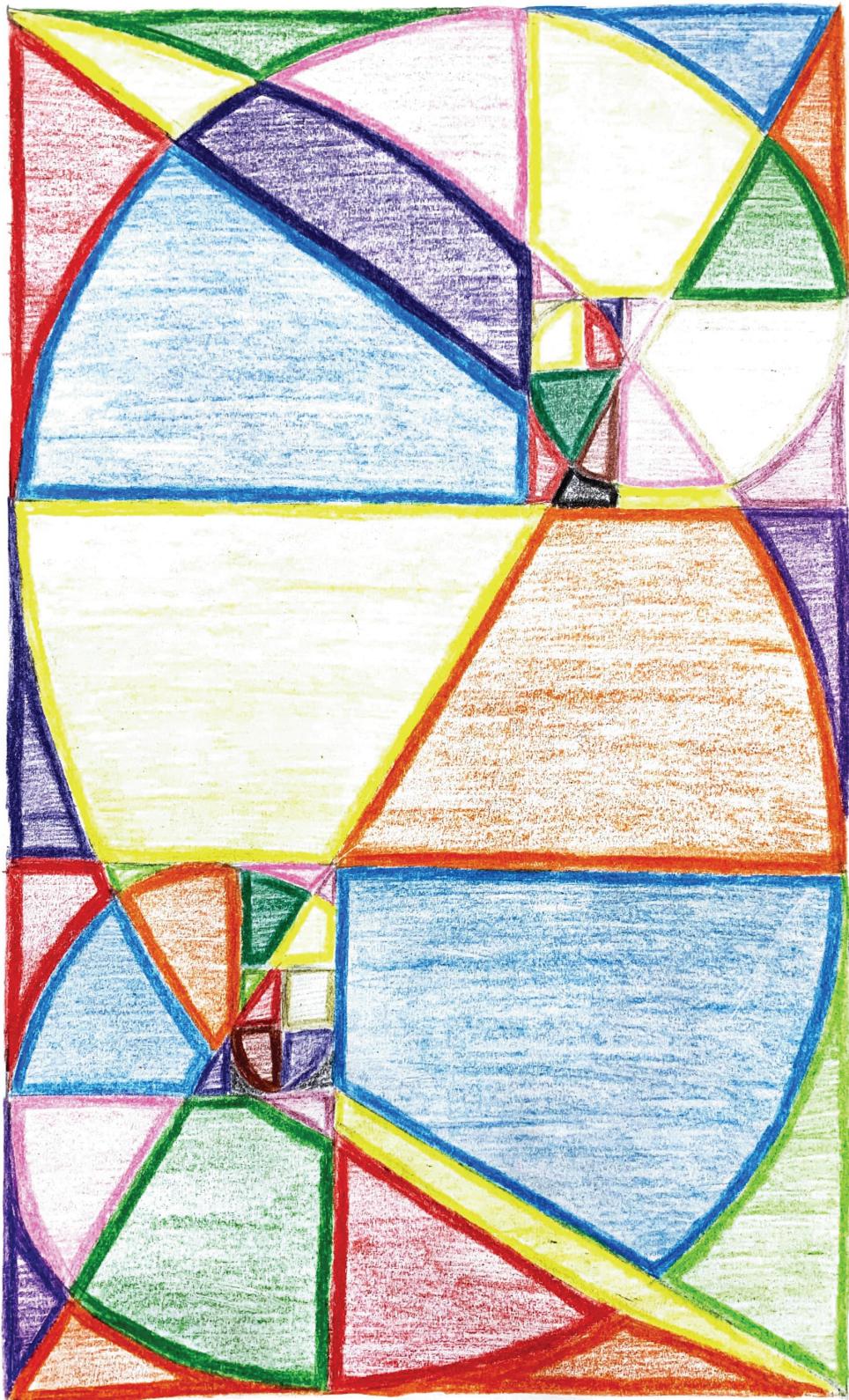


COSINE

**The Math Behind
Coronavirus**

**Alpha-The
Math**





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A Mathematical Modelling Approach

In today's time of the COVID-19 pandemic, researchers, academics and scientists worldwide are crunching the numbers when it comes to the statistics of the pandemic. Whether its algorithms, probabilities or state variables, these people are doing the math to help governments across the globe prepare for what's to come. But wait, how is MATH going to help us beat the coronavirus? The answer to that question, dear readers, is something that can perhaps be explained in a few hundred words, not a simple sentence.

It all began back in Soho, London in the September of 1854. A cholera outbreak had decimated Soho, killing 10% of the population. Medical theories asserted that the disease was spreading through "bad air" from the stinking open sewers. But one physician, John Snow, had a different theory: that cholera is spread through contaminated water. And he was just about to use mathematics to prove that he was right. Snow created an ingenious map that graphically showed the geographic spread of deaths in the outbreak and each bar on the graph represented a death at that address. This representation of the data showed that most of the deaths were tightly clustered in a specific area, crowded around the water pump at 40 Broad Street in Soho. Snow's research had led him to believe the Broad Street pump was the source of the disease, and this data backed up that theory. However, there were other pumps nearby, how could he show that it was most likely that this particular pump was the source?

