



## Estimating the Basic Reproductive Number of COVID-19 Cases in Ghana

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**Abstract.** A disease can be defined as an adverse change from a normally functional state of the living body usually characterized with or accompanied with some signs and symptoms which is differing in nature from physical injury. A pandemic is the worldwide spread of a new disease. COVID-19 is one of the global pandemic that emerged in Wuhan, China, in December 2019 and has since then spread over through the world. In Ghana, the first case of COVID-19 was reported in March 14, 2020 and has increased from just one case to over 29000 cases with over 150 deaths as at July 23, 2020. This study focuses on the estimation of the basic reproductive number,  $R_0$  using the Next Generation Method (NGM) approach. COVID-19 data in Ghana was collected and parameters were estimated using the Least-Squares Method. The basic reproductive number of Ghana is estimated to be 2.52 whilst the  $R_0$  ranges between 1.47 – 2.65 for transmission rates of 0.5 – 0.9.

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**Key Words and Phrases:** Generation Matrix Approach, COVID-19, Least-Squares Method, Transmission

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### 1. Introduction

There was a cluster of cases of pneumonia in the city of Wuhan in China in December 2019. Some of the early cases had reported visits to the seafood and live animal market or working in this market in Wuhan [28]. Research later uncovered that a newly discovered coronavirus had triggered the disease and it could be traced to this market. The disease was subsequently named COVID-19 [33]. COVID-19 spread across China and to the rest of the world. The epidemic was confirmed an international public health emergency by the World Health Organization on 30 January 2020 [25].

Coronaviruses are a very wide community of viruses. They consist of a core of genetic material enclosed by a protein-spiked lipid membrane which gives it a crown appearance. Crown is named Corona in Latin, so that's how these viruses get their name. There

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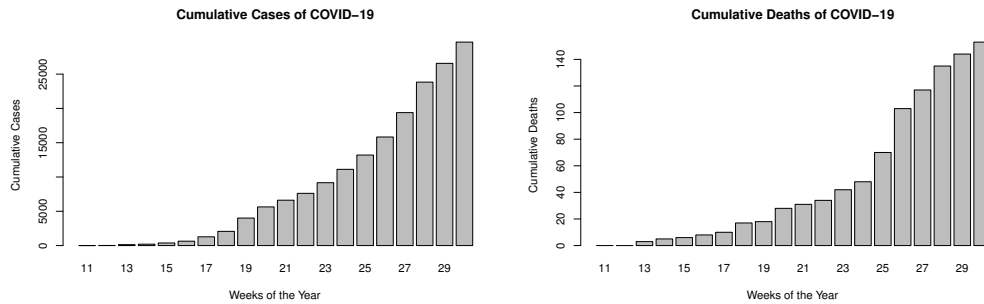


Figure 1: Weekly Representation COVID-19 Cases and Deaths in Ghana from March 14, 2020 (Week 11) to July 23, 2020 (Week 29)

are different types of coronaviruses which cause disease in humans and animals [17]. Corona viruses can cause respiratory infections ranging from the common cold, to more severe diseases. These include, the first, described in China in 2003, the Middle East Coronavirus Respiratory Syndrome- MERS Coronavirus. The other, Severe Acute Respiratory Coronavirus Syndrome (SARS-COV-2) first identified in Saudi Arabia in 2012 which is the new outbreak called COVID-19 that was first reported in December 2019 [32].

The incubation period is on average five to six days, but can range from 1 to 14 days [20]. There can be a range of symptoms, from mild to severe. Common symptoms include fever, fatigue and respiratory symptoms such as cough, sore throat, and shortness of breath [15]. The disease can spread from person to person through droplets from coughing, talking or sneezing. About 80% of cases recover from the disease without needing special treatment. Some people are at risk of serious illness, including older people or people with underlying medical problems [25].

Data shows that Asia, Europe, North and South America are worst hit by this pandemic as more cases and deaths are reported in such regions as compared to what is seen in Africa and the Oceania regions. This made researchers such as [11] to research into the role of climate in the spread of COVID-19. Possible invention of a vaccine appears to be several months (if not years) away from now. We do not lack the expertise, technology and funding for this expedition but the future is very unpredictable, leaving all of us in awful terror. This pandemic has influenced all operations in the world and has forced the world's health and data science experts to work to find possible remedies.

