

MULTISCALE MODELING OF TRANSMISSION OF MULTIDRUG-RESISTANT ORGANISMS TO REDUCE HEALTHCARE-ASSOCIATED INFECTIONS

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ABSTRACT

Healthcare-associated infections (HAIs), particularly multi-drug resistant organisms, are a major source of morbidity and mortality for patients. We developed a multiscale computational model of transmission to explore the effectiveness of interventions to reduce HAIs. We utilized a state-level patient mix database from Maryland to develop a meta-population model that simulates the movement network of patients between acute hospitals, long-term care facilities, and communities on a regional scale. On a local scale, we modeled the population at each facility and community using an epidemiological compartmental model that included susceptible, colonized, and infectious patients and their transitions between each compartment state. The local models are embedded in a multiscale model in order to simulate transmission patterns of multi-drug resistant organisms and the incidences of healthcare-associated infections for each distinct population. We then assessed the effectiveness of policy interventions, such as using an electronic patient registry or increasing active surveillance.

1 INTRODUCTION

The rise of multi-drug resistant organisms (MDRO) presents a major risk to patient safety within the healthcare environment. In particular, Carbapenem-resistant Enterobacteriaceae (CRE), which are common commensal organisms that are resistant to nearly all available antibiotics, has rapidly increased as a cause of healthcare-associated infections (HAI) in recent years (Ventola, 2015). CRE infections, which increase the odds of mortality for a patient more than 2-fold, typically occur in healthcare settings such as acute-care hospitals and long-term care facilities (Perez & Van Duin, 2013). Evidence suggests that CRE can be transmitted through direct contact between individuals or indirectly through the environment (Cheng et al., 2015). The probability of becoming infected with CRE increases greatly when a patient is colonized, *i.e.*, colonized patients can carry the pathogen and transmit the pathogen to other individuals without causing any symptoms. The most important risk factors for becoming colonized with CRE are the use of antibiotics and being hospitalized or cared for in a long-term care facility. Identifying colonized individuals and using appropriate precautions in the hospital is recognized as a means to reduce the spread of CRE.

2 MODEL STRUCTURE

Based on the epidemiology of CRE, we developed a regional model that captures the movement and population dynamics between 51 acute hospitals, 160 long-term care facilities, and 403 communities. The movement of patients in the model was informed by the Maryland Health Services Cost Review Commission (HSCRC) patient mix dataset, which compiles a database of all inpatient visits to non-federal acute-care hospitals in the state of Maryland. We combined this information with community-level population data obtained from the US Census Bureau to construct a movement network that can be characterized as an adjacency matrix that is integrated into our computational model. For each population,

we have five compartments: susceptible (S), highly susceptible due to antibiotic usage (X), undetected colonized (C), detected colonized (\hat{C}), and infected (I). Patients that are colonized and susceptible are allowed to move between the health facilities and communities. The computational model is implemented as a system of differential equations that can be solved using a numerical integration solver.

3 PRELIMINARY RESULTS

For our base model, we performed several simulations (1000 runs) with a prescribed parameter distribution based on values obtained from the literature. The parameters for each run was determined based on Latin Hypercube Sampling from a triangular distribution in order to generate parameter values that accounted for the uncertainty while still having values that are realistic according to literature. The results were compared to data on colonization and infection in Maryland hospitals (Goodman et al., 2019). The partial rank correlation coefficient (PRCC) for all parameters with respect to the number of infections and colonization in each hospital were estimated. We found that the transmission rate in the communities had the highest sensitivity to infections based on the calculated PRCC from the base run.

4 CONCLUSION

A multiscale model can capture the local as well as regional population dynamics of a healthcare system that spans a large geographical area. Using a systems approach allows us to build a simulation to consider the complex interaction between different health facilities and communities. Furthermore, employing large datasets into model development allow us to understand the relative effects of policy interventions for a single hospital versus a statewide intervention with higher fidelity to reality with respect to patient movement. The next step is to conduct experiments based on policy interventions. Numerous prevention strategies have been suggested by healthcare experts which includes recognizing CRE cases by improving surveillance (Gupta et al., 2011). Since these interventions are expensive to implement, simulation studies can help test and determine the relative feasibility and cost-effectiveness of these interventions.

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