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Evaluating Architectural Changes to Alter Pathogen Dynamics in a Dialysis Unit

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For the CDC MInD-Healthcare Group

***Abstract*—This paper presents a high-fidelity agent-based simulation of the spread of methicillin-resistant *Staphylococcus aureus* (MRSA), a serious hospital acquired infection, within the dialysis unit at the University of Iowa Hospitals and Clinics (UIHC). The simulation is based on ten days of fine-grained healthcare worker (HCW) movement and interaction data collected from a sensor mote instrumentation of the dialysis unit by our research group in the fall of 2013. The simulation layers a detailed model of MRSA pathogen transfer, die-off, shedding, and infection on top of agent interactions obtained from data. The specific question this paper focuses on is whether there are simple, inexpensive architectural or process changes one can make in the dialysis unit to reduce the spread of MRSA? We evaluate two architectural changes of the nurses' station: (*i*) splitting the central nurses' station into two smaller distinct nurses' stations, and (*ii*) doubling the surface area of the nursing station. The first architectural change is modeled as a graph partitioning problem on a HCW contact network obtained from our HCW movement data. Somewhat counter-intuitively, our results suggest that the first architectural modification and the resulting reduction in HCW-HCW contacts has little to no effect on the spread of MRSA and may in fact lead to an increase in MRSA infection counts in some cases. In contrast, the second modification leads to a substantial reduction – between 12% and 22% for simulations with different parameters – in the number of patients infected by MRSA. These results suggest that the dynamics of an environmentally mediated infection such as MRSA may be quite different from that of infections whose spread is not substantially affected by the environment (*e.g.*, respiratory infections or influenza).**

***Index Terms*—epidemiology, environmental contamination, healthcare-associated infections, disease transmission, infection control, architecture change, methicillin-resistant Staphylococcus aureus.**

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I. Introduction

A *healthcare acquired infection* (HAI) is an infection obtained in a healthcare facility during treatment for an unrelated condition. HAIs are the most common adverse events in the field of healthcare today and a significant cause of illness, death, and financial burden for patients and healthcare facilities alike. HAIs are quite prevalent: at any given time, 1 in 25 patients have an HAI [1], and the prevention of HAIs has become a major public health focus of the Centers for Disease Control and Prevention (CDC). Risk factors for HAIs include the use of invasive medical devices (*e.g.*, urinary catheters), surgery, improperly cleaned healthcare facilities, poor hand hygiene practices on the part of healthcare workers (HCWs), immunocompromised patients, and the overuse of antibiotics. Common HAIs include *Clostridium difficile* infection (CDI), methicillin-resistant *Staphylococcus aureus* (MRSA) infections, central-line associated bloodstream infections (CLABSI), pneumonia, surgical site infections, and urinary tract infections [1].

This paper focuses on the spread of MRSA among hemodialysis patients. Hemodialysis (or, more simply, dialysis) is a medical treatment that removes waste products from the bloodstream of patients with kidney failure. At the University of Iowa Hospitals and Clinics (UIHC), dialysis is performed on an outpatient basis in a specialized unit operating six days a week (excluding Sundays). Dialysis patients are particularly susceptible to HAIs because they tend to be immunocompromised due to other comorbidities, have multiple and frequent exposures to the healthcare environment, and because their care requires the use of long-term vascular access [2]. As a result, MRSA infections are much more common among dialysis patients than in the general population [3]. CDC recommendations for preventing MRSA infections

include good hand hygiene and sanitation practices [4]. Studies have shown that improved hand hygiene and surface/room cleaning effectively decrease MRSA infection rates [5]–[7]. The specific question we focus on is whether there are simple, inexpensive architectural or process changes one can make in the dialysis unit to reduce the spread of MRSA. In answering this question, we seek a better understanding of the role of the environment in the diffusion of MRSA. A one-time intervention such as an architectural change would not only complement standard hand-hygiene and cleaning policies, but could result in a long-term impact.

Spatial simulation

The results presented here are fruit of an agent-based simulation study based on ten days of fine-grained healthcare worker (HCW) movement and interaction data collected by our research group in the fall of 2013. The data were obtained by instrumenting HCWs working in a nine-chair hospital dialysis facility at the UIHC with small tracking sensor devices (see Fig. 1). The subsequent simulations replay the HCW interactions with patients, the environment, and each other, while layering a detailed model of MRSA pathogen transfer, die-off, and shedding over the agent interaction model. The simulation maintains MRSA pathogen loads on all surfaces including chairs, the nurses' station, HCW hands, and patient skin and uses a dose-response function to model the probability of a patient acquiring MRSA as a function of their pathogen load. The simulation also models the effect of HCW hand hygiene behaviors and environmental cleaning strategies. To this baseline simulation, we add two distinct architectural modifications: (*i*) splitting the central nurses' station (labeled 10 in Fig. 1) into two smaller distinct nurses' stations and (*ii*) doubling the surface area of the nursing station, in effect diluting the level of surface contamination. The first of these changes is motivated by the idea that if the nurses' station is split then HCWs will assort themselves into two groups and interactions across the two groups of HCWs at the nurses' station will be minimized. This idea of reducing contacts among HCWs is motivated by examples of "staff cohorting" used in infection control to reduce infection spread [8]. To obtain HCW partitions that could lead to the greatest reduction in HCW contact duration, we solve a graph partitioning problem on a HCW contact network obtained from our HCW movement data.

