

Dynamic analysis of a three-strain COVID-19 SEIR epidemic model with general incidence rates

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Abstract. This work deals with the global stability analysis of three-strain COVID-19 SEIR epidemic model with general incidence rates. The problem is modelled by a system of eight nonlinear ordinary differential equations describing the evolution of susceptible, exposed, infected and removed individuals. The global stability of the disease-free equilibrium is proved depending on the basic reproduction number R_0 . Furthermore, using an appropriate Lyapunov functionals, the global stability results of the endemic equilibria are established depending on the strain 1 reproduction number R_0^1 , the strain 2 reproduction number R_0^2 and the strain 3 reproduction number R_0^3 . Numerical simulations are presented in order to investigate a comparison between the model results and COVID-19 clinical data.

Introduction

The late COVID-19 caused by the severe acute respiratory syndrome-related coronavirus SARS-Cov-2 is classified as a strain of SARS-CoV-1 [1]. The classical susceptible-infected-recovered (SIR) epidemic model was first introduced in [2]. The multi-strain SEIR epidemic models, which better describes the evolution of the COVID-19 pandemic within populations, present an important tool to study this serious pandemic because they include a long incubation period and also various infection strains. The relevance of studying multi-strain models is to find out the different conditions permitting the coexistence of all acting strains. Recently, a multi-strain SEIR model with two general incidence rates are studied [3]. In this paper, we develop the study for a three-strain COVID-19 SEIR epidemic model with general incidence rates. To this end, we will consider the following three strains generalized epidemic model:

$$\begin{cases} \frac{dS}{dt} = \Lambda - f(S, I_1)I_1 - g(S, I_2)I_2 - h(S, I_3)I_3 - \delta S, \\ \frac{dE_1}{dt} = f(S, I_1)I_1 - (\gamma_1 + \delta)E_1, \\ \frac{dE_2}{dt} = g(S, I_2)I_2 - (\gamma_2 + \delta)E_2, \\ \frac{dE_3}{dt} = h(S, I_3)I_3 - (\gamma_3 + \delta)E_3, \\ \frac{dI_1}{dt} = \gamma_1 E_1 - (\mu_1 + \delta)I_1, \\ \frac{dI_2}{dt} = \gamma_2 E_2 - (\mu_2 + \delta)I_2, \\ \frac{dI_3}{dt} = \gamma_3 E_3 - (\mu_3 + \delta)I_3, \\ \frac{dR}{dt} = \mu_1 I_1 + \mu_2 I_2 + \mu_3 I_3 - \delta R, \end{cases}$$

Where (S) is the number of susceptible individuals, (E_1) , (E_2) and (E_3) are, respectively, the numbers of each latent individuals class, (I_1) , (I_2) and (I_3) are, respectively, the numbers of each infectious individuals class and (R) is the number of removed individuals. The parameter Λ is the recruitment rate, δ is the death rate of the population, γ_1 , γ_2 and γ_3 are, respectively, the latency rates of strain 1, strain 2 and strain 3, μ_1 , μ_2 and μ_3 are, respectively, the three-strain transfer rates from infected to recovered. The general incidence functions $f(S, I_1)$, $g(S, I_2)$ and $h(S, I_3)$ stand for the infection transmission rates for strain 1, strain 2 and strain 3, respectively. Our main contribution centers around the global stability of a three-strain COVID-19 SEIR epidemic model with general incidence rates.

Results and discussion

The main interest of this section is to compare the numerical simulations from our three-strain COVID-19 SEIR epidemic model with the COVID-19 clinical data. We have chosen to make this comparison concerning Moroccan clinical data during the year 2020 in the period between March 31 and June 20. We observe a good fit between the curve representing the COVID-19 clinical data and the numerical simulations resulting from our mathematical model. The impact of the quarantine strategy on controlling the infection spread is also discussed.

References

- [1] Gobalenya, A.E., Baker, S.C., Baric, R.S., de Groot, R.J., Drosten, C., Gulyaeva, A.A., and al.: The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nat. Microbiology*. **5**, 536-544 (2020)
- [2] Kermack, W.O., McKendrick, A.G.: A contribution to the mathematical theory of epidemics. *Proc. R Soc. Lond. A*. **115**, 700-721(1927)
- [3] Khyar, O., Allali, K. Global dynamics of a multi-strain SEIR epidemic model with general incidence rates: application to COVID-19 pandemic. *Nonlinear Dyn* (2020). <https://doi.org/10.1007/s11071-020-05929-4>.