

A mathematical reason to wear a face mask during a COVID-19 like pandemic

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Abstract. The new coronavirus called COVID-19 started spreading in China since the end of 2019, and shortly, it became a serious matter over the entire world, infecting millions of people and killing many of them. That virus lead researchers to looking for ways to eradicate it, the first thing being to prevent people from getting contaminated. One way someone can protect himself and others is to wear a face mask as recommended by the World Health Organization. In this paper, we give a simple mathematical model showing why everyone should wear a face mask during a COVID-19 like pandemic. In order to illustrate the situation, we carry out a short simulation work, showing how various populations can be affected. We also show the number of contamination rounds needed to contaminate the whole population if nothing is done to stop the contamination process.

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1. Introduction

The new coronavirus disease called COVID-19 is caused by the virus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and started spreading in China since the end of 2019. This has become a serious worldwide concern, especially in the most developed countries where the spread has taken most governments by surprise. Very quickly, variants of this virus also started circulating in different countries. The dominant ones are: Alpha (α) for B.1.1.7 (United Kingdom variant), Beta (β) for B.1.351 (South Africa), Gamma (γ) for P.1 (Brazil), Delta (δ) for B.1.617.2 (India), etc. Since then, many methods have been used in order to flatten the curve of

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the expansion of the virus. Washing hands, respecting a certain social distance between people and wearing face masks became famous on media and social networks.

As for the researchers, many models have been developed to appreciate and predict the spread of the virus. We can mention, e.g., Li et al. [3], who studied the transmission process of the virus and realized forward prediction and backward inference of the epidemic situation. On the other hand, Roy and Bhattacharya [7] discussed a mathematical model regarding the spread of COVID-19 in India, aiming at finding the nature of time dependence of the number of symptomatic patients, officially recorded in the country, during a certain period. They based their study on a differential equation that has been formed to find how the number of asymptomatic patients increases with time, and they discussed the impact of imposition of a countrywide lockdown and its withdrawal. In order to investigate the spread and mitigation of the COVID-19 virus in the UK, Hritonenko et al. [2] consider an integral model with finite memory using a realistic infection distribution. They construct and justify an efficient regularization algorithm for finding the transmission rate.

The research on the international epidemics and the future development trend has become a hot topic of current research, and many teams have studied the transmission law and preventive measures of the COVID-19, many leading to interesting results (see, e.g., Mizumoto and Chowell [5]; Riou and Althaus [6]; Shao and Wu [8]). However, many models that work for some areas do not work in others, and this has been the case for epidemiological models for decades.

The aim of this paper is to give a simple mathematical model showing why everyone should wear a face mask when pandemic such as COVID-19 rises. In fact, if the face masks proved to be effectively protecting from getting the virus, then wearing them is worth it, although they are uncomfortable. See Dhaene et al. [1], on which this work is based.

The layout of this work is as follows. In the next section we discuss the model when no policy is involved. In Section 3, the model involving the "wear-a-mask" (WAM) policy is discussed. In Section 4, we give results of a simulation work showing the impact of contamination on populations of various sizes and the number of rounds needed to fully contaminate those populations if nothing is done to stop the contamination process. Some concluding remarks are given in Section 5.

2. The model without any policy

Let us denote by R_0 , the basic reproduction number, that is, the average number of persons infected by a person carrying the virus in an homogeneous population where everyone is susceptible to be infected. An R_0 value greater than 1 means that the epidemic will grow, otherwise, it will reverse. Moreover, the higher the R_0 value, more contagious the disease is. Figure 1 shows the basic reproduction number, R_0 , of some of the SARS-CoV-2 variants in comparison to those of other diseases. From this figure, it appears that the basic reproduction number of Delta variant of SARS-CoV-2 is within the range 5 and 8, meaning that each infected person can infect 5 to 8 other persons. However, another recent study by Liu and Rocklöv [4] shows that the basic reproductive number, R_0 , of Delta variant varies from 3.2 to 8, with a mean of 5.08. In both cases, the Delta variant is more contagious than the original SARS-CoV-2 virus. More details can be found on UNSW Newsroom (see link in the references) [9].