Somewhat counter-intuitively, our results suggest that the first architectural modification and the resulting reduction in HCW-HCW contacts has little to no effect on the spread of MRSA. In fact, as shown in Table V, this change actually leads to a small percentage increase in the mean MRSA infection counts (for these particular parameter settings). In contrast, the second modification (increasing the surface area of the nurses' station) leads to a substantial reduction – between 12% and 22% for simulations with different parameters – in the number of patients infected by MRSA. These results suggest that the dynamics of an environmentally mediated infection such as MRSA may be quite different from that of an infection which is not substantially affected by environmental contamination (*e.g.*, respiratory infections or influenza). What seems to matter in our model critically is the *concentration* of pathogen among few individuals or surfaces. Reducing HCW-HCW contacts seems to have no effect on this and, in fact, may have the unintended effect of increasing local pathogen concentration. On the other hand, increasing the surface area of the nurses' station dilutes its pathogen load and has significant downstream effects on pathogen load on HCW hands and, in turn, pathogen load on the patient skin. This effect seems to have an analogue in the "dilution effect" studied in ecology [9].

II. HCW Movement and Interaction

In previous work, we have developed an accurate yet inexpensive and easily deployed individual movement-tracking and contact-tracing technology that directly captures the full spatiotemporal contact network of HCWs as they go about their duties [10]–[12].

A. Dialysis Unit Instrumentation

Our technology incorporates two types of elements: individual HCWs wear rechargeable *badges*, while additional line-powered *beacons* (shown as green triangles in Fig. 1) are placed in static locations to serve as spatial references. Both badges and beacons consist of commercially available wireless sensors, or *motes*. Whenever a beacon detects a badge's message, it records the unique identifier of the sender, the received signal strength index (RSSI) associated with the message, and the time the message was received. In a similar fashion, badges record timestamps and identifiers of beacons and other badges.

Four out of the 10 deployment days were short (i.e., approx 6.5 hrs, 1 shift) and the remaining six days were long (i.e., approx 14.75 hrs, 2 shifts). Badges were randomly distributed to HCWs within job categories at the start of each shift [1].

B. Extracting HCW Locations from Sensor Data

Because RSSI increases with proximity, the aggregation of time-stamped badge messages recorded by the beacons can be used to reconstruct badge positions over time, grounded in space by the known locations of the beacons. Note, however, that using badge-to-beacon RSSIs alone may not suffice, given that the human body effectively absorbs RF energy and that the physical orientation of the badge with respect to the beacon may also reduce RSSI. Thus, in addition to badge-to-beacon RSSI levels, we also incorporate the previous latent positions of each badge as well as validated (*i.e.*, confirmed by both badges) badge-to-badge sightings in our reconstruction. Our reconstruction algorithm's utility function thus combines the following three criteria: (*i*) minimize distances between badges and beacons with high badge-to-beacon RSSIs, (*ii*) minimize badge distance from its previous location, and (*iii*) minimize badge distance to other badges with high mutual

[1]Note that, because we are not collecting identifiable patient data or the mapping of badges to HCW identities, our institutional review board (IRB) has determined that this research does not meet the regulatory definition of human subjects research.

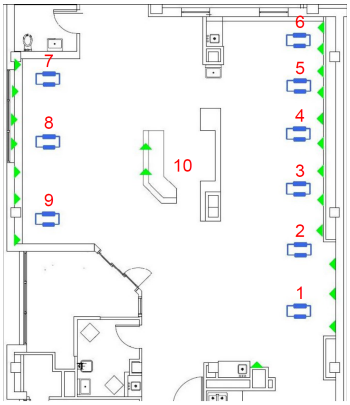


Fig. 1. **Schematic of the UIHC dialysis unit showing 9 patient chairs and the nurses' station in the central area.** There are 22 stationary sensors ("beacons"; shown as green triangles) placed in the unit to provide HCW localization. Mobile sensors ("badges") are randomly distributed within job types to HCWs at the beginning of each shift.

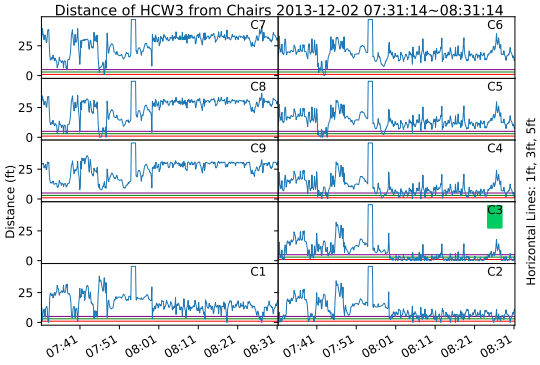


Fig. 2. **Distance with respect to time for a particular HCW from each of the nine chairs in the dialysis unit.** The nine individual chair distance plots are arranged to correspond, roughly speaking, to the position of the chairs in the dialysis unit depicted in Fig 1. The three horizontal lines in each distance plot correspond to 1ft, 3ft, and 5ft thresholds measured from the corresponding dialysis chair, and represent three different definitions of what it means for a HCW to be near a chair.

RSSI. Latent positions of these badges are taken to reflect the latent positions of their respective HCWs for the remainder of this paper.

C. Imputing Patient Dialysis Sessions from Sensor Data

Because we do not have access to patient records, we do not know when a dialysis patient is being treated, nor do we know when a dialysis chair is occupied. As modeling the spread of infection requires knowledge of HCW-patient contacts, we must first identify dialysis sessions; that is, the mapping of patients to dialysis chairs and time intervals. To do so, we exploit domain-specific knowledge about dialysis to impute the start/end times of each dialysis session while making some additional assumptions about the recurrence of each patient's treatment sessions.