In Ghana, the first case of the disease was reported in the 14 March 2020 and since then the cases of COVID-19 increased and surpassed 29000 and 150 deaths as at July 23, 2020. In this research, we investigate the basic reproductive number- the number of new individuals a single infected individual can generate- of COVID-19 in Ghana.

## 2. Methods & Model

In the study of compartmental models for infectious disease transmission, the population is divided into several compartments. These compartments are however classified

into disease and nondisease compartments. They are called disease compartments if the individuals therein are infected, and nondisease compartment if the vice versa is the case.

In this study, we consider a SEIAHR model where the population is divided into 6 compartments namely the susceptible (S), exposed (E), infectious (I), asymptomatic (A), symptomatic (H) and recovered (R) compartments. As their names suggest the individuals that would be therein share the same characteristics. Susceptible and recovered compartments are nondisease compartments. The rest of the compartments are disease compartments. The exposed compartment contains individuals that had effective contacts with infectious individuals (infected individuals, symptomatic and asymptomatic individuals) by coming into contact with exposure factors which are cough, sneezing and handshake. The total number of effective contacts at time  $t$  is given by  $\beta S(I + k_1 A + k_2 H)$  where  $\beta$ ,  $k_1$  and  $k_2$  are the transmission rates. From the exposed compartment, individuals are recruited into the infectious compartments which include the infected compartment, the symptomatic compartment and the asymptomatic compartment. An asymptomatic case reported by the laboratory is a person who is infected with COVID-19 and who does not experience symptoms. Asymptomatic transmission refers to a person transmitting the virus, who does not develop symptoms. According to recent literature on COVID-19, the asymptomatic carriers are now known to be able to transmit the virus to susceptible individuals [1, 9]. The recruitment rate from the exposed compartment into the asymptomatic compartment by the end of incubation period is given in this model as  $\delta_1 \times \omega_1$ . The symptomatic compartment includes the individuals with COVID-19 that exhibit the symptoms. The recruitment from the exposed compartment into the symptomatic compartment is also given as  $\delta_2 \times \omega_2$ . The remaining proportion out of the proportion of effective contacts after all removals (deaths, recruitment) are recruited into the infected compartment. Now it may be argued that there is no need for the infected compartment if we consider the symptomatic and asymptomatic compartments. The symptomatic compartment is hereby defined as individual carriers of COVID-19 who are demonstrating or showing symptoms identified and isolated while the infected compartment includes individuals with COVID-19 showing symptoms but are not yet identified and isolated, in other words, they are still in the susceptible population. The proportion of individuals who recover at any time  $t$  is given by  $\gamma_1 A + \gamma_2 I + \gamma_3 H$ . The infectious period for carriers in each disease compartment is given by the fraction  $\frac{1}{\gamma_i}$ . The death rate for the non-disease compartment is given as  $m_1$  as it is considered as natural death and  $m_2$  is the death rate for the disease compartments.

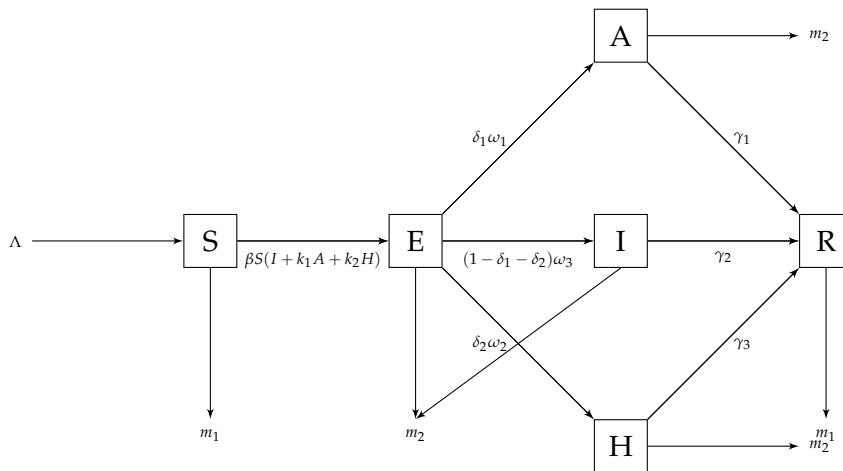


Figure 2: Schematic Diagram

The equation from this model is given below:

