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Figure R1. **Marginal posterior parameter estimates across different importation rate levels.** In both **A)** and **B)** the estimated mean and 95% CI are shown with dots and error bars around the mean. The importation rate is shown on the y-axis and is also color-coded with shades of green. Darker colors present higher values of while lighter colors have lower values as indicated in the legend. In all plots, the dashed lines show the previous parameter range introduced in the main text, the Highest and Lowest 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.

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*Figure R2****.* Identifiability, parameter estimates on simulated data.** Each figure presents the joint parameter estimates for an importation rate of **A)** γ=5, **B)** γ=10 and **C)** γ=15%. The posterior estimate is highlighted with a density plot (darker means more probable). In each subplot the true value in the first row or column sides 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 R3. **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 the 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.

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Figure R4. **Schematic for sensitivity analyses ignoring weeks at the beginning of the study period.** In all plots we depict the regions left out for data assimilation in the new inferences using gray ribbon regions as indicated in the legend. The number of weeks ignored started at 0 and increased biweekly until 16 weeks were left out. In all plots the COVID19 hospitalizations time series is presented as a black dashed line, its scale does not correspond to the scale in the plots. In **A)** is presented the weekly clinical culture data for each bacterial pathogen as dots and the monthly mean as a continuos line for better visualization. In **B)** we present the admissions, discharges and number of people hospitalized in all the hospital network (upper plot), and the number of clinical cultures (lower plot) as indicated in the legend. Continuous faded lines show the daily numbers as dashed solid lines the weekly average.

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Figure R5. **Sensitivity analyses for the beginning of the time series, and the COVID-19 period.** Mean and 95% CI marginal posterior are presented as dots and bars respectively. We used the 3 levels of the importation rate found in the literature, the **A)** highest, **B)** median and **C)** lowest as presented in the SM section **Prevalence estimates.** To facilitate comparison with the original estimate (inferences with all the time series) we highlight the mean and the 95% CI of this inference with continuous and dashed lines respectively. From left to right, we present each pathogen, and they're sorted according to their reported abundance.