**Main Manuscript for**

Option 1: Quantifying likelihoods of detection and nosocomial transmission of pathogenic bacteria in hospital settings using patient records and culture data

Option 2: Hospital traffic and surveillance determine nosocomial transmission and likelihood of detection of pathogenic bacteria in hospital settings in New York City

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Main Text

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**Abstract (313/250 words)**

Antimicrobial-resistant organisms (AMROs) are a major threat to public health. These organisms increase mortality, hospital length of stay, and in consequence healthcare-associated costs. Information on AMRO carriage rates and transmission is limited. In this work, we leverage electronic health records from a major New York City hospital system collected during 2020-2021 to support simulation-based inference of likelihoods of detection upon testing and nosocomial transmission quantities for eight pathogens. We develop an agent-based model to simulate patient traffic at the ward facility level in the hospital system, and importation from the community, nosocomial transmission, and patient spontaneous decolonization of bacteria.. The model is coupled with a Bayesian inference data assimilation algorithm to estimate the likelihood of detection upon testing and nosocomial transmission rates. We evaluate parameter identifiability for this model-inference system and investigate if the source of bias in the inference is structural identifiability or the inherent stochasticity of the model. We applied the framework to estimate both quantities for seven prevalent microorganisms species: *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus* (both sensitive, MSSA, and resistant, MRSA, phenotypes), *Staphylococcus epidermidis*, *Enterococcus faecium* and *Enterococcus faecalis*. We found nosocomial transmission for *E. coli* is negligible. We found that *MSSA* has a lower nosocomial transmission rate than *MRSA.* We found the likelihood of detection for all microorganisms, except *E. coli,* were consistently between 0.5% and 3%. , except *E. coli,* were consistently between 0.5 and 3% and mean nosocomial transmission rates between 0.15 and 0.19. This work highlights how fine-scale patient data can support simulation-based inference of epidemiological properties of microorganisms and how hospital traffic, patient contact and surveillance determine epidemiological features. Finally, we show how the design of a detailed individual-level observational model does improve parameter identifiability, compared to a population-level observational model. Evaluation of the community prevalence and transmission potential for different pathogens could ultimately support the development of in-hospital control measures that limit the spread of these pathogens.

**Main Text**

**Introduction**

Antibiotic resistance microorganisms (ABRO) are a major threat to human health worldwide and has emerged as one of the leading public threats of the 21st century 1. An estimated 4.95 million deaths were associated with bacterial ABR in 2019 globally, and mortality caused by ABR is projected to reach 10 million by 2050 2, although more rigorous projections XXX. Hospital-acquired (nosocomial) infections by bacterial pathogens including those resistant to antibiotics some with enhanced features to facilitate host-to-host transmission and survive in the environment 1 and are a major contributor to mortality, length of stay in hospital and health-care associated costs 2. Understanding the burden and spread of ABR pathogens, and microorganisms in general, within hospital settings, is critical for effective control planning and design of testing/culture protocols; however, quantification of these characteristics remains challenging due to limited observation of microorganisms carriage, difficulty assessing interventions in real-world hospital settings, and incomplete understanding of the mechanisms shaping the coexistence (both within and between hosts) of different microbial species as well as same species antibiotic-resistant and antibiotic-sensitive microorganism in hospitals 3–5. It is well-recognized and assumed in modeling studies that between-host transmission is an important driver of the maintenance of resistance in hospitals and of microorganism circulation 6, among other routes of transmission, such as environmental and of health care worker mediated transmission 4,7–11, or in the case of resistant strains within the host processes, such as horizontal gene transfer (HGT) also referred to as endogenous transmission 12,13. These mechanisms are thought to be differential per microorganisms species, across body sites as suggested by Niche theory 14–16 and heterogeneous across geographical space, although some consistency in human prevalence is expected. For example, methicillin-resistant *Staphylococcus aureus* (MRSA) is known to have a unique geographical distribution classified principally by the complex clone(s) circulating 17,18, with human prevalences from 0.4% to 10%, but the general prevalence of *S. aureus* is consistently between 20% and 50%, depending on the body sites and populations considered 19–25.

To circumvent these difficulties, mathematical models have been applied to theoretically study pathogen transmission in hospital settings, to quantify and understand the relative roles of different routes of transmission 4 or to characterize the condition of the hospital settings to sustain transmission of both resistant and sensitive strains 26. In the context of ABR, theory has been used to understand the emergence of resistance and its interplay with community-acquired infections 1,2, to evaluate antibiotic treatment protocols 28, to assess control measures to reduce nosocomial transmission 26,29–32, and has been extended recently in pair with empirical observations to assess the role of competition of different strains at the between-host level and the role of within-host microbiome pathogen interactions 33.

