

Estimation of hip dysplasia heritability using a Bayesian animal model in Rottweiler and Golden Retriever dogs registered in the Kennel Club of Perú (2014-2024)

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SUPPLEMENTARY MATERIAL

Complete MCMCglmm Model Specifications and Code With Results

This appendix provides the complete R code and model specifications used to estimate the variance components and heritability for canine hip dysplasia in Rottweiler and Golden Retriever dogs. All analyses were conducted in R (version 4.5.2) using the MCMCglmm package (Hadfield, 2010). Three independent MCMC chains were run for each model with different random seeds to ensure robust convergence assessment via the Gelman-Rubin diagnostic.

Prior specification:

```
prior_rott_bin <- list(  
  G = list(G1 = list(V = 1, nu = 5)),  
  R = list(V = 1, fix = 1)  
)
```

Model calls:

```
# Model 1: Null model
```

```
model_rott_bin_M1 <- MCMCglmm(fixed = displasia ~ 1, random = ~animal,  
  rcov = ~units, family = "categorical",  
  data = dat_rott, pedigree = ped_rott,  
  prior = prior_rott_bin, nitt = 1200000,  
  burnin = 200000, thin = 100, verbose = FALSE)
```

1. Rottweiler – Binary Trait (Affected vs. Unaffected)

For the binary trait, a threshold model with a probit link function was used (family = "categorical"). The residual variance on the liability scale was fixed at 1. The additive genetic variance was assigned a moderately informative inverse-Wishart prior ($V = 1$, $\nu = 5$). The MCMC chain was run for 1,200,000 iterations, with a burn-in of 200,000 and a thinning interval of 100.

```
# Model 2: Sex as fixed effect
model_rott_bin_M2 <- MCMCglmm(fixed = displasia ~ sex, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_rott, pedigree = ped_rott,
  prior = prior_rott_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE]
```

```
# Model 3: Age as fixed effect
model_rott_bin_M3 <- MCMCglmm(fixed = displasia ~ age, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_rott, pedigree = ped_rott,
  prior = prior_rott_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE]
```

```
# Model 4: Sex and age as fixed effects
model_rott_bin_M4 <- MCMCglmm(fixed = displasia ~ sex + age, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_rott, pedigree = ped_rott,
  prior = prior_rott_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE]
```

Model	Formula	DIC	Delta_DIC	Evidence	Selected	Mean_VA	SD_VA	Mean_h2	SD_h2	HPD_lower_h2	HPD_upper_h2	Rhat	Rhat_upper	AC_lag10	ESS
Model1	null	160.162	2.5753	Weak	No	1.8123	1.6471	0.5743	0.1486	0.2954	0.8525	1.0001	1.0003	0.198	773.052
Model2	sex	160.156	2.569	Weak	No	2.0999	3.1241	0.5854	0.1536	0.305	0.8822	1.0148	1.0152	0.4854	426.328
Model3	age	157.587	0	Weak	Yes (best DIC, but equivalence)	2.0892	2.0537	0.5978	0.1529	0.3162	0.8837	1.0068	1.0126	0.3236	615.799
Model4	sex+age	157.599	0.0123	Weak	Yes (parsimony)	2.6737	8.3067	0.6016	0.161	0.3129	0.9143	1.2743	1.5121	0.4195	375.771

2. Rottweiler – Ordinal Trait (FCI Grades A–D)

For the ordinal trait, a threshold model was fitted (family = "ordinal"). The additive genetic variance was assigned a moderately informative prior ($V = 1$, $\nu = 10$). To ensure model identifiability and adequate mixing for the ordinal structure, the residual variance prior was specified with $V = 1$ and $\nu = 1$. Due to the complexity of the ordinal model, longer chains were required: 3,000,000 iterations, a burn-in of 500,000, and a thinning interval of 1,000.

Prior specification:

```
prior_rott_ord <- list(  
  G = list(G1 = list(V = 1, nu = 10)),  
  R = list(V = 1, nu = 1)  
)
```

Model calls:

Model 1: Null model

```
model_rott_ord_M1 <- MCMCglmm(fixed = grade ~ 1, random = ~animal,  
  family = "ordinal", data = dat_rott,  
  pedigree = ped_rott, prior = prior_rott_ord,  
  nitt = 3000000, burnin = 500000, thin = 1000,  
  verbose = FALSE)
```

Model 2: Sex as fixed effect

```
model_rott_ord_M2 <- MCMCglmm(fixed = grade ~ sex, random = ~animal,  
  family = "ordinal", data = dat_rott,  
  pedigree = ped_rott, prior = prior_rott_ord,  
  nitt = 3000000, burnin = 500000, thin = 1000,  
  verbose = FALSE)
```

Model 3: Age as fixed effect

```
model_rott_ord_M3 <- MCMCglmm(fixed = grade ~ age, random = ~animal,  
  family = "ordinal", data = dat_rott,  
  pedigree = ped_rott, prior = prior_rott_ord,  
  nitt = 3000000, burnin = 500000, thin = 1000,  
  verbose = FALSE)
```

Model 4: Sex and age as fixed effects

```
model_rott_ord_M4 <- MCMCglmm(fixed = grade ~ sex + age, random = ~animal,
  family = "ordinal", data = dat_rott,
  pedigree = ped_rott, prior = prior_rott_ord,
  nitt = 3000000, burnin = 500000, thin = 1000,
  verbose = FALSE)
```

Model	Formul a	DIC	Delta_ DIC	Eviden ce	Selecte d	Mean_ VA	SD_VA	HPD_V A_Lowe r	HPD_V A_Uppe r	Mean_ h2	SD_h2	HPD_lo wer_h2	HPD_u pper_h 2	Rhat	Rhat_u pper	AC_lag 10	ESS
Model1	null	197.71	45.921	Strong	No	1.673	1.0577	0.4066	3.6418	0.5856	0.1162	0.3634	0.8059	1.0028	1.0038	-0.006	2349.1
Model2	sex	197.93	46.137	Strong	No	1.7255	1.1975	0.4333	3.8149	0.588	0.1206	0.3699	0.8326	1.0024	1.0042	-0.014	1932.5
Model3	age	193.48	41.692	Strong	No	1.8158	1.2775	0.3797	4.1256	0.5983	0.1204	0.3691	0.8332	1.0033	1.005	-0.009	1834.6
Model4	sex + age	151.79	0	Weak	Yes	1.9093	1.6043	0.428	4.348	0.6044	0.1223	0.376	0.8469	1.0059	1.0138	0.0319	1250.7

3. Golden Retriever – Binary Trait (Affected vs. Unaffected)

The specifications for the Golden Retriever binary trait were identical to those of the Rottweiler binary trait, utilising the same prior structure (v = 5 for G, fixed R) and MCMC parameters (1,200,000 iterations, 200,000 burn-in, thinning = 100).

