

where are we...

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

ABM inferences

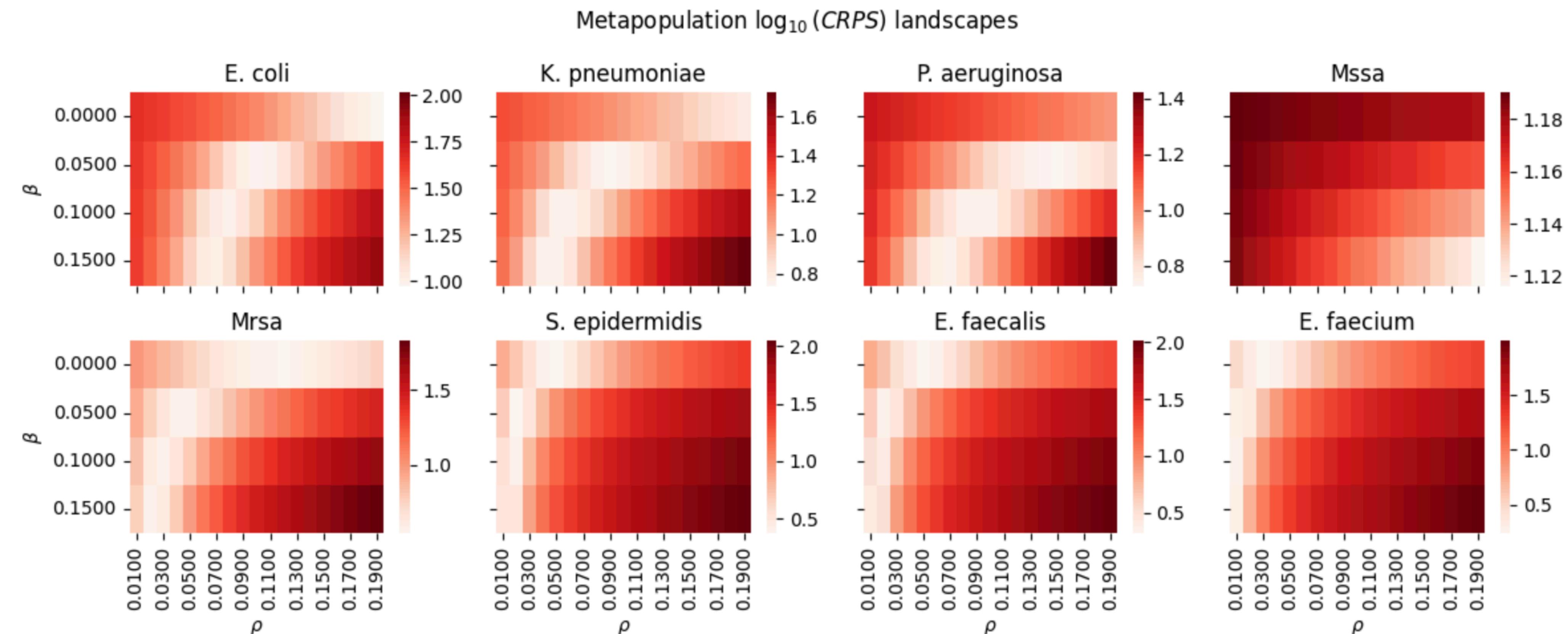
recap

- 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).

Synthetic scenarios - identifiability

Two setting of synthetic inferences

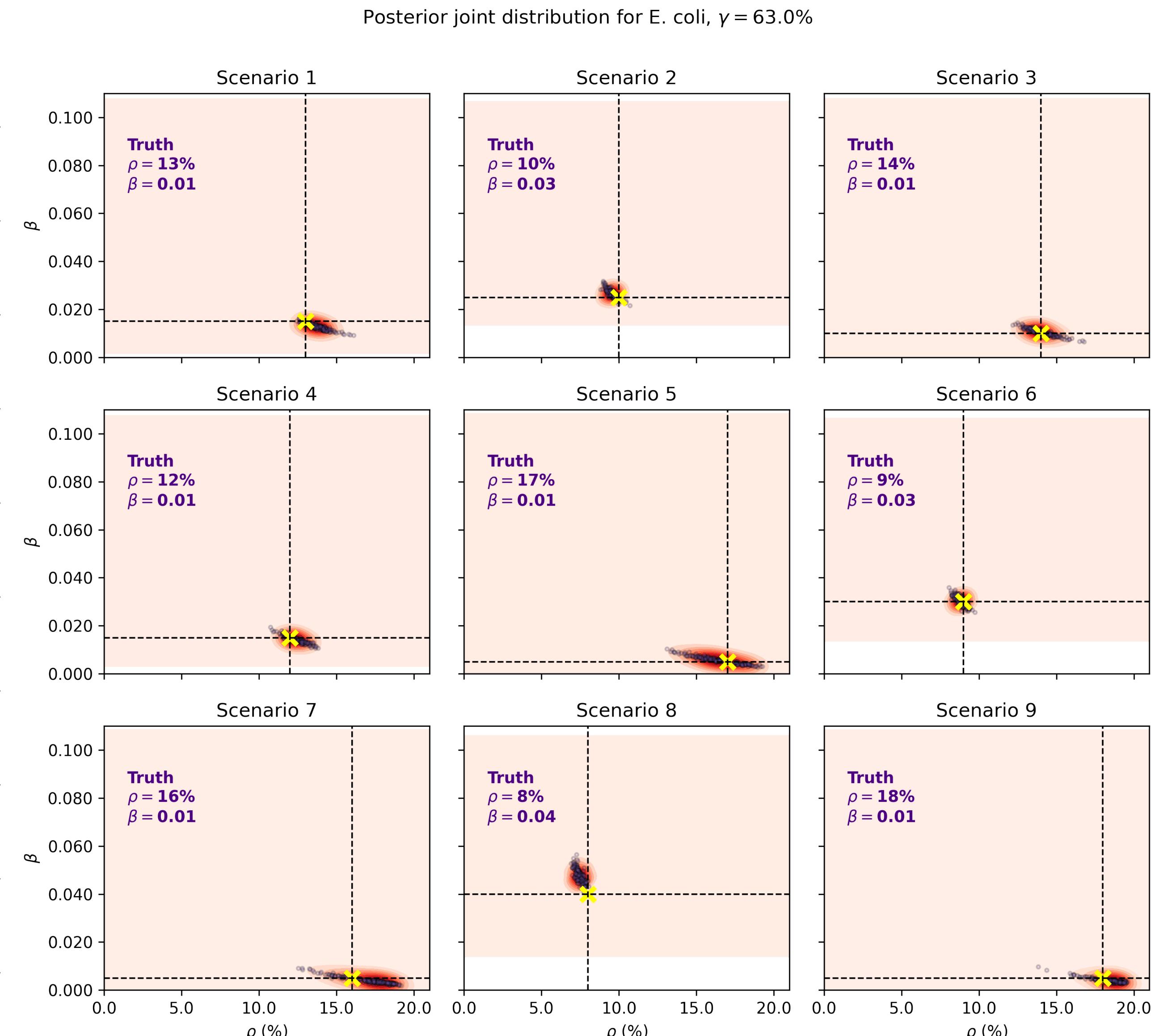
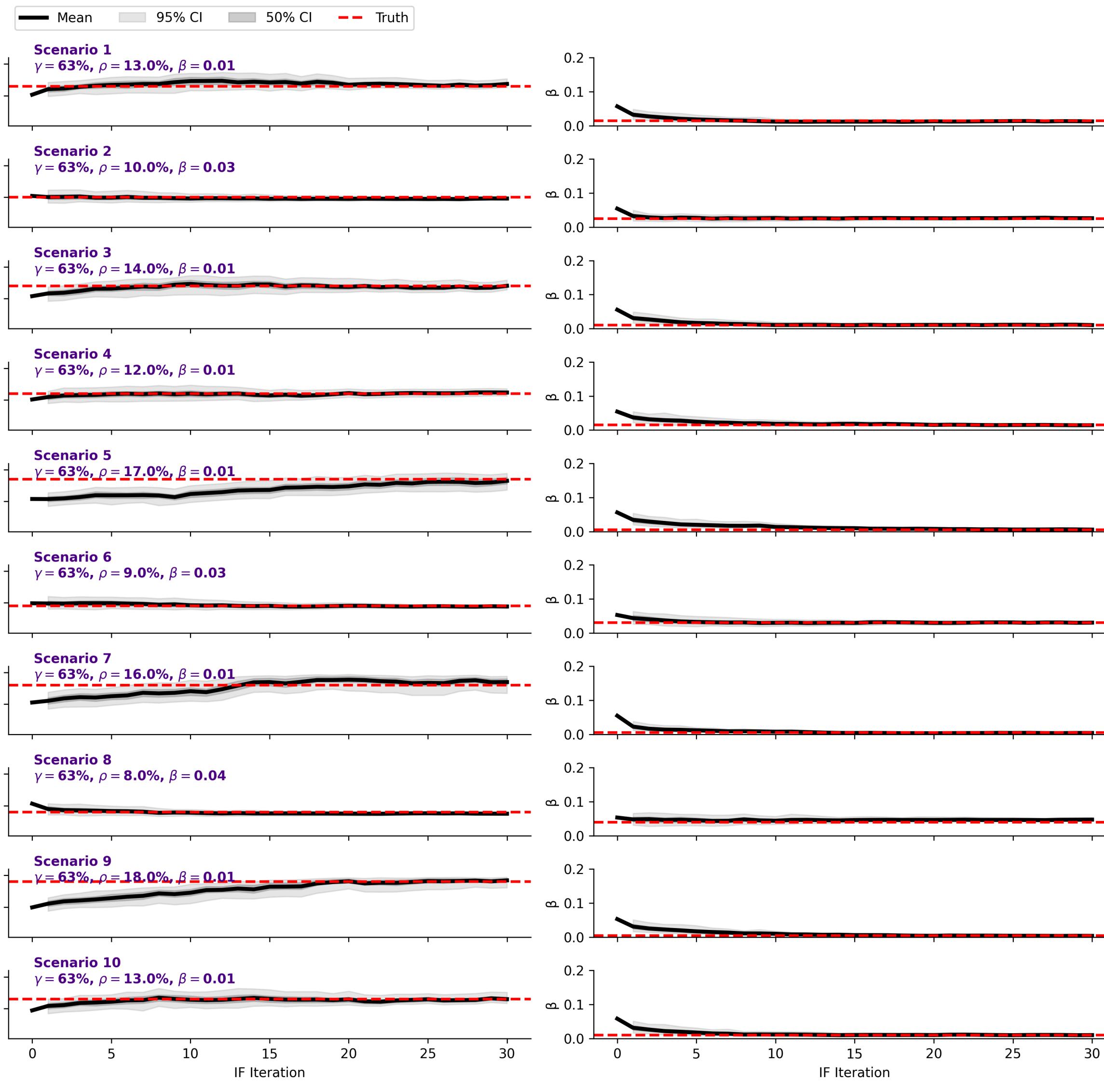
1. Inferences on truths tuple (ρ, β) that reproduced the hospital-level observations of each microorganism as quantified with the Continuous Ranked Probability Score (CRPS) - grid searches in slide 3. (**Slide 7-15**)
2. Inferences with two levels of importations $\gamma = [25\%, 50\%]$, and different combinations of ρ, β . For a total of 24 ‘not constrained’ (to the hospital level) synthetic inferences. (**Slide 16-15**)
 - $\rho \in [1\%, 5\%, 10\%, 18\%]$
 - $\beta \in [0.01, 0.05, 0.1]$

