Estimating the fitness cost and benefit of antimicrobial resistance from pathogen genomic data: Supplementary Material

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Supplementary information for detailed analysis of a single simulated dataset

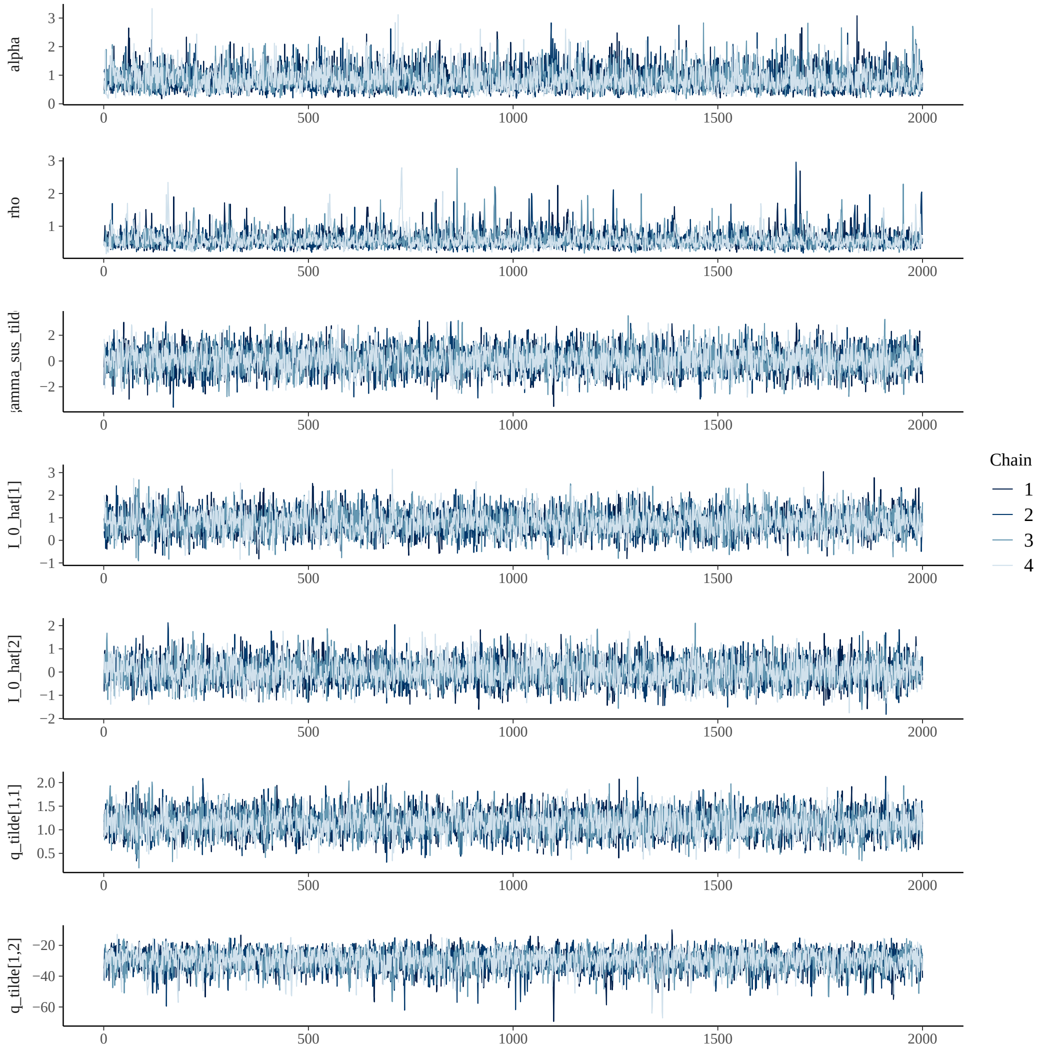

Figure S1: Traces for all parameters excluding GP inducing variables $f_1 : m$ for analysis of single simulated dataset.