Prior specification:

```
prior_gold_bin <- list(
  G = list(G1 = list(V = 1, nu = 5)),
  R = list(V = 1, fix = 1)
)
```

Model calls:

Model 1: Null model

```
model_gold_bin_M1 <- MCMCglmm(fixed = displasia ~ 1, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_gold, pedigree = ped_gold,
  prior = prior_gold_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE)
```

Model 2: Sex as fixed effect

```
model_gold_bin_M2 <- MCMCglmm(fixed = displasia ~ sex, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_gold, pedigree = ped_gold,
  prior = prior_gold_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE)
```

Model 3: Age as fixed effect

```
model_gold_bin_M3 <- MCMCglmm(fixed = displasia ~ age, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_gold, pedigree = ped_gold,
  prior = prior_gold_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE]
```

Model 4: Sex and age as fixed effects

```
model_gold_bin_M4 <- MCMCglmm(fixed = displasia ~ sex + age, random = ~animal,
  rcov = ~units, family = "categorical",
  data = dat_gold, pedigree = ped_gold,
  prior = prior_gold_bin, nitt = 1200000,
  burnin = 200000, thin = 100, verbose = FALSE]
```

Model	Formula	DIC	Delta_DIC	Evidence	Selected	Mean_VA	SD_VA	Mean_h2	SD_h2	HPD_low er_h2	HPD_upper_h2	Rhat	Rhat_upper	AC_lag10	ESS
Model1	null	299.979	3.3427	Moderate	No	2.1555	1.9339	0.6148	0.1429	0.3412	0.8796	1.0383	1.0485	0.1512	950.807
Model2	sex	299.12	2.483	Weak	No	2.3535	2.3589	0.6268	0.1454	0.3488	0.8902	1.0424	1.0455	0.2495	688.172
Model3	age	298.035	1.3981	Weak	Yes (parsimony)	2.5413	2.3706	0.6449	0.1435	0.3683	0.9053	1.0176	1.0178	0.301	589.436
Model4	sex+age	296.637	0	Weak	Yes (best DIC, but equivalen	3.3574	4.8429	0.6773	0.1456	0.3914	0.9405	1.0392	1.0527	0.534	320.363

4. Golden Retriever – Ordinal Trait (FCI Grades A–D, with D and E combined)

The specifications for the Golden Retriever ordinal trait mirrored those of the Rottweiler ordinal trait, utilising the same prior structure ($v = 10$ for G, $v = 1$ for R) and extended MCMC parameters (3,000,000 iterations, 500,000 burn-in, thinning = 1,000) to ensure adequate mixing.

Prior specification:

```
prior_gold_ord <- list(
  G = list(G1 = list(V = 1, nu = 10)),
  R = list(V = 1, nu = 1)
)
```

Model calls:

Model 1: Null model

```
model_gold_ord_M1 <- MCMCglmm(fixed = grade ~ 1, random = ~animal,
  family = "ordinal", data = dat_gold,
  pedigree = ped_gold, prior = prior_gold_ord,
  nitt = 3000000, burnin = 500000, thin = 1000,
  verbose = FALSE]
```

Model 2: Sex as fixed effect

```
model_gold_ord_M2 <- MCMCglmm(fixed = grade ~ sex, random = ~animal,
  family = "ordinal", data = dat_gold,
  pedigree = ped_gold, prior = prior_gold_ord,
  nitt = 3000000, burnin = 500000, thin = 1000,
  verbose = FALSE)
```

Model 3: Age as fixed effect

```
model_gold_ord_M3 <- MCMCglmm(fixed = grade ~ age, random = ~animal,
  family = "ordinal", data = dat_gold,
  pedigree = ped_gold, prior = prior_gold_ord,
  nitt = 3000000, burnin = 500000, thin = 1000,
  verbose = FALSE)
```

Model 4: Sex and age as fixed effects

```
model_gold_ord_M4 <- MCMCglmm(fixed = grade ~ sex + age, random = ~animal,
  family = "ordinal", data = dat_gold,
  pedigree = ped_gold, prior = prior_gold_ord,
  nitt = 3000000, burnin = 500000, thin = 1000,
  verbose = FALSE)
```

Model	Formula	DIC	Delta_DIC	Evidence	Selected	Mean_VA	SD_VA	Mean_h2	SD_h2	HPD_lower_h2	HPD_upper_h2	Rhat	Rhat_upper	AC_lag10	ESS
Model1	null	416.5119	12.3536	Strong	No	1.3103	0.7192	0.5379	0.1059	0.3468	0.7519	1.007	1.0092	-0.0199	2252.6646
Model2	sex	414.9859	10.8276	Strong	No	1.3708	0.7949	0.5455	0.1096	0.3363	0.754	1.0087	1.0126	0.014	1963.3644
Model3	age	404.1583	0	Weak	tDIC, buteq	1.5609	1.3621	0.572	0.1107	0.3597	0.7827	1.0023	1.004	-0.0166	2220.9494
Model4	sex+age	404.4227	0.2645	Weak	rsimonypre	1.6515	1.0479	0.5843	0.1132	0.3665	0.8022	1.0045	1.0056	-0.0204	1619.1962

5. Heritability Calculation and Convergence Diagnostics

For all models, heritability on the liability scale was calculated for each individual MCMC iteration as:

