ON CALIBRATING A MICROSIMULATION OF PATIENT MOVEMENT THROUGH A HEALTHCARE NETWORK

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ABSTRACT

Hospital admission and discharge dynamics facilitate pathogen transmission among individuals in communities, hospitals, nursing homes, and other healthcare facilities. We developed a microsimulation to simulate this movement, as patients are at increased risk for healthcare-associated infections, antibiotic exposure, and other health complications while admitted to healthcare facilities. Patients can also serve as a source of infection throughout the healthcare network as they move locations. This microsimulation is a base model that can be enhanced with various disease-specific agent-based health modules. We calibrated the model to simulate patient movement in North Carolina, where over 1 million hospital admissions occur annually. Each patient originated from a unique starting location and eventually transferred to another healthcare facility or returned home. Here, we describe our calibration efforts to ensure an accurate patient flow and discuss the necessary steps to replicate this model for other healthcare networks.

1 INTRODUCTION

Healthcare-associated infections (HAIs), infections patients can get while admitted to hospitals and other healthcare facilities, are a major patient safety concern and are costly to the healthcare system (Walters and Zuckerbraun (2014), Centers for Disease Control and Prevention (2011), Office of Disease Prevention and Health Promotion (2014)). Underlying conditions and their treatments, including the use of some antibiotics, can put individuals at increased risk for HAIs (World Health Organization (2011)). Previously, researchers have used system dynamic models (Durham et al. 2016) and agent-based simulations (Toth et al. 2017) to model HAI transmission within healthcare network settings. However, efforts to calibrate transmission using real, patient-level movement data from a healthcare network have not been reported. To assess the impact of HAI prevention interventions, we developed a geospatially explicit agent-based model (ABM) to simulate patient movement and HAI incidence in the regional healthcare network of UNC Health Care in North Carolina (Rhea et al. 2019). Specifically, we demonstrated the use of a *Clostridioides difficile* infection (CDI) health module, including antibiotic use, to explore the risk of CDI, currently the most common HAI in the United States. In this paper, we describe how we calibrated the location module of the ABM. This included adding parameters to achieve the desired patient movement based on a compartmental flow model. We will also discuss how this process could be used to calibrate agent movement for other networks or systems.

1.1 Model Basics

The location model consists of agents and their movement. Agents can exist at any location within the model and only have one opportunity each day to move to a new location. As we are currently modeling movement to and from facilities within a healthcare network, most agents are considered to be at home and do not move often. Specific model locations are discussed in section 3.

Modeling patient movement is essential to address several issues faced when employing a HAI microsimulation. For example, our microsimulation models patient length of stay, hospital stay history, and patient movement between facilities to achieve accurate totals for patient movement for each location. The model tracks which agents are in each facility on any given day. This allows us to model HAIs with disease transition probabilities that depend on the number of infected patients located at each facility. Using a microsimulation for location movement provides a daily granularity and a detailed individual agent history not available when using a compartmental or systems dynamics model. The biggest potential for impact when using our model is to pair it with a disease transition model, as previously described (Rhea et al. 2019).

2 MODEL AGENTS

To accurately calibrate patient movement, we used a previously-developed synthetic population (Wheaton et al. 2009) to represent the people who could be admitted to a hospital. This synthetic population, which represents people and household records for the entire United States, statistically matches the US population at the US Census block group level and has been used in previous agent-based simulations (Rogers et al. (2014), Cajka et al. (2010)). For this calibration, we used the North Carolina (NC) portion of the synthetic population, based on the 2013 US Census data, to create agents. All agents in our model contain the following characteristics:

- County: 100 NC counties
- Sex: male, female
- Age: 0-50, 50-65, 65+
- Race: white, black, other

2.1 Creating Enough Agents

The NC 2013 synthetic population consists of 9,256,781 person records. However, 29 of the 1,800 (3 ages, 3 races, 2 genders, and 100 counties: 3 * 3 * 2 * 100 = 1,800) possible demographic combinations of county, sex, age, and race were not represented in the NC 2013 synthetic population, likely due to the US Census limiting information available for demographic combinations with a low count of individuals. It was necessary that all demographic combinations be represented in the synthetic population, as this provides the means to apply patient characteristics to agents based on available hospital discharge data (UNC Sheps Center data (2015)). To ensure that all possibly demographic combinations were included, we randomly generated up to three agents for any demographic combination that had less than three agents. This action resulted in an additional 108 agents, a small number of agents which should not impact our simulation results (Jovanovic and Levy 1997).

