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CONVENTIONAL MODELLING APPROACH TO PREDICT THE DYNAMICS OF COVID-19

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ABSTRACT
The study examined transmission dynamics of COVID-19 with conventional modelling approach. We developed a mathematical model for COVID-19 pandemic as SEQIR where I, the infected compartment is partitioned in to I_r and I_u for reported and unreported group of infected individuals. Basic reproduction number has been obtained and the stability analysis was carried out. The results revealed that the disease may die out in time,

Keywords: COVID-19, Mathematical Modelling, Transmission Dynamics, infectious disease, Predict, Conventional.

INTRODUCTION

One of the major outbreaks in the early January, 2020 is the Coronavirus disease (COVID-19) which is an infectious disease that emerged in December 2019 in the city of Wuhan, China (WHO, 2020). It rapidly spreads around the country and then to many other countries of the world. This occurred very fast and in a very short period of time. Nigeria is not an exemption as being one of the countries that cases of covid-19 have been considerably increasing day-in day-out.

In February, 2020 Nigeria has recorded the first case of coronavirus which was confirmed by the Virology Laboratory of the Lagos University Teaching Hospital. This is as a result of the return of an Italian citizen on 25th February, 2020 who works in Nigeria, from Milan, Italy to Lagos, Nigeria. According to Nigeria Centre for Disease Control (NCDC), the patient was clinically stable, with no serious symptoms. He was being quarantined and managed at the infectious disease hospital in Yaba, Lagos (NCDC, Feb 28, 2020).

Kim et al. (2020) developed an age-structured mathematical model using two age groups in which they observed potential effects of school opening. They used a mathematical model that is based on susceptible-exposed-infectious-recovered (SEIR) model to describe the COVID-19 transmission dynamic. COVID-19 patients are mostly isolated after the laboratory confirmation that is why the isolated (Q) compartment is added in the model.

Cakir Z., and Basri H. S. (2020) Due to insufficient precautions taken the course of the COVID-19 pandemic manifests negative changes immediately. Consequently, individual or social precautions will be significant in terms of the course of the COVID-19 pandemic.

Ivorra B. *et al*. (2020) develop a mathematical model well adapted to COVID-19 that is not just using SIR, SEIR or any other general epidemic models which are able to estimate the number of cases, deaths and needs of beds in hospitals for intensive care.

Jia L. *et al.* (2020) present Logistic, Bertalanffy and Gompertz models which provide the statistical law of epidemiology to predict the epidemic situation of COVID-19. They used the least square method for curve fitting with mathematical optimization technique. It finds the best function match of data by minimizing the sum of squared errors. Using this method, unknown data could be easily obtained, and the sum of squares of errors between these obtained data and actual data was minimized.

Wu *et al*. (2020) introduced a susceptible-exposed-infectious-recovered (SEIR) model to describe the transmission dynamics, and anticipated the national and global spread of the disease, based on reported data from December 31, 2019 to January 28, 2020. Their result revealed that the value of the basic reproductive number for COVID-19 was estimated to give 2.68. whereas Read *et al*. (2020) reported a value of 3.1 for the basic reproductive number based on data fitting of an SEIR model, using an assumption of Poisson-distributed daily time increments.

Tang *et al.* (2020) propose a deterministic compartmental model incorporating the clinical progression of the disease, the individual epidemiological status, and the intervention measures. They found that the control reproductive number could be as high as 6.47, and that intervention strategies such as intensive contact tracing followed by quarantine and isolation can effectively reduce the control reproduction number and the transmission risk. A number of modeling studies have already been performed for the COVID-19 pandemic using SIR, SEIR and other general epidemic models. However, in this study we adapted the similar SEIR with slide additions. These additions include the use of Quarantined compartment for reported and isolated individuals who were confirmed positive. We also partition the infected class

into two compartments: I_r and $I_u$to stand for the reported and unreported cases respectively. In this scenario, individuals in I_u compartment come from exposed class directly without being isolated and could be recovered; die as a result of the disease or natural death with no any single treatment.