$$\begin{aligned}
 \frac{dS}{dt} &= \Lambda - m_1S - \beta S (I + k_1A + k_2H) \\
 \frac{dE}{dt} &= \beta S (I + k_1A + k_2H) - \delta_1\omega_1E - \delta_2\omega_2E - (1 - \delta_1 - \delta_2)\omega_3E - m_2E \\
 \frac{dI}{dt} &= (1 - \delta_1 - \delta_2)\omega_3E - (\gamma_2 + m_2)I \\
 \frac{dR}{dt} &= \gamma_2I + \gamma_1A + \gamma_3H - m_1R \\
 \frac{dA}{dt} &= \delta_1\omega_1E - (m_2 + \gamma_1)A \\
 \frac{dH}{dt} &= \delta_2\omega_2E - (m_2 + \gamma_3)H
 \end{aligned}
 \tag{1}$$

Find in table 2 the parameters and their definitions used for this study.

Basic reproduction number is a threshold parameter that measures the number of new infectives that a single infectious individual can generate [7, 13]. In the wake of this COVID-19 outbreak, this threshold parameter has been the center of research as researchers sought to measure or estimate number of people that could be infected in any population. (Some of them include the following [2, 16, 27, 31]). Mathematically, basic reproductive number ( $R_0$ ) is the spectral radius (largest eigenvalue) of the next generation matrix; [4, 5, 8, 23].

$$R_0 = \rho(FV^{-1})
 \tag{2}$$

Assume that there are  $n > 0$  disease compartments and  $m > 0$  nondisease compartments. Then a general compartmental disease transmission model can be written as

$$x' = \mathcal{F}(x, y) - \mathcal{V}(x, y); \quad y' = g(x, y)
 \tag{3}$$

Table 1: Parameter Definition

Parameter	Description
$\Lambda$	The rate at which new individuals enter the susceptible population.
$\beta$	The transmission rate.
$\delta_1$	Recruitment rate into asymptomatic compartment.
$\delta_2$	Recruitment rate into symptomatic compartment.
$(1 - \delta_1 - \delta_2)$	Recruitment rate into the infected compartment.
$\frac{1}{\omega_i}$	Incubation period for the various compartments.
$\gamma_i$	Recruitment rate into recovery compartment.
$m_1$	Natural death rate
$m_2$	COVID-19 related death rate.
$k_1$	The multiple transmissibility from asymptomatic compartment into the infectious or disease compartments
$k_2$	The multiple transmissibility from symptomatic compartment into the infectious or disease compartments

with  $g = (g_1, \dots, g_m)^T$  and  $'$  denotes the derivation with respect to time. Let  $x = (x_1, \dots, x_n)^T \in \mathcal{R}^m$  and  $y = (y_1, \dots, y_m)^T \in \mathcal{R}^n$  represent the populations in disease compartments and nondisease compartments, respectively;  $\mathcal{F} = (\mathcal{F}_1, \dots, \mathcal{F}_n)^T$  and  $\mathcal{V} = (\mathcal{V}_1, \dots, \mathcal{V}_n)^T$ , where  $\mathcal{F}_i$  represents the rate of new infections in the  $i$ th disease compartment; and  $\mathcal{V}_i$  represents the transition terms, for example, death and recovery in the  $i$ th disease compartment. Then the assumptions outlined in [6, 26] and reproduced in [22] which were made to ensure the well-posedness of the model must be met so that the next generation matrix can be defined as  $K = FV^{-1}$  and  $R_0$  is the spectral radius of  $K$  as represented in equation 2; where  $F$  and  $V$  are defined as  $n \times n$  matrix and is biologically reasonable. See [6, 26] for proof. This method of estimating  $R_0$  is called the next generation matrix (NGM) method.

However, only few of the literature written between this period on COVID-19 use this approach. Some literature used the statistical procedure for combining data from multiple studies on  $R_0$  and made their conclusions. For example [16] identified 12 researches from literature (done to suit the situations in Wuhan province in China) and found that the estimates for  $R_0$  ranged from 1.4 to 6.49, with a mean of 3.28, a median of 2.79 and inter-quartile range (IQR) of 1.16. This they found to be different from the World Health Organization (WHO) estimate for  $R_0$  which ranged between 1.4 – 2.5. However, some of these papers reviewed in this article used the NGM method for estimating this  $R_0$  measure. See similar articles [2, 12, 14, 30].

