# A few things to know about the spread of COVID-19 

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#### Abstract

The COVID-19 pandemic is currently spreading in exponential fashion outside of China. This report shows predictions from simple models that should clarify the future evolution of this pandemic. The conclusions, are that 1) the basic reproduction factor, $R_{0}$, may be as high as $5 ; 2$ ) without Containment, up to $50 \%$ of residents of large cities are Infectious at the peak of the pandemic, forcing hospitals to choose a which small fraction of patients they can treat; 3) the exponential rise of the fraction of Infectious people is followed by a slower exponential decrease; 4) by the end of an un-Contained pandemic, almost everyone will have been infected; 5) since inhabitants of countries are clustered in big cities, where encounters (hence the $R_{0}$ factor) are more frequent, the pressure on the hospitals is even greater; 6) At any given time during the current phase of exponential growth, the fraction of Infectious people is roughly 10 times what is reported; 7) there is no evidence that the virus is weakened by hot weather; 8) Containment is effective in limiting the spread, but must continue at least until end of May or early June 2020 to hope for eradication of the virus.


## 1 Introduction

This document presents my thoughts on the current Coronavirus disease 2019 (COVID-19) pandemic caused by the Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus. This should not be interpreted as the truth, but simple modeling, which may contain bad or inaccurate assumptions. The text is sparsed with mathematical equations that the non-mathematical reader can just skip. These equations are, for the most part, written in slow steps, so that readers with only moderate mathematical skills can follow them.

## 2 Mathematical formalism

The mathematical formalism can be expressed in terms of numbers of people in different categories:
Susceptibles (S) People who may catch the virus infection, without being immune to it.
Exposed (E) People who have been exposed to the virus without having become infectious.
Infectious (I) People who have caught the virus and are in an infectious stage.
Recovered (R) People who have recovered from the infection, and are no longer infectious (but could later become susceptible to a new strain of virus).

Deceased (D) Victims of the virus.
These categories follow the pattern shown in Figure 1. In a population of initial size $N$, the number of people in each pattern evidently follows

$$
\begin{equation*}
S+E+I+R+D=N . \tag{1}
\end{equation*}
$$

In the simplest homogeneous SIR model (?), several assumptions are made:


Figure 1: General progression of pandemic in categories of people

1. The Exposed population is merged into the Infectious population.
2. The Dead population is merged with the Recovered population to form the Removed population, which if they survive become immune to the virus and can no longer become susceptible.
3. The Infectious people all remain infectious for a time $T_{\mathrm{I}}$.
4. The members of the Infectious population each infect a constant number $R_{0}$ of Susceptible people through the course of their infection. $R_{0}$ is called the basic reproduction number.
5. The fraction of the population that die is very small, say less than $5 \%$, so that one can assume that the total population size $N$ is roughly constant.


Figure 2: Simplified SIR progression of pandemic in categories of people
The SIR model (Figure 2) thus involves only 3 categories of people, Susceptibles, Infectious, and Removed. It provides a good representation to outbreaks such as measles (rougeole in French), mumps (oreillons in French), and rubella (rubéole in French). Equation (1) can be simplified to

$$
\begin{equation*}
S+I+R=1, \tag{2}
\end{equation*}
$$

where $S, I$, and $R$ now represent fractions of the total population.
One can write differential equations for the temporal variations of the different populations.

$$
\left\{\begin{array}{l}
\frac{\mathrm{d} S}{\mathrm{~d} t}=-b S I  \tag{3a}\\
\frac{\mathrm{~d} I}{\mathrm{~d} t}=b S I-g I, \\
\frac{\mathrm{~d} R}{\mathrm{~d} t}=g I
\end{array}\right.
$$

Equation (3a) states that the Susceptibles are converted into Infectious when they run into an Infectious, where $b$ is the transmission rate, i.e. the (average) number of contacts between Susceptibles and Infectious that lead to the infection of the Susceptible, per Susceptible and per Infectious. Equation (3b) converts the loss of Susceptibles into a gain of Infectious, but also has a loss term to account for transition to the Removed category, either by Recovery or by Death. Here $g$ is the removal rate, so that $1 / g$ is the period (e.g. in days) that a person remains Infectious. Finally, equation (3c) expresses the loss of Infectious as a gain for the Removed. The basic reproduction number is defined as the ratio of the rates

$$
\begin{equation*}
R_{0}=\frac{b}{g} . \tag{4}
\end{equation*}
$$

Equation (4) can also be re-written as $R_{0}$ being the ratio of the infectious period to the time between infectious contacts of an Infectious with Susceptible people.

