Manuscript Number:**EPIDEMICS-D-24-00069**  
  
Manuscript title: **Estimating nosocomial transmission of micro-organisms in hospital settings using patient records and culture data**

**Editor's comments**  
**Editor 1**

I concur with the reviewers that bypassing HCWs in such modelling is quite a strong assumption... How to interpretet the estimated transmission parameters in a hospital hygiene perspective is therefore difficult. At best, the model would be changed, but at least, some discussion regarding the consequences is warranted.

Answer. Thank you for the comment. We agree that our inference of nosocomial transmission rate embeds substantial uncertainty as it models person-to-person transmission, vectored transmission by HCWs, and also fomite transmission by, for example, contact with infected devices using the same parameter. However, in the absence of data to parametrize the movement of HCWs or of the presence of environmental reservoirs we limit ourselves to patient movement data available. In the section *Understanding nosocomial transmission,* we discuss these limitations and suggest that future models explicitly and separately represent those modes of transmission.

To further discuss the consequences of our assumption we have elaborated on this issue in the discussion: ‘Fomite transmission could contribute to the nosocomial acquisition through both patient contact, for example, via the handling of uncleaned devices, or by supporting vectorial transmission by HCWs. If those modes of transmission contribute linearly to the estimated nosocomial transmission rate, then a fraction of our estimate would be attributable to that specific mode. If the contribution is non-linear, then it would be necessary to investigate the frequency of interaction and the fraction of HCWs colonized on a ward at a given time. The effects of such interactions on nosocomial transmission would be difficult to resolve without data, specifically measurements of environmental and HCW colonization.

**Editor 2**

A second point is I did not understand how the ABM formulation was essential to your results? It seems that the transmission model is Markovian and could have been simulated otherwise. In other words, you could have simulated the hospital with standard compartmental models, and I don't think that the reslts would be changed. It would be good to show whether the ABM is really of importance, or if it is just a choice for simulation.

Answer. Thanks for the comment as it allows us to further describe our model-inference approach. The preference for an ABM versus a compartmental stochastic model, which is in part choice, is described below.

1. Both the observational model, as well as the process model, use individual-level test and movement data. Together, these data resolve the specific agents who have been tested—and where they are at that time. The ABM form thus enables use of a dynamical observational model as well as parametrizes with individual-level testing sensitivity.
2. During the study period, few wards are consistently populated, and thus using, for example, a stochastic compartmental model requires aggregation of the wards to a coarser spatial scale. This also requires a different parametrization of the observational model, for example by assuming a Binomial observational model with the number of trials equal to the number of tests and the probability of testing positive proportional to the fraction of carriers inside a spatial unit.
3. The movement of patients in the ABM is as defined by the individual-level data replaying what happened and was reported in the hospital. The movement data are thus suited to be represented by an ABM framework, or some system with explicit spatial simulation, e.g. a metapopulation model. However, the use of a coarser aggregation form would require to design of an additional movement model.
4. Finally, even when another movement model of patients on a coarse spatial scale is considered it is likely that that parametrization ignores the heterogeneity in admissions and discharge rates that are time-varying. Additionally, patient length of stay was also heterogeneous across the hospital network (supplementary material Figure S6), and aggregations at any spatial scale are unlikely to represent this heterogeneity.

**Reviewers' comments**  
**Reviewer #1**  
  
**Comment 1.** A justification is missing in the methods section or supplementary material for the assumption of a Gaussian observation process.  
Answer. Thanks for this comment. We don't assume a Gaussian observational process. We did assume that the observations/assimilated data are normally distributed, as the method used for data assimilation, the ensemble adjustment Kalman filter (EAKF), models both the likelihood and prior as Gaussian, so the posterior is also Gaussian. As we only have one observation point the Gaussian approximation is suitable, because of the mathematical convenience in the data assimilation method. It indeed has been widely used in forecasting and inference of epidemiological dynamics .

However, our observational process directly observes the patient status in each ward, and it is not assumed that the number of detected carriers is drawn from a normal distribution, the simulated observations are directly observed from the number of carriers in the hospital and the individual test data we used for parametrized the inference.

**Comment 2.** The observed data is assumed to be normally distributed, should this not be a lognormal distribution? I assume you are constraining to positive values.

Answer. Thanks for the comment. The EAKF assumes the observed/assimilated data is normally distributed so the posterior can be updated with a deterministic mathematical formula. This way we only parametrize the observed data using an observational error variance (OEV, as indicated in the Supplementary Information section **Simulation-based inference framework**) that we model proportional to the data, that is to the number of positive cultures. There's no need to constrain it to positive values as the OEV enters the update deterministically. It is possible, however, that the posterior of both the parameters and the observations is outside the prior range or negative. In the process model updates, we constrain the parameters inside the specified prior range and the observations to be positive.  
  