, most existing modeling studies focus on general theoretical frameworks of ABR organisms 26–28,33–38 where empirical observations drive the modeling and provide insights on possible mechanisms behind transmission, co-existence and other processes in the hospital settings. However, for process-based models to be used as reliable tools for public health interrogation with data is essential 6. Investigations using simulation-based inference 39 tools usually rely on a single pathogen of interest such as (MRSA) 17,29,32,40, *P. aeuruginosa* 4*, C. difficil* 41*, Vancomycin-resistant enterococci* (VRE)42and used carriage detection 29,32,40,42, intensive care unit (ICU) clinical culture data 4,40 or incorporated sequencing data 41 to constrain the modeling exercises. Some of these studies are absent of interrogation about the structural identifiability of the system 1,2, some probably a consequence of designing individual-based models where the state space dimension is high and model-inference methods hard to interrogate within a mathematical framework. We suggest that investigations relying on simulation-based inference tools need to start including in their cookbook systematical assessment of the identifiability of the system, especially when relying on stochastic transmission models.

Studies on the epidemiological characteristics of multiple co-circulating organisms in a single hospital network supported by real-world data are absent. The epidemiology and transmission dynamics of healthcare-associated (HA) infections differ from community-acquired (CA) infections in a number of important ways. First, hospital networks are open systems with significant variations in the daily and weekly admission rate ranging from 23% to 52% (See Figure 1A), explained mostly by variations at the building scale in the hospital network with some ranging from 0-50% (See building traffic for Allen, Harkness Pavillion and Milstein hospitals in Supplementary Information Figure S1), and others with faster patient replacement between 80% to 150%, a consequence of admitting mostly outpatients (See Presbyterian hospital and Rest in SI Figure S1). This heterogeneity at the building scale is in turn explained by variation across the ward traffic composing each building (See SI Figure S2 ward traffic). Discharges or outflux of patients at ward facility scale follows similar patterns with some few wards per building admitting the majority of patients per week and with stable patient traffic (See Figure 1A and SI Figure S2). This heterogeneity in admissions and hospitalizations is principally dictated by ward size that was also variable at the building scale (See SI Figure S3 for ward size distribution and SI Figure S4 for the linear relationship). . In contrast, communities are closed systems with individuals moving in or out at much lower rates. Second, as many bacterial species exist as commensals on the human hosts' detection of colonization is difficult and differential by body site. Indeed, patients with infections of the bloodstream or lower respiratory tract are more likely to be detected in hospitals than those colonized at other sites 27,44. Third, facilities within a single hospital system (e.g., infusion, pediatric, emergency wards, surgical, among others) may differ substantially in their control and detection of microorganisms as well as in the hospital traffic features, a complication compounded by patient transfers between wards and hospital buildings (see SI Figure S5 for the patient transfer matrix at both spatial scales) 45,46. Fourth, a lack of observational data for communities of microorganisms spreading among patients and the environment in the same hospital system often imposes further challenges in comparing its epidemiological features. Lastly, the emergence of strains that were once confined to hospital circulation such as CA-MRSA clone-USA300 in the United States with enhanced features compared to HA-MRSA contributes to its success as a pathogen and tide up the HA-CA dynamical outcomes 1,2.

In this study, we use a process agent-based model (ABM) and patient clinical culture data for seven prevalent pathogenic bacterial species collected in a major New York City (NYC) hospital system to address these challenges. The ABM is informed by real-world patient movement in the hospital system and incorporates importation of microorganisms from the community, nosocomial transmission, patient transfer across hospital wards and decolonization via host clearance. To account for the heterogeneity of testing frequency and microorganism prevalence among facilities, we used clinical testing records to design a patient-level observational model that mimics the detection of microorganisms in hospitals. Assuming human prevalences of bacteria across humans are consistent we fixed the importation rates surveying the literature and estimated nosocomial transmission and the likelihood of detection given carriage upon testing.

We couple the ABM with a Bayesian inference algorithm, validate the system against using simulated data and estimate the likelihood of detection given carriage and nosocomial transmission rates for the eight microorganisms, which cause substantial mortality associated with AMR worldwide 2.

We explore whether bias in the inferences was inherent to structural identifiability 43 or caused by Monte Carlo error 47. We use 3 different values for the importation rates to both account for the uncertainty in prevalence and to study the sensitivity of the model-inference construct to this parameter.

**Results**

### *Empirical patterns and heterogeneity of nosocomial infections burden*

In Figure 1A, we plot weekly incidence color-coded by building for *E. coli* (total positives cultures, n=), *K. pneumoniae* (n=), *P. aeruginosa* (n=), MSSA (n=), MRSA (n=), *S. epidermidis* (n=), *E. faecalis* (n=) and *E. faecium (n=)* . We deduplicated multiple positives results during a patient visit, and consistently deduplicated them in the observational model. During the study period, the daily number of hospitalized patients fluctuated between 1,000 and 2,500 with most of the variation explained by differences in the day of the week (See solid line for daily and dashed line for weekly in Figure 1B). Daily numbers of new admissions ranged between 100 and 1,000, including outpatients. During the first COVID-19 wave in New York City, the numbers of in-patients and admissions were generally lower; after June 2020, patient traffic was higher and relatively stationary. Ward size, defined as the average occupancy per day during the study period, was heterogeneous (SI Figure S4) with the majority of wards experiencing an occupancy below 10 patients. However, a few wards (e.g., emergency rooms) could admit over 100 patients each day. Average ward size was 9 considering all the wards and 20 excluding wards with ward size equal to 1. To visualize patient traffic within each ward, we investigated temporal occupancy. Fig 1C shows the weekly number of patients relative to average occupancy for each ward and highlights the 5 most and least populated wards (see red and blue lines respectively); we only included wards with sizes greater than one for better visualization. The least populated wards were empty most of the time with irregular occupancy during the study period, whereas hospitalizations in the most populated wards were relatively stable. The relationship between newly admitted and hospitalized patients (Figures 1D and 1E) was linear and depended on ward size (see SI Figure S3). Clinical culture numbers were also heterogeneous across wards. Most cultures were sampled from a small subset of wards, as shown by the weekly number of cultures collected in each (see Fig. 1D).

