

Blouch Revision Milestones – 2023

Mark Grabowski

Reprogramming Blouch for computation speed – split off programs into their component parts. Validation results for each model shown in Model Validation Results – 2023.doc

Milestone 1: Direct effect model from Hansen (1997) for V/CV matrix

- Figures and Tables S1-S10
- Tested for increasing half-life - blouchOU_direct.stan
- Tested for multiple predictors – blouchOU_direct.stan
- Includes measurement error – blouchOU_direct_ME.stan

Milestone 2: Adaptation model

- Figures and Tables S4-14
- Tested for increasing half-life – blouchOU_adaptive.stan
- Tested for multiple predictors – blouchOU_adaptive.stan
- Includes measurement error – blouchOU_adaptive_ME.stan

Milestone 3: Combination of direct effect and adaptation model

- Figures and Tables S15-S20
- Tested for increasing half-life
- Tested for multiple predictors of both types- blouchOU_direct_adaptive.stan
- Includes measurement error - blouchOU_direct_adaptive_ME.stan

Milestone 4: Regime model

- Figures and Tables S21-S26
- Tested for increasing half-life
- Tested for an increasing number of regimes - blouchOU_reg.stan

Milestone 5: Regime model with direct effect predictors

- Figures and Tables S27-S32
- Tested for increasing half-life – blouchOU_reg_direct.stan
- Includes measurement error – blouchOU_reg_direct_ME.stan

Milestone 6: Regime model with adaptive predictors

- Figures and Tables S36-S38
- Tested for increasing half-life – blouchOU_reg_adaptive.stan
- Includes measurement error – blouchOU_reg_adaptive_ME.stan

Milestone 7: Regime and combination of direct effect and adaptation model

- Figures and Tables S39-S44
- Tested for increasing half-life - blouchOU_reg_direct_adaptive.stan
- Includes measurement error – blouchOU_reg_direct_adaptive_ME.stan

Milestone 8: Multilevel regime model – centered version

- Figures and Tables S45-S47
- Tested for increasing half-life - blouchOU_reg_mli.stan

Milestone 9: Multilevel Regime Model with Direct Effect Predictors with Measurement Error

- Figures and Tables S48-S50

- Tested for increasing half-life - blouchOU_reg_mli_direct_ME.stan
- Includes measurement error – blouchOU_reg_mli_direct_ME.stan

Milestone 10: Multilevel Regime Model with Adaptive Predictors with Measurement Error

- S51-S53
- Tested for increasing half-life – blouchOU_reg_mli_adaptive_ME.stan
- Includes measurement error – blouchOU_reg_mli_adaptive_ME.stan

Milestone 11: Multilevel Regime with Direct Effect and Adaptive Model with Measurement Error

- S54-S56
- Tested for increasing half-life
- Includes measurement error
- Tested for multiple traits

Milestone 12: Regime model with direct effect predictors with measurement error and varying slopes

- S57-S59
- Tested for increasing half-life - blouchOU_reg_direct_ME_VarSlopes.stan
- Includes measurement error - blouchOU_reg_direct_ME_VarSlopes.stan
- Tested for multiple traits - blouchOU_reg_multidirect_ME_VarSlopes.stan

Milestone 13: Regime model with Direct Effect Varying Effects and Measurement Error

- S60-S62
- Tested for increasing half-life - blouchOU_reg_direct_ME_VarEff.stan
- Includes measurement error - blouchOU_reg_direct_ME_VarEff.stan
- Tested for multiple traits - blouchOU_reg_multidirect_ME_VarSlopes.stan

Milestone 14: Regime model with Direct Effect Varying Effects and Measurement Error – non-centered

- S63-S65
- Tested for increasing half-life - blouchOU_reg_direct_ME_VarEff_nc.stan
- Includes measurement error - blouchOU_reg_direct_ME_VarEff_nc.stan
- Tested for multiple traits - blouchOU_reg_multidirect_ME_VarSlopes_nc.stan
- Very slow model

Milestone 15: Regime model with Adaptive Varying Slopes and Measurement Error

- S66-S68
- Tested for increasing half-life - blouchOU_reg_multiadaptive_ME_VarSlopes.stan
- Includes measurement error - blouchOU_reg_multiadaptive_ME_VarSlopes.stan
- Tested for multiple traits - blouchOU_reg_multiadaptive_ME_VarSlopes.stan

Milestone 16: Regime model with Adaptive Varying Effects and Measurement Error

- S69-S71
- Tested for increasing half-life - blouchOU_reg_multiadaptive_ME_VarEff.stan
- Includes measurement error - blouchOU_reg_multiadaptive_ME_VarEff.stan
- Tested for multiple traits - blouchOU_reg_multiadaptive_ME_VarEff.stan

Milestone 17: Regime model with Adaptive Varying Effects and Measurement Error – non-centered

- S72-S74
- Tested for increasing half-life - blouchOU_reg_multiadaptive_ME_VarEff.stan
- Includes measurement error - blouchOU_reg_multiadaptive_ME_VarEff.stan
- Tested for multiple traits - blouchOU_reg_multiadaptive_ME_VarEff.stan

Milestone 18: Regime model with direct and adaptive predictors with varying effects and measurement error

- S75-S77
- Tested for increasing half-life
- Includes measurement error
- Tested for multiple traits

Milestone 19: Regime model with direct and adaptive predictors with varying effects and measurement error – non-centered

- S78-S80
- Tested for increasing half-life
- Includes measurement error
- Tested for multiple traits

Blouch Revision Validation Results – 2023

Mark Grabowski

I evaluated the model's performance on data I simulated using scripts available in the Simulation Code folder on github.com. All plots were made using the Prior and Posterior Plots – Simulations.Rmd script in the Validation folder.

All data was simulated on a randomly sampled set of 50 tip species from the 10K trees primate phylogeny. This data was then analyzed using the requisite *Blouch* model, and parameter values were compared to the true parameter values. I used the set.seed() function for reproducibility and set this value to 10.

For each model I tested data simulated with the following features:

- a) Short, medium, and long half-lives
- b) Presence of measurement error. For the more advanced models the results without measurement error were not reported, though run, as validation had already been achieved in the simpler models.
- c) Increasing number of predictors including measurement error

For each model that accounts for measurement error, measurement error was added to the X and Y variables by simulating from a random normal distribution with mean=0 and standard deviation 0.01.

For the models that test hypotheses of regime placement, in addition to varying the parameters above these models tested an increasing number of regimes and a multilevel model for regimes.

All runs were using two chains were 2000 iterations per chain.

Milestone 1: Direct Effect Model without Measurement Error – blouchOU_direct.stan
 Short half-life ($hl=0.1$)

Fig. S1

Posterior Prior

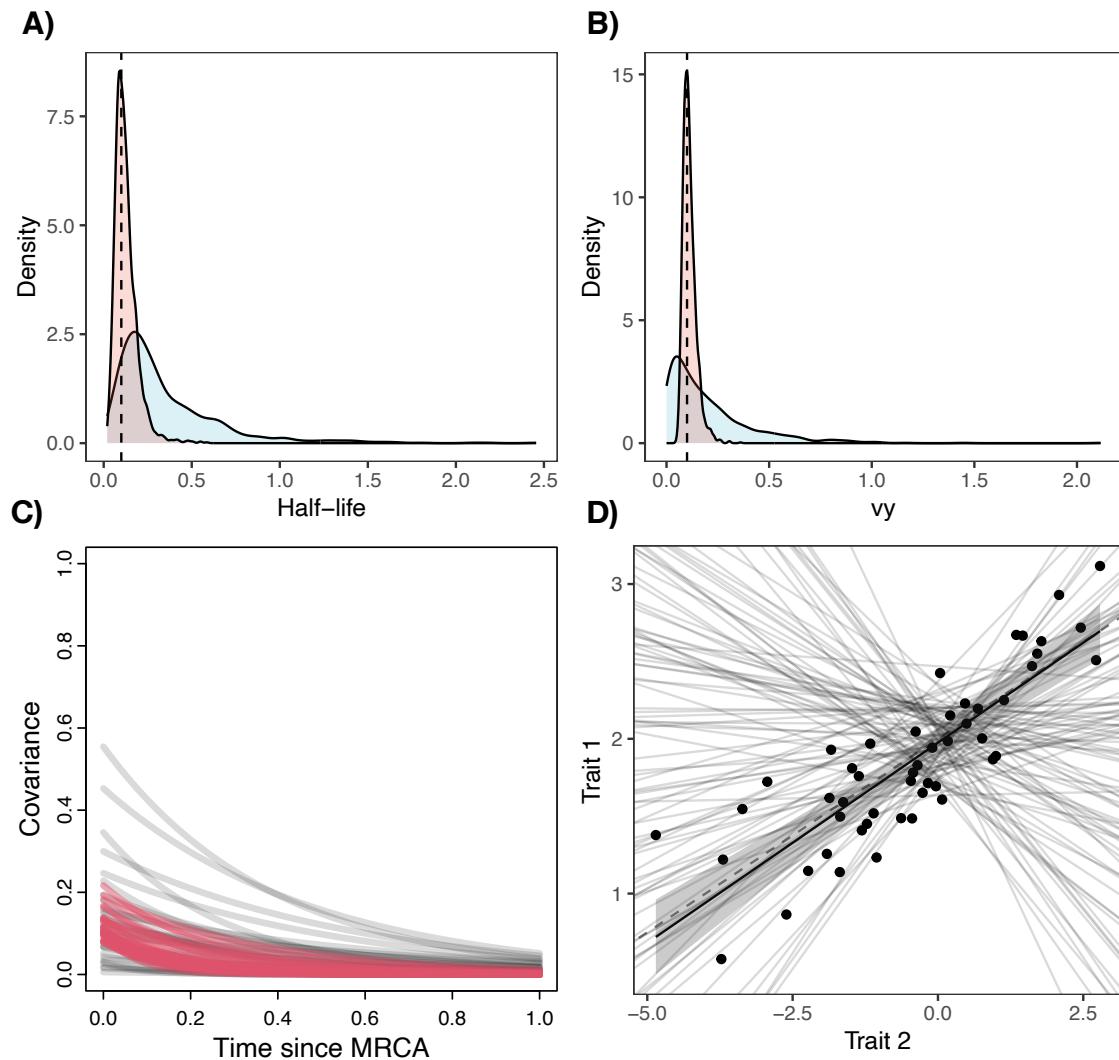


Figure S1: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of distance between taxa with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.1$, $vy=0.01$, $\alpha=2$, $\beta=(0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S1: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.13	0.00	0.06	0.04	0.08	0.11	0.15	0.28	1012	1.00
vy	0.11	0.00	0.03	0.07	0.09	0.11	0.13	0.20	1060	1.00
alpha	1.97	0.00	0.06	1.84	1.93	1.98	2.02	2.09	1456	1.00
beta[1]	0.26	0.00	0.03	0.20	0.24	0.26	0.28	0.32	1478	1.00

Medium half-life ($hl = 0.25$)

Fig. S2

Posterior Prior

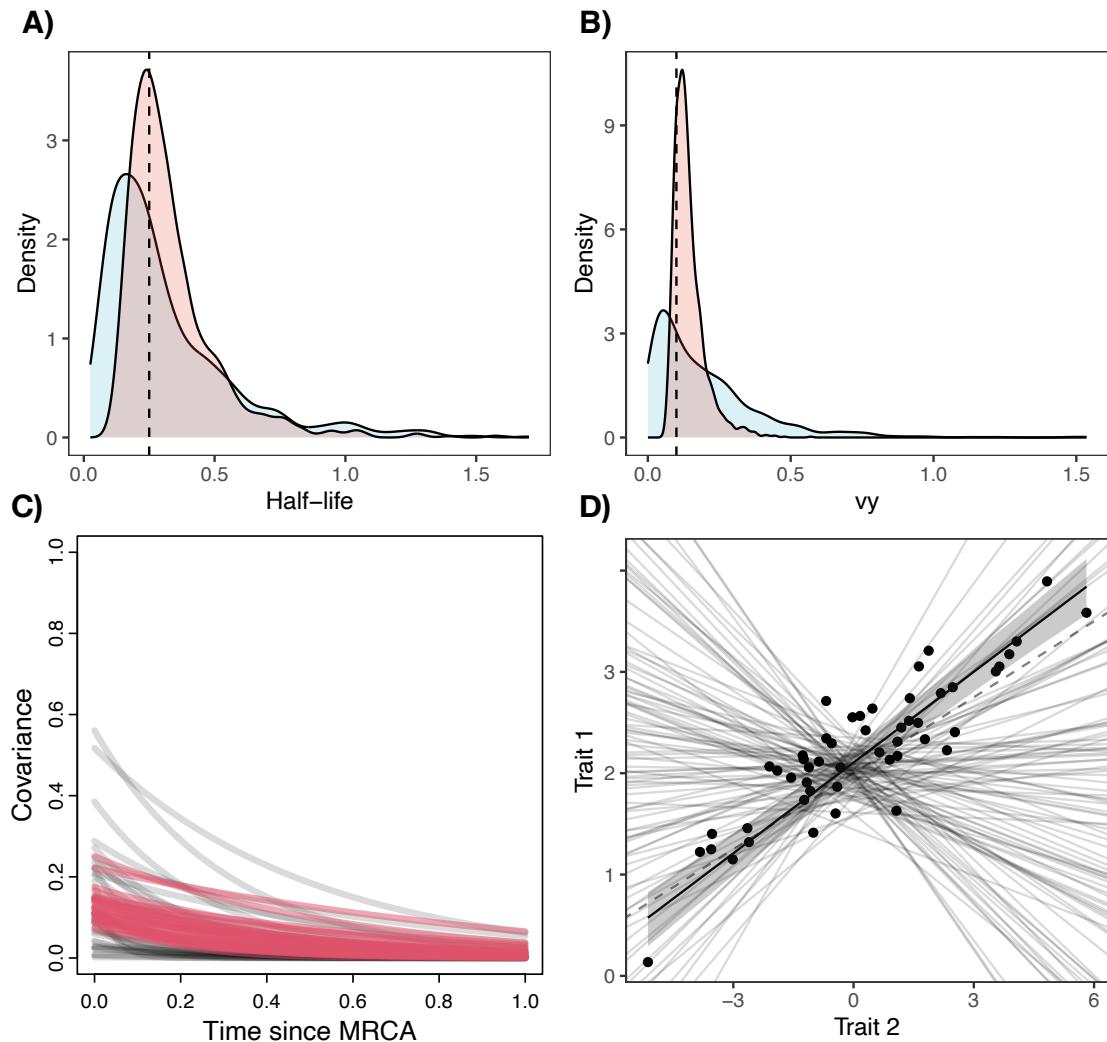


Figure S2: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of distance between taxa with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.25$, $vy=0.01$, $\alpha=2$, $\beta=(0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S2: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.33	0.01	0.18	0.14	0.22	0.29	0.39	0.80	617	1.00
vy	0.14	0.00	0.06	0.08	0.11	0.13	0.16	0.30	658	1.00
alpha	2.11	0.00	0.10	1.90	2.04	2.11	2.17	2.29	1205	1.00
beta[1]	0.30	0.00	0.03	0.25	0.28	0.30	0.32	0.35	1401	1.00

Long half-life ($hl = 0.75$)

Fig. S3

Posterior Prior

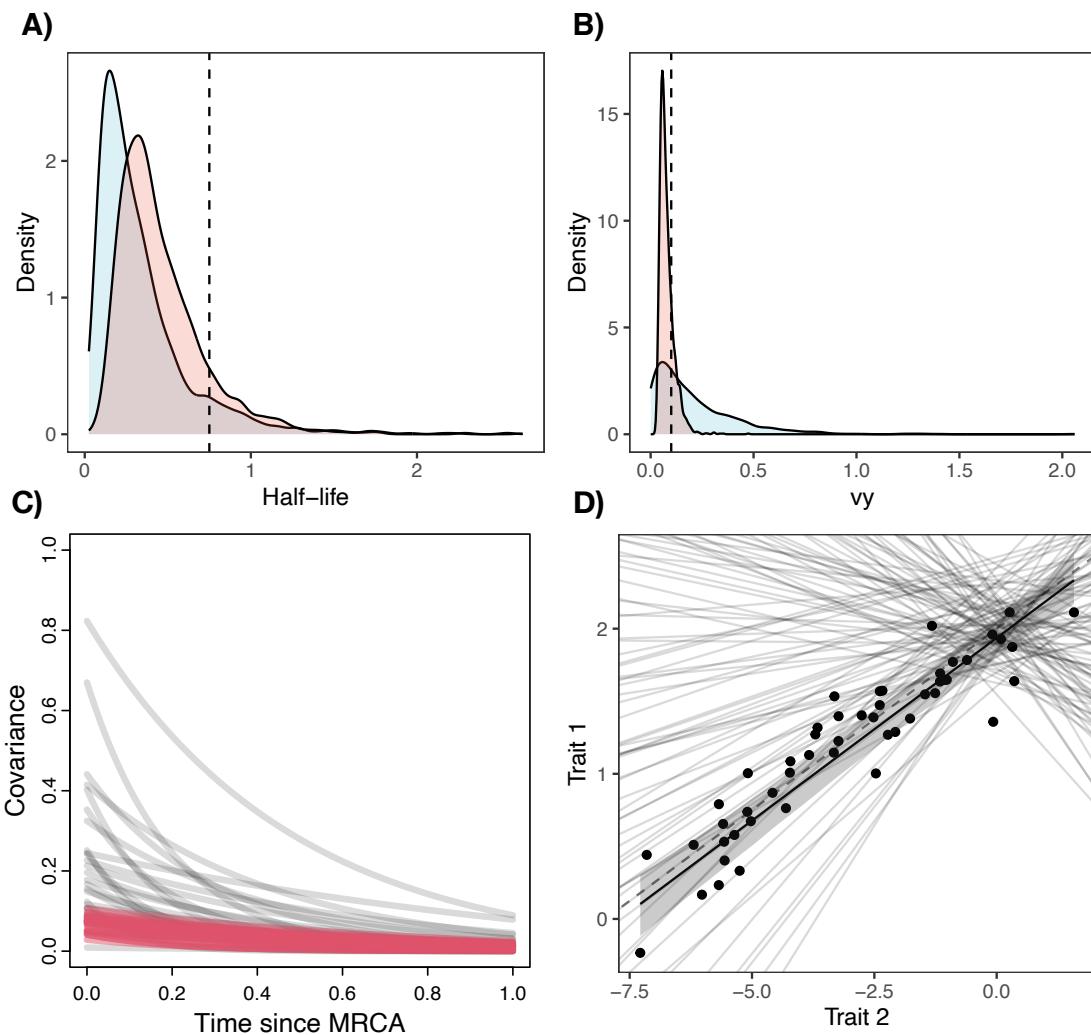


Figure S3: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.75$, $vy=0.01$, $\alpha=2$, $\beta=(0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S3: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.46	0.01	0.27	0.15	0.28	0.39	0.57	1.16	653	1.00
vy	0.08	0.00	0.04	0.04	0.05	0.07	0.09	0.17	641	1.00
alpha	1.94	0.00	0.09	1.77	1.88	1.93	1.99	2.11	1450	1.00
beta[1]	0.25	0.00	0.02	0.21	0.24	0.25	0.27	0.29	1118	1.00

Milestone 1: Direct Effect Model with Measurement Error – blouchOU_direct_ME.stan

Short half-life ($hl=0.1$)

Fig. S4

Posterior Prior

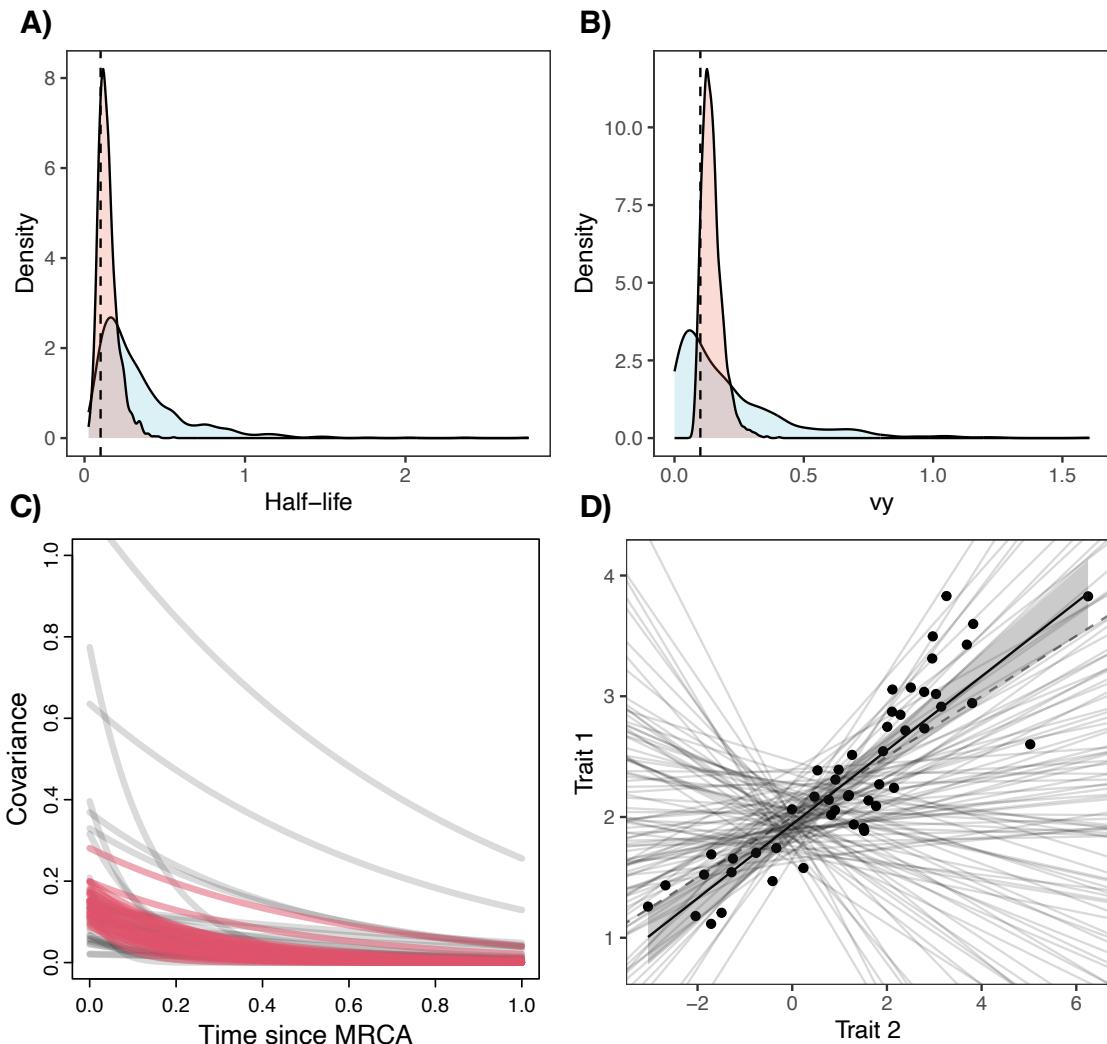


Figure S4: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.1$, $vy=0.01$, $\alpha=2$, $\beta=(0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S4: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.15	0.00	0.06	0.06	0.10	0.13	0.17	0.31	1440	1.00

vy	0.15	0.00	0.04	0.09	0.12	0.14	0.16	0.25	1470	1.00
alpha	1.94	0.00	0.08	1.77	1.89	1.94	1.99	2.11	1775	1.00
beta[1]	0.31	0.00	0.03	0.25	0.29	0.31	0.33	0.37	2015	1.00

Medium half-life ($hl=0.25$)