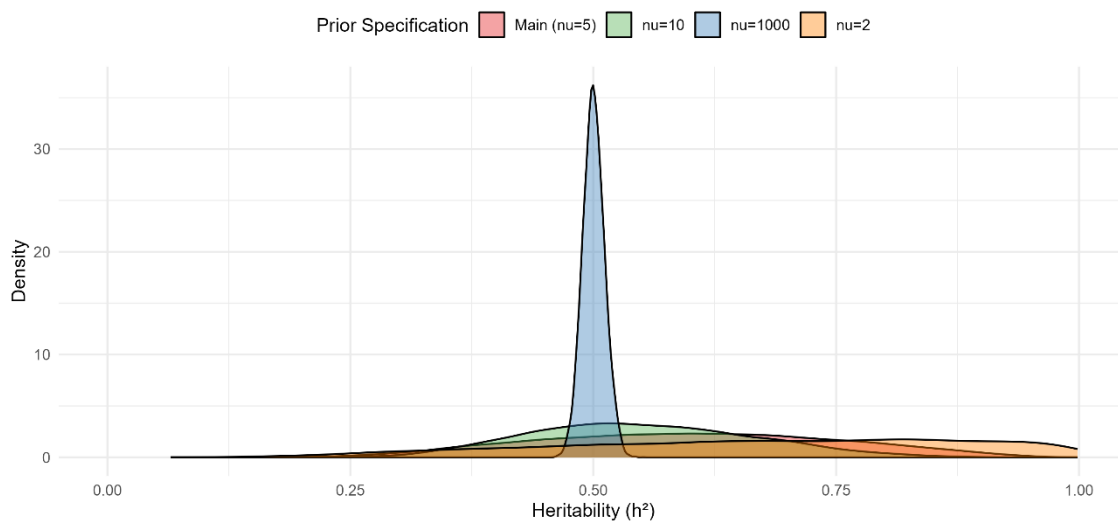
```
h2_iteration <- VA_iteration / (VA_iteration + 1)
```

Posterior means, standard deviations, and 95% highest posterior density (HPD) credible intervals were derived from the resulting distribution of h^2 values across all retained posterior samples.

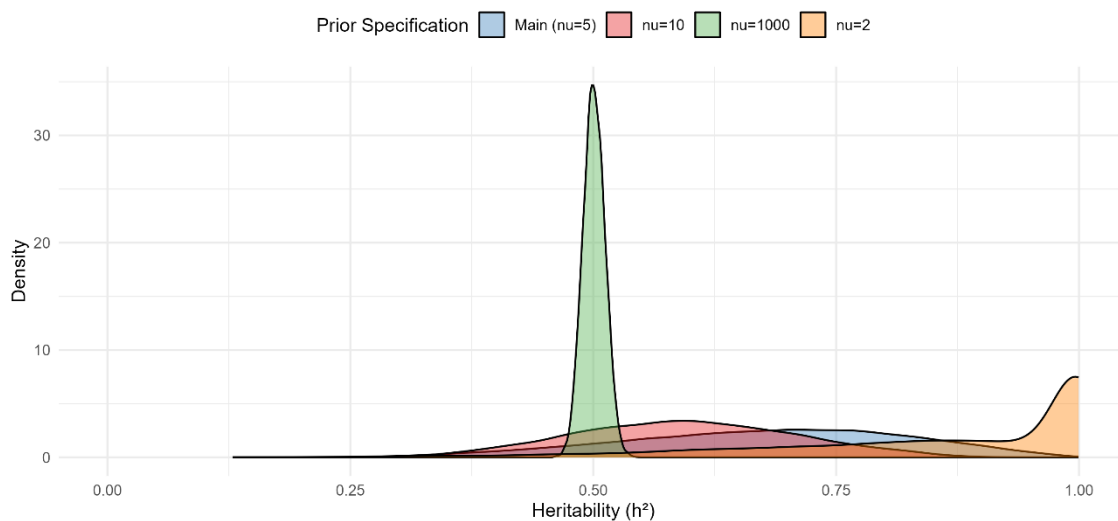
Convergence was assessed using visual inspection of trace plots from the three independent chains, autocorrelation analysis at lag 10, and the effective sample size (ESS). The potential scale reduction factor (Gelman-Rubin diagnostic, $\hat{R}$) was calculated for all variance components, with values < 1.05 indicating adequate convergence between chains.

Prior Sensitivity Analysis

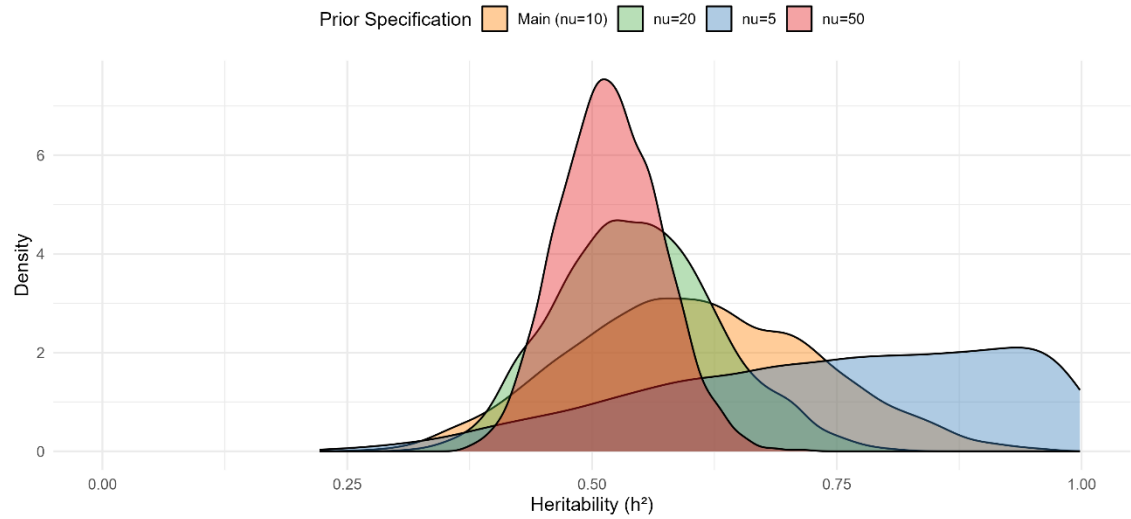
Rottweiler Binary - Prior Sensitivity Analysis