Statement of the problem

Following the index cases, as of 12th May, 2020, 146 new cases of COVID-19 have been confirmed within 20 states of Nigeria which make the total confirmed cases to 4,787. Out of which 959 were recovered and discharged while 158 deaths due to virus.

By the end of March, 2020 total confirmed cases were reported to be 139 cases, April 30, 2020 the number increased to 1932 cases. In total 4,787 persons were quarantined at some point between February 28 and May 12, 2020. However, this problem continues, people and government became afraid of the subsequent situations. Recently, around the middle of December, the daily new cases increased in alarming rate from hundreds to thousands. According to NCDC, the new confirm cases on 16th, 17th, 22nd and 23rd December are 930, 1145, 999 and 1133. Therefore, we are hereby investigating these situations and making all effort to predict and evaluate the spread of the pandemic.

Aim and objectives

The main goal of this paper is to develop a mathematical model well-tailored to COVID-19 pandemic. More specifically:

1. To develop a mathematical model for COVID-19 pandemic
2. To derive a disease free equilibrium
3. To determine the basic reproduction number
4. To (evaluate) analyses the spread of the disease analytically.

Materials and Method

1. Model formulation

Going by the characteristics of the COVID-19 pandemic, we assume that each person is in one of the following compartments:

- Susceptible- Population of the individuals that are not infected by the disease pathogen.
- Exposed- number of those individuals who are in the incubation period after being infected by the disease pathogen, and has no visible clinical signs. These individuals are infected but are not yet infectious (i.e could not pass on the disease to other people).
- Quarantined- population of individuals that are in quarantine at home or in hospital. Infected individuals in hospital (or in quarantine at home) can still infect other people.
- Infectious but reported- Population of individuals that start developing clinical signs and will be detected and reported by authorities. They are infected and can pass the disease on to other people.
- Infectious but undocumented- individuals who can infect other people and may start developing clinical signs but will not be detected and reported by authorities. They may recover or death naturally without any treatment.
- Recovered- population of individuals, who have survived the disease, are no longer infectious and have developed a natural immunity to the disease pathogen.

Assumptions

The following assumptions are used to build the model

a. The number of infected people increases proportional to both the number of infectious and the number of susceptible i.e.,$\frac{\beta SI}{N}$ with $\beta > 0$. So that number of susceptible decreases at the same rate. Here, β is called the effective infectious rate.

b. The rate of removal of infectious to recovered compartment is proportional to the number of infectious only i.e.,ΥI_u with $\Upsilon > 0$ and ρI_r with $\rho > 0$. These are called the removal rates. Therefore, $\frac{1}{\Upsilon}$ and $\frac{1}{\rho}$will be the infectious periods of the pandemic.

c. person can die at any of the compartment. Therefore, μ is taken as natural death.

a. The population is entirely Homogenous. That is everyone has equal chances of contacting the disease.

b. We also assume that there is constant birth and death rate.

Parameters

The parameters used are as follows:

β −Contact rate

δ −The rate at which an exposed individual moved to quarantined compartment

ω −The rate at which quarantined individuals move to recovery population

σ −The rate at which quarantined individuals become infected

α −The rate at which an exposed individual become infectious without being quarantined, they directly moved to the class of I_u or I_r

γ − Recovery rate for undocumented cases

ρ − Stands for the rate of successful cure of infections for reported cases (but it doesn't have permanent immunity)

ε − Represent death rate caused as a result of chronic infection of COVID-19 pandemic.