**Comment 3.** Figures are missing axis labels and alphabetic labels (e.g. A, B which are used in the figure caption) throughout the manuscript and supplementary materials. For example, in Figure 1 and Figure 4. Please add these to ensure the figures are clear.

Answer. Thanks for this. We forgot to add the labels in the last update of the manuscript. In the current submission, we have included them.  
  
**Comment 4.** Figure 4 caption refers to a legend which isn’t present. Please add and check other figures.

Answer. Thanks, in the revision we have included the caption.   
  
**Comment 5.** Figure S12 refers to ‘institutions’, this terminology is not used anywhere else in the manuscript. The distinction between institution and hospital is not clear to me, please clarify.

Answer. Thank for making noting this oversight. We have changed it to 'hospital'.

**Comment 6.** The abstract would benefit from stating that an ensemble adjustment Kalman filter is used.

Answer. We now include this information in the abstract.

**Comment 7.** A rationale is needed for using the ensemble adjustment Kalman filter method over a method more often used for inference of transmission rate parameters, such as ABC/SMC/MCMC.

Answer. The algorithm is a choice. Both SMC and EAKF have been widely in simulation-based inference of epidemiological dynamics, see for example: (1–6). Indeed, some comparisons between those are available (7–10). Due to the high dimensional state space of the problem we present that corresponds to the number of patients during the study period the EAKF is preferred as it allows a deterministic update of the prior distribution. As a consequence, fewer Monte Carlo samples are needed when compared to the other Bayesian approaches mentioned by the reviewer. Indeed, the EAKF has been for assimilation for data assimilation of other ABMs, including network models with millions of individuals (11).

**Comment 8.** The study period coinciding with peak COVID-19 cases in the city is mentioned as a limitation. Further discussion on how this might affect the study results would be beneficial. Did you consider fitting multiple transmission rates for different time periods, perhaps when different levels of restrictions were in places?

Answer. Finish  
  
**Comment 9.** A more detailed discussion is needed on the types of infectious pressure that the ABM model is not capturing, particularly the lack of hospital staff in the model. These are briefly mentioned in *Understanding nosocomial transmission*. Ideally, when modelling nosocomial transmission an ABM would either explicitly model HCWs and hospital staff as agents in the model, or implicitly include them within the force of infection. Moreover, infection dynamics could be disentangled further if other sources were considered, such as: staff infectious pressure, spatial infectious pressure from other wards (patients/staff) that may be connected, and a background infection pressure. I assume staff data was unavailable for this study?

Answer. Thank you for these comments as they allows us to further strengthen our discussion around the estimated parameters. As the reviewer intuits, HCW data were not available for this study; we implicitly represent transmission via HCWs as part of the nosocomial transmission rate parameter. This comment is similar to the comment of **Editor 1,** which the reviewer can see at the beginning of the document. We have extended our discussion in the section *Understanding nosocomial transmission* to further clarify how our nosocomial transmission rate embeds both, person-to-person, and vectored transmission via HCWs and possible transmission by contact via environmental reservoirs. We also discuss the possible contributions of these various modes to the nosocomial transmission rate.  
  
**Comment 10.** It is unclear to me why the force of infection for each ward only considers the infection/colonization status of patients in the same ward. Did you consider adding a ‘background’ transmission rate parameter which scaled with the number of infections in the hospital at that time?

Answer. Thanks for this comment. A background transmission rate might model, for example, fomite transmission, which could be represented as proportional to prevalence in the hospital. We initially attempted to estimate two transmission rates: the a person-to-person transmission rate and a second additional environmental transmission rate parameter. We were unable to accurately identify both parameters using available data. As happened with the environmental transmission we attempted to model and infer another background transmission rate is likely to make the system unidentifiable. As a consequence, we decided to combine transmission into a single parameter. The data used to inform the inference are sparse and represent only a small fraction of the prevalence and do not support inference of multiple modes of transmission. This challenge magnifies as we are considering a range of pathogenic bacteria whose natural history is poorly understood.  
  
**Comment 11.** A daily contact network was used rather than a finer-scale (e.g. hourly) to capture patient movements, was this for computational benefit? It is not clear to me if a patient was admitted into A&E and subsequently to an inpatient ward on the same day, whether they would only appear in the inpatient ward of the contact network? If so, the model may not be capturing transmission in these staging areas.

Answer. We decided to use a daily time step, both for simplicity and computational benefit.

**Comment 12.** The final three sentences of the introduction seem unnecessary and should be covered in the abstract/results and discussion.

Answer. We have deleted these sentences.   
  
