

where are we...

updates using pompjax, and the empirical prevalences from the literature.

ABM inferences

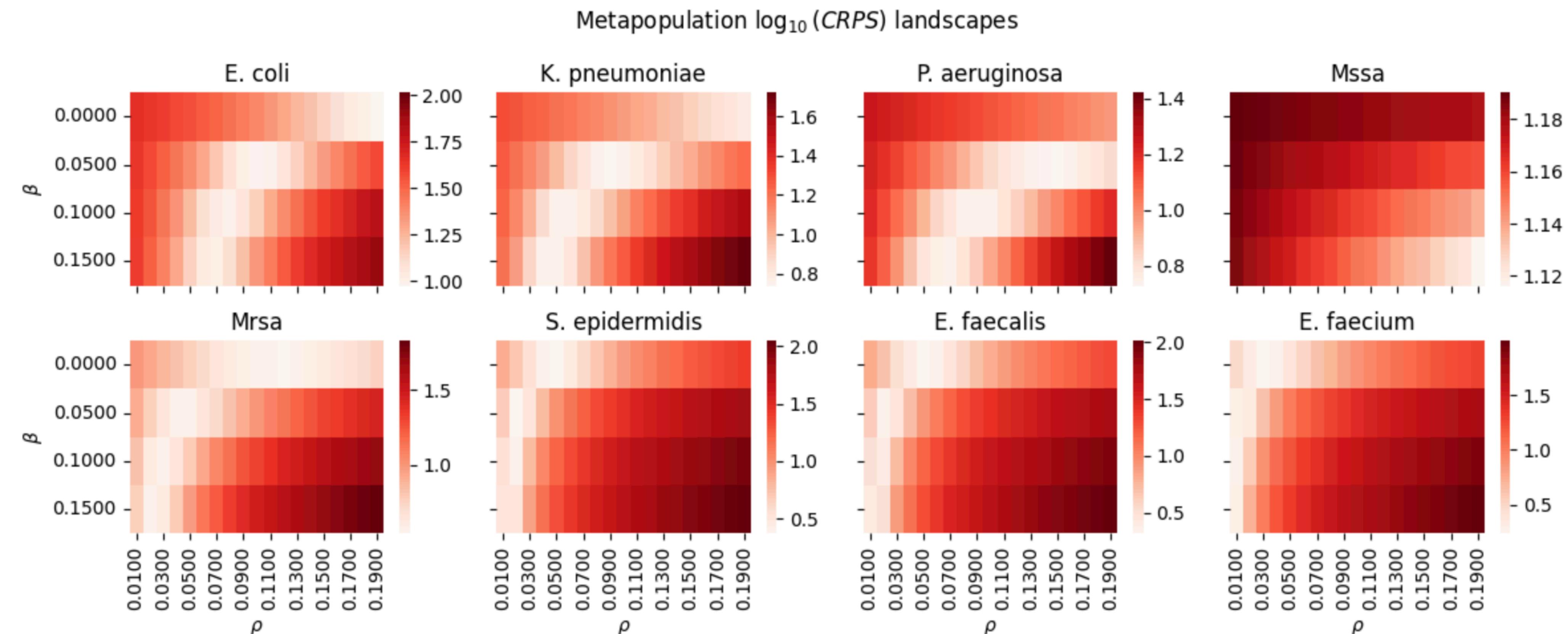
recap

- Process model at daily time scales.
- Same study period as before 01/Feb/2020 to 28/Feb/2021 (weird drop in culture after feb 2021)
- we decided to drop *C. albicans* and include *E. faecalis*, also in the top 15 of microorganism detected.

ABM inferences

Inference on synthetic data.

- as the definition of ρ is a little blurry and hard to find references I did some grid search and computed the fit to the hospital level data to ballpark the range for the different importation rates (AMRO prevalences).



ABM inferences

Inference on synthetic data.

- Using the ranges in the grid search, I selected values that already minimize the CRPS to the hospital-level observations and ran inferences on that.
 - I checked the convergence plots and the inferences seem to be working/converging.
 - The empirical prevalences range from 0.4% (MRSA), to 60.3% (E. coli), so in general, we are covering a huge range of importations from all the AMRO to test in synthetic inferences.
 - Only MRSA and *P. aeruginosa* have importations lower than 15%
 - **Results:** in general it seems that the inference is working very well (truths are falling in the posterior - even shrinking the variance). However, for low importation rates (lower than 15%) the system struggles in both β and ρ .
 - Next slides shows the posterior for the 10 scenarios for all the AMROs. Prior ranges for the inference are shown as the limit of the x-axis.
 - **Next:** If we want to report CI maybe I could remove the shrinking between iterations and see how those posterior look like.

ABM inferences

Shrinking vs Not shrinking

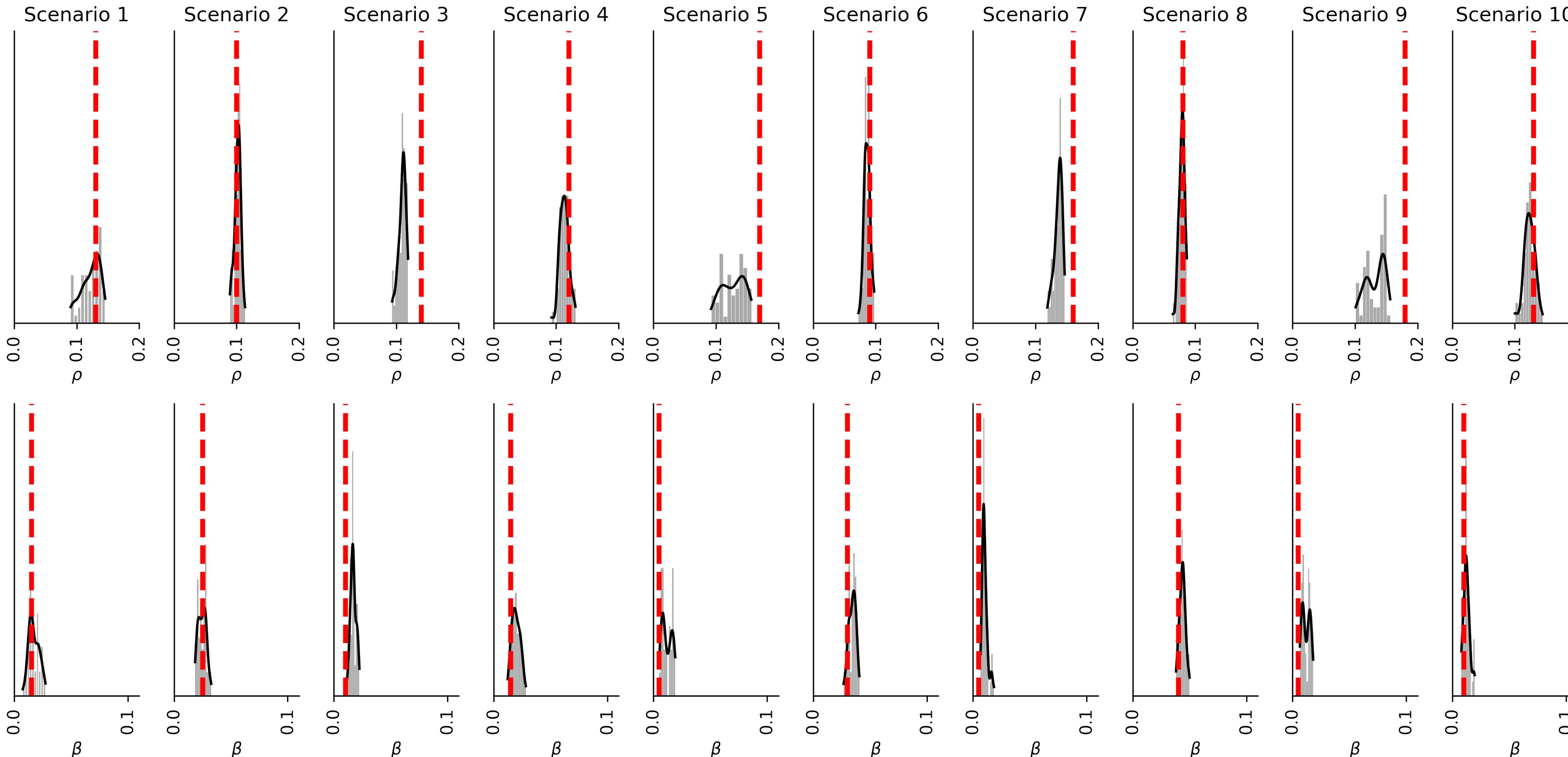
- It seems the not shrinking version is definitely working better, both captures more often the truth value and also provide a correct uncertainty.
- Results differ from the ones Rami obtained with the ABM, high importations led to a more certain estimation of β and low importations to a more uncertain estimation.
- Note, that the limits in the axes are not the prior ranges so in general the posterior is also converging towards the truth even when biased.
- Convergences plots also look to be reaching asymptotically the truth value.
- Also, as the covariance estimated by the EAKF is conserved between iterations that relation is shown in the posterior estimate (not in the original IF implementation).

**ABM inferences on synthetic data
(Previous results shrinking the
variance between IF iterations)**

Inferences on simulated observations

Two observational models;

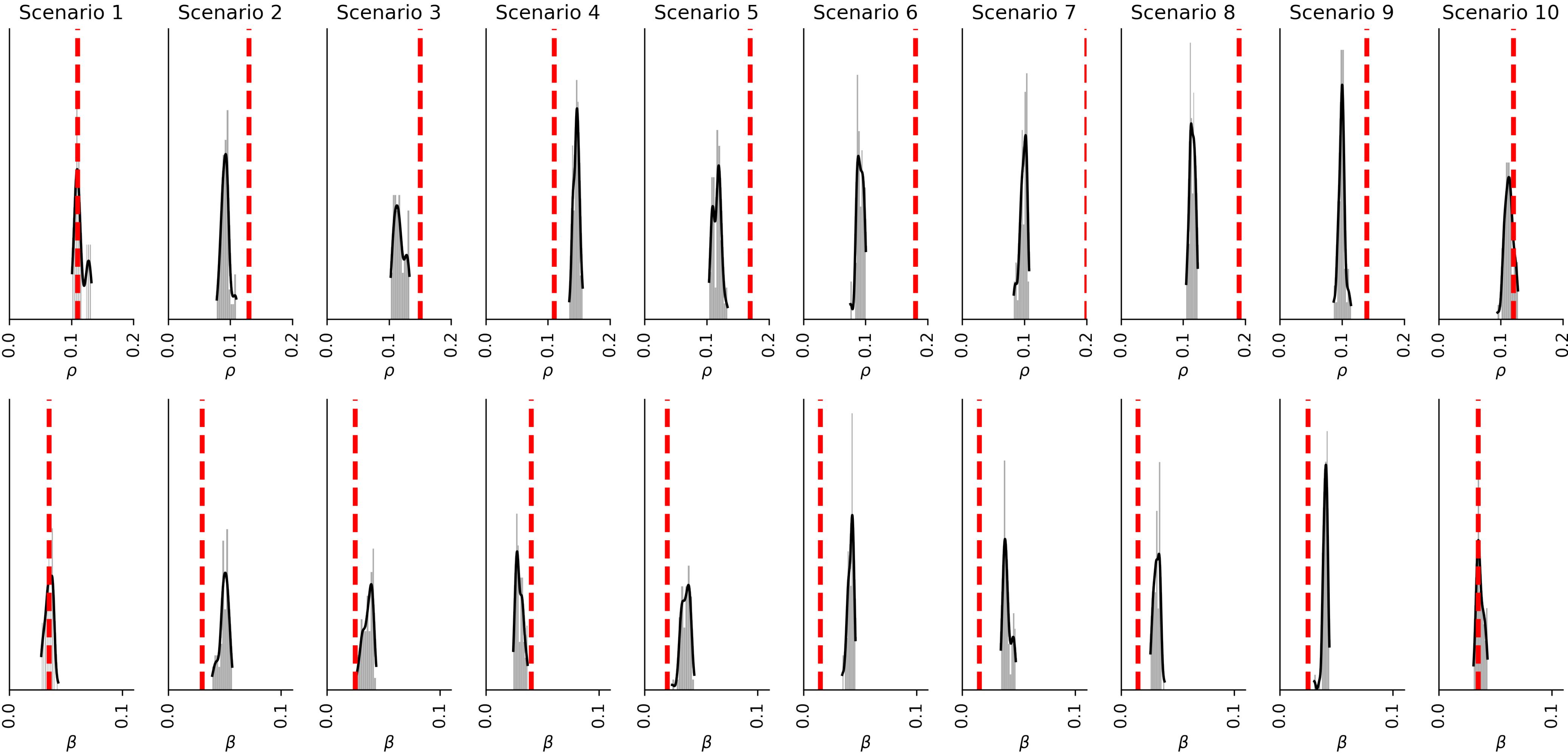
Posteriors for E. coli, $\gamma = 63.0\%$