The process model, as is an ABM, tracks the state of patients at daily time scales. Patients were either susceptible to colonization or carriers with a microorganism (See *The transmission model* in Methods). The observational model designed at the individual level allows us to map from the carriers to detected individuals via a simulated clinical culture. We parametrize the patient observational model with a likelihood of detection given carriage upon testing - (See *The individual observational model* inMethods). Data assimilation is conducted at the building level therefore we consistently aggregate simulated patient detections at this scale. Weekly and monthly incidences of positive cultures for each building are shown in Fig 1A, faded and strong solid lines respectively. We subsequently used these six building time series to perform parameter estimation.

### *Microoganism prevalence*

### We searched the literature to set the importation rate of each microorganism as a proxy of the community prevalence. Our search terms included 'prevalence', 'colonization', 'carriage rate', and used reviews for some of the microparasites that reported pooled estimates across different geographical locations. In the Supplementary Information section *Prevalence estimates* we included the different values, sources, and a small description of the study, with the geographical location and population of interest; in Table 1 we consigned a resume with the values.

### *Identifiability: synthetic simulations and inference*

To investigate the identifiability of the model-inference system, we explored inference on a simulated trajectory with known parameters. We investigated if the model inference is capable of recovering parameters fixing the importation rate to 25% and 50%, and varying the likelihood of detection upon testing and the nosocomial transmission rate uniformly covering the prior range, but without forcing the simulated carriage detection to match the observed one (Figure 1A), see SI section *Model inference framework* . The posterior parameter estimates of the inference consistently capture the true parameter values for both detection rates and nosocomial transmission rates (See Figure 2A and 2B for equal to 25 and 50% respectively). In Figure 2 we show first how the model inference is able to explore different regions of the prior range (limits of each axis), and second how the posterior captures the true parameter values. Inferences with were more biased and less sharp than inferences with , although both estimates gravitate towards the truth and only in two instances it's substantially biased, see scenarios 2 and 4 in Figure 2. We visually inspected if the marginal posterior is asymptotically reaching the true parameter values as the inference algorithm advance see SI Figure S6A and S6B.

We studied the well-posedness of the inverse problem, see Chapter 7 of 48. Inference is conducted on a single trajectory of the stochastic process, we investigated if the stochasticity has a substantial effect on the posterior inference (also referred to as Monte Carlo error). Guided by numerical results SI Figure S7A shows the goodness-of-fit can be linearly predicted by how probable the observation used to conduct inference was (Methods). This was also a function of with showing a poorer goodness-of-fit, a product of wider and slightly more biases posteriors, than for a more common inferred time series but a less pronounced relationship with the probability of observing the time series used for inference (slopes of purple line and red line respectively in SI Figure S7A). When controlled by the Monte Carlo error (see *Making sense of the bias* in Methods) we found that the goodness-of-fit decreased exponentially with the oddness of the inferred simulated nosocomial data, and it's not substantially impacted by (See SI Figure S7B).

We ran ensemble simulations with the posterior parameter estimate and compared them to the ensemble simulations with the true parameters, highlighting the observation used to conduct inference and the mean across the ensembles (See SI Figure S8A and S8B, for respectively) and found that qualitatively even biased inferences (scenario 2 and 4 in Figure 2) reproduced well both the true ensemble simulations and the nosocomial infection data used to conduct inference. We quantified the calibration displaying the reliability plot (cite) of both the posterior and truth ensemble simulation with the inferred time-series (see SI Figure S9A and S9B, for respectively) and finish this.

Last approach showed the performance of the model inference to solve the inverse problem in different regions of the prior range. We also study it's ability in parameter combinations that reproduced the microorganism's nosocomial infection data at the hospital level (aggregation across buildings of time series shown in Figure 1A). We used the middle prevalence of each bacterial microorganism reported in Table 1, see Methods for further details on the 9 scenarios selected for each pathogenic bacteria. SI Figure S10 shows the posterior estimates for each microorganism, note that the values of the parameters in the 9 scenarios for each pathogen are very similar. We found the model-inference system is able to discriminate between the scenarios. This analysis covers a broad range of prevalences from 'low' to 'high' importation rates ; 4% and 16% for *MRSA* and *K. pneumoniae* to 50% and 70% for *E. faecium* and *E. coli* respectively.