We updated the NC 2013 synthetic population to more accurately represent the actual 2015 NC population, based on the 2015 US Census estimate of 10,042,802 persons. This was necessary to ensure that our microsimulation would have enough agents to match patient movement using the available hospital discharge data, which was also from 2015. We created an additional 785,913 agents by randomly duplicating individuals from the existing population. Since we are currently using an agent's home location only for their home county, adding duplicate agents with duplicate home locations does not impact the movement in our model. The result is a pool of agents that is equal to the estimated NC population in 2015.

3 HEALTHCARE NETWORK

We developed the microsimulation based on the regional healthcare network of UNC Health Care with 14 possible locations for each agent. In the model, this regional healthcare network consists of 10 UNC Health Care-affiliated short-term acute care hospitals (STACHs), representing 10 of the 14 possible locations (nodes). All other NC STACHs (N=103 facilities) not associated with UNC Health Care were combined in our model to form a single location node (i.e. non-UNC STACHs).

The last three location nodes for the microsimulation are large nodes representing categories of locations: nursing homes (NHs), long-term acute care hospitals (LTACHs), and the community. All agents who are not in a healthcare facility are in the community. This created a total of five location types.

- Community
- UNC STACHS (10 UNC Health Care STACHs)
- Non-UNC STACHS (all other NC STACHs)
- LTACHs
- NHs

3.1 Community Movement

All agents are initialized with a *community-to-facility* probability based on their demographic characteristics (Rhea et al. 2019). Each day, the model simulates agent movement from the community using these probabilities. If an agent is randomly chosen to leave the community (based on this probability), agents move to a new facility based on probabilities of movement associated with their demographic data.

When agents are initialized, if their initial location is the community, we precompute the day that the agent will move locations for the first time. This process improves model efficiency and speed. The community-to-facility probabilities are relatively low and most agents (>90%) do not leave the community within the first year. Therefore, our model automatically skips these agents, who are predetermined to not leave the community, when assessing agent movement. These agents remain in the model and can interact with other community agents if an agent-based health module is appended to the microsimulation.

3.2 Facility Movement and Agent Initialization

Patient movement once in a healthcare facility is based on that facility and the patients demographics. The LOS and base transition probabilities are unique to each facility (Rhea et al. 2019). Along with these base transition probabilities, we made the following simplifying assumptions to help aid agent movement:

- Agents < 65 years old cannot go to an NH
- The only path to an LTACH is through an STACH
- 80% of patients moving to an STACH from a NH will return to the NH (Toth et al. 2017)
- Agents must change facilities when their LOS ends
- Non-UNC to non-UNC movement is possible; we assume a patient moved to a different non-UNC STACH

3.3 Long-Term Acute Care Hospitals

Patients leaving LTACHs will move to a new facility based on the following distribution: 47% go home, 7.1% go to an STACH, 44.9% go to a NH, and 1% will die (Toth et al. 2017).

3.4 Nursing Home

Of those leaving an NH, 25% return to the community, and 75% move to an STACH (DHHS 2013).

3.5 Initializing Starting Locations for Agents

We appended an initial location to the NC synthetic population to represent the starting location of each agent (Rhea et al. 2019). Agents can start in any of the 14 nodes described in section 3. The initiation totals are as follows:

- UNC: 2,371
- Non-UNC: 15,621
- LTACH: 301
- NH: 36,000

4   CALIBRATING PATIENT MOVEMENT

We calibrated patient movement because we are combining several sources of input data, across multiple years, and are using parameters from state and national findings. After creating the initial transition probabilities from available data, we used a compartmental flow calculation to evaluate the movement percentages obtained from the model output (Table 3). For the tables below, let UNC represent the 10 UNC Health Care STACHs, and non-UNC represent all other NC STACHs. At the community level, this calculation consists of the following steps:

- Assume all agents are in the community and calculate population totals by county, sex, age, and race (1,800 total combinations)
- Multiply each group population value by the probability an individual with those characteristics leaves the community on any given day
- Multiply these totals by the chance an individual has of going to each location type
- Sum the totals for each location and calculate movement percentages

These steps create the following tables for each demographic combination:

Table 1: Population and Daily Probability for One Demographic Combination.

Item	Value
County	Alamance
Gender	Female
Age	<50
Race	White
Population	34,465
Daily Probability	.000836
Daily Movement (number of patients)	28.8055

Table 2: Total Movement by Location Type for Table 1.

Facility Type	Probability	Daily Movement
Community	0	0
UNC	.1886	5.4321
non-UNC	.811423	23.3735
LTACH	0	0
NH	0	0

We use the following to calculate the number of individuals going from the community to each facility type, c_f, each day:

$$c_f = \sum_{i=1}^{1800} P_i * dp_i * cfp_i, \tag{1}$$

where i is the demographic type, P_i is the population, dp_i is the daily probability of leaving the community, and cfp_i is the probability of going from the community to that location type. These totals can be used to calculate the percent of patients that leave the community and go to each facility.

