Modelling COVID-19 using the Fundamentals of Fluid Dynamics

Harris Sajjad Rabbani*(1), Kofi Osei-Bonsu (2), Peter Kwame Osei-Bonsu (3), Thomas Daniel Seers (1)

(1) Department of Petroleum Engineering, Texas A&M University at Qatar, Doha, Qatar
(2) Beekin Inc, London, United Kingdom, NW3 4XL
(3) Aberdeen Royal Infirmary, NHS Grampian, Scotland

*Corresponding author: harris.rabbani@qatar.tamu.edu

As of 21st May 2020, there have been 4.89M confirmed cases worldwide and over 323,000 deaths of people who have tested positive for SARS-CoV-2. The outbreak of COVID-19, has not only caused widespread morbidity and mortality, but also led to a catastrophic breakdown in the global economy and unprecedented social disruption. To lessen the global health consequences of COVID-19, sweeping COVID-19 lockdown and quarantine measures have been imposed within many nations. These measures have significantly impacted the world's economy and in many cases has led to the loss of livelihood. Mathematical modeling of pandemics is of critical importance to understand the unfolding of transmission events and to formulate control measures. In this research letter, we have introduced a novel approach to forecasting epidemics like COVID-19. The proposed mathematical model stems from the fundamental principles of fluid dynamics, and can be utilized to make projections of the number of infected people. This unique mathematical model can be beneficial for predicting and designing potential strategies to mitigate the spread and impact of pandemics.

Keywords: COVID-19, Fluid Dynamics, Mathematical Modelling
Introduction

In December 2019, a cluster of cases of pneumonia, subsequently associated with a novel coronavirus (Severe Acute Respiratory Syndrome - Coronavirus-2, SARS-CoV-2), named Coronavirus Disease 2019 (COVID-19) by the World Health Organization (WHO), emerged in Wuhan, China. It was rapidly declared a pandemic on March 11, 2020, in view of its exponential spread worldwide\(^1\). As of 21\(^{st}\) May 2020, the WHO had reported 4.89 million confirmed cases and over 323,000 deaths globally, with the highest number of cases reported in the United States of America (USA)\(^2\). The rapid spread of the virus continues to pose a monumental global health challenge.

Clinically, infected subjects exhibit a wide range of non-specific features, from mild-to-moderate symptoms such as cough, fever and fatigue to severe, life-threatening respiratory and systemic complications. On the other hand, it has been well documented that infected persons may exhibit no symptoms at all (asymptomatic) or may be yet to manifest symptoms (pre-symptomatic), but are potentially infectious\(^3,4\). In such cases, infected individuals may be likely to maintain normal social interactions, without realizing the need for self-isolation due to the obscurity of their symptoms.

Currently, our understanding of the transmission risk is incomplete. Epidemiologic examination in Wuhan at the beginning of the outbreak identified an initial connection with a live animal seafood market, where patients had worked or visited\(^5\). As time progressed, person-to-person spread became the main mode of transmission\(^6\). Although SARS-COV-2 has been detected in non-respiratory samples such as stool and blood, transmission is primarily thought to occur through close contact, via respiratory droplets and aerosols\(^7\). The virus released in these secretions when
an infected subject coughs, sneezes, or talks can then infect another person if it makes direct contact with the mucous membranes\textsuperscript{8,9}.

Under ideal circumstances, an effective vaccine might be administered to mitigate the dire effects of the virus. Regrettably, the development of an acceptable vaccine to this end appears unlikely in the short-term. Consequently, government and public health responses have focused mainly upon non-pharmacological interventions\textsuperscript{10}. These measures include physical/social distancing to minimize the rate of person-to-person contact, frequent hand washing, the utilization of masks, gloves and other forms of personal protection equipment (PPE), mass testing, contact tracing and isolation/quarantine of persons with suspected and confirmed cases of COVID-19 infection.

Although these interventions have contributed significantly to the gradual decline of the transmission rate and by extension deaths worldwide, there are increasing concerns that the easing of these measures may result in the surge of new cases\textsuperscript{10}.

