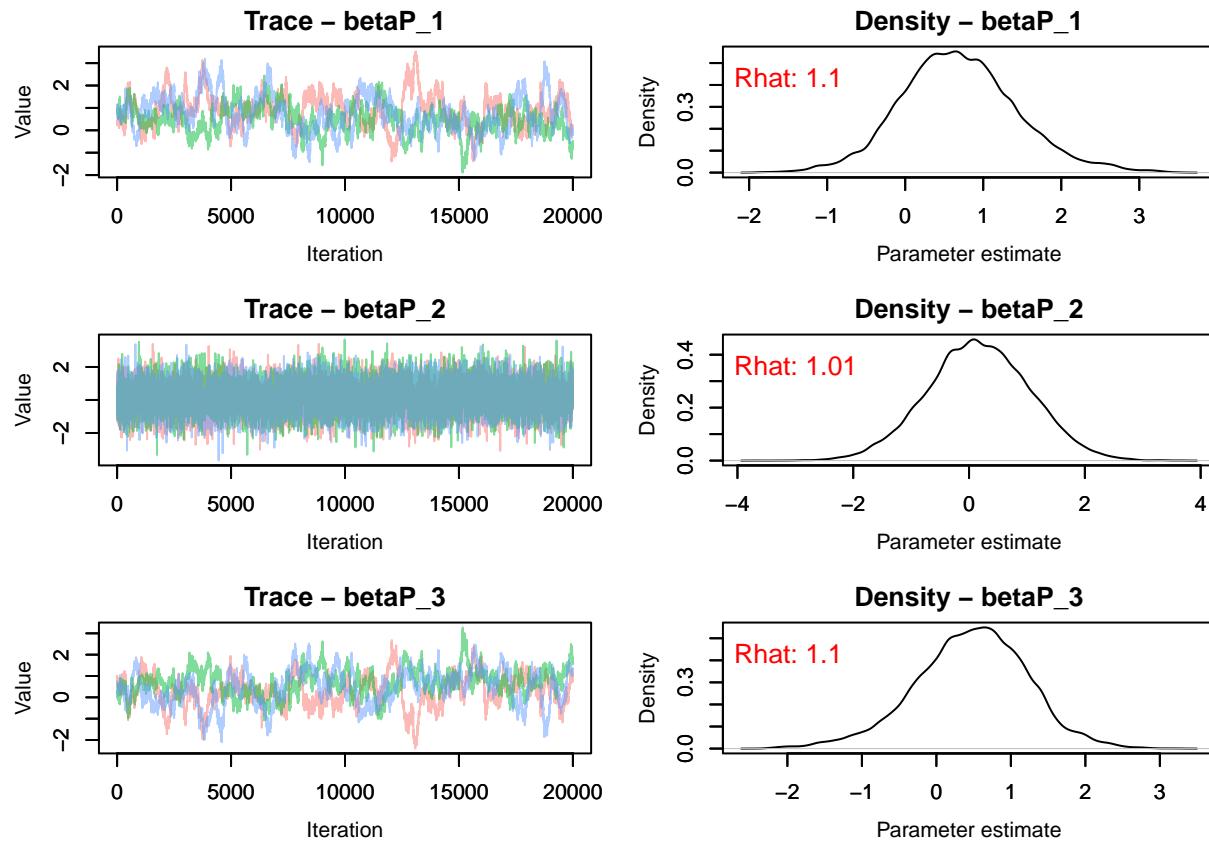


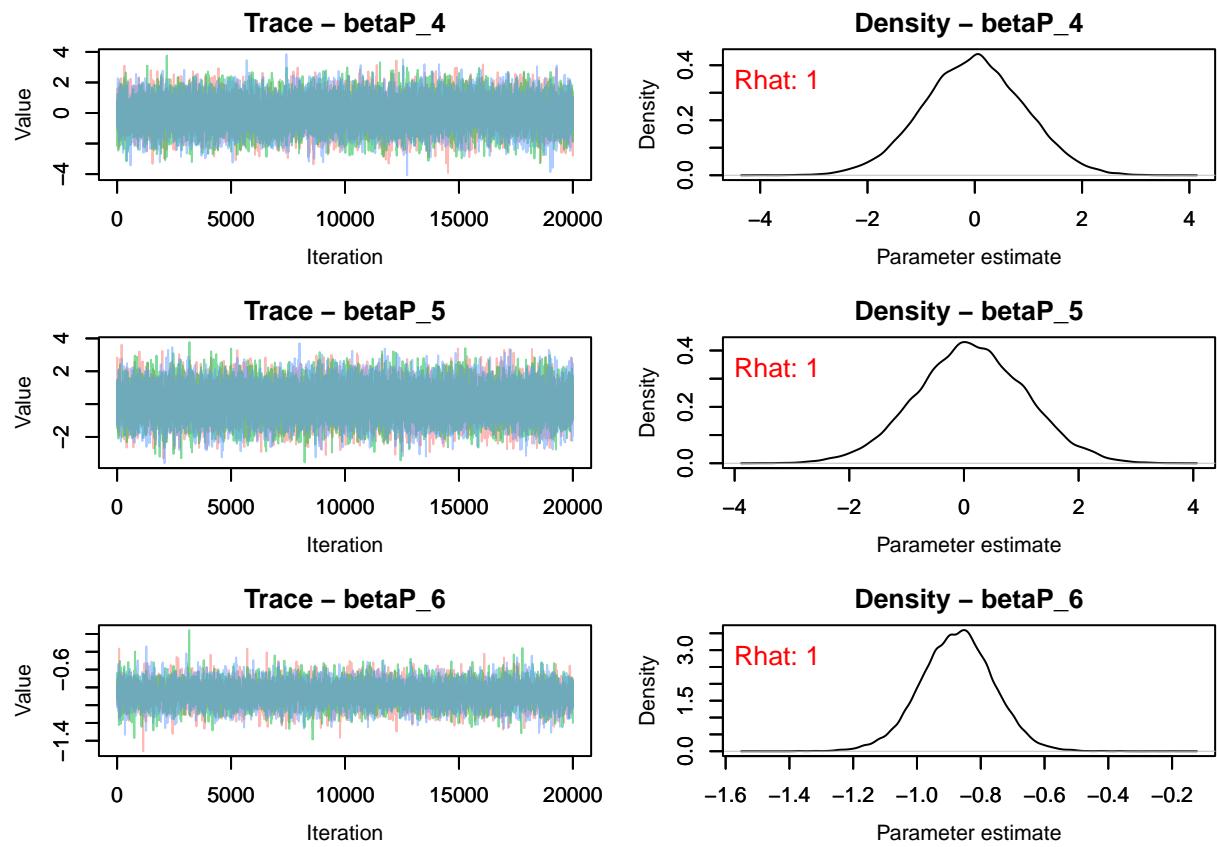
Supplemental Material 2: MCMC Diagnostics