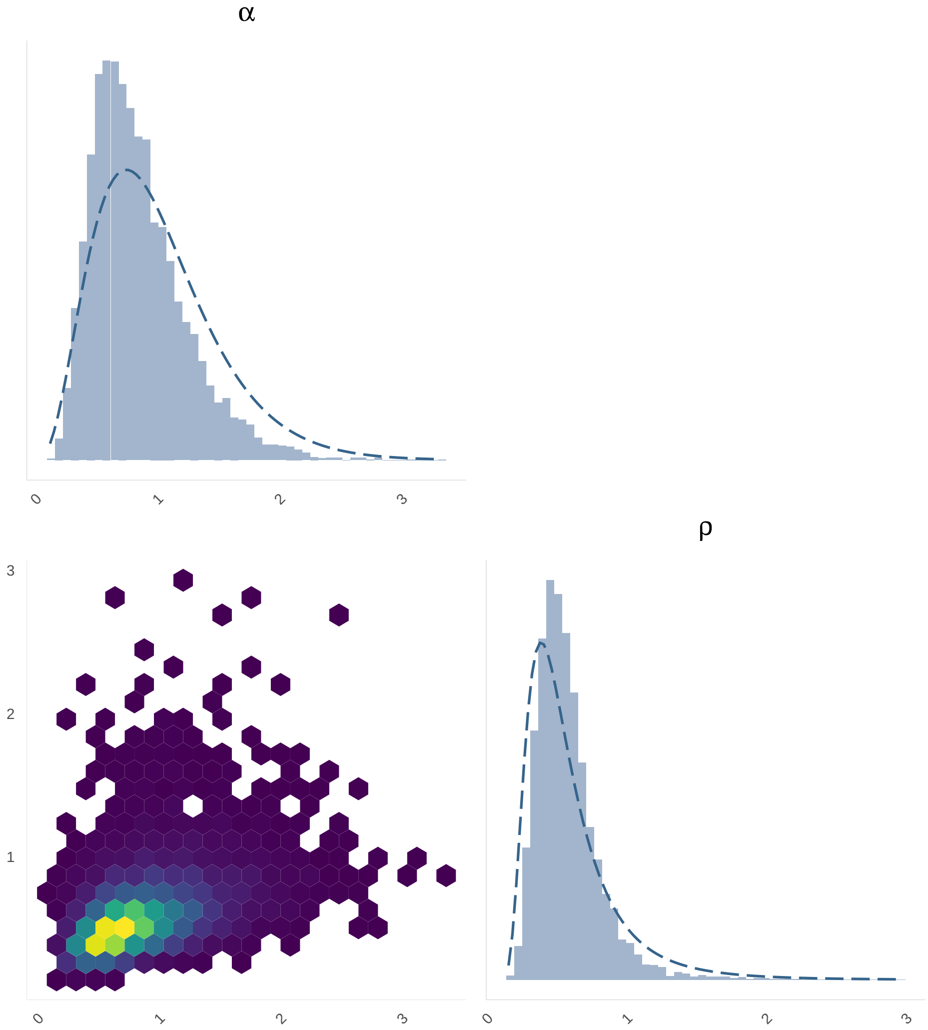

Figure S2: Marginal and joint distributions for hyperparameters ρ and α for the analysis of a single simulated dataset.