Inferences on simulated observations

Two observational models;

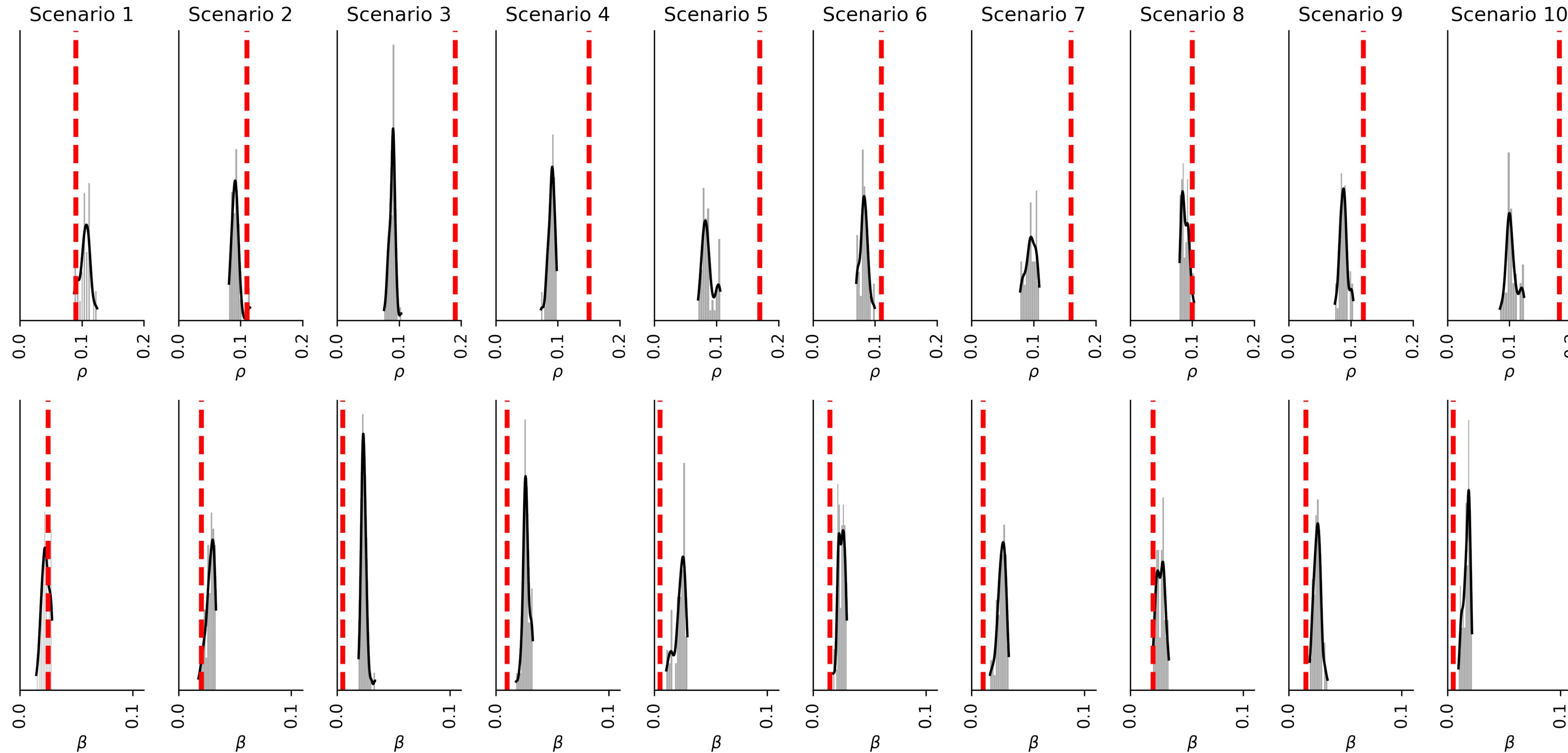
Posteriors for *P. aeruginosa*, $\gamma = 11.6\%$



Inferences on simulated observations

Two observational models;

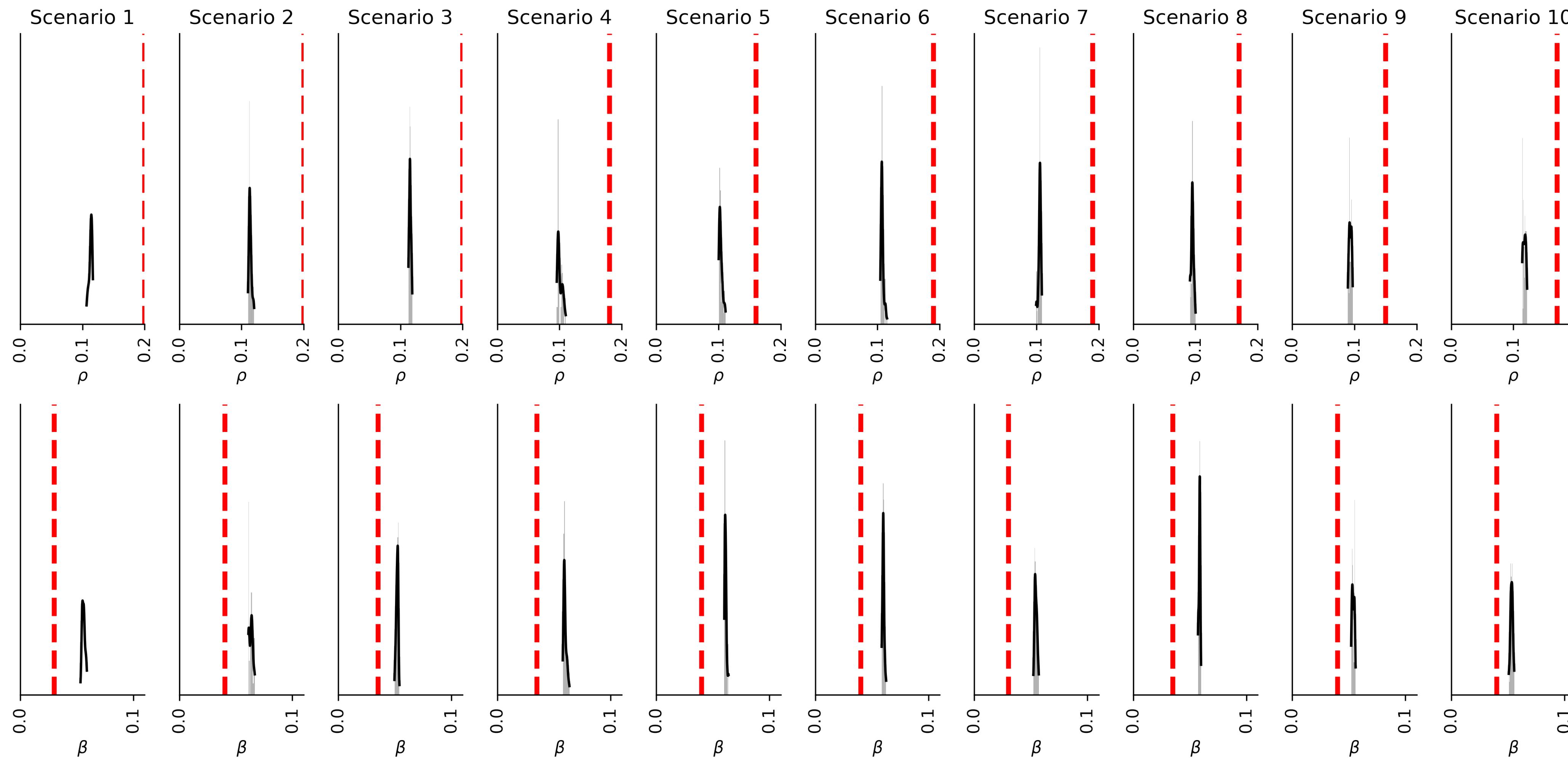
Posteriors for $K. pneumoniae$, $\gamma = 23.0\%$



Inferences on simulated observations

Two observational models;