## 3 Natural growth

We first analyze the unimpeded growth of a pandemic, that is without any efforts at containing the population to avoid transmission of the virus from Infectious people to Susceptibles, who hereafter become Infectious.

This growth can be described in several phases.

### 3.1 Exponential growth

In the early phase, the fraction of Infectious people is small, i.e. $I \ll 1$, and given equation (2), the fraction of Susceptible people is close to unity. Therefore equation (3b) becomes

$$
\begin{equation*}
\frac{\mathrm{d} I}{\mathrm{~d} t} \simeq(b-g) I=\left(R_{0}-1\right) \frac{I}{T_{\mathrm{I}}} \tag{5}
\end{equation*}
$$

Integrating equation (5) yields the evolution of the fraction of Infectious people as

$$
\begin{equation*}
I(t)=I_{i} \exp \left[\left(R_{0}-1\right) \frac{t}{T_{\mathrm{I}}}\right] \tag{6}
\end{equation*}
$$

where $I_{i}$ is the initial number of Infectious people. Equation (6) indicates that for $R_{0}>1$, there is exponential growth of the fraction of Infectious people, and equation (6) can be re-written

$$
\begin{equation*}
I(t)=I_{i} 2^{t / T_{2}} \tag{7}
\end{equation*}
$$

where $T_{2}$ is the doubling time of the number of Infectious people. Combining equations (6) and (7) gives

$$
\begin{equation*}
T_{2}=\frac{\ln 2}{R_{0}-1} T_{\mathrm{I}} \simeq \frac{0.7}{R_{0}-1} T_{\mathrm{I}} \tag{8}
\end{equation*}
$$

Conversely, if $R_{0}<1$, the fraction of Infectious people drops exponentially. If $R_{0}$ were exactly equal to unity, the fraction of Infectious people would remain constant in time.

The graphs of the time evolution of the number of Infectious people per country ${ }^{1}$ all show exponential growth for countries at this stage, except for China, where the exponential growth stage has terminated in early February.

Equation (7) can be inverted to yield

$$
\begin{equation*}
R_{0}=1+\ln 2 \frac{T_{\mathrm{I}}}{T_{2}} \simeq 1+0.7 \frac{T_{\mathrm{I}}}{T_{2}} \tag{9}
\end{equation*}
$$

[^0]

Figure 3: Basic reproduction factor, $R_{0}$, as a function of doubling time of number of infected people for different durations of the infectious stage, following equation (9)

Figure 3 illustrates how $R_{0}$ depends on both the doubling time, $T_{2}$ and on the duration of the Infectious phase, $T_{\mathrm{I}}$.

The early phases of the exponential growth often occurred with doubling times of 2 to 3 days, which, according to equation (9) and Figure 3 indicates that $R_{0}$ lies somewhere between 2.5 and 6 , depending on the duration of the contagious phase, $T_{\mathrm{I}}$. There is little information available on the value of $T_{\mathrm{I}}$, because it is very difficult to measure. A recent study (?) suggests that people infected by COVID-19 are contagious from before the symptoms appear (the incubation period) to after the symptoms disappear, which suggests that $T_{\mathrm{I}}$ should be longer than previously thought. Also, the time from onset of symptoms to death ranges from 2 to 8 weeks (?), which again suggests a very long contagious time. This suggests that COVID-19 is unusually contagious with a basic reproduction factor $R_{0}>5$. This is at the upper limit of the range of $R_{0}$ given in ?. ${ }^{2}$