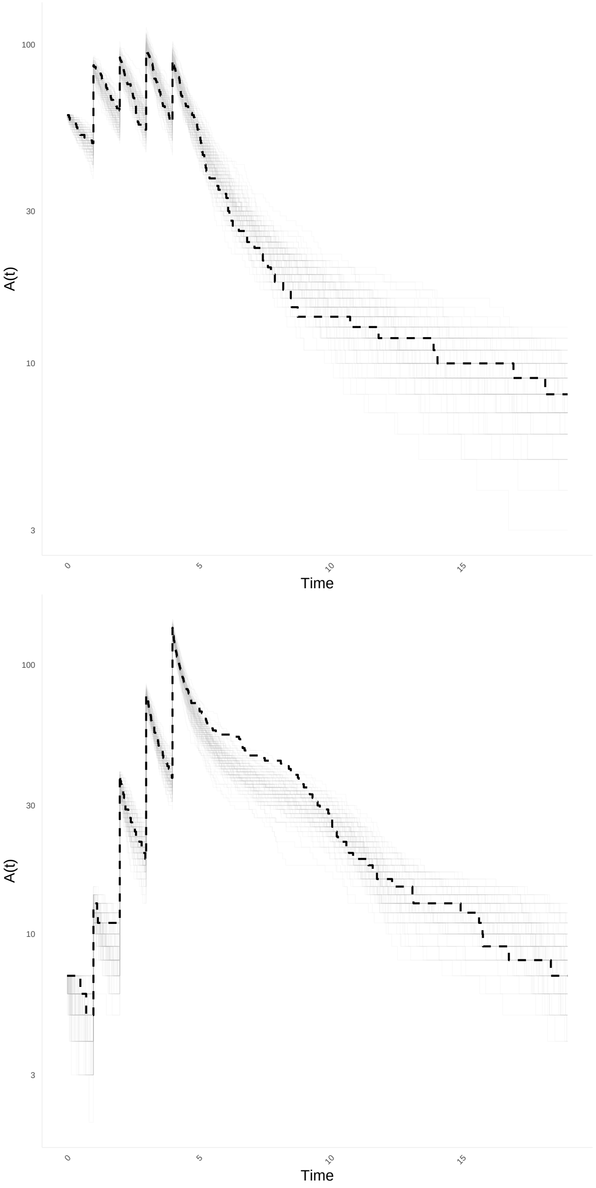

Figure S3: Posterior predictive trajectories of $A(t)$ for the susceptible (top) and resistant (bottom) lineages in the analysis of single simulated dataset.