Fig. S5

Posterior Prior

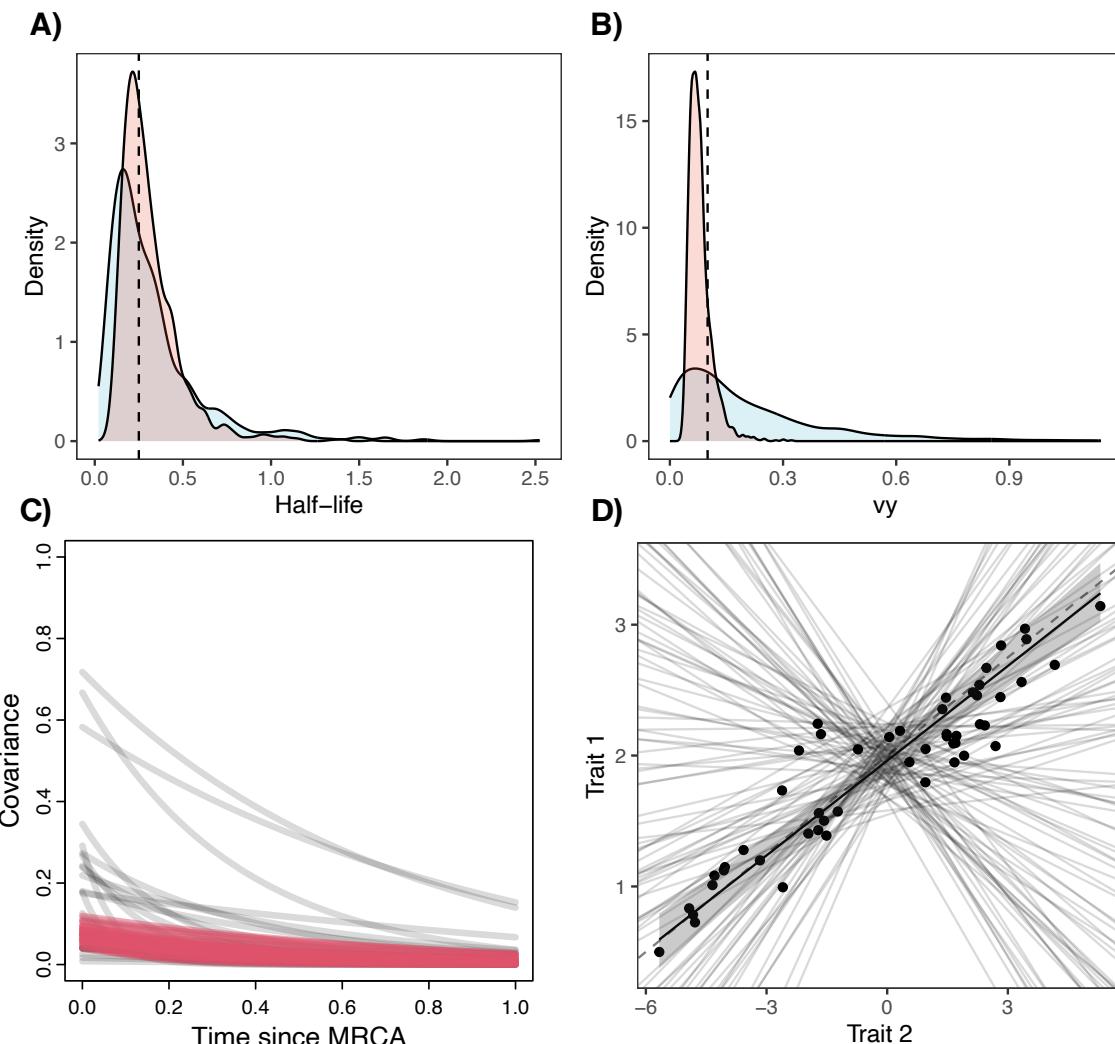


Figure S5: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.25$, $vy=0.01$, $\alpha=2$, $\beta=(0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S5: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.31	0.00	0.17	0.12	0.20	0.27	0.37	0.75	1445	1.00

vy	0.08	0.00	0.03	0.04	0.06	0.07	0.09	0.16	1509	1.00
alpha	1.96	0.00	0.07	1.82	1.91	1.96	2.01	2.12	2089	1.00
beta[1]	0.24	0.00	0.02	0.20	0.23	0.24	0.26	0.28	2967	1.00

Long half-life ($hl=0.75$)

Fig. S6

Posterior Prior

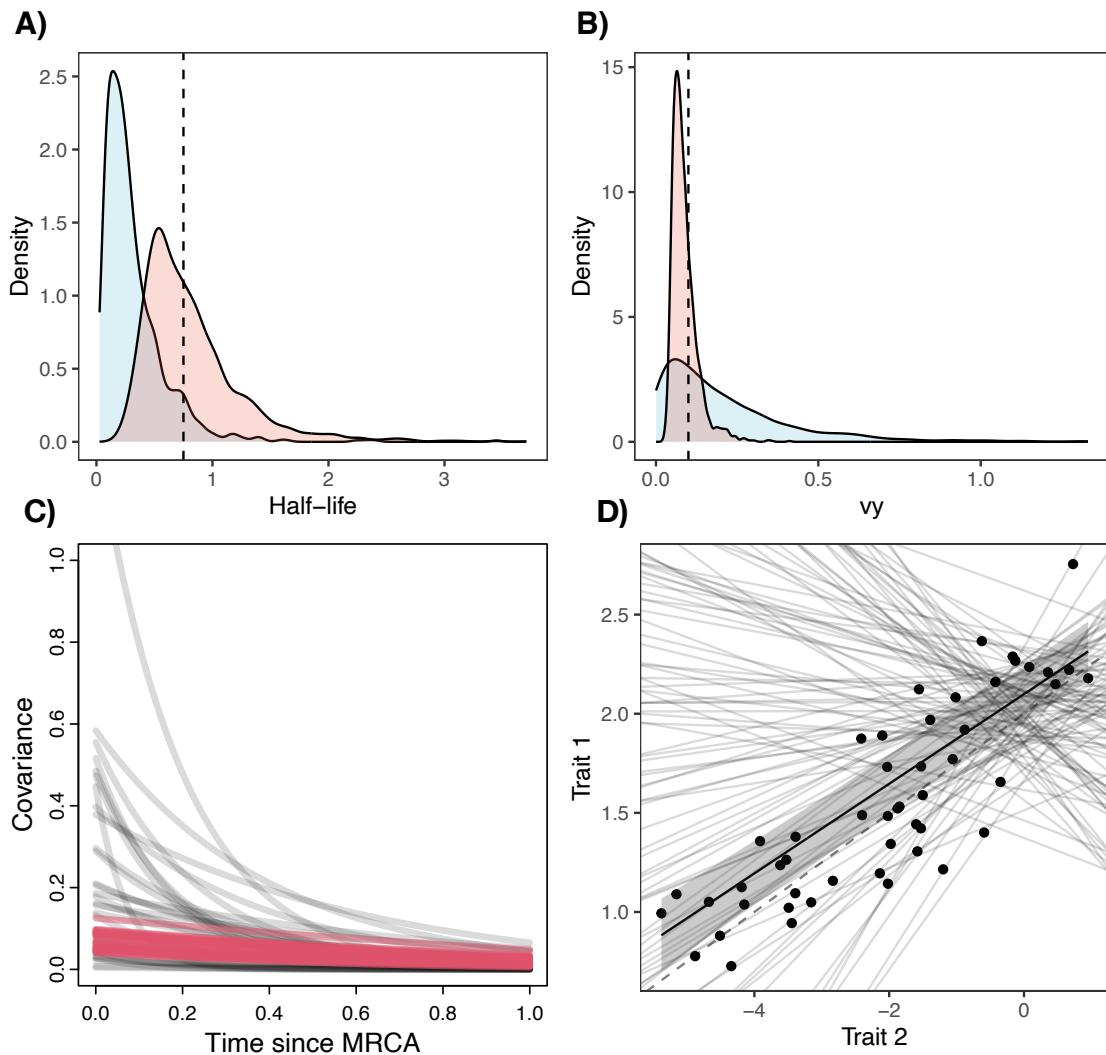


Figure S6: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.75$, $vy=0.01$, $\alpha=2$, $\beta=(0.25)$: priors were set to: $hl \sim \text{lognormal}(\text{log}(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S6: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.81	0.01	0.43	0.32	0.53	0.71	0.98	1.97	1502	1.00

vy	0.09	0.00	0.04	0.04	0.06	0.08	0.10	0.20	1374	1.00
alpha	2.10	0.00	0.09	1.92	2.04	2.10	2.16	2.28	2716	1.00
beta[1]	0.23	0.00	0.02	0.19	0.22	0.23	0.24	0.26	3101	1.00

Milestone 1: Direct Effect Model with Measurement Error and Multiple Predictors – blouchOU_direct_ME.stan

Two predictors

Fig. S7

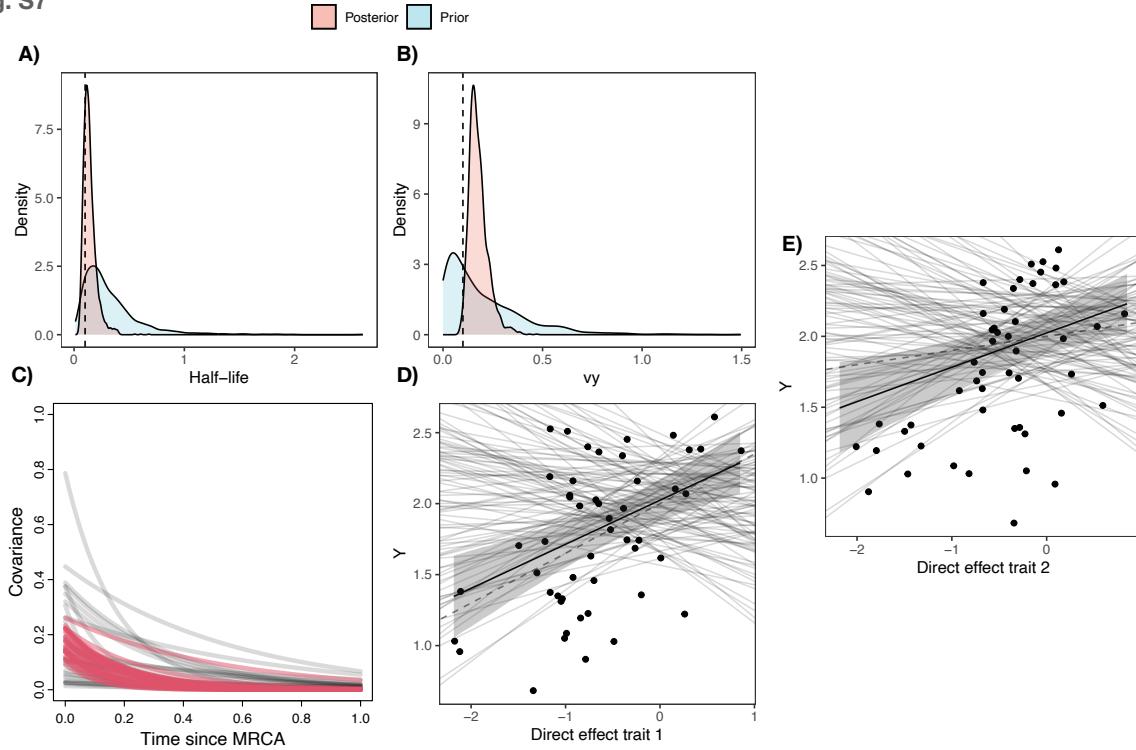


Figure S7: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: hl=0.75, vy=0.01, alpha=2, beta=(0.25): priors were set to: hl~lognormal(log(0.25),0.75); vy~exponential(5); alpha~normal(2,0.2); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S7: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.14	0.00	0.06	0.07	0.10	0.13	0.17	0.30	1851	1.00
vy	0.18	0.00	0.05	0.11	0.14	0.17	0.20	0.29	2170	1.00
alpha	2.02	0.00	0.09	1.84	1.96	2.03	2.09	2.20	3710	1.00
beta[1]	0.31	0.00	0.09	0.14	0.25	0.31	0.37	0.49	2715	1.00
beta[2]	0.24	0.00	0.09	0.07	0.18	0.24	0.30	0.42	2392	1.00

Milestone 2: Adaptive Model without Measurement Error – blouchOU_adaptive.stan

Short half-life (hl=0.1)

Fig. S8

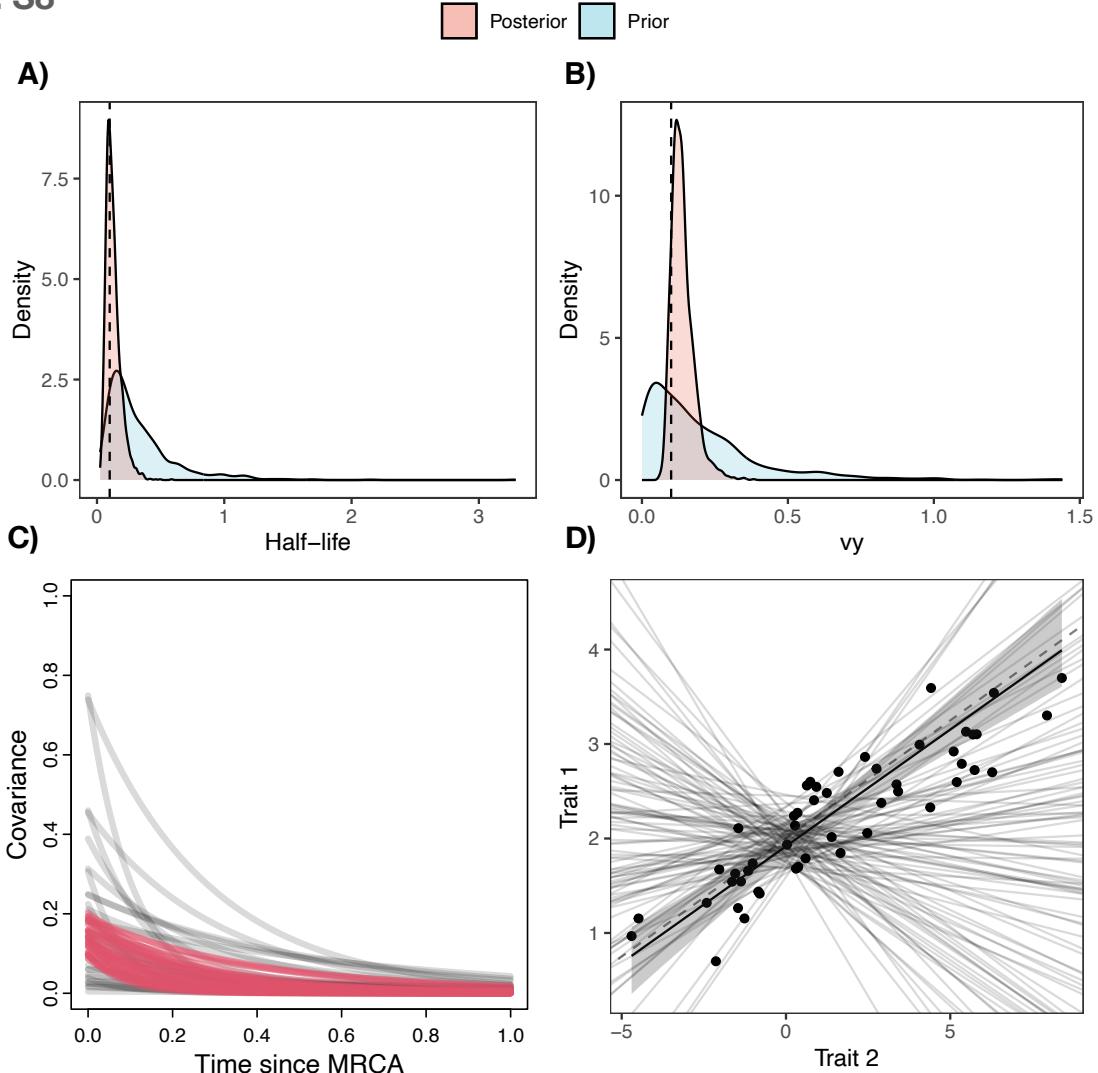


Figure S8: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: hl=0.1, vy=0.1, alpha=2, beta=(0.25): priors were set to: hl~lognormal(log(0.25),0.75); vy~exponential(5); alpha~normal(2,0.2); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S8: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.13	0.00	0.06	0.05	0.09	0.11	0.15	0.28	620	1.00
vy	0.14	0.00	0.04	0.08	0.11	0.13	0.16	0.24	726	1.00
alpha	1.92	0.00	0.09	1.75	1.86	1.92	1.97	2.10	978	1.00
beta[1]	0.25	0.00	0.04	0.19	0.22	0.24	0.27	0.34	744	1.00
beta_e[1]	0.20	0.00	0.02	0.16	0.19	0.20	0.22	0.24	1276	1.00

Medium half-life ($hl=0.25$)

Fig. S9

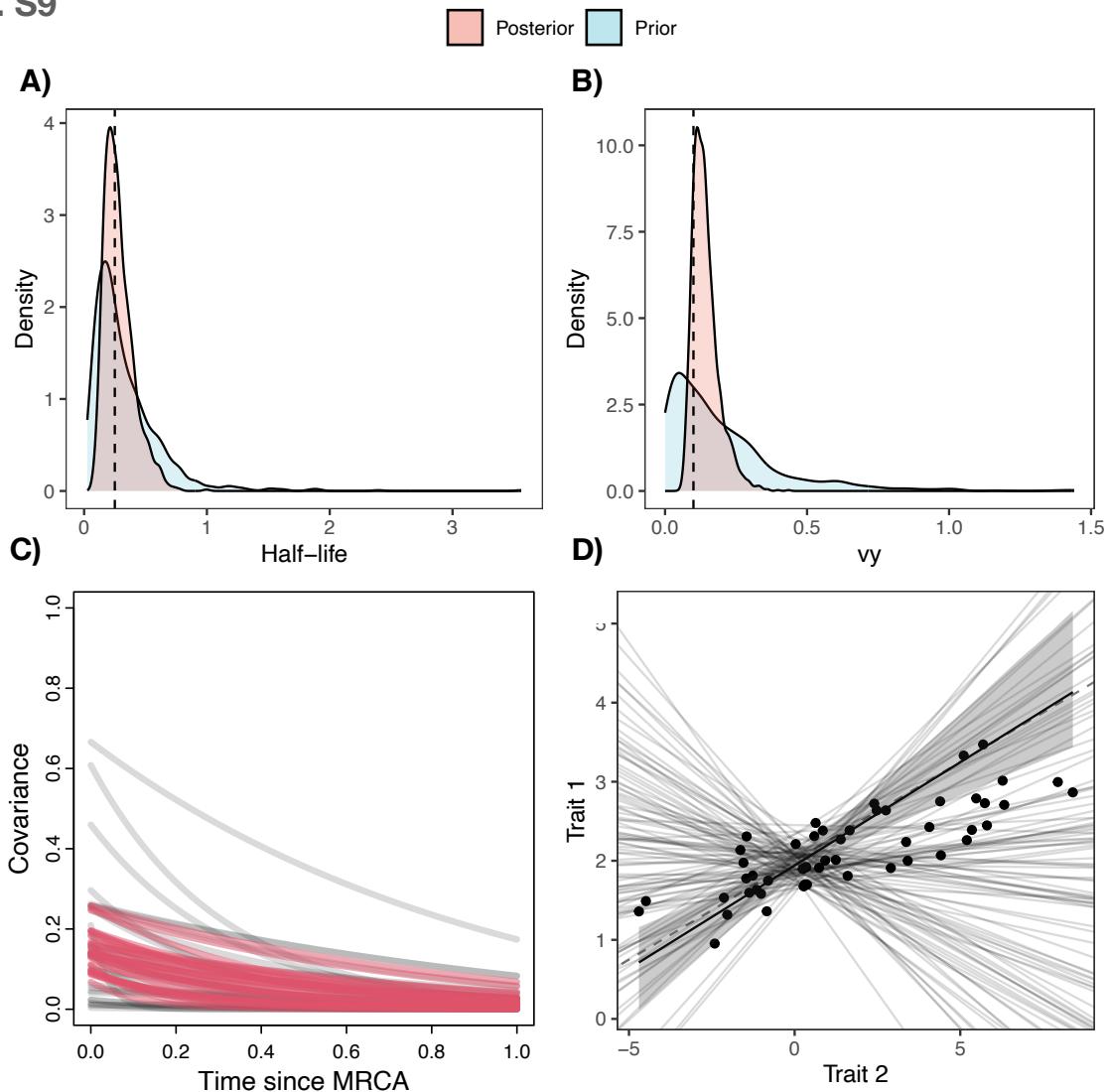


Figure S9: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $\alpha=2$, $\beta=0.25$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S9: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.28	0.01	0.12	0.12	0.19	0.26	0.35	0.59	533	1.00
vy	0.14	0.00	0.05	0.08	0.11	0.13	0.16	0.26	621	1.00
alpha	1.94	0.00	0.10	1.74	1.88	1.94	2.00	2.15	1074	1.00

beta[1]	0.26	0.00	0.07	0.17	0.21	0.25	0.30	0.42	517	1.00
beta_e[1]	0.16	0.00	0.02	0.12	0.15	0.16	0.18	0.21	1216	1.00

Long half-life ($hl=0.75$)

Fig. S10

Posterior Prior

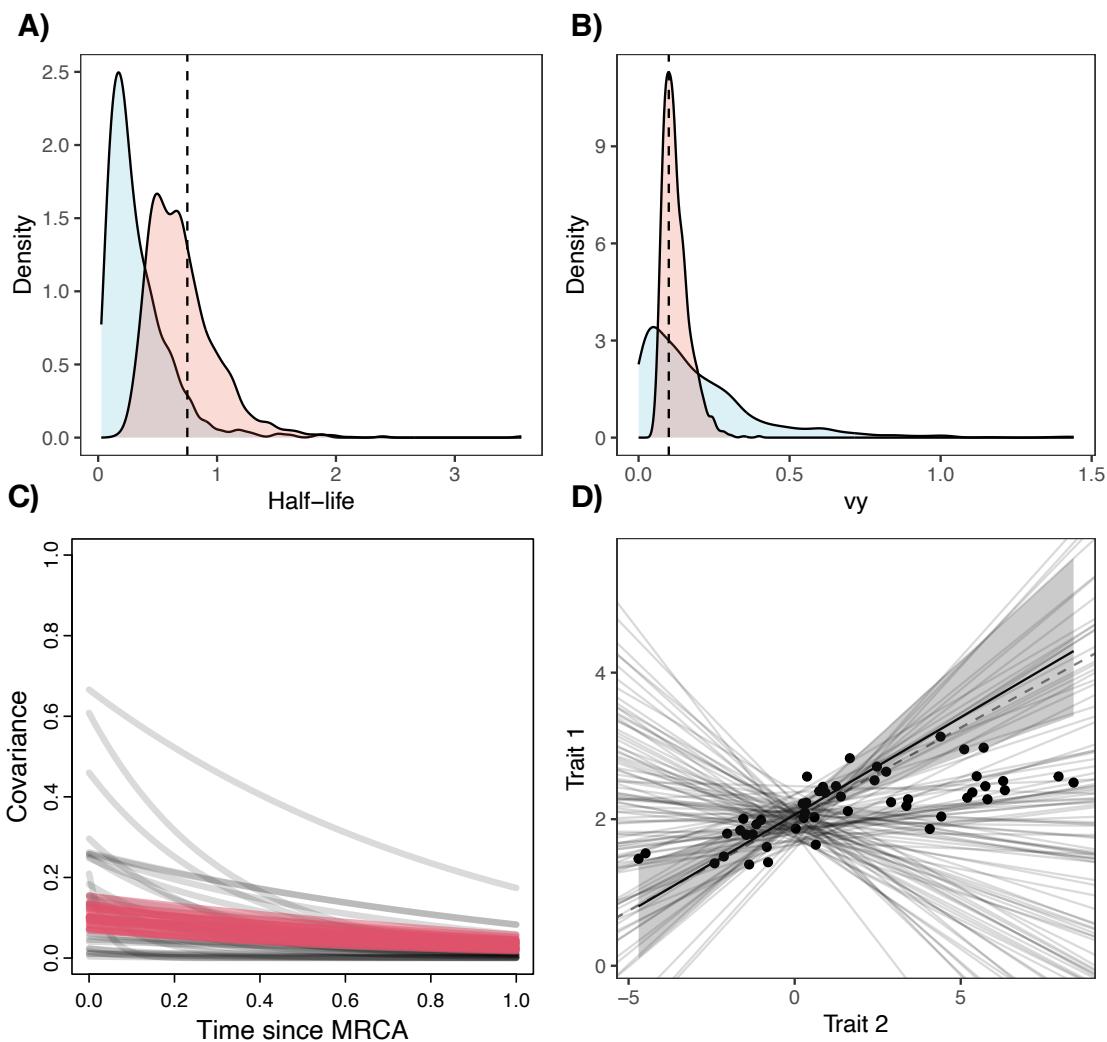


Figure S10: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.75$, $vy=0.1$, $\alpha=2$, $\beta=0.25$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S10: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
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hl	0.71	0.01	0.28	0.32	0.49	0.66	0.84	1.42	473	1.00
vy	0.12	0.00	0.04	0.07	0.09	0.11	0.15	0.23	613	1.00
alpha	2.06	0.00	0.11	1.85	1.99	2.06	2.13	2.27	1336	1.00
beta[1]	0.27	0.00	0.08	0.14	0.20	0.25	0.31	0.47	507	1.00
beta_e[1]	0.10	0.00	0.02	0.06	0.09	0.10	0.11	0.13	1960	1.00

Milestone 2: Adaptive model with measurement error - blouchOU_adaptive_ME.stan

Short half-life ($hl=0.1$)

Fig. S11

Posterior Prior

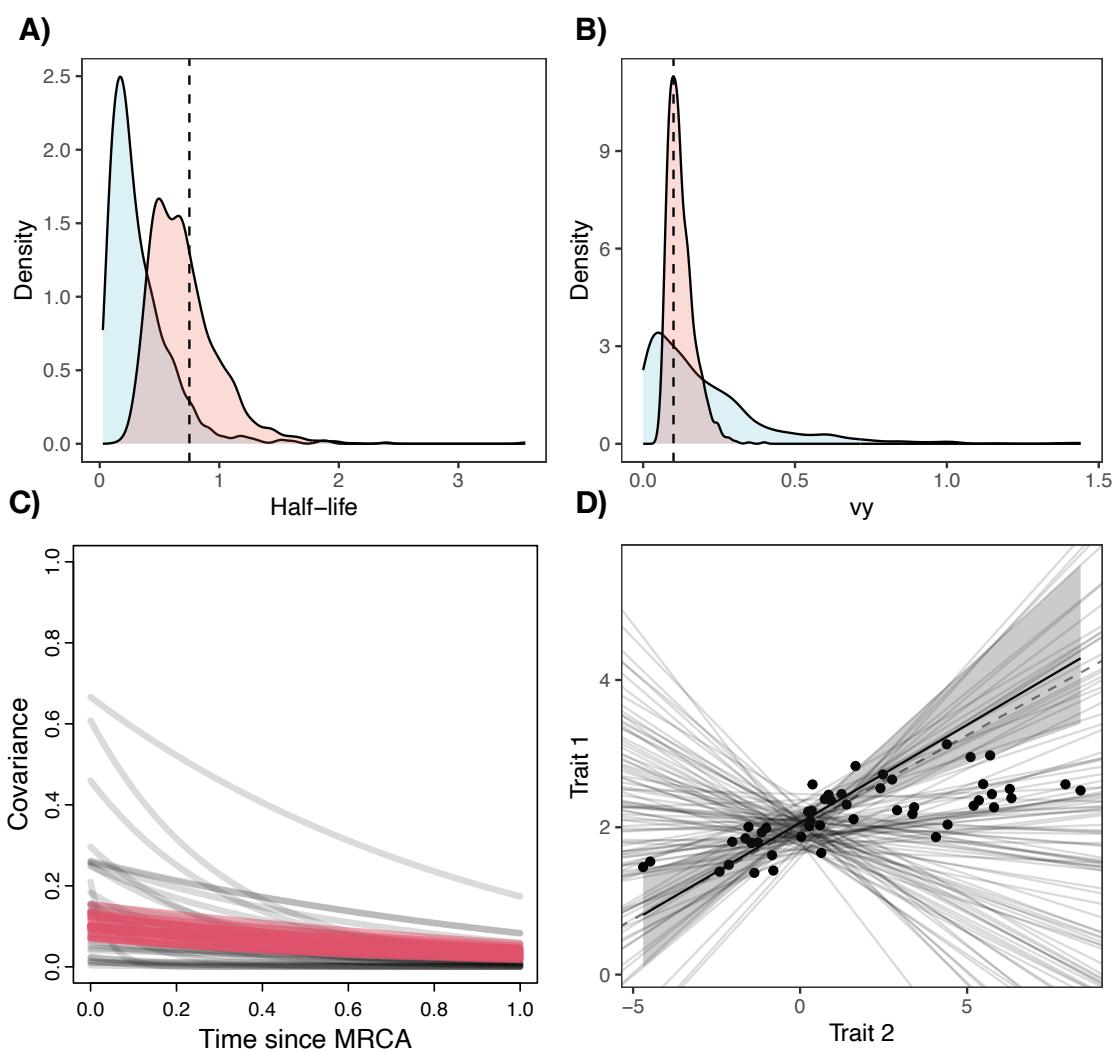


Figure S11: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.1$, $vy=0.1$, $\alpha=2$, $\beta=0.25$: priors were set to:

$hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$.
 Dotted lines in A) and B) are true values of the parameter.