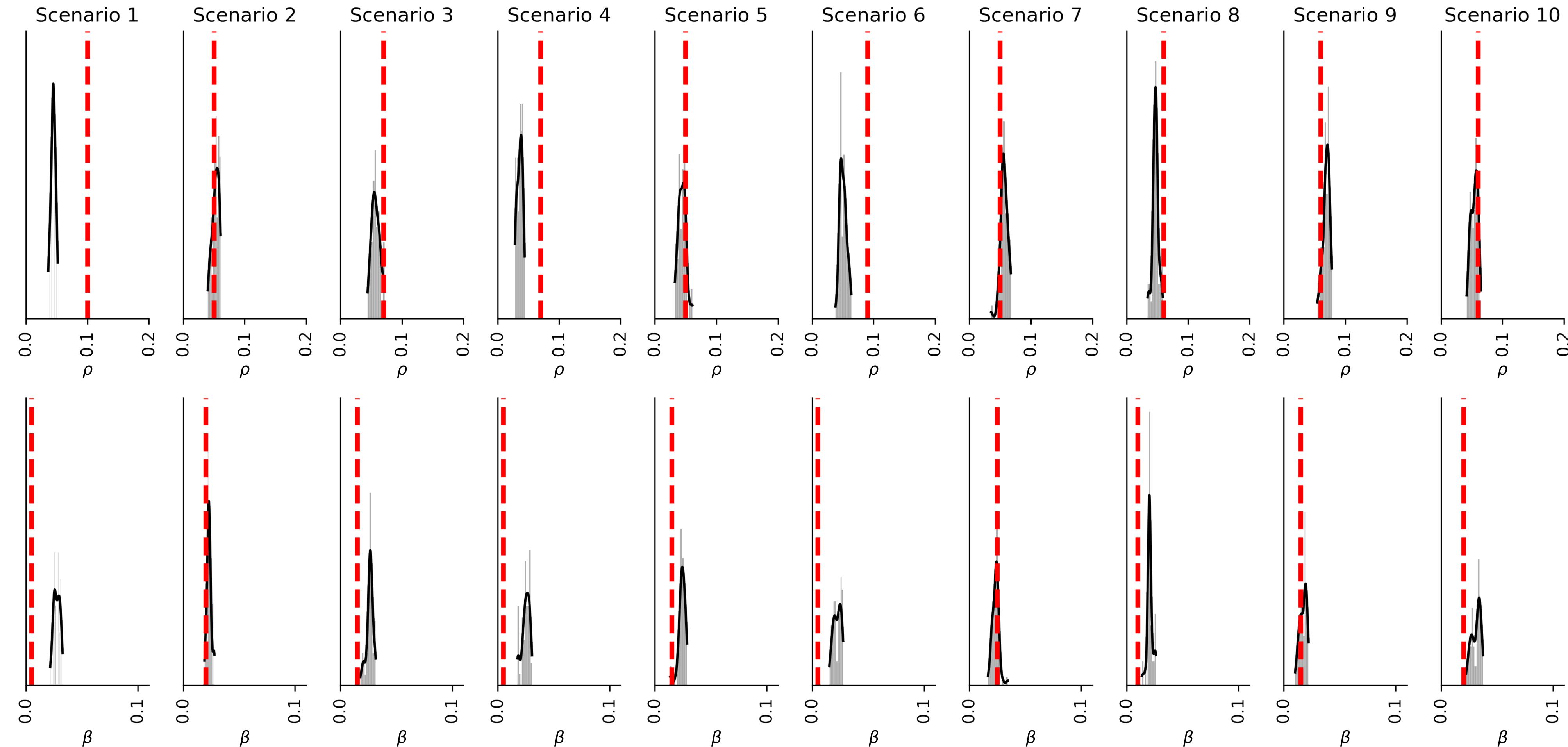
Posteriors for MSSA, $\gamma = 0.4\%$



Inferences on simulated observations

Two observational models;

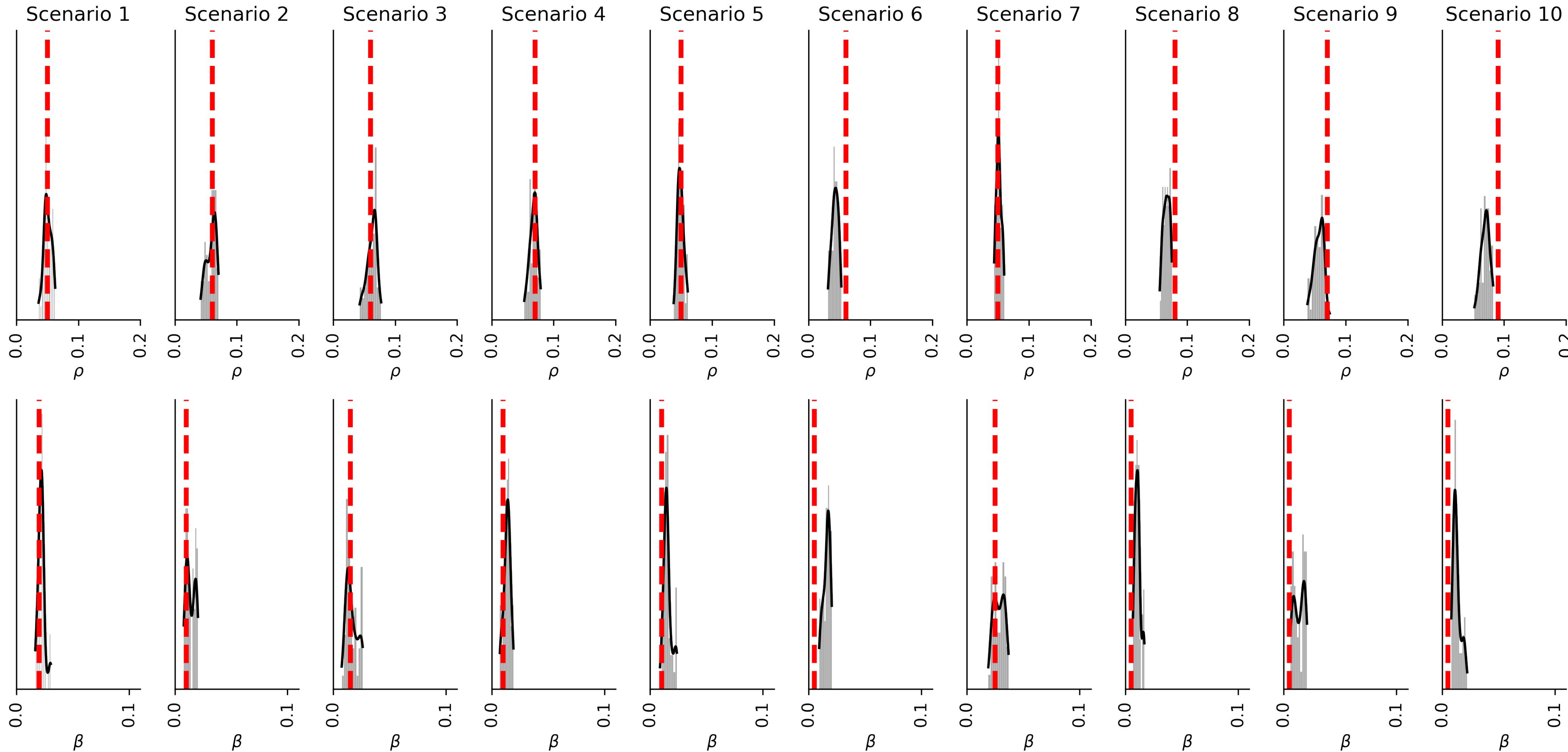
Posteriors for MRSA, $\gamma = 25.0\%$



Inferences on simulated observations

Two observational models;

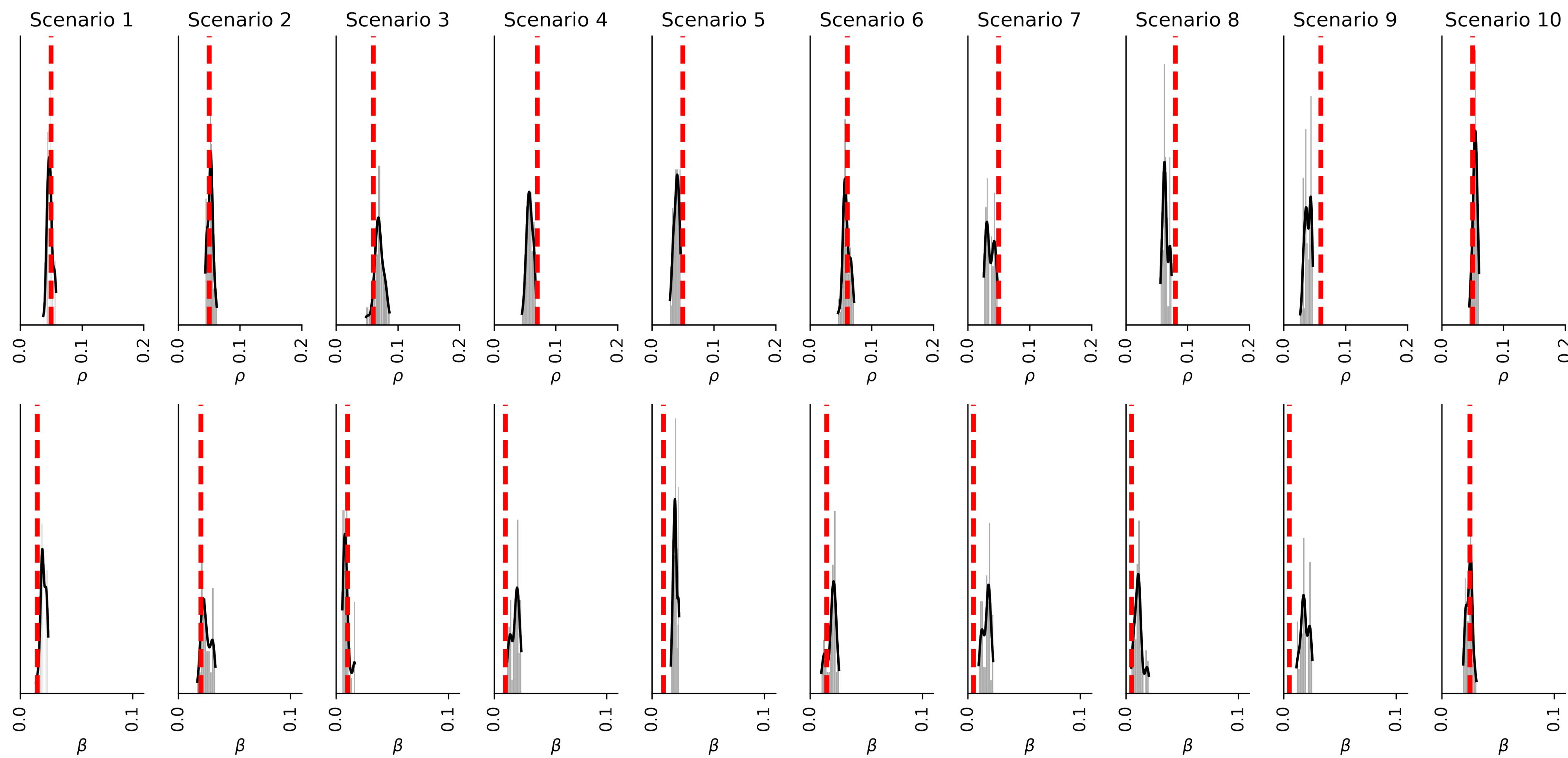
Posteriors for *S. epidermidis*, $\gamma = 58.0\%$



Inferences on simulated observations

Two observational models;