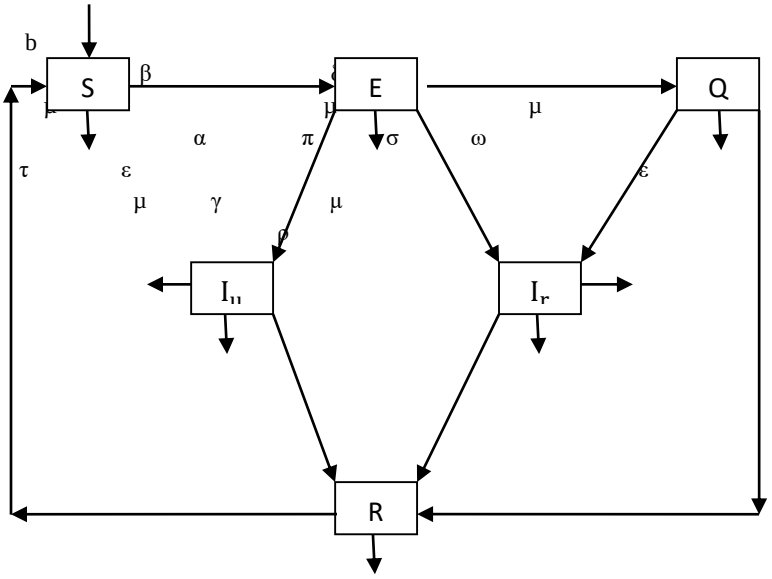
μ − Represents natural death rate

b −Proportion of incoming individuals right from birth (i.e the parameter b represents the population influx).

τ −The rate at which recovered individuals move back to susceptible compartment

R_0 − Basic reproduction number

Epidemiological diagram of the model



GOVERNING EQUATIONS

Using the above assumptions with the parameters, this model is governed by the differential equations as follows:

$$\frac{dS}{dt} = b + \tau R - \beta S(I_r + I_u) - \mu S$$

$$\frac{dE}{dt} = \beta S(I_r + I_u) - \delta E - \alpha E - \pi E - \mu E$$

$$\frac{dQ}{dt} = \delta E - \sigma Q - \omega Q - \mu Q$$

$$\frac{dI_r}{dt} = \pi E + \sigma Q - \rho I_r - \mu I_r - \varepsilon I_r$$

$$\frac{dI_u}{dt} = \alpha E - \gamma I_u - \mu I_u - \varepsilon I_u$$

$$\frac{dR}{dt} = \rho I_r + \gamma I_u + \omega Q - \tau R - \mu R$$

RESULTS

At steady states,

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dQ}{dt} = \frac{dI_r}{dt} = \frac{dI_u}{dt} = \frac{dR}{dt} = 0 \qquad 1.1$$

Hence,

$$b + \tau R - \beta S(I_r + I_u) - \mu S = 0 \qquad 1.2$$

$$\beta S(I_r + I_u) - \delta E - \alpha E - \pi E - \mu E = 0 \qquad 1.3$$

$$\delta E - \sigma Q - \omega Q - \mu Q = 0 \qquad 1.4$$

$$\pi E + \sigma Q - \rho I_r - \mu I_r - \varepsilon I_r = 0 \qquad 1.5$$

$$\alpha E - \gamma I_u - \mu I_u - \varepsilon I_u = 0 \qquad 1.6$$

$$\rho I_r + \gamma I_u + \omega Q - \tau R - \mu R = 0 \qquad 1.7$$

From (1.2): $b = S(\beta I + \mu)$

$$\therefore \quad S = \frac{b + \tau R}{\beta(I_r + I_u) + \mu} \qquad 1.8$$

Zero steady states are:

For $I_r = 0, \ and \ I_u = 0,$

$$S = \frac{b}{\mu} \quad 1.9$$

From (1.3):

$$E = \frac{\beta b(I_r + I_u)}{\mu(\delta + 2\alpha + \mu)} \quad 2.0$$

for $I_r = 0,\ and\ I_u = 0, then\ E = 0$

From (1.4):

$$Q = \frac{\delta E}{\sigma + \omega + \mu} \quad 2.1$$

for $E = 0,\ Q = 0$

From (1.5):

$$I_r = \frac{\pi E + \sigma Q}{\rho + \varepsilon + \mu} \quad 2.2$$

for $E = 0$ & $Q = 0\ then\ I_r = 0$

From (1.6):