### *Individual vs 'population'-level observational model*

We designed the observational model at the patient level making use of the richness of the dataset available and the fact that we designed a process ABM. However nosocomial infection data was assimilated at the building scale. We investigate the benefits of this approach compared to a more common 'population'-level observational model (see *The population observational model* in Methods). We used the same settings of simulated nosocomial infections detections described in the previous section, we set equal to 25 and 50% and varied the detection rate and the nosocomial transmission rate . Note the meaning of the parameter in the observational model and in the individual and population level observational model respectively is different (see Methods). SI Figure S11 shows the joint posterior parameter estimate (same as Figure 2 but for the population-level observational model) we found inferences were in general more biased and much less sharp compared to ones obtained in Figure 2, with the individual-level observational model. We also visually inspected the convergence plots (SI Figure S12) and found that the marginal posteriors are not consistently getting sharper as the algorithm advance (Methods), this lack of identifiability is magnified when compared to the convergence plots of the individual observational model (SI Figure S6).

### *Inference using real data*

We applied the model-inference system to estimate the epidemiological quantities of interest for eight different microbial bacterial pathogens. Joint posterior estimates of the likelihood of detection given carriage upon testing and nosocomial transmission rate are compared in Figure 3A, we displayed the posterior for the different values of color-coded and indicated in the legend of each subplot (Table 1). Species are sorted from the most abundant (*E. coli*) to the least (*E. faecium*) from left to right (see previous section *Empirical patterns and heterogeneity of microorganism burden* for the total numbers). We plotted the posterior estimates in the bigger plot in each subplot to show how for most species (except *MRSA*) the system is able to localize the posterior in the same region of the prior range (limits of each axis). We also plotted a zoomed version inside each subplot to highlight that the posterior inference is sensible to , i.e. both the mean (intersection of dashed lines) and the posterior estimate change (note that zoomed plots have different ranges in each axis). We found *E. coli* mean nosocomial transmission rates was the lowest across the bacterial species with mean estimates of 2.54e-3, 8.66e-4, and 9.62e-4 and the highest mean likelihoods of detection of 18.53, 18.63%, and 17.31% for community prevalences of 55%, 63% and 70% respectively (see Table 2 for confidence intervals). *E. coli* was followed by *MSSA* with mean nosocomial transmission rates of 0.141, 0.121, and 0.0994 and likelihoods of detection of 1.63%, 1.65%, and 1.58% for prevalence of 25%, 29% and 35% respectively (Table 2 for 95% CI). For the rest of the microorganisms, except *MRSA* and *E. faecalis*, we found that mean nosocomial transmission rate estimates were consistently between 0.17 and 0.19, and likelihoods of detection upon testing between 0.5% (*E. faecium)* to 2.5% (*K. pneumoniae*). Likelihoods of detection upon testing estimates match in order the abundance of bacteria but nosocomial transmission does not. For *MRSA* we found that the model inference system found two solutions, function of the value of , two with high and low for equal to 5 and 10%, and for the lowest community prevalence of 3.9% we found nosocomial transmission rate was 0.0017 and likelihood of detection upon testing was 17.15%. These results suggest that for low community prevalence there is a bifurcation in the ABM. We compiled the mean posterior estimates and 95% CI for the different values of in Table 2.

To assess the goodness-of-fit of the modeled nosocomial infection to the observed one, we simulated the dynamics using the posterior estimates of parameters and found that simulated detected nosocomial infections span the observed numbers at the hospital and building level (Figure 4A and Figure S13). We also produced reliability plots to examine whether the uncertainty in the observed data can be reproduced by model simulations (Methods). We found that the coverage of simulated CIs is slightly below expected values (under the diagonal line), indicating an uncertainty level biased low (Fig. 4B). The model simulations allow estimation of the relative contributions of importation and nosocomial transmission to the overall burden of different bacterial pathogens as well as the prevalence in the hospital.

**Discussion**

Transmission is a fundamental property that governs epidemiological dynamics and is also a step in the life cycle of bacterial pathogens 49. It is also one of the most challenging processes to understand and quantify. Estimating this property could improve understanding of the mechanism behind the risk of contagion and ultimately support improved control in healthcare systems. Nosocomial infection data have been the usual measure used to approximate and infer transmission, however it represents multiple synergies of the surveillance system. Surveillance of microorganism circulation in clinics is a product of patients that are being screened (P(culture | non-infected)) at the discretion of the clinicians and patients that present symptoms because are infected and therefore searched for pathogens (P(culture | infected)).

In this study, we used a simulation-based inference method to estimate nosocomial transmission rate to absorb the transmission process, and likelihood of detection upon testing to encapsulate surveillance in the hospital. We built the process model to evolve patient states at daily time scales and informed it with patient hospitalization records. We parametrized the risk of acquiring bacteria proportional to a nosocomial transmission rate , and the fraction of carriers an individual was contacted during the day. We designed an individual-level observational model to quantify the likelihood of detection upon testing . We assumed community-acquired carriage was at a steady state and in consequence parametrized the probability of importing a microorganism from the community or . Epidemiological observational studies show consistency in the range of human prevalences reported for each bacterial microorganism (Table 1 and SI section *prevalence estimates*), other studies have also pointed at this stability in prevalence for resistant strains of *S. pneumoniae*, and *S. aureus* 1. Ecological theory has suggested mechanistic principles should determine population density (cite), we argue that those mechanisms can also be thought to determine population density in communities of microorganisms inhabiting different body sites in humans. Armed with these experimental and theoretical arguments we set for each microorganism and studied the sensitivity of the inference to different values of this parameter taken from the observational studies.