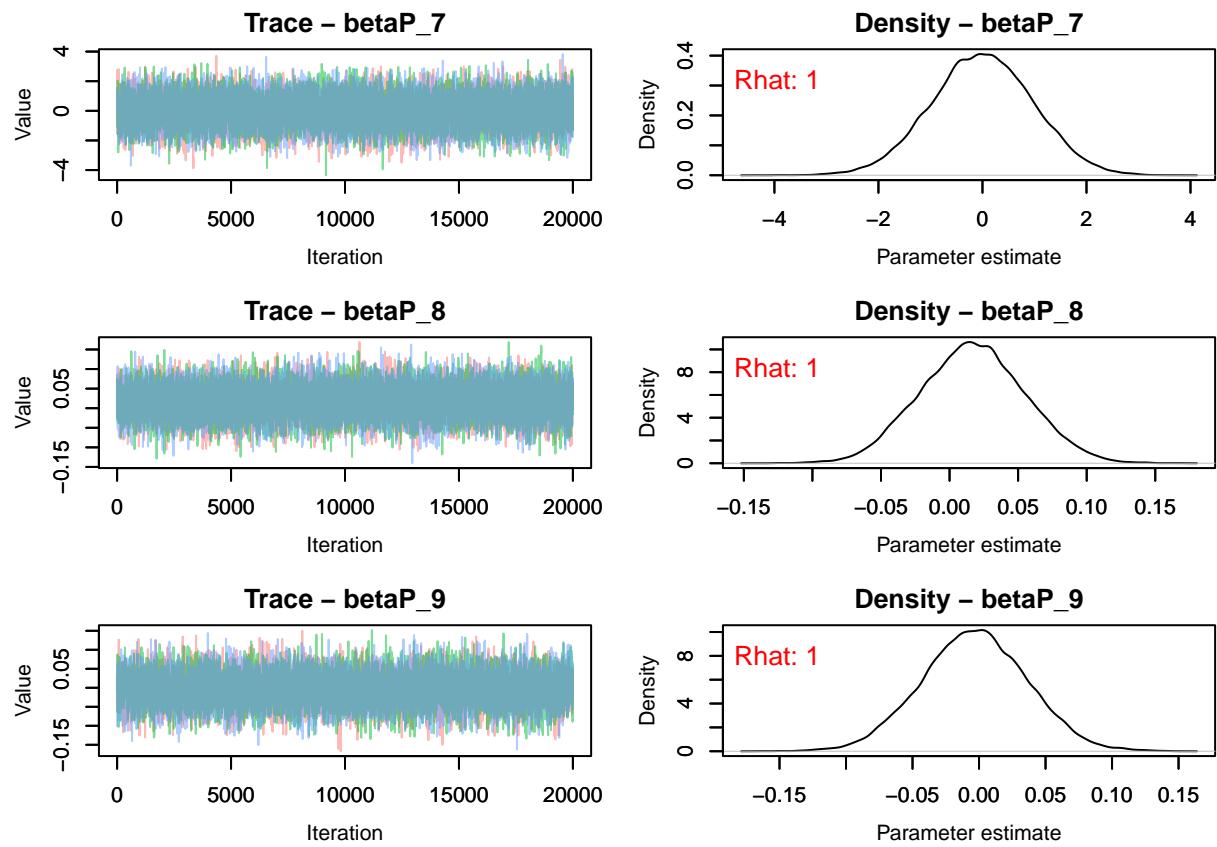
Bayesian Multivariate Longitudinal Model for Immune Responses to Leishmania - a Tick Borne Coinfection Study

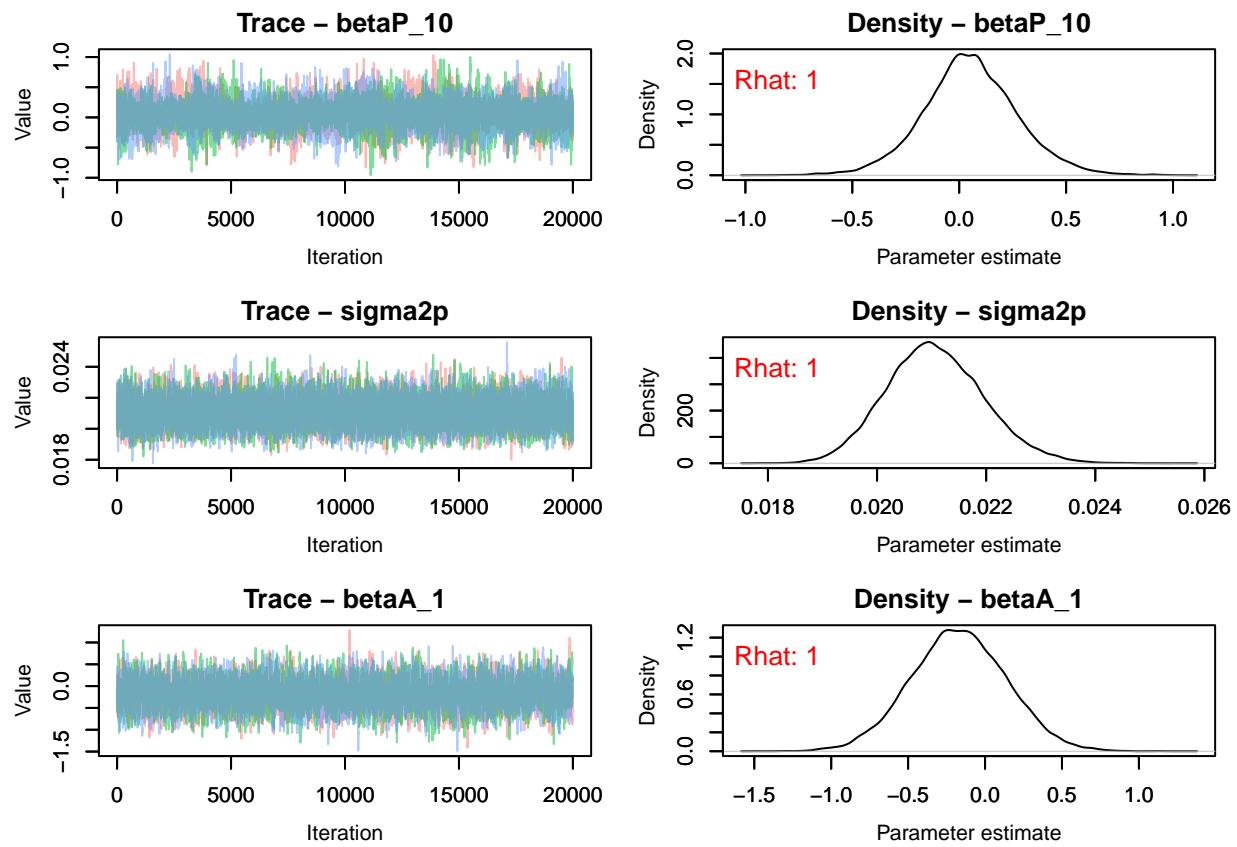
Felix M. Pabon-Rodriguez, Grant D. Brown, Breanna M. Scorza, Christine A. Petersen

