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Global stability of some continuous and nonstandard discretization models for the Ebola virus disease with fast and slow transmissions

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Mathematical models for the Ebola Virus Disease (EVD) were, until recently, mostly based on the fast/direct transmission route, which involves contact with blood or body fluid and objects that have been contaminated by body fluid. The fact that in almost all outbreaks of the EVD in Africa, the index case became infected through contact with infected animals, such as fruit bats and primates, makes the environment a no negligible channel for slow/indirect transmission of the disease.

In this talk, we incorporate both direct and indirect transmission routes in the setting of SIR-type models that are developed gradually. Firstly, we add two compartments (for dead individuals and for the environment) in order to capture infection through the manipulation of deceased individuals before burial as well as contaminated environment. Secondly, we enrich the first model with self-protection measures reflected by the addition of classes of vaccinated and trained individuals.

For the two models, we prove that the disease-free equilibrium is globally asymptotically stable (GAS) whenever the basic reproduction number is less than or equal to unity, and unstable when this threshold number is greater than 1. In the latter case, the existence of at least one endemic equilibrium (EE) (for the second model) and of a unique EE (for the first model), which are locally asymptotically stable (LAS) is shown, together with the fact that the unique EE is GAS in the absence of shedding and manipulation of deceased human individuals before burial. At the endemic level, it is shown that the number of infectious individuals is much smaller than that obtained in the absence of any intervention.

In a final step, we construct nonstandard finite difference schemes that are dynamically consistent with respect to the above features of the continuous models.

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