

Supplemental Material 2: MCMC Diagnostics

Bayesian Hierarchical Model for Immune Responses to Leishmania - a Tick Borne Coinfection Study

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MCMC Diagnostics. The following R output provides the Gelman-Rubin diagnostic and traceplots for the model parameters considering the 3 full MCMC chains (20,000 iterations each) after 5,000 iterations were discarded as burn-in. The Rhat value shown in the density plots (right side) represent the point estimate for the Gelman-Rubin diagnostic. The value 1.1 is used as a threshold, as explained in the main text. Therefore, we say that a factor of 1.1 or below indicates that the parameter has reached a level of convergence, which was achieved by all parameters in the model.





