$$I_u = \frac{\alpha E}{\gamma + \varepsilon + \mu} \quad 2.3$$

for $E = 0,\ I_u = 0$

From (1.7):

$$R = \frac{\rho I_r + \gamma I_u + \omega Q}{\mu + \tau} \quad 2.4$$

for $I_r = 0, I_u = 0\ and\ Q = 0$, then $R = 0$

Hence the Disease Free Equilibrium (DFE) is when

$S^\star = \frac{b}{\mu},\ \ E^\star = 0,\ \ Q^\star = 0,\ \ I_r^* = 0,\ \ I_u^* = 0,\ \ R^\star = 0$

Now, the non-zero steady states(endemic equilibrium) are obtained as follow:

From (1.5), $E = \frac{I_r(\rho + \varepsilon + \mu)}{\pi} - \sigma Q$ where $Q = \frac{\delta E}{\sigma + \omega + \mu}$

Substitute for the value of Q, it gives

$$E = \frac{I_r(\rho + \varepsilon + \mu)(\sigma + \omega + \mu)}{\pi(\sigma + \omega + \mu) + \delta\sigma} \quad 2.5$$

Also,

From (1.6),

$$E = \frac{I_u(\gamma + \varepsilon + \mu)}{\alpha} \quad 2.6$$

Equating equations (2.5) and (2.6) we have

$$\frac{I_r}{I_u} = \frac{\{\pi(\sigma + \omega + \mu) + \delta\sigma\}(\gamma + \varepsilon + \mu)}{\alpha(\rho + \varepsilon + \mu)(\sigma + \omega + \mu)}$$

That is,

$$I_r = \{\pi(\sigma + \omega + \mu) + \delta\sigma\}(\gamma + \varepsilon + \mu)$$

And

$$I_u = \alpha(\rho + \varepsilon + \mu)(\sigma + \omega + \mu)$$

Now, substitution for I_r and I_u in equations (1.8) and (2.0) we get

$$S = \frac{b}{\beta\{\pi(\sigma + \omega + \mu)[\gamma + \rho + 2\varepsilon + 2\mu] + \delta\sigma(\gamma + \varepsilon + \mu)\} + \mu - \tau} \quad 2.7$$

And

$$E = \frac{\beta b\{\pi(\sigma + \omega + \mu)[\gamma + \rho + 2\varepsilon + 2\mu] + \delta\sigma(\gamma + \varepsilon + \mu)\}}{\mu(\delta + 2\alpha + \mu)} \quad 2.8$$

Substitute for the value of E {from equation (2.8)} in equation (2.1) to get

$$Q = \frac{\beta\delta b\{\pi(\sigma + \omega + \mu)[\gamma + \rho + 2\varepsilon + 2\mu] + \delta\sigma(\gamma + \varepsilon + \mu)\}}{\mu(\delta + 2\alpha + \mu)(\sigma + \omega + \mu)} \quad 2.9$$

Substitute for the values of E and Q {from equation (2.8) and (2.9) respectively} in equation (2.2) to get

$$I_r = \frac{\{\alpha(\sigma + \omega + \mu)[\gamma + \rho + 2\varepsilon + 2\mu] + \delta\sigma(\gamma + \varepsilon + \mu)\}[\beta\alpha b(\sigma + \omega + \mu) + \beta\delta\sigma b]}{\mu(\delta + 2\alpha + \mu)(\sigma + \omega + \mu)} \quad 3.0$$

Substitute for the value of E {from equation (2.8)} in equation (2.3) to get

$$I_u = \frac{\beta\alpha b\{\alpha\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}}{\mu(\delta+2\alpha+\mu)(\gamma+\omega+\mu)} \quad 3.1$$