### 3.2 Peak of pandemic

The pandemic reaches a peak, because Infectious people run out of Susceptibles to contaminate. This peak is naturally defined when the fraction of Infectious people reaches its maximum, i.e. $\mathrm{d} I / \mathrm{d} t=0$. Since equation (3b) can be re-written as

$$
\begin{equation*}
\frac{\mathrm{d} I}{\mathrm{~d} t}=\left(R_{0} S-1\right) \frac{I}{T_{\mathrm{I}}}, \tag{10}
\end{equation*}
$$

the peak occurs when $S=S_{\text {peak }}=1 / R_{0}$, and the fraction of people who have caught the virus at this time (Infectious plus Removed), is

$$
\begin{equation*}
Z_{\text {peak }}=1-S_{\text {peak }}=1-\frac{1}{R_{0}} . \tag{11}
\end{equation*}
$$

For $R_{0}=2$ to 5 , equation (11) leads to $\mathbf{5 0 \%}$ to $\mathbf{8 0 \%}$ of the population having been contaminated at the peak of the pandemic, and more by the end as we shall see in Sect. 3.4 below.

[^1]
### 3.3 Post-peak exponential decrease

After the peak, the fraction of Susceptibles is very roughly constant, and equation (10) can be approximated as

$$
\begin{equation*}
\frac{\mathrm{d} I}{\mathrm{~d} t} \simeq(b S-g) I=\left(R_{0} S-1\right) \frac{I}{T_{I}} \tag{12}
\end{equation*}
$$

which is similar to equation (5), with the extra constant $S$ term. The solution of equation (12) is an exponential decrease of the fraction of Infectious

$$
\begin{equation*}
I(t)=I_{j} \exp \left[\left(S R_{0}-1\right) \frac{\left(t-t_{j}\right)}{T_{I}}\right] \tag{13}
\end{equation*}
$$

where $t_{j}$ is a reference time, $I_{j}=I\left(t_{j}\right)$ is te fraction of Infecytious at this reference time. For $S<1 / R_{0}$, equation (13) can be re-written as

$$
\begin{equation*}
I(t)=I_{j} 2^{-t / T_{2}} \tag{14}
\end{equation*}
$$

where $T_{2}$ is now the halving time of the number or fraction of Infectious people. Combining equations (13) and (14) produces

$$
\begin{equation*}
T_{2}=\frac{\ln 2}{1-R_{0} S} T_{I} \simeq \frac{0.7}{1-R_{0} S} T_{I} \tag{15}
\end{equation*}
$$

One should note that the ratio of halving to doubling times is easily obtained by combining equations (8) and (15):

$$
\begin{equation*}
\frac{T_{2}^{\text {halving }}}{T_{2}^{\text {doubling }}}=\frac{R_{0}-1}{1-R_{0} S_{\mathrm{final}}} \tag{16}
\end{equation*}
$$

The halving time is at best (shortest) equal to $R_{0}-1$ times the doubling time. For $R_{0}=3$, the halving time is at least twice the doubling time. We shall see below that $S_{\text {final }}$ is much lower than unity, so the halving time is close to that limit.

### 3.4 End of pandemic

The pandemic ends when the fraction of Infectious people is significantly decreased by the Recoveries or Deaths. A this stage, one can estimate the fraction $Z_{\text {final }}$ of people who have caught the virus can be found as follows.

Equations (3a) and (3b) combine to

$$
\begin{equation*}
\frac{\mathrm{d} S}{\mathrm{~d} t}+\frac{\mathrm{d} I}{\mathrm{~d} t}=-g I=-\frac{b}{R_{0}} I=\frac{1}{R_{0}} \frac{1}{S} \frac{\mathrm{~d} S}{\mathrm{~d} t} . \tag{17}
\end{equation*}
$$

Equation (17) can be integrated to yield

$$
\begin{equation*}
\left(S_{\text {final }}-S_{\text {initial }}\right)+\left(I_{\text {final }}-I_{\text {initial }}\right)=\frac{1}{R_{0}} \ln \left(\frac{S_{\text {final }}}{S_{\text {initial }}}\right) . \tag{18}
\end{equation*}
$$

