A Model for COVID-19 with Control Measures and Mobility

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Abstract

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1. Introduction

2. Results

3. Discussion

4. Methods

4.1. Baseline mathematical models

We use a deterministic compartmental model that is an extension of the SEIR model [citation] in which we include current experience with SARS-CoV-2. We partition the total population [citation] into susceptible individuals ($S(t)$), exposed individuals ($E(t)$), Asymptomatic, undetected and infected individuals ($A(t)$), Symptomatic, undetected, and infected individuals ($I(t)$), Asymptomatic, diagnosed and infected individuals ($Q(t)$), Symptomatic, diagnosed, and infected individuals ($H(t)$), individuals with acute symptoms and in critical care ($C(t)$), and recovered ($R(t)$) and deceased ($D(t)$), see Figure 1.

The transmission dynamics of COVID-19 in the basic model is given by the following deterministic system of nonlinear differential equations (1)-(10):

$$\frac{dE}{dt} = q + \beta(t)\left(I + \kappa A + \omega Q + \rho H\right)\frac{S}{N} - \sigma E - v, \tag{1}$$

$$\frac{dI}{dt} = s + \alpha\sigma E + \nu A - \left(\eta + \theta + \lambda\right) I - x, \tag{2}$$

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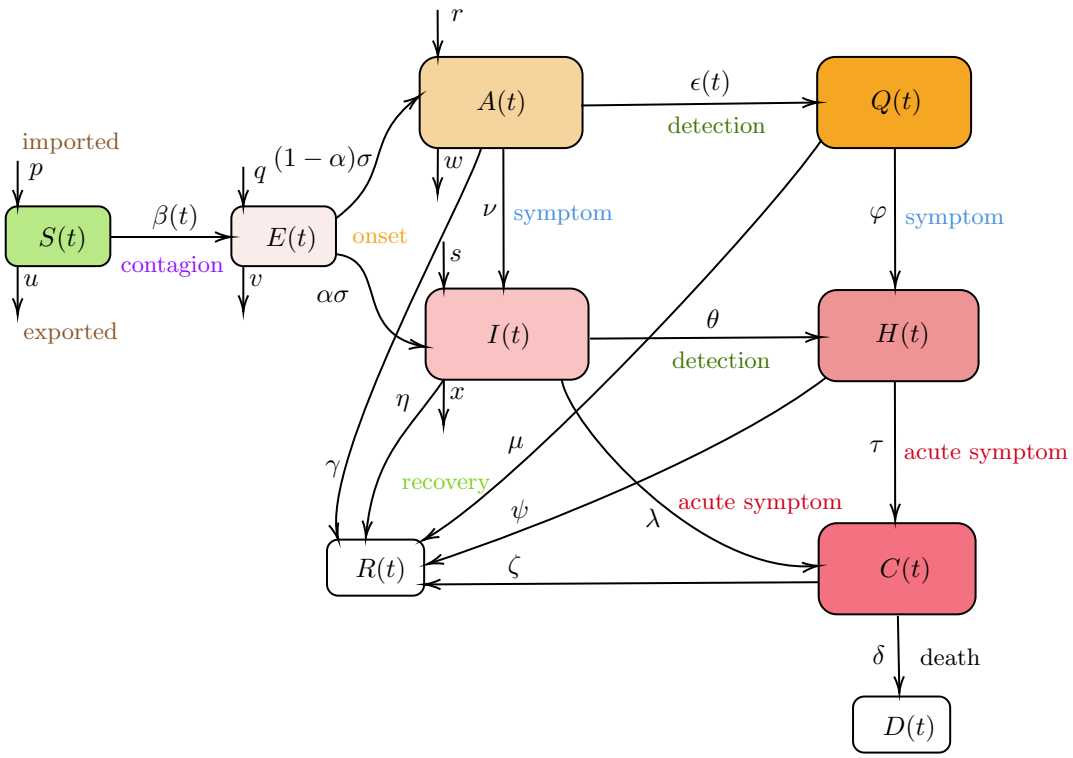

Figure 1: The model consists of following bins: susceptible $S(t)$,, exposed $E(t)$, asymptomatic $A(t)$, symptomatic $I(t)$, quarantined $Q(t)$, isolated $H(t)$, deceased ($D(t)$ and recovered $R(t)$ individuals in a population of $N(t) = S(t) + E(t) + A(t) + I(t) + Q(t) + H(t) + R(t) + D(t)$ individuals.

$$\frac{dA}{dt} = r + (1-\alpha)\,\sigma E - (\epsilon(t) + \nu + \gamma)\,A - w, \tag{3}$$

$$\frac{dQ}{dt} = \epsilon(t)A + (\varphi + \mu)\,Q, \tag{4}$$

$$\frac{dH}{dt} = \theta I + \varphi Q - (\tau + \psi)\,H, \tag{5}$$

$$\frac{dC}{dt} = \tau H + \lambda I - (\delta + \zeta)\,C, \tag{6}$$

$$\frac{dD}{dt} = \delta C, \tag{7}$$

$$\frac{dR}{dt} = (\eta I + \gamma A + \mu Q + \psi H + \zeta C)\,, \tag{8}$$

$$\frac{dS}{dt} = p - \beta(t)\,(I + \kappa A + \omega Q + \rho H)\,\frac{S}{N} - u, \tag{9}$$

where,

$$N(t) = S(t) + E(t) + A(t) + I(t) + Q(t) + H(t) + R(t) + D(t), \tag{10}$$

is the total population.

