
LUYAO ZHAO, University of New Brunswick

A Unified Mathematical Study of Four Within-Host Mycobacterium tuberculosis Models

Tuberculosis infection within a host is shaped by interactions among uninfected macrophages, infected macrophages, and extracellular *Mycobacterium tuberculosis* (MTB). In this poster, we develop and compare four within-host MTB models within a unified three-dimensional framework. The models share the same infection and bacterial-production structure, but differ in how they represent macrophage maintenance, local proliferation, local crowding, and macrophage-mediated bacterial loss. For each model, we derive the nontrivial disease-free equilibrium and compute the basic reproduction number R_0 using the next-generation matrix method. A unified Lyapunov approach is then used to establish global stability of the disease-free equilibrium when $R_0 \leq 1$, under suitable biological assumptions.

We further study the existence and local stability of positive equilibria, which represent persistent chronic infection states. The analysis shows how different modeling assumptions change the threshold conditions for infection persistence and the stability of chronic infection. In addition, Hopf bifurcation analysis with respect to the infection rate β illustrates that increasing infection efficiency may destabilize the positive equilibrium and generate oscillatory dynamics in infected cells and extracellular bacterial load. Numerical simulations are used to support the analytical results and to compare stable, unstable, and oscillatory regimes. Overall, this work highlights how local macrophage regulation, external cell recruitment, and bacterial clearance mechanisms jointly shape MTB persistence and within-host infection dynamics.