**Reviewer #2**

This is an interesting paper and the methods are well explained. However, by focussing on carriage, particularly in the case of *E. coli*, I worry that the conclusions are not helpful or informative and this needs to be addressed and discussed in more detail. The model does not distinguish between commensal bacteria and pathogenic or resistant bacteria and the message that *E. coli* is not commonly transmitted in hospital settings is likely not true, and is in fact an artefact of the model structure that only allows for a single colonization event with *E. coli*. While all models are abstractions, this issue cannot be ignored.  
  
Here is a list of comments, please also see annotations in the PDF document attached (if you can't get the attached file, inquire with the journal).

**Comment 1.** There is no definition of what is classed as a nosocomial case in the underlying data. Many cases that are considered community acquired based on days in hospital before infection is detected are in fact potentially related to a previous hospital event. Is this included in the definition of nosocomial used here?  
Answer. Thanks for these comments. In the first paragraph of the discussion, we wrote *"The patient-level clinical culture data mostly represent infection. Clinical culture samples were targeted at one body site and were typically obtained on patients presenting symptoms, suggestive of infection at a specific site and a preponderate use of clinical cultures for diagnosis rather than surveillance."* In addition, in the section *Understanding effective sensitivity* we mention that surveillance is mostly targeted to infected patients: "*Surveillance of micro-organism infection and colonization in patients is primarily the product of clinician-directed collection of cultures for infection-compatible clinical symptoms (i.e. fever, dysuria, or cough).*"

The study hospital system is a clinical setting in which most carriage is detected by diagnosis and not by screening. To clarify this further, we now include a sentence in the Methods section *Data: Clinical cultures*: "Cultures were collected mostly at the discretion of clinicians as part of diagnosis in order to confirm infection ".

**Comment 2.** Are some sites more likely to be sampled than others, therefore effecting the estimated prevalence in the underlying data?  
Answer. There are some wards in which patients were cultured more often, see Figure 1D and SI Figure S12. Our observational model accounts for the effect of different sampling across wards in the hospital network. Indeed, as our observational model uses the number of clinical cultures at the individual level we are accounting for the likelihood of diagnosis given infection, which is differential across wards. It is possible however that wards have different surveillance settings: i.e. they differ on the amount of screening and diagnostic. Those differences are not modeled and could bias the estimate of the effective sensitivity . However, most of the nosocomial data used to inform the inference were typically clinician ordered for patients suspected to be infected. In the SM we show that under a scenario in which screening is negligible high values of could only be obtained with high values of the ratio between diagnosis given infection and probability of testing (i.e. high values of , see SM Fig S11) combined with high values of the infection to clearance ratio . This ratio, , would suggest that infection rates given carriage would need to be much faster than carriage clearance, which is unlikely. It also suggests that even when and the infection-to-clearance ratio varies within wards, it is unlikely that this will result in substantially different effective sensitivity values.

**Comment 3.** The parameters underlying the model are drawn from literature outside of the region being simulated. While I appreciate that this is a limitation that cannot be avoided when there are no available data, a full sensitivity analysis should be performed on these parameters to determine the impact that they have. For example some of the *E. coli* estimates for community carriage are very high and this reduces the impact of nosocomial transmission in this model framework where patients already carrying *E. coli* cannot be infected again. A sensitivity analysis is essential here as it is highly unlikely these results hold true for antibiotic-resistant *E. coli* which likely have a much lower prevalence in the community. I also feel that this point should be drawn out in the discussion. The introduction talks about ABRO, but this is a very different problem to what is being modelled in this paper.  
Answer. Thanks for this comment, as it allows us to refine the relationship between the community prevalence and the estimated nosocomial transmission. In the previous analysis, we selected 3 values of the importation rate spanning values found in the literature worldwide. The inferred parameters with such parametrization of the importation rate were presented in Figure 3. We now present inferences by using only the highest value reported in the literature , and fractions of this value (). For all bacterial pathogens we varied between 1 and 0.3, with steps of 5%. The result of those inferences is presented in Figure R1 below. In each subplot, we highlight the previous ranges of importation rates (from lowest to highest reported in the literature) with green dashed lines. We found that within the previous region considered our results are consistent with the findings presented: all bacterial pathogens, except *E. coli* and MSSA*,* span similar ranges of both the nosocomial transmission rate and the effective sensitivity. In Figures R2 and R3 we present the nosocomial transmission rate and the effective sensitivity as a function of the importation rate. We investigate if a linear fit accounts for changes in the estimated parameters by fitting a linear regression to the mean parameter estimates. We use the coefficient of determination to investigate if the changes in the parameter estimates are accounted for by those in the community prevalence . We also present the estimated uncertainty by the inference method as error bars but don't use them in the regression analysis.