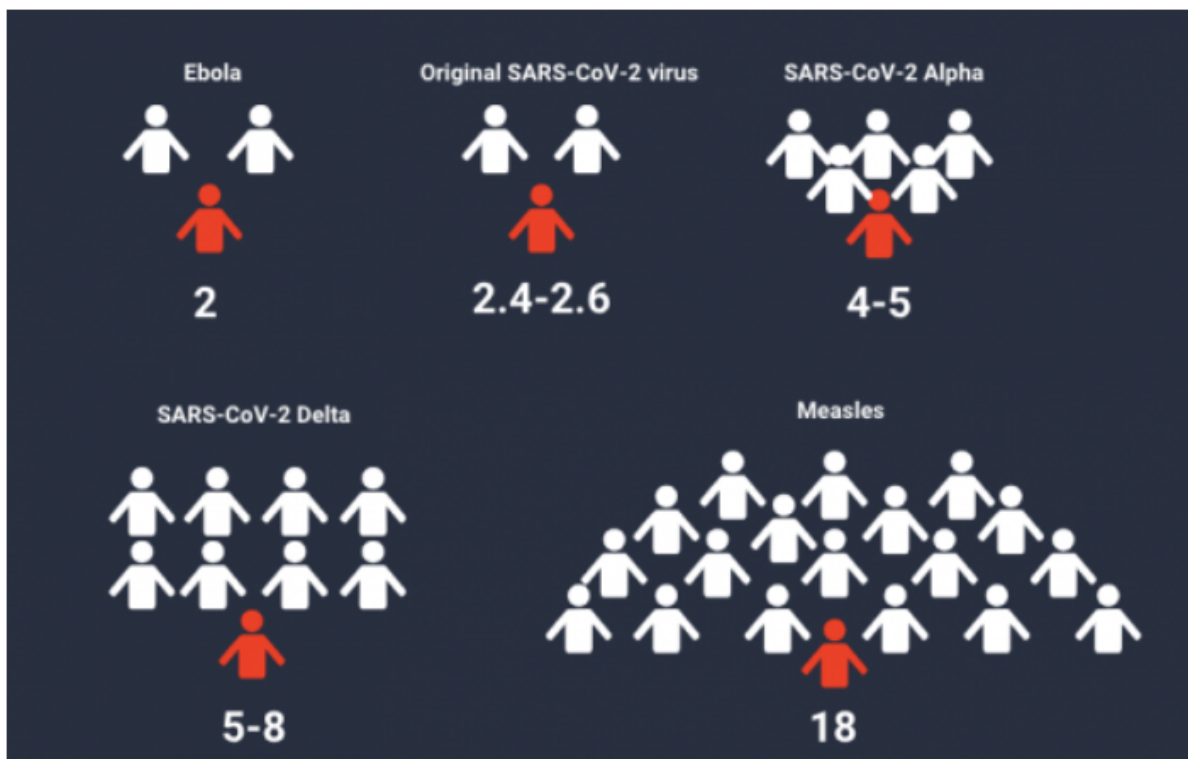


Figure 1: The basic reproduction number, R_0 , of some of the SARS-CoV-2 variants in comparison to those of other diseases. Source: Imperial College London, Lancet, Australian Government.

With a reproduction number of R_0 , an infected person can infect on average R_0 persons, making a total of $1 + R_0$ infected persons. Each one of the R_0 infected persons will infect on average R_0 other persons, yielding $1 + R_0 + R_0^2$ infected persons. The new infected ones will further infect on average R_0 others each, making in total $1 + R_0 + R_0^2 + R_0^3$, and so on.

Suppose that the above process where infected people are infecting others happens n times. Then after n infection rounds, the total number of infected people, which we denote by $M(R_0, n)$, will be equal to $1 + R_0 + R_0^2 + R_0^3 + \dots + R_0^n$. By remarking that the terms of this expression follow a geometric progression of common ratio R_0 and first term 1, $M(R_0, n)$ becomes:

$$M(R_0, n) = \frac{1 - R_0^{n+1}}{1 - R_0}. \quad (2.1)$$

Since $M(R_0, n)$ can be decimal, we will consider the integer part where necessary to account for the fact that we deal with a discrete variable (number of persons).