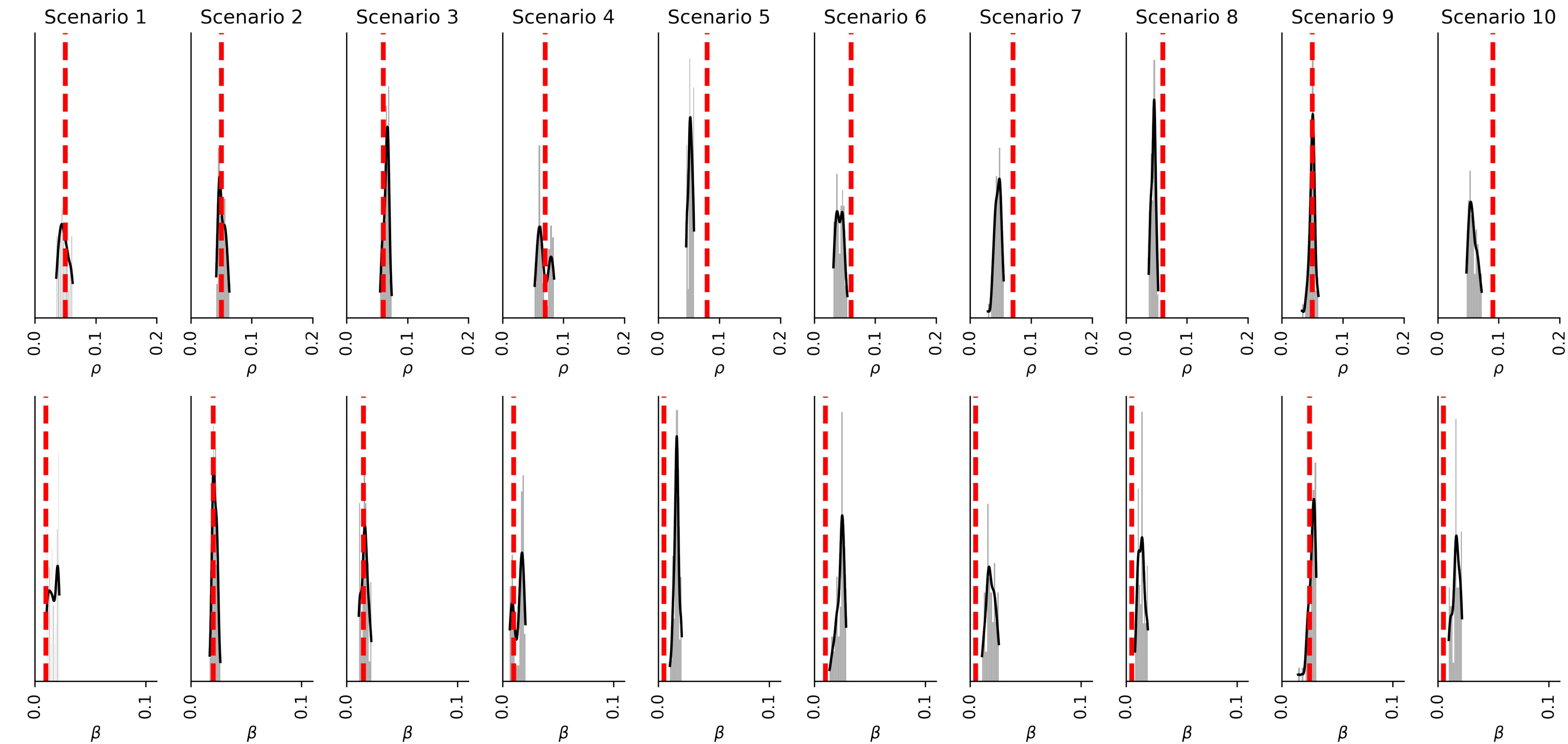
Posteriors for $E. faecalis$, $\gamma = 47.6\%$



Inferences on simulated observations

Two observational models;

Posteriors for E. faecium, $\gamma = 40.6\%$

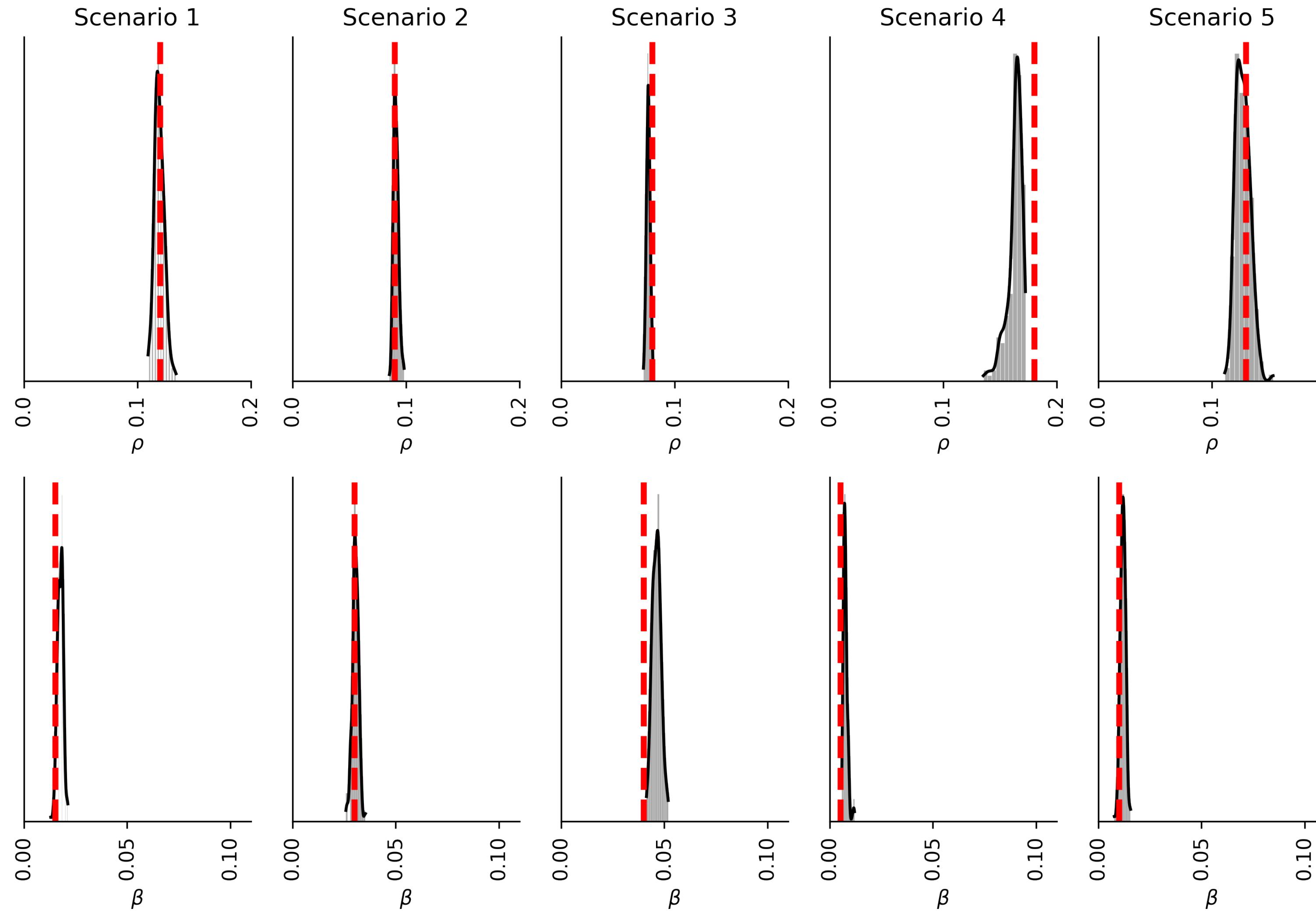


**ABM inferences on synthetic data
(Previous results NOT shrinking the
variance between IF iterations)**

Inferences on simulated observations

E. coli

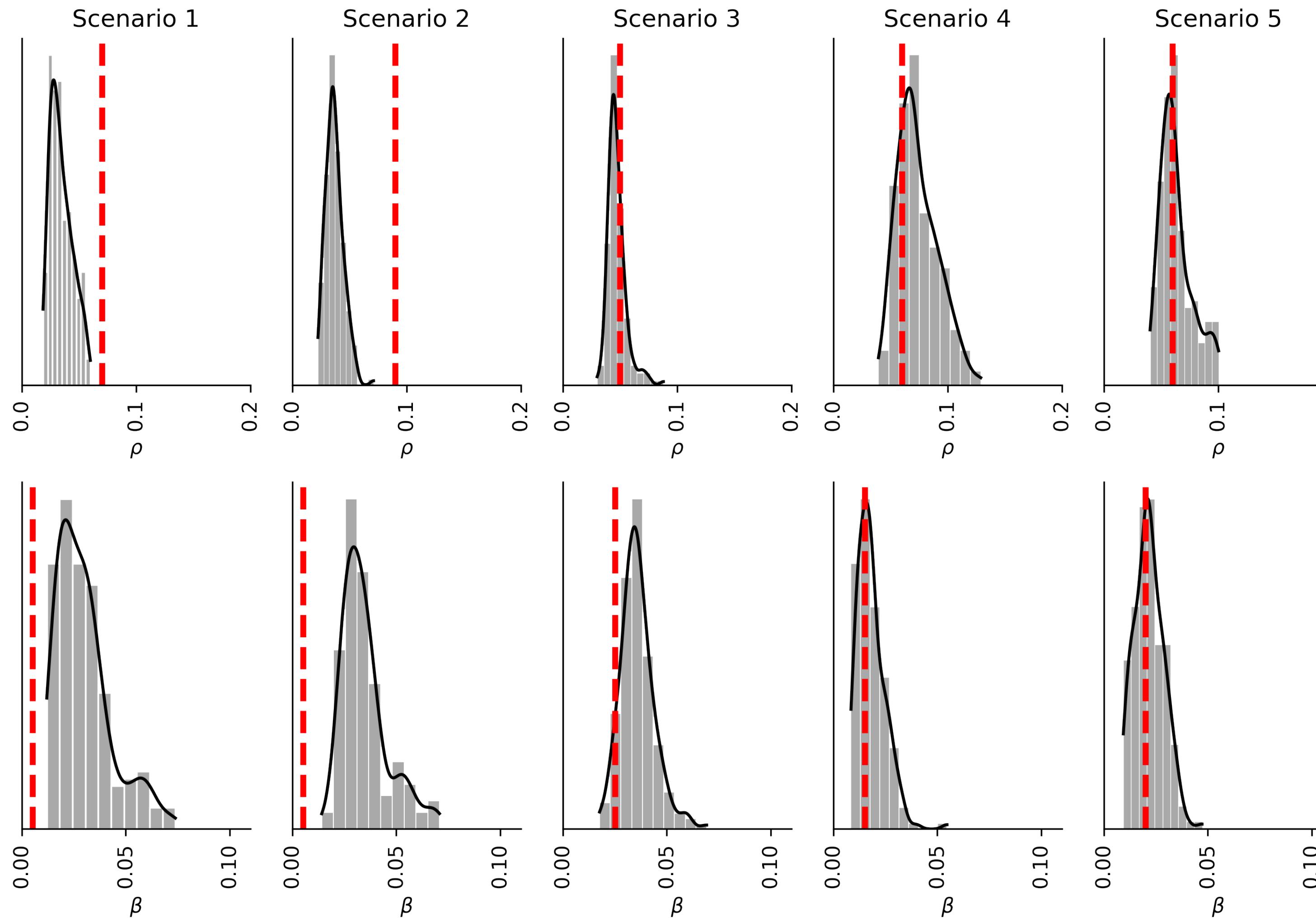
Posteriors for E. coli, $\gamma = 63.0\%$



