Mathematical model for the study of effectiveness in therapy in Tuberculosis

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Abstract: In this work we propose a mathematical model of Tuberculosis (TB) with drug resistance to a first and second line of treatment and taking into account the influence of HIV and Diabetes mellitus treatments. We find the basic reproduction number ($\mathfrak{R}_0$) for the sub-model with TB and HIV and the sub-model with TB and Diabetes, and for the general model and we present results that link it to local stability at the infection-free equilibrium point. We perform computational experiments in scenarios presented in bibliographies in order to study the behavior of the model and extend it to real scenarios. We show the influence that HIV and Diabetes have on the resistance to the first and second line of treatment for tuberculosis. **Keywords**: Diabetes, HIV, model, Tuberculosis.

Introduction

Tuberculosis (TB) is one of the top 10 causes of death worldwide and is a chronic bacterial infectious disease caused by Mycobacterium Tuberculosis. The are six types of multidrug-resistant TB (MDR-TB). MDR-TB and, more recently, extensively resistant TB (XDR-TB) threater TB control, and cause alarm of future non-effective TB drugs [1]. The TB is the second deadliest disease due to a single infectious agent only after HIV/AIDS. Another disease that is associated with the control and efficacy of treatment is Diabetes Mellitus. Mathematical modelling of HIV/TB co-infections have been reported by several researchers [2]. In the last few decades, several mathematical models are proposed to better comprehend the patterns of TB and Diabetes [3]. The objective of this work is to present a mathematical model for to study the influence of HIV and Diabetes and its treatments on resistance to TB treatment.

Methods

The model was designed using ordinary differential equations. The figure (6.5) shows the flow diagram of the model. The $\mathfrak{R}_0$ was studied for submodels that relate HIV and Diabetes to TB and general using the next-generation matrix method. A theoretical study of the model including existence, uniqueness and postivity of the solution, among other mathematical results, was carried out. For the computational experimentation was used

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data of bibliographies (some real and others estimated in the texts) and MATLAB-R2017a was used for programming.

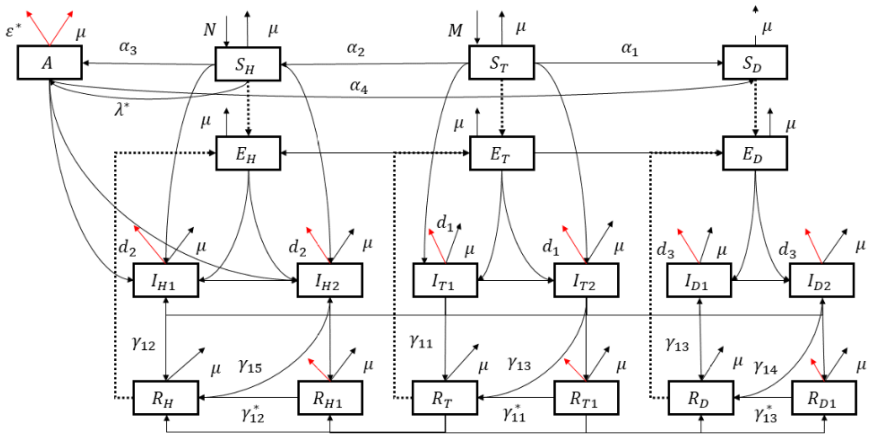

Figure 6.5: Model structure. The subindices H, D and T represent, with HIV+, with diabetes and free of these diseases. Susceptible begin in S_H, S_D, S_T and A (people with HIV who are using treatment) and move to E_H, E_D and E_T, exposed compartment, I_{H1}, I_{D1}, I_{T1}, sensitive to TB or I_{H2}, I_{D2}, I_{T2}, resistant to the first line of treatment after having contact with a infected (TB). From I_{H1}, I_{D1}, I_{T1} can enter the recovered state R_H, R_D and R_T or become resistant to the first line of treatment. From the resistant compartment to the first line can be moved to recovered or to resistant to the second line (R_{H1},R_{D1},R_{T1}) depending on the effectiveness or not of the treatment. From R_{H1},R_{D1} and R_{T1} we assume that they can recover or die. From the recovered state they return to the exposed state by having only partial immunity. In all dynamics there is the possibility of becoming infected with HIV or of developing Diabetes.

Discussion

Among the results obtained in the computational experimentation is that, the cases of tuberculosis with HIV have a greater chance of recovering from cases that have TB with Diabetes. Diabetes patients who become infected with TB have a greater chance of developing resistant TB than those who are HIV+ (with and without treatment). Patients with HIV recover before being resistant to the first line of treatment in greater proportion to those with diabetes. In the scenario studied, the $\Re_0$ for the TB/Diabetes submodel is greater than the TB/HIV submodel, which represents that Diabetes has great influence in the dynamics of the TB.

References

[1]G. Delogu and G. Fadda. *The biology of mycobacterium tuberculosis infection*, Mediterr. J. Hematol. Infect. Dis, 16(5), 2013. DOI: 10.4084/MJHID.2013.070. heoret. Biol, 6(4), 197-205, 2011. DOI: 10.3934/mbe.2009.6.815.

[2]L-IW. Roeger and Z. Feng and C. Castillo-Chavez. *Modelling TB and HIV co-infections*. Math. Biosci. Eng, 16(4), 815-837, 2009. DOI: 10.3934/mbe.2009.6.815.

[3]C. Coll and A. Herrero and E. Sanchez and N. Thome. *A dynamic model for a study of diabetes*, Math Comput Model, 50(5-6),713-16, 2009. DOI: 0.1016/j.mcm.2008.12.027.