The estimate for the nosocomial transmission rates for *E. coli* are consistent until values drop below importation rates of 40%, a drop of more than 50% of the initial highest value . We find a similar pattern for the estimated effective sensitivity of this pathogen. We found that the importation rate explains inferred changes of both the nosocomial transmission rate () and the effective sensitivity (). However, as mentioned the relation is non-linear with importation rate values below 40% causing an increase in and a decrease in . For higher importation values the estimates remain unchanged. This result is of interest when contrasted with the relation obtained for the other microbial bacterial pathogens. For all the other microbial pathogens we find only one of the estimated parameter changes as a function of the importation rate. Specifically, the nosocomial transmission rate was found to be explained by changes in the importation rate for *E. faecalis* () and *E. faecium* (). Contrasted with the non-linear and thresholded relationship found for the nosocomial transmission rate for *E. coli*, for the enterococcus species the decay in is well explained by an increase in . For the rest of the bacteria, *K. pneumoniae ()*, *P. aeruginosa* (), and MSSA () the effective sensitivity changes as a function of the importation rate but the nosocomial transmission rate does not. The relationship is non-linear and displays a threshold pattern with values below 50% of the highest importation rate for *P. aeruginosa* and *K. pneumoniae*. For MSSA however, the decay of is well explained by an increase in , thus displaying a linear relationship.

Zooming into the estimated mean values on the lowest and highest importation rates and on the suggested threshold one obtains the following numbers: For *E. coli* the mean estimates of increase from the highest importation rate to the lowest, . As suggested by the relationships presented (Figure R2 and R3) that change is compensated with a change in the opposite direction of . When compared to the estimated values before the threshold the changes are of and . Following the same exercise for *K. pneumoniae*, *P. aeruginosa* which exhibits a non-linear thresholded curve but only for one obtains and respectively.

These results together show a robust estimate of the nosocomial transmission rate , and the effective sensitivity spanning a broader range of importation rates compared to the one presented in the main text. We also show that the trade-off between the transmission and detection rates could be non-linear exhibiting a threshold in which decreases in importation rates cause a change in the estimated quantity until it drops below a value. However, those changes are small and captured by the inferred uncertainty during the inference (error bars in Figures R3 and R4).

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Figure R1. **Marginal posterior parameter estimates across different importation rates levels.** **A)** nosocomial transmission rate and **B)** effective sensitivity .In both **A)** and **B)** the parameter estimates mean and 95% CI are shown with dots and error bars around the mean. The importation rate is shown in the y-axis and it is also color-coded with shades of green. Darker colors present higher values of while lighter colors lower values as indicated in the legend. In all plots, the dashed lines show the previous parameter range introduced in the main text, the High and Low values found in the literature review presented in the Supplementary Material **Prevalence estimates**. Bacterial pathogens are sorted from upper to lower proportional to the reported abundance and match the order presented in SM Figure S13.