[29] contributed to this space by using stochastic Markov Chain Monte Carlo (MCMC) methods with Gibbs sampling and non-informative flat prior, using posterior distribution to estimate that the  $R_0$  for COVID-19 in the Wuhan city alone is averagely 2.68 with a 95% CI(2.46 – 2.87). They also inferred from this study that the disease doubling time was averagely 6.4 days with 95% CI(5.8 – 7.1). Since its publication till today, we have seen all the study predictions accomplished as the disease continues to wreak much havoc in

many other countries. [21] used mathematically dynamic compartmental model (5 compartments namely susceptible individuals, asymptomatic individuals during the incubation period, infectious individuals with symptoms, isolated individuals with treatment and recovered individuals), they estimated the  $R_0$  using nonlinear least squares method. They found that the average basic reproductive number in Wuhan was 6.49 with a 95% CI(6.31 – 6.66).

### 2.1. Basic Properties

**Theorem 1.** *Suppose that  $\Omega$  is the solution set for the system ???. Let the initial data set be  $S(0) \geq 0, E(0) \geq 0, I(0) \geq 0, A(0) \geq 0, H(0) \geq 0$  and  $R(0) \geq 0 \in \Omega$ , then the solution set  $S(t), E(t), I(t), A(t), H(t)$  and  $R(t)$  is positive for all  $t > 0$ .*

*Proof.* From the system 1, the following inequalities

$$\begin{aligned}
 \frac{dS}{dt} &\geq -m_1S - \beta S (I + k_1A + k_2H) \\
 \frac{dE}{dt} &\geq -\delta_1\omega_1E - \delta_2\omega_2E - (1 - \delta_1 - \delta_2)\omega_3E - m_2E \\
 \frac{dI}{dt} &\geq -(\gamma_2 + m_2)I \\
 \frac{dR}{dt} &\geq -m_1R \\
 \frac{dA}{dt} &\geq -(m_2 + \gamma_1)A \\
 \frac{dH}{dt} &\geq -(m_2 + \gamma_3)H
 \end{aligned}
 \tag{4}$$

are true. From the first inequality in 4

$$\begin{aligned}
 \frac{dS}{dt} &\geq -(m_1 + \beta (I + k_1A + k_2H))S \\
 \frac{dS}{S} &\geq -(m_1 + \beta (I + k_1A + k_2H))dt \\
 \int \frac{dS}{S} &\geq - \int (m_1 + \beta (I + k_1A + k_2H))dt \\
 \ln S &\geq -(m_1 + \beta (I + k_1A + k_2H))t + c \\
 S(t) &\geq S_0e^{-[m_1+\beta(I+k_1A+k_2H)t]} > 0
 \end{aligned}
 \tag{5}$$

where  $S(0) = S_0$  is the initial condition for the susceptible compartment. From the second

inequality in 4,

$$\begin{aligned}
 \frac{dE}{dt} &\geq -(\delta_1\omega_1 + \delta_2\omega_2 + (1 - \delta_1 - \delta_2)\omega_3 + m_2)E \\
 \frac{dE}{E} &\geq -(\delta_1\omega_1 + \delta_2\omega_2 + (1 - \delta_1 - \delta_2)\omega_3 + m_2)dt \\
 \int \frac{dE}{E} &\geq - \int (\delta_1\omega_1 + \delta_2\omega_2 + (1 - \delta_1 - \delta_2)\omega_3 + m_2)dt \\
 \ln E &\geq -(\delta_1\omega_1 + \delta_2\omega_2 + (1 - \delta_1 - \delta_2)\omega_3 + m_2)t + c \\
 E(t) &\geq E_0 e^{-(\delta_1\omega_1 + \delta_2\omega_2 + (1 - \delta_1 - \delta_2)\omega_3 + m_2)t} > 0
 \end{aligned} \tag{6}$$

where  $E(0) = E_0$  is the initial condition for the exposed compartment. From the third inequality in 4,