Substitute for the values of I_r from (3.0), I_u from (3.1) and Q from (2.9) in equation (2.4) to get

$$R = \left[\rho\{[\pi(\sigma+\omega+\mu)+\delta\sigma](\gamma+\varepsilon+\mu)\}+\gamma\{\alpha(\rho+\varepsilon+\mu)\}+\frac{\beta\omega\delta b\{\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}}{\mu(\delta+2\alpha+\mu)(\sigma+\omega+\mu)}\right] \div (\mu + \tau) \quad 3.2$$

Hence the Epidemic Equilibrium (EE) is when

$$S^* = \frac{b}{\beta\{\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}+\mu-\tau}$$

$$E^* = \frac{\beta b\{\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}}{\mu(\delta+2\alpha+\mu)}$$

$$Q^* = \frac{\beta\delta b\{\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}}{\mu(\delta+2\alpha+\mu)(\sigma+\omega+\mu)}$$

$$I_r^* = \frac{\{\alpha(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}[\beta\alpha b(\sigma+\omega+\mu)+\beta\delta\sigma b]}{\mu(\delta+2\alpha+\mu)(\sigma+\omega+\mu)}$$

$$I_u^* = \frac{\beta\pi b\{\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}}{\mu(\delta+2\alpha+\mu)(\gamma+\omega+\mu)}$$

$$R^* = \left[\rho\{[\alpha(\sigma+\omega+\mu)+\delta\sigma](\gamma+\varepsilon+\mu)\}+\gamma\{\alpha(\rho+\varepsilon+\mu)\}+\frac{\beta\omega\delta b\{\pi(\sigma+\omega+\mu)[\gamma+\rho+2\varepsilon+2\mu]+\delta\sigma(\gamma+\varepsilon+\mu)\}}{\mu(\delta+2\alpha+\mu)(\sigma+\omega+\mu)}\right] \div (\mu + \tau)$$

Basic reproduction number.

The basic reproduction number is denoted by R_0. It is an important parameter that is used to study the behaviour of epidemiological models. It is defined as the average number of secondary infections infected by an individual during an effective period provided that, all members of the population are susceptible. It determinewhether or not, an infection will spread through a given population.

We apply the next generation matrix technique by Dirissche and Watmough(2005) to obtain the basic reproduction number, R_0, by considering the infected compartments of the system (1.1) to (1.6). That is equation (1.2), (1.3), (1.4) and (1.5).

$$\frac{dx}{dt} = F_i(x) - V_i(x)$$

Where

$$F_i(x) = \begin{bmatrix} F_1 \\ F_2 \\ F_3 \\ F_4 \end{bmatrix} = \begin{bmatrix} \beta S(I_r + I_u) \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

And

$$V_i(x) = \begin{bmatrix} V_1 \\ V_2 \\ V_3 \\ V_4 \end{bmatrix} = \begin{bmatrix} \beta S(I_r + I_u) - \delta E - \alpha E - \pi E - \mu E \\ \delta E - \sigma Q - \omega Q - \mu Q \\ \pi E + \sigma Q - \rho I_r - \mu I_r - \varepsilon I_r \\ \alpha E - \gamma I_u - \mu I_u - \varepsilon I_u \end{bmatrix}$$

Now evaluating the Jacobian matrix of $F_i(x)$ and $V_i(x)$at disease free equilibrium, we obtain

$$F = \begin{bmatrix} 0 & 0 & \beta\frac{b}{\mu} & \beta\frac{b}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} A & 0 & 0 & 0 \\ -\delta & B & 0 & 0 \\ -\pi & -\sigma & C & 0 \\ -\alpha & 0 & 0 & D \end{bmatrix}$$

