Modeling tuberculosis transmission in urban cities through agent-based simulation: the case of Barcelona

Extended Abstract[†]

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ABSTRACT

Tuberculosis remains one of the world's deadliest infectious diseases. About one-third of the world's population is infected with tuberculosis bacteria. Understanding the dynamics of transmission at different spatial scales is critical to progress in its control. We present an agent-based model for tuberculosis epidemics in Barcelona, which has an observatory on this disease. Our model considers high heterogeneity within the population, including risk factors for developing an active disease, and it tracks the individual behavior once diagnosed. We incorporated the immunodeficiency and smoking/alcoholism, as well as the individual's origin (foreigner or not) for its contagion and infection as risks factors. We implemented the model in Netlogo, a useful tool for interaction with physicians. However, the platform has some computational limitations, and we propose a solution to overcome them.

CCS CONCEPTS

• **Computing methodologies → Agent / discrete models**; Computing methodologies → Modeling methodologies

KEYWORDS

Tuberculosis, agent-based simulation, epidemics

1 INTRODUCTION

Today, Tuberculosis (TB) is still one of the major humankind threats, being the first cause of death by an infectious disease worldwide. TB is a communicable chronic infectious disease that every year affects 10 million people worldwide and kills 2 million. European cities today face a significant challenge to control TB infection and spread. Europe spends over €5 billion yearly only in the treatment of TB ill population. This amount is considered to be less than 10% of the actual cost of the disease [1]. One of the major problems is that this process is very silent, causing a delay in its diagnosis. The main reason for this delay is the absence of knowledge on the factors and circumstances driving an infected person to develop the disease. Thus, there is a need for decision support tools to provide solutions that will allow the definition of better resilience strategies for TB-related interventions.

Current proposed simulation works address TB modeling from an SEIR (top-down) perspective. However, SEIR models do not take into account the intrinsic heterogeneity of TB dynamics and consider homogeneous conditions, which is unlikely. As an alternative, we use Agent-Based Modeling (ABM) to observe how the dynamics of the global system emerge from the low-level interactions. ABM is particularly useful for projecting a population by answering "what if" questions such as the effect of a certain policy on the spread of a disease in a target group. In this paper, we present an ABM for TB epidemics in the city of Barcelona (Spain). Our model simulates the dynamics of the population and the transmission of the disease among a heterogeneous population. Data were obtained from national statistics and the Tuberculosis Investigation Unit in Barcelona. The model was developed in Netlogo [2], a user-friendly tool that has proven to be useful in our interaction with physicians. The implementation with this tool should facilitate its use by non-modelers such as health services workers and tuberculosis control units. The main drawback of this platform is that it is highly time-consuming. In our work, we propose a computing solution to this problem by collectively treating individuals that do not require explicit control (healthy subpopulation). We show the capability of the new model in providing equivalent results to those obtained with the original model with a considerable reduction in the computing time. This strategy is an important innovation that may be used in epidemiological studies of other diseases. Moreover, the model is robust enough to be calibrated to any other region.

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