

A mathematical model of malaria and tuberculosis co-dynamics
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This work addresses the co-dynamics between Malaria and Mycobacterium Tuberculosis using deterministic model, which incorporates many of the essential biological and epidemiological features of the two diseases. A useful epidemic threshold parameter is computed for the two submodels that is Malaria only and TB only models as well as the full model. The existence and stability of the system is analyzed for the disease-free and endemic equilibrium points based on this threshold parameter \mathcal{R}_s , say, $s = M$ or TB , with M representing malaria and TB for tuberculosis. The disease-free equilibrium point is locally asymptotically stable when the reproduction number $\mathcal{R}_s < 1$ and the disease will always die out. For $\mathcal{R}_s > 1$, the disease-free equilibrium becomes unstable and the endemic equilibrium exists and is locally asymptotically stable. The global stability of the steady states does not hold due to the phenomenon of backward bifurcation. The two submodels undergo backward bifurcation, and consequently, the condition $\mathcal{R}_s < 1$ is necessary, but not sufficient to curtail the epidemics. The dual malaria-TB only model has no positive endemic equilibrium (EE) whenever the reproductive number for the dual Malaria-TB co-infection only $\mathcal{R}_T < 1$, - its disease free equilibrium (DFE) is globally asymptotically stable (GAS) whenever $\mathcal{R}_{MT}^d < 1$. Simulations of the submodels and full model are carried out in order to determine whether the two diseases will co-exist. Finally, we perform sensitivity analysis on the key parameters that drive the disease dynamics in order to determine their relative importance to disease transmission and prevalence.