**inferences with truths that
reproduced the synthetic
observations**

Very challenging IMO 

Inferences on simulated observations

E. coli



Inferences on simulated observations

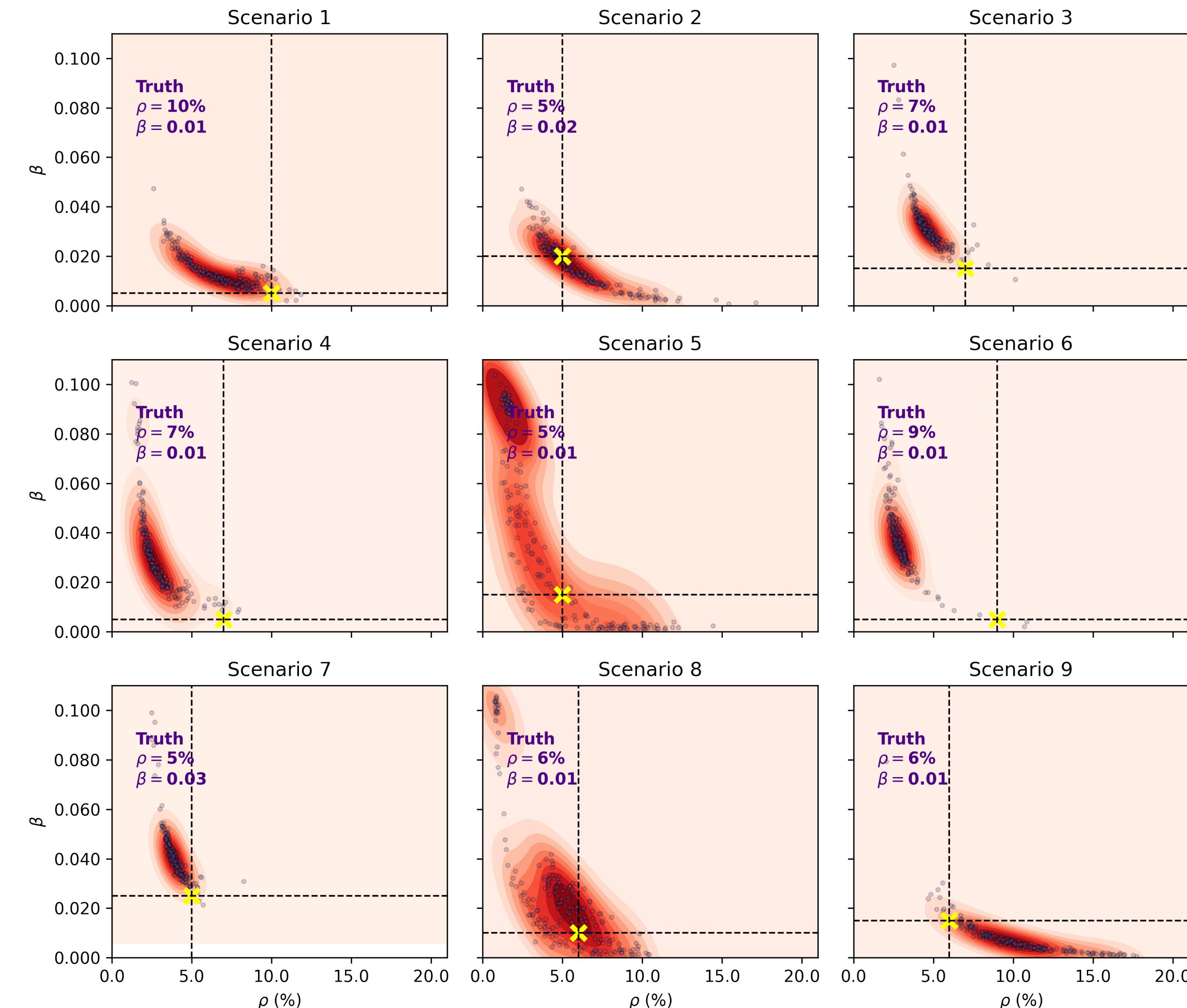
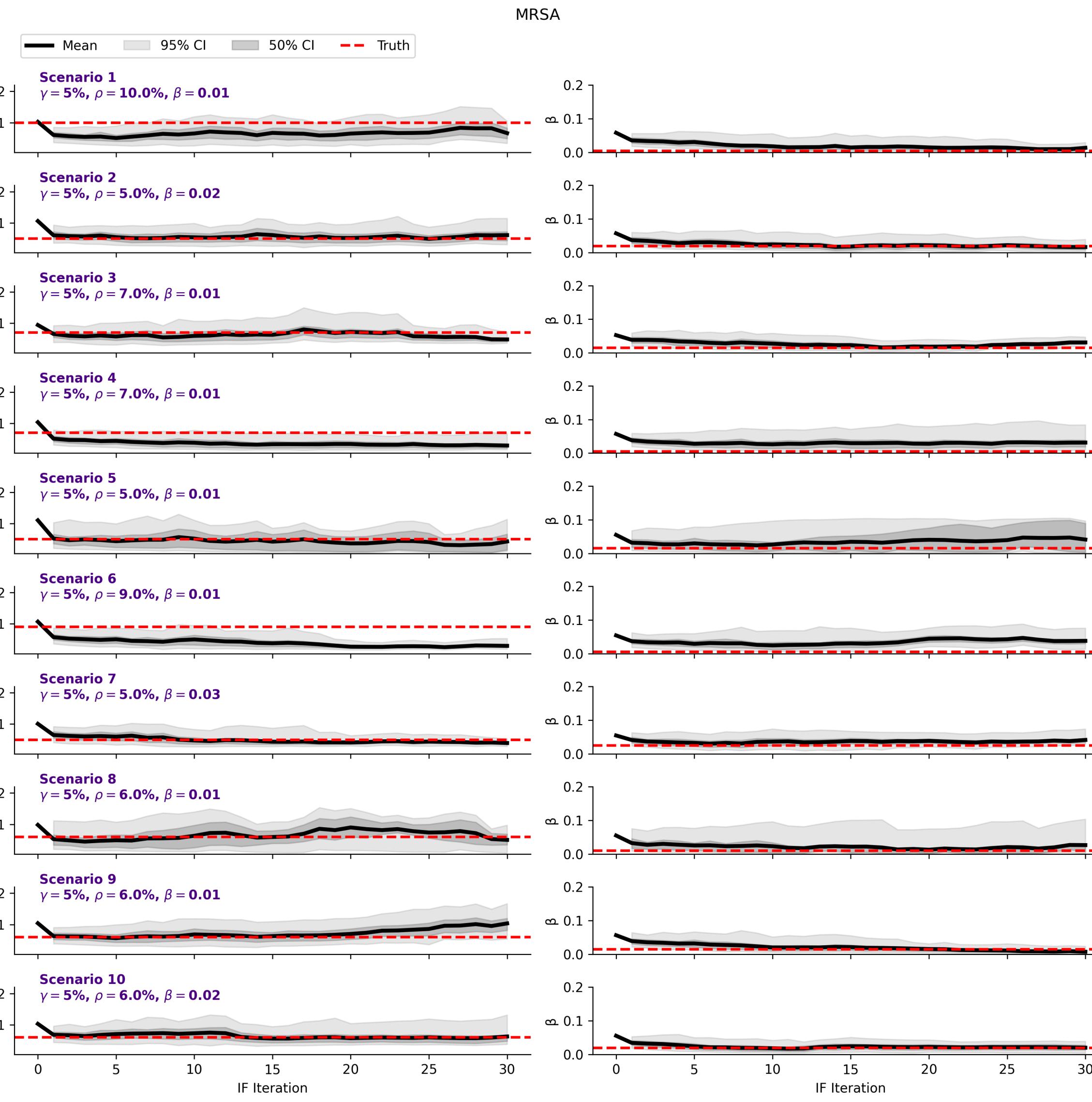
MSSA

