A mathematical model for understanding the spread of COVID-19 in Saudi Arabia with access to vaccination

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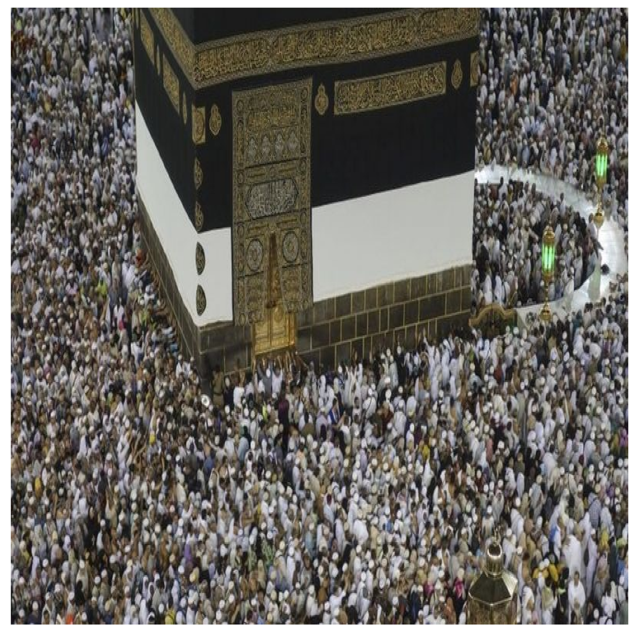
Abstract

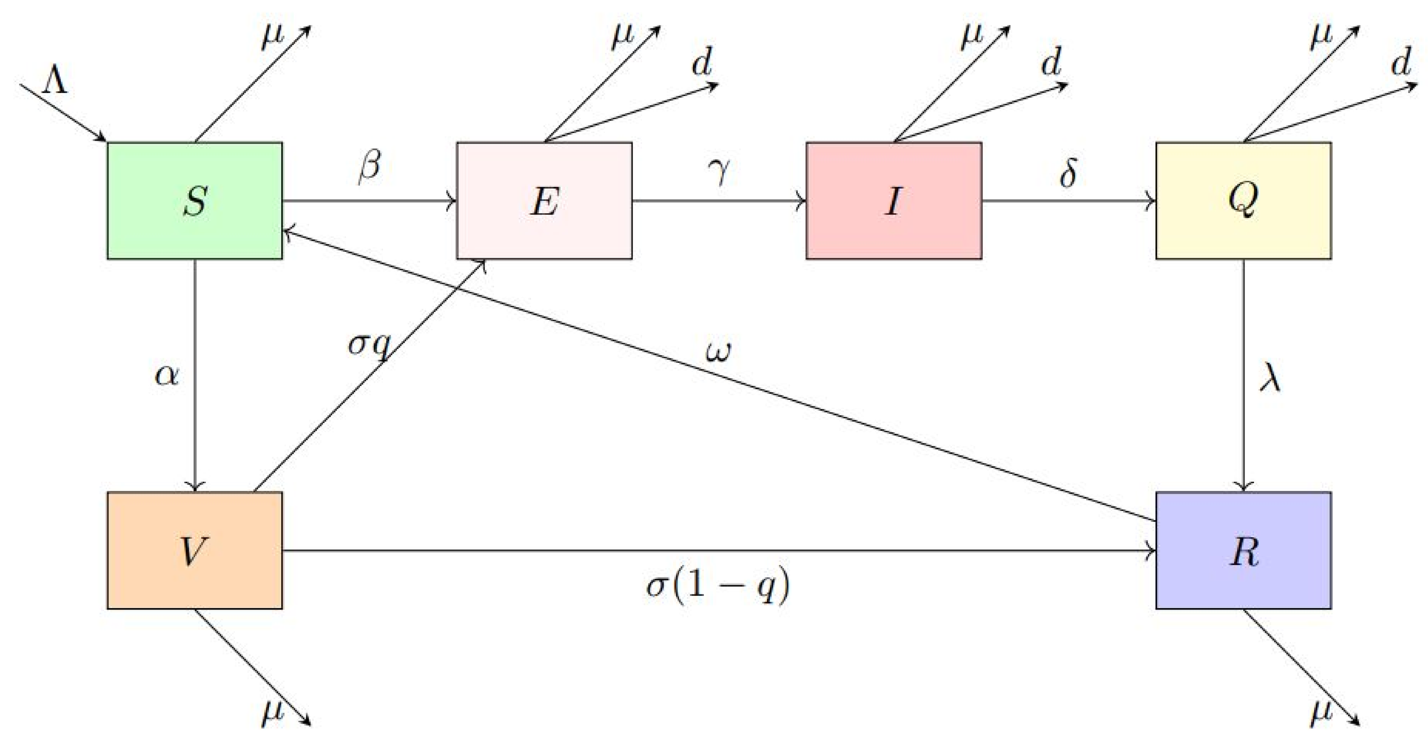
In this research paper, an extended SEIR model to study the spread of COVID-19 in the Kingdom of Saudi Arabia (KSA) with vaccination is proposed. Specifically, a mathematical analysis is carried out to illustrate the non-negativity, boundedness, epidemic equilibrium, existence, and uniqueness of the endemic equilibrium, and the basic reproduction number of the proposed model was calculated. Furthermore, MATLAB was used in the implementation of the numerical simulation of the model, and actual data of COVID-19 cases and vaccinations was used to validate our numerical model.

