

The global stability of an epidemiological model with n strain "all coronavirus mutations"

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- The new idea of our article is to divide people infected to the coronavirus (Covid-19) into a lot categories, so that each category expresses a mutant of the disease, each infected with a covid-19 mutation will be noted by I_i such that $i = 1, 2, \dots$ therefore we can say that each index i represents such a mutation of the disease. As for the recovery booth, we also divided it into two categories, one for people who have completely recovered without showing any side effects R_T and the other for people who have not been completely recovered R_{NT} such as people who still have no sense of smell and taste.
- In our model, the population studied is divided into a certain number of compartments which form a partition of the entire population at a given moment, a given individual necessarily belongs to one and only one of the compartments. The dynamics of the epidemic causes individuals to move from one compartment to another, which explains the construction of the equations of our new model.
- In our model there are several strains, each strain possessing in each case a mutation at a basic reproduction rate R_{0i} ; then our model needs a single basic reproduction rate R_0 to properly control the disease so that's why we take the maximum rates, that is to say we have a rate which contains the maximum quantities of transmission of the disease.
- We have added the source of the method used in Section 4.2 for determining the R_0 and we have explained the meaning of i in the text above.
- We have added text conclusion.
- We have corrected all spelling and clarification errors.