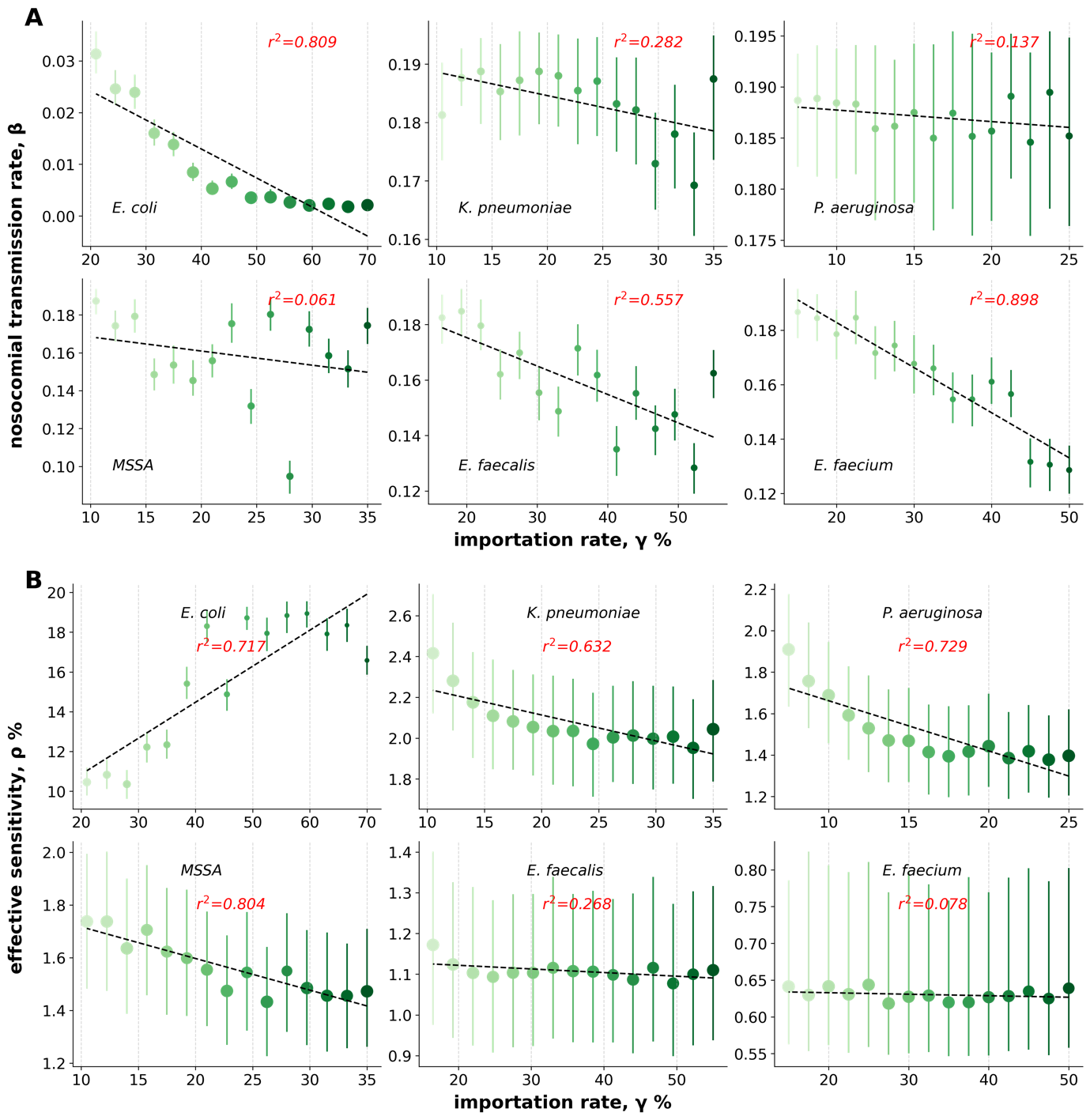


Figure R2. **Relationship between the parameter estimates and the importation rate . A)** nosocomial transmission rate and **B)** effective sensitivity . In each subplot, we present the mean parameter estimate with dots and the 95% CI using error bars. We used the same color scheme introduced in Figure R1, darker colors indicate a higher importation rate while lighter colors a lower one. The size of the dots corresponds to opposite parameter, in **A)** they depict the effective sensitivity and in **B)** the nosocomial transmission rate. A linear regression is shown as a dashed black line and the coefficient of determination is presented inside each subplot red. The bacterial pathogens are sorted from left to right and upper to lower plots according to their reported abundance.

**Comment 4.** limitations could be addressed by a global sensitivity analysis as suggested.  
Answer. Thanks for the comment as it allows us to point to the reviewer to some of the inferences we have done and some others we present in the current submission. In the inferences we presented in the previous submission, we first investigated the effect of readmission. For this, we tracked the patient's state even when discharged from the hospital and presented the result of these inferences in Supplementary Material Figure S13. The discussion of these results was presented in the paragraph *Limitations: heterogeneity in carriage duration and readmission*.

We conducted synthetic inferences: parameter estimates on simulated data with two levels of community prevalence . The posterior joint density was presented in Figure 2, and calibration simulation with the estimated parameters was compared to that with the true parameters and presented in SM Figure S9. These results showed we were able to estimate both , and the calibration to the observed data was as good as the one obtained with simulations with the true parameters. As the reviewer(s) point, some of the microbial pathogens have community prevalences of between 15 and 35% (*K. pneumoniae*), or between 5 to 15% (MRSA). These ranges are considered the lowest to highest community prevalences we found in studies worldwide. To further investigate the sensitivity of the parameter estimates to the importation rate parameter we conducted synthetic inference with . We used 3 different levels of detection rates, varying the effective sensitivity , and 3 different levels of nosocomial transmission . Note that the values found for the effective sensitivity span those inferred for the microbial pathogens. To show that the inference is robust to low transmission regimes we selected values of lower than those inferred for the pathogenic bacteria. In the 3 Figures below, Figures R4-R6, we present the posterior joint distribution for those each community prevalence. We find a consistent pattern regardless of the community prevalence: the simulation-based inference method accurately identifies the parameters when the nosocomial transmission rate and the effective sensitivity is not the lowest. Even when or are in the lowest value selected for the synthetic inferences, or , we find the system can locate the region of the truth value. However, the posterior does not always capture the truth (yellow crosses). This result is because if the posterior didn't have information of the assimilated data it would result in an estimate in the middle of the prior range and/or with some uncertainty around it. To further show this localization around the truth in Figure R7 we present the convergence plots of the synthetic inferences with or . We found that across iterations of the Iterated Filtering, the marginal posterior estimates asymptotically gravitate toward the true parameter values. We also find that the effective sensitivity is better estimated than the nosocomial transmission rate in this lower transmission and lower detection regimen.