Inferences on simulated observations

MSSA

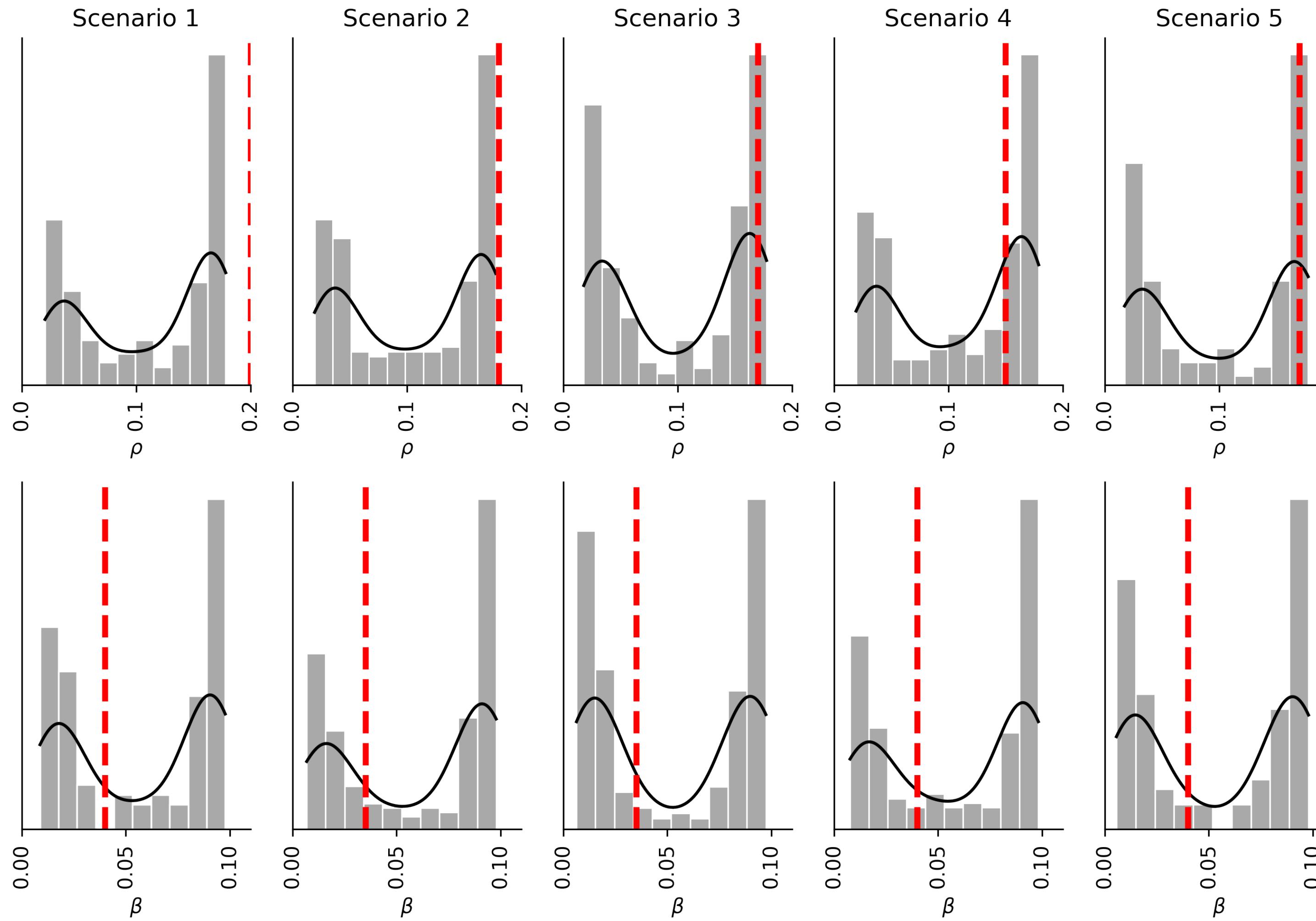
Posteriors for MRSA, $\gamma = 25.0\%$



Inferences on simulated observations

MRSA

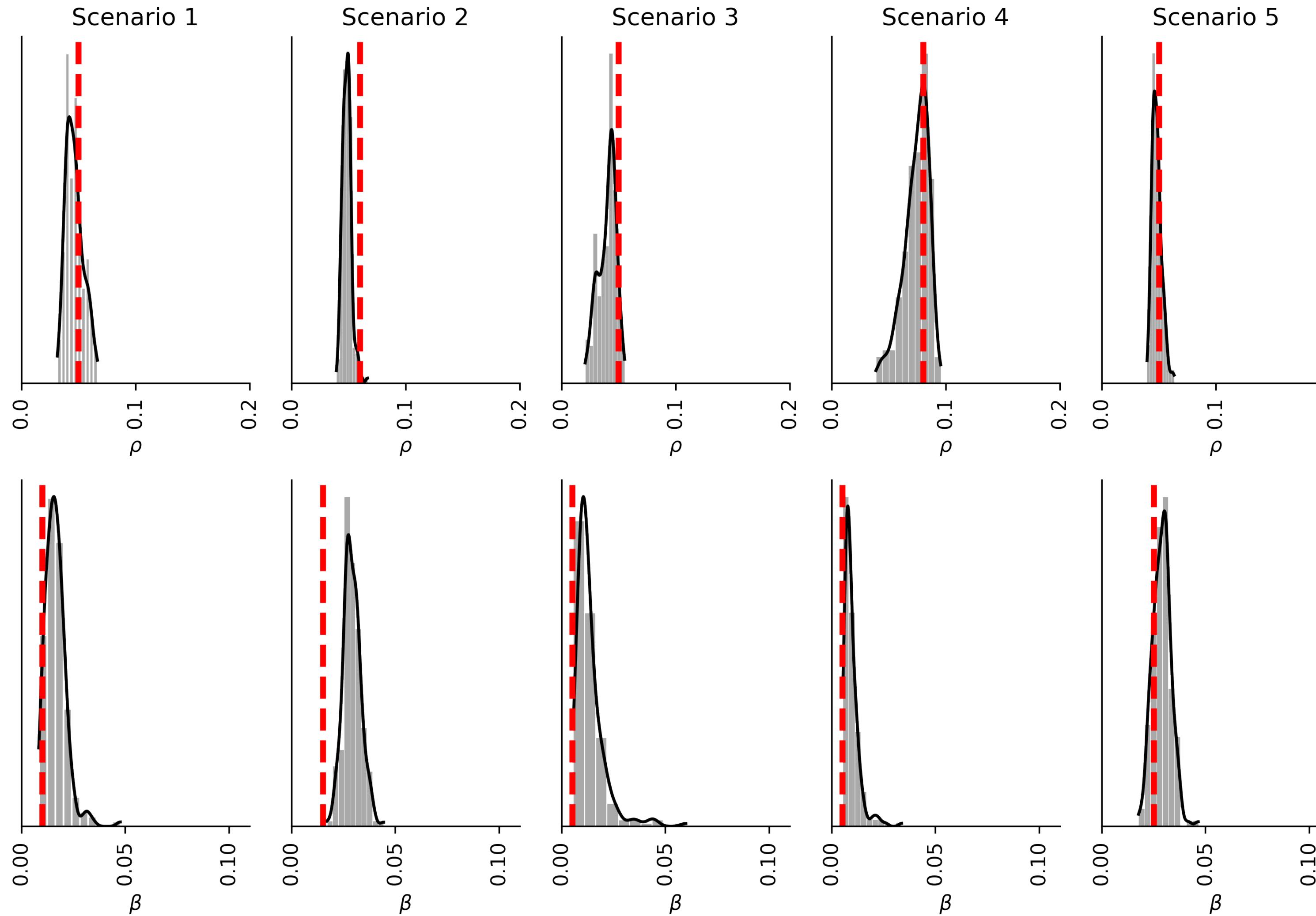
Posteriors for MSSA, $\gamma = 0.4\%$



Inferences on simulated observations

E. faecalis

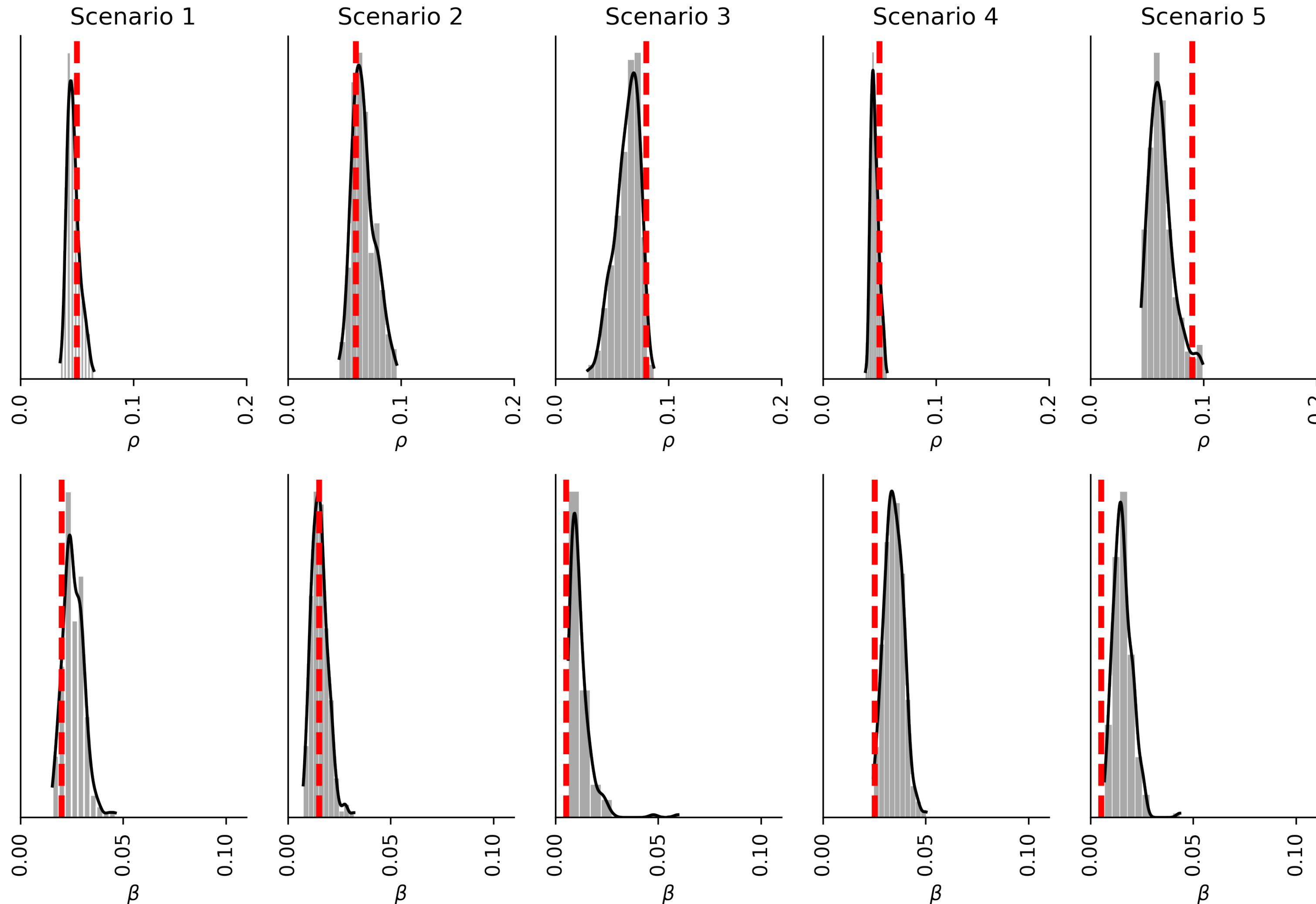
Posteriors for E. faecalis, $\gamma = 47.6\%$