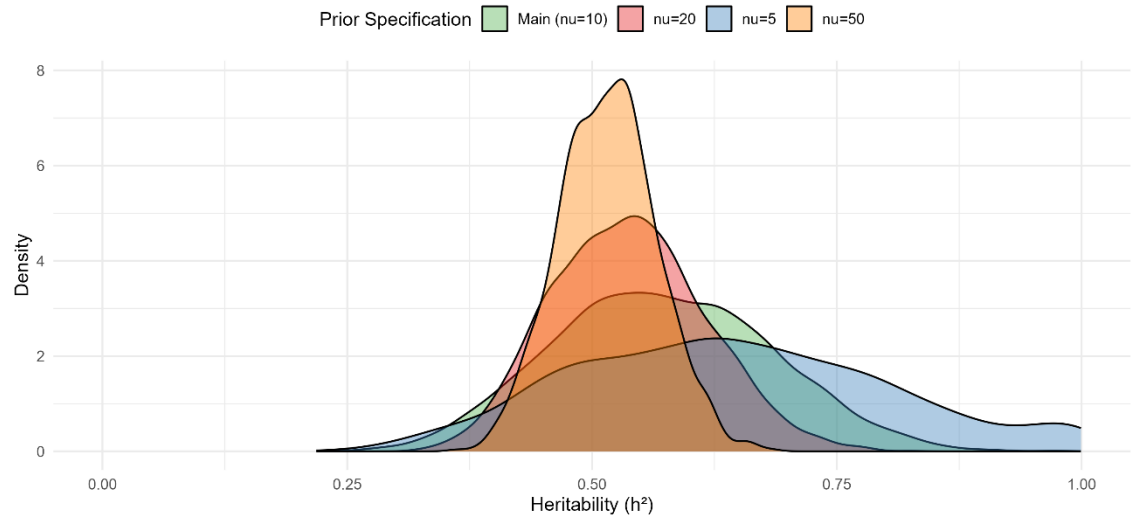
Golden Retriever Binary - Prior Sensitivity Analysis