Community movement calibration was straight-forward. As the community has such a large base, it is not necessary to determine where an agent was before arriving in the community. For all heathcare facilities, however, patients must have come into that facility from some other location. We made simplifying assumptions to help this calibration process. For STACHs and NHs, we assumed patients came from the community. For LTACHs, we assumed the patients came from an STACH, and that those STACH patients came from the community. Using these assumptions, we calculated movement to and from each location with the following:

$$unc_f, non\_unc_f, nh_f = \sum_{i=1}^{1800} P_i * dp_i * cfp_i * f_1 f_2 p_i \tag{2}$$

$$ltach_f = \sum_{i=1}^{1800} P_i * dp_i * (cfp(non\_unc)_i + cfp(unc)_i) * f_1 f_2 p_i \tag{3}$$

where $f_1 f_2 p_i$ is the probability of moving from the current facility type to the new facility type. After these calculations, we have estimates for which percent of patients leaving each location will end up in the other location types.

Table 3: Compartmental Percentages for Patient Movement.

From Location	To: Community	To: UNC	To: non-UNC	To: LTACH	To: NH
Community	0%	12.34%	87.03%	0%	0.62%
UNC	88.08%	1.40%	1.86%	0.32%	8.34%
non-UNC	88.05%	0.26%	3.01%	0.32%	8.33%
LTACH	77.93%	0.88%	6.22%	0%	14.97%
NH	25%	9.32%	65.68%	0%	0%

Table 4: Overall Target Percentages for Patient Movement.

From Location	To: Community	To: UNC	To: non-UNC	To: LTACH	To: NH
Community	0%	13.41%	85.97%	0%	0.62%
UNC	90.62%	3.20%	4.13%	0.34%	1.61%
non-UNC	90.68%	0.59%	6.64%	0.34%	1.61%
LTACH	47.47%	0.89%	6.22%	0%	45.35%
NH	25%	9.32%	65.68%	0%	0%

The largest difference between the compartmental percentages, Table 3, and the overall target percentages, Table 4, are highlighted in grey. Note that the target percentages for Table 4 were computed using a combination of UNC de-identified patient-level hospital discharge data (July 1, 2016-June 30, 2017), the LTACH discharge distribution (Toth et al. 2017), and the nursing home discharge distribution (DHHS 2013). Although Table 3 and Table 4 should have lined-up without calibration, there are several reasons

why they are different. The UNC patient-level data is only available for 7 of the 10 UNC system hospitals, forcing us to make assumptions about the remaining 3 hospitals that data was not available for. The non-UNC STACHs only had data available at an aggregate level, not broken down by the demographics used for UNC STACHs. And finally, most of the aggregated LTACH and NH data were not specific to NC. For example, the LTACH discharge distributions (Toth et al. 2017) were from a single study and North Carolina's LTACHs are different in size, location, and patient population.

4.1 Adjusting Model Input

The input data that controls agent-movement is a 25,200 (14 facilities x 2 sexes x 3 races x 3 age groups x 100 counties) by 19 (current facility, sex, race, age group, county, and 14 possible destinations) lookup table that contains the probabilities of moving from one facility to another based on an agent's demographics. In order to calibrate to Table 4, we adjusted transition probabilities in this lookup table until our compartmental flow model matched our target percentages. Each location was treated slightly differently, as described below.

4.1.1 The Community

Following the steps described in section 4 for the community, we obtained the following table:

Table 5: Calibrating Community Movement.

To Location	Daily Movement	Percent	Target Value	Target Percent
Community	0	0%	0	0%
UNC	1,806.67	12.34%	1,962.2	13.41%
non-UNC	12,738.82	87.03%	12,583.27	85.97%
LTACH	0	0%	0	0%
NH	91.20	0.62%	91.198	0.62%

Target Percent in Table 5 was multiplied by the sum of the *Daily Movement* column to determine the *Target Value*. For this particular target, we are not moving enough patients from the community to UNC STACHs. We adjusted this by slowly increasing the probability of moving from the community to a UNC STACH for all demographic combinations until the percent and target percent were within 0.1%. The remaining facilities (non-UNC, LTACH, and NH) were then reduced by the same percentage, such that each group's percentages add to 100%. We repeat this process for the other locations, as needed, keeping the community to UNC STACH probabilities constant because they have already been updated.

4.1.2 Other Facilities

Calibrating facility specific movement is similar to calibrating the community movement. However, in some cases additional steps must be considered. For example, consider the UNC calibration values:

Table 6: Calibrating Movement from UNC STACHs.