Supplementary information for resistance parameter recovery

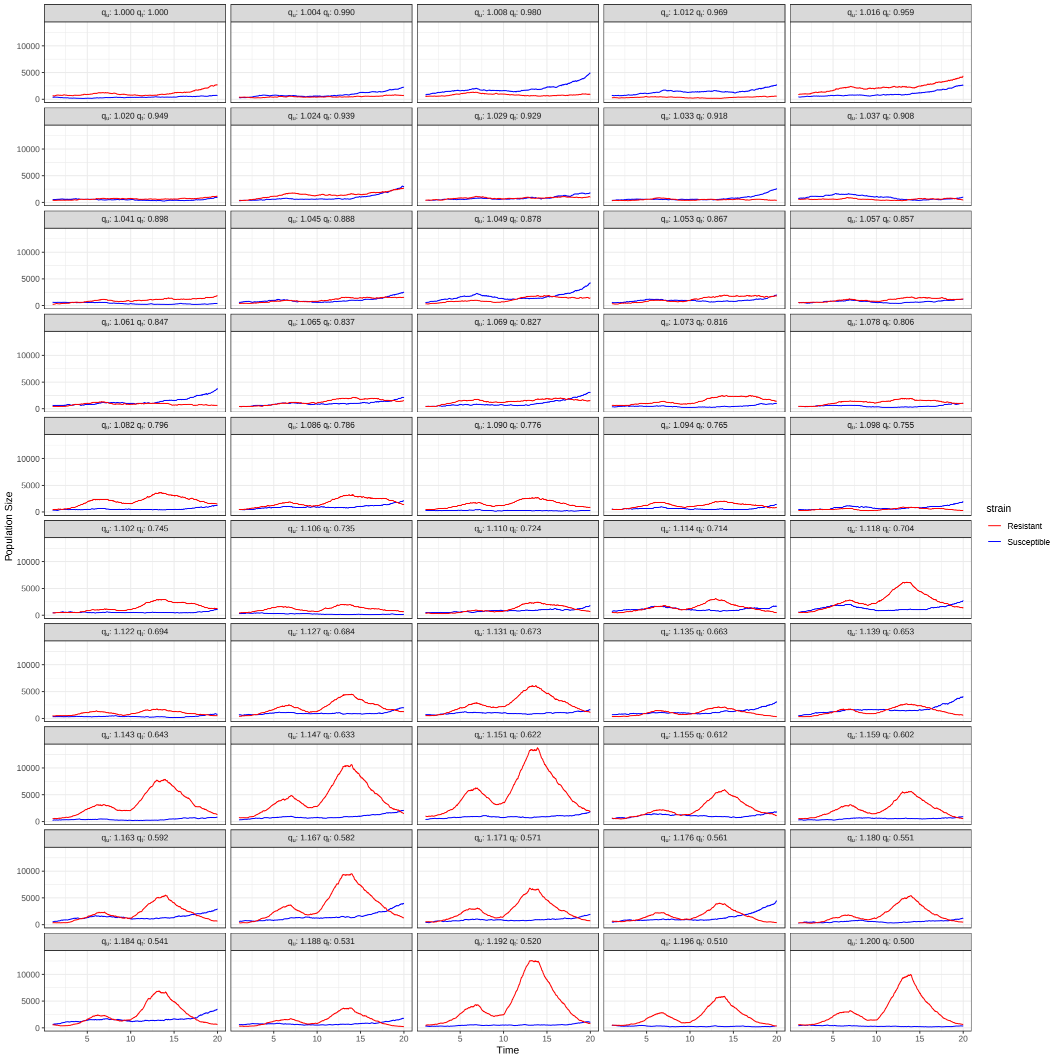

Figure S4: Trajectories of observed lineages used for parameter recovery validation.

Supplementary information for analysis of *Neisseria gonorrhoeae* dataset

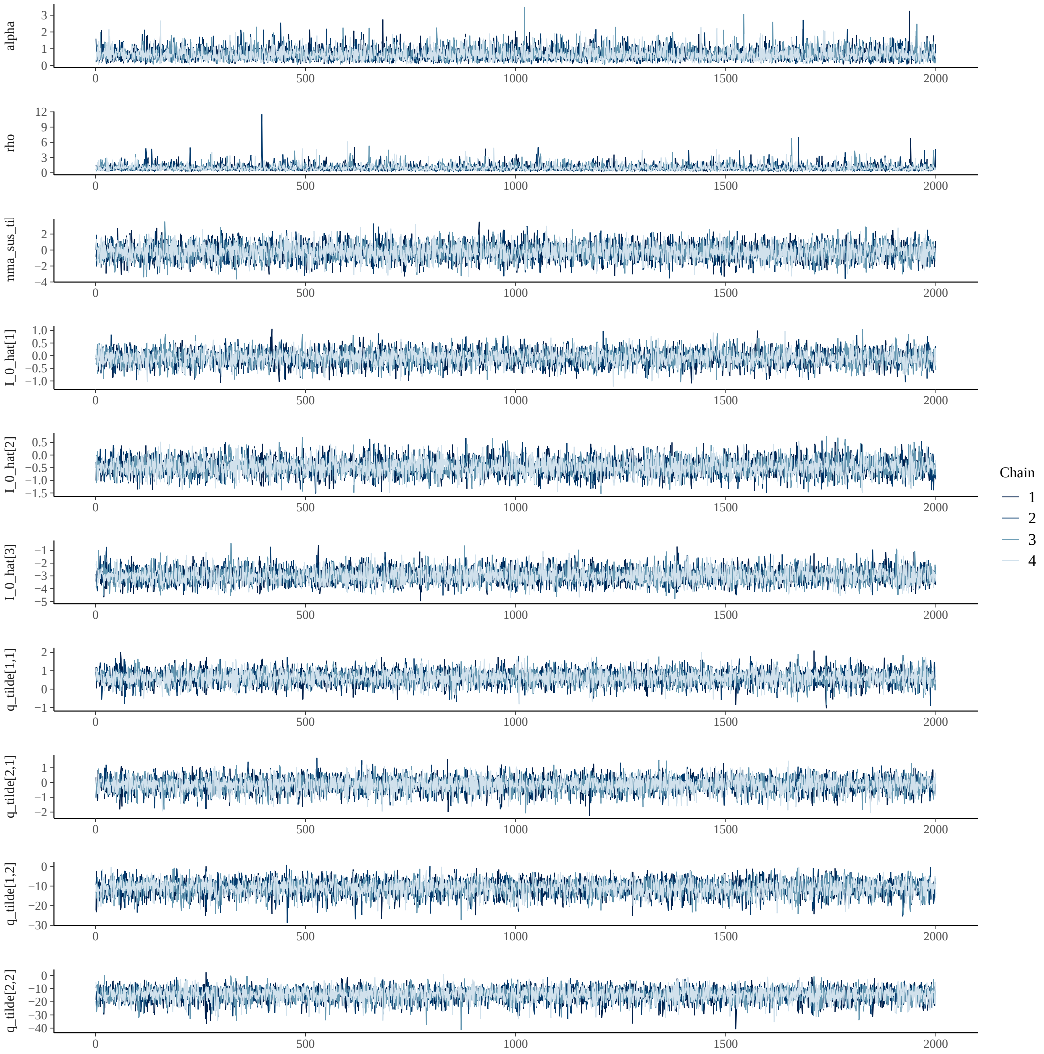

Figure S5: Traces for all parameters excluding GP inducing variables $f_1 : m$ for the analysis of *N. gonorrhoeae*.