We assumed the decolonization rate was constant for all microorganisms, however is known for example that *S. pneumoniae* bacterial clearances are strain dependent 1. Host clearance rates for the bacteria studied in this work are reported between 5 months to 2 years 1,2 (cite Cooper, Sen, K pneumoniae and *E coli*). We derived a mathematical expression based on the mean-field approximation of the system and showed that the system is not sensitive to the value for the decolonization rate given the fast replacement of patients in the hospital system. Specifically, we computed the basic reproductive number , and found is the product between the nosocomial transmission rate and the average duration of a carrier inside the hospital, the inverse of the discharge rate plus the clearance rate (SI section *The ordinary differential equation*). In SI Figure S14 we plotted the distribution of discharge rates at hospital and building level and in SI Figure S15 the distribution of time in hospital obtained from the patient records, in average a person spent 3.85 days in the hospital, and 3.17, 4.18, 6.22, 5.05, 1.25 and 1.85 days in Allen Hospital, Harkness Pavilion, Milstein Hospital, Mschony, Presbyterian Hospital and Rest respectively. There is at least one order of magnitude of difference between the discharge rate and the clearance rate and therefore .

The record of observed nosocomial infection (Figure 1A) is a stochastic realization among an ensemble of possible outcomes of an underlying stochastic process. In order to evaluate the ability of the system to infer key epidemiological parameters we studied how the oddness of the observation used to conduct inference, aggregated weekly incident nosocomial infection data, and as demonstrated in the previous experiments it impacts the inference of epidemiological parameters but in general good inferences are made. We applied the model inferences to estimate the epidemiological properties of eight co-circulating bacterial pathogens. We found that hospital traffic, patient contact network and surveillance of microorganism in hospitals appears to dictate the epidemiological features of most of the co-circulating bacteria. Mean nosocomial transmission rates of all pathogens except *E. coli* and *MSSA* were consistently between 0.15 and 0.19 and likelihood of detection given carriage from 0.57% to 2.51%. We found that while *E. coli* has the highest likelihood of detection (mean estimates from 17.31% to 18.53%), it has the lowest nosocomial transmission rate almost negligible suggesting that most nosocomial infections can be associated with infections with host commensal strains that do not contribute to transmission, which has been reported empirically 50.

We found nosocomial transmission rates of *S. aureus* phenotypes were different, suggesting a difference in the fitness of the two strains. It has been assumed principally in modeling studies that resistance generates a decrease in fitness with respect to the sensitive strain, making it less transmissible 1,5,26,34,36. The emergence of CA-MRSA with an equal level of resistance as HA-MRSA without an observed compromise in fitness 44 violates this assumption. We found *MSSA* has a lower nosocomial transmission rate than *MRSA*. A simple model of competition between resistant and sensitive strains would predict that as the ratio between nosocomial transmissions between strains the resistant strain should outcompete the sensitive strains 38,51 that is not the case observed empirically (Figure 1A). Split into resistant and sensitive phenotypes could possibly be the most important categorization clinically 52 however is agnostic to the number of resistant genes carried by each. Within-host dynamics between these two 5,52 including an accurate representation of the levels of resistance in each, loss and gain of resistance genes through means of HGT, and interactions between CA-MRSA and HA-MRSA strains 36,44 intertwined by the fast dynamical nature of hospital traffic could help to understand estimated differences in the nosocomial transmission rates and ultimately be a more accurate representation of the processes shaping the co-existence of *S. aureus* strains in the hospital. *S. aureus* and *S. epidermis* inhabit the nasal nares as commensal, these overlap in their ecological niche produce negative feedback between the population dynamics within the host ('competitive release') of both species (cite) and possibly ramify up to hospital-level dynamics of these two. Lastly, polymicrobial infections with *P. aeruginosa* and *S. aureus* are considered to be harmful to their host resulting in worst healthcare outcomes. In turn, *in-vitro* experiments have shown that *P. aeruginosa* outcompetes *S. aureus* possibly modulating the individual risk of contagion as well as hospital-level observed carriage of each 53.

We used an individual-based computational model to enrich the dynamical representation of patient movement across the hospital network using patient records in a major New York City hospital network. The ABM captures multiple sources of heterogeneity (e.g., patient length of stay, contact patterns, individual observational model, etc.) that otherwise cannot be represented by compartmental models but we sacrifice an accurate representation of the underlying biological details making each microparasitic infection unique. Our aim was, in consequence, to understand the general similarities and provide a first attempt to quantify the epidemiological properties of communities of circulating bacteria among patients in hospitals. We show that while bacterial species have different levels of importation rates nosocomial transmission rate across species was similar suggesting similar modes of transmission for all. We were able to accurately reproduce the observed nosocomial infection data across the hospital and building levels. Our model absorbs both direct and indirect modes of transmission in the same parameter . Fast dynamics of patient traffic and replacement of patients within daily to weekly timescales points to transmission possibly dominated by indirect modes of transmission, that do not depend on host-to-host contact, especially environmental or fomite as well as HCW-mediated transmission 1–7. In fact, the Center for Disease Control and Prevention (CDC) healthcare infection control webpage 55,56 highlights the environment, surfaces and devices, as a common reservoir of germs in healthcare places and hand washing, cleaning and disinfection of shared medical devices as important control measures to diminish the risk of contagion. How does fomite transmission impact nosocomial transmission? (linearly or non-linearly) and the timescales of bacterial clearance rates (survival times) in the environment will also be relevant questions to ask and where data-driven modeling could substantially contribute, by its power to explore a wide range of functional forms between fomite and nosocomial transmission. Other limitations of the current study include the absence of information on the demographics, age profiles and co-morbidities of patients in the hospital network that are known to have differential susceptibility to bacterial acquisition and infection (cite), which we therefore do not model.