Table S11: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.13	0.00	0.06	0.05	0.09	0.12	0.16	0.29	1336	1.00
vy	0.14	0.00	0.04	0.08	0.11	0.13	0.15	0.24	1520	1.00
alpha	1.92	0.00	0.08	1.76	1.87	1.92	1.97	2.09	3457	1.00
beta[1]	0.25	0.00	0.04	0.19	0.22	0.24	0.27	0.34	1620	1.00
beta_e[1]	0.20	0.00	0.02	0.16	0.19	0.20	0.21	0.24	2871	1.00

Medium half-life ($hl=0.25$)

Fig. S12

Posterior Prior

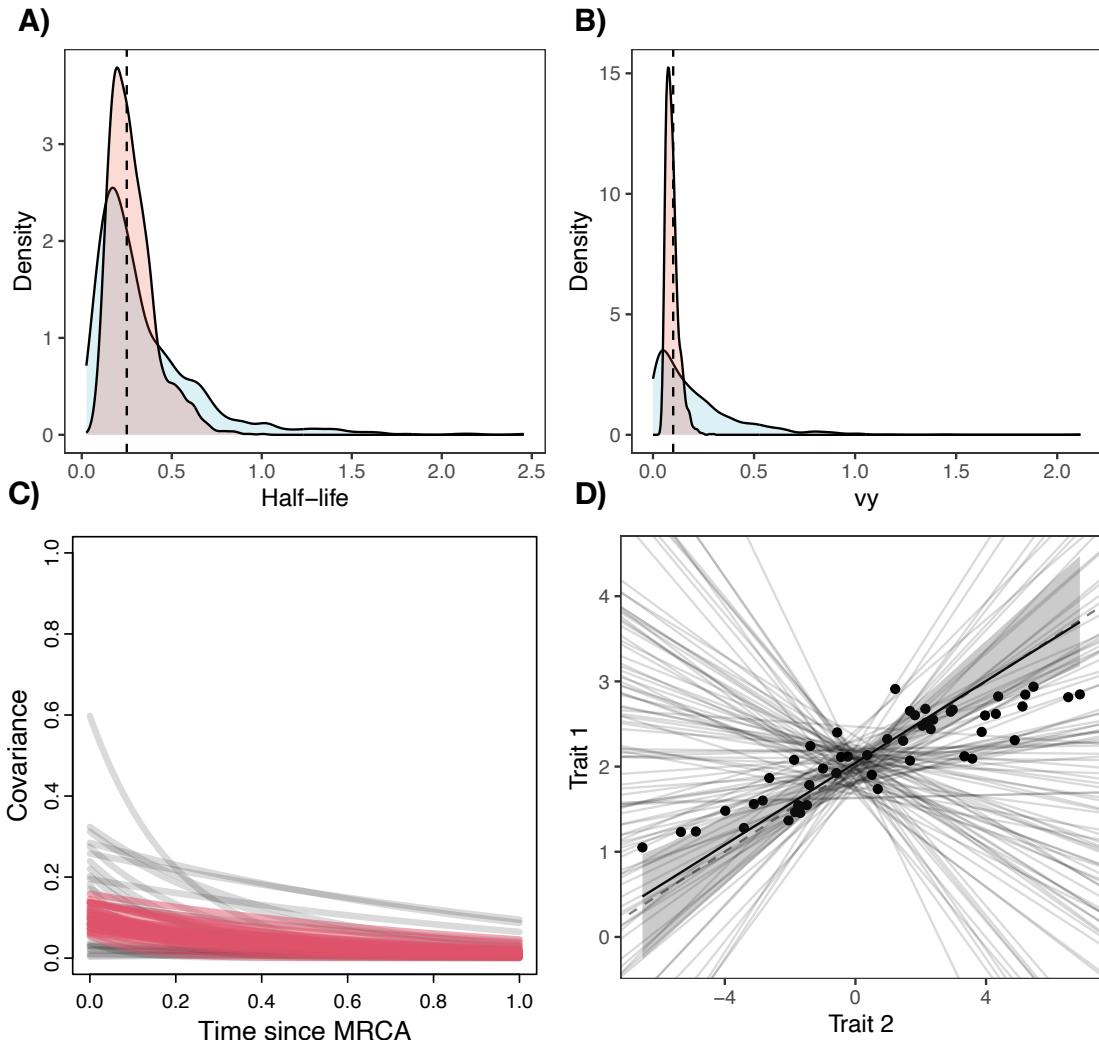


Figure S12: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for

adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $\alpha=2$, $\beta=0.25$: priors were set to: $hl \sim \text{lognormal}(\text{log}(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S12: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.28	0.00	0.13	0.11	0.19	0.26	0.34	0.62	1355	1.00
vy	0.09	0.00	0.03	0.05	0.07	0.09	0.11	0.18	1554	1.00
alpha	2.04	0.00	0.08	1.87	1.99	2.04	2.10	2.20	3629	1.00
beta[1]	0.24	0.00	0.06	0.16	0.20	0.23	0.27	0.40	1424	1.00
beta_e[1]	0.15	0.00	0.02	0.11	0.14	0.15	0.16	0.19	2002	1.00

Long half-life ($hl=0.75$)

Fig. S13

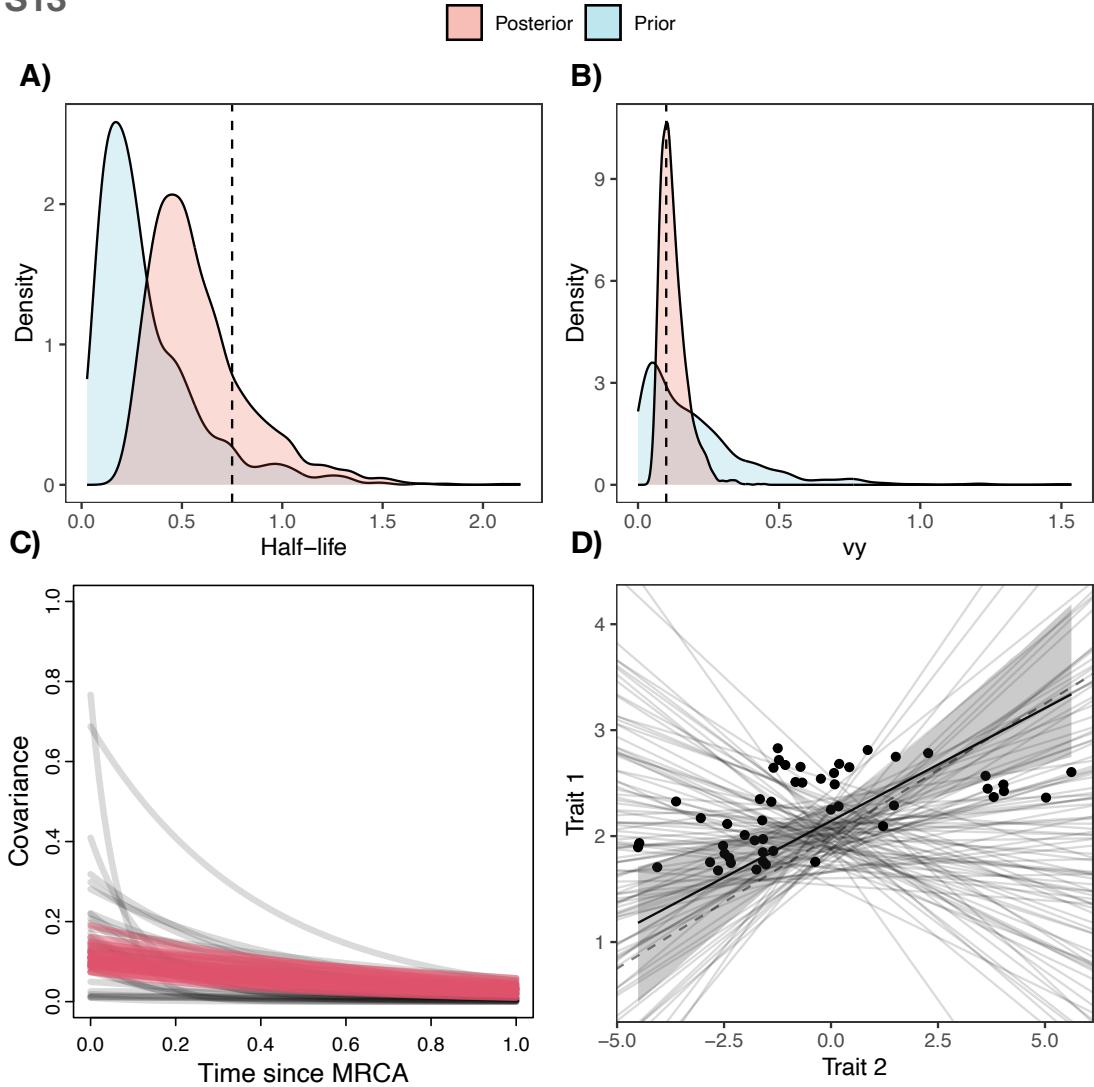


Figure S13: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: hl=0.25, vy=0.1, alpha=2, beta=0.25: priors were set to: hl~lognormal(log(0.25),0.75); vy~exponential(5); alpha~normal(2,0.2); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S13: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.59	0.01	0.26	0.26	0.41	0.53	0.70	1.25	1534	1.00
vy	0.13	0.00	0.05	0.06	0.09	0.11	0.15	0.24	1565	1.00
alpha	2.14	0.00	0.11	1.92	2.08	2.15	2.21	2.35	4073	1.00
beta[1]	0.21	0.00	0.08	0.09	0.15	0.20	0.26	0.40	1797	1.00
beta_e[1]	0.09	0.00	0.02	0.04	0.07	0.09	0.10	0.13	2049	1.00

Milestone 2: Adaptive Model with Measurement Error and Multiple Predictors – blouchOU_adaptive_ME.stan

Two traits

Fig. S14

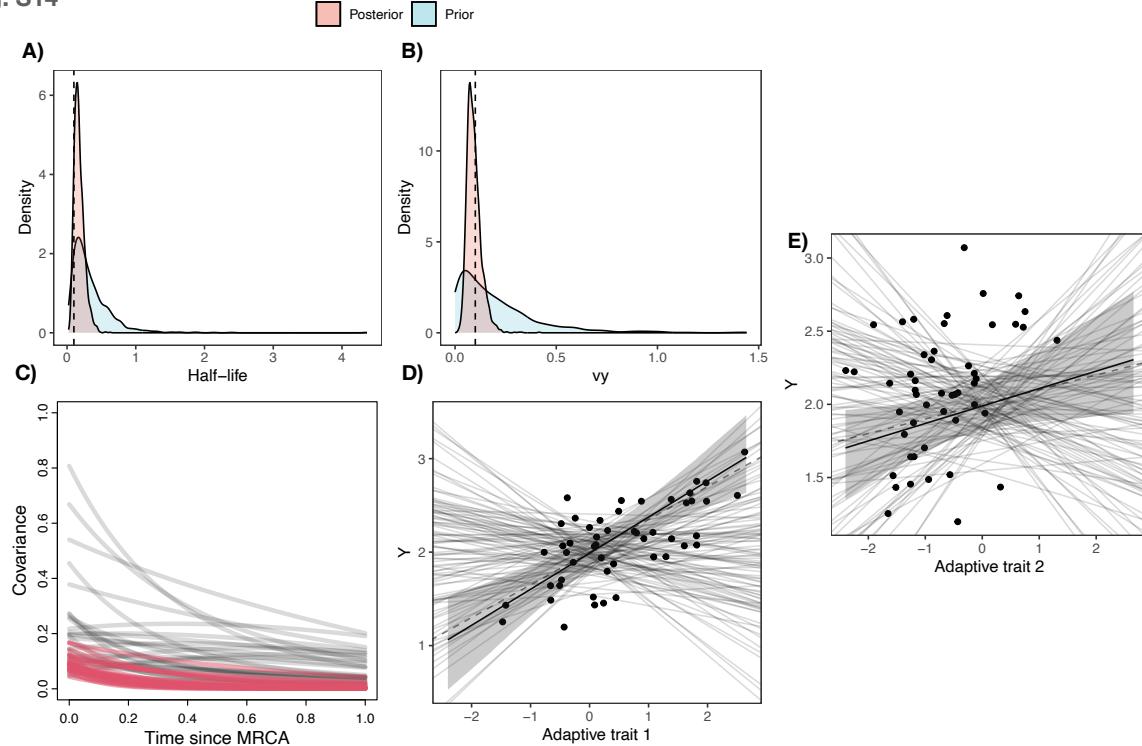


Figure S14: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: hl=0.1, vy=0.1, alpha=2, beta=(0.35,0.1); priors were set to: hl~lognormal(log(0.25),0.75); vy~exponential(5); alpha~normal(2,0.2); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S14: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.18	0.00	0.07	0.07	0.12	0.16	0.22	0.35	2384	1.00
vy	0.09	0.00	0.04	0.04	0.07	0.09	0.11	0.17	3266	1.00
alpha	1.99	0.00	0.10	1.78	1.92	1.99	2.06	2.18	4078	1.00
beta[1]	0.39	0.00	0.11	0.20	0.31	0.38	0.45	0.63	2959	1.00
beta[2]	0.12	0.00	0.08	0.01	0.06	0.11	0.17	0.31	2234	1.00
beta_e[1]	0.29	0.00	0.07	0.15	0.24	0.29	0.33	0.42	2840	1.00
beta_e[2]	0.09	0.00	0.06	0.00	0.04	0.08	0.12	0.22	2273	1.00

Milestone 3: Combination of direct effect and adaptation predictor model without measurement error – blouchOU_direct_adaptive.stan

Short half-life ($hl=0.1$)

Fig. S15

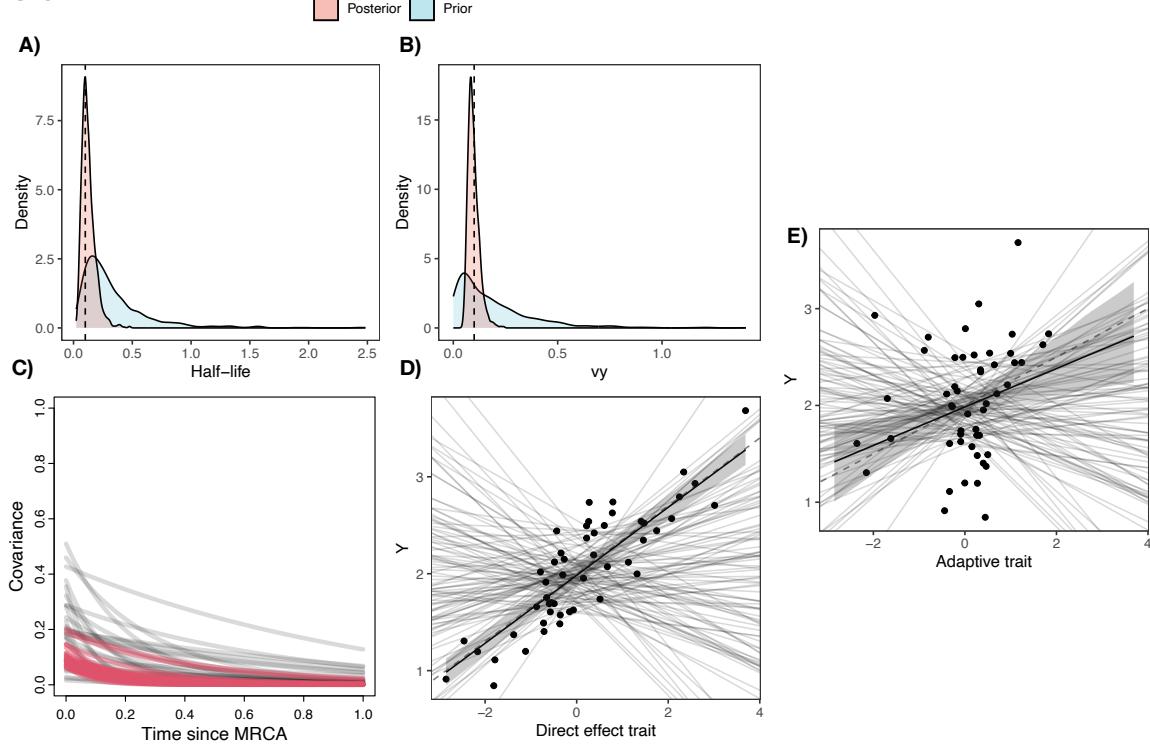


Figure S15: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model and adaptive model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.1$, $vy=0.1$, $\alpha=2$, $\beta=(0.35, 0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S15: Summary table for half-life = 0.1. Direct effect model slope is first beta, adaptive model is second, and beta_e is evolutionary slope.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.13	0.00	0.06	0.05	0.09	0.11	0.15	0.27	811	1.00
vy	0.10	0.00	0.03	0.06	0.08	0.09	0.11	0.16	978	1.00
alpha	1.98	0.00	0.07	1.86	1.94	1.98	2.02	2.13	1490	1.00
beta[1]	0.35	0.00	0.02	0.31	0.34	0.35	0.36	0.39	2183	1.00
beta[2]	0.20	0.00	0.09	0.04	0.14	0.19	0.25	0.39	1511	1.00
beta_e[1]	0.16	0.00	0.06	0.03	0.12	0.16	0.20	0.29	2013	1.00

Medium half-life ($hl=0.25$)

Fig. S16

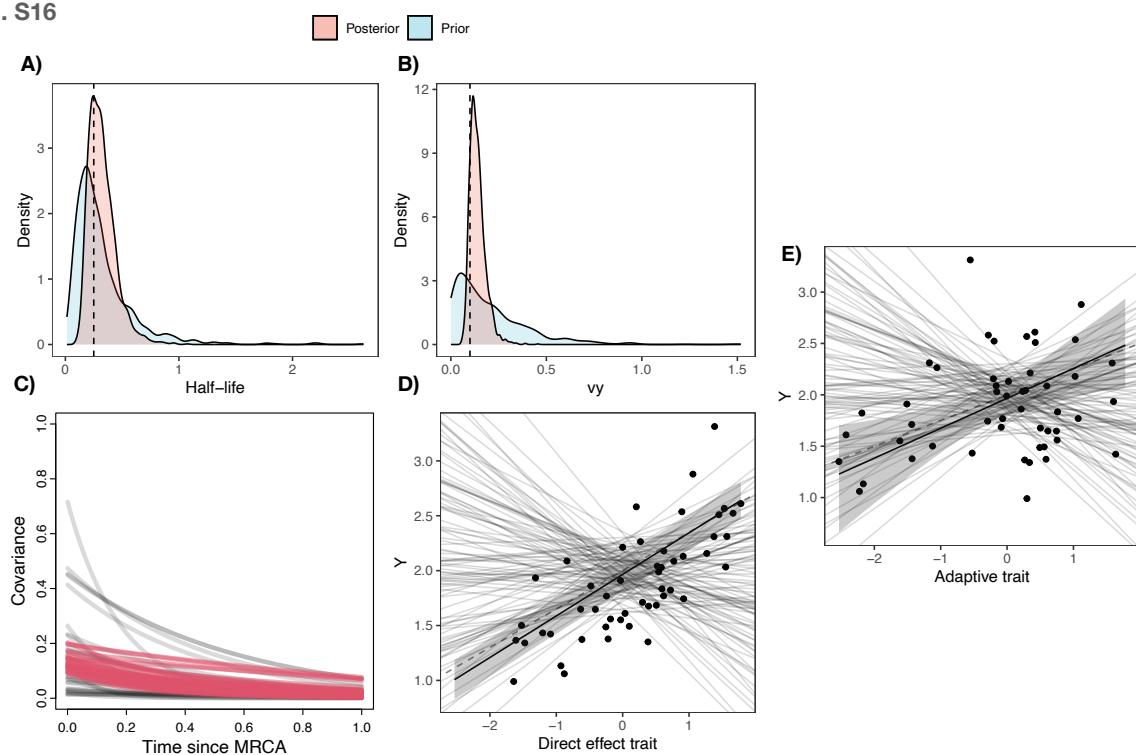


Figure S16: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model and adaptive model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $\alpha=2$, $\beta=(0.35,0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S16: Summary table for half-life = 0.25. Direct effect slopes are the first beta, followed by adaptation slopes, and evolutionary slopes last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.32	0.00	0.12	0.16	0.24	0.30	0.39	0.62	959	1.00
vy	0.14	0.00	0.04	0.08	0.11	0.13	0.16	0.24	1100	1.00
alpha	1.97	0.00	0.10	1.77	1.90	1.97	2.03	2.17	1629	1.00
beta[1]	0.38	0.00	0.02	0.34	0.37	0.38	0.39	0.42	1521	1.00
beta[2]	0.29	0.00	0.13	0.05	0.20	0.28	0.37	0.57	1365	1.00
beta_e[1]	0.17	0.00	0.07	0.03	0.13	0.17	0.22	0.30	1758	1.00

Long half-life ($h=0.75$)