Lastly, we investigate the inference of the parameters by using lower values of the importation rate for each microbial pathogen as indicated in the previous comment of the reviewer, ***comment 3***.

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*Figure R4****.* Identifiability, parameter estimates on simulated data.** Joint posterior estimates for importation rate γ=5%. The posterior estimate is highlighted with a density plot (darker means more probable). In each subplot the true value used for simulating the stochastic trajectory to infer is highlighted in the title of each scenario and with a yellow cross at the intersection of the two black dashed lines. The x-axis shows the effective sensitivity ρ (%) and the y-axis the nosocomial transmission rate β. Note that in all subplots the prior range is the limits of each axis, ρ increments from left to right and β from upper to lower plots.

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*Figure R5.* **Identifiability, parameter estimates on simulated data.** Joint posterior estimates for importation rate γ=10%. The posterior estimate is highlighted with a density plot (darker means more probable). In each subplot, the true value used for simulating the stochastic trajectory to infer is highlighted in the title of each scenario and with a yellow cross at the intersection of the two black dashed lines. The x-axis shows the effective sensitivity ρ (%) and the y-axis the nosocomial transmission rate β. Note that in all subplots the prior range is the limits of each axis, ρ increments from left to right and β from upper to lower plots.

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*Figure R6.* **Identifiability, parameter estimates on simulated data.** Joint posterior estimates for importation rate γ=15%. The posterior estimate is highlighted with a density plot (darker means more probable). In each subplot, the true value used for simulating the stochastic trajectory to infer is highlighted in the title of each scenario and with a yellow cross at the intersection of the two black dashed lines. The x-axis shows the effective sensitivity ρ (%) and the y-axis the nosocomial transmission rate β. Note that in all subplots the prior range is the limits of each axis, ρ increments from left to right and β from upper to lower plots.

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Figure R7. **Convergence plots of inferences for synthetic data with low and .** Marginal posterior parameter estimates for importation rate of **A)** 5 **B)** 10 and **C)** 15%.In each panel left subplots present the convergence for the effective sensitivity , and the right subplots for the nosocomial transmission rate . In each row of each panel the truth value is indicated in an inset text, the truths are also highlighted as dashed red lines in each subplot as indicated in the legend. The convergence of the marginal posterior distribution is presented for the mean (black line) and the 95 and 50% credible intervals as indicated in the legend.

**Comment 5.** The layout of the manuscript is excellent and the subheadings are very clear and make the manuscript very easy to navigate. However the writing in this manuscript feels rushed and is confusing in places. The manuscript would benefit from a thorough readthrough and edit by someone less familiar with it's content.  
Answer. Jeff and Sen what can I say here? I think we have had multiple rounds of edits over the manuscript, do you think we still need some more edits?

**Reviewer #3**

I feel the article applies interesting methodology and a lot of technical interesting work has been performed, but still, I wonder how much added value the manuscript has to the existing literature. The biological conclusions, that *E. coli* spreads not very well and MRSA reasonably well in hospital environments is not new and I do not trust the numerical values too much.  
  
**Comment 1.** My impression is that fixing the importation rate is quite a big assumption. Especially when the amount of data is limited, as is the case as primarily infection data are being used, differentiation between importation and transmission is difficult as both are positively related to a high prevalence. A choice of the importation rate based on the literature, from many different countries, can have quite some impact on the transmission parameter as is seen in the sensitivity analysis.

Answer. We agree with the reviewer that using importation from other locations is a big assumption. For that reason, we selected values that spanned the lowest, median, and highest values we found in the literature across the globe. We discussed this in detail in the section *Heterogeneity and steady state of community prevalence*, and further discussed some consistencies in the values reported worldwide. Without additional data to parametrize the model-inference system with information from New York City, specifically northern Manhattan, it is suspect to pick one value. Despite importation rates spanning a range of reported values worldwide, we find consistency in the estimated values for both the nosocomial transmission rate and the effective sensitivity (see **Comment 3** of **Reviewer 2**).   
  
