alpha\beta$) and this is negative inhibiting growth. We now have:

$$\frac{dp}{dt} = \alpha p - \gamma p^2 \tag{12}$$

This can be written as:

$$\frac{dp}{dt} = kp\left(1 - \frac{p}{k'}\right) \tag{13}$$

$$\left(k' = {}^{\alpha}/_{\gamma}, {}^{k}/_{k'} = {}^{\alpha}/_{p}\right)$$

This has form of Riccati equation, with solution (Zelikin, 2000):

$$p = \frac{k'}{1 + Ae^{-kt}} \tag{14}$$

where A is a constant of integration. This gives rise to a S – shaped curve with inflection point I at $\frac{1}{2}k'$, and upper asymptote at $p = k'$ (figure 1).

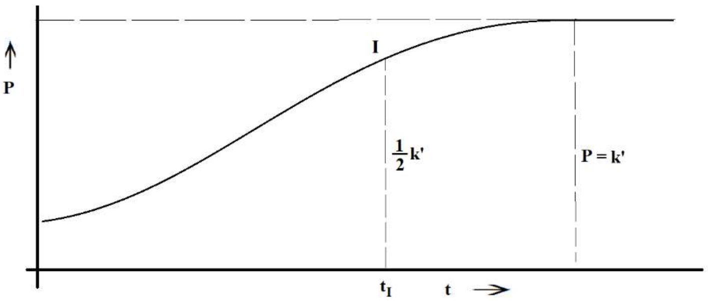

Figure 1: Growth and flattening of the curve

$t_I = I = \frac{1}{2}k'$, $I =$ Point of inflection, $p = [t_I, p_I]$, where, $t_I = \frac{1}{k} logA$, $p_I = \frac{1}{2}k'$ at the inflection point.

Turning point t_I depends on k and A, and p asymptotically reaches k'. Number of curves can be drawn for different values of $k' = {}^{\alpha}/_{\gamma}$, ${}^{k}/_{k'} = {}^{\alpha}/_{p}$. As there are no ways of theoretically estimating α, γ, A, etc. empirical data of different regions (countries) with data on rate of growth of p with t, can be used to deduce the constants by fitting the curve.

At present it is not clear if the inflection point has been reached in many of the regions. A more generalized equation with γ (and α) as functions of time is:

$$\frac{dp}{dt} = \gamma(t)p(p - \epsilon) \tag{15}$$

With solution $p = \frac{\in}{1+Ae^{\phi(t)}}$

$$\phi(t) = \epsilon \int_0^t \phi'(t)dt\,;\ \phi' = {}^{d\phi}/_{dt} \tag{16}$$

The $\phi(t)$ function varying continuously between $\infty, -\infty$ as t varies between t_a and t_b. Points of inflection found from,

$$\phi^1(t) + \phi^2(t)(2p - \epsilon) = 0 \tag{17}$$

(i.e. $\frac{d^2p}{dt^2} = 0$)

The equation (12) gives rise to an S-shaped curve that flattened asymptotically with time scales for turning (inflection) points, as seen from figure 1. The first term in equation (12) gives rise to an initial exponential growth. This is still continuing in many places, including cities like Delhi. We also have growing number of cases in many countries, for instance, right now number of cases in India is increasing steadily at about ten thousand per day (as of mid-June 2020). The second term in equation (12), which is the damping term that has yet to dominate in several places.

However we do want the number of cases to drop and not just have a flattened curve. This can happen if the second term in equation (12) dominates. So we have:

$$\frac{dp}{dt} = -\gamma p^2 \qquad (18)$$

$$-\frac{dp}{p^2} = \gamma dt \qquad (19)$$

This gives, $\frac{1}{p_0} - \frac{1}{p} = \gamma(t - t_0)$ (20)

Here again p_0 is the initial number at t_0. This gives a relation:

$$p \propto \frac{1}{t} \qquad (21)$$

The time taken for p_0 to fall to $\frac{1}{2}p_0$ (or for $p = \frac{p_0}{n}$, $n > 1$) can be estimates from equation (20).

So the two limits are, the exponential growth (first term in equation (12) dominates) followed by steady decline (second term in equation (12) dominates). Thus we have three cases:

1. Rise (first term dominates)
2. Flatten (both terms present)
3. Decline (second term dominates)
4.

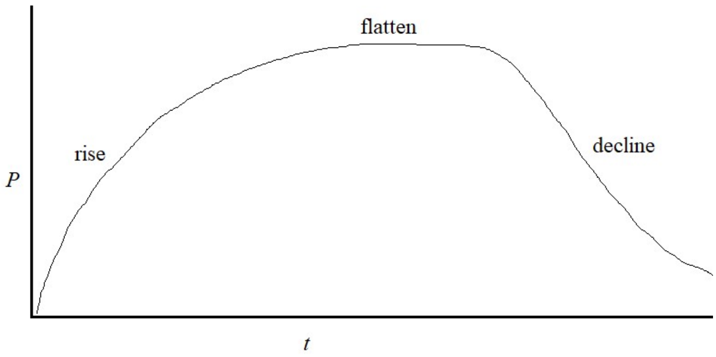

Figure 2: Rise, flattening, and decline of the curve

In fact this plot is similar to the number of daily cases reported by certain countries like Australia and New Zealand.

Thus we now have a more complete picture of the evolution of the virus – rise, flattening, and decline (Sivaram, Arun, Kiren, 2020). Actual data in each area can be used to predict the declines.

5. Diffusion equation for virus spread

A suitable diffusion equation for space and time dependence of the number of droplets (containing viruses) is (within a hotspot region):

$$\frac{dN}{dt} = \frac{v}{\lambda_s}(R-1)N + \frac{\lambda v}{3}(\nabla^2 N) \qquad (22)$$

N is the number density (number per unit volume), v is the average droplet velocity (as estimated from equation (4)), the number of viruses per droplet can be estimates. R is the multiplying factor $(R > 1)$, could be 3 or more, for each virus encounter. λ is the mean free path

and λ_s is the mean free path of the virus at the hotspot, estimated in section 3. This implies average time taken between encounters as $\lambda_s/v = \tau$, time constant.

The above diffusion equation can be solved by standard separation of variables method. The general solution is given as:

$$N_s(r,t) = N(0)\exp[(k/\tau)t]\left[\frac{\sin(r/r_n)}{r}\right] \tag{23}$$

k is a constant, $N(0)$ is the initial number density, r_n is the extent (radius) of the hotspot. Equation (23) gives the number density both as a function of time and distance away from an 'active region'. Note the exponential increase and $(\sin r\,)/r$ factor. If τ becomes large, i.e. encounter times become longer and longer, exponential becomes small and $\sin(r/r_n)$ dominates. N can also be taken as population of people, each person transmitting or receiving droplets (each with viruses). So we can solve for virus density as also density of people infected.

6. Conclusions

In this work we discuss some quantitative models for the spread of viruses such as the Corona virus and look at the science behind the 'social distancing' between individuals that could reduce the rate of spread by increasing the time scale for propagation. We have also modelled the growth, flattening and decay of the curve and these models match with those observed in various countries. With this model we have a more complete picture of the evolution of the virus

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