In pandemic situations where data could be sparse, mathematical modelling can be a powerful tool to understand and predict the course of the outbreak in order to inform the development of potential control strategies\textsuperscript{11,12}. The most frequently used framework in the case of human transmissions is the so-called SIR model\textsuperscript{13}. According to this model, the individuals are categorized into three groups: susceptible $S$, infected $I$ and recovered $R$. Mathematically, the transition of individuals among these three groups is computed using the Ordinary Differential Equation (ODE) to predict the overall behavior of the number of infected persons. Several, more complex variants of the SIR model have been developed in an attempt to capture the transmission dynamics of pandemics more accurately. Particularly in the case of COVID-19, several modifications have been made to the SIR framework to consider the number of deceased\textsuperscript{14} and the effect of public health containment policies\textsuperscript{15}, including the fraction of undocumented infections and their contagiousness\textsuperscript{16}. Wu et
al.\textsuperscript{17} utilized available data to model the case fatality risks of symptomatic persons in Wuhan, China. Giordano et al.\textsuperscript{18} further extended the model to distinguish between detected and undetected cases and the level of severity of the manifested symptoms during the course of the outbreak.

In this article, we introduce a novel approach to forecasting disease outbreaks, specifically COVID-19, using the fundamental principles of fluid dynamics. In this model, we consider a carrier of the virus as a fluid containing a dissolved ionic species (Figure 1). With this intuition, we attempt to derive a simplified theoretical model using the well-known Fluid Transport Equation to predict the transmission and propagation of COVID-19. Our model was validated using COVID-19 data from 16 countries provided by EU Open Data portal\textsuperscript{19} (as of 8\textsuperscript{th} June 2020), showing an excellent match between the data set and model predictions. We further discuss the mitigating strategies for controlling the COVID-19 pandemic optimally, based on our model parameters.

![Figure 1: Shows analogy between the transportation of ions through fluid and spread of virus through infected human. (a) Schematic showing movement of ions in the fluid. b) Cartoonish representation of infected individual\textsuperscript{20}.
]
Analytical Modelling

Using the fluid transport equation, we derived the following mathematical model to predict the infected cases of COVID-19. The details concerning the derivation of mathematical model are provided in the methods section.

\[ \phi^n = \alpha \phi^o + \gamma e^{\phi^o} - \phi^o \beta + \phi^o \]  

(1)

The number of infected cases is given by Equation 1 where \( \phi \) is the ratio of total infected cases \( I \), over the initial number of susceptible people \( S^0 \) (assumed as the entire population of the area); \( \alpha \) an interaction factor which takes into account the transmission of infection due to person-to-person contact; \( \gamma \) the growth of the virus within individual and \( \beta \) the efficacy of the public health intervention strategy. The subscripts \( n \) and \( o \) refer to the new and old cases respectively. The detailed description of fitting parameters used to solve the analytical model (Equation 1) is given in Table 1.

Table 1: Definition of fitting parameters that are used to solve the presented analytical model.

| Parameters | Physical Description |
|------------|----------------------|
| \( \alpha \) | Interaction factor, which takes account of the transmission of infection from person to person. Increase in \( \alpha \) is an indication of more frequent interaction of infected individuals with the population, whereas low \( \alpha \) values are indicative of social isolation of infected individuals. |
| \( \gamma \) | The growth or activity of the virus within an individual. Can be linked to the severity of symptoms or how early symptoms are manifested. |
| \( \beta \) | Describes the effectiveness of public health intervention measures. This may include widespread testing and contact tracing. |
Figure 2 compares our model predictions for the number of infected cases with recorded data for 16 countries. The computation was performed using MATLAB with the code provided in the supplementary information. Overall, the model (Equation 1) is able to capture the trend of the cumulative number of cases and also forecast future numbers. As observed in Figure 2, Australia shows the lowest number of infected cases. In contrast, some European countries (reported in Figure 2 and 3) and the USA have been heavily affected by the COVID-19, showing cases in excess of 100,000. In addition to the number of recorded cases, our model captures the faster recovery of Austria, China and Australia (given by the gradient of the curve) which is consistent with the reported data.
Mathematical basis for Mitigation Strategy for COVID-19

We have demonstrated from Figure 2 that the proposed model is able to capture the course of the pandemic in different countries. We further analyze the parameters of our model to evaluate the efficacy of the mainstream mitigation strategies that have been adopted to combat COVID-19. In this section we illustrate mathematically why widespread testing, isolation of infected individuals along with contact tracing are important intervention mechanisms to curb the pandemic.