Since $S_{\text {initial }} \simeq 1$ and $\left(I_{\text {final }}-I_{\text {initial }}\right) \ll 1$, equation (18) leads to

$$
\begin{equation*}
Z_{\mathrm{final}}=1-S_{\mathrm{final}} \simeq-\frac{1}{R_{0}} \ln \left(1-Z_{\mathrm{final}}\right) \tag{19}
\end{equation*}
$$

or equivalently

$$
\begin{equation*}
Z_{\text {final }}=1-\mathrm{e}^{-R_{0} Z_{\text {final }}} . \tag{20}
\end{equation*}
$$

Figure 4 shows the solution of equation (20) in terms of $R_{0}$ (top panel) or of the Infectious duration, $T_{\mathrm{I}}$ (bottom panel). The final fraction of people infected at some point by the virus is as high as $\mathbf{8 0 \%}, \mathbf{9 4 \%}$, or $\mathbf{9 9 \%}$, for $R_{0}=2,3$, or 5 , respectively.

Since the fatality rate among those who have been contaminated at one point is estimated to be between $1 \%$ and $5 \%,{ }^{3}$ then the percentage of people in a country who die from the virus is $\mathbf{1 \%}$ to $\mathbf{5 \%}$, assuming that no Containment measures are taken, as shown in Figure 5.

[^2]

Figure 4: Final fraction of contaminated population versus $R_{0}(\mathbf{t o p})$ or versus $T_{\mathrm{I}}$ (Bottom).

### 3.5 Full evolution

The full evolution, with no measures of Containment (Sect. 5 below discusses Containment), obtained by solving the system of differential equations (3a)-(3c) is shown in Figure 6. The top panel highlights the different evolution of the Susceptibles, Infectious and Removed populations, for $T_{2}=3$ days and for three choices of $T_{I}$ (hence of $R_{0}$ ). The fraction of Susceptibles (never contaminated) decreases slowly from unity then rapidly, finally reaching a plateau at $5 \%$ to $15 \%$ in roughly 1 month of time. The fraction of Infectious first rises rapidly, in fact exponentially, then reaches its maximum and then decreases exponentially for lack of Susceptible people to infect. The fraction of Removed rises exponentially and reaches a plateau near $100 \%$. The longer the duration of the Infectious stage of individuals, the longer is the exponential rise of Infectious people, and the later and higher is the peak fraction of Infectious. For our choice of 3-day doubling time, as observed in most countries before effective measures of Containment, the peak occurs when as many as half to $70 \%$ of the population have been infected at one point. And, according to Figure 6, the maximum fraction of Infectious people at a given time is as high as $18 \%$ to $34 \%$, depending on the Infectious duration, $T_{\mathrm{I}}$.


Figure 5: Final percentage of deaths, for different fatality rates

## 4 Clustering

Unfortunately for the decision-makers, the parameter $R_{0}$ is not uniform among the population. In large cities, Infectious people will meet more Susceptibles and contaminate more of them than in small villages. And even within cities, people in some occupations have more close encounters with others, for example medical doctors who consult with up to 4 patients per hour.

I propose to neglect this second issue and assume that in a given zone, $R_{0}$ is the same for everyone. My clustering model has 3 zones:

1. A village, O, that is the Origin (foyer in French) of the infection in the country;
2. Cities, C;
3. The rest of the country side, V, made of small Villages similar to the foyer of infection.

We then have to follow 9 parameters, $S_{\mathrm{O}}, I_{\mathrm{O}}$, and $R_{\mathrm{O}}$ for the populations (not fractions) of the Origin, $S_{\mathrm{C}}, I_{\mathrm{C}}$, and $R_{\mathrm{C}}$ for the populations of the Cities, and $S_{\mathrm{V}}, I_{\mathrm{V}}$, and $R_{\mathrm{V}}$ for the populations of the other Villages. The population $N_{\mathrm{O}}=S_{\mathrm{O}}+I_{\mathrm{O}}+R_{\mathrm{O}}$ of the Origin represents a fraction $F_{\mathrm{O}}$ of the population $N$ of the entire country, while the population $N_{\mathrm{C}}=S_{\mathrm{C}}+I_{\mathrm{C}}+R_{\mathrm{C}}$ of the cities is $F_{\mathrm{C}}$ that of the country, with the remaining $N_{\mathrm{V}}=N-N_{\mathrm{O}}-N_{\mathrm{C}}$ in the other villages, i.e. $F_{\mathrm{O}}+F_{\mathrm{C}}+F_{\mathrm{V}}=1$.