Fig. S17

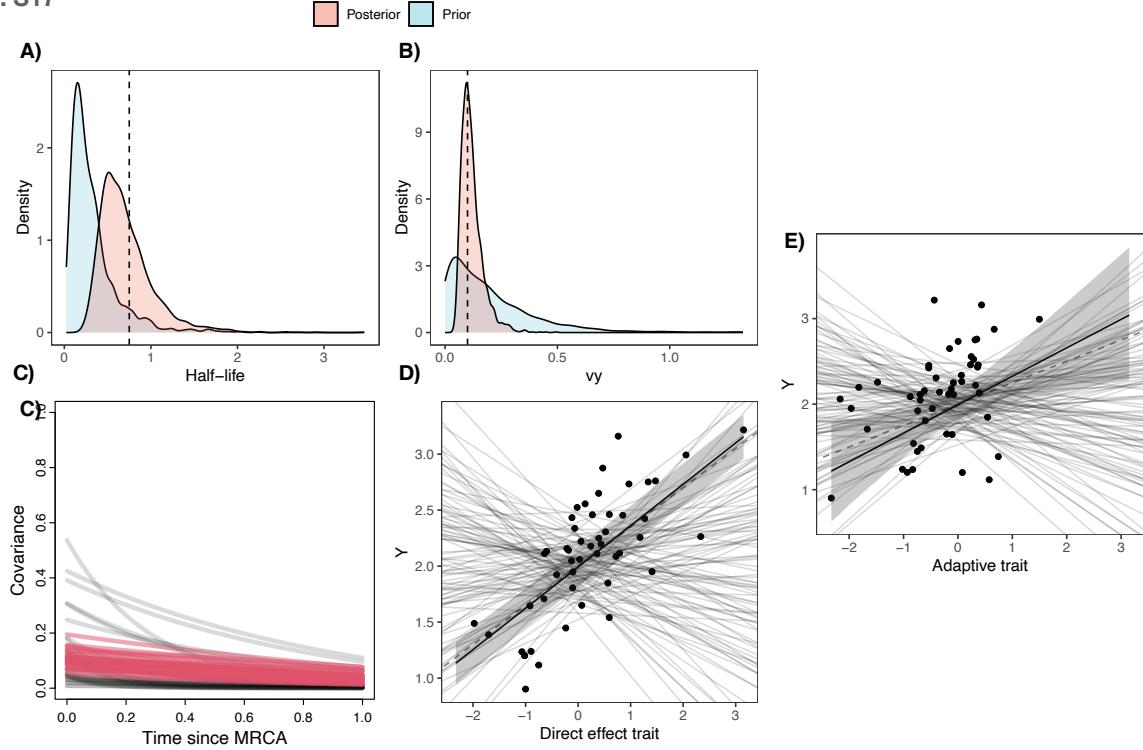


Figure S17: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model and adaptive model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.75$, $vy=0.1$, $\alpha=2$, $\beta=(0.35,0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S17: Summary table for half-life = 0.75. Direct effect slopes are the first beta, followed by adaptation slopes, and evolutionary slopes last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.71	0.01	0.31	0.33	0.50	0.65	0.85	1.52	1045	1.00
vy	0.12	0.00	0.05	0.06	0.09	0.11	0.14	0.25	990	1.00
alpha	1.99	0.00	0.11	1.77	1.92	2.00	2.06	2.20	1656	1.00
beta[1]	0.37	0.00	0.02	0.33	0.36	0.37	0.38	0.41	1661	1.00
beta[2]	0.33	0.00	0.15	0.03	0.24	0.33	0.43	0.65	1696	1.00
beta_e[1]	0.13	0.00	0.06	0.01	0.09	0.13	0.17	0.24	1685	1.00

Milestone 3: Combination of Direct effect and Adaptation Predictor model with Measurement Error – blouchOU_direct_adaptive_ME.stan

Short half-life ($hl=0.1$)

Fig. S18

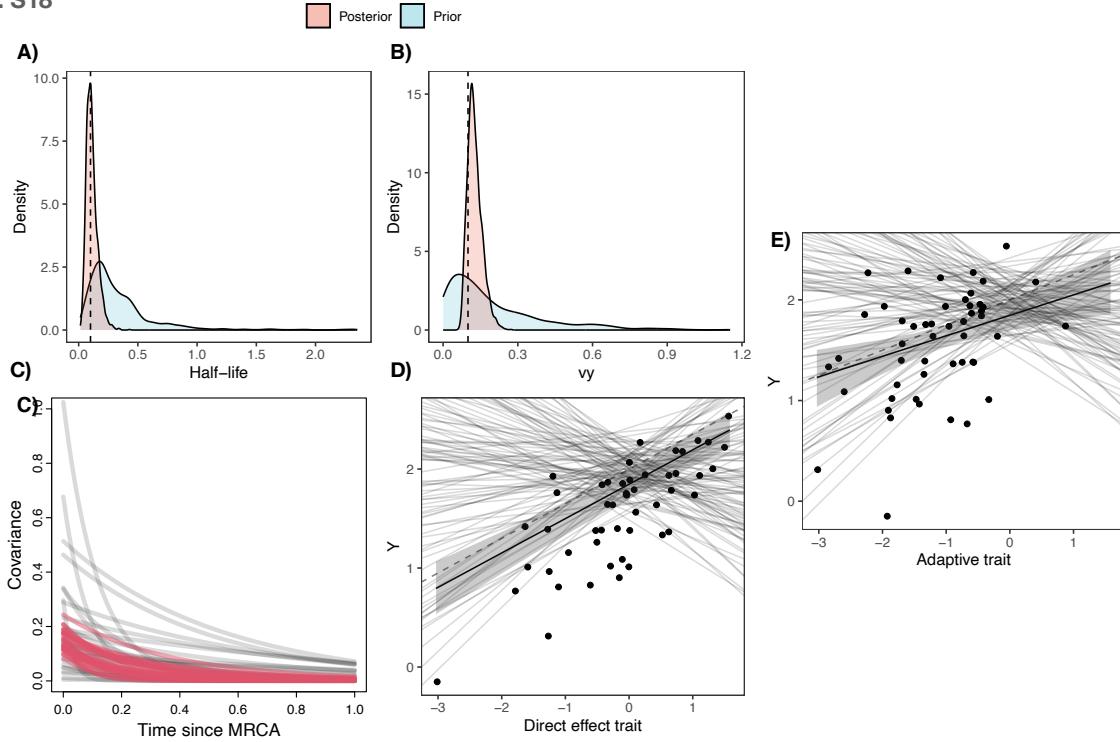


Figure S18: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model and adaptive model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: hl=0.1, vy=0.1, alpha=2, beta=(0.35,0.25): priors were set to: hl~lognormal(log(0.25),0.75); vy~exponential(5); alpha~normal(2,0.2); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S18: Summary table for half-life = 0.1. Direct effect slopes are the first beta, followed by adaptation slopes, and evolutionary slopes last (beta_e[1]).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.11	0.00	0.05	0.04	0.08	0.10	0.14	0.23	1828	1.00
vy	0.13	0.00	0.03	0.08	0.11	0.12	0.14	0.20	2317	1.00
alpha	1.85	0.00	0.10	1.66	1.78	1.84	1.91	2.04	2590	1.00
beta[1]	0.35	0.00	0.04	0.26	0.32	0.35	0.38	0.43	3058	1.00
beta[2]	0.20	0.00	0.08	0.06	0.15	0.20	0.25	0.37	2231	1.00
beta_e[1]	0.17	0.00	0.06	0.05	0.13	0.17	0.21	0.30	2213	1.00

Medium half-life (hl=0.25)

Fig. S19

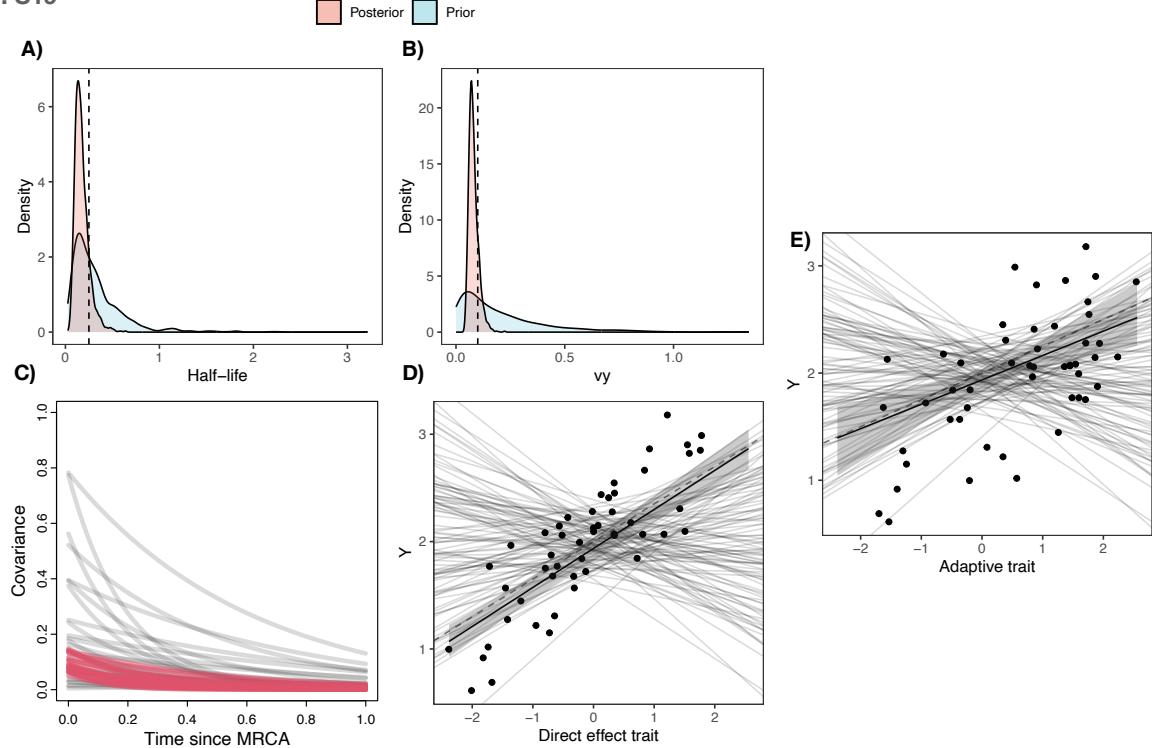


Figure S19: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model and adaptive model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: hl=0.25, vy=0.1, alpha=2, beta=(0.35,0.25): priors were set to: hl~lognormal(log(0.25),0.75); vy~exponential(5); alpha~normal(2,0.2); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S19: Summary table for half-life = 0.25. Direct effect slopes are the first beta, followed by adaptation slopes, and evolutionary slopes last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.18	0.00	0.08	0.07	0.12	0.16	0.21	0.37	1553	1.00
vy	0.08	0.00	0.02	0.05	0.07	0.08	0.09	0.13	1553	1.00
alpha	1.94	0.00	0.07	1.81	1.89	1.93	1.98	2.06	3117	1.00
beta[1]	0.36	0.00	0.03	0.30	0.34	0.36	0.39	0.43	4522	1.00
beta[2]	0.23	0.00	0.08	0.10	0.18	0.22	0.27	0.41	2372	1.00
beta_e[1]	0.17	0.00	0.05	0.08	0.14	0.17	0.20	0.27	2598	1.00

Long half-life (hl=0.75)

Fig. S20

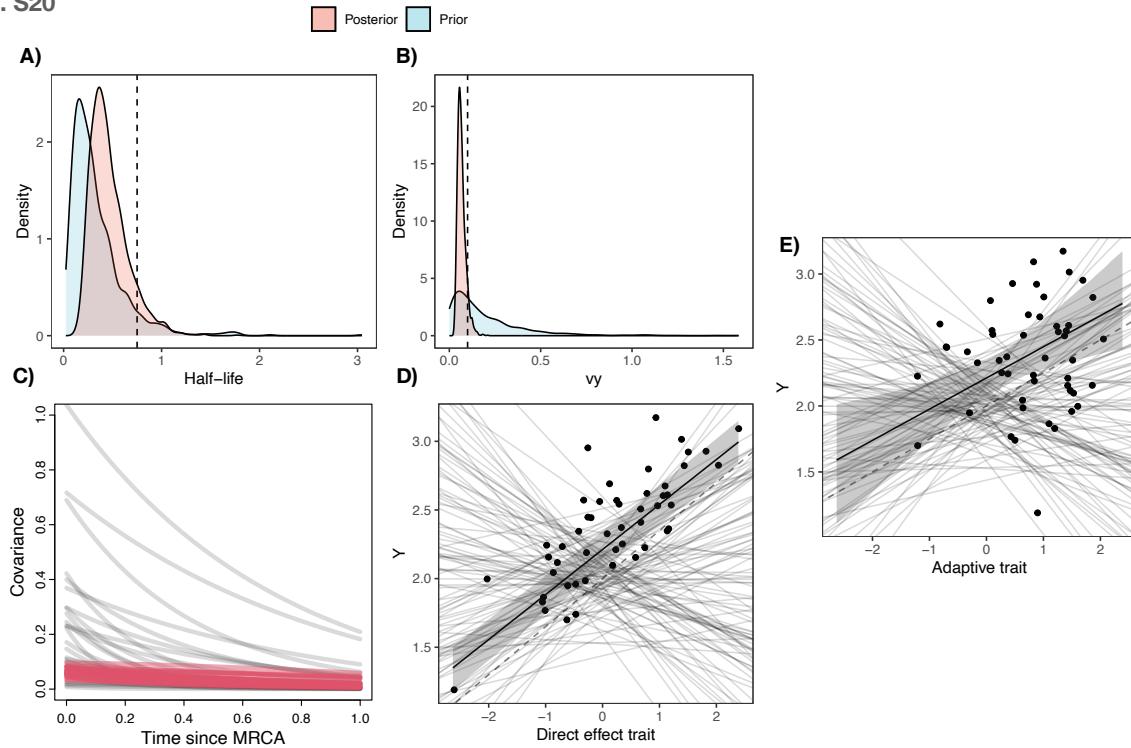
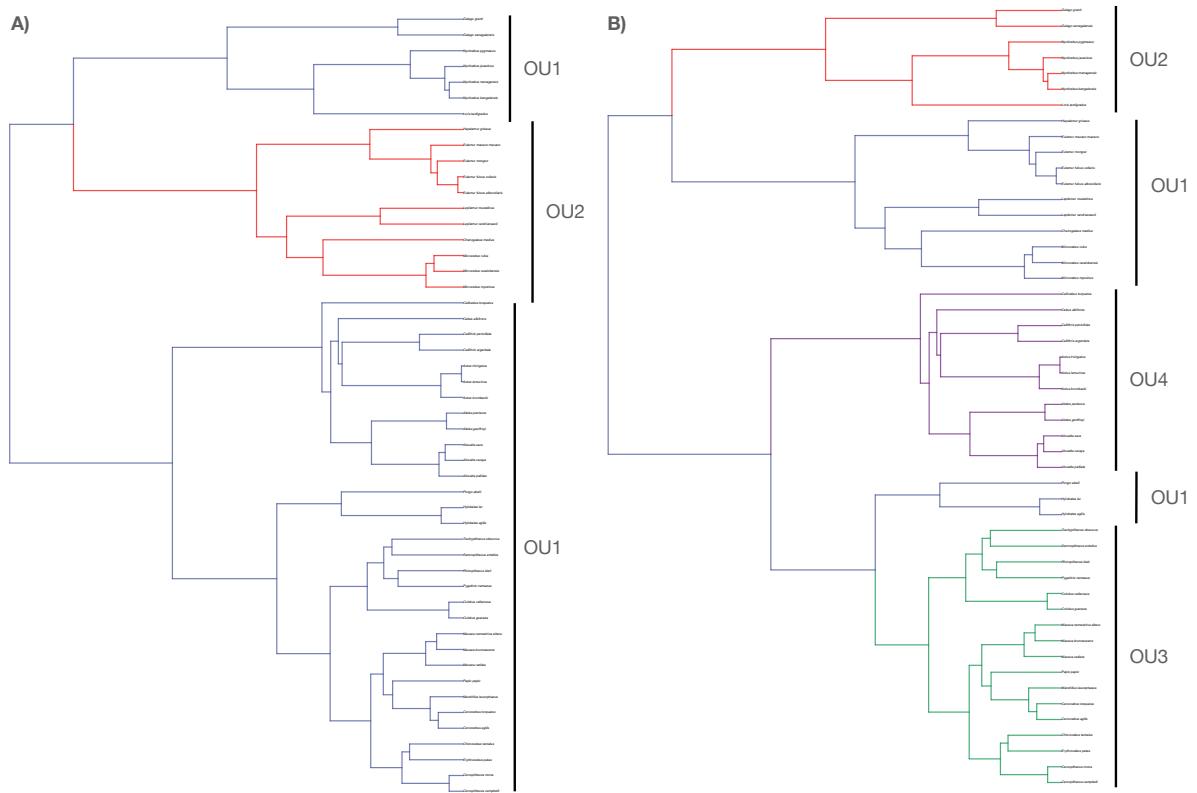


Figure S20: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D,E) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model and adaptive model, with priors in light grey. Species values are shown in the dark circles, with dotted line showing true parameter values of intercept and slope. For this simulation parameter values were set to: $hl=0.75$, $vy=0.1$, $\alpha=2$, $\beta=(0.35,0.25)$: priors were set to: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(5)$; $\alpha \sim \text{normal}(2, 0.2)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S20: Summary table for half-life = 0.75. Direct effect slopes are the first beta, followed by adaptation slopes, and evolutionary slopes last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.47	0.00	0.20	0.21	0.33	0.42	0.56	0.96	2599	1.00
vy	0.07	0.00	0.02	0.04	0.05	0.06	0.08	0.12	2420	1.00
alpha	2.21	0.00	0.09	2.03	2.16	2.21	2.27	2.38	3954	1.00
beta[1]	0.33	0.00	0.02	0.29	0.32	0.33	0.34	0.36	5025	1.00
beta[2]	0.24	0.00	0.10	0.07	0.17	0.23	0.29	0.46	2154	1.00
beta_e[1]	0.11	0.00	0.04	0.04	0.09	0.11	0.14	0.19	2091	1.00

Milestone 4: Regime Model without other predictors – blouchOU_reg.stan
Regime placement: Two (left) and four (right) regimes



Two regimes

Short half-life ($hl=0.1$)

Fig. S21

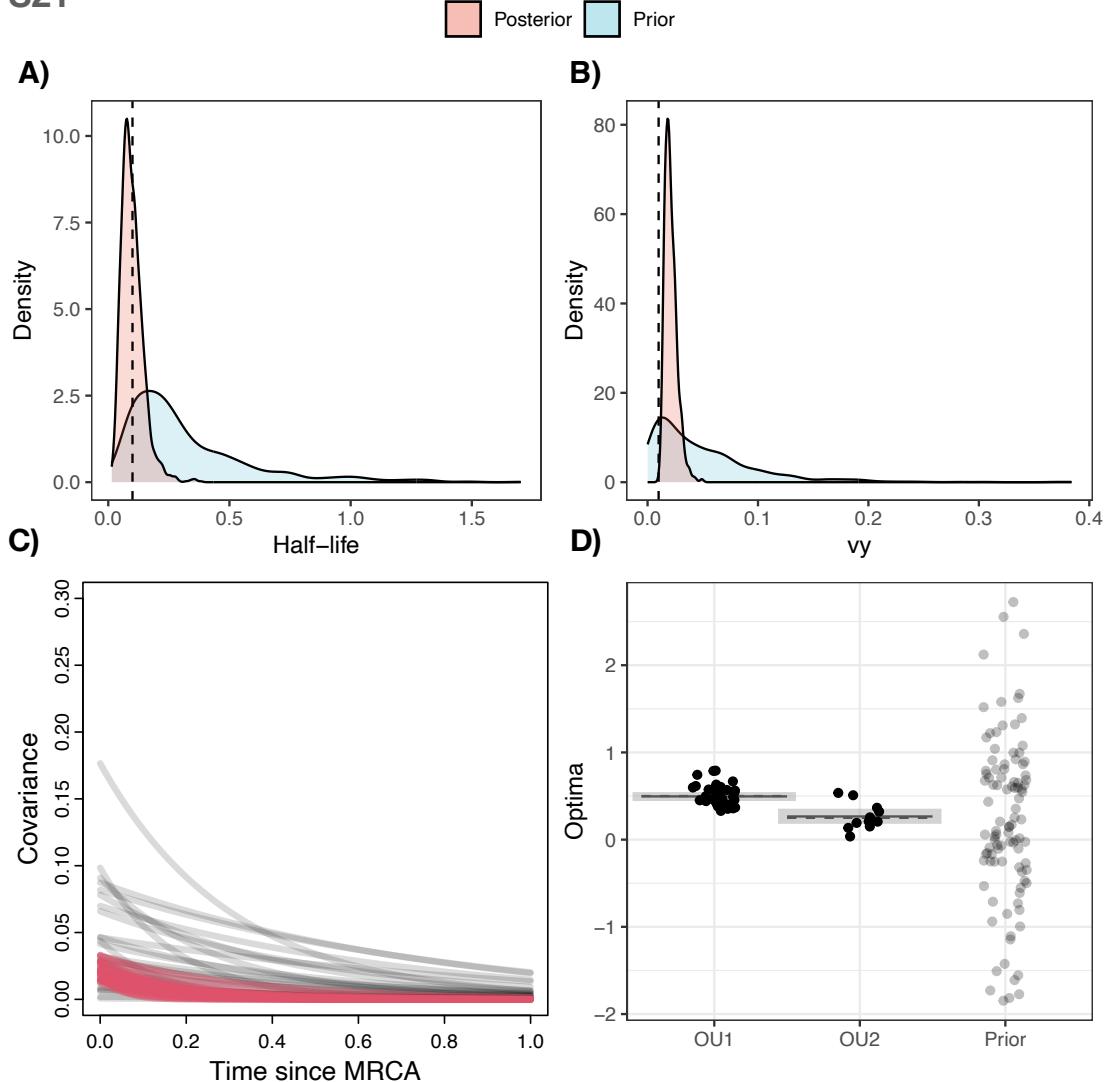


Fig. S21: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark great and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(0.5,0.25); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,1).

Table S21: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.10	0.00	0.05	0.04	0.07	0.09	0.12	0.23	854	1.00
vy	0.02	0.00	0.01	0.01	0.02	0.02	0.02	0.04	825	1.00
optima[1]	0.50	0.00	0.03	0.42	0.48	0.50	0.52	0.56	1283	1.00
optima[2]	0.26	0.00	0.06	0.15	0.23	0.27	0.30	0.37	1221	1.00

Medium half-life (hl=0.25)

Fig. S22

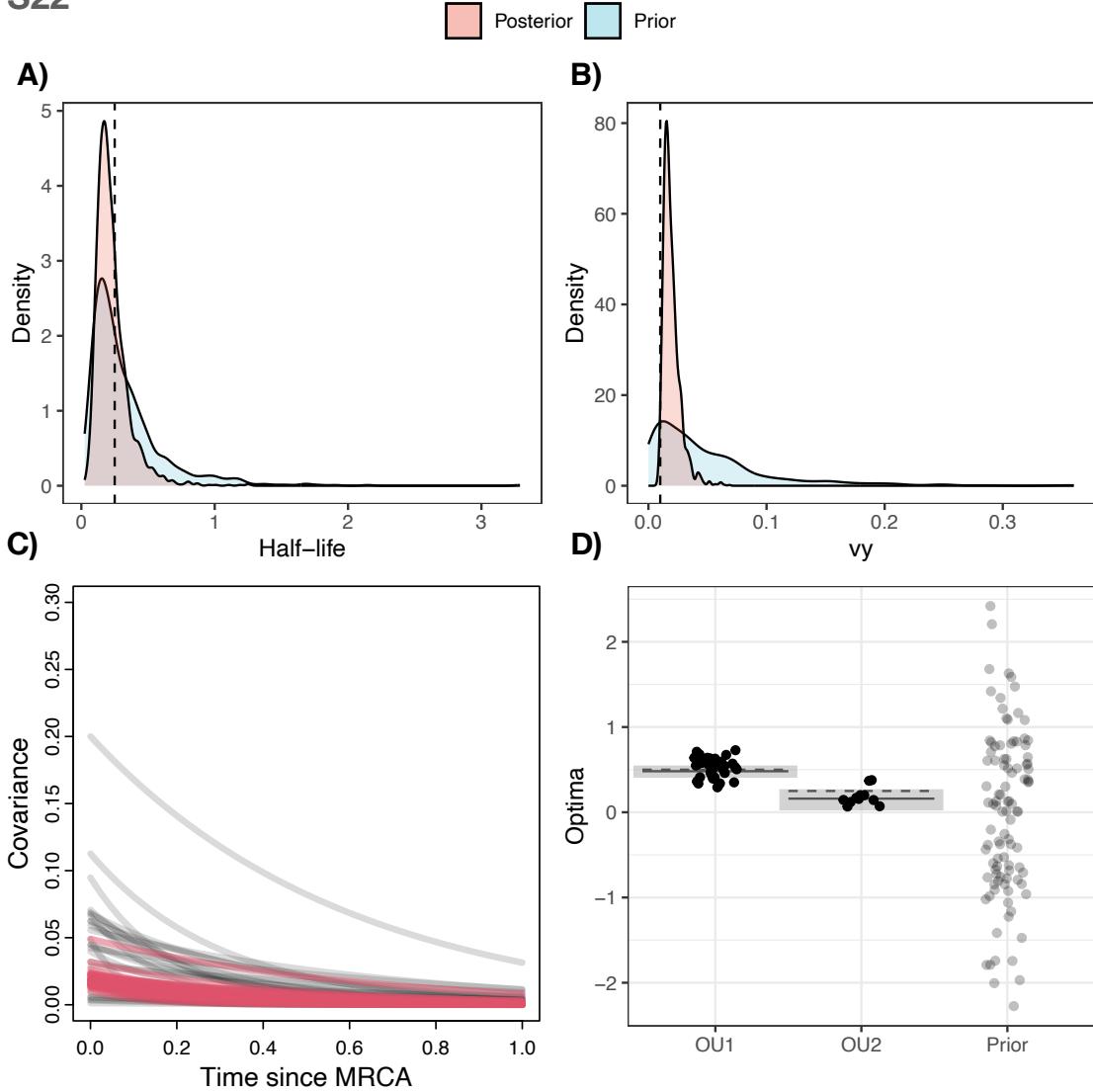


Fig. S22: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark grey and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(0.5,0.25); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,1).