**Comment 2.** Also, I find the assumption of a constant transmission parameter in all wards and all hospitals rather unrealistic? I expect that there will be at least a three-fold difference between wards (with ICUs among the wards with the highest transmission parameters). How should we interpret the average transmission parameter which is calculated in this study?  
Answer. We use a single parameter to model the transmission rate from infected to susceptible patients. However, by creating a daily contact network we are capturing heterogeneity in contact in time. In a typical epidemiological model, the force of infection is proportional to a transmission rate that embeds the probability of transmission upon contact, times the number of contacts. Our modeling approach, by using the individual-level patient data, is discriminating the number of contacts in time. However as the reviewer suggests control measures are different between wards. Our estimate presents a weighted average across the hospital network, but we are controlling by the time-varying nature of the contacts. In future studies consideration of differential control measures across the hospital network might reveal differential spread across the hospital. However, without additional data to support the parametrization of control measures introduction and inference of more parameters will make the system unidentifiable.

**Comment 3.** Why are the analyses to determine identifiability of the parameters only done with importation rates of 25% and 50%? A lower value of 5% or 10% seems to reflect the situation for MRSA and Pseudomonas better.  
Answer. Thanks for the suggestion as it allows us to further investigate the identifiability of the simulation-based inference system we presented. In **Comment 4** of **Reviewer 2** we extended our discussion introduced in the main text. We investigated the identifiability of the parameters using simulated data with importation rate values of 5, 10 and 15% as the reviewer suggested (Figures R1-R4). We found we were able to accurately identify the parameters.

**Comment 4.** I find the choice of the time period a bit strange, a relatively short time period is chosen to ensure that the admission prevalence is more or less constant, but the time period does overlaps with the COVID-19 epidemic which had a big impact on processes in the hospital. Moreover, from Figure 1 I conclude that the number of hospitalized patient is zero at the start of the study? It seems that only data are used from the starting date onwards, but this means that patients already present in the hospital at the starting data are not part of the estimation process, which means that in the first weeks/months, the prevalence will be relatively low. This can also be seen form the empirical colonization data. I think only the data should be used from the moment the hospital size is in its stable distribution as the initial data do not represent a stable situation.  
Answer.

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**Reviewer's Responses to Questions**

Note: In order to effectively convey your recommendations for improvement to the author(s), and help editors make well-informed and efficient decisions, we ask you to answer the following specific questions about the manuscript and provide additional suggestions where appropriate.  
  
1. Are the objectives and the rationale of the study clearly stated?  
  
Please provide suggestions to the author(s) on how to improve the clarity of the objectives and rationale of the study. Please number each suggestion so that author(s) can more easily respond.

Reviewer #1: Yes, these are clearly stated.

Reviewer #2: Yes, the study aims to quantify the nosocomial transmission rates of key pathogens and determine their effective detection rate.

Reviewer #3: Yes. Although the assumptions could be stated a bit earlier. Mentioning in the introduction that a frequency-dependent transmission model per ward with the same transmission parameter per ward is used would be helpful to understand the model.

2. If applicable, is the application/theory/method/study reported in sufficient detail to allow for its replicability and/or reproducibility?  
  
Please provide suggestions to the author(s) on how to improve the replicability/reproducibility of their study. Please number each suggestion so that the author(s) can more easily respond.

Reviewer #1: Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:  
The supplementary materials provided detailed explanations of the model and the model code is available.

Reviewer #2: Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:

Reviewer #3: Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:

3. If applicable, are statistical analyses, controls, sampling mechanism, and statistical reporting (e.g., P-values, CIs, effect sizes) appropriate and well described?  
  
Please clearly indicate if the manuscript requires additional peer review by a statistician. Kindly provide suggestions to the author(s) on how to improve the statistical analyses, controls, sampling mechanism, or statistical reporting. Please number each suggestion so that the author(s) can more easily respond.

Reviewer #1

Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:  
Yes, a few minor points:  
  
1) A justification is missing in the methods section or supplementary material for the assumption of a Gaussian observation process.  
  
2) The observed data is assumed to be normally distributed, should this not be a lognormal distribution? I assume you are constraining to positive values.

Reviewer #2: Mark as appropriate with an X:  
Yes [] No [X] N/A []  
Provide further comments here:  
  
There is no definition of what is classed as a nosocomial case in the underlying data. Many cases that are considered community acquired based on days in hospital before infection is detected are in fact potentially related to a previous hospital event. Is this included in the definition of nosocomial used here?  
  
Are some sites more likely to be sampled than others, therefore effecting the estimated prevalence in the underlying data?  
  
The parameters underlying the model are drawn from literature outside of the region being simulated. While I appreciate that this is a limitation that cannot be avoided when there are no available data, a full sensitivity analysis should be performed on these parameters to determine the impact that they have. For example some of the E coli estimates for community carriage are very high and this reduces the impact of nosocomial transmission in this model framework where patients already carrying E coli cannot be infected again. A sensitivity analysis is essential here as it is highly unlikely these results hold true for antibiotic resistant E coli which likely have a much lower prevalence in the community. I also feel that this point should be drawn out in the discussion. The introduction talks about ABRO, but this is a very different problem to what is being modelled in this paper.