Re-running with the new prevalences

Inferences on simulated observations

MRSA

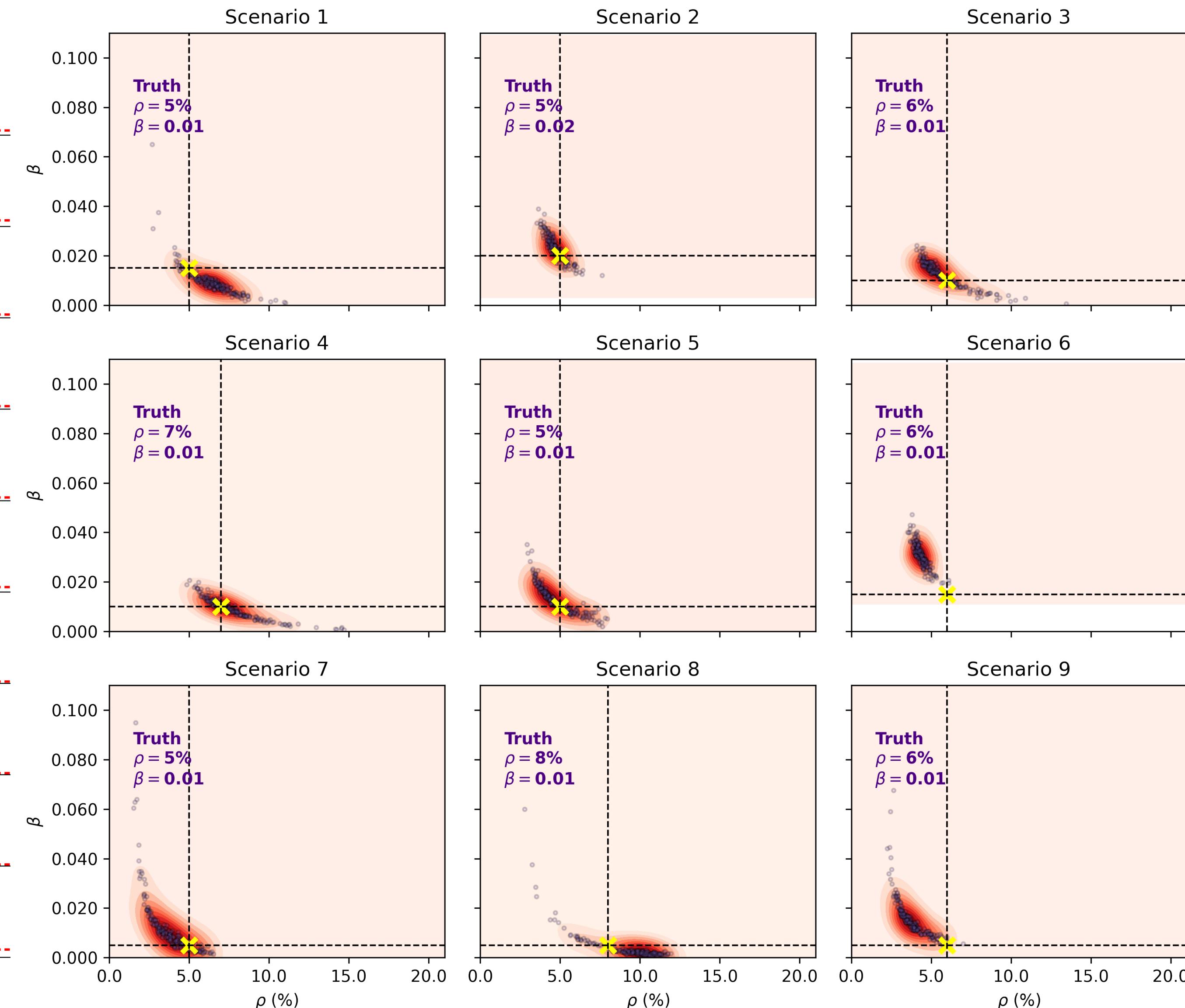
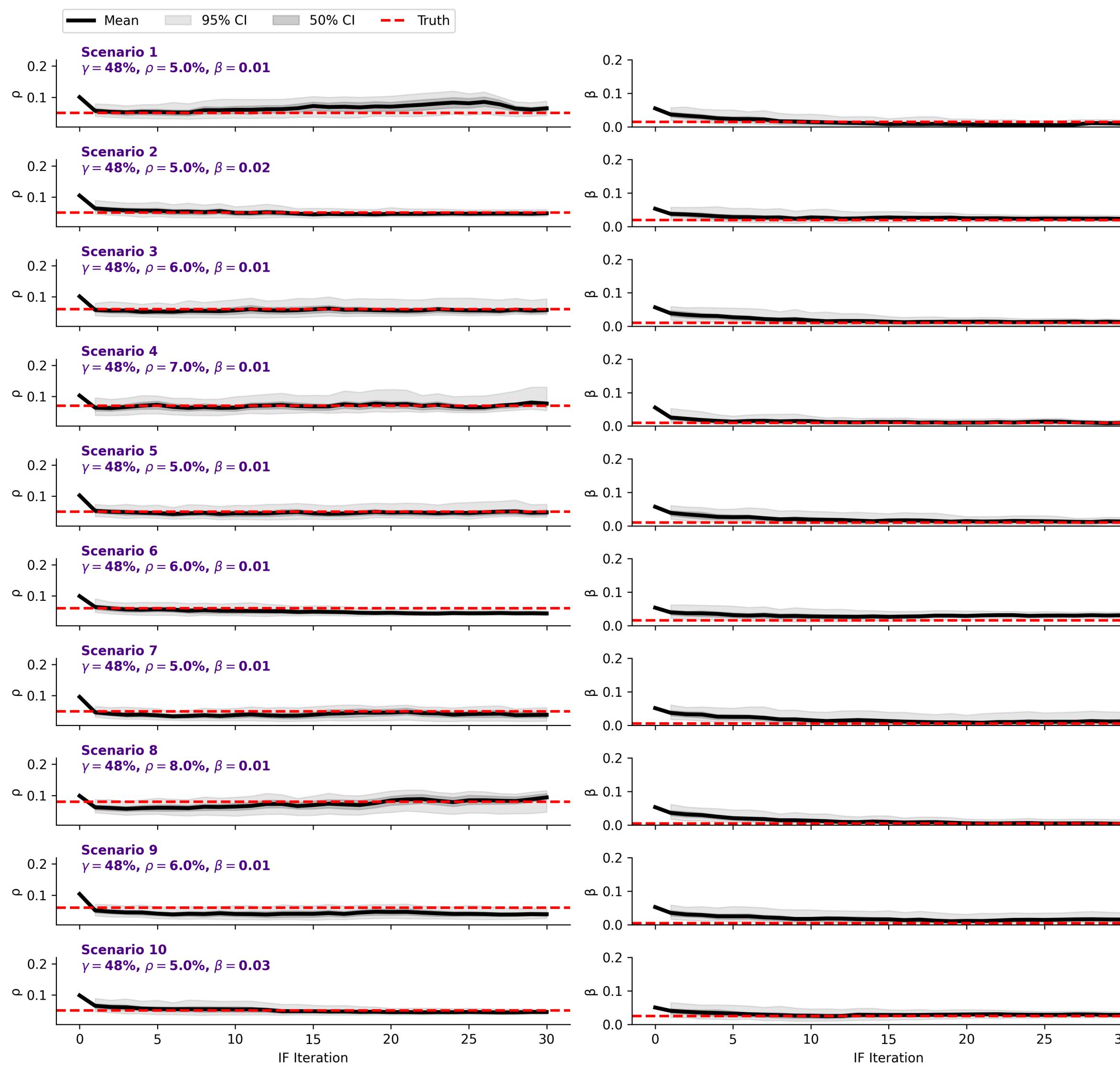
Posterior joint distribution for MRSA, $\gamma = 5.0\%$