We can derive the number of infection rounds needed to contaminate a population of size N as:

$$n = \frac{\ln\left(\frac{1 - N + R_0 N}{R_0}\right)}{\ln(R_0)}. \quad (2.2)$$

As it can be seen from equation (2.1), the number of contaminations depends on two parameters: the reproduction number, R_0 , and the number, n , of infection rounds. However, we can note that, for a fixed value of the infection rounds, a small change in R_0 values will produce a huge impact on the number of contaminations. In order to illustrate this idea, let us compare the number of contaminations for a disease with $R_0 = 1.9$ with that of a disease with $R_0 = 2$ after $n = 20$ rounds. We get $M(1.9, 20) = 793564$ and $M(2, 20) = 2097151$. We

can see that although epidemics with basic reproduction numbers 1.9 and 2 might look similar to each other, the latter is vastly a much more severe disease.

3. The model with "wear-a-mask" (WAM) policy

Let us now assume that there is a policy where everybody in the population wears a mask in public areas. Suppose this policy reduces the basic reproduction number from R_0 to $R_0 \times p$, where $p \in (0, 1)$. Then after n rounds of contaminations, the total number of contaminated persons is:

$$M_p(R_0, n) = \frac{1 - (R_0 \times p)^{n+1}}{1 - (R_0 \times p)}. \quad (3.1)$$

The number of rounds needed to contaminate a population of size N is therefore:

$$n = \frac{\ln\left(\frac{1 - N + R_0 \times p \times N}{R_0 \times p}\right)}{\ln(R_0 \times p)}. \quad (3.2)$$

Obviously, since $p < 1$, we have $M_p(R_0, n) < M(R_0, n)$, meaning that the policy will reduce the number of contaminations.

Table 1 to Table 4 show the impact of the reproduction number, R_0 , on the number of contaminations $M(R_0, n)$ and $M_p(R_0, n)$ and the comparison of these numbers for various values of R_0 (ranging from 4 to 8), p ($p = 0.5, 0.7, 0.8, 0.9$) and fixed values of n ($n = 5, 10, 15, 20$). From these tables, we conclude that a relatively small difference in the basic reproduction number, R_0 , will have a huge impact on the total number of infections, $M(R_0, n)$ and $M_p(R_0, n)$, after a sufficient number of transmission of the virus. Particularly, from $n = 15$ we observe an exponential increase on $M(R_0, n)$ and $M_p(R_0, n)$.

Table 1: Impact of R_0 ($R_0 = 4$ to 8) on $M(R_0, n)$ and $M_p(R_0, n)$ and comparison of these numbers of contaminations for $p = 0.5$ and fixed n ($n = 5, 10, 15, 20$).

			$n = 5$	$n = 10$	$n = 15$	$n = 20$
$p = 0.5$	$R_0 = 4$	$M(R_0, n)$	1365	1398101	1.431656e+09	1.466016e+12
		$M_p(R_0, n)$	63	2047	65535	2097151
		M_p/M	4.62%	0.15%	0%	0%
	$R_0 = 5$	$M(R_0, n)$	3906	12207031	3.814697e+10	1.192093e+14
		$M_p(R_0, n)$	162	15894	1552204	151582450
		M_p/M	4.15%	0.13%	0%	0%
	$R_0 = 6$	$M(R_0, n)$	9331	72559411	5.642220e+11	4.387390e+15
		$M_p(R_0, n)$	364	88573	21523360	5230176601
		M_p/M	3.90%	0.12%	0%	0%
$R_0 = 7$	$M(R_0, n)$	19608	329554457	5.538822e+12	9.309098e+16	
	$M_p(R_0, n)$	734	386196	202837711	106534169022	
	M_p/M	3.74%	0.12%	0%	0%	
$R_0 = 8$	$M(R_0, n)$	37449	1227133513	4.021071e+13	1.317625e+18	
	$M_p(R_0, n)$	1365	1398101	1431655765	1466015503701	
	M_p/M	3.64%	0.11%	0%	0%	

Table 2: Impact of R_0 ($R_0 = 4$ to 8) on $M(R_0, n)$ and $M_p(R_0, n)$ and comparison of these numbers of contaminations for $p = 0.7$ and fixed n ($n = 5, 10, 15, 20$).