Rottweiler Ordinal - Prior Sensitivity Analysis

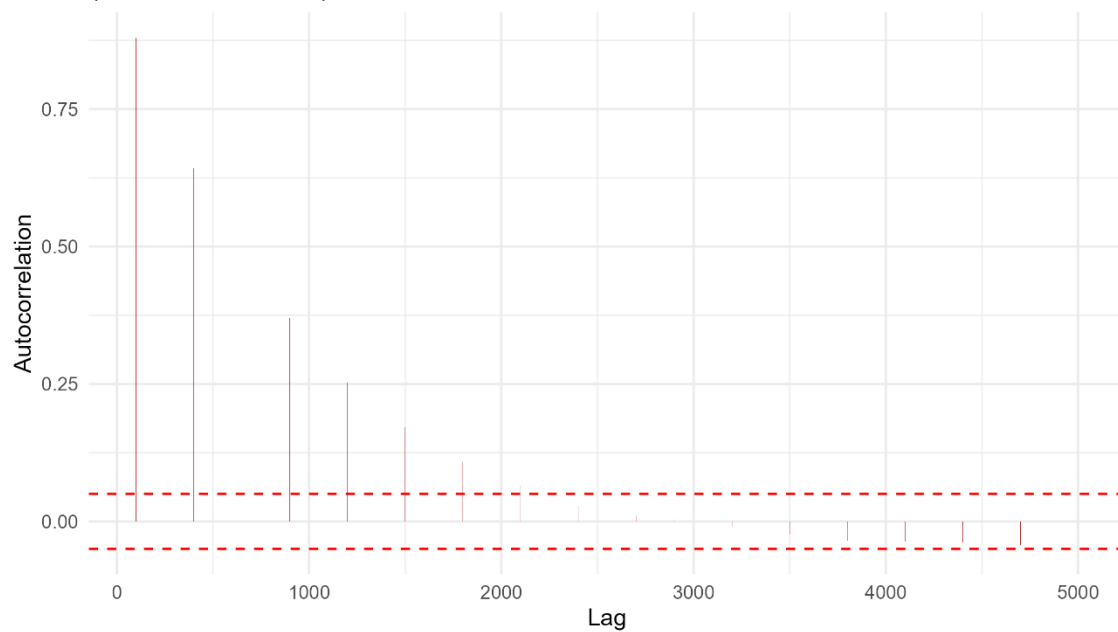


Golden Retriever Ordinal - Prior Sensitivity Analysis

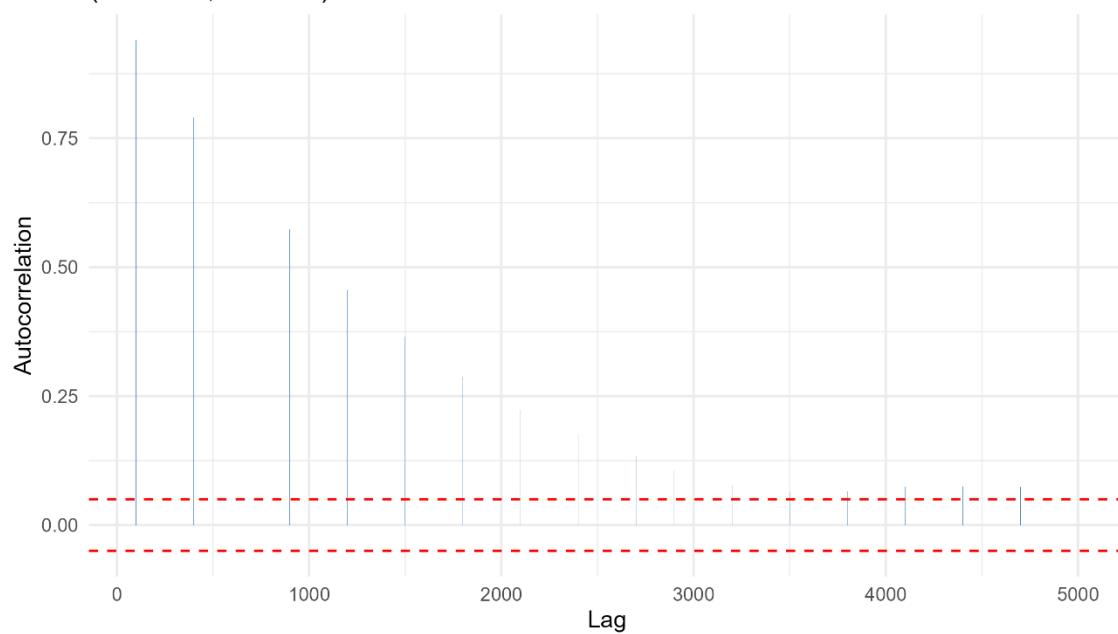


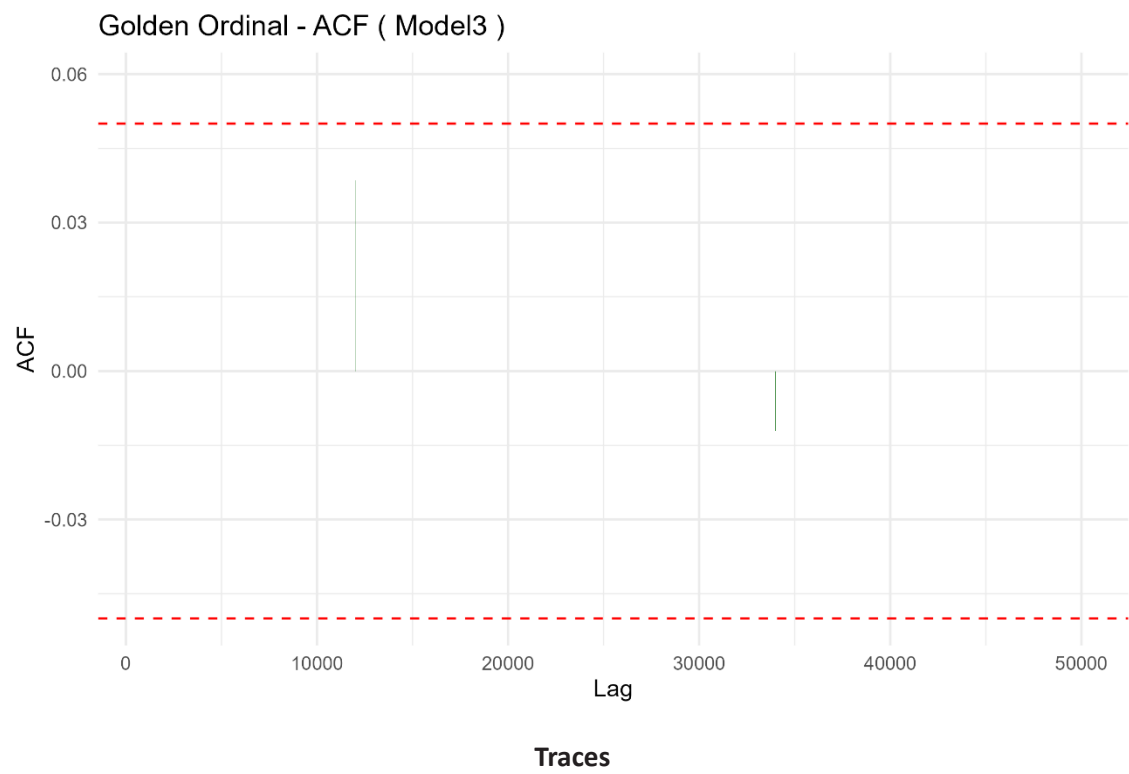
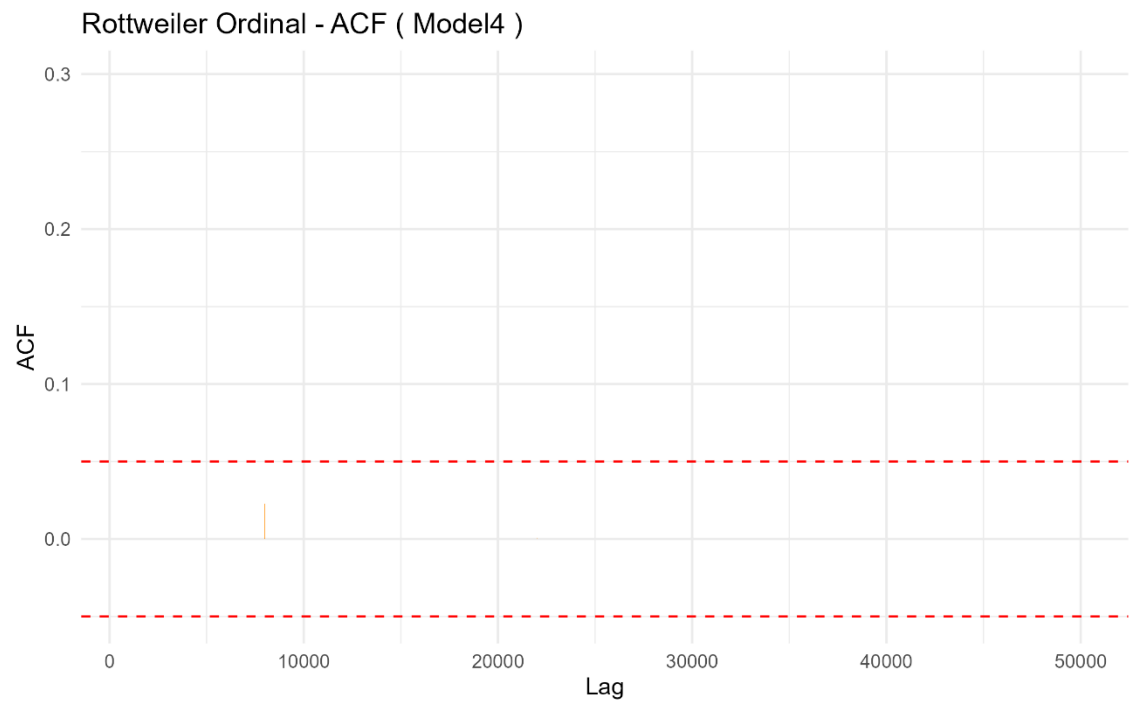
Autocorrelation Analysis (Best DIC)