His next ingenious step was to represent the time it took to travel to the Broad Street pump on his map and to calculate who was most likely to use each water pump in the area. Snow drew a curve on the map that marked the points where the Broad Street pump was at equal walking distance from neighboring water pumps. If you lived inside this curve the Broad Street pump is your nearest source of water. Almost all the deaths marked on the map lay inside this curve and anecdotal evidence explained the few cases that did not.

This brilliant mathematical device is called a Voronoi diagram. In the simplest of cases, if given a finite set of points $\{p_1 \dots p_n\}$ in the Euclidean plane then each site P_k is simply a point, and its corresponding Voronoi cell R_k consists of every point in the Euclidean plane whose distance to P_k is less than or equal to its distance to any other P_k . Each



such cell is obtained from the intersection of half-spaces, and hence it is a convex polygon. The line segments of the Voronoi diagram are all the points in the plane that are equidistant to the two nearest sites.

Though the first mathematical model or the first algorithms for such models are believed to have been invented back in 30,000 B.C. predominantly by Babylon, Egypt and India, it was John Snow's model that set the tone for future mathematical models. And it's these models that today's mathematicians are creating and constantly studying.

If you consider a mathematical model for the current pandemic, like the S-I-R (susceptible, infected and recovered) by the Singapore University of Technology and Design, you would have to factor in various constants such as confirmed cases, tests conducted, deaths recorded, but since nothing like this has ever happened, some of the inputs would also be variables and it is due to these variables that even a super futuristic AI mathematical model would not be able to give an absolutely accurate figure as to when the pandemic will come to an end.



-Anannya Sharma

Nash Embedding Theorem

There was a film a few years ago starring Russell Crowe as John Nash, it was called "A Beautiful Mind". There is also a book that is based on Nash's life story written by Sylvia Nasar. You may have heard of him because of his work in economics, for which he won a Nobel Prize. That was for Game Theory. He analysed what are called non-zero-sum games, which was a big deal back in the 1950s when people were worried about nuclear conflict. He is really well known amongst mathematicians as well for his serious pure math work that he did in a subject called differential geometry. But this kind of geometry is very different from the geometry learned at high school. It is not like trigonometry or Pythagoras found in the higher secondary textbooks. Rather, it is about topics like surfaces, curvature and smoothness. I would like to talk about something that is not very well known that is the Nash Embedding Theorem.

It's about how you can realise abstract curved surfaces as subsets of Euclidean space that we live in. The first we can think about is a torus (doughnut shaped object). You can imagine that the surface is quite squidgy and has the same surface as that of a doughnut and so topologically it is equivalent. As seen in the image, it has got some distances (grids) marked on its surface. You can measure the distance as marked on the surface but intrinsically it has its own idea of what the distance is.

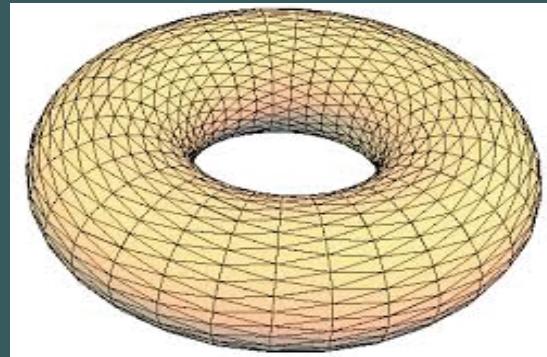
It was noticed that if we bent the torus one side the rectangles would become thinner and longer on one side and the same with the other.

What Nash was interested in was whether we could find a way to put it in a three-dimensional space in such a way that the distances agree with the distances traced along the surface.

If I have a curved surface in three-dimensional space, it is already equipped with a distance (where we can take any two points and trace many curves between them and take the shortest distance between them as the distance). This notion of distance is called a Riemannian metric. We can also have an abstract surface which is already equipped with a Riemannian metric and we want to know if it comes from a way you can put the surface in a three-dimensional space.

If we create a Möbius band with a piece of rectangular paper, you will notice that the paper only bends in one direction at a time and cannot look like a part of a sphere. Any way that we are going to embed this Möbius band on three-dimensional space, it will always be isometric. Isometry is the property that the distances on the paper are the ones that you would get from the shortest distance between two points along a three-dimensional space.

In the torus, I would get a shorter distance going



on the inside and a longer distance going on the outside. There is a natural metric on a torus called the flat torus where it is difficult to embed it in a smooth way into three-dimensional space.