Further, the current work exploits the availability of individual-level patient records to estimate the transmission properties of pathogenic bacteria in hospital settings. Individual-level data and models can be employed in future research to understand the impact of individual-level interventions on disease control, as the ones highlighted by the CDC. An example might be to test counterfactual scenarios of individual-level interventions that replace infections caused by resistant strains with infections caused by sensitive strains in order to quantify the impact of resistance at the hospital level 1.

**Materials and Methods**

### *Overview*

To estimate key epidemiological characteristics of AMROs, we developed an ABM to simulate the dynamics of these organisms in hospital settings. The model was informed by patient hospitalization and culture data from electronic healthcare records collected between February 1 2020 and February 28 2021. We coupled the ABM with a Bayesian inference algorithm and, using simulated outbreaks, validated the ability of this ABM inference system to identify importation and nosocomial transmission rates. We then assimilated the real-world lab-confirmed positive case data and estimated the importation and nosocomial transmission rates for eight co-circulating organisms. Using these estimated parameters and the ABM, we were able to reproduce the time series of positive cases for six clusters of wards in the hospital system. The estimated importation rates and nosocomial transmission rates were compared for the eight organisms.

### *Data*

Data for this study derives from 3 hospitals of a Northern Manhattan Hospital System, including a quaternary care center, pediatric hospital, and community hospital. The hospitals contain 221 wards of different types including emergency, infusion, cardiology, pediatrics, etc. Hospitalization and clinical culture data were collected during the study period from February 1 2020 to February 28 2021. The hospitalization data include admission, discharge, and transfer of patients within the hospital system. The dates and wards in which each patient stayed during hospitalization were used to construct a time-evolving contact network. Clinical culture records were available for the eight most prevalent organisms in the hospital system: *Eschericia coli*, *K. pneumoniae* *Pseudomonas aeruginosa*, methicillin-susceptible *S. aureus* (MSSA), MRSA, *Staphylococcus epidermidis*, *Enterococcus faecalis* and *Enterococcus faecium*. The date and patient associated with each test were used to inform the observation model (see Methods below). We plotted the number of tests across the 3 hospitals and it's buildings (Figure S1) and in the wards in each hospital (Figure S12), which show a similar order in cultures across the hospital but substantial heterogeneity inside the hospital at the ward scale.

### *The transmission model*

We used an ABM to simulate transmission in the study hospital system 1. For the ABM, the patient-to-patient daily contact networks were constructed using hospitalization records. Two patients staying in the same ward on the same day were connected in the contact network as they are expected to have close contact and care from the same hospital workers who might facilitate transmission of microbial species. Due to patient movement (admission, discharge, and transfer), the contact network is time-varying and was updated daily. We assumed each patient is either susceptible (S) or colonized (C). Patients in contact on a given day (those who shared the same ward) can be and converted to carriers proportional to the number of patients in the ward carrying a particular microorganism. We model the force of infection in ward , , following the law of mass action, as described below. We assumed colonized patients can spontaneously decolonize and become susceptible after a decolonization period days 31. Colonization in hospitals can be attributed to two mechanisms: importation from the community and nosocomial transmission. Specifically, we defined these two processes as follows:

1. **Importation from the community:** Using hospital admission records, we assumed a newly admitted patient is colonized with a particular pathogen with an importation probability . The number of patients admitted from the community is shown in Figure 2B. We treated all admissions independently but keep track of re-admission on consecutive days. However, if patients were admitted on consecutive days we assumed their colonization status did not change. As a consequence, the number of admitted, colonized patients on day , , among all admitted patients on day , , can be computed as:
2. **Nosocomial contact transmission:** We defined a force of infection for each ward as . The force of infection is proportional to the number of individuals carrying the pathogen in a given ward on day , denoted by . We defined a frequency-dependent transmission rate per ward as , where is the average ward daily occupancy (Density distribution shown in Supplementary Information Figure S1). The force of infection per ward is computed as:

Thus, the force of infection per ward, or probability of colonization for susceptible individuals staying in ward at time , is given by , and the transition equations governing the change of state for a patient, , residing in ward during time are given by:

where is the decolonization period of patient and is a random variable with uniform distribution as indicated previously.