I also assume that some fraction of the people from one zone make round-trip visits to the other zone. This leads to Infectious from one zone contaminating the Susceptibles from other zones.

Therefore the rate of change of the number of Susceptibles from one zone is the sum of 3 terms:

1. contaminations from Infectious of their zone;
2. contaminations from Infectious people visiting from other zones;


Figure 6: Top: Evolution of fractions of Susceptibles (solid), Infectious (dashed) and Removed (dotted), for 3 assumed durations of the Infectious. Bottom: Evolution of total cases (solid) and (current) Infectious (dashed). Both panels assume doubling time $T_{2}=3$ days and Infectious duration $T_{\mathrm{I}}=5,7$, or 10 days, which for $T_{2}=3$ days amounts to $R_{0}=2.2,2.6$, and 3.3.
3. contaminations from Infectious people from other zones, when visiting their zone.

With these assumptions one can write the differential equations of our clustering SIR model as in equations (24a)-(24i) of Appendix A.

Figure 7 shows the evolution of such a 3 -zone clustered country. The infection spreads rapidly to other Villages, then almost immediately to Cities, whose greater promiscuity, hence larger $R_{0}$ factor, leads to a faster relative rise in number of Infectious. The number of Infectious in the country has two peaks: in Cities after 45 days, and in Villages after 270 days. Moreover, while up to $10 \%$ of the inhabitants of the Origin and of Villages are Infectious at the peak of their respective epidemics, the peak fraction of Infectious is as high as $\mathbf{5 0 \%}$ in the Cities.

## 5 Containment

The top panel of Figure 8 displays the effects of a 90 -day period of Containment that reduces $R_{0}$ from 3 to 0.5 . The figure indicates that Containment represents a delay in the Contamination, but the final cumulative fraction of Contaminated people remains the same. Indeed, while


Figure 7: Evolution of Infectious cases in 3-zone clustered country, where $R_{0}=5$ in cities (total population of 20 million) and $R_{0}=1.5$ elsewhere, without Containment. The simulation assumes that $20 \%$ of people in the Origin and in other Villages travel regularly to Cities and $10 \%$ of the inhabitants of the Origin village to other Villages. The dashed horizontal lines represent the total population of each of the 3 zones. The bottom panel is a zoom at early times.

Containment does reduce drastically the Number of Infectious (decreasing portion of red line), the Infectious rises exponentially (seen linearly in logarithmic $y$ axis) as soon as Containment is ended. The post-Containment period matches the evolution of the No-Containment case (dashed lines), but with the delay of the Containment period.

With Containment, equation (16) becomes

$$
\begin{equation*}
\frac{T_{2}^{\text {halving }}}{T_{2}^{\text {doubling }}}=\frac{R_{0}^{\text {initial }}-1}{1-R_{0}^{\text {Containment }} S_{\text {Containment }}} \simeq \frac{R_{0}^{\text {initial }}-1}{1-R_{0}^{\text {Containment }}} \tag{21}
\end{equation*}
$$

where $R_{0}^{\text {Containment }}<1<R_{0}^{\text {initial }}$. According to equation (21) and illustrated in Figure 9, the ratio of halving to doubling time is 4 for $R_{0}^{\text {initial }}=3$ and $R_{0}^{\text {Containment }}=0.5$ (a wild guess). Equation (21) indicates that even with complete Containment ( $R_{0}^{\text {Containment }}=0$ ), the halving time will be at least $R_{0}^{\text {initial }}-1 \simeq 2$ times the initial doubling time.


Figure 8: Effect of Containment (during times shown as gray shaded region) on fractions of cumulative cases and of Infectious. The Infectious duration is assumed to be 7 days. The basic reproduction number is $R_{0}=3$ before and after Containment, and $R_{0}=0.5$ (top) or 0 (bottom) during Containment. The dashed and solid curves show the cases without and with Containment.