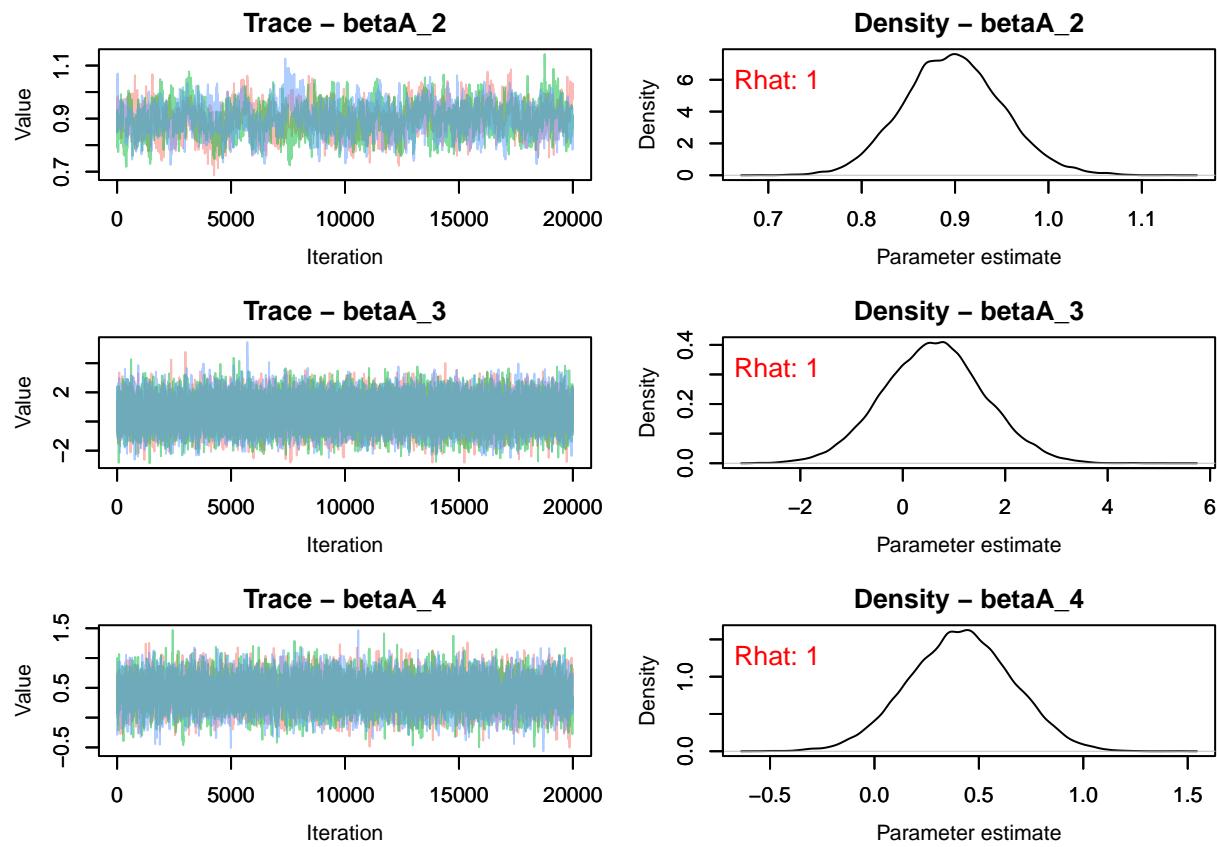
MCMC Diagnostics 1. The following R output provides the Gelman-Rubin diagnostic and traceplots for the model parameters considering the 3 full MCMC chains (20,000 iterations each) after 5,000 iterations were discarded as burn-in. The Rhat value shown in the density plots (right side) represent the point 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.