Table S22: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.23	0.01	0.13	0.08	0.15	0.20	0.28	0.55	495	1.00
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	512	1.00
optima[1]	0.48	0.00	0.05	0.38	0.46	0.49	0.51	0.56	855	1.00
optima[2]	0.16	0.00	0.09	-0.02	0.12	0.17	0.21	0.30	685	1.00

Long half-life ($hl=0.75$)

Fig. S23

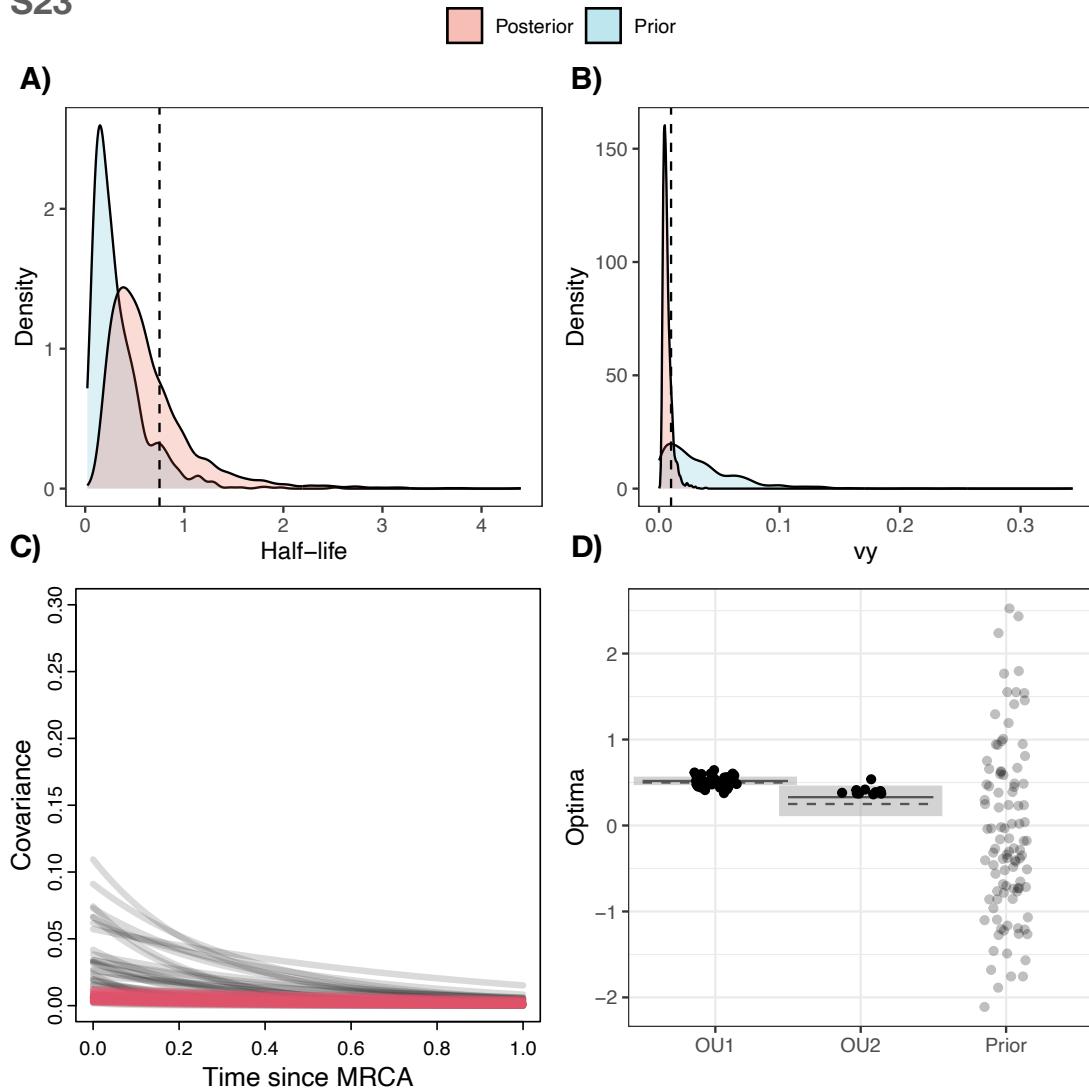


Fig. S23: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark great and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: $hl=0.75$, $vy=0.01$, $optima=(0.5,0.25)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $\beta \sim \text{normal}(0, 1)$.

Table S23: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	1.01	0.05	0.88	0.23	0.46	0.72	1.25	3.24	358	1.00
vy	0.01	0.00	0.01	0.00	0.01	0.01	0.02	0.05	355	1.01
optima[1]	0.49	0.00	0.04	0.40	0.47	0.50	0.52	0.59	941	1.00
optima[2]	0.10	0.01	0.28	-0.64	0.01	0.19	0.28	0.42	375	1.00

Four regimes

Short half-life ($hl=0.1$)

Fig. S24

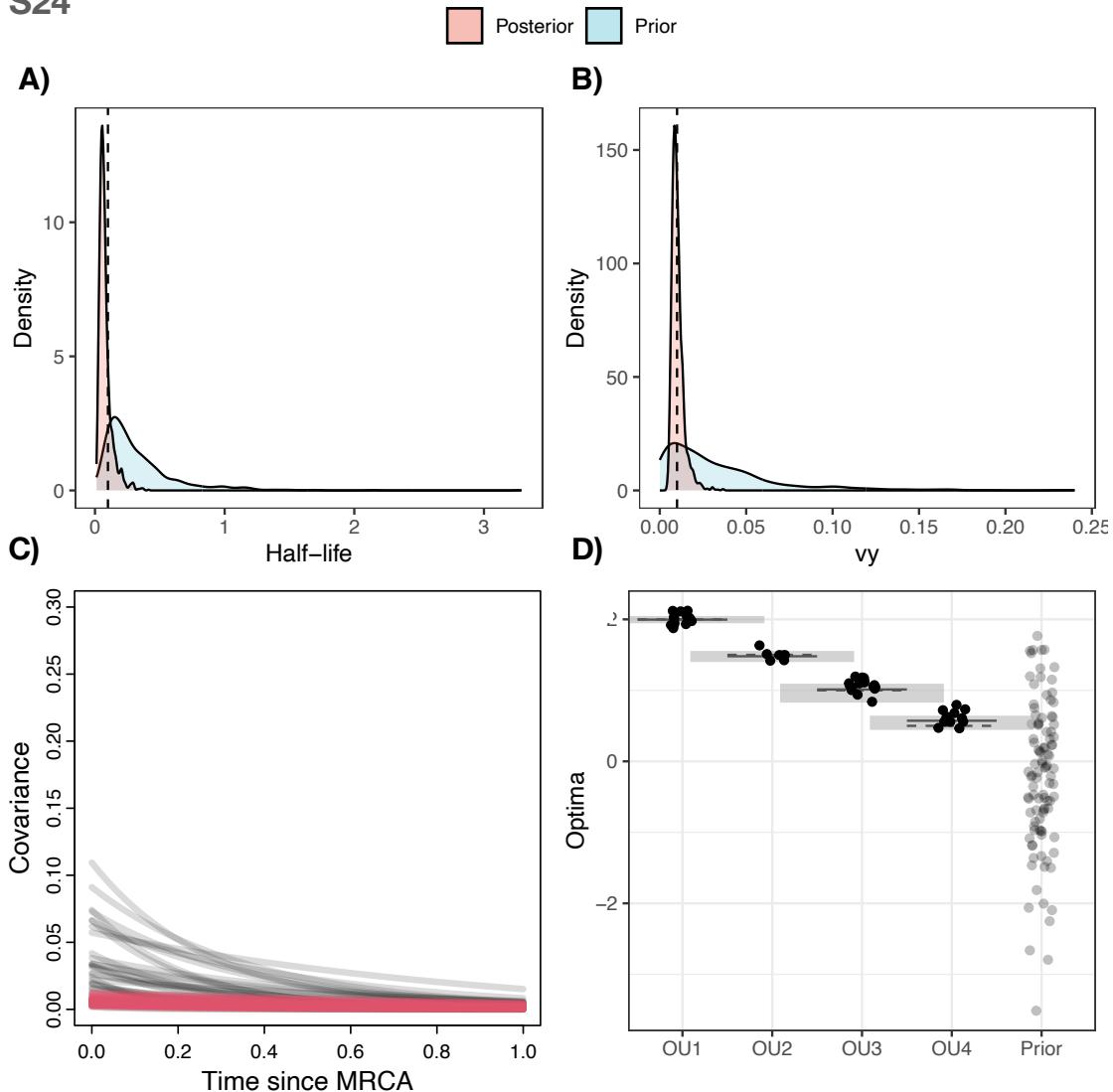


Fig. S24: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark grey and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: $hl=0.1$, $vy=0.01$, $optima=(2.0, 1.5, 1.0, 0.5)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(0, 1)$.

Table S24: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.08	0.00	0.05	0.02	0.05	0.07	0.09	0.21	155	1.01
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	223	1.01

optima[1]	2.00	0.00	0.03	1.93	1.98	2.00	2.02	2.06	1484	1.00
optima[2]	1.48	0.00	0.05	1.37	1.45	1.48	1.51	1.57	879	1.00
optima[3]	1.01	0.01	0.11	0.68	1.01	1.04	1.07	1.11	143	1.01
optima[4]	0.57	0.01	0.08	0.36	0.56	0.59	0.61	0.65	150	1.01

Medium half-life ($hl=0.25$)

Fig. S25

Posterior Prior

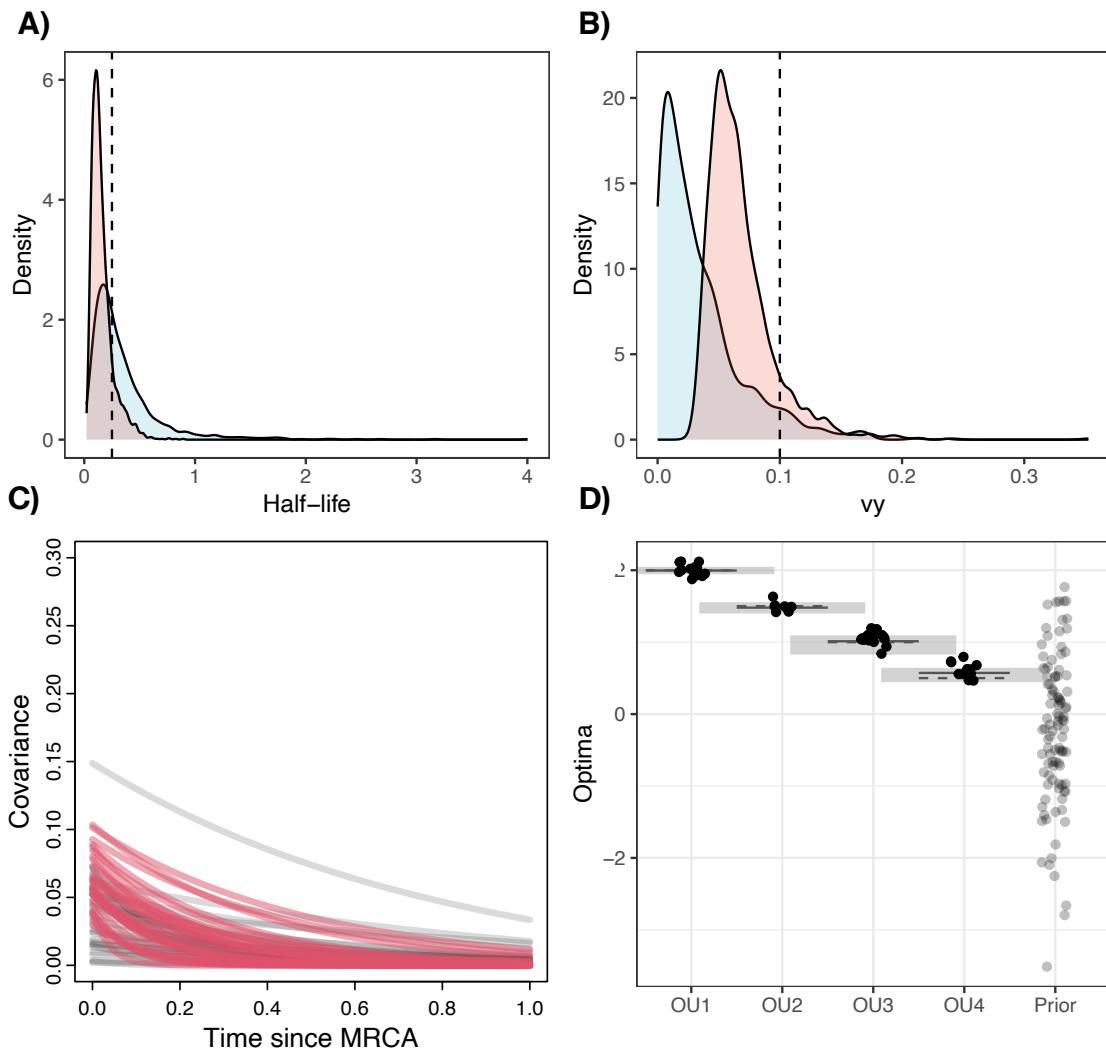


Fig. S25: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark great and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: $hl=0.25$, $vy=0.01$, $optima=(2.0, 1.5, 1.0, 0.5)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(0, 1)$.

Table S25: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.16	0.01	0.10	0.05	0.09	0.13	0.20	0.44	269	1.01
vy	0.07	0.00	0.03	0.04	0.05	0.06	0.08	0.14	295	1.01
optima[1]	1.95	0.00	0.10	1.73	1.89	1.95	2.01	2.13	970	1.00
optima[2]	1.56	0.01	0.16	1.22	1.49	1.58	1.66	1.81	778	1.00
optima[3]	1.16	0.01	0.27	0.43	1.09	1.23	1.32	1.45	379	1.01
optima[4]	0.51	0.01	0.25	-0.17	0.45	0.57	0.65	0.79	372	1.01

Long half-life (hl=0.75)

Fig. S26

Posterior Prior

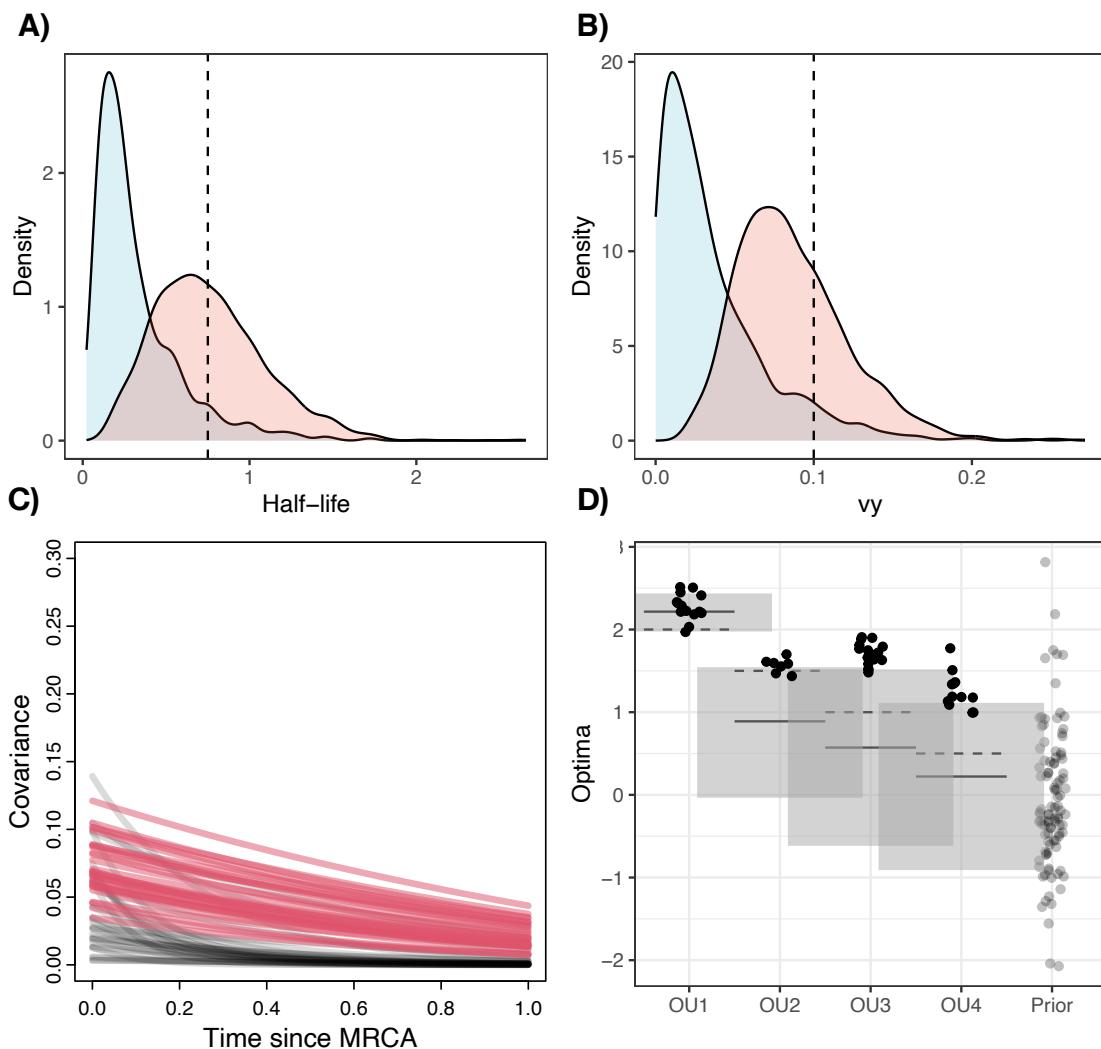


Fig. S26: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark great and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5,1.0,0.5); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(0,1).

Table S26: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.76	0.02	0.33	0.22	0.51	0.72	0.95	1.49	350	1.00
vy	0.09	0.00	0.03	0.03	0.06	0.08	0.11	0.17	425	1.00
optima[1]	2.22	0.00	0.14	1.92	2.13	2.23	2.31	2.48	1079	1.00
optima[2]	0.89	0.02	0.52	-0.37	0.60	0.98	1.28	1.61	501	1.00
optima[3]	0.57	0.03	0.68	-0.93	0.15	0.67	1.08	1.63	608	1.00
optima[4]	0.22	0.03	0.65	-1.23	0.19	0.31	0.71	1.21	488	1.00

Milestone 5: Combination Regime with Direct Effect Model without Measurement Error

Short half-life (hl=0.1)

Fig. S27

Posterior Prior

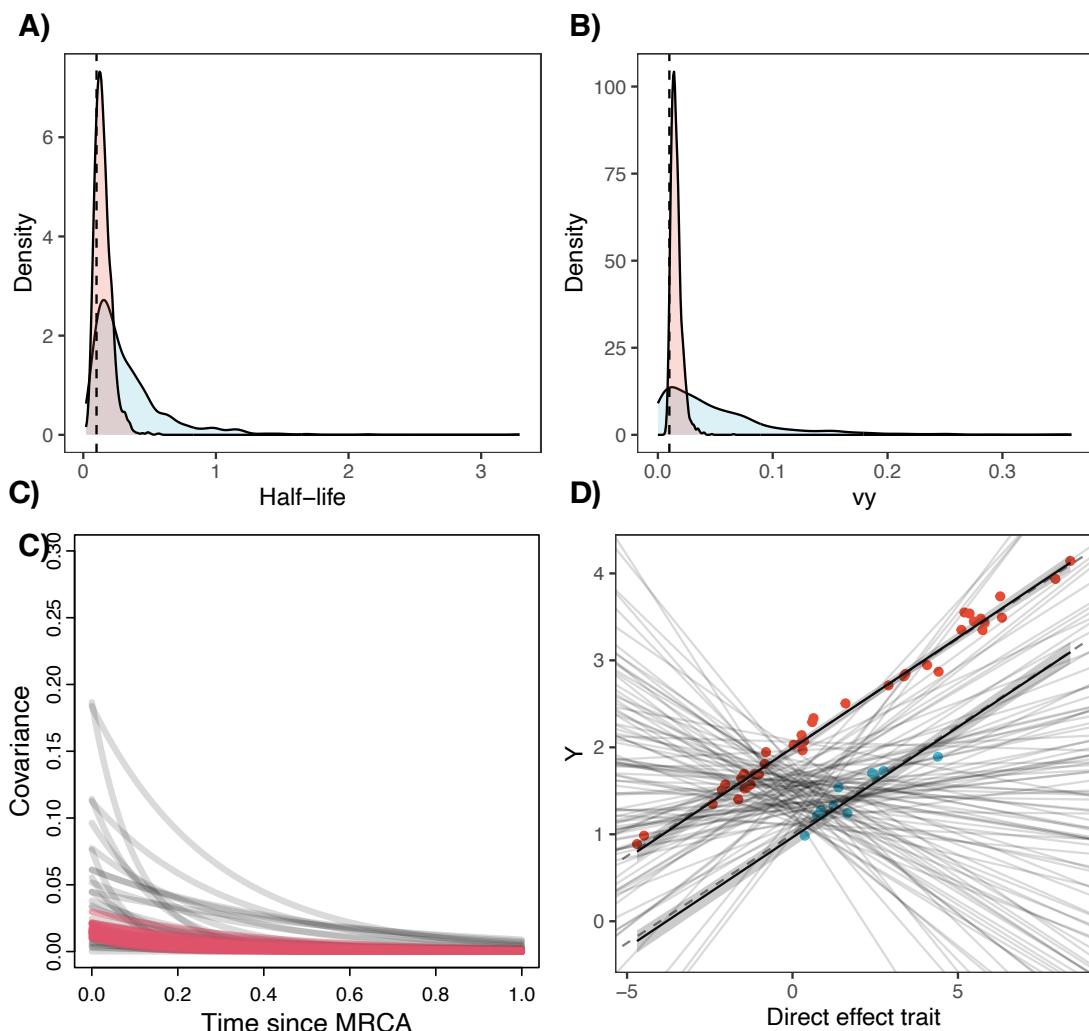


Fig. S27: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D)

Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(1.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S27: Summary table for half-life = 0.1. Direct effect slope is the first beta.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.15	0.00	0.06	0.06	0.11	0.14	0.18	0.31	651	1.00
vy	0.02	0.00	0.00	0.01	0.01	0.02	0.02	0.03	830	1.00
optima[1]	1.99	0.00	0.04	1.91	1.97	1.99	2.02	2.06	911	1.00
optima[2]	0.96	0.00	0.06	0.82	0.93	0.97	1.01	1.07	1111	1.00
beta[1]	0.25	0.00	0.01	0.24	0.25	0.25	0.26	0.27	983	1.00

Medium half-life (hl=0.25)