Inferences on simulated observations

E. faecalis

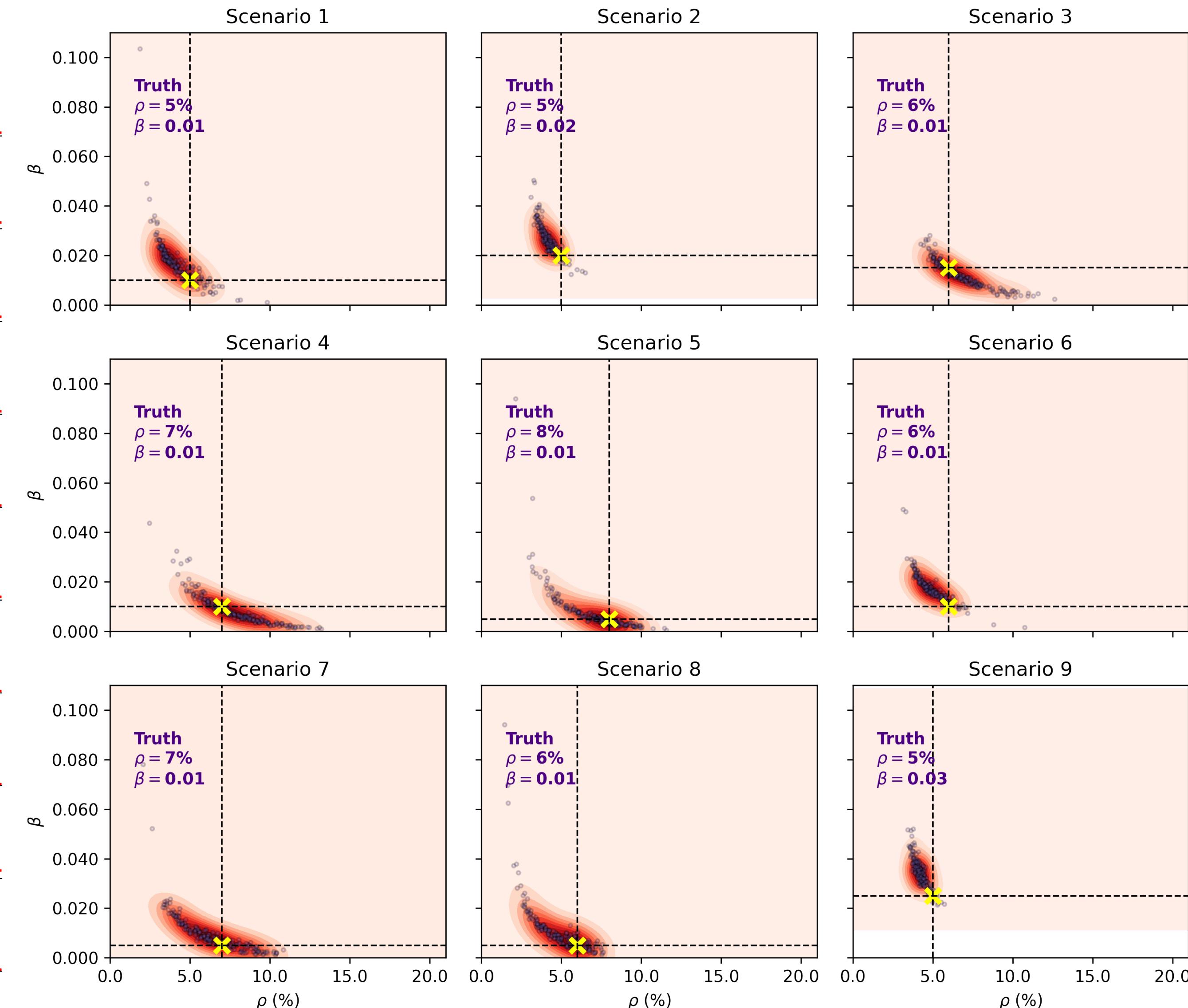
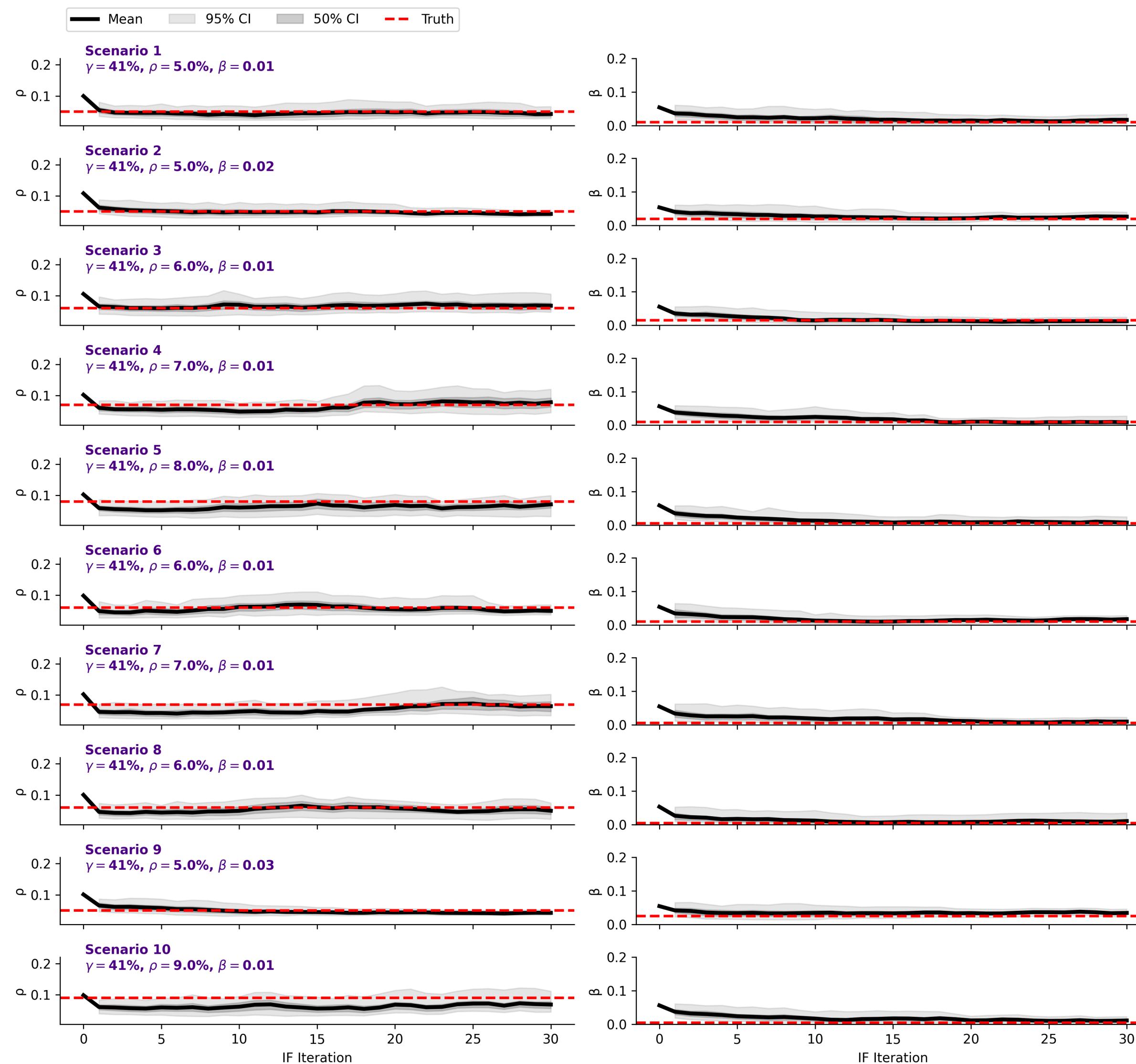
Posterior joint distribution for E. faecalis, $\gamma = 47.6\%$



Inferences on simulated observations

E. faecium

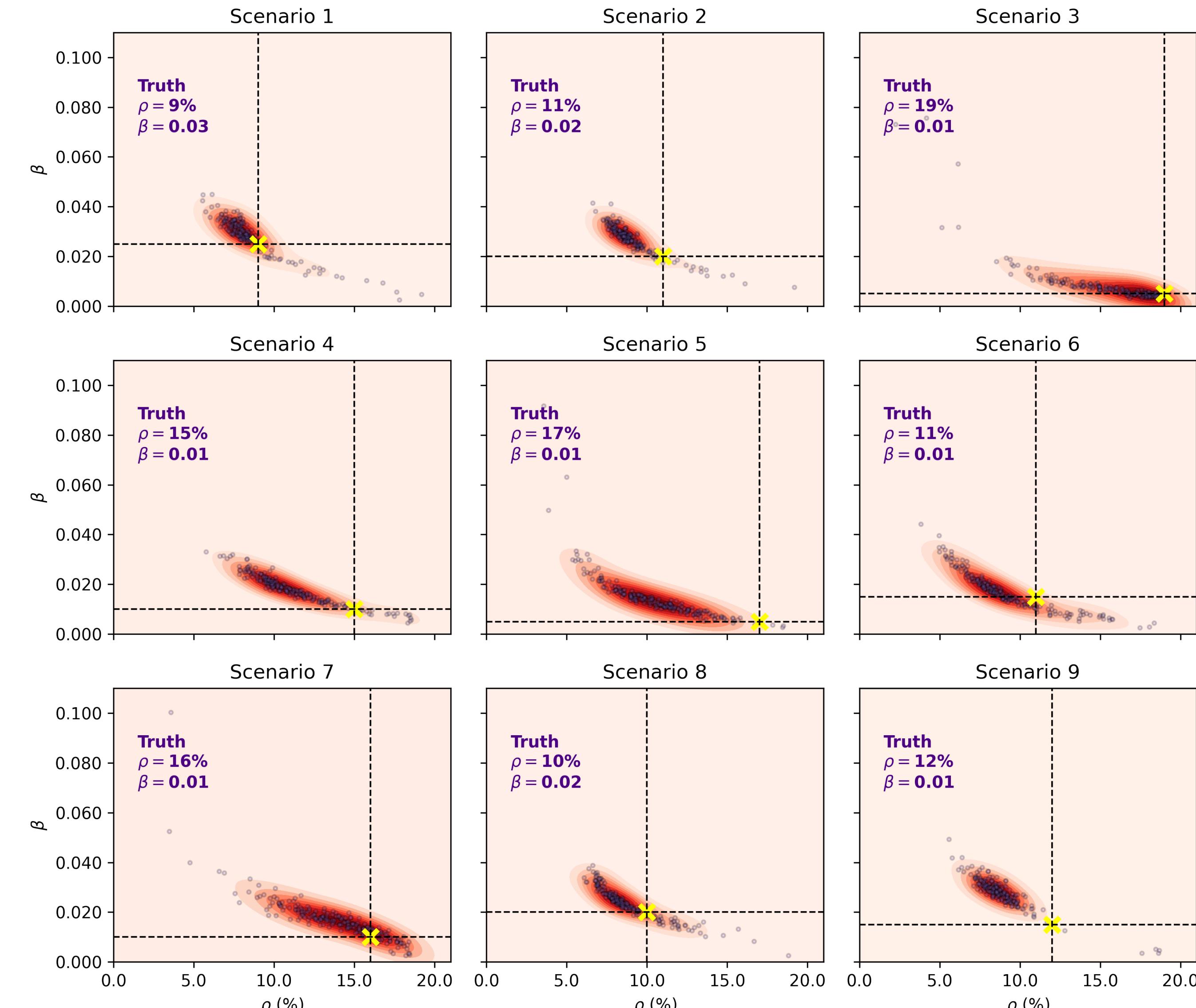
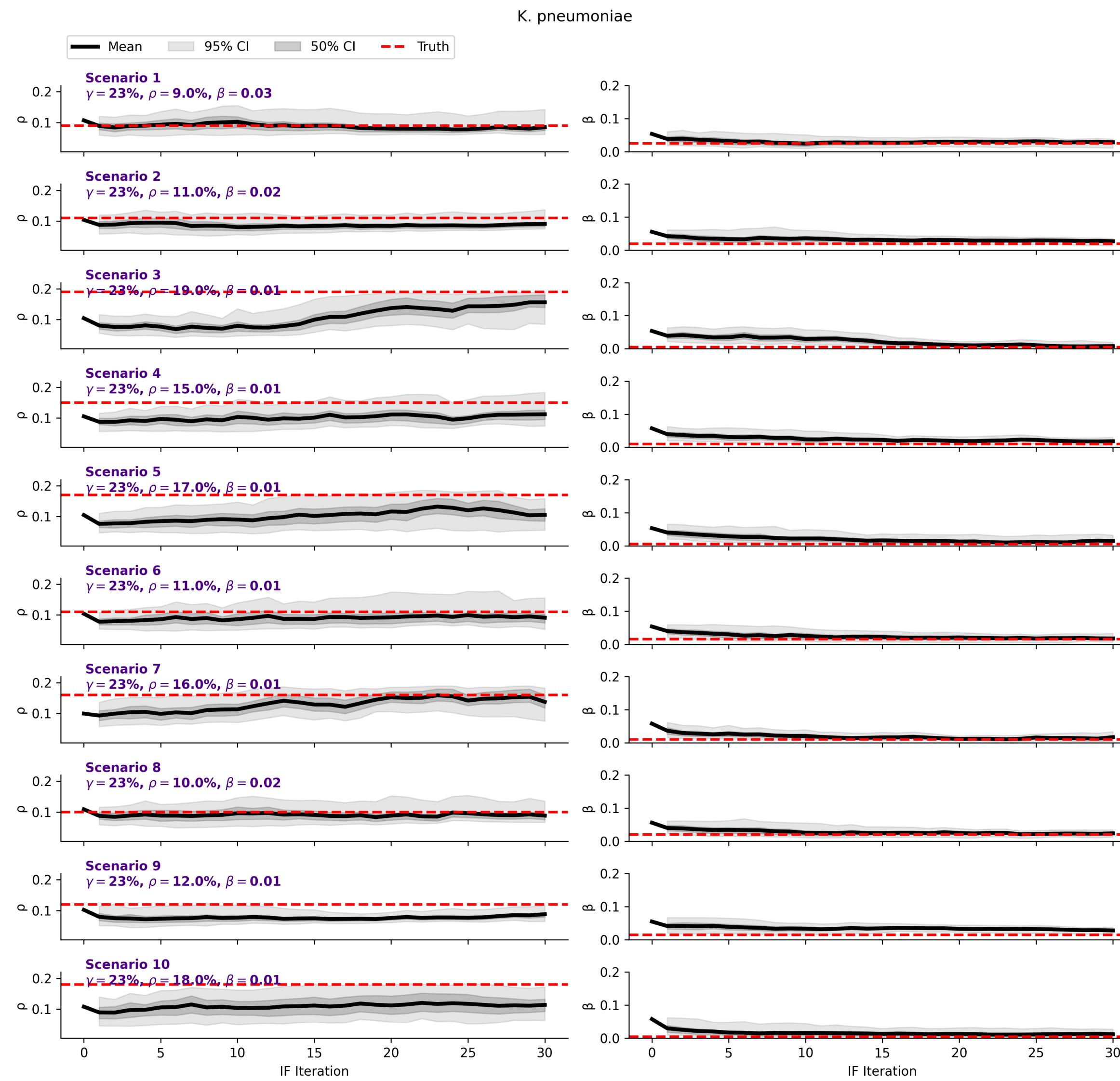
Posterior joint distribution for E. faecium, $\gamma = 40.6\%$