$$\begin{aligned}
 \frac{dI}{dt} &\geq -(\gamma_2 + m_2)I \\
 \frac{dI}{I} &\geq -(\gamma_2 + m_2)dt \\
 \int \frac{dI}{I} &\geq - \int (\gamma_2 + m_2)dt \\
 \ln I &\geq -(\gamma_2 + m_2)t + c \\
 I(t) &\geq I_0 e^{-(\gamma_2 + m_2)t} > 0
 \end{aligned} \tag{7}$$

where  $I(0) = I_0$  is the initial condition for the infectious compartment. From the fourth inequality in 4,

$$\begin{aligned}
 \frac{dR}{dt} &\geq -m_1R \\
 \frac{dR}{R} &\geq -m_1dt \\
 \int \frac{dR}{R} &\geq - \int m_1dt \\
 \ln R &\geq -m_1t + c \\
 R(t) &\geq R_0 e^{-m_1t}
 \end{aligned} \tag{8}$$

where  $R(0) = R_0$  is the initial condition for the recovered compartment. From the fifth inequality in 4,

$$\begin{aligned}
 \frac{dA}{dt} &\geq -(\gamma_1 + m_2)A \\
 \frac{dA}{A} &\geq -(\gamma_1 + m_2)dt \\
 \int \frac{dA}{A} &\geq - \int (\gamma_1 + m_2)dt \\
 \ln A &\geq -(\gamma_1 + m_2)t + c \\
 A(t) &\geq A_0 e^{-(\gamma_1 + m_2)t} > 0
 \end{aligned} \tag{9}$$

where  $A(0) = A_0$  is the initial condition for the asymptomatic compartment. From the sixth inequality in 4,

$$\begin{aligned} \frac{dH}{dt} &\geq -(\gamma_3 + m_2)H \\ \frac{dH}{H} &\geq -(\gamma_3 + m_2)dt \\ \int \frac{dH}{H} &\geq - \int (\gamma_3 + m_2)dt \\ \ln A &\geq -(\gamma_3 + m_2)t + c \\ H(t) &\geq H_0 e^{-(\gamma_3 + m_2)t} > 0 \end{aligned} \tag{10}$$

where  $H(0) = H_0$  is the initial condition for the symptomatic compartment. Hence the proof.

### 2.2. Basic Reproduction Number, $R_0$

$\mathcal{F}$  is the rate of new infections which can be taken from the susceptible compartment whilst  $\mathcal{V}$  is the rate of transition from one compartment to the other. These are represented below.

$$\mathcal{F} = \begin{pmatrix} \beta S(I + k_1 A + k_2 H) \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

$$\mathcal{V} = \begin{pmatrix} (\delta_1 \omega_1 + \delta_2 \omega_2 + (1 - \delta_1 - \delta_2) \omega_3 + m_2) E \\ -(1 - \delta_1 - \delta_2) \omega_3 E + (\gamma_2 + m_2) I \\ -\delta_1 \omega_1 E + (m_2 + \gamma_1) A \\ -\delta_2 \omega_2 E + (m_2 + \gamma_3) H \end{pmatrix}$$

Using the NGM approach which is spelled in the earlier parts of this article, we find the threshold parameter. It can be shown that, the disease free equilibrium (DFE) of the system 1 is

$$\left( \frac{\Lambda}{m_1}, 0, 0, 0, 0, 0 \right).$$

From the  $\mathcal{F}$  and  $\mathcal{V}$  above,  $F$ ,  $V$  and  $V^{-1}$  can be deduced and represented as follows:

$$F = \begin{bmatrix} 0 & \beta \frac{\Lambda}{m_1} & \beta k_1 \frac{\Lambda}{m_1} & \beta k_2 \frac{\Lambda}{m_1} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} (\delta_1 \omega_1 + \delta_2 \omega_2 + (1 - \delta_1 - \delta_2) \omega_3 + m_2) & 0 & 0 & 0 \\ -(1 - \delta_1 - \delta_2) \omega_3 & (\gamma_2 + m_2) & 0 & 0 \\ -\delta_1 \omega_1 & 0 & (\gamma_2 + m_1) & 0 \\ -\delta_2 \omega_2 & 0 & 0 & (\gamma_2 + m_3) \end{bmatrix}$$