## 6 Strategic choices

### 6.1 National and regional strategies

### 6.1.1 Should the population be Contained?

Given the observed fatality rate between $1 \%$ and $5 \%$, and that the peak fraction of Infectious people is between $14 \%$ and $33 \%$ in a homogeneous model (Figure 6) or as high as $50 \%$ in Cities in a clustered model (top panel of Figure 7), the authorities feel obliged to treat the serious Infectious cases. But since roughly $20 \%$ of the Infectious cases are life-threatening, the moral decision to treat all serious cases implies that at one point of time as many as $7 \%$ of the entire population ( $10 \%$ in Cities) will be hospitalized (roughly one-quarter of these in intensive care). These huge fractions of peak demands for hospitalizations and of intensive care are well beyond the capacities of any country. Therefore, all governments face the following dilemma:

- Treat only a fraction of the cases. This leads to choices of who should be treated, which be


Figure 9: Ratio of Containment halving time to Pre-Containment doubling time
considered as immoral by a large fraction of the population.

- Contain the spread of the pandemic. This has dire consequences on 1) the economy, and 2) the health of the remaining population. In fact, one could worry that a long Containment period would indirectly cause more deaths than the roughly one million expected from the COVID-19 virus in a country of 65 million, from inadequate access to medical facilities and personnel of people who are ill from other causes than the virus.

The only reason for Containment is to gain time in hope that the virus weakens during the hot Summer days, or that an effective and safe vaccine becomes widely available.

### 6.1.2 When should Containment be instituted?

The analysis of the pandemic by national or regional authorities is difficult in the early exponentialgrowth phase, because of two factors:

1. not all Infectious people report their illness;
2. those who do report their illness, do it with a delay corresponding to the incubation period plus the period where their signs of illness are not deemed threatening.

Denoting this delay as $T_{\text {delay }}$, and assuming that it is the same for all Infectious people, then the actual number of cases is

$$
\begin{equation*}
I_{\text {reported }}(t)=I\left(t-T_{\text {delay }}\right)=I_{i} 2^{\left(t-T_{\text {delay }}\right) / T_{2}}=2^{-T_{\text {delay }} / T_{2}} I(t) . \tag{22}
\end{equation*}
$$

i.e.

$$
\begin{equation*}
I(t)=2^{T_{\text {delay }} / T_{2}} I_{\text {reported }} \tag{23}
\end{equation*}
$$

Equation (23) indicates that the number of reported cases is hugely underestimated. In China, the arrival of the symptoms pre-dated the diagnosis of the virus by typically $T_{\text {delay }}=7$ days (?, see


Figure 10: Effect of time delay on measured number of cases (semi-log plot)
also ?). Equation (23) indicates that there are 5 to 11 times more cases than reported if the doubling time is 3 or 2 days, respectively (see ?). This underestimation of the number of cases is even more important if, as many think, the Infectious stage begins before the first symptoms. So, when you venture into the street, you should consider that at least 10 times the official ratio of contaminated to total population are effectively Infectious, and multiply by another factor of 2 or more if you live in a city, where people run into one another more frequently, hence Infectious people contaminate Susceptibles at a faster rate (i.e. cities have higher $R_{0}$ than rural areas).

### 6.1.3 When should Containment be lifted?

There are three criteria to lift the containment:

1. when the virus is eradicated;
2. when the Summer season hopefully decreases the strength of the virus.
3. when an effective and safe vaccine becomes widely available;

The eradication of the virus could be expected following the exponential decrease of the Infectious population, predicted in equations (13) and (14), and computed in Figure 6 and especially Figure 8. In particular, Figure 8 shows that for a country of population around 65 million (e.g. France, the United Kingdom, Italy), the time to have the fraction of Infectious to fall below 1 over 65 million is 150 days for $R_{0}^{\text {Containment }}=0.5$ or a minimum of 75 days for $R_{0}^{\text {Containment }}=0$. Empirically, the residents of the Hubei province of China (where the outbreak begun) had to wait 50 days after the start of Containment (a strictly-enforced lockdown) to see zero new cases on 18 March 2020. But the number may rise again, and there are still some Infectious people. So the Containment period in Hubei whose population is 60 million) should probably last $50+15=65$ days, which is not too far off from our estimate of 75 days. Therefore, in such countries, the absolute minimum duration of Containment is 2 or 2.5 months. This brings us to end of May or early June 2020.