4.1.1. Susceptible individuals: $S(t)$

In our model, the susceptible individuals gets exposed to infection, and move to exposed group $E(t)$, from coming in contact with an infected individual, who may be symptomatic, asymptomatic, quarantined, or isolated. $\beta(t)$ is the baseline infectious contact rate, which can vary with time or assumed constant for the analysis of our baseline model. We assume that a person who is infected with symptom, and is not isolated, has the basic transmission coefficient of $\beta(t)$, that is changing over time. Based on [1, 2], we define $\beta(t)$ to have a value β_0 till time t_0 and then as a decreasing function with respect to time t, to reaching $\beta_{\min}$.

$$\beta(t) = \begin{cases} \beta_0 & t < t_0 \\ \beta_{\min} + (\beta_0 - \beta_{\min})\,e^{-r(t-t_0)} & t \geq t_0 \end{cases} \tag{11}$$

We would like to note that in certain countries, stringency measures were in place at an earlier stages of the epidemic and was relaxed over time leading to a higher contact rate. Under such scenario, we use value β_0.

Our model incorporates some facets of mobility, whereby, we recruit a inflow of susceptible individuals into the region at a rate p, and also consider an outflow with a rate u. It is well known that such inflow of travelers in the community including regional migration, immigration and emigration has lead to faster spread of the contagion [Citation]. A similar inflow and outflow has been amended to exposed, symptomatic and asymptomatic but undetected compartments, namely $E(t), A(t), I(t)$. In the absence of an effective screening test,

and when it was observed that in the wake of governmental stringency measure, people tried to flee regions that are under stricter measures, individuals from these groups carried contagion to other geographic regions [citation].

We assume that the asymptomatic individuals infect with a lower contact rate ($\kappa < 1$) than the symptomatic individuals. Once someone symptomatic is diagnosed, they can only infect healthcare workers and this lower contact rate is captured by the parameter ($\rho < 1$). Similarly, quarantined individuals have much lower contact rate of ($\omega < 1$). Overall rate of change for the susceptible population is thus defined by equation (9).

4.1.2. Exposed individuals: $E(t)$

Individuals in compartment E, are exposed to the virus, and are not contagious during a period of latent time. An individual in E becomes infectious, and moves to compartment A as asymptomatic or to I as symptomatic. We assume that σ is the transition rate from exposed to infectious, and a fraction α of them show symptoms. Overall rate of change for the exposed population is thus defined by equation (1).

4.1.3. Symptomatic individuals: $I(t)$

Symptomatic individuals can get diagnosed (θ) and be isolated, or show acute symptoms and be hospitalized (λ), or can recover at the rate η. It has been observed that $\eta \geq \gamma$, where symptomatic individuals recover at faster rate than asymptomatic individuals, and asymptomatic individuals have longer duration of viral shedding [3]. Overall rate of change is given by equation (2).

4.1.4. Asymptomatic individuals: $A(t)$

Asymptomatic individuals can enter into population with rate r, and then can migrate out at rate w. Asymptomatic individuals can eventually show symptoms and move to I at rate ν or can have a positive diagnosis and move to quarantine. We model testing of asymptomatic population as a function of time as the community testing process ramps up. Testing rate has been captured as $\epsilon(t)$. Finally, they can recover at the rate γ. Overall rate of change is given by equation (3).

4.1.5. Quarantined individuals: $Q(t)$

Quarantined individuals are asymptomatic population after diagnosis and they have very low contact rate ($\omega < 1$). This is mostly by infecting the other family members or by breach of protocol. They however, may develop symptoms and move to H or recover. Overall rate of change is given by equation (4).

4.1.6. Isolated individuals: $H(t)$

Isolated individuals are showing symptoms and has been either home isolated or has been hospitalized. They can pass the infection to a limited number of health care professional or caregiver (ρ). They can become critical and require treatments in intensive care (τ), and a large number of them recover (ψ). Overall rate of change is given by equation (5).

Parameter	Description	Range	Reference
β_0	abc def	0.5 days	[5]
σ	abc def	0.5 days	[5]
α	abc def	0.5 days	[5]
ν	abc def	0.5 days	[5]
$\epsilon(t)$	abc def	0.5 days	[5]
φ	abc def	0.5 days	[5]
θ	abc def	0.5 days	[5]
τ	abc def	0.5 days	[5]
λ	abc def	0.5 days	[5]
γ	abc def	0.5 days	[5]
η	abc def	0.5 days	[5]
μ	abc def	0.5 days	[5]
ψ	abc def	0.5 days	[5]
ζ	abc def	0.5 days	[5]
δ	abc def	0.5 days	[5]

Table 1: Data Source

4.1.7. Critical, Recovered and Deceased individuals: $C(t), R(t), D(t)$

These counters collect information on population that are critical, recovered or have deceased. Overall rate of change is given by equations (6) - (8). We assume that recovered individuals possess lasting immunity against SARS-CoV-2 over the period of simulation.

4.2. Baseline epidemiological parameters

In this section we describe the estimated values of various parameters based on the current literature. It has been noted in the litrature that the clinical course of the disease is typically quite long. Average total duration of illness has been estimated to be three weeks in [4]. [5] [3] [6]

Authors' contributions

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