Where

A= $\delta + \alpha + \pi + \mu_E$

B= $\sigma + \omega + \mu_Q$

C= $\rho + \mu I_r + \varepsilon$

D=$\gamma + \mu I_u + \varepsilon$

We find the inverse of V, that is

$$V^{-1}=\frac{1}{ABC}\begin{bmatrix} BCD & BCD & 0 & 0 \\ \delta CD & ACD & 0 & 0 \\ \delta\sigma D & ABD & ABD & 0 \\ 0 & -\sigma AC & 0 & ABC \end{bmatrix}=\begin{bmatrix} \frac{D}{A} & \frac{D}{A} & 0 & 0 \\ \delta\frac{D}{A} & \frac{D}{B} & 0 & 0 \\ \frac{\delta\sigma D}{ABC} & \frac{D}{C} & \frac{D}{C} & 0 \\ 0 & \frac{-\sigma}{B} & 0 & 1 \end{bmatrix}$$

Now

$$FV^{-1}=\begin{bmatrix} 0 & 0 & \beta\frac{b}{\mu} & \beta\frac{b}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}\begin{bmatrix} \frac{D}{A} & \frac{D}{A} & 0 & 0 \\ \delta\frac{D}{A} & \frac{D}{B} & 0 & 0 \\ \frac{\delta\sigma D}{ABC} & \frac{D}{C} & \frac{D}{C} & 0 \\ 0 & \frac{-\sigma}{B} & 0 & 1 \end{bmatrix}$$

$$=\begin{bmatrix} \beta\frac{b\delta\sigma D}{\mu ABC} & \beta\frac{bD}{B\mu} & \beta\frac{D}{\mu C} & \beta\frac{b}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

Therefore we evaluated the characteristic equation $|FV^{-1}-\lambda|=0$ of the equation

$$\begin{vmatrix} \beta\frac{b\delta\sigma D}{\mu ABC}-\lambda & \beta\frac{bD}{B\mu} & \beta\frac{D}{\mu C} & \beta\frac{b}{\mu} \\ 0 & -\lambda & 0 & 0 \\ 0 & 0 & -\lambda & 0 \\ 0 & 0 & 0 & -\lambda \end{vmatrix}$$

Observe that $\lambda_2=\lambda_3=\lambda_4$ and $\lambda_1=\beta\frac{b\delta\sigma D}{\mu ABC}$

Therefore,

$$R_0=\beta\frac{b\delta\sigma(\gamma+\mu I_u+\varepsilon)}{\mu(\delta+\alpha+\pi+\mu_E)(\sigma+\omega+\mu_Q)(\rho+\mu I_r+\varepsilon)}$$

If $R_0<1$, then on average an infected individual produces less than one new infected individual over the course of its, infectious period, and the infection cannot grow. Conversely, if $R_0>1$, then each individual produces, on average, more than one new infection, and the disease can invade the population (Dirissche and Watmough, 2005).

Stability Analysis of Disease-Free Equilibrium

We find out that the Jacobian of F about X^* at disease free equilibrium is

$$\begin{bmatrix} -\mu-\lambda & 0 & 0 & \beta\frac{d}{\mu} & \beta\frac{d}{\mu} & \tau \\ 0 & -(\delta+\alpha+\pi+\mu_E)-\lambda & 0 & 0 & 0 & 0 \\ 0 & \delta & -(\sigma+\omega+\mu_Q)-\lambda & 0 & 0 & 0 \\ 0 & \pi & \sigma & -(\rho+\mu I_r+\varepsilon)-\lambda & 0 & 0 \\ 0 & \alpha & 0 & 0 & -(\gamma+\mu I_u+\varepsilon)-\lambda & 0 \\ 0 & 0 & \omega & \rho & \gamma & -(\tau+\mu)-\lambda \end{bmatrix}$$

Noticing the form of the Jacobian, we immediately have that all the eigenvalues of the characteristics polynomials have negative real part, thus implying asymptotic stability as applied in Ssematimba(2005) and Benyah(2008).

CONCLUSION

In this researchthe transmission dynamics of COVID-19 with conventional modelling approach has been studied. We developed a mathematical model for COVID-19 pandemic. The analytic result of the study revealed that there are certain situations when the disease will no longer be active to infect new individuals.That is if the basic reproduction number R_0 is brought to strictly less than unity, reducing the number of unreported cases. Further research may include simulation analysis.

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