At the start of a dialysis session, a HCW will necessarily spend some time connecting the patient to the dialysis machine [13]. Each session lasts for three to four hours [14], and, at the end of the session, a HCW again must attend to the patient in order to disconnect the machine. We can use these extended interactions between HCW and patient at the beginning and end of each dialysis sessions along with temporal constraints on session duration and knowledge of the number of patients treated per week to impute the likeliest pattern of dialysis sessions. Fig. 2 is an example of one particular HCW's distance from each of the nine dialysis chairs over the course of the morning of Day 10; we can clearly see a period of extended interaction between this particular HCW and a presumed patient in chair 3 from 8:00 to 8:25 in the morning.

We train a machine learning system to recognize the patterns of extended interaction that typify the beginning or end of a dialysis session in our HCW location data. We cast the problem as a binary classification problem: we manually select 32 distance profiles, ranging from 7.5 minutes to 28.5 minutes in length as positive examples and then generate a training set by sliding a 7.5 minute (56 8-second timesteps) window over the examples to generate 2196 equal length positive training examples. Negative training examples consist of distance sequences of the same length from the next closest chair and from randomly selected sequences that do not fit the desired pattern; these negative instances are further augmented with random noise to improve the robustness of the model, resulting in a total of 4392 negative training examples. We held back 20% of the 6588 training instances, and then trained a multilayer perceptron on the remaining 80% of the instances using mini-batch gradient descent. Finally, applying the classifier to all of our HCW/chair data, we generated a set of daily patient sessions on long days by selecting entry and exit times randomly from several candidates of predicted patterns. The average delivered treatment time of 227 (std. dev. 21 min) roughly matched the average conventional hemodialysis treatment duration [14]. Between 13 to 20 patient sessions were detected by our system for the 6 long deployment days.

III. Simulating the Spread of MRSA in the Dialysis Unit

We next perform a series of agent-based simulations that explore the impact of our architectural design changes on the transmission of MRSA over a fixed period of time. A simulation consists of multiple replicates, where each replicate replays a single day of HCW-patient, HCW-HCW and HCW-environment interactions derived from the HCW location data just described. Each interaction represents an opportunity for pathogen exchange with another HCW, patient or environmental surface according to a stochastic model of pathogen transmission. Under certain conditions, a patient becomes infected, and begins to shed pathogen which can subsequently be spread to other patients in the same fashion. By varying the structure of these interactions in accordance with our proposed architectural changes, we can compare the impact of these changes on the outcome of interest (here, the mean number of infected patients over a collection of replicates). We implemented the simulator in Python and allowed simulation

replicates to run on multiple cores. A 30-day simulation runs in 2.5 seconds for each core on Intel(R) Xeon(R) CPU E5-2683 v4 @ 2.10GHz.

A. Patient Scheduling and Disease Model

For each simulation, we pick a long day and repeatedly replay the interactions of all HCWs and all patients present in the dialysis unit on that day. The results presented in this paper are obtained by replaying Day 10 (a long day) during which 11 HCWs were present and there were 20 dialysis sessions. This implies a cohort of 40 patients divided into two equal groups. We assume that each group of 20 patients dialyzes three times per week, on either a Monday-Wednesday-Friday or a Tuesday-Thursday-Saturday dialysis schedule (the unit does not operate on Sunday), for a total of 520 dialysis sessions over 30 days, or 13 dialysis sessions per patient in just over four weeks. Patients are randomly assigned to chairs on a particular shift (morning, afternoon, and evening) each day in the simulation.

Patients adhere to a simple Susceptible-Infected-Susceptible (SIS) model [15]. On the first simulated day, a single patient in the morning session is randomly identified as *infected*; all other patients are initially assumed to be *susceptible*. An infected patient continuously sheds pathogen at the shedding rate α [5]; we assume this pathogen immediately settles on nearby surfaces, including the patient's skin, the hands of any HCW who is presently in contact with the patient, and the patient's chair. After 10 days, a patient returns to the susceptible state. HCWs do not adhere to the SIS model; they never become infected, but can instead be *colonized*, serving to transfer pathogen within the simulation.

B. Pathogen Transfer Model

Pathogen transfer occurs via 5 different types of *contacts*: (*i*) HCW-patient, (*ii*) HCW-HCW, (*iii*) HCW-chair, (*iv*) patient-chair, and (*v*) HCW-nurses' station. We measure contacts in 8-second quanta (based on the granularity of our sensor data), and in most cases a contact is said to occur between two entities if they are separated by a distance of at most 1 ft. The single exception to this rule concerns HCW-HCW contacts, where an additional parameter τ_{hcw} denotes the fraction of times (sampled uniformly at random) that the presence of two HCWs within 1 ft of each other represents an effective contact. The τ_{hcw} parameter reflects the fact that while HCWs are likely to pass close to one another in the course of their duties, most of these interactions do not involve any actual touching or exchanging of physical objects that may transfer pathogen between them.

Each contact between two entities A and B results in some quantity of MRSA pathogen being transferred bidirectionally between the entities [5]. Specifically, the volume of pathogen transferred from A to B is the volume of pathogen in the contact area of A times the transfer efficiency between surfaces of A and B (and vice-versa). We operationalize this principle by making two assumptions: (*i*) contact between HCWs and other entities occurs only via HCW hands and (*ii*) pathogen is always spread uniformly over all the surfaces we model (*i.e.*, HCW hands, patients' skin, chair surfaces, and the surface of the nurses' station). With these assumptions, we can simulate MRSA transfer during contacts by tracking the volume of MRSA pathogen on different surfaces. We use $MRSA_{hcw\ i}$, $1 \leq i \leq 11$, $MRSA_{pt\ j}$, $1 \leq j \leq 40$, $MRSA_{ch\ k}$, $1 \leq k \leq 9$, and $MRSA_{ns}$ to denote the volume of pathogen on the hands of HCW i, the skin of patient j, the surface of chair k, and the surface of the nurses' station, respectively.

