A Simple Mathematical Model for Ebola in Africa

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In 2014, an outbreak of Ebola virus (Ebola) decimated people in western Africa. With more than 16000 clinically confirmed cases, and approximately 70% case mortality, it was, out of the twentieth Ebola threats since 1976, the deadliest. In almost all the outbreaks, the index case (first patient) became infected through contact with an infected animal (hunted for food), such as a fruit bat or primate (apes, monkeys).

The virus can be spread to others via direct contact (through broken skin or mucous membranes in, the eyes, nose, or mouth) with: (1) blood or body fluids (including but not limited to urine, saliva, sweat, feces, vomit, breast milk, and semen); (2) objects (needles, syringes) that have been contaminated with body fluids; (3) infected fruit bats or primates. As reported in [1], 10% and 3% of the *Ebola-Zaire* virus type, survived on glass and plastic surfaces, respectively, after 14 days at 4°C. Moreover, 0.1-1% of Ebola virus particles remained viable for up to 50 days at 4°C [2].

In this talk, we propose a deterministic model which focuses both on the direct (route 1) and environmental (routes 2, 3) transmission routes. It is a SIR model with an additional environmental compartment regarded as the pool of Ebola viruses. This latter class is motivated; firstly by the consumption of bushmeat and fruit bats; second by the poor living and sanitary conditions of people in Ebola outbreak areas in Africa. The full model has only a unique endemic equilibrium which is locally asymptotically stable (LAS), while the model without provision of viruses has two equilibria: the disease-free equilibrium which is globally asymptotically stable (GAS) and the endemic equilibrium which is LAS.

[1] K. Bibby et al., *Ebola Virus Persistence in the Environment: State of the Knowledge and Research Needs*, Environ. Sci. Technol. Lett. 2015**(2)**, 2–6.

[2] T. J. Piercy et al., *The survival of filoviruses in liquids, on solid substrates and in a dynamic aerosol*, J. Appl. Microbiol. 2010, 109 **(5)**, 1531–1539.