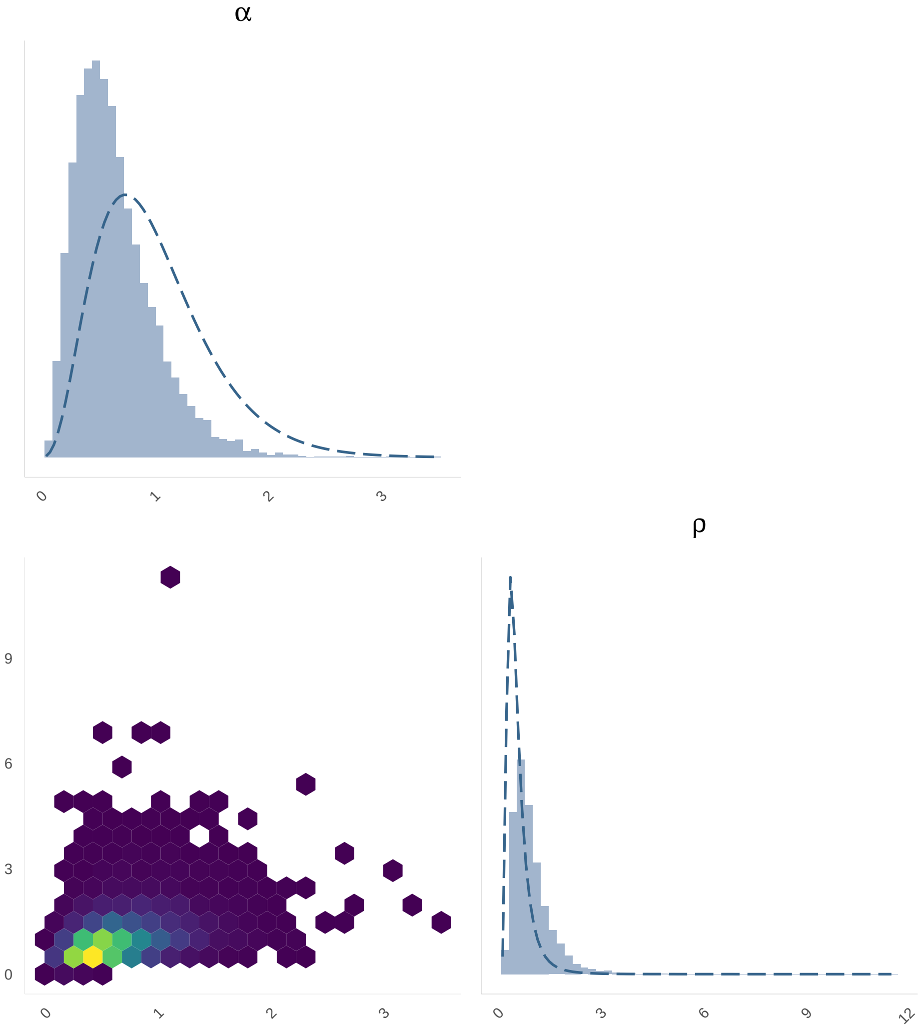

Figure S6: Marginal and joint distributions for hyperparameters ρ and α for the analysis of *N. gonorrhoeae*.