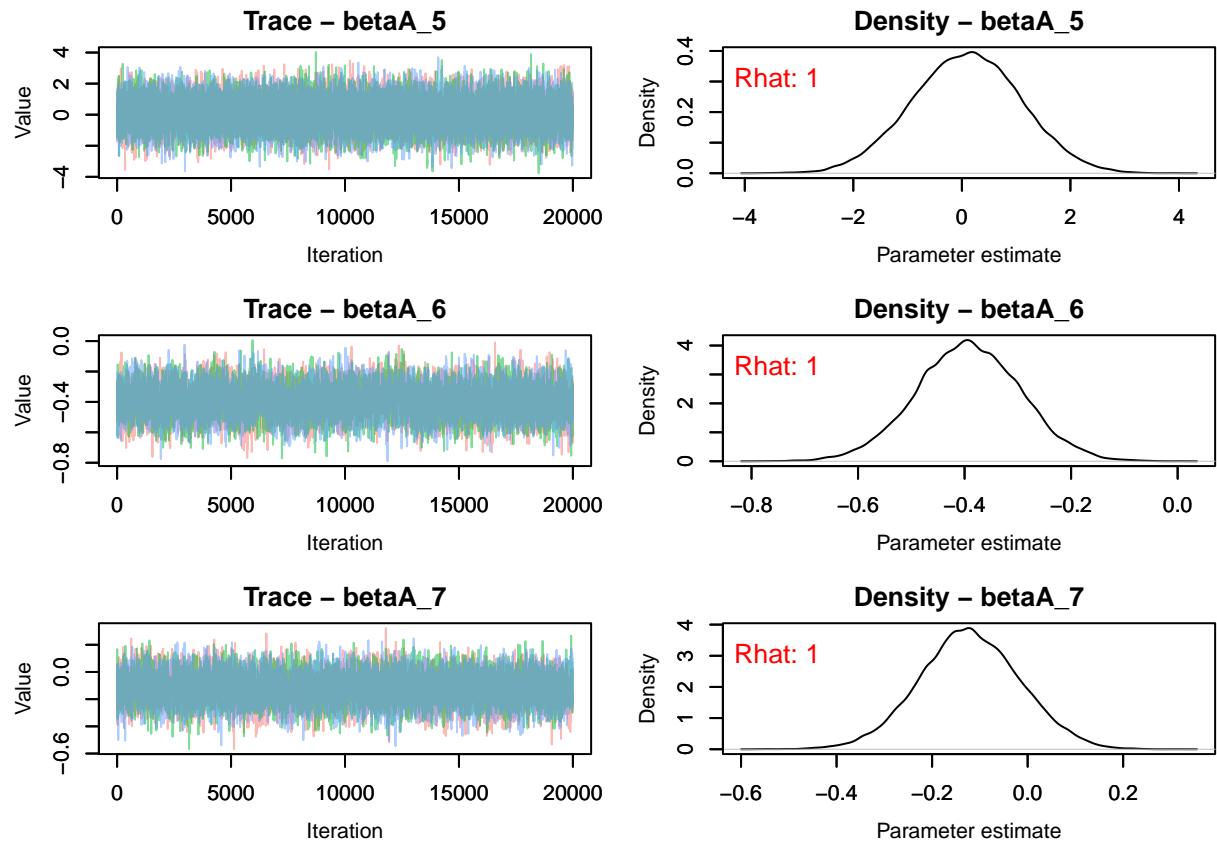


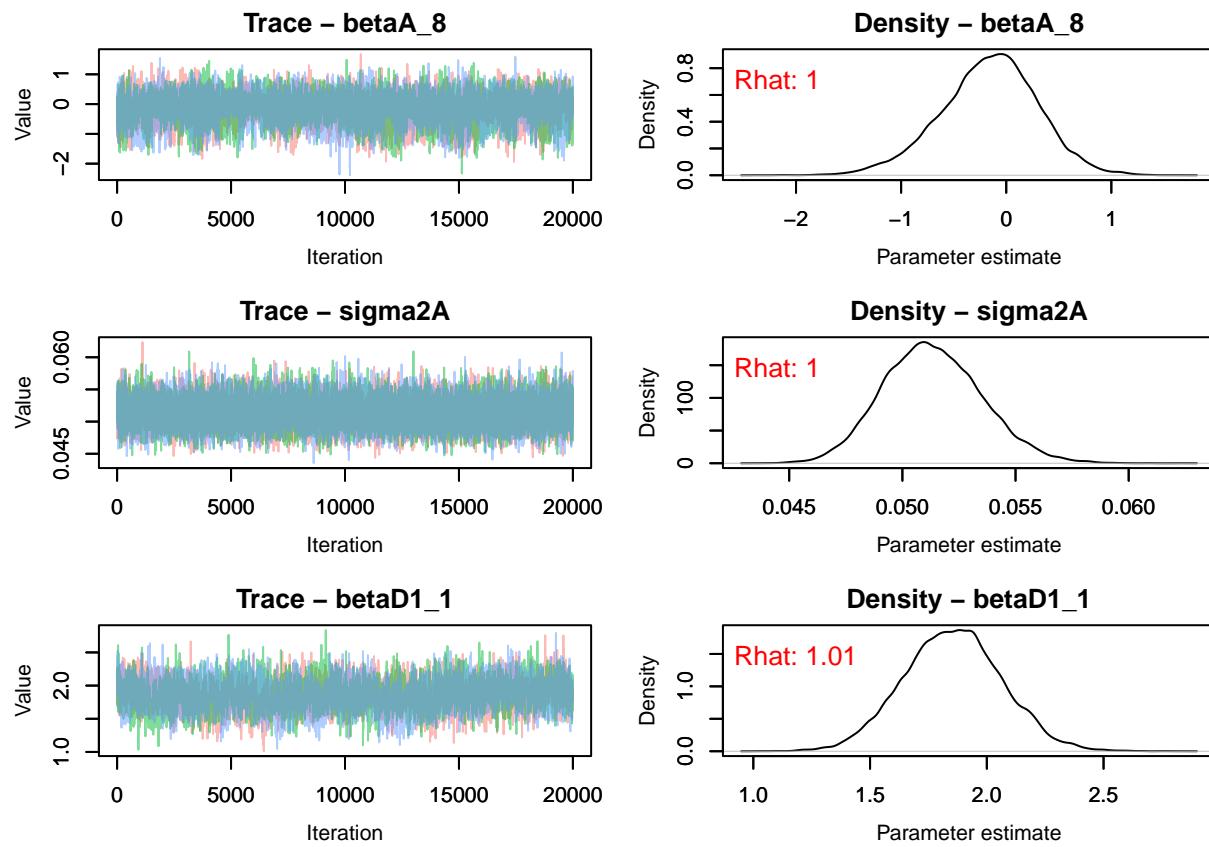


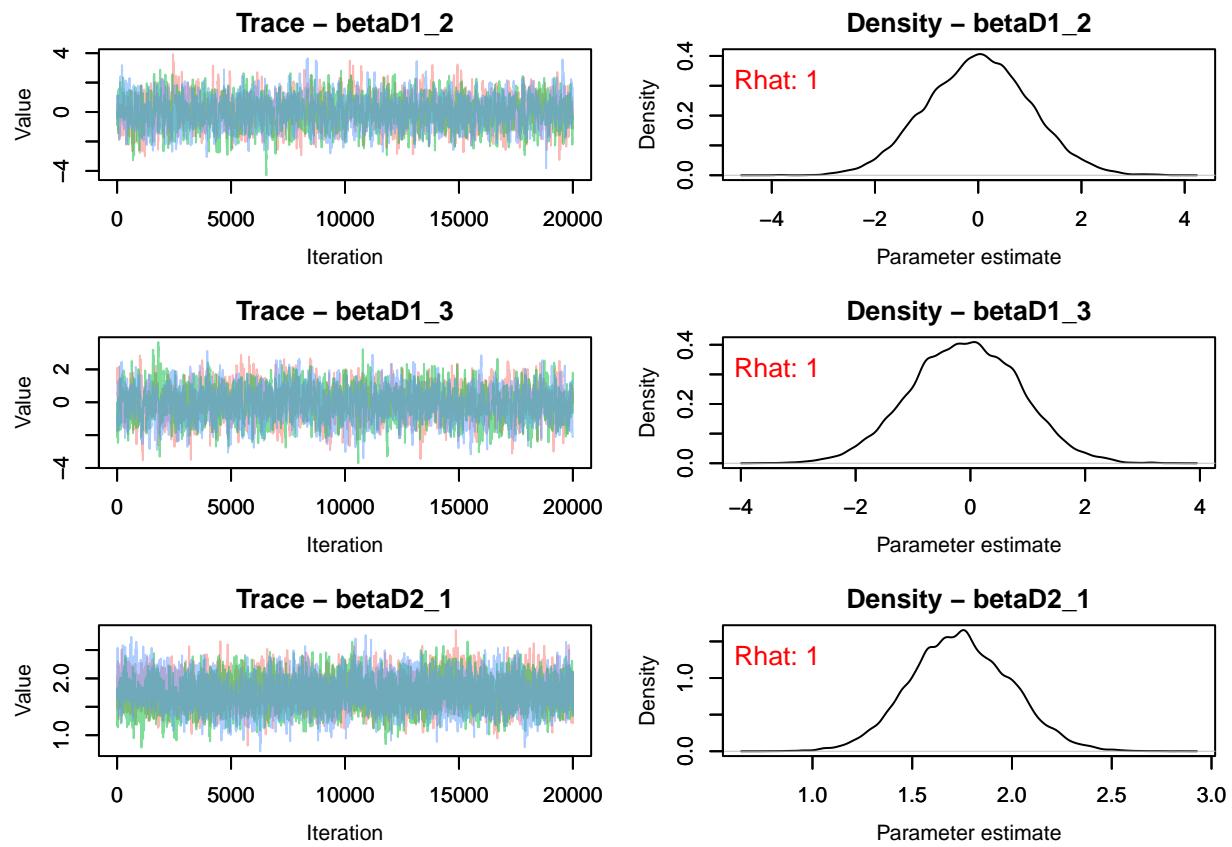


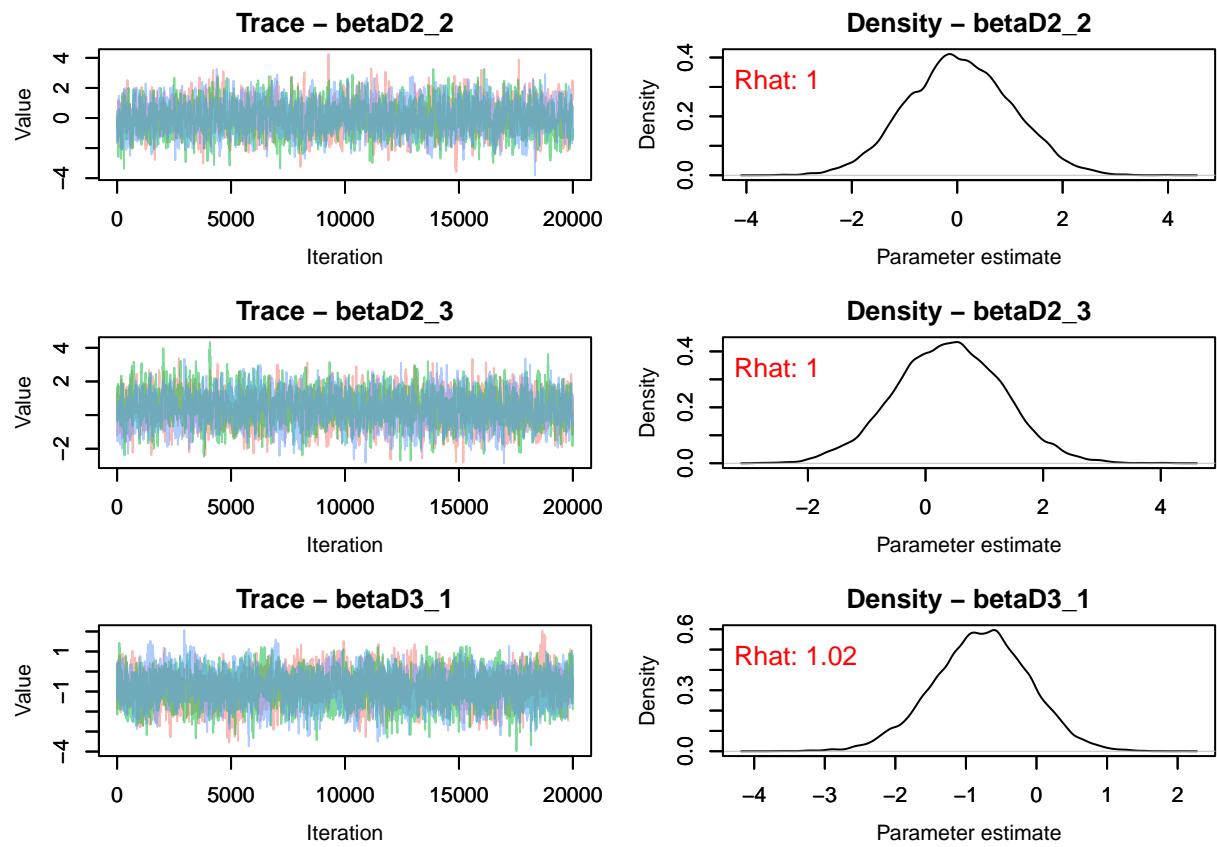


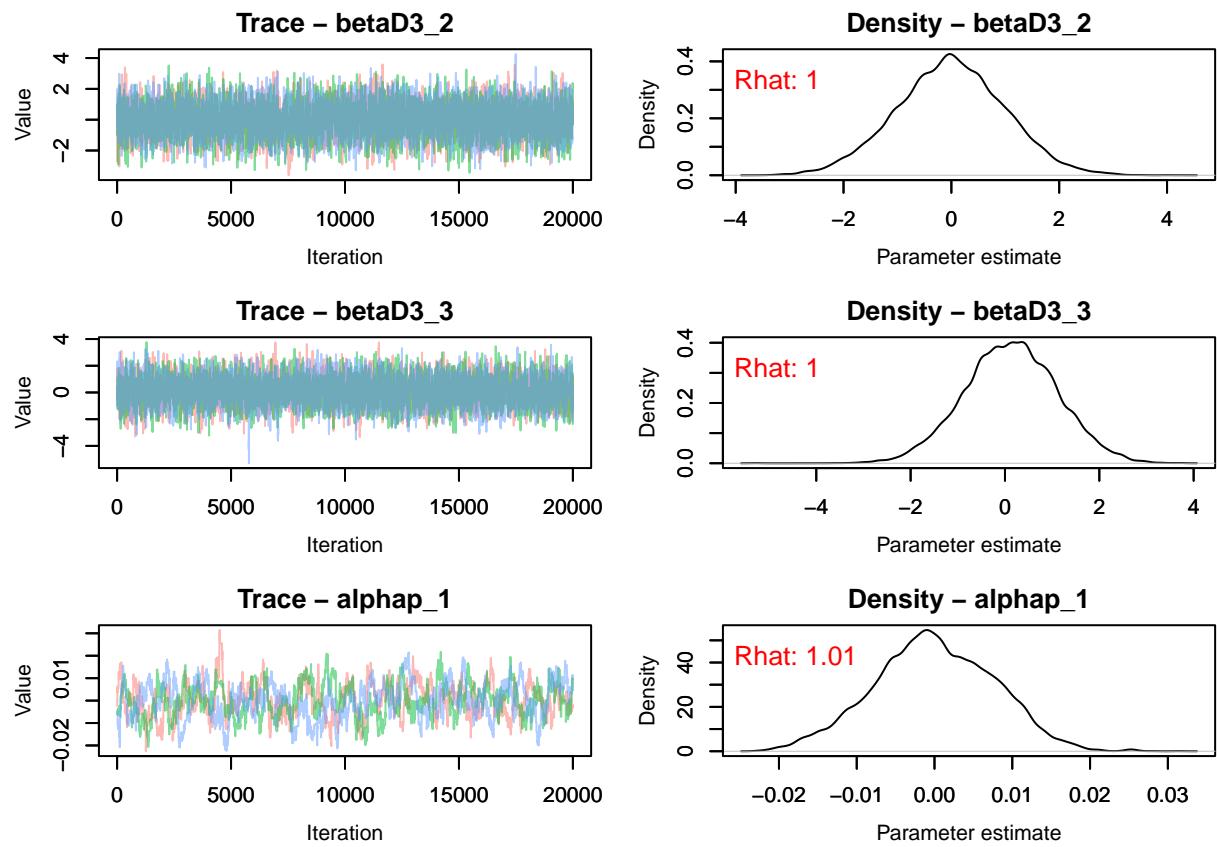


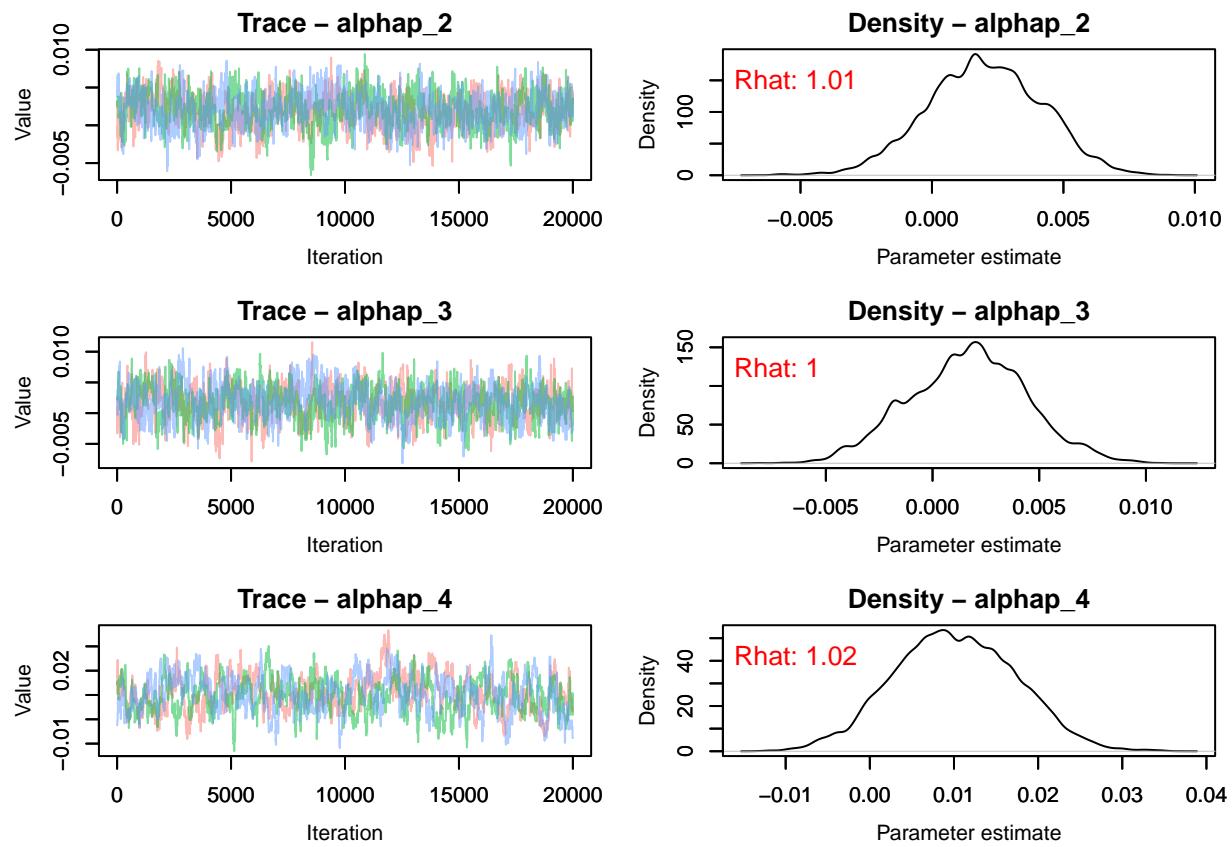


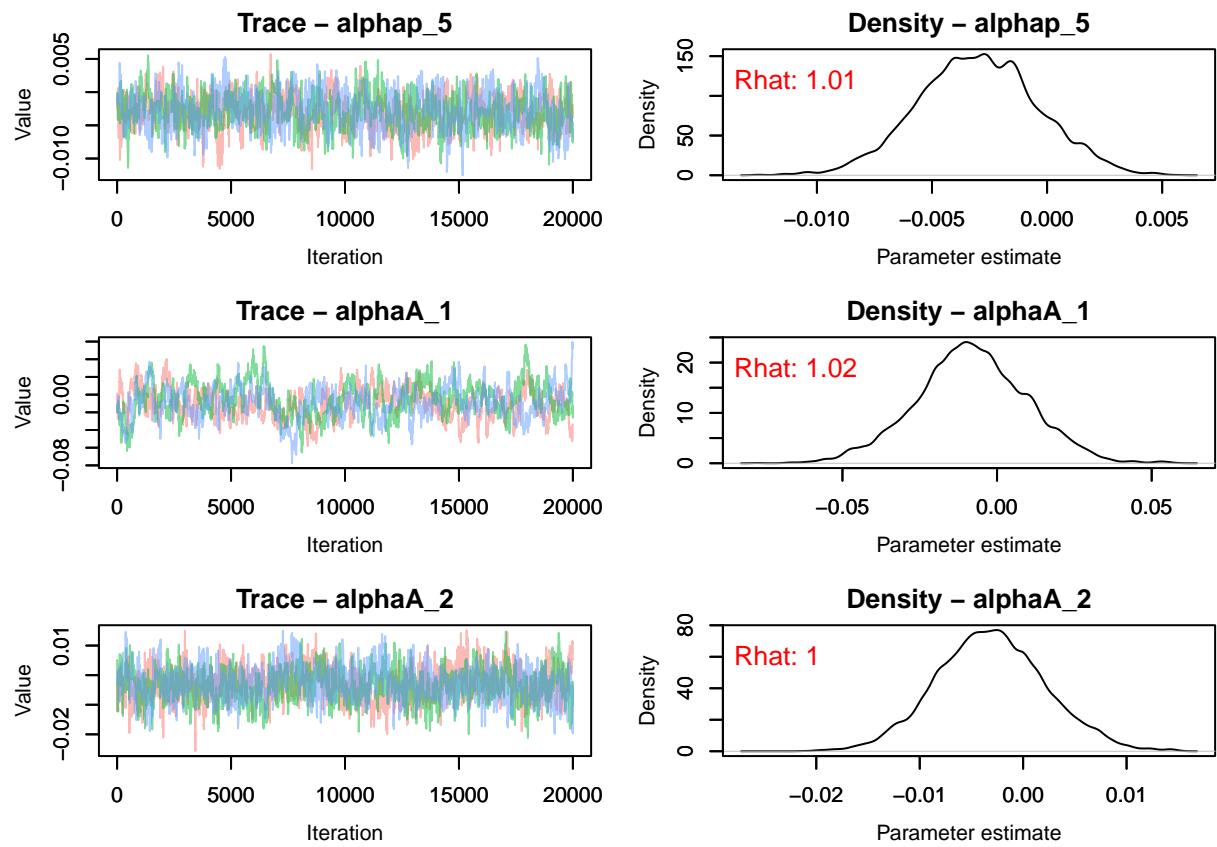


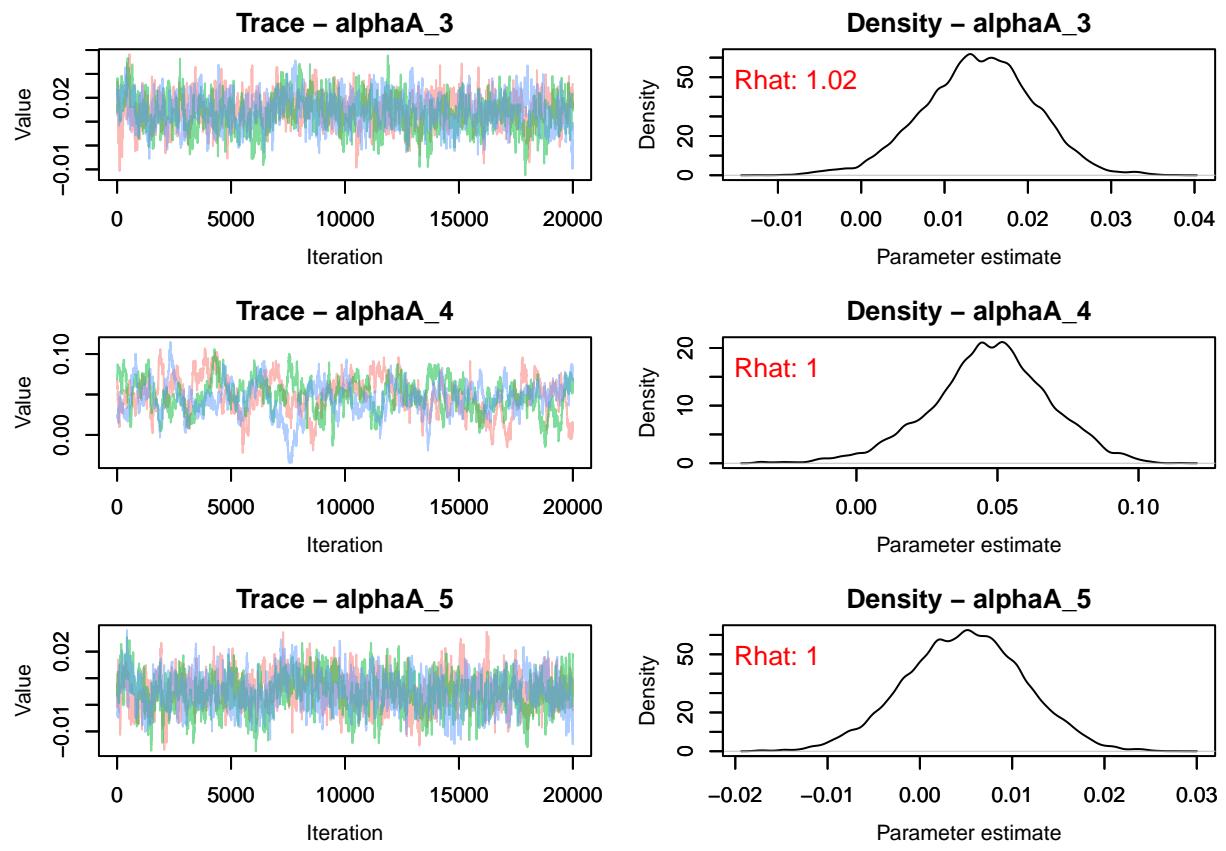


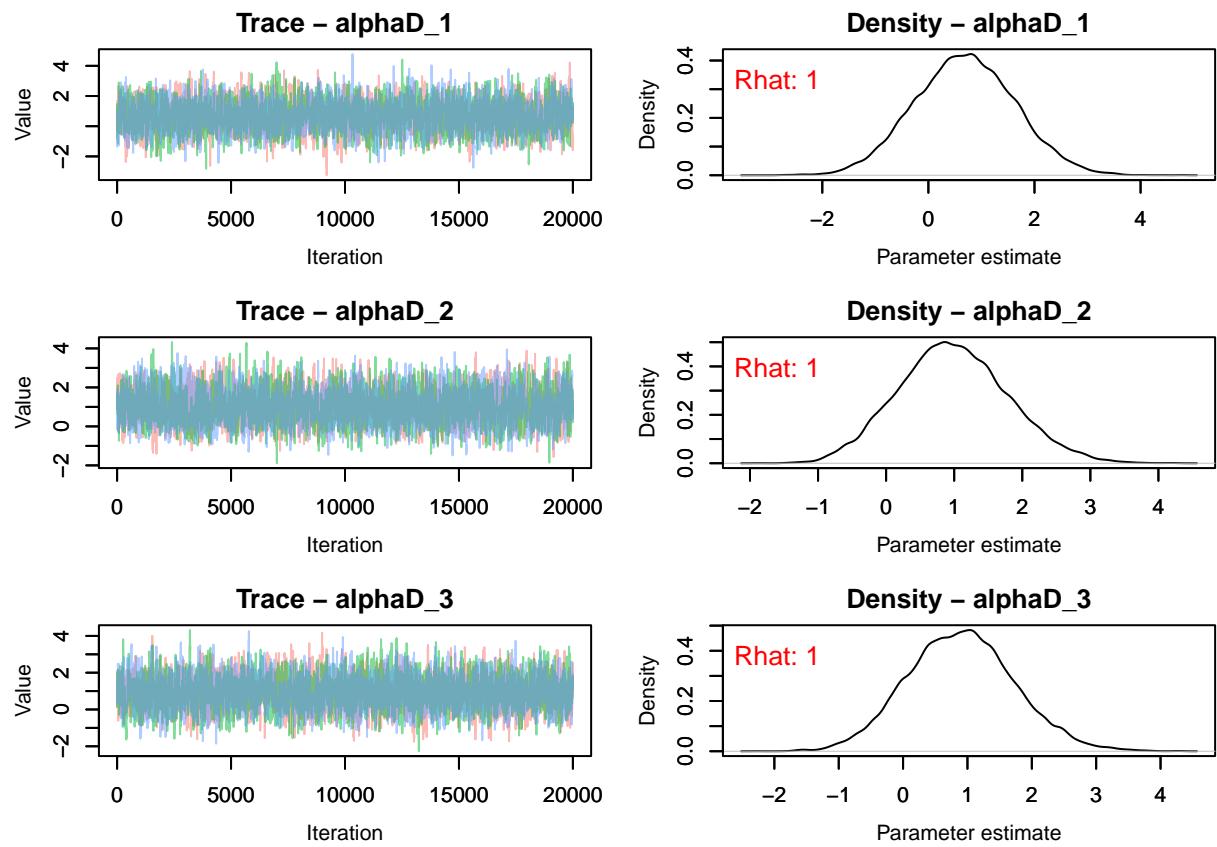