Fig. S28

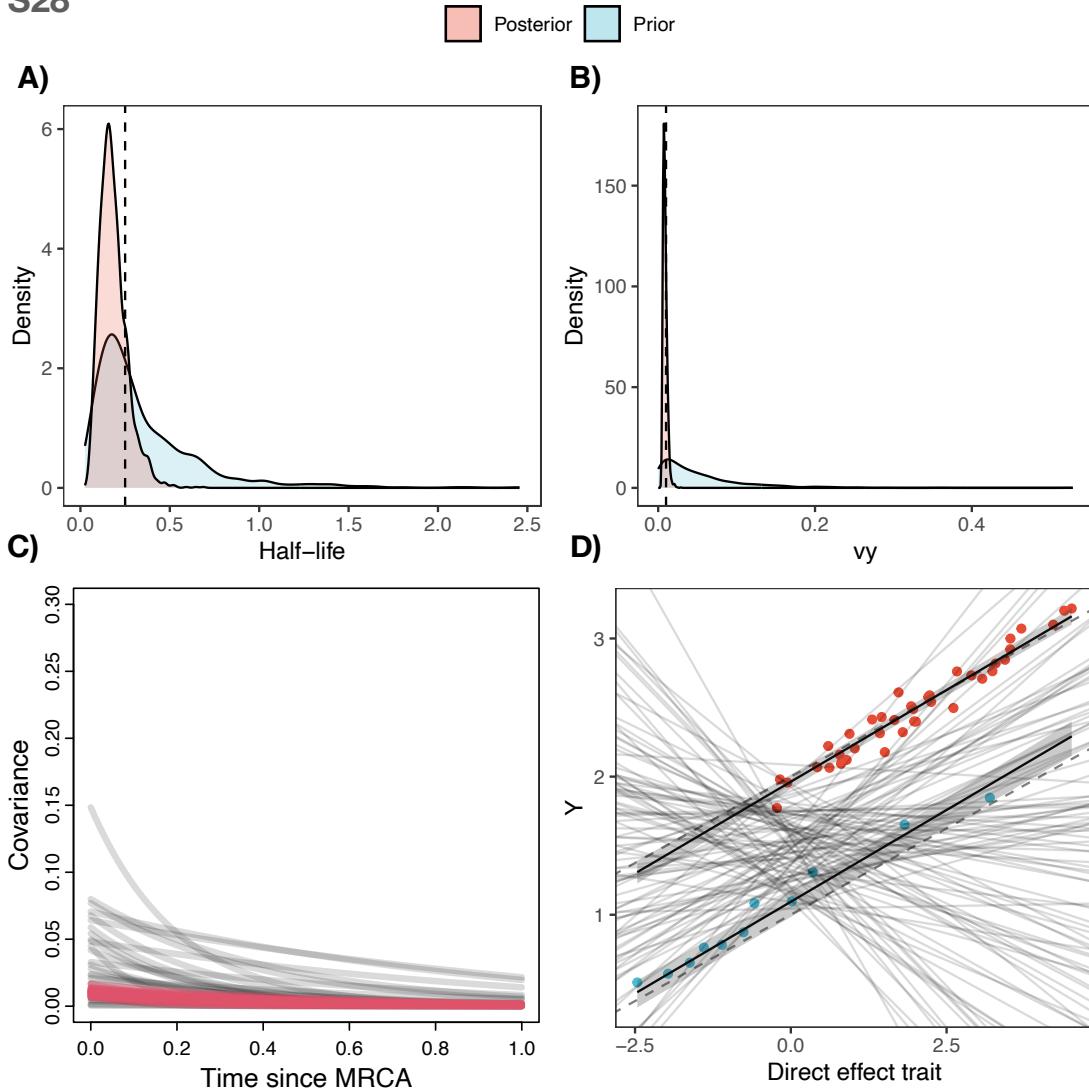


Fig. S28: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(1.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S28: Summary table for half-life = 0.25. Direct effect slope is the first beta.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.18	0.00	0.08	0.07	0.13	0.17	0.22	0.38	691	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.01	743	1.00
optima[1]	1.96	0.00	0.03	1.90	1.94	1.96	1.98	2.03	1009	1.00
optima[2]	1.09	0.00	0.06	0.94	1.07	1.10	1.13	1.18	960	1.00
beta[1]	0.27	0.00	0.01	0.25	0.26	0.27	0.27	0.29	1392	1.00

Long half-life ($hl=0.75$)

Fig. S29

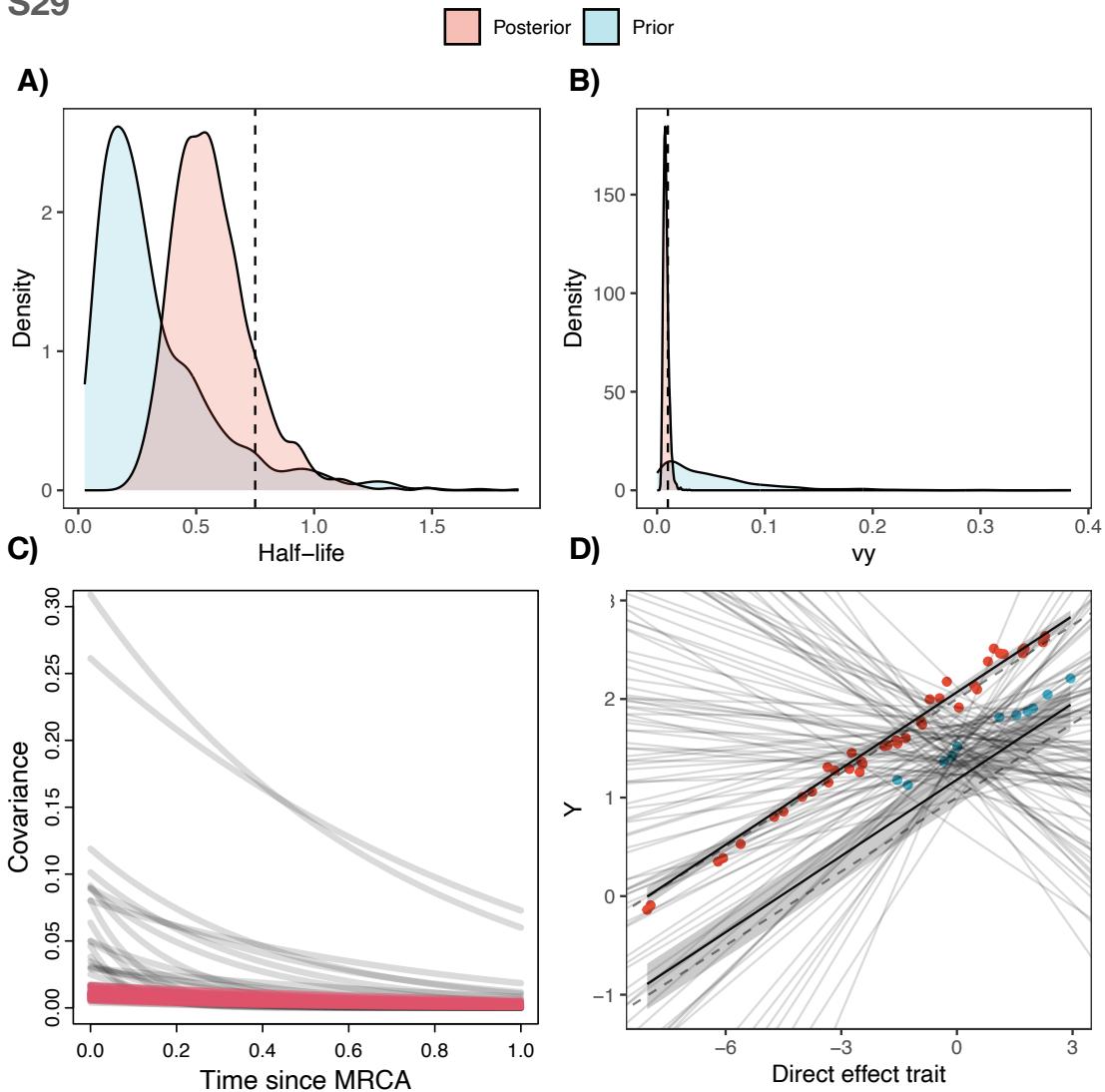


Fig. S29: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: $hl=0.75$, $vy=0.01$, $optima=(1.5,0.25)$, $\beta=0.25$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(1.5, 0.5)$, $\beta \sim \text{normal}(0, 0.25)$.

Table S29: Summary table for half-life = 0.75. Direct effect slope is the first beta.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.57	0.01	0.17	0.31	0.45	0.55	0.66	0.97	791	1.01
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.01	859	1.01
optima[1]	2.07	0.00	0.04	1.99	2.05	2.07	2.09	2.14	1281	1.00
optima[2]	1.18	0.00	0.14	0.86	1.10	1.20	1.28	1.41	907	1.00

beta[1]	0.26	0.00	0.01	0.24	0.25	0.26	0.26	0.27	1526	1.00
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Milestone 5: Combination Regime with Direct Effect Model with Measurement Error

Short half-life ($hl=0.1$)

Fig. S30

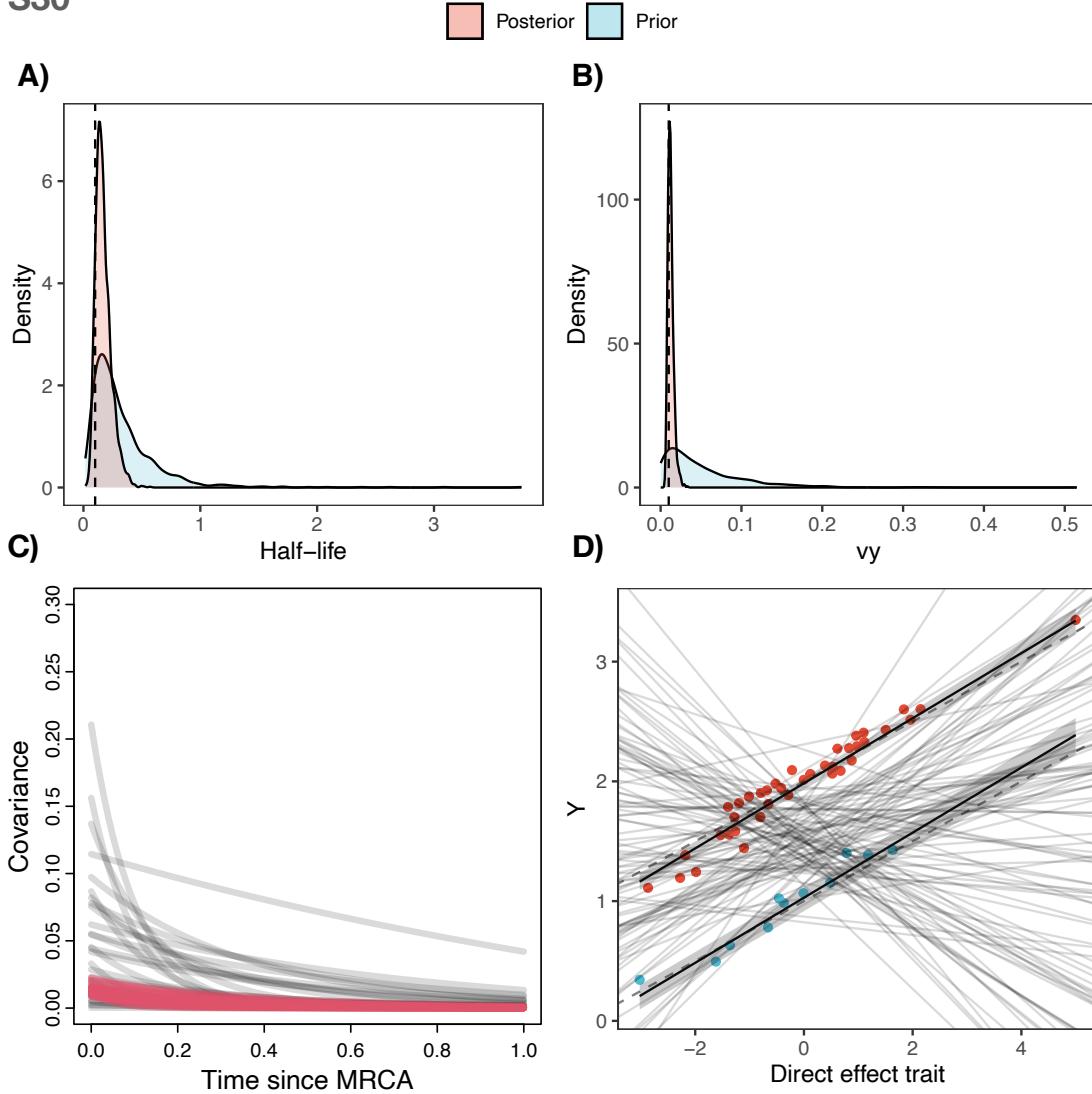


Fig. S30: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: $hl=0.1$, $vy=0.01$, optima=(1.5,0.25), beta=0.25; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; optima $\sim \text{normal}(1.5, 0.5)$, beta $\sim \text{normal}(0, 0.25)$.

Table S30: Summary table for half-life = 0.1. Direct effect slope is the first beta.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.17	0.00	0.07	0.07	0.12	0.16	0.21	0.34	962	1.00

vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	1084	1.00
optima[1]	1.98	0.00	0.03	1.91	1.97	1.99	2.00	2.04	1396	1.00
optima[2]	1.03	0.00	0.06	0.88	1.00	1.03	1.07	1.13	1298	1.00
beta[1]	0.27	0.00	0.01	0.25	0.26	0.27	0.28	0.29	1630	1.00

Medium half-life (hl=0.25)

Fig. S31

Posterior Prior

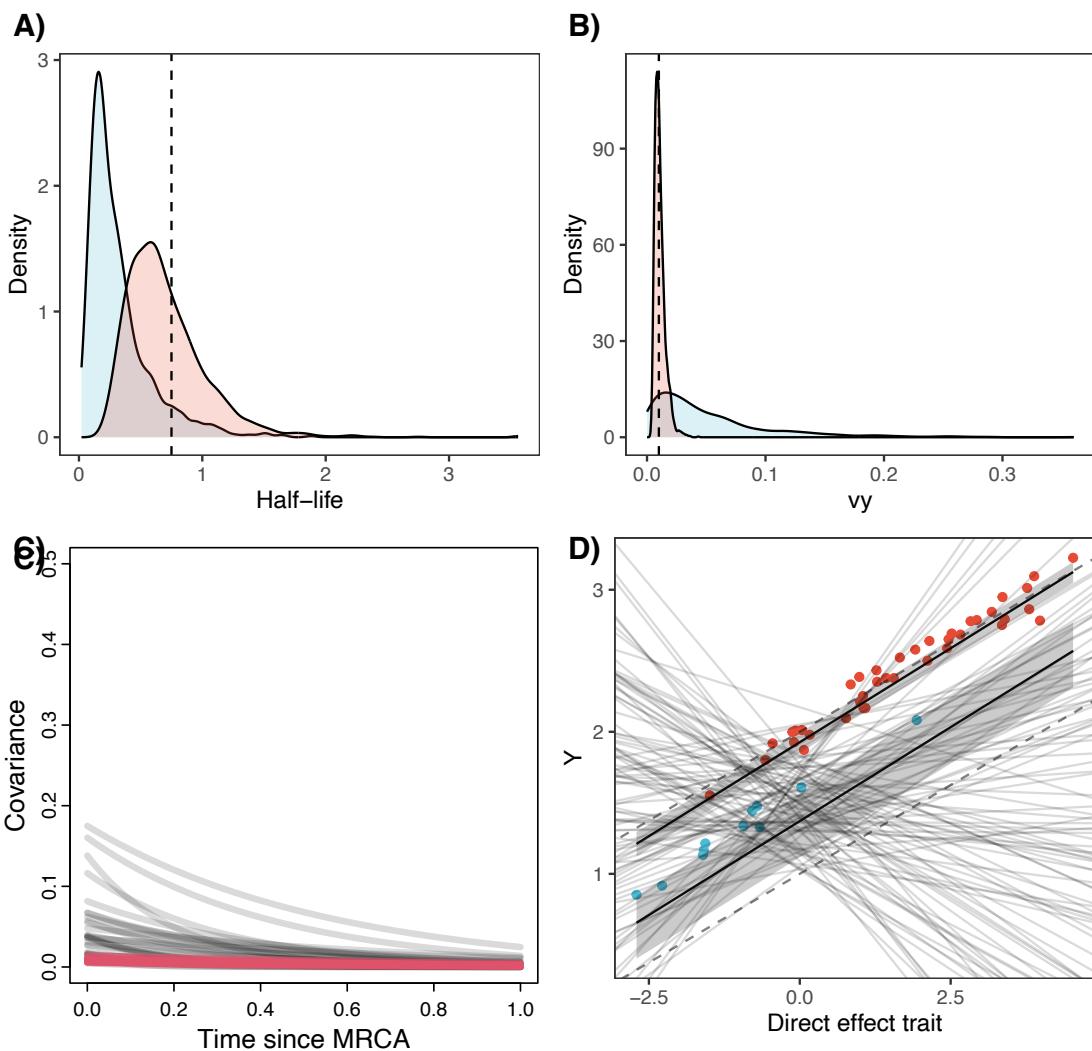


Fig. S31: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(1.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S31: Summary table for half-life = 0.25. Direct effect slope is the first beta.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
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hl	0.26	0.00	0.09	0.12	0.19	0.24	0.31	0.48	1422	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	1589	1.00
optima[1]	1.97	0.00	0.03	1.89	1.95	1.97	1.99	2.03	2401	1.00
optima[2]	0.99	0.00	0.09	0.77	0.94	1.00	1.05	1.12	1723	1.00
beta[1]	0.25	0.00	0.01	0.23	0.24	0.25	0.25	0.26	3417	1.00

Long half-life (hl=0.75)

Fig. S32

Posterior Prior

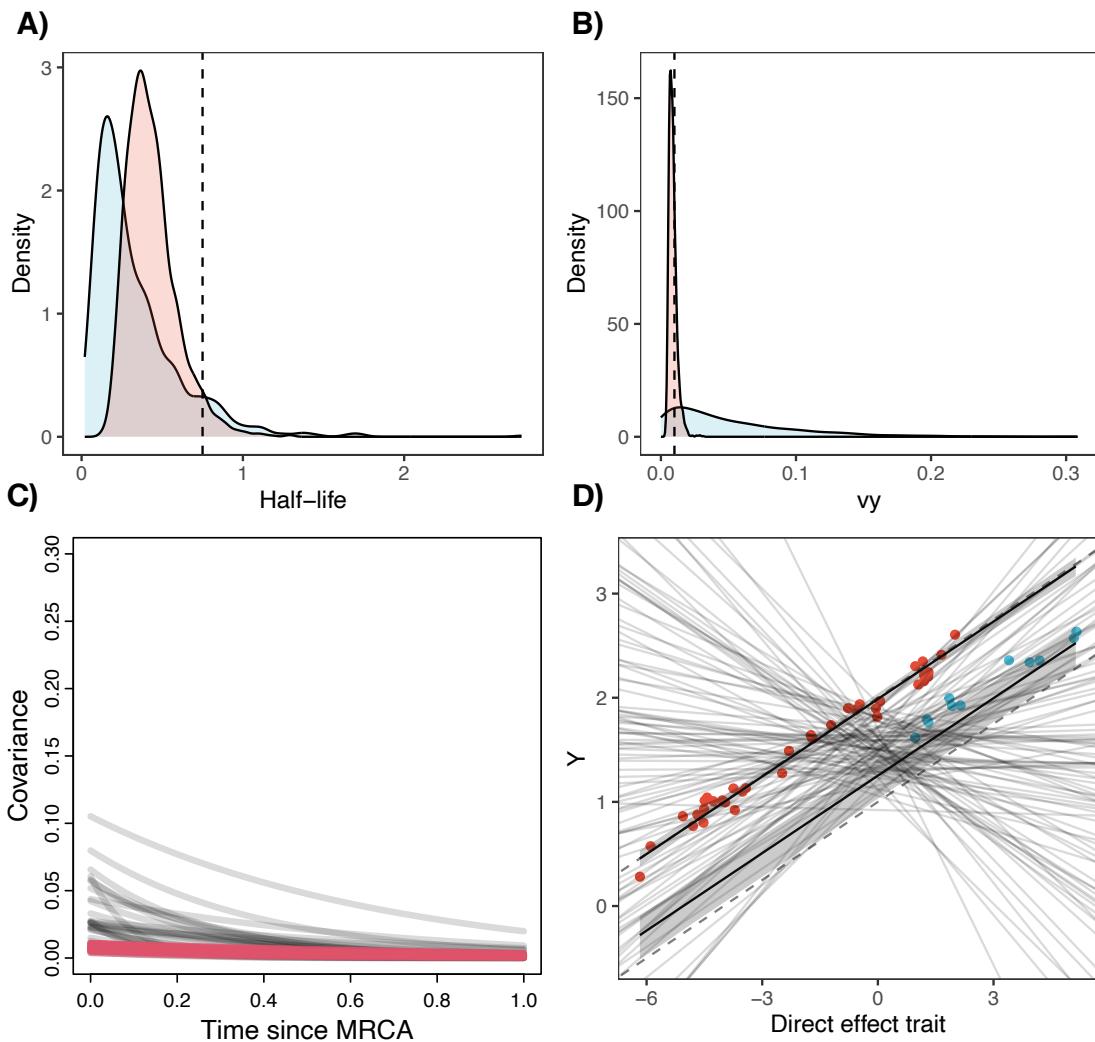


Fig. S32: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.0), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S32: Summary table for half-life = 0.75. Direct effect slope is the first beta.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.70	0.01	0.31	0.28	0.47	0.64	0.86	1.46	1159	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	1123	1.00
optima[1]	1.93	0.00	0.05	1.83	1.90	1.93	1.96	2.01	2411	1.00
optima[2]	1.37	0.00	0.14	1.06	1.29	1.39	1.47	1.59	1830	1.00
beta[1]	0.26	0.00	0.01	0.25	0.26	0.26	0.27	0.28	3348	1.00

Milestone 6: Regime model with Adaptive Predictors without Measurement Error

Short half-life ($hl=0.1$)

Fig. S33

■ Posterior ■ Prior

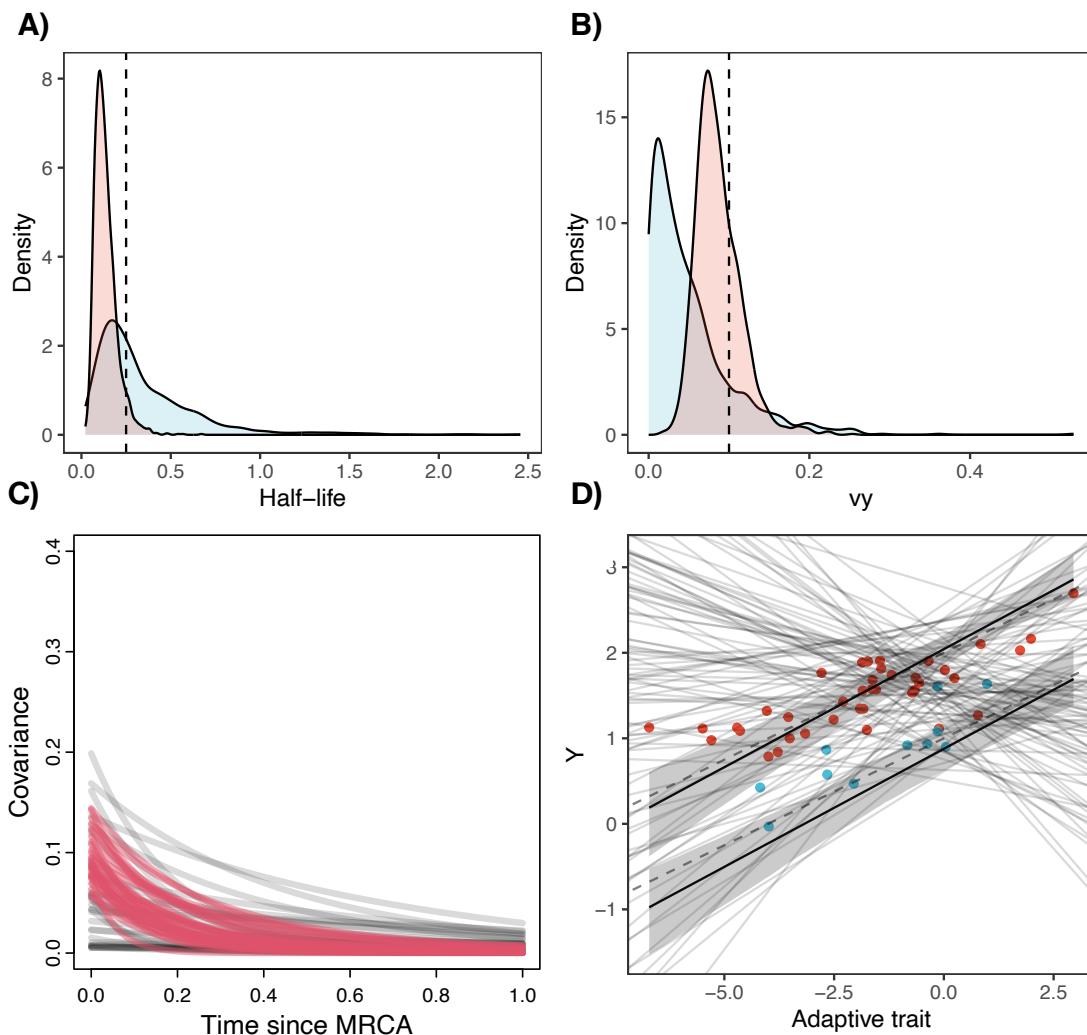


Fig. S33: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: $hl=0.1$, $vy=0.1$, $\text{optima}=(1.5,0.25)$, $\text{beta}=0.25$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $\text{optima} \sim \text{normal}(1.5, 0.5)$, $\text{beta} \sim \text{normal}(0, 0.25)$.