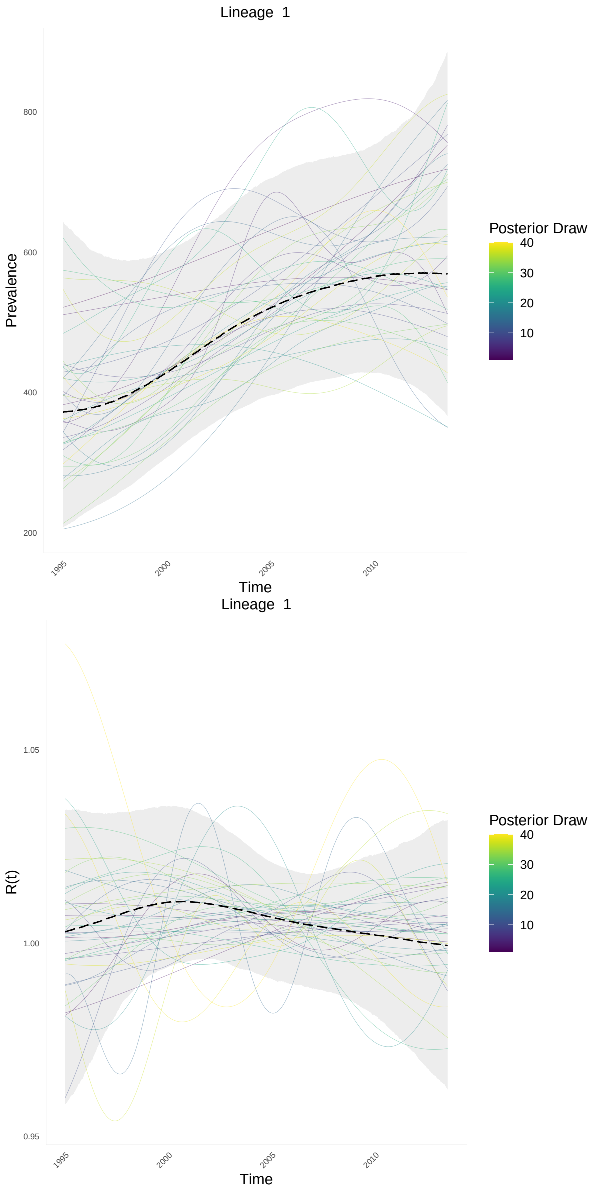

Figure S7: Estimated susceptible lineage dynamics for *N. gonorrhoeae*.

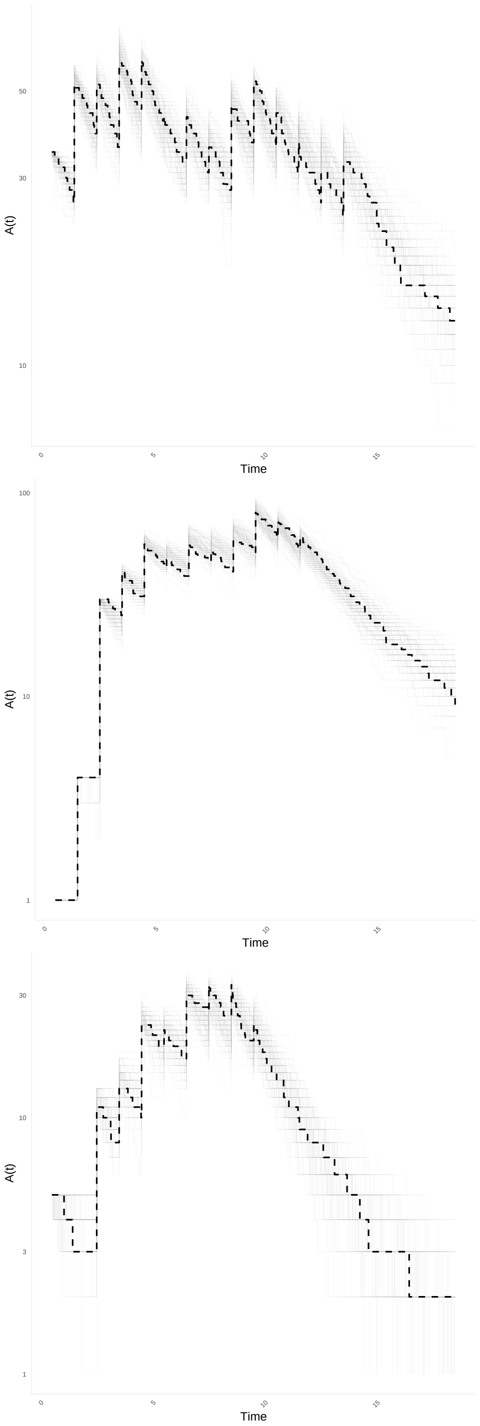

Figure S8: Posterior predictive trajectories of $A(t)$ for the susceptible lineage (top), resistant lineage 1 (middle) and resistant lineage 2 (bottom) of *N. gonorrhoeae*.