Introduction



On March 2, 2020, the first case of COVID-19 infection that is caused by the novel coronavirus called SARS-COV-2 was reported in the Kingdom of Saudi Arabia (KSA). Since the first case, the infected number of cases continued to grow rapidly which made the Saudi government take several measures including putting restrictions on travel to and from KSA. Some examples include restrictions on holy cities Makkah and Madinah, closure of the two Ground Mosques on March 6, 2020 for over 2 months which limited the Hajj of several visitors for within the kingdom pilgrimage, suspension of travel, and imposition of a curfew on the cities from March 23 to May 28, 2020. By September 2020, KSA reported 334,605 cases, with over 4700 deaths. As the disease dynamics progressed and vaccinations started to become available to the KSA population, there was a need to study how the vaccination impacted the spread of the disease which is the focus of this work.

Flow Diagram and Mathematical Model



$$\frac{dS}{dt} = \Lambda - \beta SI + \omega R - \epsilon_1 S$$
$$\frac{dE}{dt} = \beta SI + \sigma qVI - \epsilon_2 E$$
$$\frac{dI}{dt} = \gamma E - \epsilon_3 I$$
$$\frac{dQ}{dt} = \delta I - \epsilon_4 Q$$
$$\frac{dR}{dt} = \lambda Q + \sigma(1-q)V - \epsilon_5 R$$
$$\frac{dV}{dt} = \alpha S - \sigma qVI - \sigma(1-q)V - \mu V$$

where $\epsilon_1 = \alpha + \mu, \epsilon_2 = \gamma + \mu + d, \epsilon_3 = \delta + \mu + d, \epsilon_4 = \lambda + \mu + d, \epsilon_5 = \mu + w$.

Analysis of the Model

Theorem 1. *Let the initial condition* $\{S(0), E(0), I(0), Q(0), R(0), V(0)\} \geq 0$. *Then the solutions Model above are non-negative in* $[0, \infty)$.

Theorem 2. *All solutions of the proposed system are bounded inside the region* $\left\{\mathcal{X}(t) \in \mathbf{R}^6 : 0 \leq N(t) \leq \frac{\Lambda}{\mu}\right\}$.

Theorem 3. *The basic reproduction number* $\mathcal{R}_0 = \mathcal{R}_0^1 + \mathcal{R}_0^2$ *where,*

$$\mathcal{R}_0^1 = \frac{\gamma\beta S_0}{(\gamma+\mu+d)(\delta+\mu+d)}$$
$$\mathcal{R}_0^2 = \frac{\sigma qV_0}{(\gamma+\mu+d)(\delta+\mu+d)}$$

Proof. Let $X = (E, I)^T$. Then, $X' = f(X) - w(X)$ where, $f(X) = \{\beta SI + \sigma qVI, 0\}$ and let $w(X) = \{\epsilon_2 E, \epsilon_3 I - \gamma E\}$. Then the Jacobian of each becomes,

$$F = \begin{pmatrix} 0 & \beta S^0 + \sigma qV^0 \\ 0 & 0 \end{pmatrix} \qquad W = \begin{pmatrix} \epsilon_2 & 0 \\ -\gamma & \epsilon_3 \end{pmatrix}.$$

$$\implies FW^{-1} = \begin{pmatrix} \frac{\gamma(\beta S_0 + \sigma qV_0)}{\epsilon_2\epsilon_3} & \frac{\beta S_0 + \sigma qV_0}{\epsilon_3} \\ 0 & 0 \end{pmatrix}.$$

To find the eigenvalues, we set $\det(FW^{-1} - \lambda I) = 0$. The basic reproduction number is the dominant eigen value given by:

$$\mathcal{R}_0 = \frac{\gamma(\beta S_0 + \sigma qV_0)}{\epsilon_2\epsilon_3}$$
$$= \frac{\gamma\beta S_0}{(\gamma+\mu+d)(\delta+\mu+d)} + \frac{\sigma qV_0}{(\gamma+\mu+d)(\delta+\mu+d)}$$