Inferences on simulated observations

E. faecium

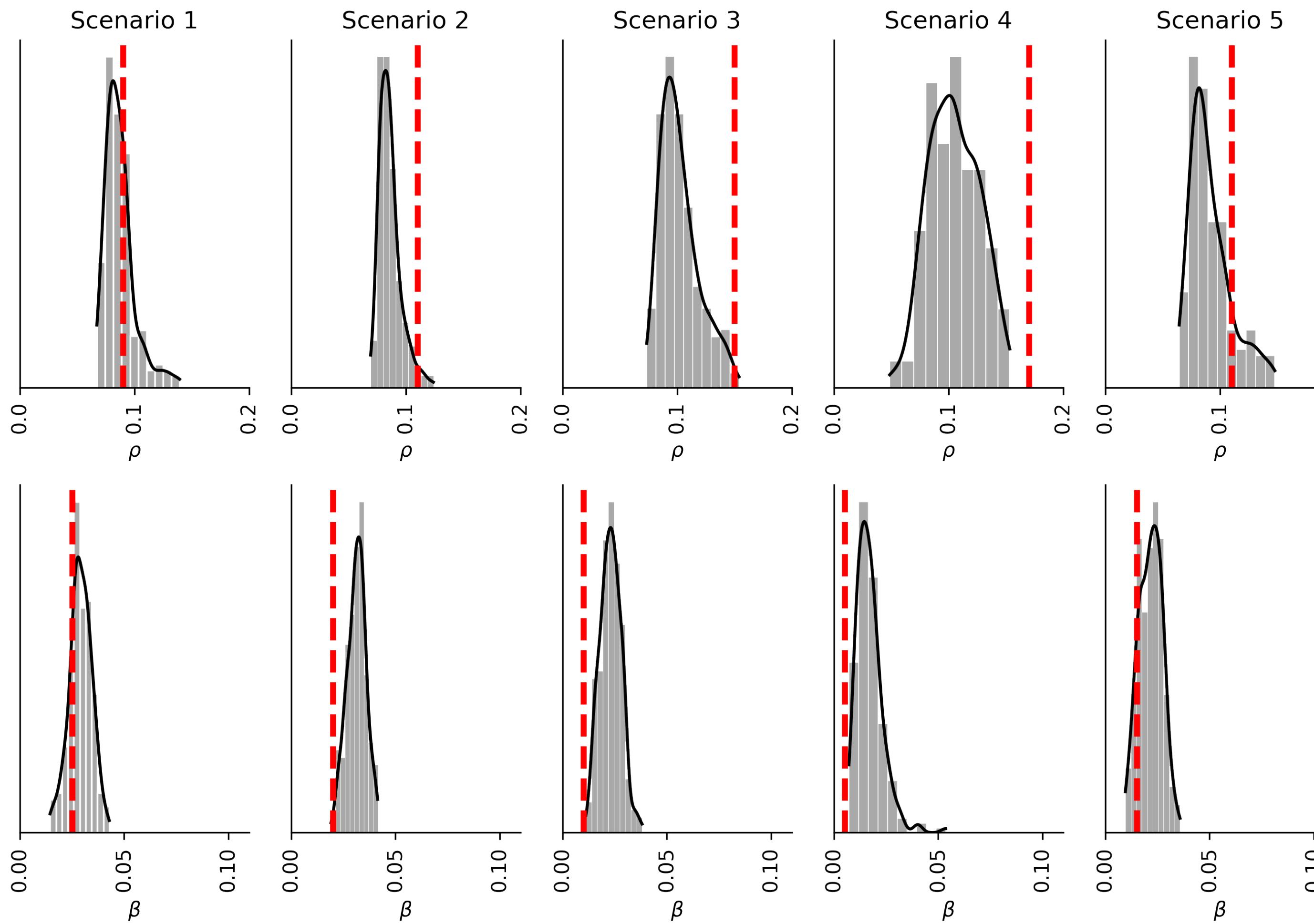
Posteriors for E. faecium, $\gamma = 40.6\%$



Inferences on simulated observations

K. pneumoniae

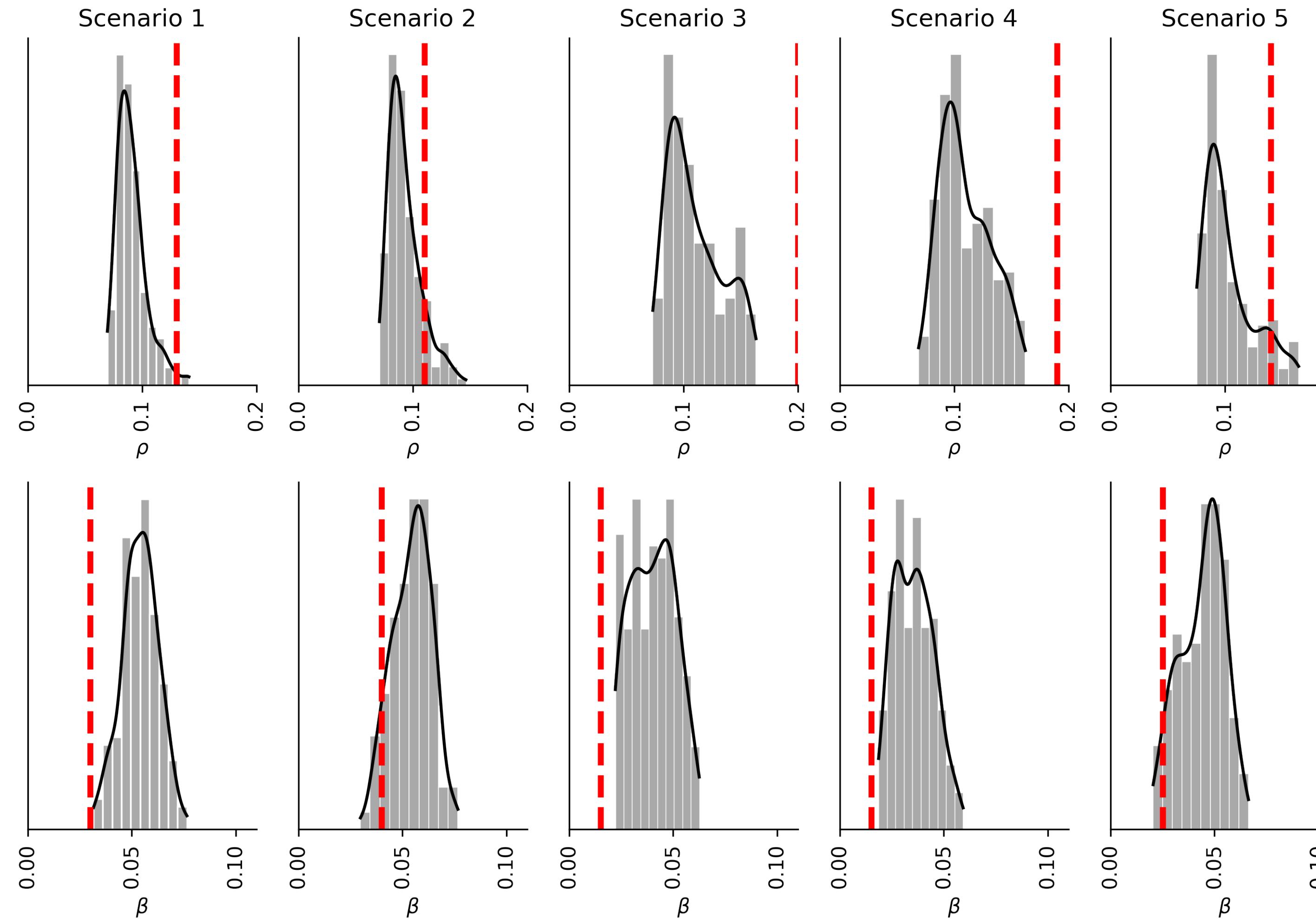
Posteriors for *K. pneumoniae*, $\gamma = 23.0\%$



Inferences on simulated observations

P. aeruginosa

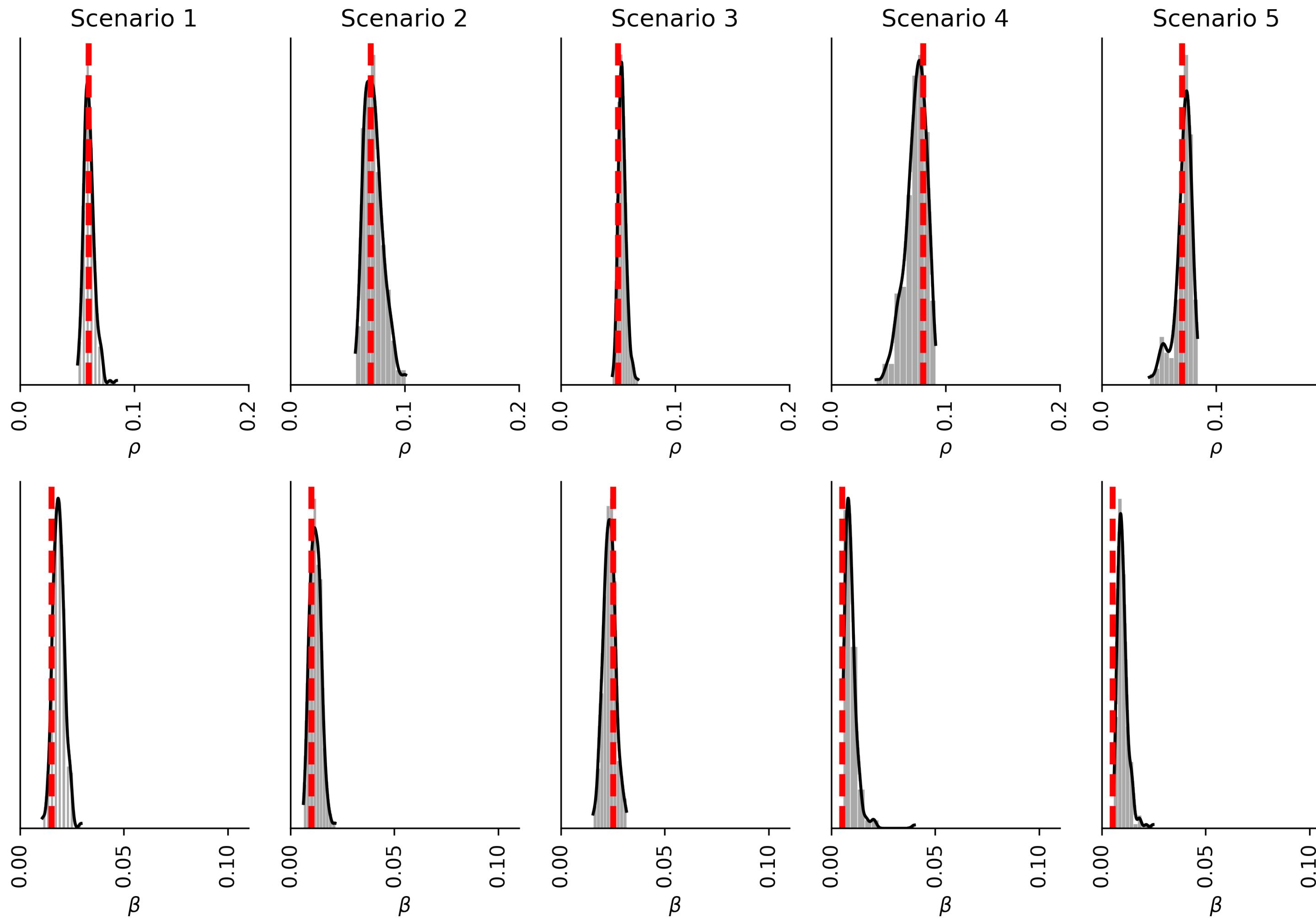
Posteriors for *P. aeruginosa*, $\gamma = 11.6\%$