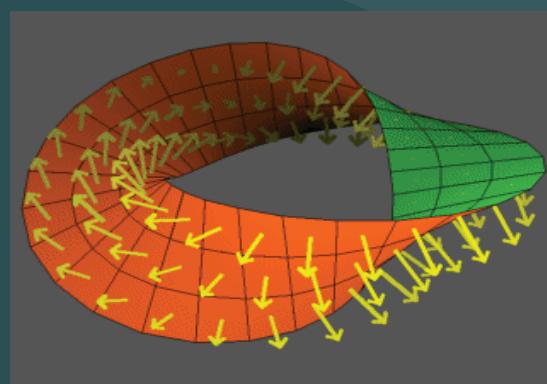
Nash proved that if you were to embed it in a slightly irregular way, then you could even embed the flat torus into three-dimensional space. Nash's condition was that the normal vectors should continuously move around the surface while bending the torus. He was able to do this, which resulted in a very counterintuitive result.

Nash came to the conclusion that a compact m -dimensional Riemannian manifold can be embedded isometrically in $\{m*(3m+11)\}/2$ dimensional Euclidean space. There was a condition about the type of embedding -- how regular it can be (how many times can you differentiate the coordinate functions). The technical term for this is 'C $^\infty$ ' which means, to make the three-dimensional structure as smooth as you can you can differentiate the coordinate functions infinite number of times. For a tire (torus shape) we have got $m=2$ since it is a surface and can go in two different directions at right angles.

$\{m*(3m+11)\}/2$, we get

$\{2*(6+11)\}/2 = (2*17)/2 = 17$ dimensions

So according to the Nash equilibrium we would require a 17-dimensional Euclidean space for the tire.



Maths and the Death Rate

This year certainly started off with a bang with the outbreak of the worldwide coronavirus pandemic. This virus is said to have originated from Wuhan in China and has practically spread throughout the world and has triggered country wide lockdowns and practically brought life -- as we know it -- to a standstill. Whenever such a pandemic occurs, one of the first things that everyone tries to calculate to get a rough estimate of the severity is the death rate.

While initially the topic of the mortality rate related to COVID-19 seems relatively simple and straightforward it is actually quite the opposite.

If you are like me, you probably thought the mortality rate is just the total number of deaths divided by the total number of cases in the world. So, for 29th of June 2020 the total cases are 10,272,028 and the total number of deaths is 504,952 and the mortality rate from this general idea comes out to be about 4.91%. While this seems quite reasonable and you think to yourself, "what's the big deal?", a quick search on worldometers.info will show you that the total death rate is 8%. So what happened here? Well the death rate for the entire world the way we calculated might be quite sensible and reasonable if the pandemic was already over. However, since the pandemic is still going on, this formula is quite naïve and misleading. The actual rate depends on several factors. These include variables like location, age, strand of the virus infecting the person and several other factors. Another major factor that needs to be taken into account is the fact that not all cases are reported. In fact, according to a study in New York the actual number of cases in New York are 1.7 million, which is about 10 times the 166,883 reported cases. This is due to a number of causes including being asymptomatic and just the general belief in people that they can treat themselves at home. The total death rate also increases steeply due to a number of underlying medical conditions like obesity, diabetes, hypertension, malignancy, lung diseases which all need to be taken into account while calculating the mortality rate. Yet another factor that affects the rate is the age of the patient. The mortality rate is higher for people above 65 years. In fact, about 75% of the total deaths in the USA were people who were above 65 years.

So how do we actually calculate the death rate in an ongoing pandemic? The formula that would be used is $CFR = \text{deaths at day } x / \text{cases at day } x - \{T\}$ (where T = average time period from case confirmation to death)

This would constitute a fair attempt to use values for cases and deaths belonging to the same group of patients. One issue can be determining whether there is enough data to estimate T with precision, but it is certainly not $T = 0$ (what is implicitly used when applying the formula current deaths / current cases to determine the death rate during an ongoing outbreak).

Let's take, for example, the data at the end of February 8, 2020: 813 deaths (cumulative total) and 37,552 cases (cumulative total) worldwide.

If we use the formula (deaths / cases) we get:

$$813 / 37,552 = 2.2\% \text{ (flawed formula).}$$

With a conservative estimate of $T = 7$ days as the average period from case confirmation to death, we would correct the above formula by using February 1 cumulative cases, which were 14,381, in the denominator:

$$\text{Feb. 8 deaths} / \text{Feb. 1 cases} = 813 / 14,381 = 5.7\% \text{ (correct formula, estimating } T=7\text{).}$$

This seems much closer to the rate today too.

T could be estimated by simply looking at the value of (current total deaths + current total recovered) and pair it with a case total in the past that has the same value.

This just gives us a general idea of how the scientist and governments try to calculate the mortality rate.