Inferences on simulated observations

K. pneumoniae

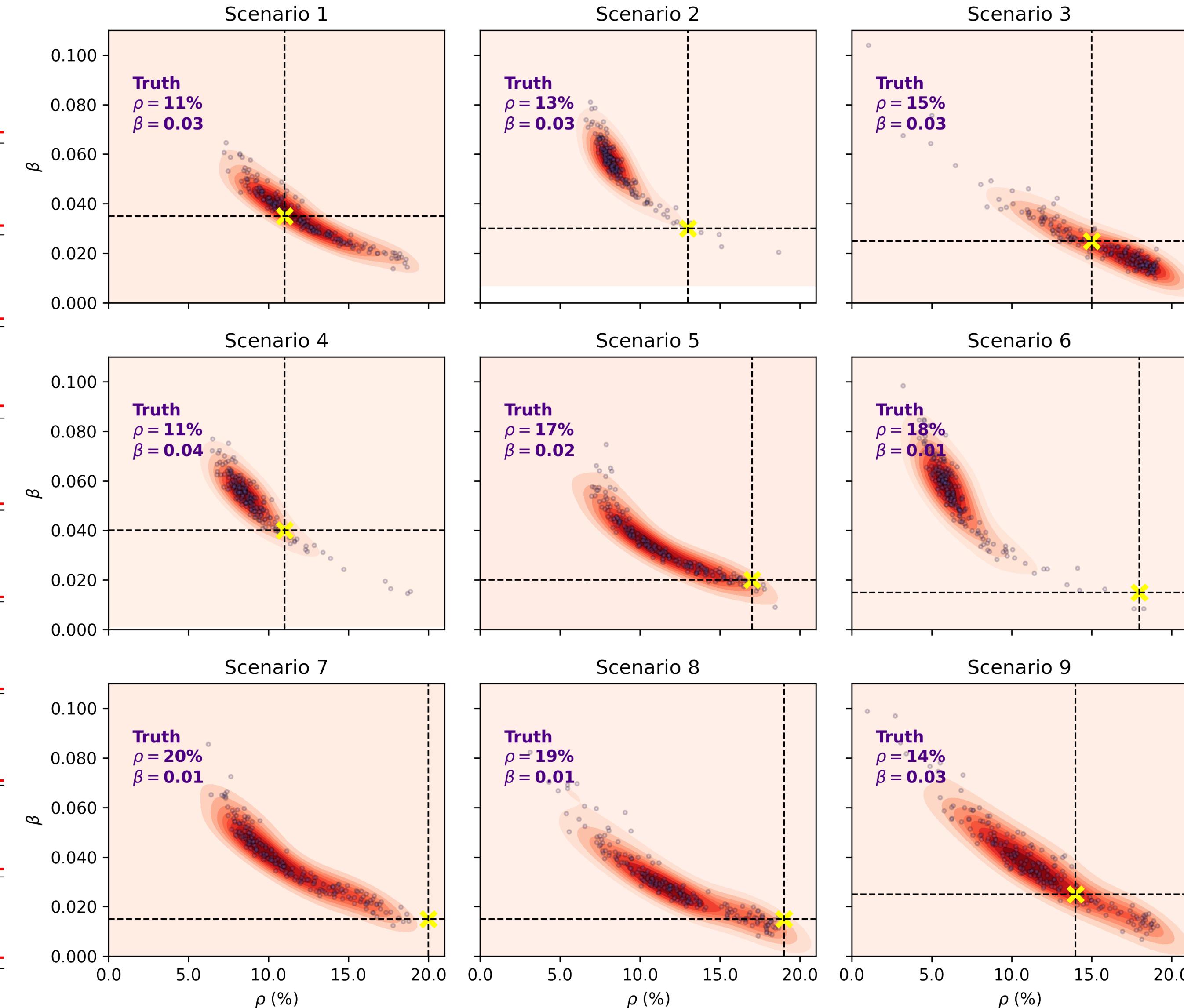
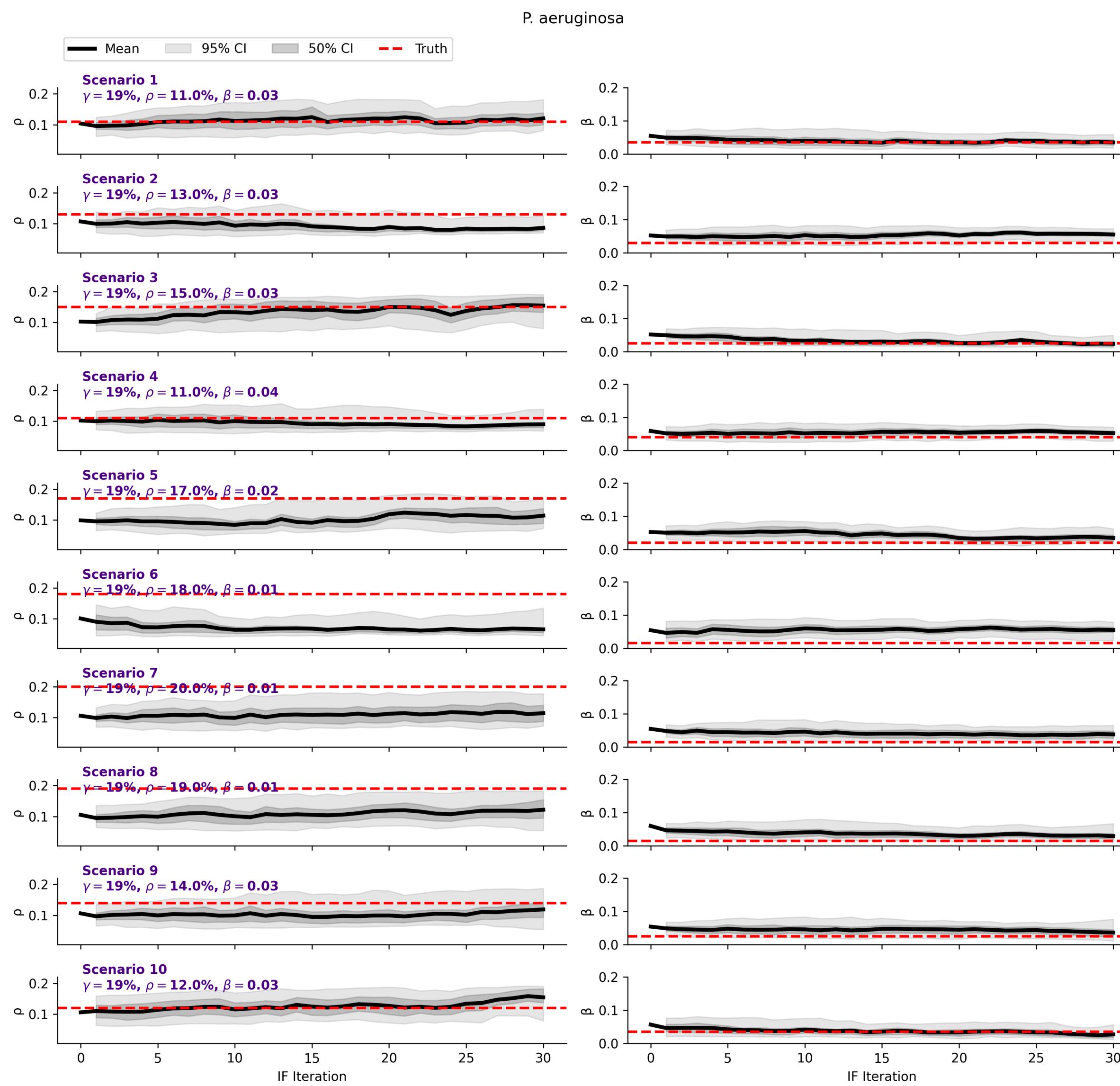
Posterior joint distribution for *K. pneumoniae*, $\gamma = 23.0\%$