$$V^{-1} = \begin{bmatrix} \frac{1}{(1-\delta_1-\delta_2)(\omega_3+\delta_1\omega_1+\delta_2\omega_2+m_2)} & 0 & 0 & 0 \\ B_1 & \frac{1}{m_2+\gamma_2} & 0 & 0 \\ B_2 & 0 & \frac{1}{m_2+\gamma_1} & 0 \\ B_3 & 0 & 0 & \frac{1}{m_2+\gamma_3} \end{bmatrix}$$

where  $B_1, B_2$  and  $B_3$  are

$$\begin{aligned} B_1 &= \frac{(\delta_2 + \delta_1 - 1) \omega_3}{(m_2 + \gamma_2) (\delta_2 \omega_3 + \delta_1 \omega_3 - \omega_3 - \delta_2 \omega_2 - \delta_1 \omega_1 - m_2)}, \\ B_2 &= \frac{\delta_1 \omega_1}{(m_2 + \gamma_1) ((1 - \delta_1 - \delta_2) \omega_3 + \delta_1 \omega_1 + \delta_2 \omega_2 + m_3)} \text{ and} \\ B_3 &= \frac{\delta_2 \omega_2}{(m_2 + \gamma_3) ((1 - \delta_1 - \delta_2) \omega_3 + \delta_1 \omega_1 + \delta_2 \omega_2 + m_3)} \end{aligned} \tag{11}$$

so that the spectral radius  $R_0 = \rho(FV^{-1})$  of the matrix  $FV^{-1}$  is

$$\begin{aligned} R_0 &= \frac{\beta \Lambda (1 - \delta_2 - \delta_1) \omega_3}{m_1 (m_2 + \gamma_2) ((1 - \delta_1 - \delta_2) \omega_3 + \delta_1 \omega_1 + \delta_2 \omega_2 + m_2)} \\ &+ \frac{\beta \Lambda k_1 \delta_1 \omega_1}{m_1 (m_2 + \gamma_1) ((1 - \delta_1 - \delta_2) \omega_3 + \delta_1 \omega_1 + \delta_2 \omega_2 + m_2)} \\ &+ \frac{\beta \Lambda k_2 \delta_2 \omega_2}{m_1 (m_2 + \gamma_3) ((1 - \delta_1 - \delta_2) \omega_3 + \delta_1 \omega_1 + \delta_2 \omega_2 + m_2)} \end{aligned}$$

### 2.3. Parameter Estimation

Before we estimate the value of the basic reproductive number  $R_0$ , we must first estimate the associated parameters. Some of these parameters including  $\beta$  were estimated using least-squares method and observed data, while some others like  $m_1$  and  $\Lambda$  are fixed values estimated for each year in the country.  $\beta$  is the transmission rate and is estimated to be 0.857. In an earlier study, the transmission rate was estimated to be in the range of  $6.038 \times 10^{-8} - 0.8038$  [3] whilst [19] predicted that it could even rise up to 0.87 at the peak of the disease infections in Ghana.

In our study, we find that a small change in the transmission results in a relatively significant change in the basic reproductive number. Therefore we investigate the dynamics of the basic reproductive number as the transmission rate is sandwiched between 0.5 and 0.9 with a step size of 0.01.  $k_1$  and  $k_2$  represent the transmission rates for the symptomatic and susceptible and asymptomatic and susceptible individuals respectively. This is estimated using least square method and the available data as at 23rd July 2020.

$\omega_i$  is the period of incubation. Hitherto, it is known that it takes between 1 to 14 days for an exposed individual to become infectious so that,  $\frac{1}{\omega_i}$  becomes a rate at which expose individuals are getting infectious. For this study, we pegged  $\omega$  to be 10 days. It has also been published that in Ghana, only 18% of the COVID-19 infections are symptomatic, whilst 82% are asymptomatic (Accessed on the July 23, 2020 on <https://www.graphi>

c.com.gh/news/general-news/82-per-cent-of-ghana-s-covid-19-active-cases-are-asymptomatic-ghs.html). Based on the least-square parameter estimation from the data collected however,  $\delta_1$ , which is the recruitment rates into the asymptomatic compartment is calculated to be 0.08019 so that  $\delta_1 \times \omega_1 = 0.8019$ .