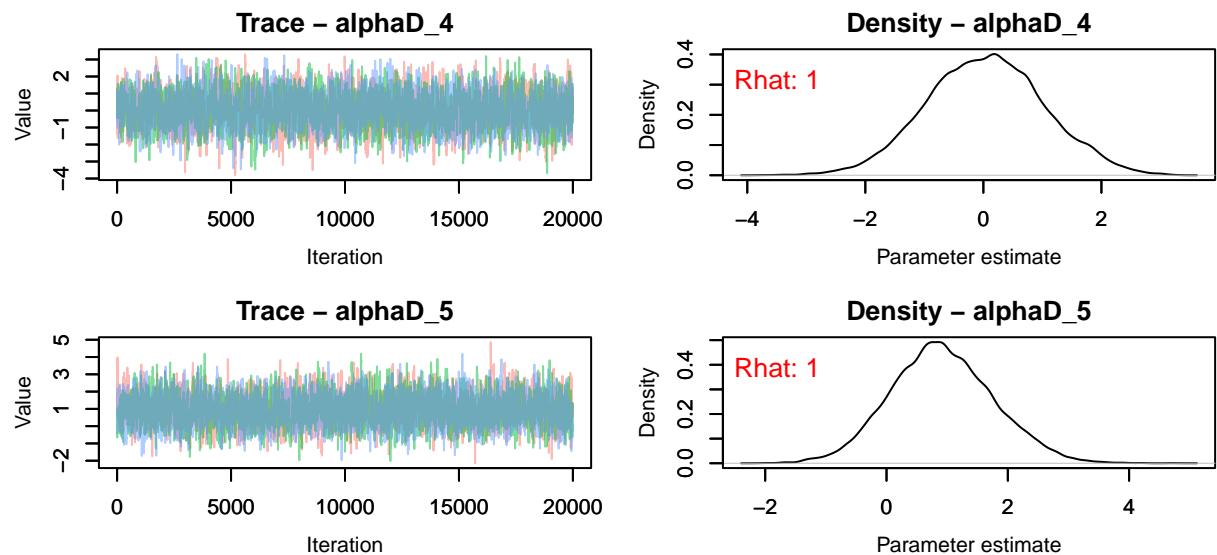












MCMC Diagnostics 2. We computed the Monte-Carlo Standard Error (MCSE), which is a measure of the precision of the posterior distribution obtained from a MCMC algorithm. The purpose of MCSE is to provide a measure of the accuracy of the estimate of the posterior distribution, which is the distribution of the parameters of interest after taking into account the data and prior