Inferences on simulated observations

P. aeruginosa

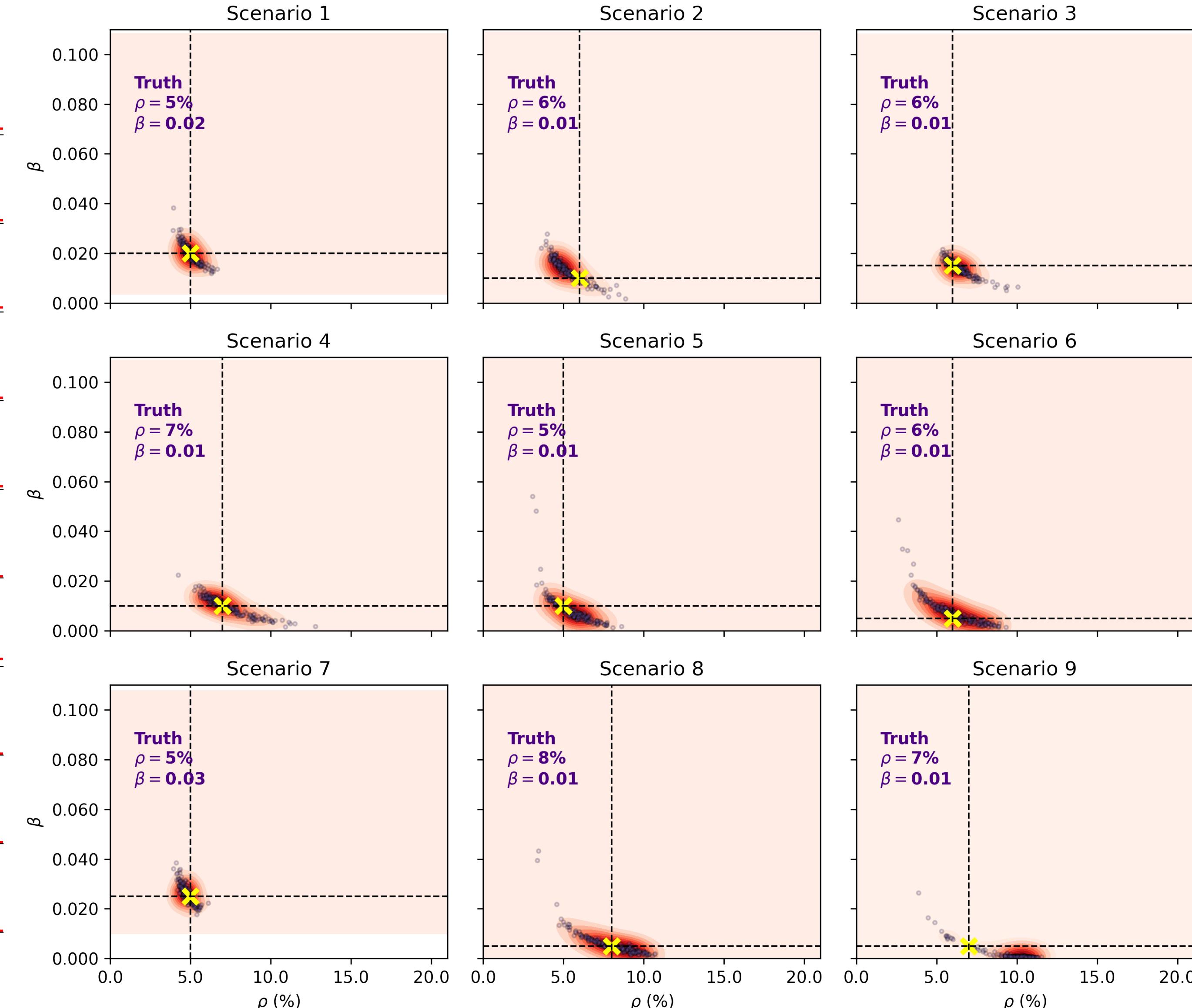
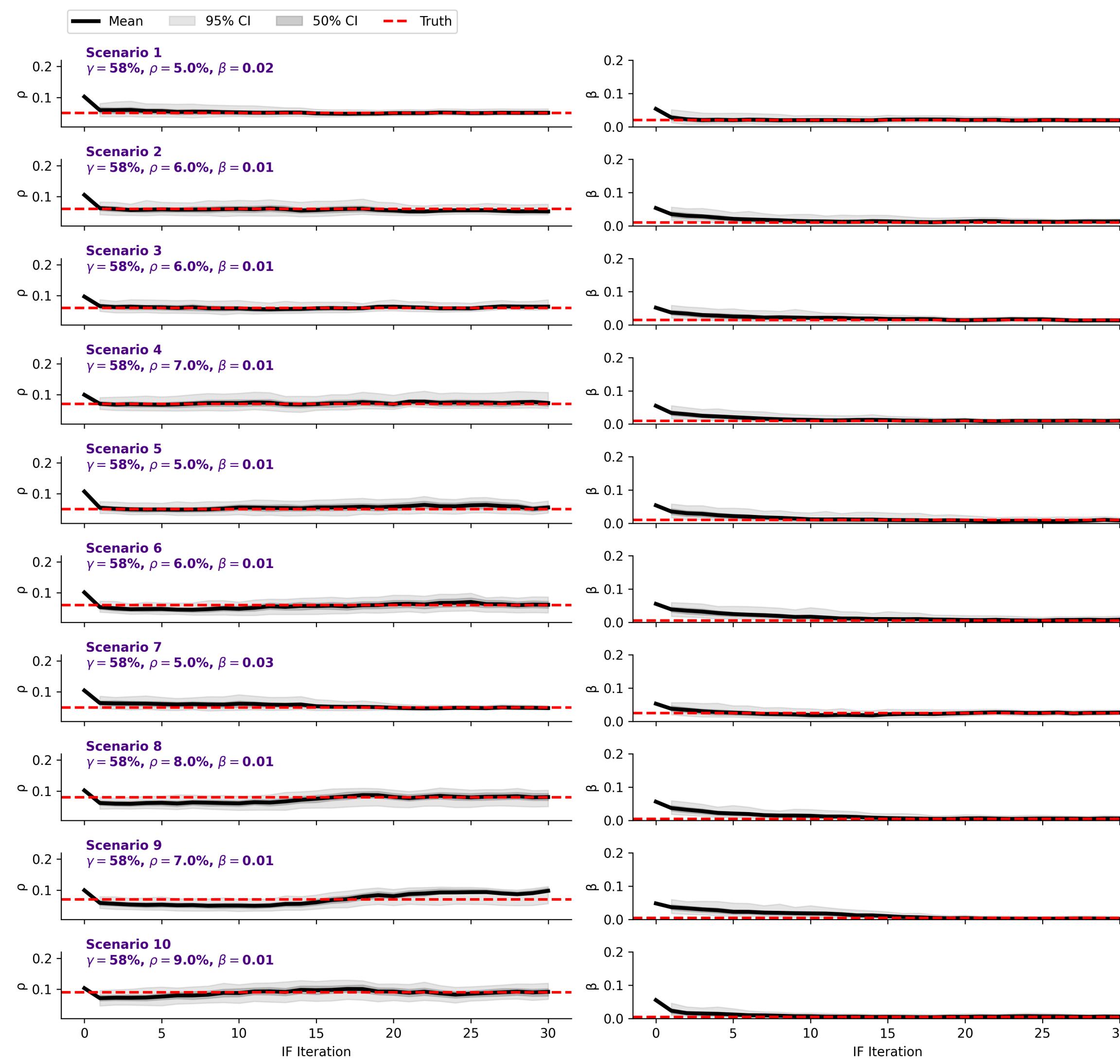
Posterior joint distribution for *P. aeruginosa*, $\gamma = 18.8\%$



