

ABSTRACT

Human immunodeficiency virus and *Mycobacterium Tuberculosis* infections are two major world's public health problems especially in developing countries. Worldwide, 13 % of TB cases are estimated to be co-infected with HIV and about a third of 33 million people living with HIV are infected with the bacterium that causes TB. Deterministic models developed by Carlos *et al*, Gumel *et al* and Mukandavire *et al* estimated the basic reproduction number of HIV and TB co-infection as a single output value by treating each of the parameter input as a constant value. In this research, we develop a deterministic model using Ordinary Differential Equations (ODE) in order to estimate parameter estimates of basic reproduction number R_{ht} for HIV and TB co-infection by treating each parameter input as a random variable with a corresponding probability distribution. The next generation matrix method is used to derive an expression of basic reproduction number R_{ht} for HIV and TB co-infection. Probability distribution of R_{ht} is computed with the random effects in the parameters using Windows for Bayesian Inference Using Gibbs Sampling (WinBUGS) in Markov Chain Monte Carlo (MCMC) and R software. The results from probabilistic simulation of the basic reproduction number R_{ht} for HIV and TB co-infection shows that when each parameter is treated as a random variable, variance of R_{ht} can be computed unlike using deterministic approach where each parameter is treated as a constant value hence not possible to compute for the variance of R_{ht} . For future research work, appropriate non negative distributions can be incorporated in estimating the basic reproduction number R_{ht} for HIV and TB co-infection.