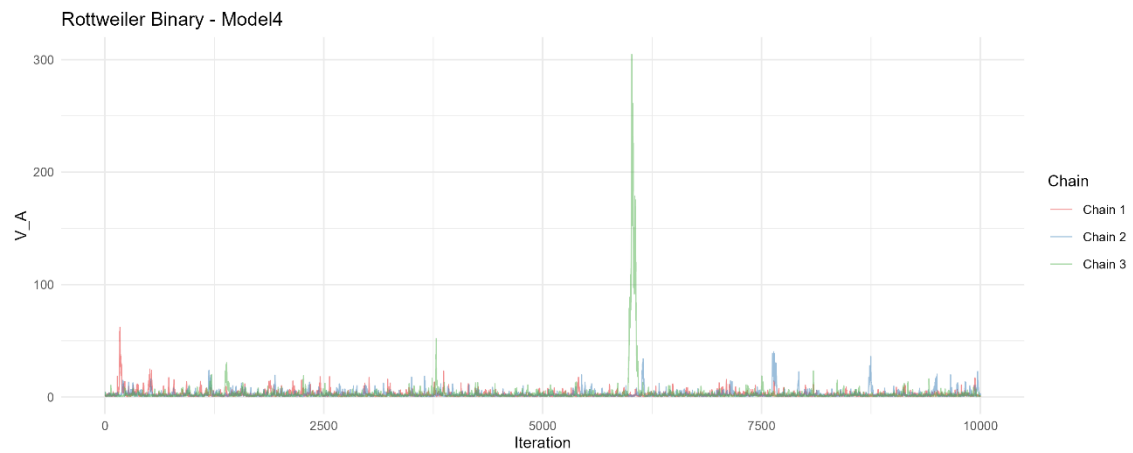
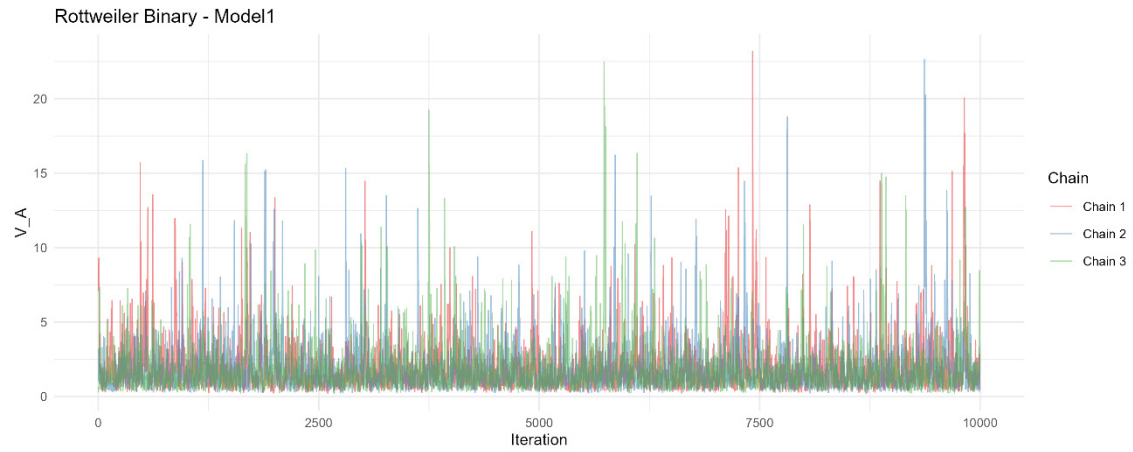
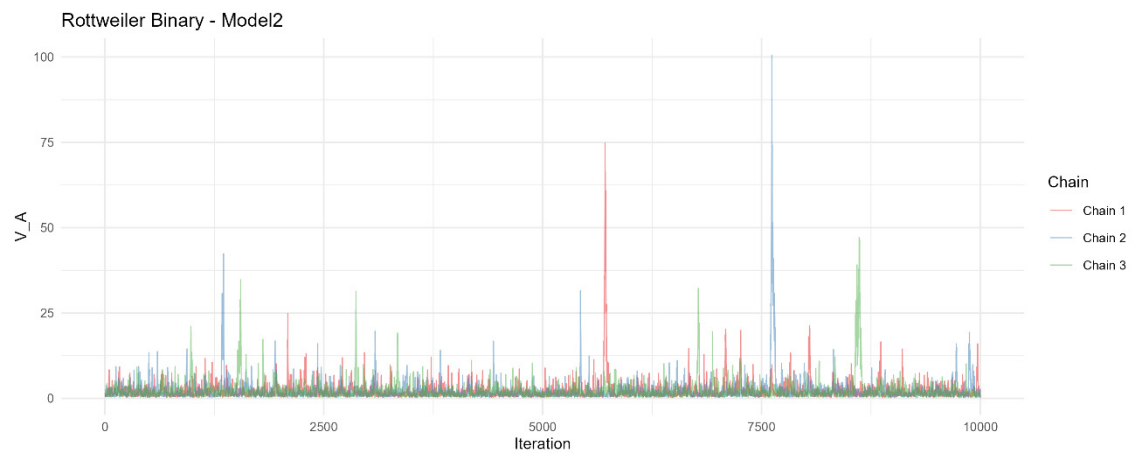
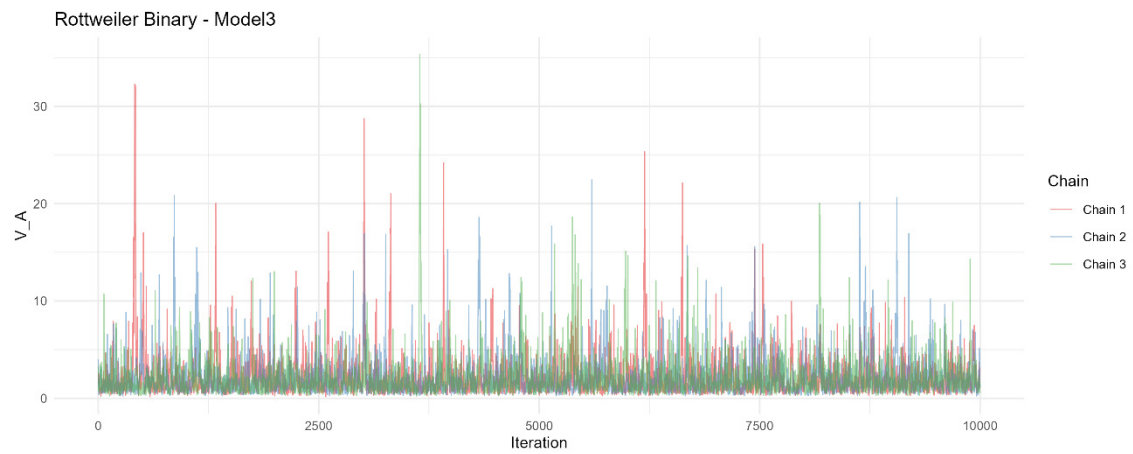
Rottweiler Binary - Autocorrelation
(Model3 , Chain 1)