Table S33: Summary table for half-life = 0.1. Estimated optima are followed by adaptation slope (beta), and evolutionary slope (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.14	0.00	0.06	0.05	0.09	0.12	0.16	0.29	713	1.00
vy	0.09	0.00	0.03	0.04	0.07	0.08	0.10	0.15	1639	1.00
optima[1]	2.04	0.00	0.11	1.81	1.98	2.04	2.11	2.25	1827	1.00
optima[2]	0.88	0.00	0.17	0.56	0.77	0.87	0.98	1.23	1754	1.00
beta[1]	0.28	0.00	0.04	0.21	0.25	0.27	0.30	0.38	700	1.00
beta_e[1]	0.22	0.00	0.02	0.18	0.21	0.22	0.24	0.27	1688	1.00

Medium half-life (hl=0.25)

Fig. S34

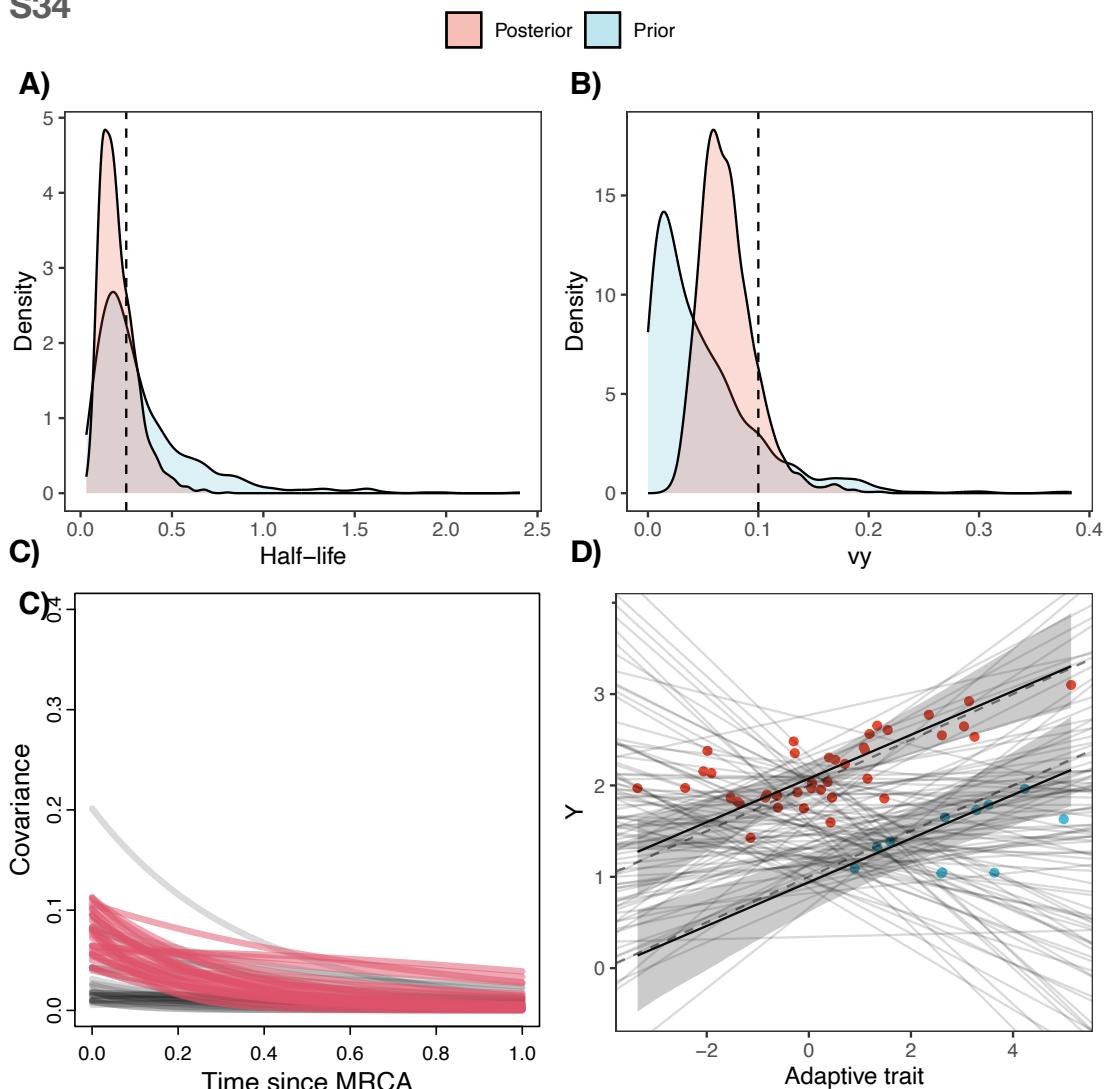


Fig. S34: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this

simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $optima=(1.5,0.25)$, $\beta=0.25$; Priors: $hl \sim \text{lognormal}(\text{log}(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(1.5, 0.5)$, $\beta \sim \text{normal}(0, 0.25)$.

Table S34: Summary table for half-life = 025. Estimated optima are followed by adaptation slope (beta), and evolutionary slope (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.20	0.00	0.10	0.07	0.13	0.18	0.26	0.47	745	1.00
vy	0.07	0.00	0.03	0.03	0.05	0.07	0.09	0.13	1038	1.00
optima[1]	2.08	0.00	0.12	1.83	2.01	2.08	2.15	2.30	1341	1.00
optima[2]	0.94	0.01	0.21	0.51	0.81	0.95	1.08	1.31	1150	1.00
beta[1]	0.24	0.00	0.07	0.14	0.19	0.23	0.27	0.40	774	1.00
beta_e[1]	0.17	0.00	0.03	0.11	0.15	0.17	0.19	0.22	1303	1.00

Long half-life ($hl=0.75$)

Fig. S35

Posterior Prior

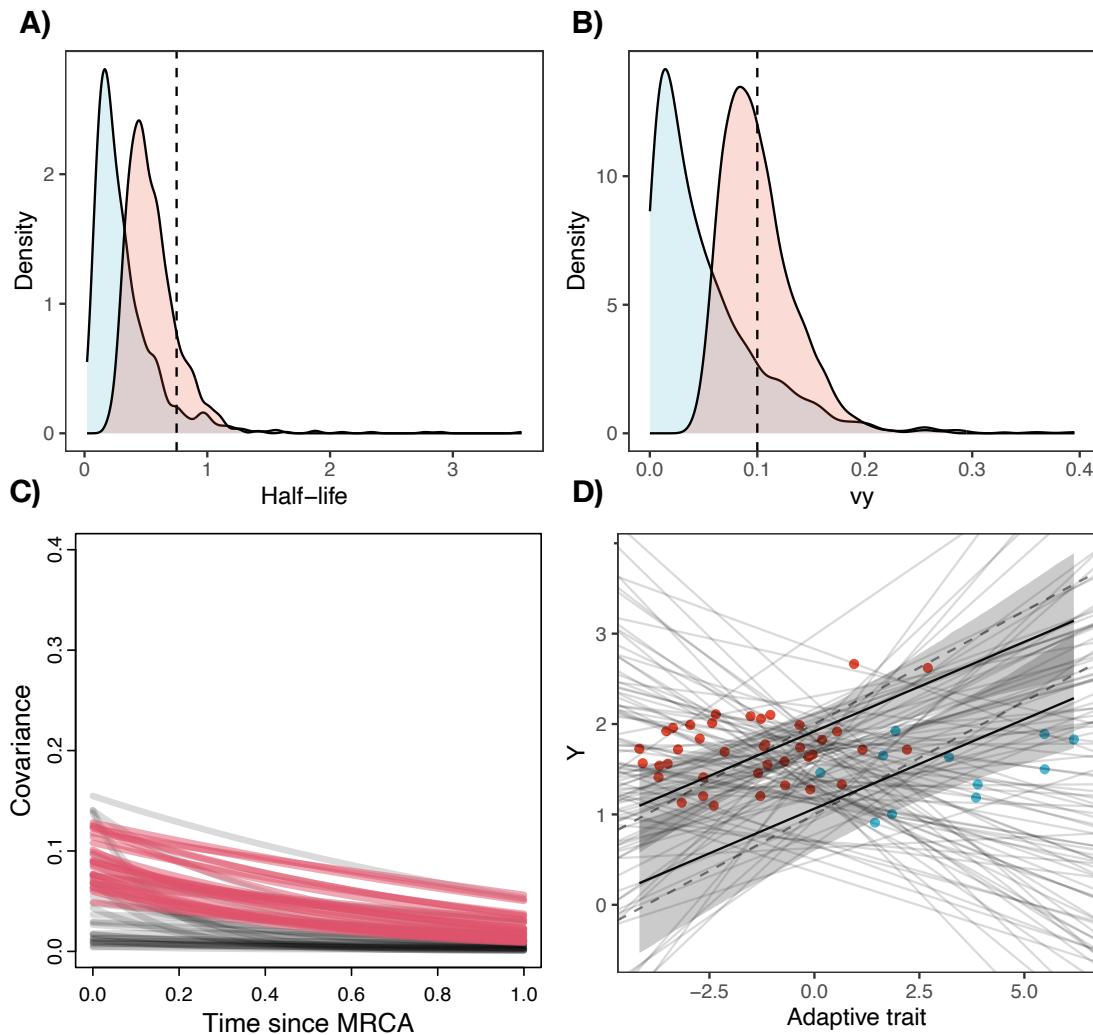


Fig. S35: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.1, optima=(1.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S35: Summary table for half-life = 0.75. Estimated optima are followed by adaptation slope (beta), and evolutionary slope (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.55	0.01	0.20	0.28	0.40	0.51	0.65	1.02	989	1.00
vy	0.10	0.00	0.03	0.05	0.08	0.10	0.12	0.18	1189	1.00
optima[1]	1.92	0.00	0.14	1.62	1.82	1.92	2.02	2.18	1447	1.00
optima[2]	1.06	0.01	0.29	0.48	0.87	1.06	1.26	1.63	1341	1.00
beta[1]	0.20	0.00	0.06	0.09	0.15	0.19	0.23	0.34	1135	1.00
beta_e[1]	0.09	0.00	0.02	0.05	0.07	0.09	0.10	0.13	2076	1.00

Milestone 6: Regime model with Adaptive Predictors with Measurement Error

Short half-life (hl=0.1)

Fig. S36

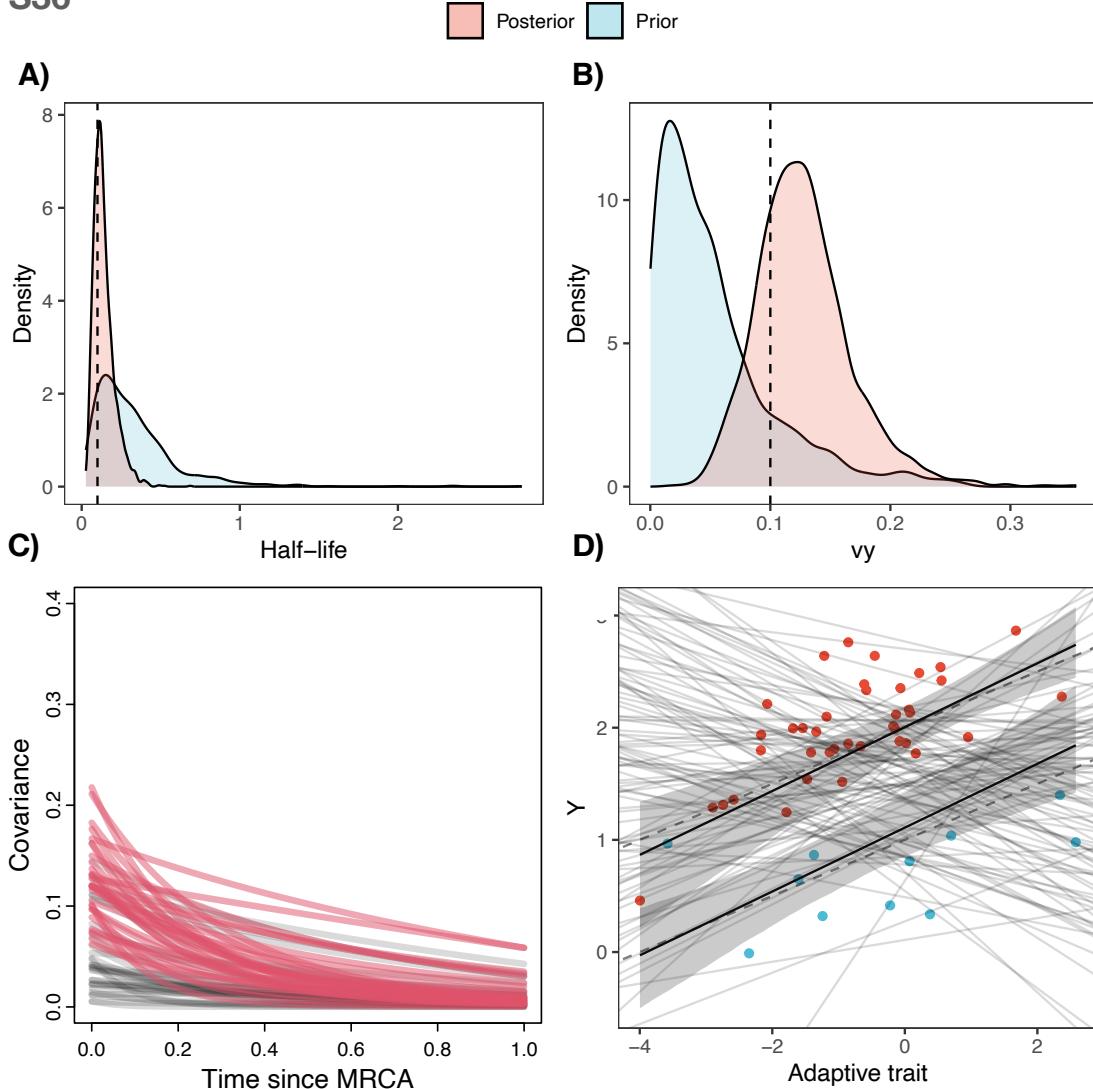


Fig. S36: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.1, optima=(1.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S36: Summary table for half-life = 0.1. Estimated optima are followed by adaptation slope (beta), and evolutionary slope (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.14	0.00	0.07	0.05	0.09	0.13	0.17	0.31	1495	1.00
vy	0.13	0.00	0.04	0.06	0.10	0.12	0.15	0.22	2839	1.00
optima[1]	2.00	0.00	0.13	1.73	1.93	2.02	2.09	2.22	2144	1.00
optima[2]	1.11	0.00	0.17	0.80	0.99	1.10	1.21	1.49	2540	1.00
beta[1]	0.28	0.00	0.08	0.16	0.23	0.28	0.33	0.46	1734	1.00

beta_e[1]	0.22	0.00	0.05	0.14	0.19	0.22	0.25	0.31	2415	1.00
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Medium half-life ($hl=0.25$)

Fig. S37

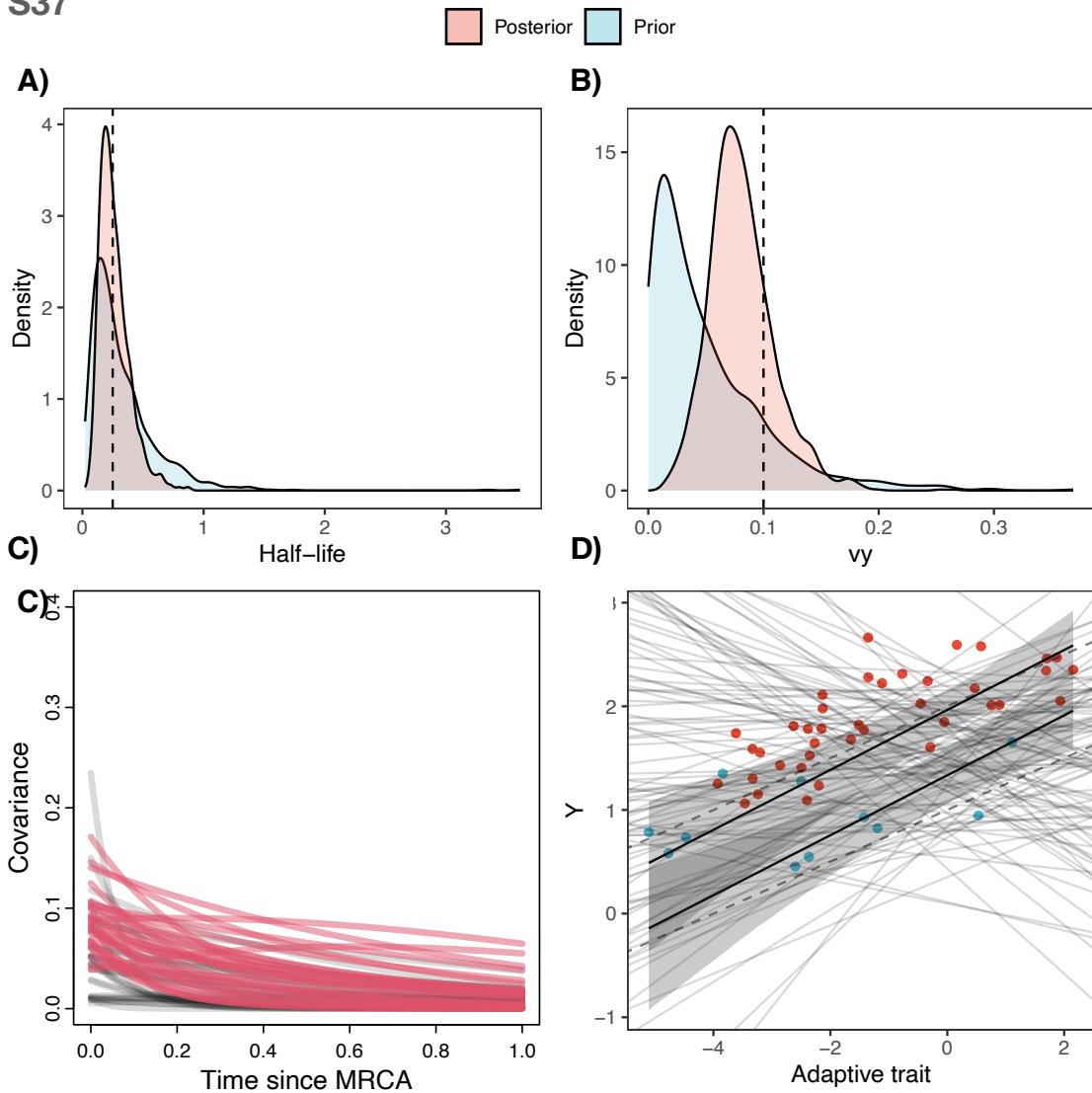


Fig. S37: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $optima=(1.5,0.25)$, $\beta=0.25$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(1.5, 0.5)$, $\beta \sim \text{normal}(0, 0.25)$.

Table S37: Summary table for half-life = 0.25. Estimated optima are followed by adaptation slope (beta), and evolutionary slope (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
-----------	------	---------	----	-------	-----	-----	-----	--------	-------	------

hl	0.26	0.00	0.13	0.10	0.18	0.24	0.33	0.59	902	1.00
vy	0.08	0.00	0.03	0.03	0.06	0.08	0.10	0.15	1867	1.00
optima[1]	1.97	0.00	0.13	1.69	1.89	1.97	2.05	2.21	2280	1.00
optima[2]	1.33	0.00	0.17	0.99	1.22	1.33	1.45	1.66	2505	1.00
beta[1]	0.29	0.00	0.08	0.17	0.23	0.28	0.33	0.49	834	1.00
beta_e[1]	0.18	0.00	0.03	0.13	0.16	0.18	0.20	0.24	2008	1.00

Long half-life (hl=0.75)

Fig. S38

Posterior Prior

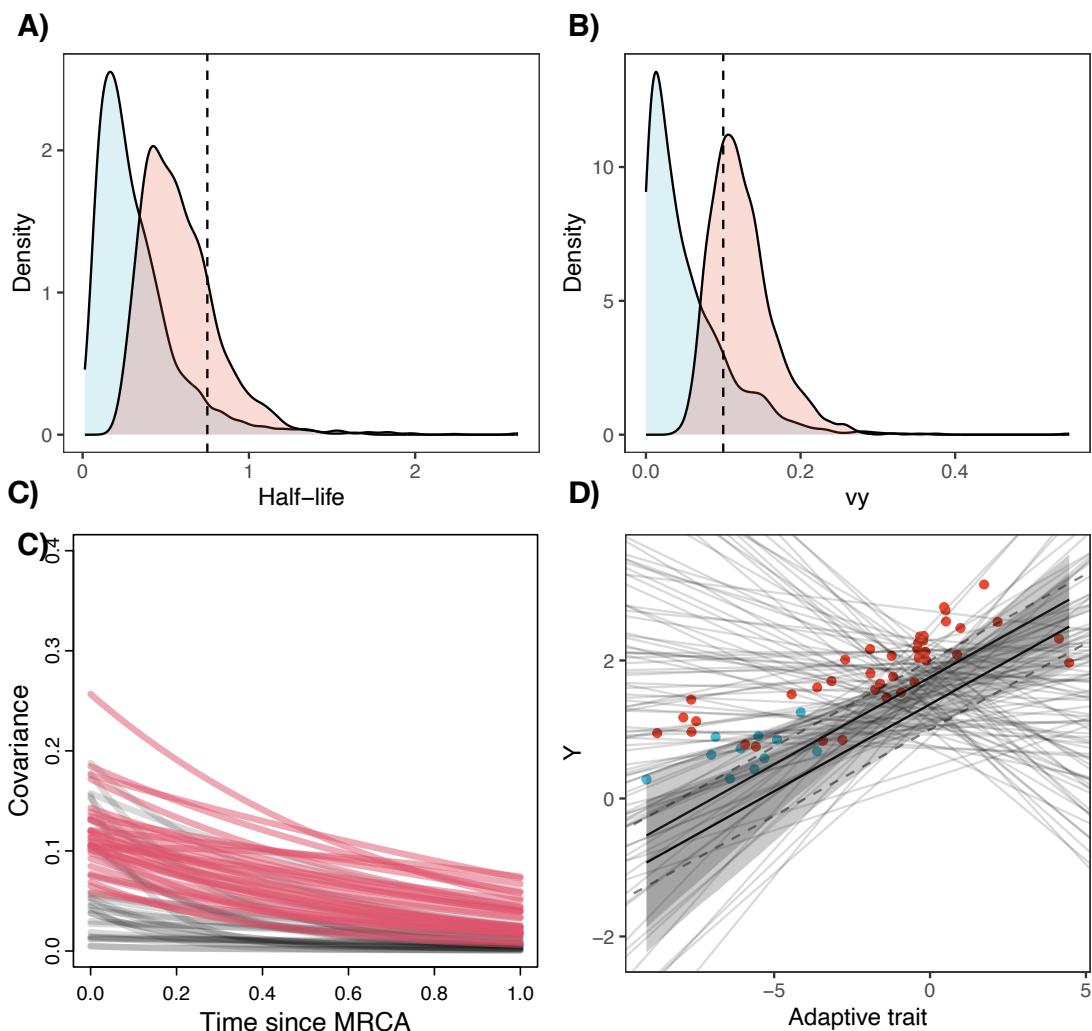


Fig. S38: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptation model with estimated optima, with priors in light grey. Species values are shown in the dark circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.1, optima=(1.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25).