### *The individual observational model*

Colonized patients may develop clinical infections due to the invasion of typically sterile body sites such as blood. At other body sites (i.e. respiratory and urinary tract) the presence of pathogens may indicate both infection or colonization, depending on additional clinical variables 1,26. Other individuals carrying pathogens may be discovered through routine screening or cultures ordered discretionarily by clinicians for patients without clinical manifestations. In the ABM, we did not explicitly distinguish between colonized and clinically infected patients. Instead, we applied an observational model to detect carriers. This observational model represents the detection probability for clinical cultures taken from individuals in the hospital network during the study period; it captures the heterogeneous observation of microorganisms across wards. Weekly number of cultures across hospital wards and weekly number of admitted patients have a strong positive correlation (cultures are proportional to admissions) (Figure 1D-E).

A key challenge in colonization detection is that cultures collected from one body site may miss colonization of other sites even though the patient carries the bacterium. For instance, blood cultures of a patient colonized by *E. coli* in the urinary tract will likely test negative, and this patient may not neccesarily present symptoms (Seth Blumberg told us - Sen and I - this, but I did not found any reference. Should we just leave the guess there?). This compounded with differential detection of screening and diagnosis makes the parametrization challenging. To define our observational model, we therefore estimated the ‘effective sensitivity’ of detecting colonization upon testing defined by the culture data, i.e. the probability of identifying carriage given that the patient is carrying a particular microorganism. This effective sensitivity not only represents culture test sensitivity, in the strict sense, but also the likelihood a specimen will be taken from a colonized site (and capture bacteria) given colonization or infection exists anywhere on a patient. The defined observational model indicates the likelihood that a colonized patient is detected given the effective sensitivity is .

### *The population-level observational model*

### *Hospital-level observational model*

Due to substantial testing heterogeneity, observations of positive cultures were dominated by a few wards with a disproportionately large number of tests. To facilitate use of more granular observations at the sub-hospital level while avoiding excessive noise, we used the building aggregation to sum the number of nosocomial infection data and perform inference. SI Figure SX shows the number of test at the building scale, we merge buildings composed mostly by outpatients and with few test into a aggregation named 'Rest'. The number of transfers between wards is shown in SI Figure SX2. Wards within each identified building have more frequent within-cluster transfers than cross-cluster transfers.

### *Inference*

Inference for dynamic and latent variables and parameters is often treated as a filtering problem, in which the state space is sequentially estimated as observations become available 59,60. This framework has been applied to many infectious diseases, including influenza, dengue, malaria, cholera, Ebola, enterovirus D68, and COVID-19 61–70, typically using compartmental models that represent transmission dynamics with a set of ordinary differential equations (ODEs). However, there are fewer instances in which filters have been used in conjunction with ABMs, possibly due to the considerably higher dimension of the state space for these models 17. For this ABM system, we solve the inverse problem without solving the filtering problem and therefore only estimate parameters, i.e., infer the likelihood of detection given carriage upon testing and the nosocomial transmission rate , without re-adjusting the state space.

We use the ensemble adjustment Kalman filter (EAKF 59 or EnKF ), which assumes both the prior and the observations are normally distributed. Compared to other data assimilation techniques, the EAKF is amenable for use with high-dimensional models such as numerical weather models (cite). We assimilated weekly observations of total numbers nosocomial infection detections for microorganisms 59 using an iterated filtering framework (IF). Iterated filtering for dynamical systems was proposed in the context of epidemiology using particle filters or sequential Monte Carlo 71,72 (we based most of our implementation on those algorithms), but has also been proposed in the context of inverse problems using Kalman filters 48,73. The implementation of the IF-EAKF in Python was made using the packages NumPy and SciPy 74,75. Further details and hyperparameters for this implementation are available in the Supplementary Information.

### *Identifiability: Synthetic simulations and inference*

To verify that the model-inference system is able to accurately estimate the two key epidemiological parameters, we first investigated the identifiability of the system using simulated nosocomial detections (i.e., the ability of the framework to infer the parameters when they are known). We generated synthetic observations of incident microorganism colonization using the ABM and assigned importation and nosocomial transmission rates. The synthetic observations were then assimilated into the full model-inference system to assess system ability to accurately estimate the parameters.

### *Inference using real-world data*

We next used actual weekly observations for the six ward clusters to infer community importation and nosocomial transmission rates for all eight microbial species. The model-inference framework was applied to each species separately with the assumption that no ecological interaction exists among species. The primary observational model uses culture data from all body sites; however, we also performed sensitivity analyses in which we restricted the observation of positives to particular body sites. Specifically, we estimated parameters using positive observations excluding one body site at a time. A detailed description of the number of specimens used and the number of cultures across ward clusters is shown in the Supplementary Information.

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**References**

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**Figures and Tables**

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**Figure 1. Empirical colonization of microbial organisms, hospital admissions and testing.** **A)** Nosocomial infection data for pathogenic bacteria studied, faded dots are the weekly incident and solid lines the monthly incident detections, from left to right and top to bottom: *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *MSSA*, , *MRSA*, *S. epidermis,* *E. faecali* and *E. faecium*. **B)** Numbers of in-hospital patients (red) and admitted patients (blue) during the study period at daily resolution (weekly variability is evident). **C)** Numbers of in-hospital patients normalized by ward size (average occupancy per day during the study period); blue lines show the 10 most populated wards, green lines the 10 least populated, and the remaining wards are shown in gray in the background **D)** Heatmap showing the number of weekly cultures in each ward during the study period. **E)** Heatmap plot showing the number of patients admitted weekly to each ward during the study period.