			$n = 5$	$n = 10$	$n = 15$	$n = 20$
$p = 0.7$	$R_0 = 4$	$M(R_0, n)$	1365	1398101	1.431656e+09	1.466016e+12
		$M_p(R_0, n)$	267	46074	7929686	1364728160
		M_p/M	19.56%	3.30%	0.55%	0.09%
	$R_0 = 5$	$M(R_0, n)$	3906	12207031	3.814697e+10	1.192093e+14
		$M_p(R_0, n)$	735	386196	202837711	1,06534e+11
		M_p/M	18.79%	3.16%	0.53%	0.09%
	$R_0 = 6$	$M(R_0, n)$	9331	72559411	5.642220e+11	4.387390e+15
		$M_p(R_0, n)$	1715	2241776	2929804677	3,829e+12
		M_p/M	18.38%	3.09%	0.52%	0.09%
	$R_0 = 7$	$M(R_0, n)$	19608	329554457	5.538822e+12	9.309098e+16
		$M_p(R_0, n)$	3549	10025182	28318658314	7,99932e+13
		M_p/M	18.09%	3.04%	0.51%	0.09%
	$R_0 = 8$	$M(R_0, n)$	37449	1227133513	4.021071e+13	1.317625e+18
		$M_p(R_0, n)$	6704	36924146	203353e+11	1,11993e+15
		M_p/M	17.90%	3.01%	0.51%	0.08%

Table 3: Impact of R_0 ($R_0 = 4$ to 8) on $M(R_0, n)$ and $M_p(R_0, n)$ and comparison of these numbers of contaminations for $p = 0.8$ and fixed n ($n = 5, 10, 15, 20$).

			$n = 5$	$n = 10$	$n = 15$	$n = 20$
$p = 0.8$	$R_0 = 4$	$M(R_0, n)$	1365	1398101	1.431656e+09	1.466016e+12
		$M_p(R_0, n)$	487	163766	5.495117e+07	1.843855e+10
		M_p/M	35.68%	11.71%	3.84%	1.26%
	$R_0 = 5$	$M(R_0, n)$	3906	12207031	3.814697e+10	1.192093e+14
		$M_p(R_0, n)$	1365	1398101	1.431656e+09	1.466016e+12
		M_p/M	34.95%	11.45%	3.75%	1.23%
	$R_0 = 6$	$M(R_0, n)$	9331	72559411	5.642220e+11	4.387390e+15
		$M_p(R_0, n)$	3218	8201060	2.089663e+10	5.324544e+13
		M_p/M	34.49%	11.30%	3.70%	1.21%
	$R_0 = 7$	$M(R_0, n)$	19608	329554457	5.538822e+12	9.309098e+16
		$M_p(R_0, n)$	6704	36924146	2.033530e+11	1.119930e+15
		M_p/M	34.19%	11.20%	3.67%	1.20%
	$R_0 = 8$	$M(R_0, n)$	37449	1227133513	4.021071e+13	1.317625e+18
		$M_p(R_0, n)$	12725	136642548	1.467188e+12	1.575381e+16
		M_p/M	33.98%	11.14%	3.65%	1.20%



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Table 4: Impact of R_0 ($R_0 = 4$ to 8) on $M(R_0, n)$ and $M_p(R_0, n)$ and comparison of these numbers of contaminations for $p = 0.9$ and fixed n ($n = 5, 10, 15, 20$).