In practice, governments should not lift Containment as soon as the number of Infectious appears to be nil, but wait a few days to make sure that the few missing cases of Infectious move to the Removed category, otherwise they will re-infect the population with exponential growth. The Containment
measures could be lifted in steps lasting a week each, so as to monitor the evolution of the number of Infectious people.

There is also the hope that the COVID-19 virus will weaken when the hot Summer days arrive. The one hot-Summer country in the Southern hemisphere whose medical quality is at the level of Europe and North America is Australia. The doubling time of the cases (Infectious + Removed in our parlance) is also roughly 3 days (?). While the fraction of cases in Australia is 5 times lower than in France it is as much as half that of the United Kingdom. So, there seems to be little relief of the pandemic from hot weather.

Finally, if the virus cannot be eradicated, our hope lies in an effective and widely distributed vaccine. Vaccines usually take over a year to fully develop and certify, which would keep us in Containment until February or March 2021. However, there is some hope for a shorter wait, as a COVID-19 vaccine has begun Phase 1 trials, in record time (?).

## 7 Conclusions

It is very difficult to accurately predict the spread of a pandemic like that of the COVID-19 coronavirus. This report highlights the spread of a pandemic in a given mid-size country from simple modeling in cases of a homogeneous population, showing how a more clustered population changes the spread. It also shows the effects and limits of Containment of the population. At best, the Containment will last until late May or early June, but perhaps many months more. The effects on the economy will be huge.

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## A 3-zone model equations

In our 3-zone model, involving the Origin village ( O ), the Cities $(\mathrm{C})$ and the other Villages ( V ), the equations of the variations of the populations of each category in each zone (not the fractions) can be written by considering

