Stability and sensitivity analysis of Be-CoDiS, an epidemiological model to predict the spread of human diseases between countries

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The Ebola virus disease is a lethal human and primate disease that requires a particular attention from the international health authorities due to important recent outbreaks in some Western African countries and isolated cases in Europe and North-America. Regarding the emergency of this situation, various decision tools, such as mathematical models, were developed to assist the authorities to focus their efforts in important factors to eradicate Ebola. In a previous work (see [1]), we proposed an original deterministic spatial-temporal model, called Be-CoDiS (Between-Countries Disease Spread), to study the evolution of human diseases within and between countries by taking into consideration the movement of people between geographical areas. This model was validated by considering numerical experiments regarding the 2014-16 West African Ebola Virus Disease epidemic. In this article, we propose to perform a stability analysis of Be-CoDiS. Our first objective is to study the equilibrium states of simplified versions of this model, limited to the cases of one or two countries, and to determine their basic reproduction ratios. Then, we perform a sensitivity analysis of those basic reproduction ratios regarding the model parameters. Finally, we validate the obtained results by considering numerical experiments based on data from the 2014-16 West African Ebola Virus Disease epidemic.

References

[1] B. Ivorra, D. Ngom, and A. M. Ramos, *A mathematical model to predict the risk of human diseases spread between countries-validation and application to the 2014-2015 ebola virus disease epidemic*, Bulletin of Mathematical Biology, 77(9):1668-1704, 2015.