-Shaurya Mann XII E



The Math Behind Social Distancing



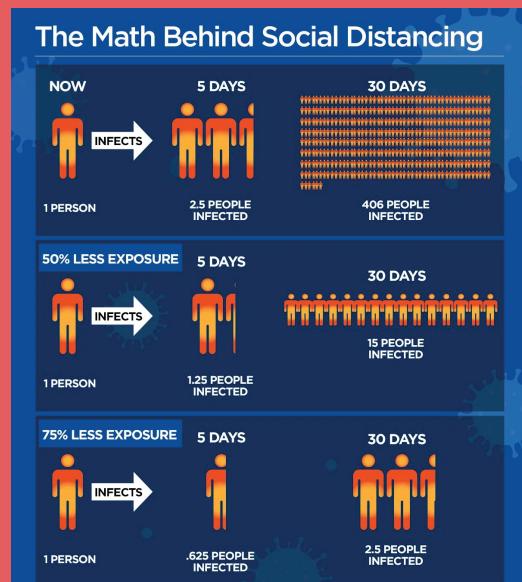
As scientists and healthcare professionals continue to develop a vaccine for COVID-19, there is another, more readily available tool i.e. Social Distancing.

Social distancing – involving measures taken to reduce physical contact – is the first line of defence for containing an infectious disease like COVID-19. That's because these infections spread when people cough, sneeze, or touch surfaces on which the virus resides.

Due to this coronavirus threat, we have all become familiar with the term "flattening the curve". Most of us have seen illustrative curves and have some knowledge of this concept. We all accept the need to flatten the curve to control the spread of the virus, which we are told is best achieved by "social distancing".

A key determinant of the curve is the "basic reproduction number". This number is usually denoted by R. It is the estimation of the average number of people who will catch the virus from a single infected person, during the outbreak of an infectious disease.

It has been estimated that each infected person infects between two and three others in a largely uninfected population. Later it gives rise to exponential growth in the number of infected cases.



Using a summation formula makes it possible to estimate the number of new infections over a 30 day period, across three scenarios.

Scenario	5 Day Period	30 Day Period
No social distancing practiced	1 person infects 2.5* others	406 people infected as a result
50% reduction in social exposure	1 person infects 1.25* others	15 people infected as a result
75% reduction in social exposure	1 person infects 0.625* others	2.5 people infected as a result

The above figure shows only hypothesized data, not real data.

The figure shows an estimation that the basic reproduction number (R_0) of COVID-19 will be 2.5 -- on average, an infected individual will spread the disease to 2.5 other people.

An infected person unknowingly spreads COVID-19 over the median five day incubation period. After this period, the person begins to develop symptoms and immediately, the self-quarantine period starts.

Now a medical professional or public health official may ask you to self-isolate in the following situations:

- Self-quarantine is where you don't feel infected, but you may be. This could be because someone near you has been infected, or because you have recently travelled.

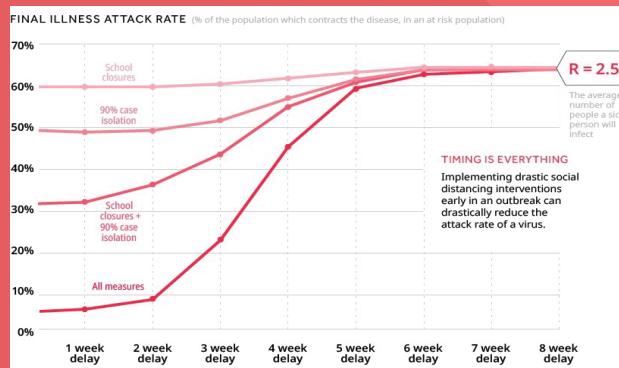
- Mandatory self-isolation is where you have tested positive for infection, and a doctor considers you well enough to stay at home (as opposed to hospital isolation).

This means that when an infected person reduces their physical contact with others by 50%, they also spread the disease by an amount 50% less.

The distancing measures are:

Measure	Details
School closure	Teachers and students spent weekday daytime cycles at home, rather than at school.
Increased case isolation	Upon becoming symptomatic, adults (90%) and children (100%) would self quarantine for the duration of the infection.
Workplace non-attendance	Each day, a person had a 50% chance of staying home instead of attending their workplace.
Community contact reduction	Individuals reduced their physical contact with community members by half, each day.
Combination of all four	All four measures combined.

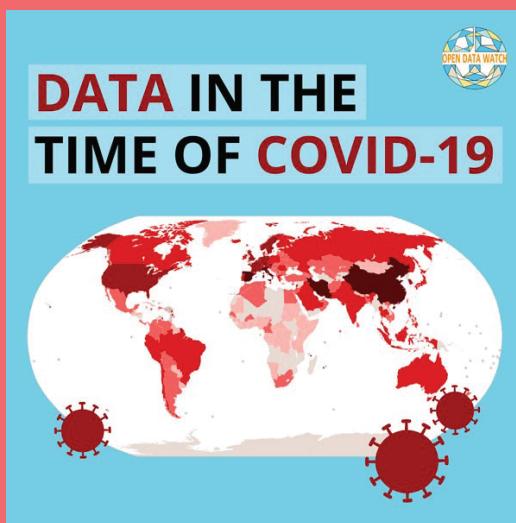
Community of 30,000 people and an epidemic with $R=2.5$, are charted below. We can define the final illness attack rate as the share of people from an at risk population who ultimately catch the disease.