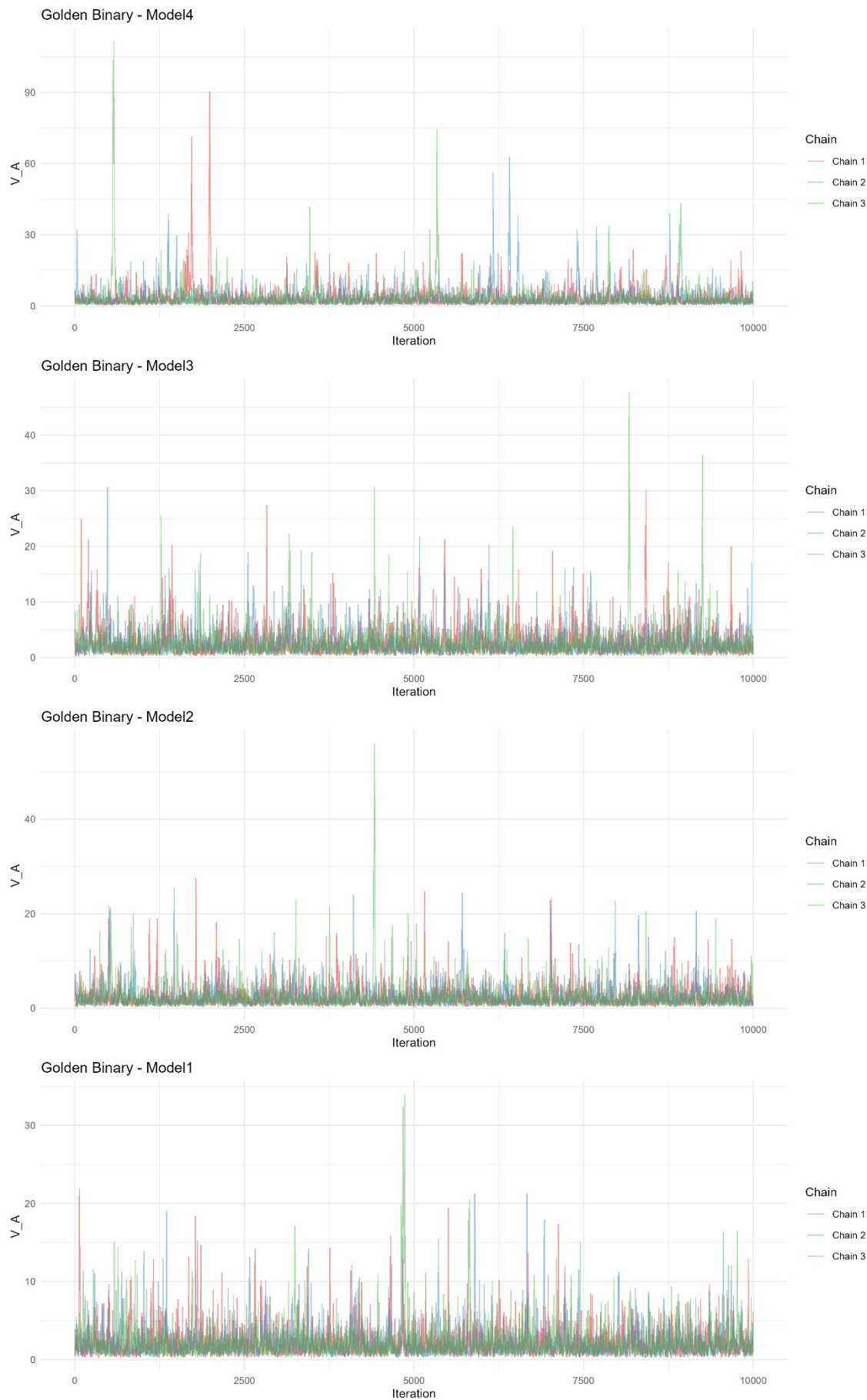


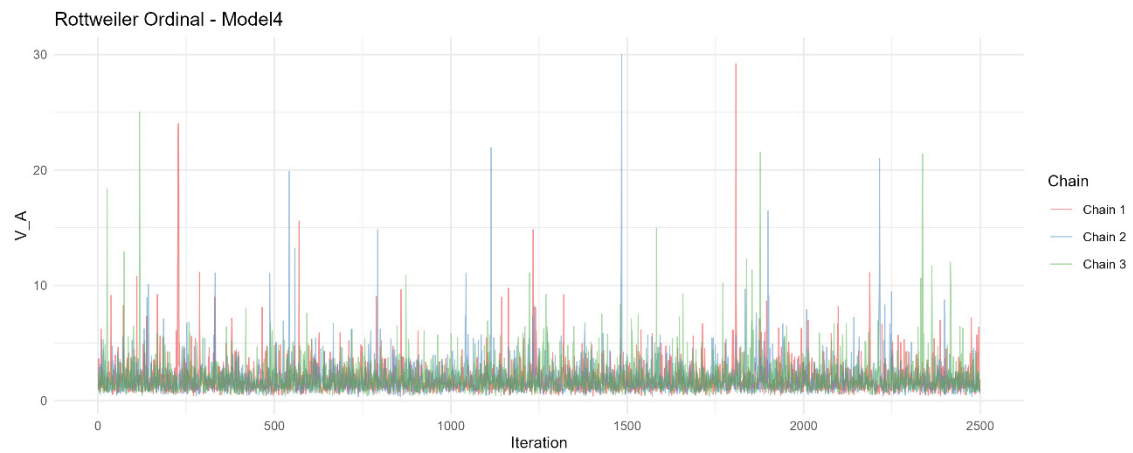
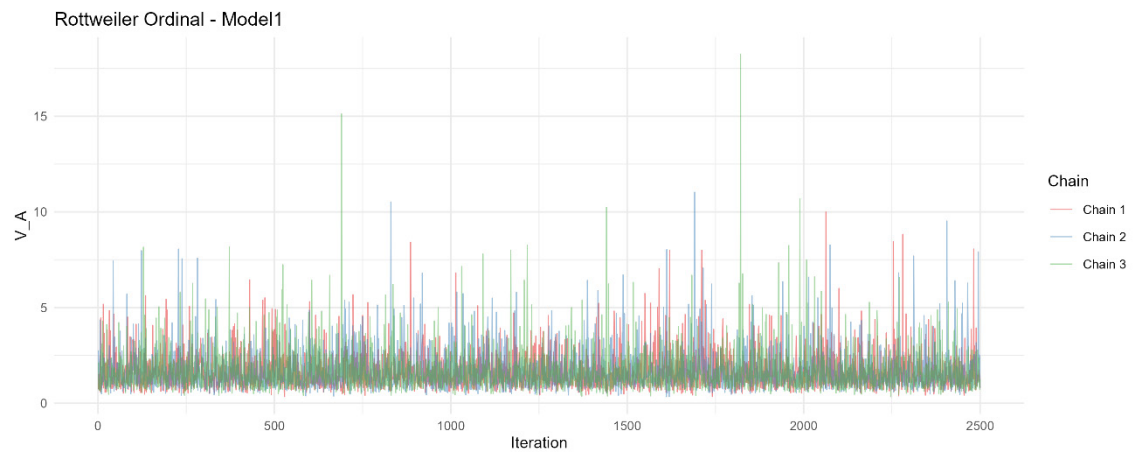
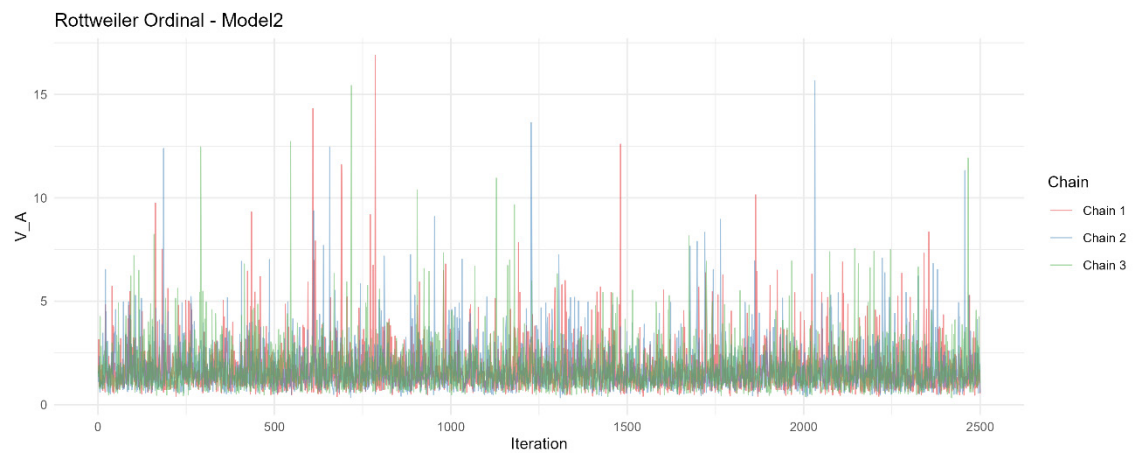