Inferences on simulated observations

S. epidermidis

Posteriors for *S. epidermidis*, $\gamma = 58.0\%$

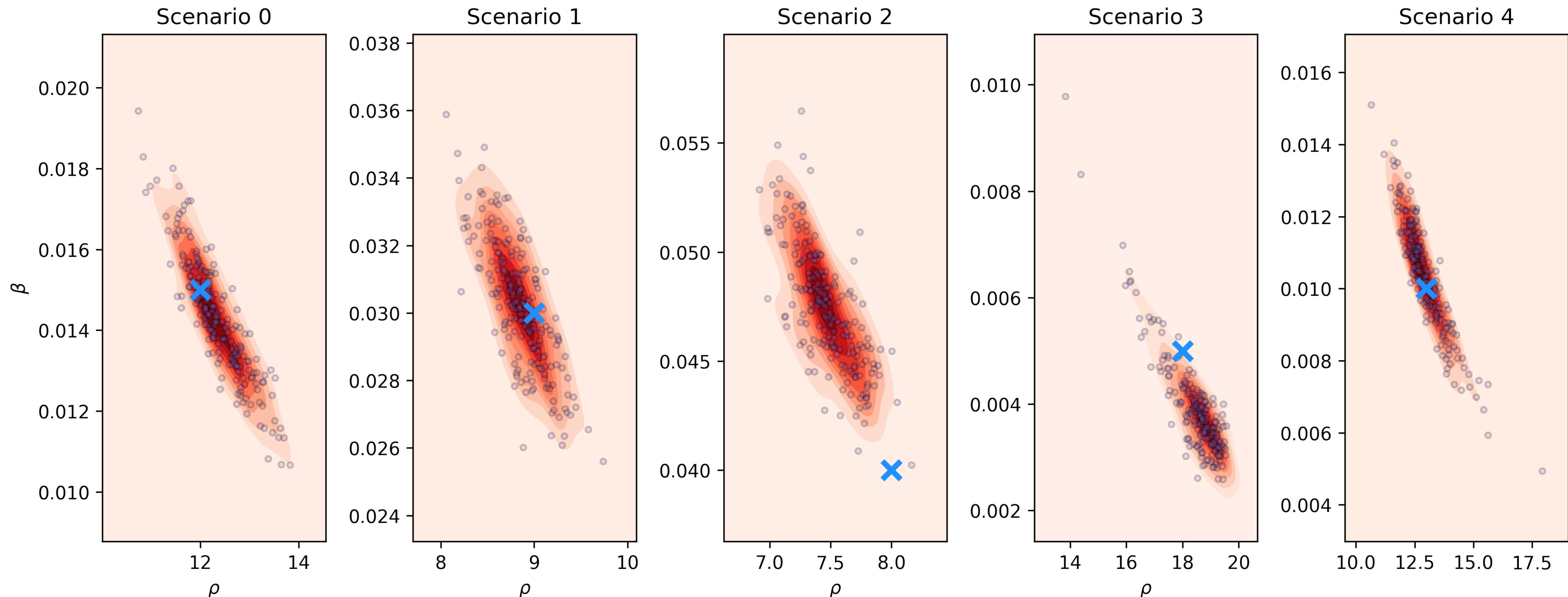


**ABM inferences on synthetic data
(Previous results NOT shrinking the
variance between IF iterations)**

Inferences on simulated observations

E. coli

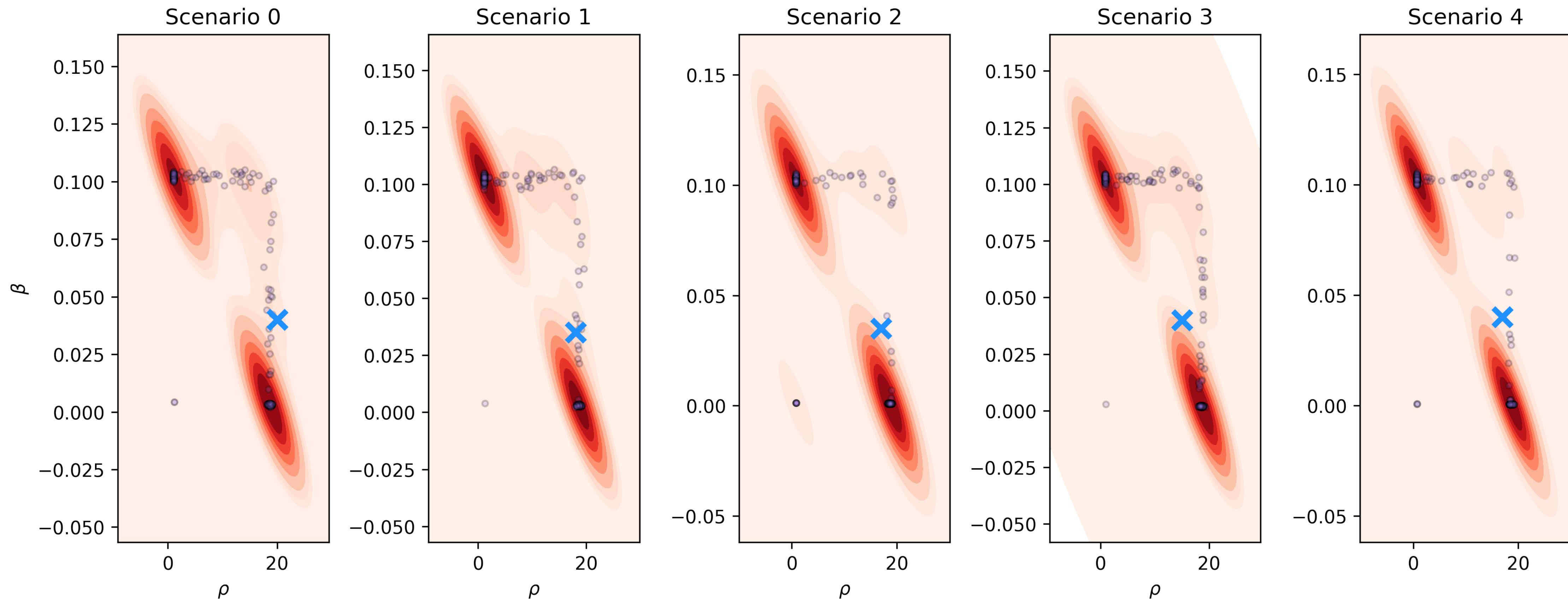
Posterior joint distribution for E. coli, $\gamma = 63.0\%$



Inferences on simulated observations

MSSA

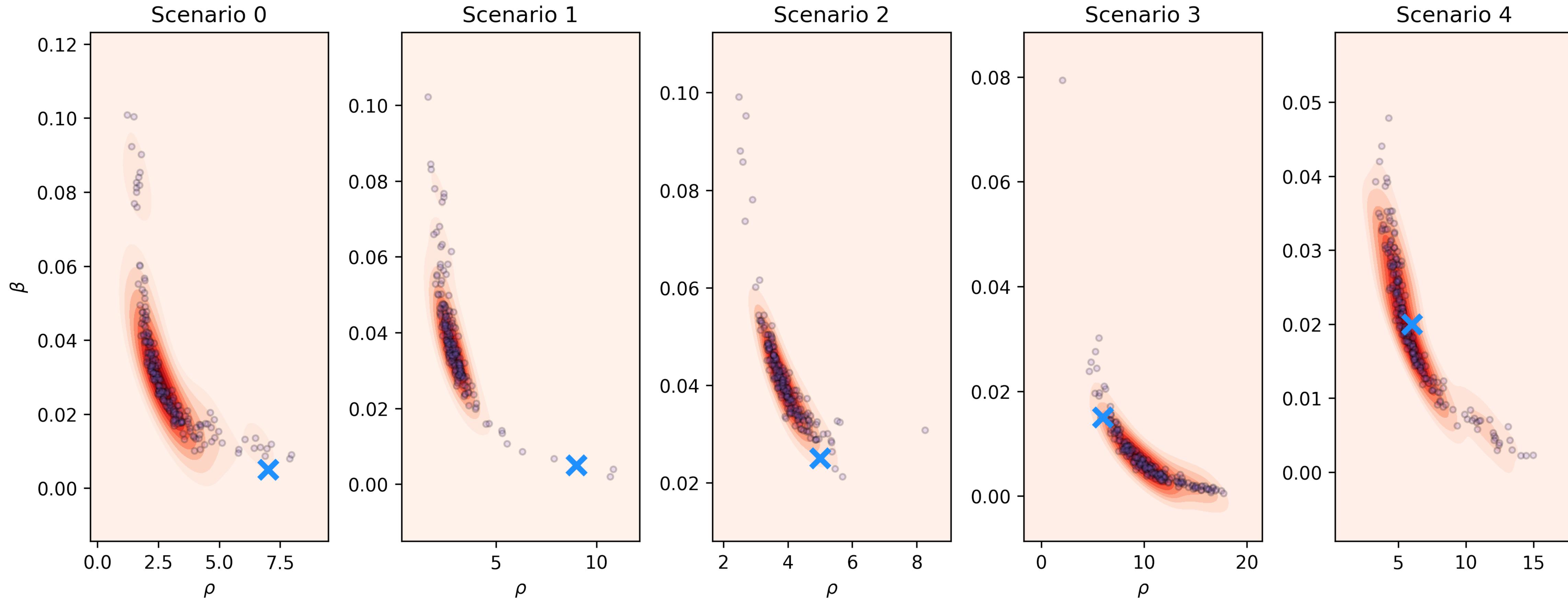
Posterior joint distribution for MSSA, $\gamma = 0.4\%$



Inferences on simulated observations

MRSA

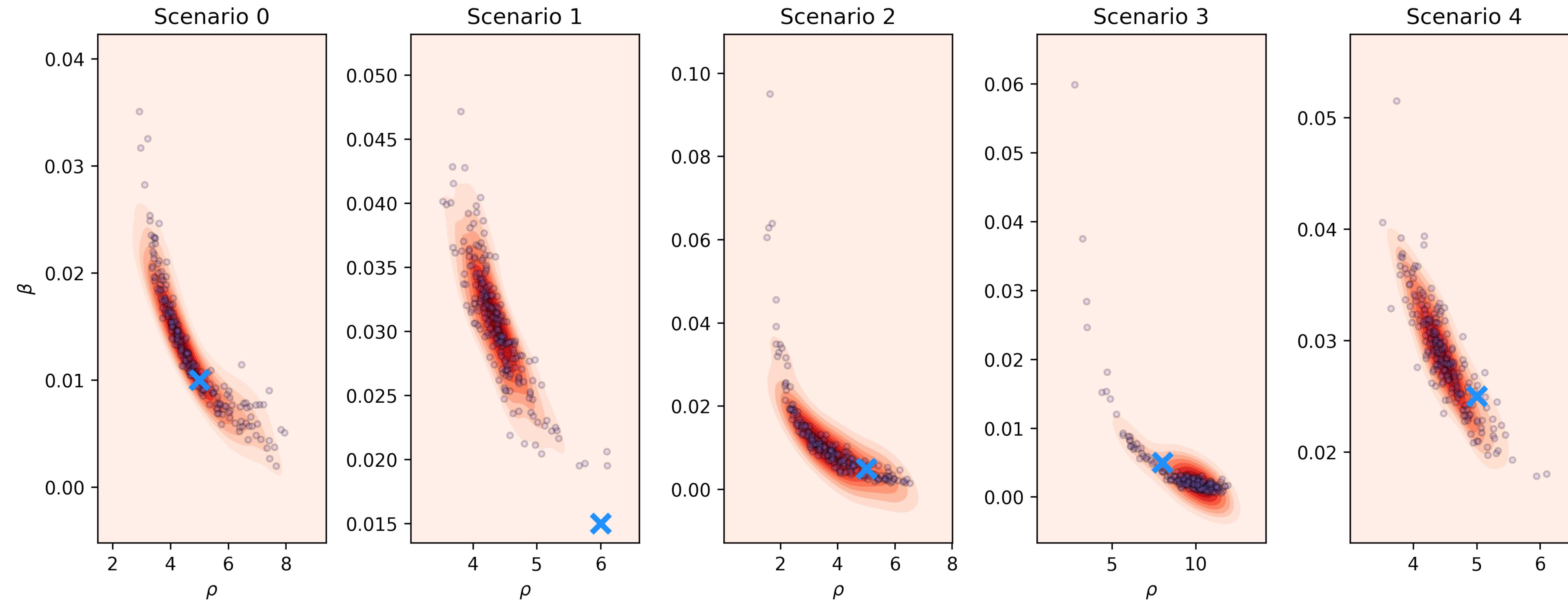
Posterior joint distribution for MRSA, $\gamma = 25.0\%$