To Location	Current Value	Percent	Target Value	Target Percent
Community	1591.32	88.08%	1655.53	92.64%
UNC	25.34	1.40%	58.40	3.23%
non-UNC	33.52	1.86%	77.21	4.27%
LTACH	5.85	0.32%	6.23	0.35%
NH	150.64	8.34%	9.29	0.51%

The *Target Percent* in Table 6 does not match the overall target percentages from Table 4 because we made the simplifying assumption that 80% of patients moving to an STACH from a NH will return to the

NH. This is a forced movement in the model, and the model input data has not been updated to reflect this. The calibration process we implement here accounts for this forced patient movement and is why the naturally-occurring UNC STACH to NH percentages are lower than the overall targets. The target percent in Table 6 was corrected to reflect that our model will automatically move some patients from an STACH to a NH.

Each facility had minor similar minor corrections. For example, as hospital patients being automatically returned to NHs if they were originally from an NH. However, each location type followed a similar process for calibration.

4.2 Agent Death

Currently, agent death does not play a large role in results of a model run. However, when modeling certain HAIs, death due to these infections might be more relevant than all-cause death. However, we still incorporated all-cause death in our mode, paying particular attention to agents dying outside of the community (Rhea et al. 2019).

5 MODEL RESULTS

On average across the 15 model runs, there were almost 970,000 total hospitals visits.

Table 7: Agent Movement Totals for One Model Run.

From Location	To: Community	To: UNC	To: non-UNC	To: LTACH	To: NH
Community	0	121,157 ± 384	774,021 ± 993	0	5,913 ± 62
UNC	117,784 ± 321	3,728 ± 64	5,491 ± 72	430 ± 18	1,643 ± 37
non-UNC	758,783 ± 1,078	4,662 ± 52	56,790 ± 255	2,831 ± 47	10,946 ± 103
LTACH	1,615 ± 31	25 ± 5	181 ± 12	0	1,283 ± 103
NH	3,884 ± 68	1,324 ± 46	10,322 ± 115	0	0

Converting the totals in Table 7 to percentages by facility type will match the target percentages discussed in section 4. Throughout the model, the five facility types are generally at a steady state. The average number of people in each facility type is displayed below.

Table 8: Model Steady State Averages.

From Location	Target	Model Output
Community	9,983,084	9,981,076
UNC	2,371	1,740
non-UNC	15,621	11,813
LTACH	301	307
NH	36,000	36,244

The hospital totals are lower than expected, likely becuase we did not include newborns, which are approximately 10% of hospital stays (UNC Sheps Center data (2015)). We are accurately modeling the hospital length of stay and the number of hospital patients, which indicates that the targets for UNC and non-UNC might be too high.

6 MICROSIMULATION USE-CASES

Although our model is technically a microsimulation, as agents are independent and do not interact with each other, use-cases that include agent-interactions can be incorporated (e.g ABMs where agents interact at the same facility). The microsimulation can also be adapted to accommodate any number of facilities, facility connections, and patients. As detailed data become available for additional NC hospitals, updates

to the input transition files can also be incorporated. Similarly, if facility data were available for another state, or a sub-network of facilities, these data could be used to inform the model.

For example, the model can be used to assess the impact of limiting patient flow to a specific facility, limiting movement between facilities, and removing a facility from a network altogether. This could occur if a single STACH in the network partially closes and can only accept a fraction of all patients that arrive, while the remaining patients are diverted to other facilities.

This microsimulation serves as a framework for agent flow, which can provide public health and healthcare stakeholders with valuable information about patient movement throughout a healthcare network. However, within each agent, a natural history submodel can be implemented, providing the ability to study specific HAIs (Rhea et al. 2019). As a result, we can replicate the process of disease acquisition, spread, and recovery in a relatively realistic environmental setting. Model output can include incidence of infection at all location nodes. Through epidemiologic simulations, our model can be used to evaluate the impact of various infection prevention interventions on the incidence of HAIs. These interventions could include reduction in the use of antibiotics that increase the risk of acquiring some HAIs and early identification and isolation of asymptomatic colonized persons who could unknowing be spreading HAI pathogens. Results of these simulations could be used to inform public health and healthcare policy with regard to HAI prevention.

7 CONCLUSION

The creation of a calibrated, microsimulation of patient movement through a healthcare network allows researchers to explore patient flow, assess the risk of diseases, and to simulate interventions. Our micro-simulation framework is disease agnostic and can serve as a base model for disease-specific health modules. The location module itself is capable of simulating over 10 million synthetic agents in NC and producing over 1 million realistic hospital admissions. Using patient-level data, we can determine how long patients stay, and where patients move after their visit is completed.

When running disease-specific models, movement timing, length of stay, and the patients within each facility can effect disease transition. Our location model provides this background movement, keeping track of which agents are at each facility, allowing for increased granularity in a disease -specific state model.

8 ACKNOWLEDGMENTS

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