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Dynamic Structure and Local Analysis of a Multi-Stage Tuberculosis Model with Therapeutic Resistance

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Abstract

Tuberculosis (TB) remains one of the leading causes of infectious mortality worldwide, particularly due to the emergence and spread of drug-resistant strains. In this work, we propose and rigorously analyze a deterministic compartmental model structured into eight classes: susceptible (S), exposed (E), latent (L), drug-sensitive infectious (Is), drug-resistant infectious (Ir), treated sensitive (Ts), treated resistant (Tr), and recovered (R).

We develop a complete mathematical study including: (i) the proof of well-posedness of the system, (ii) the explicit analytical computation of the basic reproduction number R_0 using the next-generation matrix method, (iii) a detailed spectral analysis of the Jacobian at the disease-free equilibrium, (iv) a rigorous center-manifold reduction in a neighborhood of the critical threshold $R_0 = 1$, (v) the explicit computation of the quadratic and cubic coefficients characterizing the bifurcation, (vi) the complete asymptotic expansion of all infectious and non-infectious compartments near the epidemic threshold, and (vii) the formal proof of the absence of backward bifurcation.

The results show that the model admits a unique forward transcritical bifurcation, excluding any sub-threshold bistability. The analytical expression of R_0 highlights the combined effects of resistance, treatment rates, and latent transitions on epidemic dynamics. This study provides a robust theoretical framework for the mathematical assessment of TB control strategies.

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