Inferences on simulated observations

S. epidermidis

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

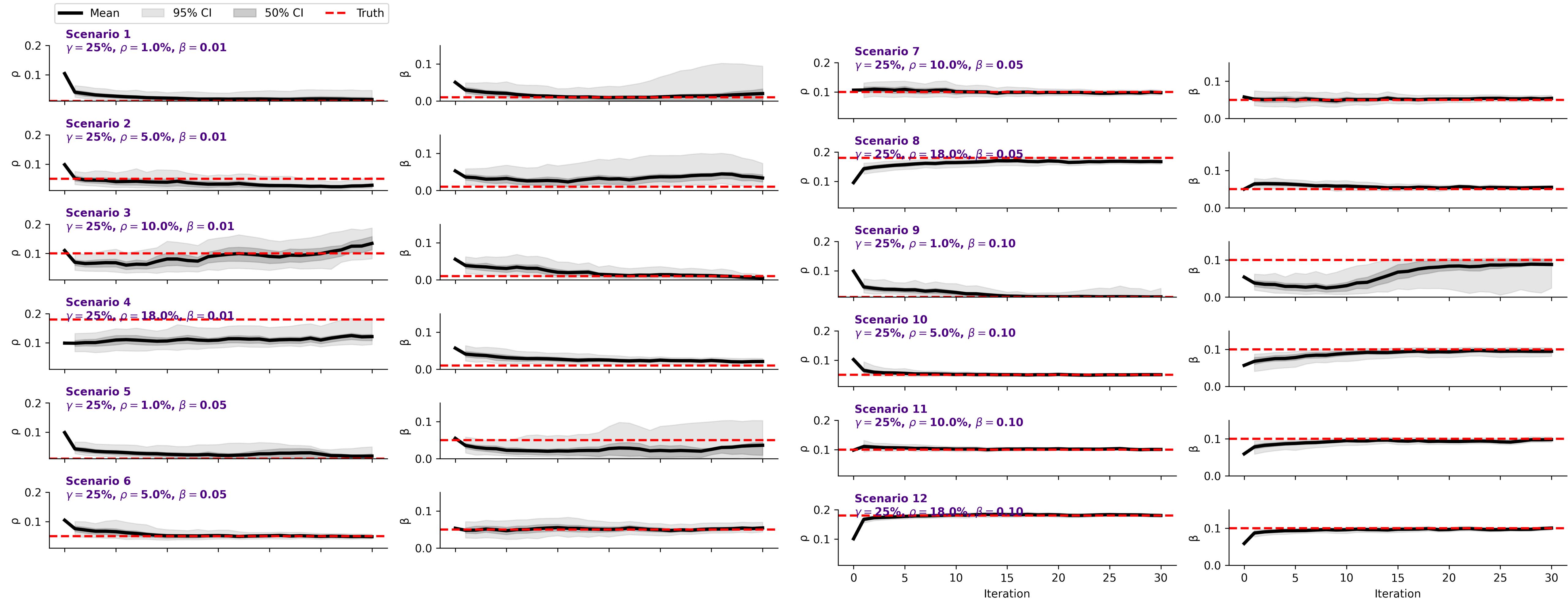


Inferences on a broader range

Jeff's request

Broad synthetic inferences

Convergence plots - $\gamma = 25\%$

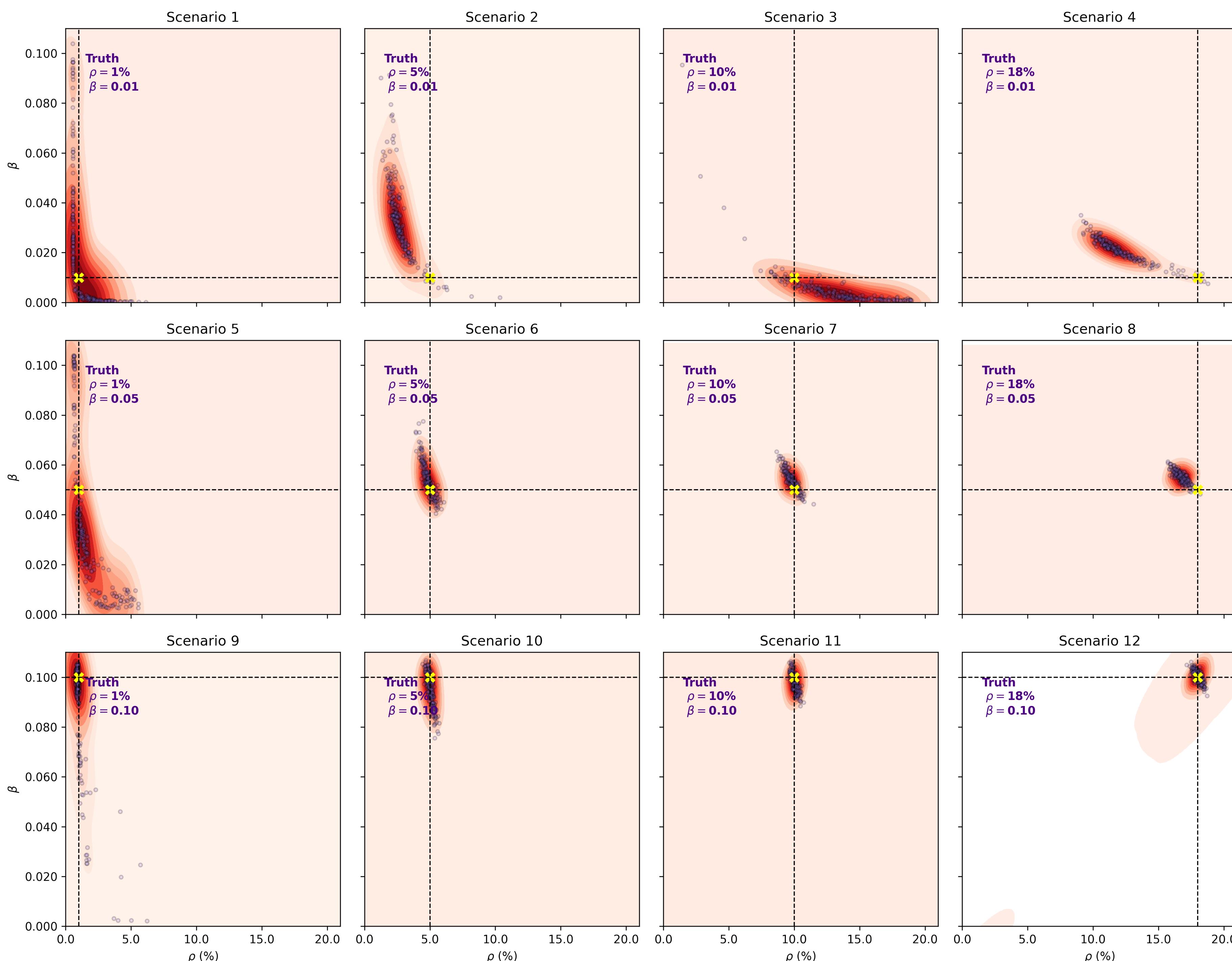


Broad synthetic inferences

Joint posterior

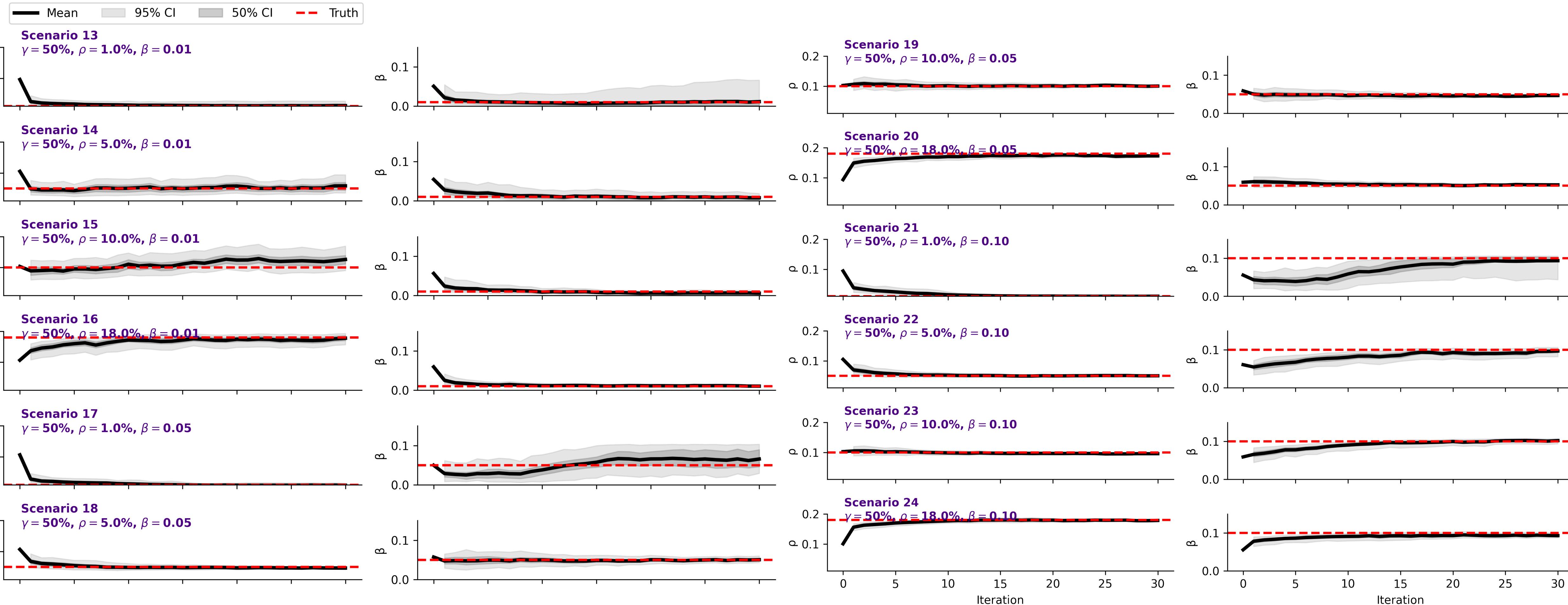
$\gamma = 25\%$

- Prior ranges shown in the axis.
- β increases per row
- ρ varies per column
- Truth as **X** cross and intersection of lines.