Results showed that when no action was taken, 65% of the population contracted the disease. However, if a combination of all four distancing measures were implemented instead, the attack rates were:
 •45% (distancing begins after a 4 week delay)
 •21% (distancing begins after a 3 week delay)
 •7% (distancing begins after a 2 week delay)

Now it is clear that social distancing is more effective

CHALLENGES FACED BY RESEARCHERS IN COLLECTING AND ANALYSING COVID-19 DATA DURING THE PANDEMIC



The Covid-19 pandemic is a worldwide phenomenon that has brought with it a huge wave of panic. This wave of panic is immensely increased by the spread of misinformation. Misinformation can be very harmful if it is spread on a large scale. Also, insufficient or incorrect information about something as large as this pandemic causes speculations, which leads to chaos and panic. Thus, in such hectic times, it is the responsibility of statisticians and data analysts to provide accurate and trustworthy information to the public, so as to "fight panic with information". In the process of doing so, there are a lot of methodological challenges faced by the people providing us with the data we see.



One of these challenges is merging and managing relevant data collected from large multi-centre hospitals. Data collection must also be done in a standardised way, and following international protocols such as ISARIC (International Severe Acute Respiratory and emerging Infection Consortium) and LEOSS (Lean European Open Survey on SARS-CoV-2 Infected Patients). Artificial Intelligence and complex deep learning

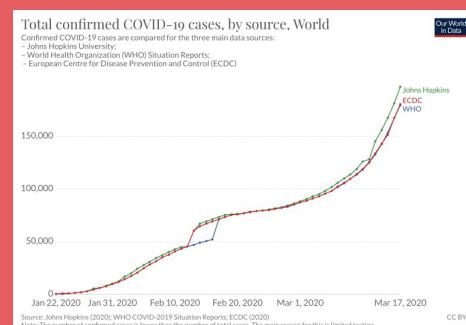
algorithms might be some suitable ways to tackle this. Then, it is also required to distinguish between active (still hospitalized) and closed (discharged or dead) COVID-19 cases.

Also, data needs to be analysed in a standardised manner. Statisticians and data analysts are required to develop suitable analytical strategies to analyse collected data.

Communicating this analysed data to the public is also very challenging, especially in hectic times such as these. Statisticians must also present the data in a very clear and transparent manner. A research such as this is also time-dependent. Rapid flow of accurate information is very crucial in fighting the difficulties that arise with the pandemic. Thus, the researchers must update, track, monitor, analyse and present data real-time

Additionally, while reporting, the quality and transparency of the articles and data must be maintained, which further challenges the writers and statisticians, who are already working on deadlines. Sometimes these challenges are overwhelming, and result in inconsistencies and contentions to the reported numbers that reach the media. And as a result, different sources show slightly different numbers.

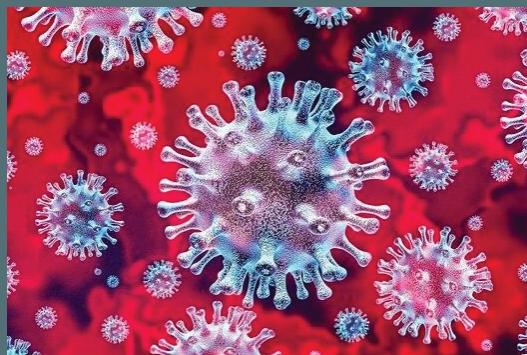
In conclusion, we learn that there is a lot of hard-work and detailed research behind the beautiful graphs and tables that we see. A large number of challenges are faced by all the people involved in the long process of producing, gathering, analysing, reporting and publishing this data.



R

Five months ago, the phrase “R number” didn’t mean much to anyone except epidemiologists and infectious disease experts. But as the coronavirus pandemic has raced around the world, infecting millions and killing hundreds of thousands, just keeping up with the news is starting to feel like taking a crash course in infectious disease epidemiology.

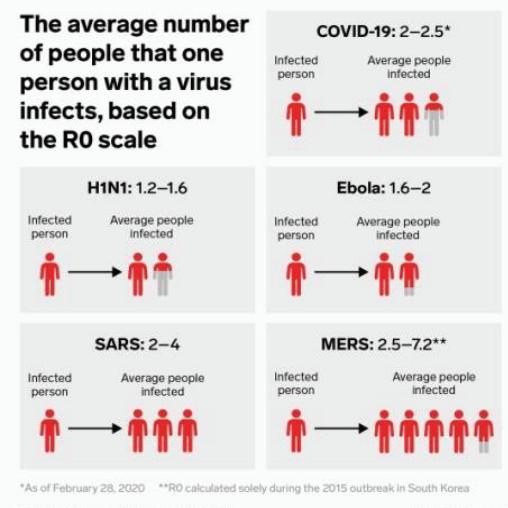
This once-obscure term – R – is only going to become more important over the coming months. As governments across the world ease lockdown restrictions, the government advisors will be keeping a very close look at the R of the outbreak. If it starts heading up, it could mean that the relaxed social distancing measures are increasing the rate of transmission. If it goes too high, then governments may have to consider tightening restrictions again.