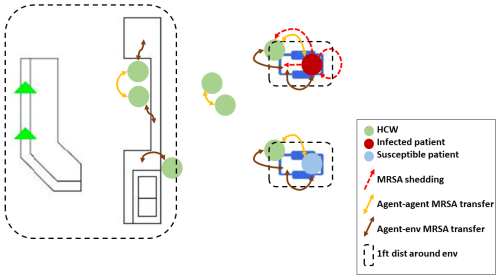


Fig. 3. **Diagram of the simulation model.** Circles represent agents in the simulation (green: HCW, red: infected patient, blue: susceptible patient) and compartments surrounded by black dashed lines are environments (left: nurses station, right: chairs). Arrows represent pathogen transfer (red dashed arrow: shedding of an infected patient, yellow arrow: contacts between agents, brown arrow: contacts between agents and the environment).

An example should help make this process clear. Consider the case where HCW i comes in contact with patient j (Fig. 3 shows all the possible transfer types used in our simulations). Letting $\rho_{sk\text{-}sk}$ denote skin-to-skin transfer efficiency of the MRSA pathogen, A_h denote the surface area of a hand, and A_{pt} denote the surface area of a patient, we see that $\rho_{sk\text{-}sk} \cdot MRSA_{hcw\ i}$ is the amount of MRSA transfered from HCW i's hand to patient j's skin, while $\rho_{sk\text{-}sk} \cdot MRSA_{pt\ j} \cdot A_h/A_{pt}$ is the amount of MRSA transfer from patient j's hand to HCW i's hand. In the latter expression, A_h/A_{pt} denotes the fraction of the patient's skin surface that is in contact with the HCW's hands and therefore, thanks to our uniform pathogen mixing assumption, $MRSA_{pt\ j} \cdot A_h/A_{pt}$ is the volume of pathogen on patient j that has the potential to be transferred to HCW i's hands. It should be noted that A_h and A_{pt} are considered identical for all hands and all patients respectively. See Table I for formulae for the volume of pathogen transfer for all 5 types of contacts.

C. Pathogen Reduction Model

MRSA is introduced into the simulation by shedding of pathogen from the initially infected patient, and subsequently increased by the addition of other infected patients. In a similar fashion, MRSA pathogen can also be removed from the simulation via three distinct mechanisms: (*i*) HCWs performing hand hygiene, (*ii*) environmental cleaning, and (*iii*) natural decay. Every HCW starts the day with clean hands and accumulates pathogen over the course of the day. We use λ to denote the fraction of $MRSA_{hcw\ i}$ removed from HCW i's hands by performing hand hygiene [16]. In the simulation,

we view the arrival of a HCW at a patient's chair or the nurses' station as a hand hygiene opportunity. We assume that all HCWs share the same hand hygiene compliance rate γ [12]. In a similar fashion, we use ϵ to denote the fraction of pathogen removed from surfaces when cleaned [17] (note that chairs are cleaned after each dialysis session, while the nurses' station is cleaned only at the end of the day). Finally, MRSA pathogen naturally decays at a rate of μ_{sk} from skin and a rate of μ_{np} from non-porous surfaces (such as chairs and the nurses' stations) [5]. And while patients do not dialyze on Sunday, our simulations do apply this natural decay process every seventh day.

D. Disease State Transition Model

Colonization, or the presence of MRSA pathogen on a patient's skin, may result in the patient becoming infected. We model this process using dose-response functions that define the probability of infection $f(MRSA_{pt\ j})$ for patient j in terms of $MRSA_{pt\ j}$, the volume of MRSA pathogen present on patient j's skin [5], [18]. In our simulations, we used two different dose-response models: (*i*) a *linear* model and (*ii*) an *exponential* model. The linear model has the form $f(x) = \pi x$ where π is the *infectivity* of a pathogen. This model assumes a linear relationship between the volume of pathogen and the probability of an individual transitioning from susceptible to infected. In contrast, the exponential model has the form $f(x) = 1 - e^{-\pi x}$, which assumes that each pathogen can infect an individual independent of other pathogens [18]. For the simulations, we used $\pi \in \{\frac{1}{5M}, \frac{1}{7.5M}\}$ because these values produce an infection rate consistent with the observed MRSA infection statistic in a dialysis unit [3]. An infected patient can shed pathogen for days or weeks [7], but usually sheds for less than ten days if treated [19]. We assume that infected patients transition from infected to susceptible after 10 days.

This completes the description of our baseline model. Table III shows all the parameters used in the baseline simulation along with their values and in most cases, sources for these values.

IV. Modeling Architectural Changes

We propose two simple, low-cost architectural changes to the dialysis unit and evaluate their impact on MRSA diffusion.

TABLE I
VOLUME OF PATHOGEN TRANSFER

MRSA Transfer Between Entities		
Source	***Target***	***MRSA Transfer (Source to Target)***
HCW i patient j	patient j HCW i	$\rho_{sk\text{-}sk} \cdot MRSA_{hcw\ i}$ $\rho_{sk\text{-}sk} \cdot MRSA_{pt\ j} \cdot A_h / A_{pt}$
HCW i HCW l	HCW l HCW i	$\rho_{sk\text{-}sk} \cdot MRSA_{hcw\ i}$ $\rho_{sk\text{-}sk} \cdot MRSA_{hcw\ l}$
HCW i chair k	chair k HCW i	$\rho_{sk\text{-}np} \cdot MRSA_{hcw\ i}$ $\rho_{sk\text{-}np} \cdot MRSA_{ch\ k} \cdot A_h / A_{ch}$
patient j chair k	chair k patient j	$\rho_{sk\text{-}np} \cdot MRSA_{pt\ j} \cdot A_h / A_{pt}$ $\rho_{sk\text{-}np} \cdot MRSA_{ch\ k} \cdot A_h / A_{ch}$
HCW i nurses' station	nurses' station HCW i	$\rho_{sk\text{-}np} \cdot MRSA_{hcw\ i}$ $\rho_{sk\text{-}np} \cdot MRSA_{ns} \cdot A_h / A_{ns}$

These simple architectural changes suffice to help us better understand the role of the environment in MRSA diffusion.