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**Figure 2. Identifiability, posterior estimates.** Joint posterior estimates for **A)** importation rate =25% and **B)** =50%. The posterior estimate is highlighted with a density plot (darker means more probable), and posterior ensemble members are shown as purple dots. In each subplot the true value used for simulating the stochastic trajectory to infer is highlighted in the title of each scenario, with a yellow cross and the intersection of the two black dashed lines. x-axis shows the likelihood of detection upon testing (%) and y-axis the nosocomial transmission rate . Note that in both **A)** and **B)** the prior range is the limits of each axis, increments from upper to lower plots and from left to right.

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**Figure 3. Posterior parameter estimates.** Joint estimates for the likelihood of detection upon testing (%) (x-axis) and the nosocomial transmission rate (y-axis). Importation rate values for sensitvity analysis are color-coded with high, medium and low prevalences, and indicated in each subplot. Color-coded dashed lines show the mean estimates, and posterior is shown with both a density plot (darker indicates more probable) and with the posterior ensemble members plotted as dots.

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**Figure 4. Hospital level fit (not used for data assimilation):** **A)** Ensemble simulation of modeled nosocomial infections detections with posterior parameter estimates, solid lines show the mean and ribbons the 95% CI and are color-coded. Importation rate is highlighted in the legend and color-coded for high, medium and low prevalences. Weekly nosocomial infection data is plotted with red dots. **B)** Reliability plot (Methods). Hospital-level fit with 4 different confidence intervals (25%, 50, 75%, 95%). Importation rate is color-coded. The black dotted line is the reference perfect calibration.

**Table 1.** Human prevalence range from the literature, we present the 3 values used in the inferences (SI *Prevalence estimates)*.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Importation rate, (%)** | **Nosocomial transmission rate**  **Mean (95% CI)** | **Likelihood of detection (%)**  **Mean (95% CI)** |
| *E. coli* | 55 | 2.54E-03 (1.72E-03, 3.58E-03) | 18.53 (17.30, 19.43) |
|  | 63 | 8.66E-04 (3.78E-04, 1.58E-03) | 18.63 (17.85, 19.23) |
|  | 70 | 9.62E-04 (4.06E-04, 1.73E-03) | 17.31 (16.33, 18.02) |
| *K. pneumoniae* | 15 | 0.187 (0.180, 0.194) | 2.51 (2.36, 2.65) |
|  | 23 | 0.189 (0.180, 0.195) | 2.14 (1.98, 2.29) |
|  | 35 | 0.181 (0.165, 0.193) | 2.05 (1.92, 2.17) |
| *P. aeruginosa* | 11.6 | 0.189 (0.183, 0.194) | 1.93 (1.78, 2.07) |
|  | 18.8 | 0.190 (0.182, 0.195) | 1.61 (1.47, 1.75) |
|  | 25. | 0.187 (0.178, 0.194) | 1.55 (1.43, 1.67) |
| *MSSA* | 25 | 0.141 (0.122, 0.164) | 1.63 (1.47, 1.79) |
|  | 29 | 0.121 (0.103, 0.140) | 1.65 (1.49, 1.81) |
|  | 35 | 9.94E-02 (8.43E-02, 0.116) | 1.58 (1.40, 1.73) |
| *MRSA* | 10 | 0.170 (0.136, 0.184) | 1.38 (1.21, 1.60) |
|  | 3.9 | 1.70E-02 (9.16E-03, 2.74E-02) | 17.15 (12.48, 18.96) |
|  | 5 | 0.182 (0.168, 0.190) | 1.96 (1.72, 2.19) |
| *S. epidermidis* | 58 | 0.171 (0.117, 0.190) | 1.24 (1.12, 1.35) |
|  | 75 | 0.174 (0.134, 0.190) | 1.21 (1.10, 1.33) |
|  | 90 | 0.173 (0.107, 0.189) | 1.23 (1.12, 1.36) |
| *E. faecalis* | 36 | 0.167 (0.121, 0.186) | 1.05 (0.96, 1.17) |
|  | 47.6 | 0.149 (9.69E-02, 0.182) | 1.07 (0.96, 1.19) |
|  | 55.0 | 0.159 (0.101, 0.185) | 1.09 (0.96, 1.21) |
| *E. faecium* | 36.8 | 0.182 (0.163, 0.192) | 0.58 (0.54, 0.63) |
|  | 40.6 | 0.179 (0.147, 0.191) | 0.57 (0.54, 0.65) |
|  | 50.0 | 0.178 (0.123, 0.193) | 0.58 (0.54, 0.66) |

**Table 2.** **Posterior estimates**. Mean posterior estimates for the eight pathogen; the value for the importation rate γ is shown in the second column. Nosocomial transmission rates β is presented as rate per day in the third column and likelihoods of detection upon testing in the fourth column.