

1125-92-1288

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*Incorporating Antibiotic Resistance in the Modeling of TB in the US.* Preliminary report.

According to WHO, one third of the world's population is infected with tuberculosis (TB), with drug resistance posing another challenge to the management of TB. Strains resistant to the most common drugs for treatment (e.g. isoniazid, rifampin) are already widespread. To address the issue, we constructed a mathematical compartmental model described by differential equations showing the transmission of TB in the US. The model encompasses four strains of different resistance to antibiotics, while taking into consideration immigration, which greatly contributes to the excessive transmission of latent TB. We fitted parameters to recent CDC data on TB morbidity and mortality, producing reliable fits, by generating random parameter values within the ranges obtained from real-world data. We then algorithmically adjusted parameter values to better fit CDC and census data in three categories (total US population, active cases of TB, total TB deaths). Our focus now is improving the algorithm by understanding the its behavior of through tests, which show that the order in which the parameter space is investigated may affect the results of the simulation, and that the stop rule of the algorithm is effective. The final goal is to use the model to identify effective strategies against TB. (Received September 15, 2016)