Broad synthetic inferences

Convergence plots - $\gamma = 50\%$

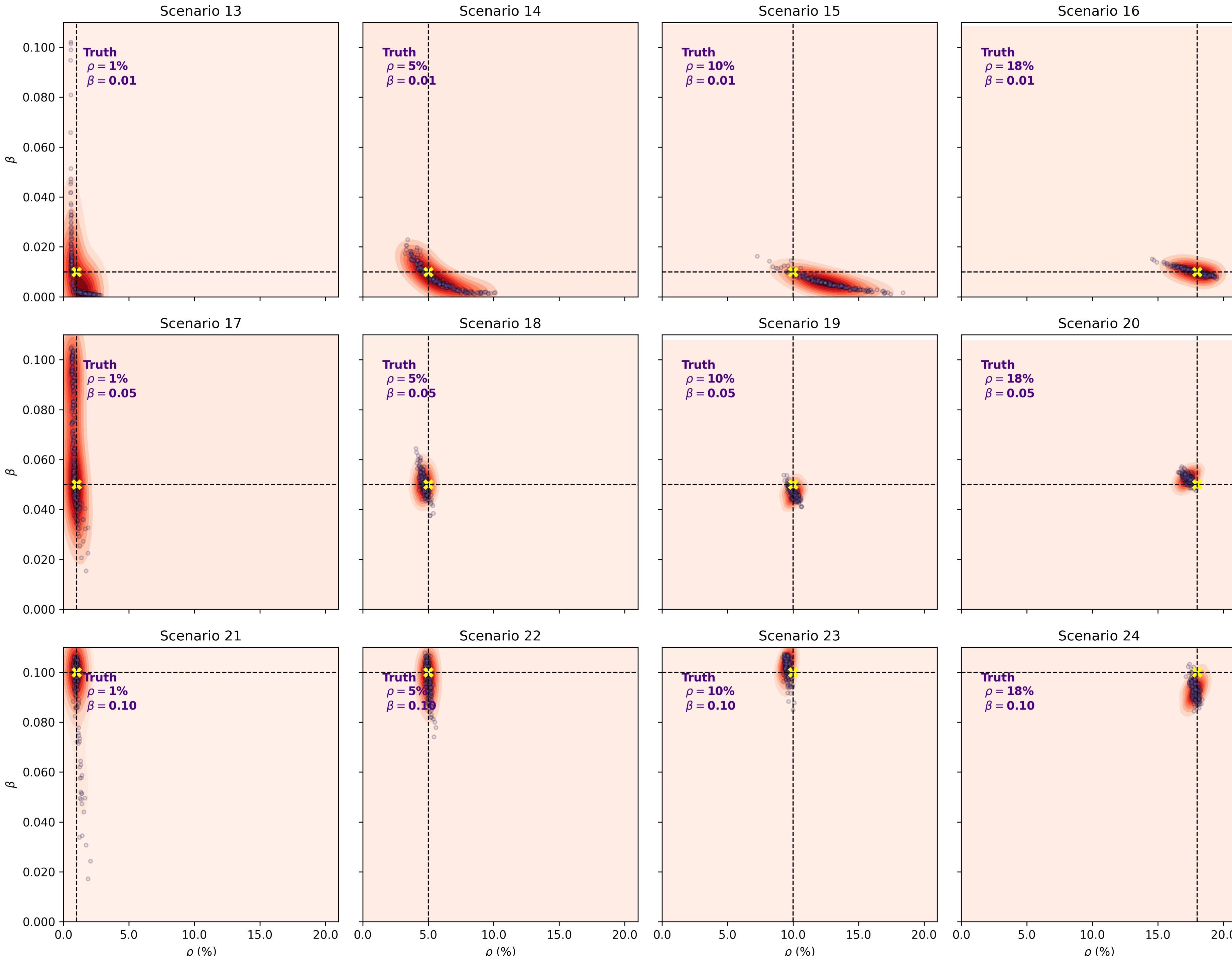


Broad synthetic inferences

Joint posterior

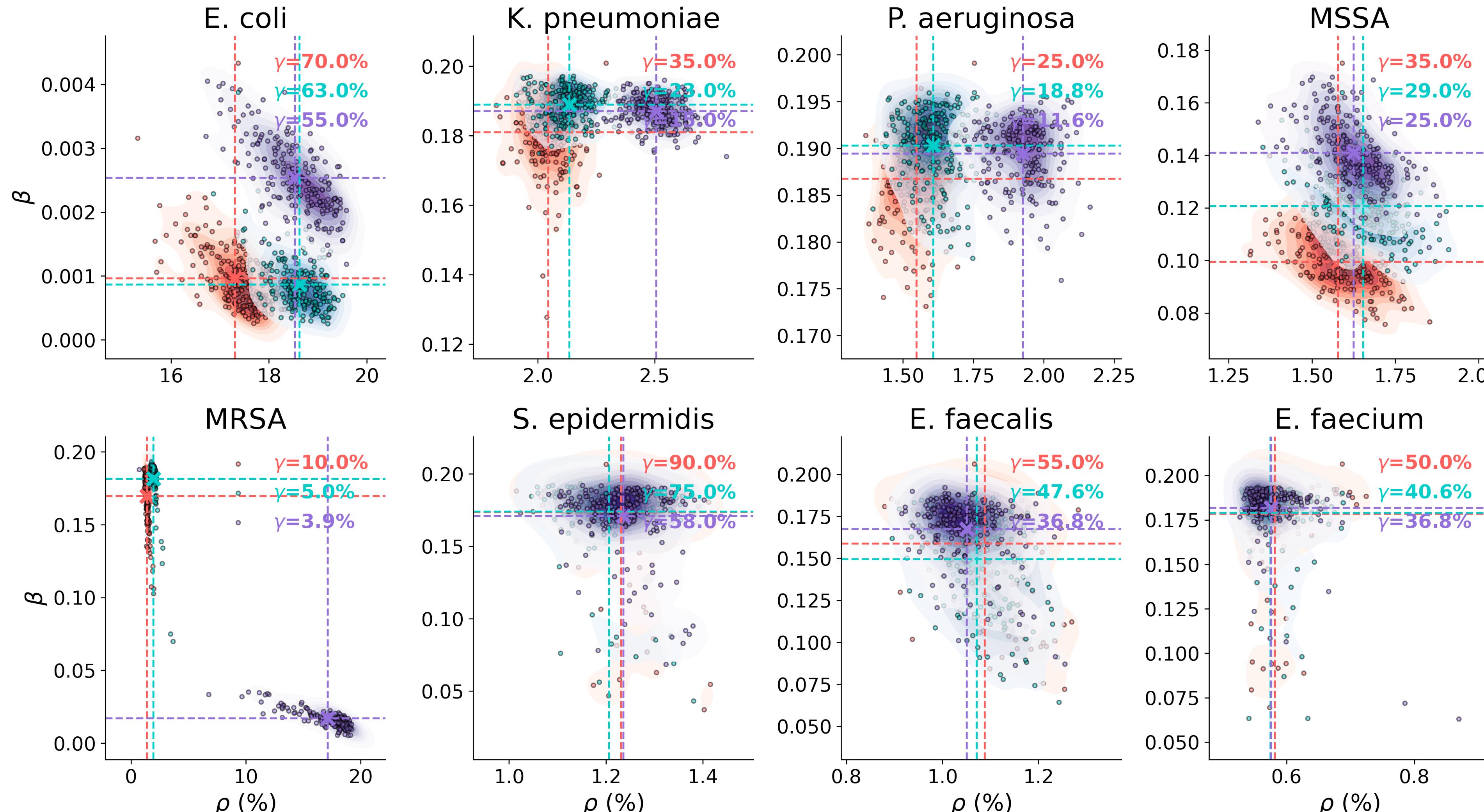
$\gamma = 50\%$

- Prior ranges shown in the axis.
- β increases per row
- ρ varies per column
- Truth as **X** cross and intersection of lines.



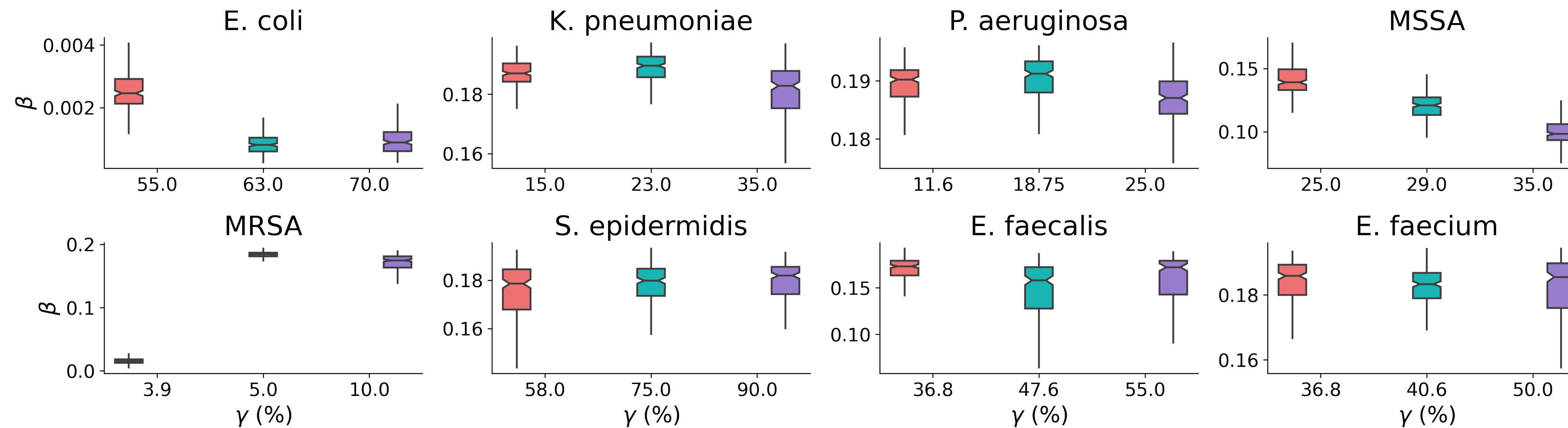
Inferences with different prevalences

Posterior joint distribution



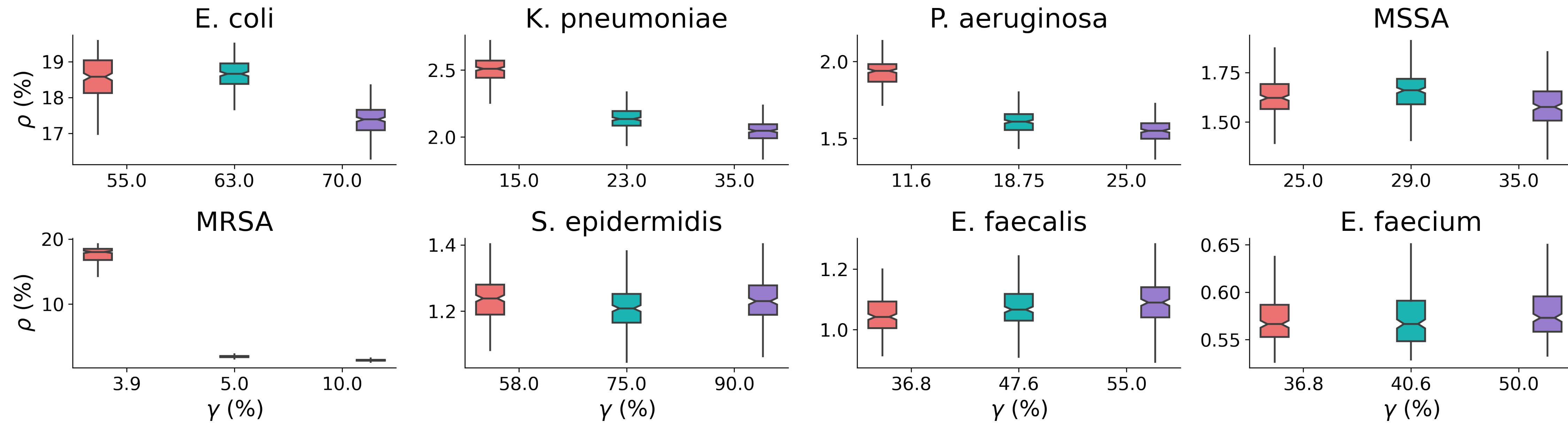
Inferences with different prevalences

Boxplots on nosocomial transmission rate β



Inferences with different prevalences

Boxplots on effective sensitivity ρ



Why are some inferences biased?

**My guess: Stochasticity of the system a.k.a.
Monte Carlo error**

- Each synthetic inference is conducted on a single stochastic trajectory $y^i = [y_1^i, y_2^i, \dots, y_T^i]$.
- We know the distribution of possible y_i , so if we know how far was y_i from the distribution of possible trajectories Y , we could explain biases in the inference?
 - Not need to compute a lot of inferences (expensive with the ABM).
 - We can understand the impact of the parameters on the bias too, more than knowing how they impact the uncertainty in the estimates.

Distances

- Distance between a posterior estimate Θ and truth θ_T (point)
 - The posterior can be parametrized with a vector of means μ_Θ , and a covariance matrix C_Θ
 - Distance between posterior and truth: Just a norm scaled with the covariance (Mahalanobis distance (?) according to Wikipedia)
 - $D_1 = |\mu_\Theta - \theta_T|_{C_\Theta} = \sqrt{(\mu_\Theta - \theta_T)^T C_\Theta^{-1} (\mu_\Theta - \theta_T)}$
 - Distance between inferred observation and set of possible observations (continuous ranked probability score).
 - $D_2 = CRPS(Y, y_i)$

What should we expect?

- The more common the observation (lower CRPS) the lower the distance between the posterior and the truth (less bias)
- Probably depends on importation rates γ , other guess: the higher the prevalence less error in the posterior (?).

Result