By further mathematical analysis, we derived the epidemic growth factor \( G \) (Equation 2), which describes the impact of key parameters influencing the extent of the pandemic. The detailed derivation of Equation 2 is provided in the methods section.

\[
G = \alpha + \beta e^{\beta - 1}
\]  

(2)

It follows from Equation 2 that for a given country, a high value of \( G \) indicates a more severe epidemic. \( \varepsilon \) is the ratio of total number of infected cases at the initial phase of epidemic over the total number of initial susceptible people \( S^0 \). It can be seen from Equation 2 that as interaction factor \( \alpha \rightarrow 0 \), the epidemic growth factor reduces, indicating that to minimize the spread of the disease, \( \alpha \) must be reduced by social distancing and the isolation of infected persons. Figure 3 shows the influence of \( \alpha \) on the trend of infected cases. It can be observed from Figure 3 that as \( \alpha \) reduces the number infected cases reduces and the plateau is slightly delayed. This agrees with the strict social distancing and lockdown measures implemented by several countries in order to control the spread of the virus.
Figure 3: Describes the effect of $\alpha$ on the trend of COVID-19 infected cases. The base case shows the France data. One can see that with the subsequent reduction in $\alpha$ which corresponds to social isolation of infected individual the growth of epidemic can be suppressed.

Interestingly, Equation 2 predicts that for a given $\alpha$, an increase in $\beta$ (parameter linked to mitigation strategy) will lead to a decrease in the growth factor $G$. In contrast to $\alpha$, a relative increase in $\beta$ is favorable to optimally control the spread of an epidemic. Practically, this suggests widespread testing, contact tracing, and isolation of infected persons coupled with high quality medical resources will result in the deceleration of the spread of the epidemic. It is important to note that both increase in $\alpha$ and $\beta$ will result in an increase in the total number of infected cases. Therefore, as $\alpha$ represents the transmission of virus due to human-human contact, an increase will reflect an increase in the total number of both symptomatic and asymptomatic cases that may be left undetected. Conversely, an increase in $\beta$ will also result in an increase in the number of reported infected individuals, due to a robust public health mitigation strategy that includes widespread
testing and contact tracing. We have also shown the relationship between $\alpha$ and $\beta$ for various countries (Figure 4), affirming that high $\beta$ resulted in the isolation of the infected individuals and buffered transmission rates.

Figure 4. Relationship of $\beta$ against $\alpha$. Indicating decrease in $\alpha$ as $\beta$ increases. Overall this suggests that widespread testing and contact tracing results in social isolation of infected individuals.

**Conclusion**

In this article we present a novel approach for modelling and forecasting the course of COVID 19 using fundamental principles of fluid transport. The model considers the infected individual as a fluid containing species such as ions which spread in the direction of fluid flow. The model was validated with recorded data for 16 countries. Our model produced an excellent match with the data in most cases. Mathematical analysis of our model parameters demonstrated why social
distancing, widespread testing and contact tracing is the optimum strategy for fighting the pandemic.

Methods

Mathematical model

Ignoring the advective flux the traditional fluid transport equation is written as\(^2\)

\[
\frac{\partial c}{\partial t} = D \nabla^2 c + R
\]  

\(\frac{\partial c}{\partial t}\) relates to the rate of change in the concentration of species \(c\) in fluid, \(D\) is the diffusive flux of species, \(\nabla^2\) is the Laplace indicating spatial coordinates and \(R\) is the net growth of species. Following our intuition that a fluid is a carrier of species such as salts, an infected individual could also be conceptualized as the carrier of the virus. Utilizing this approach we substitute \(c\) with \(\emptyset\) which represents the ratio of total infected cases \(I\), over the initial number of susceptible people \(S^o\) (assumed as the total population of the specific region), and \(R\) as \(mexp(-\emptyset) + \frac{\partial \emptyset}{\partial t}\).

\[
\frac{\partial \emptyset}{\partial t} = d \nabla^2 \emptyset + mexp(-\emptyset) + \frac{\partial \emptyset}{\partial t}
\]