A. Splitting the Nurses' Station into Two Stations

The first simple architectural change we consider is to split the nurses' station NS into two stations NS_1 and NS_2, each with surface area half of the surface area of NS. This change is motivated by the idea that HCWs will assort themselves into two-equal-size groups and interaction across the two groups of HCWs at the nurses' station will be minimized. As a result, MRSA pathogen transfer across the groups is substantially reduced. We hypothesize that this architectural change will reduce mean infection counts. This idea is motivated by examples of "staff cohorting" used in infection control to reduce infection spread [8].

To implement this change in the simulation, we partition the HCWs equitably into two groups H_1 and H_2 and assign H_i to NS_i, $i = 1, 2$. Each contact between a HCW $h \in H_i$ and NS in the original simulation is replaced by a contact between h and NS_i. Also, each contact between $h \in H_1$ and $h' \in H_2$ that occurs at NS is removed, modeling the fact that HCWs h and h' now visit different nurses' stations. We evaluate three methods for partitioning the HCWs equitably into H_1 and H_2. The first two methods are motivated by the aim of maximizing the duration of contact between HCWs in H_1 and HCWs in H_2 so that when we delete all contacts between H_1 and H_2, this will result in the greatest reduction of contact duration between the HCWs. We formalize this idea via the MaxBisection problem which takes as input an edge-weighted graph $G = (V, E)$ and whose output is required to be a partition (V_1, V_2) of the vertex set such that $|V_1| = \lceil |V|/2 \rceil$, $|V_2| = \lfloor |V|/2 \rfloor$ and the weight the edges in $\{\{u, v\} \mid u \in V_1, v \in V_2\}$ is maximized. Let G_{ns} (respectively, G_{all}) be the HCW contact graph whose vertices are HCWs and each of whose edges $\{h, h'\}$ are weighted by the total contact duration between h and h' that occurs at the nurses' station (respectively, anywhere in the unit).

1) Solve MaxBisection on G_{ns} and used the returned partition.
2) Solve MaxBisection on G_{all} and used the returned partition.
3) Partition the HCWs into two (roughly) equal-sized groups and picked uniformly at random from the $\binom{11}{5}$ possible grouping of HCWs into five and six members.

The first two grouping strategies require *a priori* information on HCW mobility, whereas the random strategy is independent of HCW mobility and is easier to implement in practice.

B. Doubling the Surface Area of the Nurses Station

In our simulation model, we assume that MRSA spreads uniformly on surfaces whenever MRSA transfer between entities occur. Based on this assumption, increasing the surface area of the nurses' station has the effect of diluting MRSA concentration at the nurses' station. In our second, simple architectural change, we double the surface area of the nurses'

station. Note that we do not split the nurses' station when we make this architectural change. We hypothesize that doubling the surface of the nurses' station will reduce mean MRSA infection counts.

The specific policies we implement based on the architectural changes are summarized in Table II.

V. Results

There are several sources of stochasticity in our simulation model, namely (*i*) chair placement of initially infected patient, (*ii*) chair placement of remaining patients, (*iii*) dampening of HCW-HCW contacts based on parameter τ_{hcw}, (*iv*) HCW hand hygiene compliance based on parameter γ, (*v*) infectivity of patients according to the probability given by the dose-response function, and (*vi*) variation (by a few minutes) of patient entry and exit times at chairs. To account for this stochasticity, we report statistics over 1000 replicates of each simulation. Fig. 4 shows the distribution of infection counts, *i.e.*, the number of additional infected patients beyond the initially infected patient, over the 1000 simulation replicates performed using the baseline simulation parameters in Table III. The mean and median infection counts for the baseline simulation are 3.287 and 2 respectively with a std. dev. of 4.129.

Fig. 5 contains four plots comparing mean infection counts from simulations using the five different policies mentioned above. The simulations in Fig. 5a use the baseline simulation parameters, whereas the remaining figures are obtained by varying one parameter each relative to the baseline. In Fig. 5b, we replace the exponential dose-response function with a linear dose-response function. In Fig. 5c we use $\tau_{hcw} = 0.5$ instead of $\tau_{hcw} = 0.05$, *i.e.*, we assume that 50% of HCW-HCW contacts are "touch" contacts as opposed to just 5%. In Fig. 5d we use a higher infectivity of $\pi = \frac{1}{5M}$ instead of $\pi = \frac{1}{7.5M}$. Infection counts are cumulative over 30 days, and the count per day is averaged over 1000 simulation replicates for each policy, which are depicted as line graphs. For the random HCW grouping policy, we repeat this procedure ten times – each repetition likely yielding a different partition of the HCWs. We show the distribution of the mean infection counts over ten random HCW groups with an associated boxplot showing the distribution over the ten repetitions.

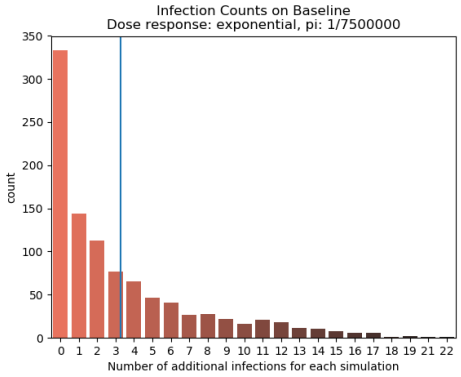


Fig. 4. **Distribution of infection counts in 1000 repetitions of the baseline simulation using the model parameters in Table III.** The mean and median infection counts on the baseline simulation are 3.287 and 2, respectively with a std. dev. of 4.129. The mean infection count is depicted as a vertical line.