information. MCSE is calculated by estimating the standard deviation of the MCMC samples of the posterior distribution, which provides a measure of the variability in the posterior estimates due to the Monte Carlo sampling process. This value is then divided by the square root of the effective sample size (ESS), which is the number of independent samples that the MCMC algorithm generates. For the parameters in the model, we obtained MCSE values between 0.00001 and 0.04177, with mean of 0.01210 and median of 0.00659.

Parameter	MCSE
betaP_1	0.0416
betaP_2	0.0126
betaP_3	0.0418
betaP_4	0.0127
betaP_5	0.0126
betaP_6	0.0023
betaP_7	0.0123
betaP_8	0.0005
betaP_9	0.0006
betaP_10	0.0041
sigma2p	0.0000
betaA_1	0.0074
betaA_2	0.0023
betaA_3	0.0126
betaA_4	0.0051
betaA_5	0.0133
betaA_6	0.0016
betaA_7	0.0020
betaA_8	0.0073
sigma2A	0.0000
betaD1_1	0.0059
betaD1_2	0.0366
betaD1_3	0.0330
betaD2_1	0.0055
betaD2_2	0.0346
betaD2_3	0.0303
betaD3_1	0.0167
betaD3_2	0.0213
betaD3_3	0.0216
alphap_1	0.0004
alphap_2	0.0001
alphap_3	0.0001
alphap_4	0.0004
alphap_5	0.0001
alphaA_1	0.0010
alphaA_2	0.0002
alphaA_3	0.0003
alphaA_4	0.0011

alphaA_5	0.0003
alphaD_1	0.0287
alphaD_2	0.0234
alphaD_3	0.0241
alphaD_4	0.0304
alphaD_5	0.0237