What is R?

R refers to the “effective reproduction number” and, basically put, it’s a way of measuring an infectious disease’s capacity to spread. The R number signifies the average number of people that one infected person will pass the virus to.

The R number isn’t fixed, but can be affected by a range of factors, including not just how infectious a disease is but how it develops over time, how a population behaves, and any immunity already possessed thanks to infection or vaccination. Location is also important: a densely populated city is likely to have a higher R than a sparsely populated rural area.



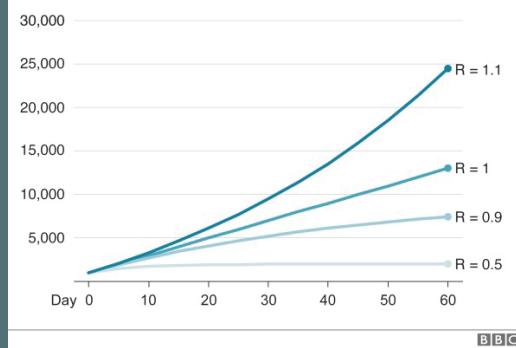
Why do we need an R of less than 1?

An R figure that is even slightly over 1 can lead quickly to a large number of cases due to exponential growth.

Here’s how that works. Say a disease has an R of 1.4. This may seem like a manageable figure, but a glance at the figures quickly proves that isn’t the case. An R of 1.4 would see 100 people infect 140, who would in turn infect 196, who would infect 275. In four rounds of infection, the number of people with the virus would quadruple (approximately). Mathematicians call this phenomenon exponential growth, and it explains why coronavirus infected so many people all over the world so quickly.

Conversely, an R of less than 1 means that the virus will eventually peter out – the lower the R, the more quickly this will happen. An R of 0.5 means that 100 people would infect only 50, who would in turn infect 25, who would then infect 13. As the number of cases drops and ill people either die or recover, the virus will be brought under control – as long as the R can be kept low.

How 1,000 cases would increase under different infection rates



How do we measure it?

There are lots of different ways of calculating R. Scientists have been looking at the genome of the virus to see how it changes as it infects new people. They can also look at death and hospitalisation figures to get a sense of how many people have contracted the disease. The problem is that most of these methods involve looking into the past to some degree. People who unfortunately die from coronavirus will have been infected weeks before, so using that data to calculate R can only tell you how widely the disease was infecting people several weeks ago.



The math of physical distance

Till six months ago, life coaches all over the world were advocating the healing power of touch, the warmth of a hug, and the power of staying together. Not anymore! It's as if the world has turned upside down suddenly. Wherever you go now, people are scurrying away from each other, refusing to shake hands, appalled at the idea of touching anything and the buzz word is "social distancing". By now we've all heard of it. Yes, yes, it's the distance we have to maintain from each other at social gatherings. But it's a misnomer. It's not the social distance, but the physical distance that we should maintain! Physical distance to be practised during the corona times has been prescribed at different lengths in different countries. On an average 1.5 to 2.0 meters is taken as a good distance to curb the spread of the bacteria.

So how does physical distancing work? The short answer is networks. All of us, in our daily lives, interact with dozens of people. Those people interact with other people, who interact with others, forming a large network that connects everyone in our society.

If we are infected, we can easily pass the virus on to other people. The average number of people we pass it on to is called the 'reproduction number', or R.

Every virus has a basic reproduction number or R₀. This is the value of R before we begin physical distancing.

As an example below, R₀ is three: one person will pass it to an average of three people. Those three people will spread it to three other people in the next round, and so on.

At the tenth round, from just one original person, 59,049 people (3¹⁰) will be infected, with 88,573 cases in total.

Round	0	1	2	3	4	5	6	7	8	9	10	Total Cases
(R ₀ =3)	1	3	9	27	81	243	729	2187	6561	19,683	59,049	88,573

With physical distancing we could (for example) get this down to an average of two people (R=2).

Therefore, at the tenth round, only 1024 people (2¹⁰) will be infected, with 2047 cases in total.

Round	0	1	2	3	4	5	6	7	8	9	10	Total Cases
(R=2)	1	2	4	8	16	32	64	128	256	512	1024	2047

SARS-CoV-2, the virus that causes COVID-19, is currently thought to have an R₀ of between 2 and 3.3, though this number is

dynamic. A future vaccine or treatment for COVID-19 may give us a lower value of R.