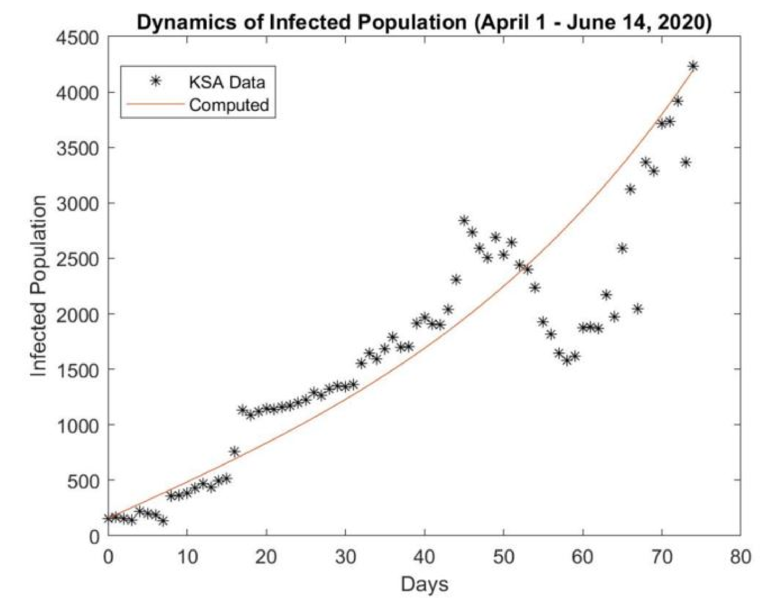
□

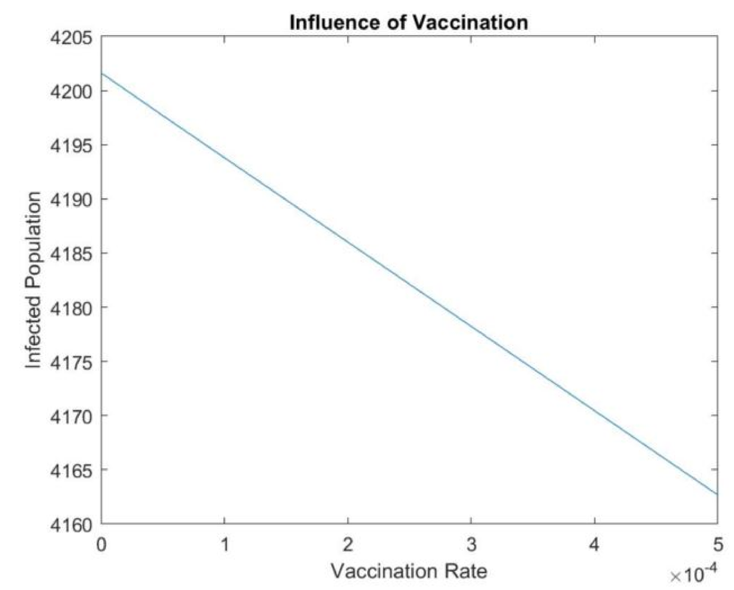
Theorem 4. *The disease-free equilibrium* X^0 *is locally asymptotically stable if* $\mathcal{R}_0 < 1$, *and unstable if* $\mathcal{R}_0 > 1$.

Computational Experiments

Table 1: Definition and value of parameters in the model

Parameter	Definition	Value
Λ	New births and new residents	2300
β	Transmission Rate	6e-9
γ	Rate at which Exposed individuals become Infected	0.00325
δ	Rate at which Infected individuals become Quarantined	1e-5
λ	Rate at which Quarantined individuals become Recovered or Died	1e-5
ω	Rate at which Recovered individuals become Symptomatic individual	1e-10
μ	Natural death Rate	3e-5
σ	Vaccine efficacy	1e-7
α	Vaccination Rate	5e-7
d	death rate due to COVID-19	3.423e-7
q	Function of Exposed individuals out of Vaccinated individual	0.001





Conclusions and Future Research

In this work, we develop a novel mathematical model to study the role of the vaccine in controlling the spreading of the COVID-19 in the KSA. The proposed model consists of six compartments: Susceptible individuals (S) who either may interact withe Exposed (E) or some of them may become vaccinated individual(V), infected individual (I) who will go to Quarantine (Q), and the Recovered population (R). The mathematical analysis of the model was conducted and the numerical simulation was performed to validate the model with the real data from KSA.

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