Our main discovery is that, somewhat counter-intuitively, splitting the nurses' station into two stations does not much affect mean infection counts. However, doubling the surface area of the nurses' station substantially reduces infection counts for all four simulations in Fig. 5 (a t-test on the 1000 replicates of policy 0 and policy 4 for the 4 simulations in Fig. 5a yielded p-values 0.030, 0.041, 0.001, and 2.14e−7 respectively).

Table IV shows the probability of an *outbreak* for various policies and parameter settings, where an outbreak is defined as a simulation having an attack rate larger than 0.05 (more than two additionally infected patients) [20]. Doubling the surface area of the nurses' station reduced the probability of an outbreak compared to other policies.

TABLE II
Nurses Station Architecture Change Policies

Policy	Architecture Change	HCW Grouping
0	None (baseline)	No Grouping
1	Split into two stations	Random Grouping
2	Split into two stations	Max Bisection on G_{ns}
3	Split into two stations	Max Bisection on G_{all}
4	Double the surface area	No Grouping

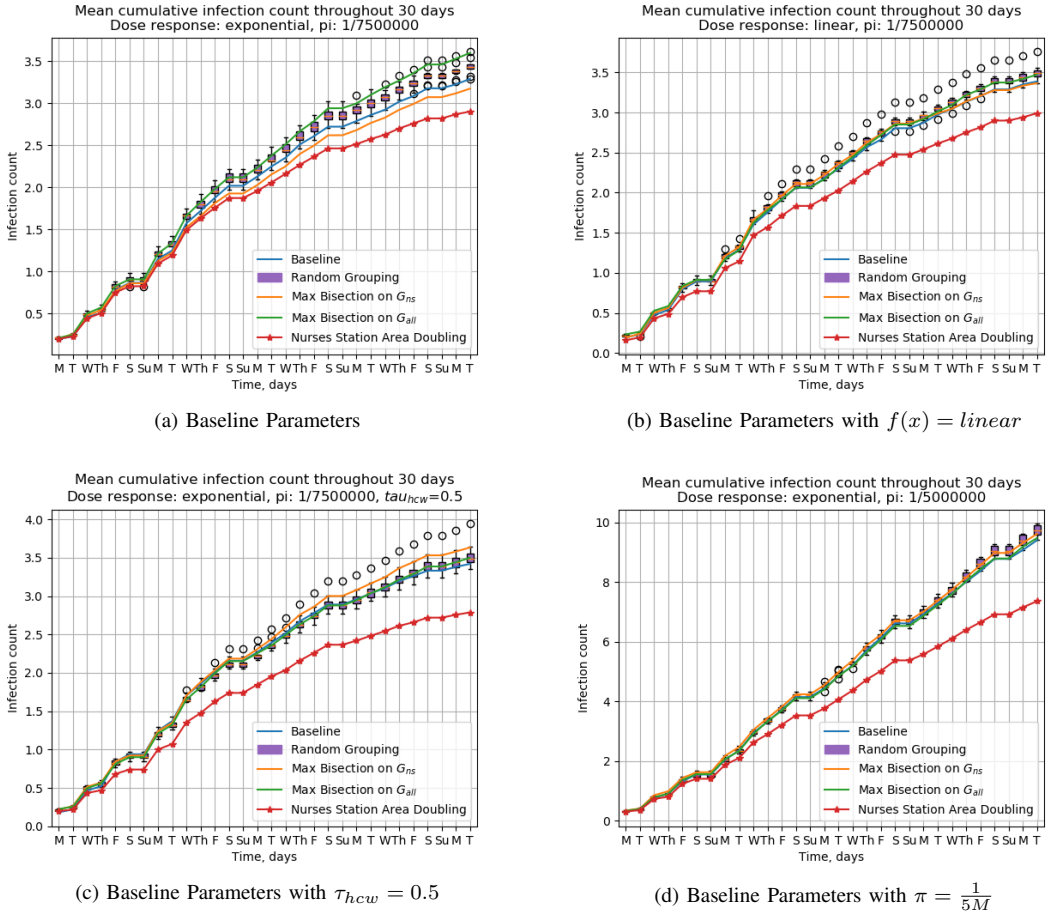
TABLE III
Baseline Simulation Parameters

Parameter	Symbol	Value	Ref
Shedding rate ($cfu/cm^2/8s$)	α	0.001333	[5]
Die-off rate on skin ($/8s$)	μ_{sk}	0.000471	[5]
Die-off rate on environments ($/8s$)	μ_{np}	0.000027	[5]
Transfer efficiency: skin-skin	$\rho_{sk\text{-}sk}$	0.35	[5]
Transfer efficiency: skin-env	$\rho_{sk\text{-}np}$	0.4	[5]
Area of patient's exposed skin (cm^2)	A_{pt}	2000	[5]
Area of HCW's exposed skin (cm^2)	A_{hcw}	150	-
Area of hand contact surface (cm^2)	A_h	150	[5]
Area of chair surface (cm^2)	A_{ch}	3600	-
Area of nurses' station (cm^2)	A_{ns}	41000	-
Decontamination efficacy	ϵ	0.5	[17]
Hand hygiene compliance	γ	0.279	[12]
Hand hygiene efficacy	λ	0.83	[16]
Rate of HCW-HCW contact	τ_{hcw}	0.05	-
Infection duration	d	10	[7]
Dose-response function	$f(x)$	$exponential$	[18]
MRSA Infectivity	π	$\frac{1}{7.5M}$	-