Reviewer #3: Mark as appropriate with an X:  
Yes [] No [] N/A []  
Provide further comments here:

4. Could the manuscript benefit from additional tables or figures, or from improving or removing (some of the) existing ones?  
  
Please provide specific suggestions for improvements, removals, or additions of figures or tables. Please number each suggestion so that author(s) can more easily respond.

Reviewer #1:

1) Figures are missing axis labels and alphabetic labels (e.g. A, B which are used in the figure caption) throughout the manuscript and supplementary materials. For example, in Figure 1 and Figure 4. Please add these to ensure the figures are clear.  
  
2) Figure 4 caption refers to a legend which isn’t present. Please add and check other figures.  
  
3) Figure S12 refers to ‘institutions’, this terminology is not used anywhere else in the manuscript. The distinction between institution and hospital is not clear to me, please clarify.

Reviewer #2: No

Reviewer #3: No

5. If applicable, are the interpretation of results and study conclusions supported by the data?  
  
Please provide suggestions (if needed) to the author(s) on how to improve, tone down, or expand the study interpretations/conclusions. Please number each suggestion so that the author(s) can more easily respond.

Reviewer #1: Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:

Reviewer #2: Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:

Reviewer #3: Mark as appropriate with an X:  
Yes [X] No [] N/A []  
Provide further comments here:  
  
The estimation procedure in itself is correct, but I have problems with several assumptions of the model.

6. Have the authors clearly emphasized the strengths of their study/theory/methods/argument?  
  
Please provide suggestions to the author(s) on how to better emphasize the strengths of their study. Please number each suggestion so that the author(s) can more easily respond.

Reviewer #1: Yes, the importance of modelling nosocomial transmission, particularly of bacterial pathogens is clear, as are the study findings. A few minor comments regarding the inference methodology:  
  
1) The abstract would benefit from stating that an ensemble adjustment Kalman filter is used.  
  
2) A rationale is needed for using the ensemble adjustment Kalman filter method over a method more often used for inference of transmission rate parameters, such as ABC/SMC/MCMC.

Reviewer #2: Yes.

Reviewer #3: Yes

7. Have the authors clearly stated the limitations of their study/theory/methods/argument?  
  
Please list the limitations that the author(s) need to add or emphasize. Please number each limitation so that author(s) can more easily respond.

Reviewer #1: 1) The study period coinciding with peak COVID-19 cases in the city is mentioned as a limitation. Further discussion on how this might affect the study results would be beneficial. Did you consider fitting multiple transmission rates for different time periods, perhaps when different levels of restrictions were in places?  
  
2) A more detailed discussion is needed on the types of infectious pressure that the ABM model is not capturing, particularly the lack of hospital staff in the model. These are briefly mentioned in Understanding nosocomial transmission.  
  
Ideally when modelling nosocomial transmission an ABM would either explicitly model HCWs and hospital staff as agents in the model, or implicitly include them within the force of infection. Moreover, infection dynamics could be disentangled further if other sources were considered, such as: staff infectious pressure, spatial infectious pressure from other wards (patients/staff) that may be connected, and a background infection pressure. I assume staff data was unavailable for this study?  
  
  
3) It is unclear to me why the force of infection for each ward only considers the infection/colonization status of patients in the same ward. Did you consider adding a ‘background’ transmission rate parameter which scaled with the number of infections in the hospital at that time?  
  
  
4) A daily contact network was used rather than a finer-scale (e.g. hourly) to capture patient movements, was this for computational benefit? It is not clear to me if a patient was admitted into A&E and subsequently to an inpatient ward on the same day, whether they would only appear in the inpatient ward of the contact network? If so, the model may not be capturing transmission in these staging areas.

Reviewer #2: Yes, but some of these limitations could be addressed by a global sensitivity analysis as suggested.

Reviewer #3: Yes

8. Does the manuscript structure, flow or writing need improving (e.g., the addition of subheadings, shortening of text, reorganization of sections, or moving details from one section to another)?  
  
Please provide suggestions to the author(s) on how to improve the manuscript structure and flow. Please number each suggestion so that author(s) can more easily respond.

Reviewer #1: The manuscript flows well, just one very minor point:  
1) The final three sentences of the introduction seem unnecessary and should be covered in the abstract/results and discussion.

Reviewer #2: Yes.  
The layout of the manuscript is excellent and the subheadings are very clear and make the manuscript very easy to navigate. However the writing in this manuscript feels rushed and is confusing in places. The manuscript would benefit from a thorough readthrough and edit by someone less familiar with it's content.

Reviewer #3: No

9. Could the manuscript benefit from language editing?

Reviewer #1: No

Reviewer #2: Yes

Reviewer #3: No

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