Table 2: Parameter Definition

Parameter	Value	Source
$\beta$	0.857	Estimated
$\delta_1$	0.08019	Estimated
$\delta_2$	0.00712	Estimated
$\omega_i$	10	Cited <sup>†</sup>
$\gamma_i$	0.95	Estimated
$m_1$	0.0072	<a href="https://www.macrotrends.net/countries/GHA/ghana/death-rate">https://www.macrotrends.net/countries/GHA/ghana/death-rate</a>
$m_2$	0.05	Estimated
$k_1$	0.15	Estimated
$k_2$	0.12	Estimated

†

### 3. Results and Discussions

Using our estimated parameters in the table 2.3 with the estimated transmission rate 0.857, the basic reproductive number,  $R_0 = 2.52$ . This means that, one infectious person is likely to infect 2.52 new ones. However, it is observed that, a little impulse in the transmission rates results in a relatively bigger response in the reproductive number. That is, a little increase of 0.01 one in the transmission rate results in averagely 0.0294 increase in the basic reproductive number,  $R_0$ . The  $R_0$  value ranges between 1.47 and 2.65 for transmission rates ranging between 0.5 and 0.9. When transmission rate reaches 0.8038 which was determined in earlier studies in Ghana [3], the reproductive number is estimated to be 2.36. This results will be consistent with the  $R_0$  estimated by [19].

Remember that [19] predicted that the transmission rate could reach 0.87 at the peak of the disease infection. When transmission rate reaches 0.87,  $R_0$  becomes 2.56. See figure 3 for the graphical representation. When transmission rates reduces to 0.5 for instance,  $R_0$  decreases to 1.47. This would be consistent with the study done by [24] who had  $R_0$  to be in the range 95% CI(1.45 – 1.75). It is very important to add that, when transmission rate  $\beta \leq 0.34$ , then the  $R_0 < 1$ . This can only be achieved when we educate more people to observe the COVID-19 protocols. That is, observing social distance in wearing nose mask, cleaning their hands with sanitizer, including identifying and isolating COVID-19 patients, both the symptomatic and asymptomatic individuals.

†Citation in table 2.3 <sup>1</sup>[10, 18]

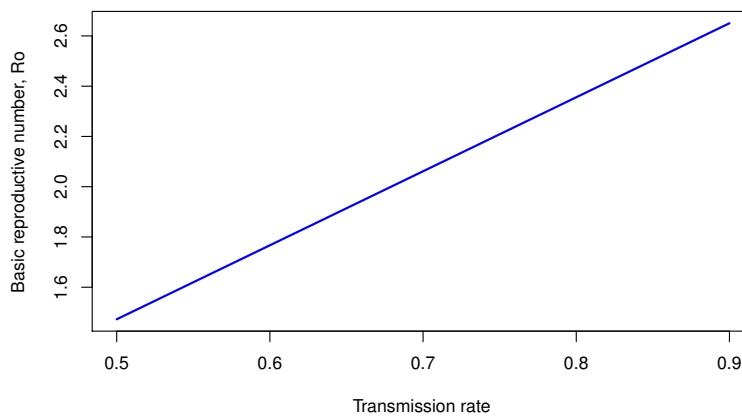


Figure 3: Graphical representation of the changes in  $R_0$  as transmission rate changes

#### 4. Conclusion

In this study we considered an SEIAHR compartmental model where the population has been compartmentalized into susceptible, exposed, infectious, asymptomatic, symptomatic and recovered compartments. The next generation matrix approach is used to determine the threshold parameter,  $R_0$ . Associated parameters were estimated from the data acquired from WHO COVID-19 data for Ghana using the least-squares approach. The reproductive number is estimated to be 2.52 as transmission rates in Ghana stands at 0.857. Furthermore, when transmission rate is sandwiched between 0.5 – 0.9, the basic reproductive number ranges between 1.47 – 2.65. However, for the disease to be contained and die out from the system, then  $\beta \leq 0.34$  so that the  $R_0 < 1$ . This can only be realized when we educate the populace to respect all the COVID-19 protocols and to understand that adhering to these protocols doesn't only protect them from COVID-19 but protects others especially the aged, children and those with severe underlying health conditions from contacting COVID-19.

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