TABLE IV
Probability of an Outbreak while using different policies[a]

Parameters	*Policy0*	*Policy1*	*Policy2*	*Policy3*	*Policy4*
Baseline (Fig. 5a)	0.410	0.416	0.377	0.432	**0.367**
$f(x) = linear$ (Fig. 5b)	0.405	0.422	0.411	0.422	**0.355**
$\tau_{hcw} = 0.5$ (Fig. 5c)	0.413	0.424	0.422	0.430	**0.362**
$\pi = \frac{1}{5M}$ (Fig. 5d)	0.657	0.678	0.679	0.663	**0.608**

[a]Outbreak if an attack rate for a simulation is larger than 0.05 [20]



(a) Baseline Parameters

(b) Baseline Parameters with $f(x) = linear$

(c) Baseline Parameters with $\tau_{hcw} = 0.5$

(d) Baseline Parameters with $\pi = \frac{1}{5M}$

Fig. 5. **Cumulative infection counts for four different parameter settings.** Fig. 5a uses the baseline simulation parameters; the remaining plots are obtained by changing one parameter value each from the baseline parameters. Five different graphs are present in each plot (blue line: baseline policy, purple boxplot: random grouping policy, orange line: max bisection on G_{ns}, green line: max bisection on G_{all}, and red stared line: nurses station area doubling).

In supplementary material [21] we provide the results of a number of additional simulations, showing that our results are robust. Specifically, using other long days (besides Day 10) as the basis for simulations does not change our results. Neither does using other values of the parameter τ_{hcw} (rate of HCW-HCW contact).

A. Discussion

The fact that a reduction in HCW-HCW contacts that results from the first architectural change does not consistently reduce MRSA spread is an important take away from our work.

TABLE V
PERCENTAGE CHANGES IN MEAN INFECTION COUNTS OF DIFFERENT POLICIES[a]

Parameters	*Policy1*	*Policy2*	*Policy3*	*Policy4*
Baseline (Fig. 5a)	1%	-3%	9%	**-12%**
$f(x) = linear$ (Fig. 5b)	11%	-1%	3%	**-12%**
$\tau_{hcw} = 0.5$ (Fig. 5c)	7%	6%	2%	**-19%**
$\pi = \frac{1}{5M}$ (Fig. 5d)	4%	2%	1%	**-22%**

[a]Percentage changes are relative to that of *Policy0*.

This result suggests that the dynamics of an environmentally mediated infection such as MRSA may be quite different from that of other infections, such as respiratory infections or influenza in which environmental contamination may not play a substantial role. The result also cautions against the unintended consequences of reducing HCW interactions. In seeking an explanation for this finding, we note that the exponential dose-response function $f(x) = 1 - e^{-\pi \cdot x}$ is concave and therefore subadditive, i.e., $f(x_1) + f(x_2) \geq f(x_1 + x_2)$. Thus the expected number of infections is higher when the pathogen load "mixes" among patients, leading to loads x_1 and x_2 at two patients rather than $x_1 + x_2$ at a single patient. We expect to see more "mixing" in the baseline simulation relative to the simulation with the first architectural change and due to the above-mentioned property of the dose-response function, we expect to see more infection in the baseline simulation. However, this is not what we observe and this implies that there are other factors at play that counter the role of "mixing" of pathogen loads. Our hypothesis is that the extra HCW-HCW contacts in the baseline simulation are playing a role in spreading more MRSA among the HCWs and on the nurses'

station, thereby reducing the overall MRSA load on patients. We aim to test this hypothesis in future work.

The fact that increasing the surface area of the nurses' station plays a significant role in reducing MRSA spread is another important take away from our work. Our hypothesis is that increasing the nurses' station area dilutes pathogen load at the nurses' station, which has significant downstream effects on pathogen load on HCW hands and, in turn, pathogen load on the patient skin. Another way to view this phenomenon is that a larger nurses' station is a larger reservoir for pathogen, thereby diluting the volume of pathogen that reaches patients. This effect seems to have an analogue in the "dilution effect" studied in ecology [9]. We aim to test this hypothesis in future work, as well, by measuring pathogen loads on various surfaces over the course of our simulations.

B. Limitations

Studies have shown that HCWs play a significant role in the spread of HAIs and that hands of HCWs act as vectors for pathogen transmission [22]. However, it is unclear if the role of HCWs in this process is just as a vector or whether HCWs could serve as a source of pathogen shedding. Albrich et al. [23] show that among 33,000 HCWs, 4.6% carry MRSA and these colonized HCWs may be viewed as the source of MRSA transmission. Our simulation model view HCWs as vectors of MRSA transmission only. MRSA dynamics could change if our simulations allow HCWs to start shedding MRSA in the dialysis unit.

Additional careful sensitivity analysis over the parameter space is needed before our results can be considered robust. For example, our model assumes that patients start shedding MRSA at a fixed level immediately after they get infected. However, the amount and duration of MRSA shedding, as well as the point in time at which an infected patient starts shedding, may differ from patient to patient.

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REFERENCES

[1] Office of Disease Prevention and Health Promotion at health.gov, "Overview: Health care-associated infections," https://health.gov/hcq/prevent-hai.asp.

[2] ——, "National action plan to prevent health care-associated infections: Road map to elimination," https://health.gov/hcq/prevent-hai-action-plan.asp.

[3] J. Schieszer, "Invasive MRSA hits dialysis patients," *Renal and Urology News*, December 2007.

[4] Centers for Disease Control and Prevention (CDC), "Methicillin-resistant Staphylococcus aureus (MRSA): General information," https://www.cdc.gov/mrsa/community/index.html.