			$n = 5$	$n = 10$	$n = 15$	$n = 20$
$p = 0.9$	$R_0 = 4$	$M(R_0, n)$	1365	1398101	1.431656e+09	1.466016e+12
		$M_p(R_0, n)$	837	506237	306102350	1,85088e+11
		M_p/M	61.25%	36.21%	21.38%	12.63%
	$R_0 = 5$	$M(R_0, n)$	3906	12207031	3.814697e+10	1.192093e+14
		$M_p(R_0, n)$	2372	4377938	8078526911	1,49072e+13
		M_p/M	60.73%	35.86%	21.18%	12.51%
	$R_0 = 6$	$M(R_0, n)$	9331	72559411	5.642220e+11	4.387390e+15
		$M_p(R_0, n)$	5635	25874900	1,18808e+11	5,45527e+14
		M_p/M	60.38%	35.66%	21.06%	12.43%
	$R_0 = 7$	$M(R_0, n)$	19608	329554457	5.538822e+12	9.309098e+16
		$M_p(R_0, n)$	11797	117076619	1,16191e+12	1,15312e+16
		M_p/M	60.16%	35.53%	20.98%	12.39%
	$R_0 = 8$	$M(R_0, n)$	37449	1227133513	4.021071e+13	1.317625e+18
		$M_p(R_0, n)$	22470	434776209	8,41256e+12	1,62776e+17
		M_p/M	60.00%	35.43%	20.92%	12.35%

Another aspect that is worth highlighting is that these tables clearly indicate the positive impact of the policy on the contamination rate. As an example (see Dhaene et al. [1]), let us suppose that the factor p is equal to 90%. This means that wearing face masks reduces the basic reproduction number by 10%. At step 20 of a chain of 20 rounds of infections, the number of infected people under the wear-a-mask policy is only about 12% of the number of people that would have been infected without introducing that policy (Table 4).

Instead of 90%, let us now look at what happens if the factor p equals 80%, which means that wearing masks reduces the reproduction number by 20%. In this case we find that after 20 steps, the number of infected people is reduced to 1.2% of the original number of infected people (Table 3).

4. Simulations

In this section, we carry out a short simulation work to show how various populations can be affected by the virus. We also show the number of infection rounds needed to contaminate the whole population if nothing is done to stop the contamination process. In order to achieve this, we have considered populations of sizes $N = 100, 1000, 5000, 10000, 100000, 1000000, 3000000$, and 5000000 . For the basic reproduction number, we take $R_0 = 4$. The results are given in Tables 5.

Table 5: Number of rounds needed to contaminate the full population for different values of p (0.3, 0.5, 0.7, 0.9, 1) and $R_0 = 4$.

Population size	Rounds with No policy	Rounds with WAM policy			
	$p = 1$	$p = 0.9$	$p = 0.7$	$p = 0.5$	$p = 0.3$
100	3.12	3.34	4.05	5.66	15.70
1000	4.78	5.14	6.28	8.97	28.09
5000	5.94	6.40	7.84	11.29	36.89
10000	6.44	6.94	8.52	12.29	40.69
100000	8.10	8.73	10.75	15.61	53.32
1000000	9.76	10.53	12.99	18.93	65.95
3000000	10.55	11.39	14.06	20.52	71.97
5000000	10.92	11.79	14.55	21.25	74.78

It is clear from this table that, for fixed value of p , the number of rounds needed to contaminate the full population increases as the population size increases. Moreover, for fixed population size, the number of rounds required to contaminate that population decreases as the value of p increases.

5. Concluding remarks

This work clearly illustrate the importance of wearing masks to fight the COVID-19 and similar diseases. We have seen that the reproduction number can be considerably reduced if a "wear-a-mask" policy is made and especially if people respect it. Simulation results show that the infection process is slowed down with the WAM policy, and this could allow more time to researchers to find cure or vaccines to completely eradicate the virus.

The models considered are, of course, too simple to explain and take into account all effects of wearing masks or not. For example, mandating mask protection could make people become less cautious about social distancing, and this could reduce the positive effects of wearing masks. Therefore, wearing a face mask with the intention to decrease the infection rate will only be fully effective if it is surrounded by a sufficient educative support and combined with other regulations. Further, the models should not be applied for any number of infection rounds because when a high proportion of the population becomes immune, the reproduction number will automatically go down.

While we focused on the WAM policy, it is clear that similar observations as the ones we made also hold for any other strategy that adapts the number of infected people. We suggest that people wear masks all the time, even if they have been infected and recovered or if they have been vaccinated. In fact, although approaches of solutions are being obtained, different variants of the virus are springing out, and the available solutions may not be efficient against them.

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