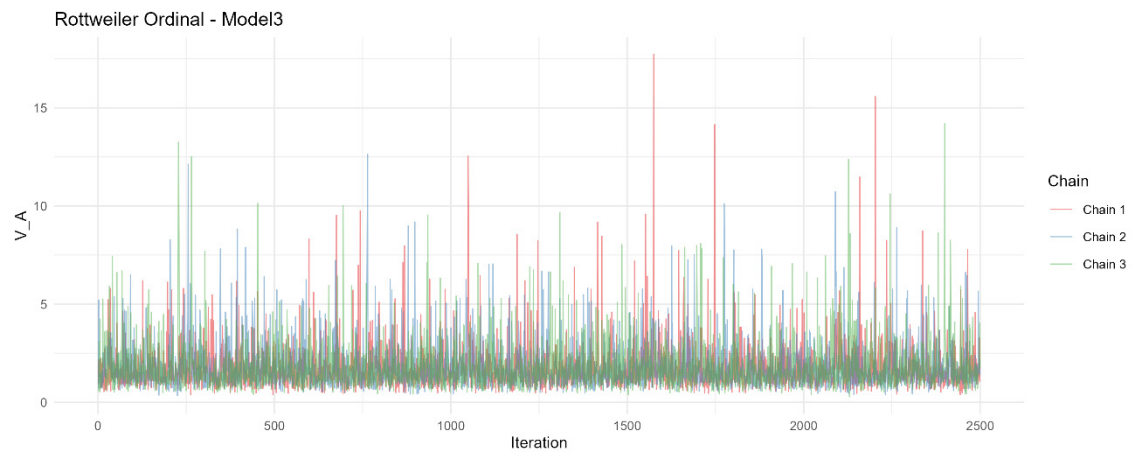
Golden Retriever Binary - ACF
(Model4 , Chain 1)













Golden Retriever Ordinal - Model4 - Trace Plot V_A (3 chains)