So should we work towards reducing the value of R? Absolutely. But why? Because "the earlier the better". The following simple mathematical model will explain this theory.

Consider two simple scenarios where the same level of physical distancing (R=2) is applied, but at different times—at 100 cases or at 500 cases—and look at seven weeks of transmission. Contrast both of these with a scenario with no distancing.

This is a highly simplified model, assuming that all transmission takes place in one week, and that no person recovers within 7 weeks.

With a limited number of ICU beds, if even ten per cent of these cases are serious enough to require intensive care, the starting time could mean the difference between life and death. When we started physical distancing at 500 cases, we ended with 6350 serious cases requiring ICU beds. When we started at 100 cases, we ended with 1270 serious cases requiring ICU beds.

The significance therefore, of controlling the exponential growth rate cannot be underestimated, and is the key to dampening the speed of the spread of infectious diseases.

Without social distancing, the virus will not be subdued, and the hospital system will not be able to cope. Infections would still taper off at some point, as the virus runs out of population to infect, but not before damage to the health system has been incurred.

Scenario	Physical Distancing	New Cases Week 1	New Cases Week 2	New Cases Week 3	New Cases Week 4	New Cases Week 5	New Cases Week 6	New Cases Week 7	TOTAL CASES	ICU cases (10%)
Without distancing	None (R=R ₀ =3)	100	300	900	2700	8100	24,300	72,900	109,300	10,930
	One third (R=2)	500	1000	2000	4000	8000	16,000	32,000	63,500	6,350
	One third (R=2)	100	200	400	800	1600	3200	6400	12,700	1,270



Prophetic Math Modelling to Track COVID-19



Nearly 3 months after being declared a pandemic by WHO, COVID-19 still has a deathly grip on most countries around the globe. While some countries have been able to contain the spread, the numbers of confirmed cases are still soaring in many others, including India. In such a situation, it becomes crucial to predict the extent towards which such a situation can unfold. This is especially important for hospitals and other healthcare institutions, which are already scrambling for medical supplies.

Mathematical modelling using available data, has been proven as a useful tool in such situations, where such estimates can serve as the basis for making policies regarding lockdowns and distribution of medical resources. With the help of past data, mathematical modelling can help predict the number of cases that may occur in the future.

This article summarises the model used by Qasim, M., et al., Data model to predict prevalence of COVID-19 in Pakistan. The model uses the rate at which the number of patients increased previously to estimate how the number of cases will rise in the future. Moreover, it can also estimate the maximum and minimum bound of cases, giving an approximate range of number of confirmed cases by a certain date.

Method:

To derive this model,

Let y_i represent the number patients reported at i th day

Then, we define the ratio x_i as

$$x_i = y_{(i-1)}/y_{(i-1)} + y_i$$

Where, $(i - 1)$ represents the previous day and the current day is denoted by i .

Note that when $x_i \rightarrow 0$, $y_i \rightarrow \infty$ (number of cases would increase drastically) and when $x_i \rightarrow \infty$, $y_i \rightarrow 0$ (not many new cases within the given time).

Thus, the lower bound of cases can be obtained by taking the maximum value of x_i

The x_i is calculated for all $i = 1, \dots, n$, where n is the total number of days for which estimation is performed.

The mean of all x_i is calculated as

$$\bar{x} = \sum_{i=1}^n (x_i)/n$$

Let d_i represent the total deaths and r_i be the count of patients that have recovered until i days. Then the expected number of patients at day i was modelled as

$$y_i = (y_{i-1} - d_{i-1}) (1/\eta - 1) - R_{i-1} \dots (A)$$

Though this expression does seem daunting at first, it can be understood by taking $i=1$, i.e. estimating the number of cases in day 1 provided that accurate data for day 0 of the pandemic is available.

Then,

$$x_1 = (y_0)/(y_0 + y_1) \text{ and, } x_0 = 0 \text{ (because there could not have been any cases before the first day)}$$

$$\text{As a result, } \eta = (x_1 + x_0)/1 = x_1 = (y_0)/(y_0 + y_1)$$

And equation (A) will reduce to:

$$y_1 = (y_0 - d_0) ((y_1)/(y_0)) - R_0$$

Thus, we can infer that if no deaths occurred, then the equation would provide the number of new cases while also taking into account the number of recoveries. Note that it has been assumed that a patient once dead, cannot spread the virus.

It is evident that this method of modelling cannot always be accurate. Modelling relies heavily on accurate past data, which is not always available. Moreover, it cannot take into account random major events that increase or decrease the number of cases drastically (like sudden initiation of a lockdown), and a separate model would have to be created before and after the event took place to provide a precise picture. However, mathematical modelling has been proved to be accurate enough to predict the path of a pandemic with only marginal errors.