[5] N. Plipat, I. H. Spicknall, J. S. Koopman, and J. N. Eisenberg, "The dynamics of methicillin-resistant Staphylococcus aureus exposure in a hospital model and the potential for environmental intervention," *BMC infectious diseases*, vol. 13, no. 1, p. 595, 2013.

[6] H. Lei, R. M. Jones, and Y. Li, "Exploring surface cleaning strategies in hospital to prevent contact transmission of methicillin-resistant Staphylococcus aureus," *BMC Infectious Diseases*, vol. 17, no. 1, p. 85, Jan 2017. [Online]. Available: https://doi.org/10.1186/s12879-016-2120-z

[7] J. Coia, G. Duckworth, D. Edwards, M. Farrington, C. Fry, H. Humphreys, C. Mallaghan, D. Tucker, J. W. P. of the British Society of Antimicrobial Chemotherapy *et al.*, "Guidelines for the control and prevention of meticillin-resistant Staphylococcus aureus (MRSA) in healthcare facilities," *Journal of hospital infection*, vol. 63, pp. S1–S44, 2006.

[8] E. M. Jochimsen, L. Fish, K. Manning, S. Young, D. A. Singer, R. Baker, and W. R. Jarvis, "Control of vancomycin-resistant enterococci at a community hospital: Efficacy of patient and staff cohorting," *Infection Control & Hospital Epidemiology*, vol. 20, no. 2, pp. 106–109, 1999.

[9] K. A. Schmidt and R. S. Ostfeld, "Biodiversity and the dilution effect in disease ecology," *Ecology*, vol. 82, no. 3, pp. 609–619, 2001.

[10] T. Herman, S. Pemmaraju, A. Segre, P. Polgreen, D. Curtis, J. Fries, C. Hlady, and M. Severson, "Wireless applications for hospital epidemiology," in *1st Association for Computing Machinery International Workshop on Medical-Grade Wireless Networks*, New Orleans, LA, May 18 2009, pp. 45–50.

[11] P. Polgreen, C. Hlady, M. Severson, A. Segre, and T. Herman, "Method for automated monitoring of hand hygiene adherence without radio-frequency identification," *Infection Control and Hospital Epidemiology*, vol. 31, no. 12, pp. 1294–1297, December 2010, [PMID: 20973724].

[12] M. N. Monsalve, S. V. Pemmaraju, G. W. Thomas, T. Herman, A. M. Segre, and P. M. Polgreen, "Do peer effects improve hand hygiene adherence among healthcare workers?" *Infection Control & Hospital Epidemiology*, vol. 35, no. 10, pp. 1277–1285, 2014.

[13] The National Institute of Diabetes and Digestive and Kidney Diseases Health Information Center, "Hemodialysis," https://www.niddk.nih.gov/health-information/kidney-disease/kidney-failure/hemodialysis.

[14] M. B. Rivara, S. V. Adams, S. Kuttykrishnan, K. Kalantar-Zadeh, O. A. Arah, A. K. Cheung, R. Katz, M. Z. Molnar, V. Ravel, M. Soohoo *et al.*, "Extended-hours hemodialysis is associated with lower mortality risk in patients with end-stage renal disease," *Kidney international*, vol. 90, no. 6, pp. 1312–1320, 2016.

[15] H. W. Hethcote, "The mathematics of infectious diseases," *SIAM Rev.*, vol. 42, no. 4, pp. 599–653, Dec. 2000. [Online]. Available: http://dx.doi.org/10.1137/S0036144500371907

[16] E. Girou, S. Loyeau, P. Legrand, F. Oppein, and C. Brun-Buisson, "Efficacy of handrubbing with alcohol based solution versus standard handwashing with antiseptic soap: randomised clinical trial," *Bmj*, vol. 325, no. 7360, p. 362, 2002.

[17] O. Sherlock, N. O'Connell, E. Creamer, and H. Humphreys, "Is it really clean? An evaluation of the efficacy of four methods for determining hospital cleanliness," *Journal of Hospital Infection*, vol. 72, no. 2, pp. 140–146, 2009.

[18] A. F. Brouwer, M. H. Weir, M. C. Eisenberg, R. Meza, and J. N. S. Eisenberg, "Dose-response relationships for environmentally mediated infectious disease transmission models," *PLOS Computational Biology*, vol. 13, no. 4, pp. 1–28, 04 2017. [Online]. Available: https://doi.org/10.1371/journal.pcbi.1005481

[19] 2019 MRSA Research Center, The University of Chicago, "Frequently asked questions about MRSA," http://mrsa-research-center.bsd.uchicago.edu/patients_families/faq.html.

[20] S. Li, J. N. Eisenberg, I. H. Spicknall, and J. S. Koopman, "Dynamics and control of infections transmitted from person to person through the environment," *American journal of epidemiology*, vol. 170, no. 2, pp. 257–265, 2009.

[21] Hankyu Jang, Samuel Justice, Philip M. Polgreen, Alberto M. Segre, Daniel K. Sewell, Sriram V. Pemmaraju, "Supplementary material," https://compepi.cs.uiowa.edu/archive/jang19sup.pdf.

[22] D. Pittet, B. Allegranzi, H. Sax, S. Dharan, C. L. Pessoa-Silva, L. Donaldson, J. M. Boyce *et al.*, "Evidence-based model for hand transmission during patient care and the role of improved practices," *The Lancet infectious diseases*, vol. 6, no. 10, pp. 641–652, 2006.

[23] W. C. Albrich and S. Harbarth, "Health-care workers: source, vector, or victim of MRSA?" *The Lancet infectious diseases*, vol. 8, no. 5, pp. 289–301, 2008.