

Qualitative analysis of two strain HIV model in the presence of antiretroviral treatment

B. Abdulra'uf Bello*, B.I.S. van der Ventel and F. Nyabadza

University of Stellenbosch

belloab@sun.ac.za

SAMS Subject Classification: ODE's and Dynamical Systems

We present a comprehensive deterministic mathematical model for HIV, which includes wild-type and drug-resistant strain. The model consists of a system of ordinary differential equations describing the transmission dynamics of HIV in the presence of antiretroviral therapy (ART). The principle objective is to assess the dynamics of the two strains and identify the key epidemiological factors. We carried out an extensive analytical and numerical analysis. We determined the basic reproductive numbers for each strain (R_{0R} and R_{0W}) and perform an uncertainty and sensitivity analysis on the reproduction numbers. The model has a disease free equilibrium which is globally asymptotically stable whenever both reproduction number is less than unity. This asymptotic global stability is shown using comparison theorem. Using the Center of manifold theorem we showed the existence and stability of drug-resistant only boundary equilibrium and wild-type only boundary equilibrium. The result shows that wild-type only boundary equilibrium exist and it is locally asymptotically stable whenever $R_{0R} < 1 < R_{0W}$ and that drug-resistant only boundary equilibrium exist and it is locally asymptotically stable whenever $R_{0W} < 1 < R_{0R}$. The model can have a coexistence equilibrium whenever both reproduction number are greater than unity. Simulation results suggest that treatment rate, risky behavior, rate of development of resistant strain and fitness of resistant strain are key epidemiological factors that either increase or decrease HIV prevalence.