$$
\left\{\begin{align*}
\frac{\mathrm{d} S_{\mathrm{O}}}{\mathrm{~d} t}= & -\frac{S_{\mathrm{O}}}{T_{\mathrm{I}} N_{\mathrm{O}}}\left[R_{0}^{\mathrm{O}}\left(I_{\mathrm{O}}+\frac{f_{\mathrm{C} \rightarrow \mathrm{O}} I_{\mathrm{C}}}{1+f_{\mathrm{C} \rightarrow \mathrm{O}} I_{\mathrm{C}}}+\frac{f_{\mathrm{V} \rightarrow \mathrm{O}} I_{\mathrm{V}}}{1+f_{\mathrm{V} \rightarrow \mathrm{O}} I_{\mathrm{V}}}\right)\right. \\
& \left.+\left(R_{0}^{\mathrm{C}} \frac{f_{\mathrm{O} \rightarrow \mathrm{C}} I_{\mathrm{C}}}{1+f_{\mathrm{O} \rightarrow \mathrm{C}} I_{\mathrm{C}}}+R_{0}^{\mathrm{V}} \frac{f_{\mathrm{O} \rightarrow \mathrm{~V}} I_{\mathrm{V}}}{1+f_{\mathrm{O} \rightarrow \mathrm{~V}} I_{\mathrm{V}}}\right)\right],  \tag{24a}\\
\frac{\mathrm{d} I_{\mathrm{O}}}{\mathrm{~d} t}= & -\frac{\mathrm{d} S_{\mathrm{O}}}{\mathrm{~d} t}-\frac{I_{\mathrm{O}}}{T_{\mathrm{I}}},  \tag{24b}\\
\frac{\mathrm{~d} R_{\mathrm{O}}}{\mathrm{~d} t}= & \frac{I_{\mathrm{O}}}{T_{\mathrm{I}}},  \tag{24c}\\
\frac{\mathrm{~d} S_{\mathrm{C}}}{\mathrm{~d} t}= & -\frac{S_{\mathrm{C}}}{T_{\mathrm{I}} N_{\mathrm{C}}}\left[R_{0}^{\mathrm{C}}\left(I_{\mathrm{C}}+\frac{f_{\mathrm{O} \rightarrow \mathrm{C}} I_{\mathrm{O}}}{1+f_{\mathrm{O} \rightarrow \mathrm{C}} I_{\mathrm{O}}}+\frac{f_{\mathrm{V} \rightarrow \mathrm{C}} I_{\mathrm{V}}}{1+f_{\mathrm{V} \rightarrow \mathrm{C}} I_{\mathrm{V}}}\right)\right. \\
& \left.+\left(R_{0}^{\mathrm{O}} \frac{f_{\mathrm{C} \rightarrow \mathrm{O}} I_{\mathrm{O}}}{1+f_{\mathrm{C} \rightarrow \mathrm{O}} I_{\mathrm{O}}}+R_{0}^{\mathrm{V}} \frac{f_{\mathrm{C} \rightarrow \mathrm{~V}} I_{\mathrm{V}}}{1+f_{\mathrm{C} \rightarrow \mathrm{~V}} I_{\mathrm{V}}}\right)\right],  \tag{24d}\\
\frac{\mathrm{d} I_{\mathrm{C}}}{\mathrm{~d} t}= & -\frac{\mathrm{d} S_{\mathrm{C}}}{\mathrm{~d} t}-\frac{I_{\mathrm{C}}}{T_{\mathrm{I}}},  \tag{24e}\\
\frac{\mathrm{~d} R_{\mathrm{C}}}{\mathrm{~d} t}= & \frac{I_{\mathrm{C}}}{T_{\mathrm{I}}},  \tag{24f}\\
\frac{\mathrm{~d} S_{\mathrm{V}}}{\mathrm{~d} t}= & -\frac{S_{\mathrm{V}}}{T_{\mathrm{I}} N_{\mathrm{V}}}\left[R_{0}^{\mathrm{V}}\left(I_{\mathrm{V}}+\frac{f_{\mathrm{O} \rightarrow \mathrm{~V}} I_{\mathrm{O}}}{1+f_{\mathrm{O} \rightarrow \mathrm{~V}} I_{\mathrm{O}}}+\frac{f_{\mathrm{C} \rightarrow \mathrm{~V}} I_{\mathrm{C}}}{1+f_{\mathrm{C} \rightarrow \mathrm{~V}} I_{\mathrm{C}}}\right)\right. \\
& \left.+\left(R_{0}^{\mathrm{O}} \frac{f_{\mathrm{V} \rightarrow \mathrm{O}} I_{\mathrm{O}}}{1+f_{\mathrm{V} \rightarrow \mathrm{O}} I_{\mathrm{O}}}+R_{0}^{\mathrm{C}} \frac{f_{\mathrm{V} \rightarrow \mathrm{C}} I_{\mathrm{C}}}{1+f_{\mathrm{V} \rightarrow \mathrm{C}} I_{\mathrm{C}}}\right)\right],  \tag{24~g}\\
\frac{\mathrm{d} I_{\mathrm{V}}}{\mathrm{~d} t}= & -\frac{\mathrm{d} S_{\mathrm{V}}}{\mathrm{~d} t}-\frac{I_{\mathrm{V}}}{T_{\mathrm{I}}}  \tag{24h}\\
\frac{\mathrm{~d} R_{\mathrm{V}}}{\mathrm{~d} t}= & \frac{I_{\mathrm{V}}}{T_{\mathrm{I}}} . \tag{24i}
\end{align*}\right.
$$

Equations (24b), (24e), and (24h) for the Infectious all resemble equation (3b), and equations (24c), (24f), and (24i) for the Removed all resemble equation (3c). On the other hand equations (24a), (24d), and ( 24 g ) include extra terms relative to equation (3a), namely the infections from Infectious visitors from another zone ( 2 nd and 3rd terms of the 1st parentheses), and the infections occurred when traveling to another zone (both terms of 2 nd parentheses).


[^0]:    ${ }^{1}$ These graphs can be seen in ?, with data provided by the European Centre for Disease Prevention and Control (ECDC) at https://www.ecdc.europa.eu/sites/default/files/documents/COVID-19-geographic-disbtribution-worldwide-2020-03-14_1.xls.

[^1]:    ${ }^{2}$ Note that the article giving the upper limit of $R_{0}=4.82$ has been withdrawn, as the authors indicate they wish to update it.

[^2]:    ${ }^{3}$ The global fatality rate at 18 March 2020 is $4.4 \%(?)$, but may be lower given unreported (usually mild) cases.