In above equation, \(d\) represents the flux of infected individuals, \(mexp(-\emptyset)\) is the growth of virus within infected individual, and \(\frac{\partial \emptyset}{\partial t}\) suggests temporal changes in the epidemic activity due to medical interventions. Discretizing Equation 4 using FTCS (Forward Time Centered Space) method results in;

\[
\frac{\emptyset^n_i - \emptyset^o_i}{\Delta t} = d \left[ \frac{\emptyset_{i+1}^o - 2\emptyset_i^o + \emptyset_{i-1}^o}{\Delta x^2} + \frac{\emptyset_{i+1}^o - 2\emptyset_i^o + \emptyset_{i-1}^o}{\Delta y^2} + \frac{\emptyset_{i+1}^o - 2\emptyset_i^o + \emptyset_{i-1}^o}{\Delta z^2} \right] + mexp(\emptyset_i^o) + \frac{\emptyset_i^{n-o}}{\Delta t}
\]
We further simplify Equation 5 by equating $\emptyset_{i+1}^o = 0$, $\emptyset_{i-1}^o = 0$ and $\emptyset_i^{\beta^n} = 0$. In order to nondimensionalize Equation 5 we substitute $2d\Delta t\left[\frac{1}{\Delta x^2} + \frac{1}{\Delta y^2} + \frac{1}{\Delta z^2}\right]$ and $m\Delta t$ with $\alpha$ and $\gamma$ respectively. This results in the derivation of final equational form, which relates the increase in the infected cases $\emptyset_i^n - \emptyset^o$ with the transfer of virus due to human-human interaction, $\alpha\emptyset_i^o$, the growth or the activity of virus within infected individual, $\gamma e^{-\emptyset_i^0}$, and mitigation strategies, $\emptyset_i^{o\beta}$.

$$\emptyset_i^n = \alpha\emptyset_i^o + \gamma e^{-\emptyset_i^0} - \emptyset_i^{o\beta} + \emptyset^o \quad (6)$$

Derivation of growth Factor

For the derivation of the growth factor we sum the effects together reported in Equation 6 that are responsible for controlling the pandemic resulting in

$$A = \alpha\emptyset + \gamma e^{-\emptyset} + \emptyset^\beta \quad (7)$$

As during the initial phase of pandemic $\emptyset \approx 0$, consequently, we can substitute $\emptyset$ as $\epsilon$ and equate $e^{-\emptyset} = 1$. This results in Equation 8.

$$A = \alpha\epsilon + \gamma + \epsilon^\beta \quad (8)$$

The subsequent derivation of $A$ with respect to $\epsilon$ results in

$$\frac{dA}{d\epsilon} = \alpha + \beta \epsilon^{\beta-1} \quad (9)$$

where $\frac{dA}{d\epsilon}$ is the growth factor $G$ as given in Equation 2.
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Data Availability

The data presented in this manuscript will be available freely via sending a request to the corresponding author.

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Supplementary information

The MATLAB code employed for the fitting the data and predicting the course of COVID-19.

%Start with the guess values of the fitting parameters
guess = [1.2, 0.01, 1.0e-4];
goalie = optimset('MaxFunEvals', 1000000);
% fitting the model to the data
C = fminsearch @optimization, guess, options);
d = readtable('Data.xlsx', 'basic', true);
f = d.France;
s = f(1);
I = f(2);
t = 200;
phi = zeros(t, 1);
phi(1) = I/s;
cases = zeros(t, 1);
cases(1) = phi(1)*s;
for i = 2:t
    phi(i) = phi(i-1) + (C(2)*(phi(i-1))) + C(3).*exp(-phi(i-1)) - ((phi(i-1)).^(C(1)));
cases(i) = phi(i)*s;
end

% Optimization function used for fitting the model to data
function [error] = optimization(C)
d = readtable('Data.xlsx', 'basic', true);
f = d.France;
s = f(1);
I = f(2);
t = length(f(2:end)) - sum(isnan(f(2:end)));
phi = zeros(t, 1);
phi(1) = I/s;
cases = zeros(t, 1);
cases(1) = phi(1)*s;
for i = 2:t
    phi(i) = phi(i-1) + (C(2)*(phi(i-1))) + C(3).*exp(-phi(i-1)) - ((phi(i-1)).^(C(1)));
cases(i) = phi(i)*s;
end
a = f(2:t+1);
error = (cases-a).^2;