Inferences on simulated observations

E. faecalis

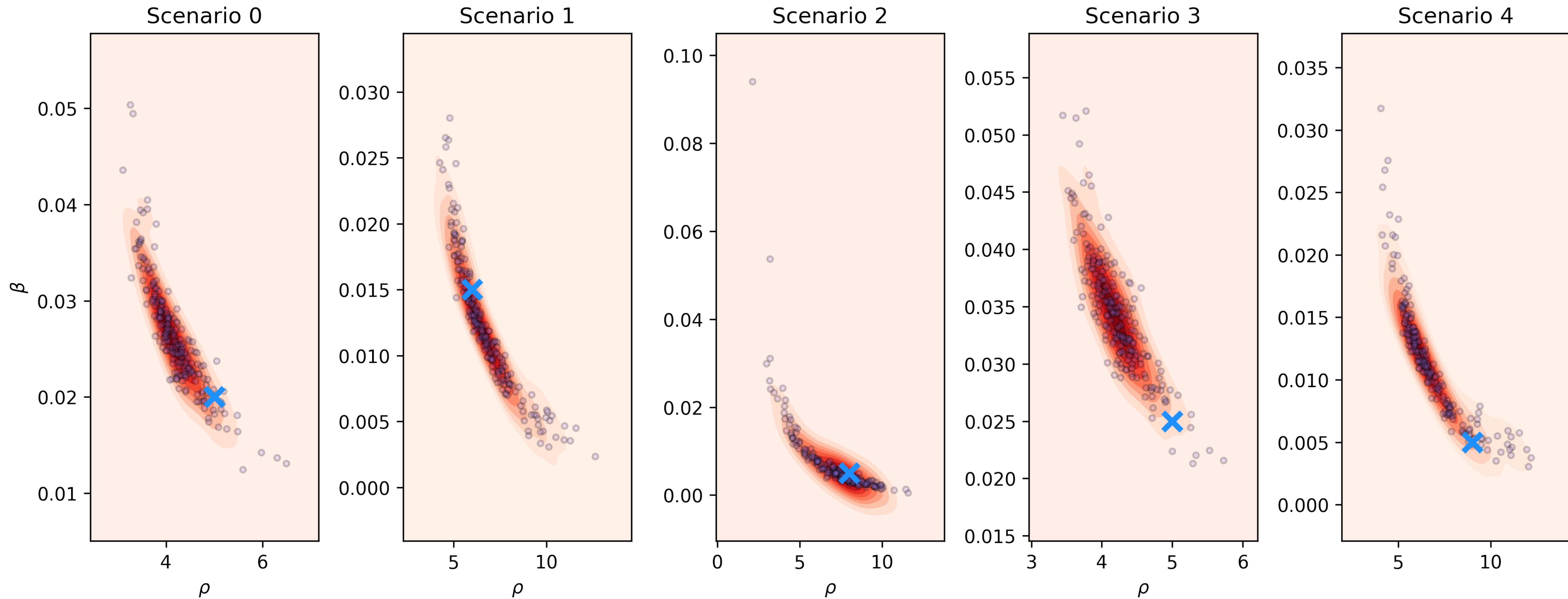
Posterior joint distribution for *E. faecalis*, $\gamma = 47.6\%$



Inferences on simulated observations

E. faecium

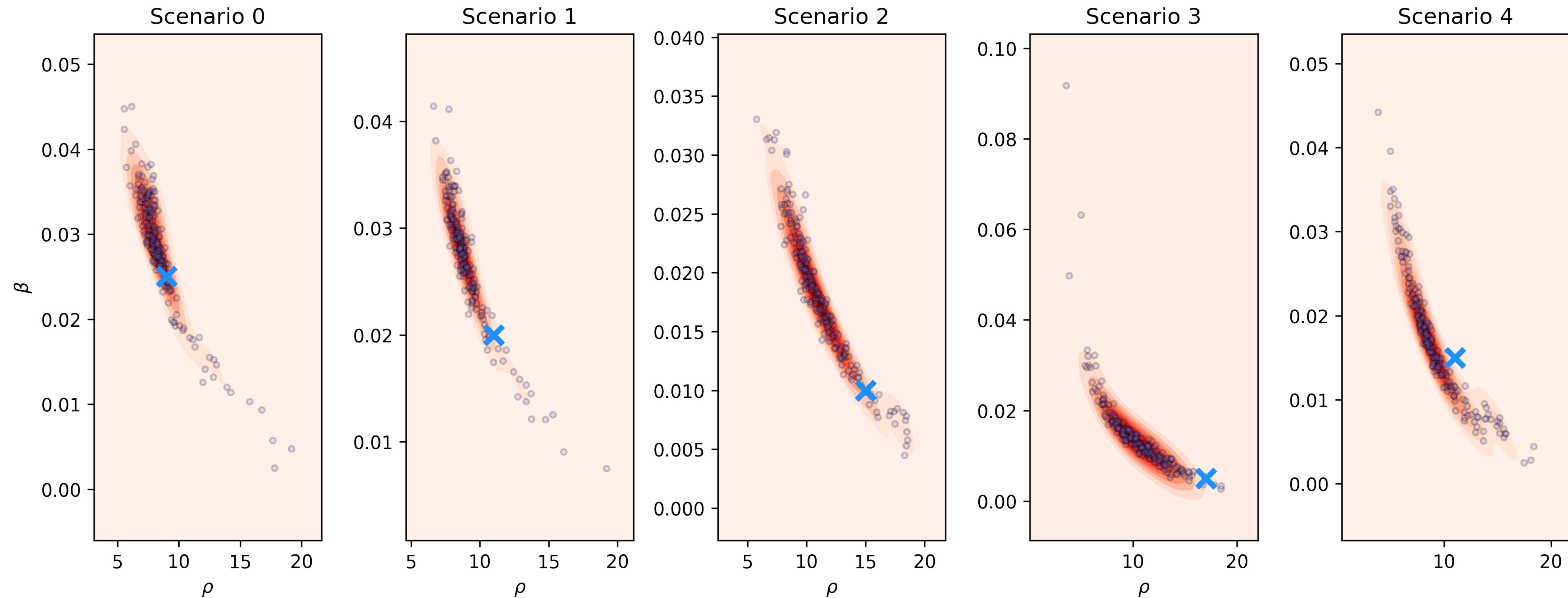
Posterior joint distribution for E. faecium, $\gamma = 40.6\%$



Inferences on simulated observations

K. pneumoniae

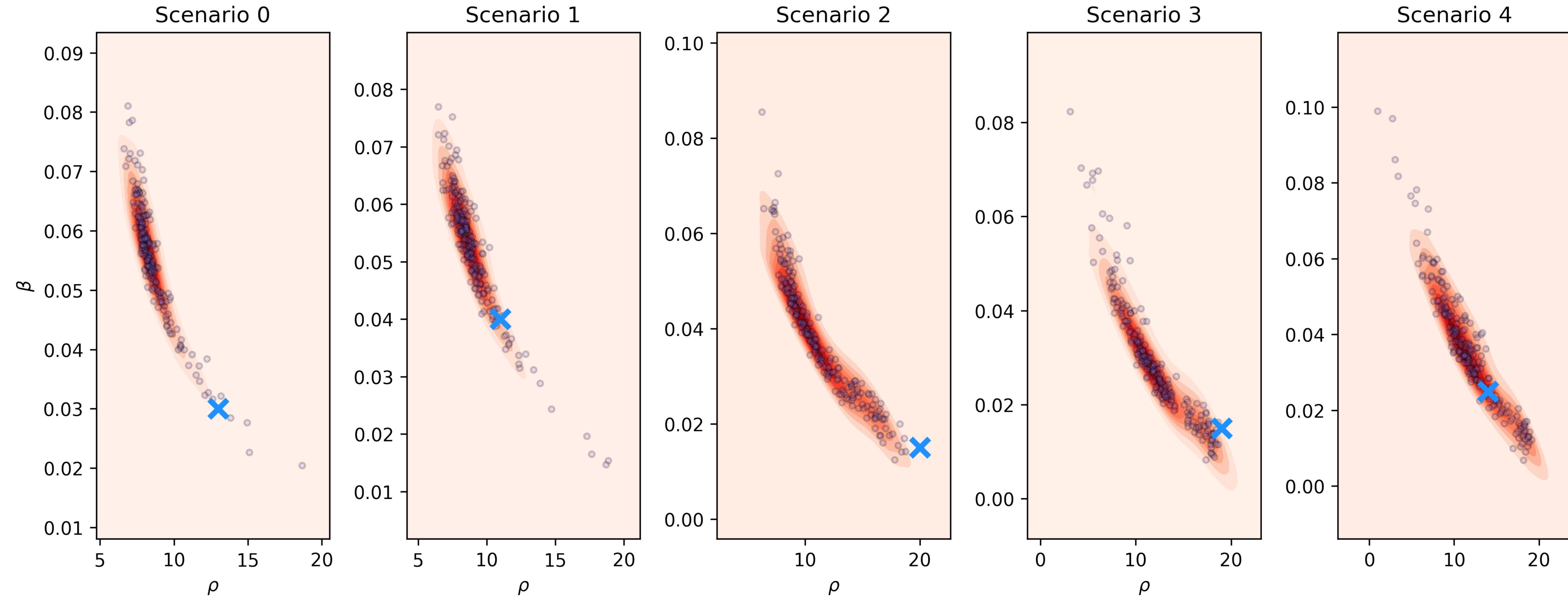
Posterior joint distribution for *K. pneumoniae*, $\gamma = 23.0\%$



Inferences on simulated observations

P. aeruginosa

Posterior joint distribution for *P. aeruginosa*, $\gamma = 11.6\%$



Inferences on simulated observations

S. epidermidis

Posterior joint distribution for *S. epidermidis*, $\gamma = 58.0\%$