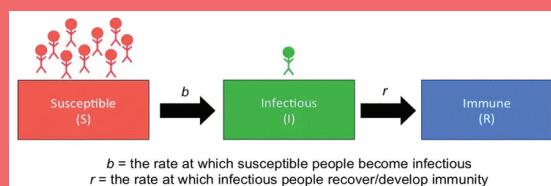
Though coming up with a real solution to the complex equation of this epidemic seems difficult, at least we have math to help us along the way.

S.I.R. Model

Maths in daily life is a concept we're all familiar with. But when our daily lives change, that is, our routines change in accordance with the situations around us, maths always finds a way to weasel its importance into our life. This is the case with the ongoing pandemic. Maths plays an extremely important role in the calculation and determination of infected persons. The S.I.R. Model is one such effective model to aid these calculations.

The S.I.R. Model is a dynamical systems model, used to make certain predictions during an epidemic. The origin of the S.I.R. Model traces back to the early 20th century, with notable works being that of Kermack and McKendrick in 1927. The general population is divided into three compartments- S(susceptibles), I(infectives) and R(removed).

Susceptibles are the individuals who are prone to the disease. Infectives are the individuals who are infected and are capable of spreading the disease to other individuals. Removed are the individuals who are not capable of spreading the disease to Susceptibles. They may be infected or healthy individuals who have either recovered from the disease and have thus developed immunity against it, have been isolated so they cannot transmit the disease, or have died. If an individual has recovered from the disease but hasn't developed immunity against it and is at the risk of getting infected again, they go back to the Susceptibles compartment.

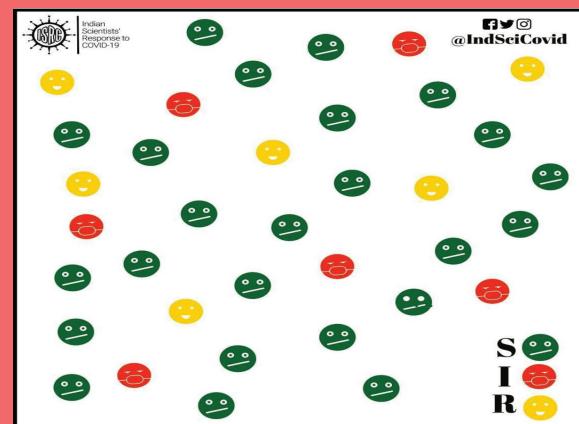


The aim of the model is to determine the number of persons falling under each category, and thus making predictions about the duration of the epidemic, the rates of infection and recovery, estimation of various epidemiological parameters and the public health interventions that may affect the outcome of the epidemic.

For all calculations under the S.I.R. Model, time(t) is the function of the state variables S , I and R . To represent that the number of susceptible, infectious and removed individuals may vary over time (even if the total population size remains constant), we make the precise numbers a function of t (time): $S(t)$, $I(t)$ and $R(t)$.

To determine the dynamics of the S.I.R. Model, mathematical equations show how an individual goes from susceptible to infective to removed.

A susceptible individual can get infected only



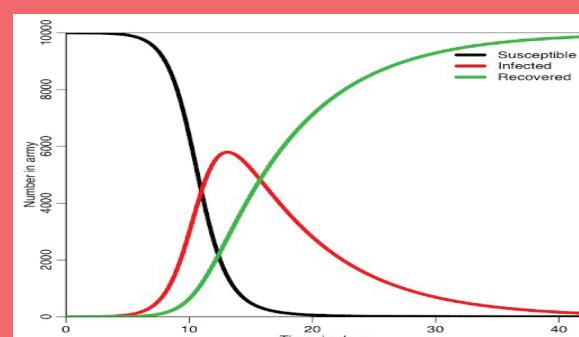
by coming in contact with an infective. Thus, the rate of transmission depends on $S(t)$ and $I(t)$, i.e., the $S \rightarrow I$ rate is directly proportional to $S(t)$ and $I(t)$. Taking β as the constant of proportionality, the $S \rightarrow I$ rate at time t is $\beta S(t)I(t)$.

This parameter β combines two effects-the likelihood that a susceptible and an infective will interact and the likelihood that such an interaction will lead to disease transmission. A greater value of β will correspond to a society where people have a lot of social interactions, and the disease is highly contagious. Such a combination will maximize the infection rates. A smaller value of β will correspond to reclusive individuals, and a disease that is difficult to transmit. This combination would minimize the infection rate.

The number of removed individuals depends on the number of infectives. Thus, the rate of recovery depends on $I(t)$, i.e., the $I \rightarrow R$ rate is directly proportional to $I(t)$. Let the parameter γ be the constant of proportionality so that the recovery rate is $\gamma I(t)$.

γ captures how quickly a person recovers from a disease. If the value of γ is small, then an infected person will stay infected for a long time and might have the opportunity to infect others. If the value of γ is large, the illness is brief.

To include the specific logistics of each disease, there are variations of the S.I.R. Model. But the main aim of each variation is to classify the general population into three categories, around which all further healthcare planning revolves.



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