A Novel Computational Agent-Based Model for the Outbreak, Spread, and Containment of Tuberculosis

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Although tuberculosis (TB) is the second leading cause of death from an infectious disease, affecting approximately one-third of the world's population in some way, little is known about TB epidemiology in a macroscopic population. This research aims to address this issue through the creation of a novel computational Agent-Based Model (ABM) that investigates spatial and temporal progression of TB, as well as the development of containment strategies. The test case chosen for this study was the slum of Kibera in Nairobi, Kenya. The necessary geospatial and socio-demographic information was obtained to create the environment and simulate realistic human behavior. Schelling Segregation and SEIR submodels helped define social networks and TB dynamics, while specific TB transmission equations were independently derived from literature. The ABM and its processes were verified, validated, and tested using established VV&T techniques. Less than an 8.5% variance in real-world case fatality rate was found, thus giving the ABM statistical credibility as a realistic predictive tool. Model results show that TB epidemics progress in a staircase pattern of emergence and stabilization. Furthermore, geospatial analysis using ArcGIS (ex. IDW Interpolation) suggests that TB spreads primarily through hotspots. Population demographic analyses further reveal which age groups contribute to the spread and which are most negatively impacted. Containment strategy experiments were successfully performed to pre-diagnose TB in the most efficient and cost-effective way. Results, lessons and the model itself can easily be incorporated into current health policies to mitigate TB's future negative impact. This project also shows the strength of ABMs in computational epidemiology studies.

Awards Won:

Second Award of $2,000