Table S38: Summary table for half-life = 0.75. Estimated optima are followed by adaptation slope (beta), and evolutionary slope (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.58	0.00	0.22	0.27	0.42	0.55	0.70	1.11	1996	1.00
vy	0.12	0.00	0.04	0.07	0.10	0.12	0.14	0.22	2349	1.00
optima[1]	1.76	0.00	0.16	1.42	1.66	1.76	1.86	2.04	4239	1.00
optima[2]	1.36	0.00	0.21	0.95	1.22	1.36	1.51	1.77	4877	1.00
beta[1]	0.25	0.00	0.08	0.14	0.20	0.24	0.29	0.44	2194	1.00
beta_e[1]	0.11	0.00	0.02	0.06	0.09	0.11	0.12	0.15	2918	1.00

Milestone 7: Combination Regime with Direct and Adaptive Predictor Model without Measurement Error

Short half-life (hl=0.1)

Fig. S39

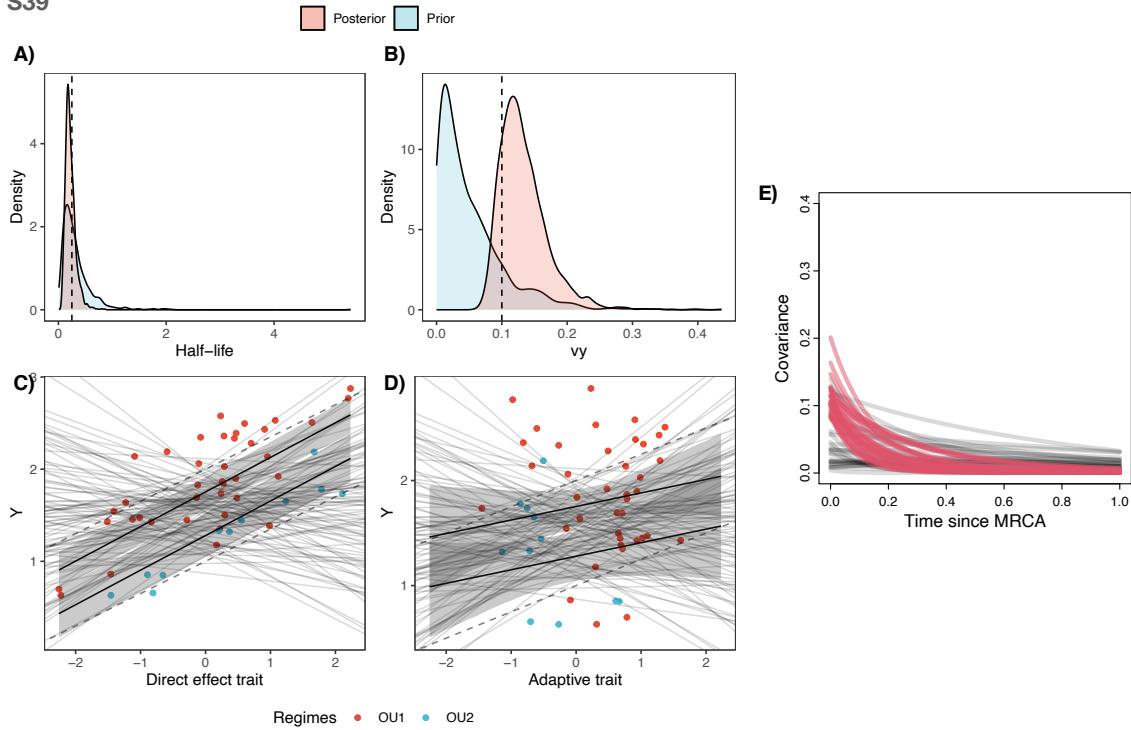


Figure S39: Prior vs. posterior for A) Half-life, B) vy, C,D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for C) direct effect and D) adaptive models by estimated optima, with priors in light grey. Species values are shown in the dark circles; and E) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line). For this simulation parameter values were set to: hl=0.1, vy=0.1, alpha=2, optima=(2,1), beta=(0.35,0.25); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.25); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S39: Summary table for half-life = 0.1. Direct effect slope is the first beta, followed by adaptation slope, and evolutionary slope last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.11	0.00	0.05	0.04	0.07	0.10	0.13	0.22	809	1.00
vy	0.10	0.00	0.03	0.06	0.08	0.10	0.11	0.17	1095	1.00
optima[1]	1.95	0.00	0.08	1.78	1.90	1.95	1.99	2.09	1613	1.00
optima[2]	1.16	0.00	0.12	0.94	1.08	1.15	1.24	1.41	1820	1.00
beta[1]	0.33	0.00	0.04	0.24	0.30	0.33	0.36	0.41	1576	1.00
beta[2]	0.21	0.00	0.08	0.06	0.16	0.21	0.26	0.39	1457	1.00
beta_e[1]	0.18	0.00	0.06	0.06	0.14	0.18	0.22	0.31	1795	1.00

Medium half-life ($hl=0.25$)

Fig. S40

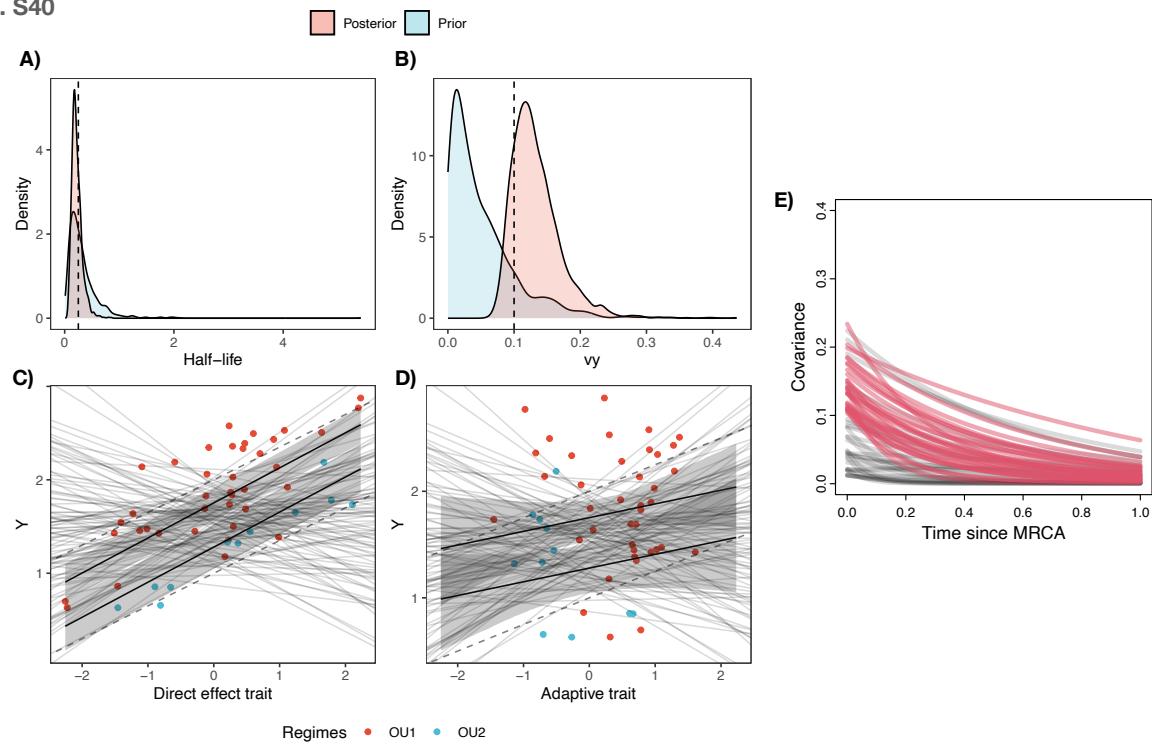


Figure S40: Prior vs. posterior for A) Half-life, B) vy, C,D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for C) direct effect and D) adaptive models by estimated optima, with priors in light grey. Species values are shown in the dark circles; and E) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line). For this simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $\alpha=2$, $optima=(2,1)$, $\beta=(0.35,0.25)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(1.5, 0.25)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S40: Summary table for half-life = 0.25. Direct effect slope is the first beta, followed by adaptation slope, and evolutionary slope last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.22	0.00	0.10	0.09	0.16	0.20	0.27	0.46	1102	1.00
vy	0.13	0.00	0.04	0.08	0.11	0.13	0.15	0.23	1303	1.00

optima[1]	1.75	0.00	0.11	1.51	1.69	1.76	1.82	1.95	1390	1.00
optima[2]	1.28	0.00	0.15	0.99	1.17	1.28	1.38	1.59	1871	1.00
beta[1]	0.38	0.00	0.03	0.32	0.36	0.38	0.39	0.43	2457	1.00
beta[2]	0.13	0.00	0.12	-0.09	0.05	0.12	0.20	0.38	1722	1.00
beta_e[1]	0.09	0.00	0.08	-0.07	0.04	0.09	0.14	0.24	2230	1.00

Long half-life ($hl=0.75$)

Fig. S41

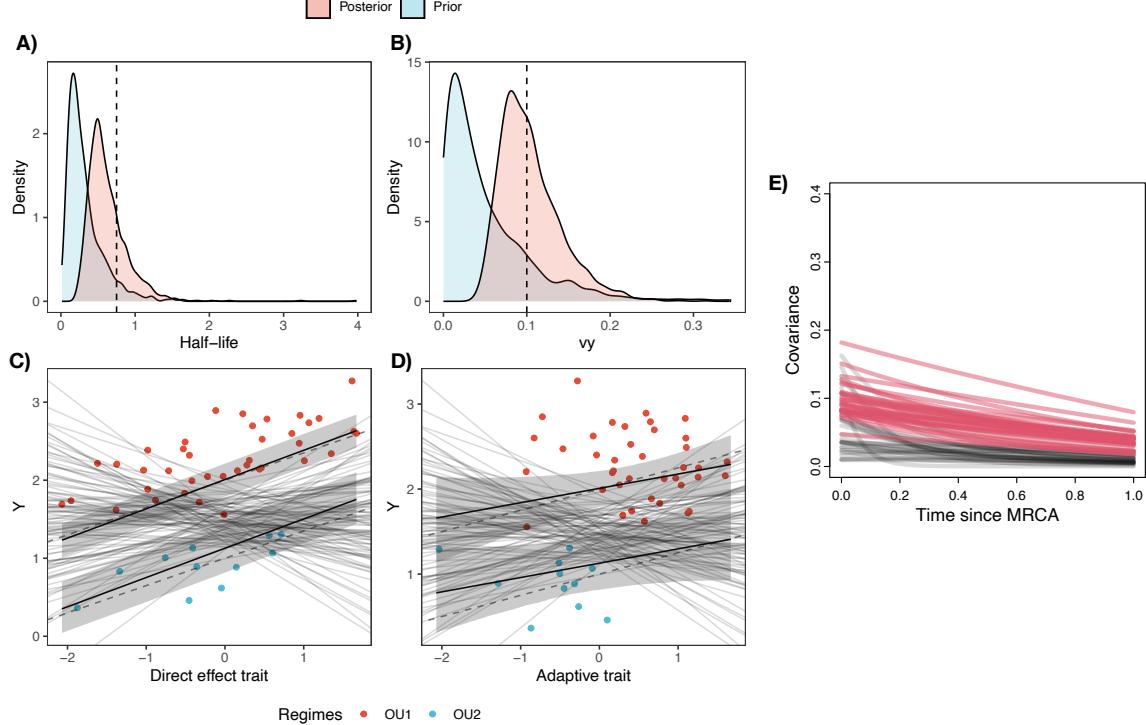


Figure S41: Prior vs. posterior for A) Half-life, B) vy, C,D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for C) direct effect and D) adaptive models by estimated optima, with priors in light grey. Species values are shown in the dark circles; and E) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line). For this simulation parameter values were set to: $hl=0.75$, $vy=0.1$, $\alpha=2$, $optima=(2,1)$, $\beta=(0.35,0.25)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(1.5, 0.25)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S41: Summary table for half-life = 0.75. Direct effect slope is the first beta, followed by adaptation slope, and evolutionary slope last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.62	0.01	0.25	0.29	0.45	0.57	0.74	1.22	884	1.00
vy	0.10	0.00	0.04	0.05	0.08	0.10	0.12	0.19	868	1.00
optima[1]	2.01	0.00	0.13	1.72	1.92	2.02	2.10	2.25	1223	1.00
optima[2]	1.13	0.01	0.21	0.74	0.99	1.11	1.26	1.56	1334	1.00
beta[1]	0.38	0.00	0.01	0.35	0.37	0.37	0.38	0.40	1384	1.00
beta[2]	0.17	0.00	0.13	-0.06	0.08	0.17	0.25	0.42	1458	1.00

<u>beta_e[1]</u>	0.07	0.00	0.05	-0.03	0.03	0.07	0.10	0.17	1970	1.00
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Milestone 7: Combination Regime with Direct and Adaptive Predictor Model with Measurement Error

Short half-life (hl=0.1)

MISSING

Figure S42: Prior vs. posterior for A) Half-life, B) vy, C,D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for C) direct effect and D) adaptive models by estimated optima, with priors in light grey. Species values are shown in the dark circles; and E) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line). For this simulation parameter values were set to: hl=0.1, vy=0.1, alpha=2, optima=(2,1), beta=(0.35,0.25); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.25); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S42: Summary table for half-life = 0.1. Direct effect slope is the first beta, followed by adaptation slope, and evolutionary slope last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.17	0.00	0.07	0.07	0.12	0.15	0.20	0.35	1730	1.00
vy	0.11	0.00	0.03	0.07	0.09	0.10	0.12	0.18	1699	1.00
optima[1]	1.91	0.00	0.09	1.71	1.85	1.91	1.97	2.07	2209	1.00
optima[2]	1.25	0.00	0.15	0.93	1.15	1.25	1.35	1.55	3351	1.00
beta[1]	0.38	0.00	0.03	0.32	0.36	0.38	0.40	0.43	4508	1.00
beta[2]	0.27	0.00	0.12	0.05	0.19	0.27	0.34	0.54	3335	1.00
beta_e[1]	0.21	0.00	0.08	0.04	0.15	0.21	0.26	0.36	3586	1.00

Medium half-life (hl=0.25)

Fig. S43

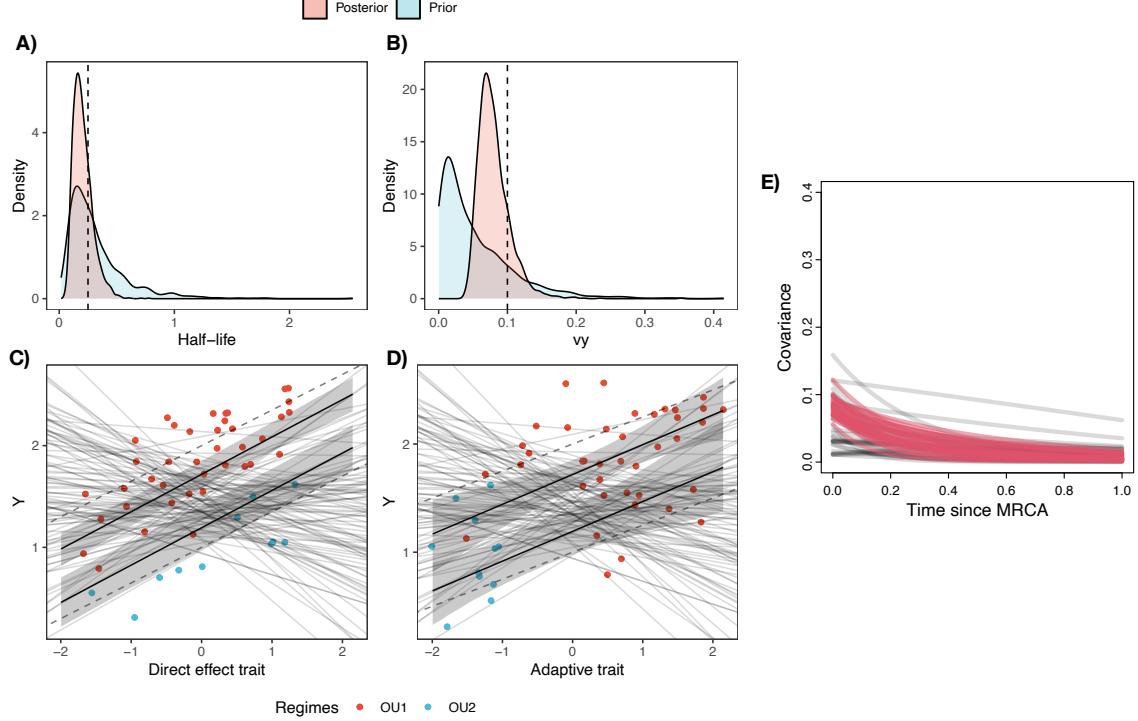


Figure S43: Prior vs. posterior for A) Half-life, B) vy, C,D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for C) direct effect and D) adaptive models by estimated optima, with priors in light grey. Species values are shown in the dark circles; and E) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line). For this simulation parameter values were set to: hl=0.25, vy=0.1, alpha=2, optima=(2,1), beta=(0.35,0.25); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.25); beta~normal(0,0.25). Dotted lines in A) and B) are true values of the parameter.

Table S43: Summary table for half-life = 0.25. Direct effect slope is the first beta, followed by adaptation slope, and evolutionary slope last (beta_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.21	0.00	0.08	0.09	0.14	0.19	0.25	0.41	2189	1.00
vy	0.08	0.00	0.02	0.05	0.06	0.08	0.09	0.13	2064	1.00
optima[1]	1.72	0.00	0.09	1.55	1.66	1.72	1.77	1.88	3544	1.00
optima[2]	1.19	0.00	0.14	0.93	1.11	1.19	1.28	1.47	3986	1.00
beta[1]	0.37	0.00	0.03	0.31	0.35	0.37	0.39	0.42	6602	1.00
beta[2]	0.28	0.00	0.09	0.12	0.22	0.27	0.33	0.47	3083	1.00
beta_e[1]	0.20	0.00	0.05	0.09	0.16	0.19	0.23	0.31	3904	1.00

Long half-life (hl=0.75)

Fig. S44

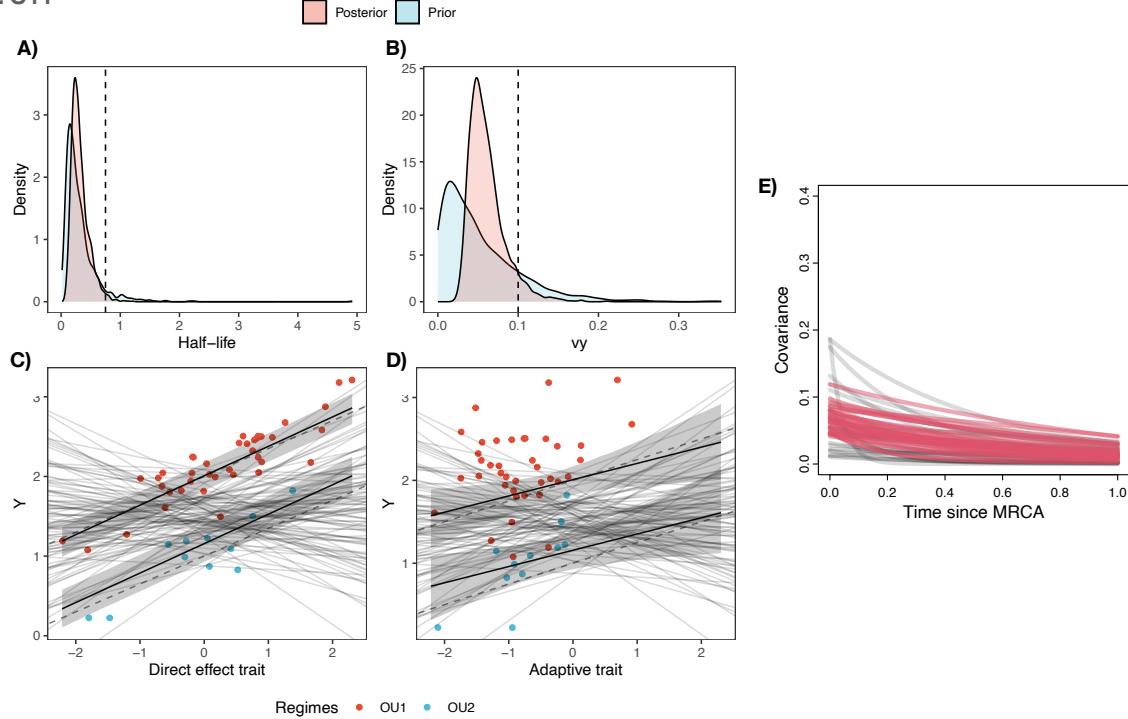


Figure S44: Prior vs. posterior for A) Half-life, B) vy , C,D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for C) direct effect and D) adaptive models by estimated optima, with priors in light grey. Species values are shown in the dark circles; and E) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line). For this simulation parameter values were set to: $hl=0.25$, $vy=0.1$, $\alpha=2$, $optima=(2,1)$, $\beta=(0.35,0.25)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima \sim \text{normal}(1.5, 0.25)$; $\beta \sim \text{normal}(0, 0.25)$. Dotted lines in A) and B) are true values of the parameter.

Table S44: Summary table for half-life = 0.75. Direct effect slope is the first beta, followed by adaptation slope, and evolutionary slope last (β_e).

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.32	0.00	0.15	0.12	0.22	0.29	0.39	0.69	1486	1.00
vy	0.06	0.00	0.02	0.03	0.05	0.06	0.07	0.12	1550	1.00
optima[1]	2.01	0.00	0.11	1.77	1.94	2.02	2.09	2.20	2562	1.00
optima[2]	1.16	0.00	0.15	0.87	1.06	1.16	1.25	1.44	3315	1.00
beta[1]	0.37	0.00	0.02	0.33	0.36	0.37	0.38	0.41	4870	1.00
beta[2]	0.20	0.00	0.10	0.00	0.13	0.19	0.26	0.42	3260	1.00
beta_e[1]	0.12	0.00	0.06	0.00	0.08	0.12	0.16	0.23	3224	1.00

Milestone 8: Multilevel Regime Model with Four Regimes – centered version Short half-life ($hl=0.1$)

Fig. S45

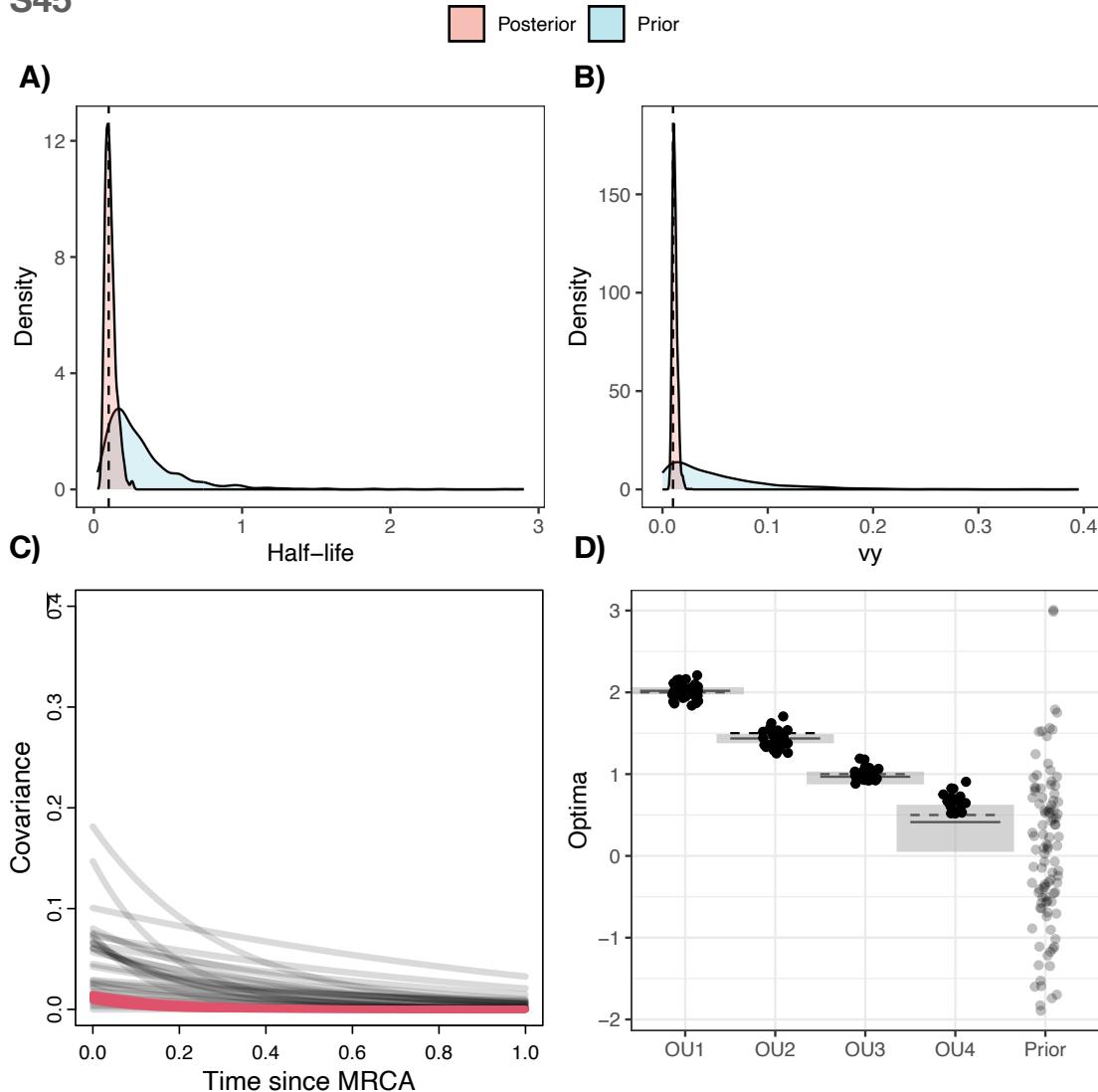


Figure S45: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark great and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2,1.5,1.0,0.5); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima_bar~normal(0,1); sigma~exponential(5).

Table S45: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.11	0.00	0.04	0.06	0.08	0.10	0.13	0.20	479	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	627	1.00
optima[1]	2.02	0.00	0.03	1.96	2.00	2.02	2.04	2.07	1078	1.00
optima[2]	1.44	0.00	0.04	1.36	1.41	1.44	1.46	1.50	814	1.00
optima[3]	0.97	0.00	0.05	0.84	0.95	0.97	1.00	1.04	643	1.00
optima[4]	0.41	0.01	0.19	-0.07	0.33	0.46	0.55	0.65	460	1.00
optima_bar	1.10	0.01	0.30	0.48	0.93	1.12	1.30	1.66	1111	1.00

sigma	0.60	0.01	0.18	0.33	0.47	0.57	0.69	1.02	1193	1.00
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Medium half-life ($hl=0.25$)

Fig. S46

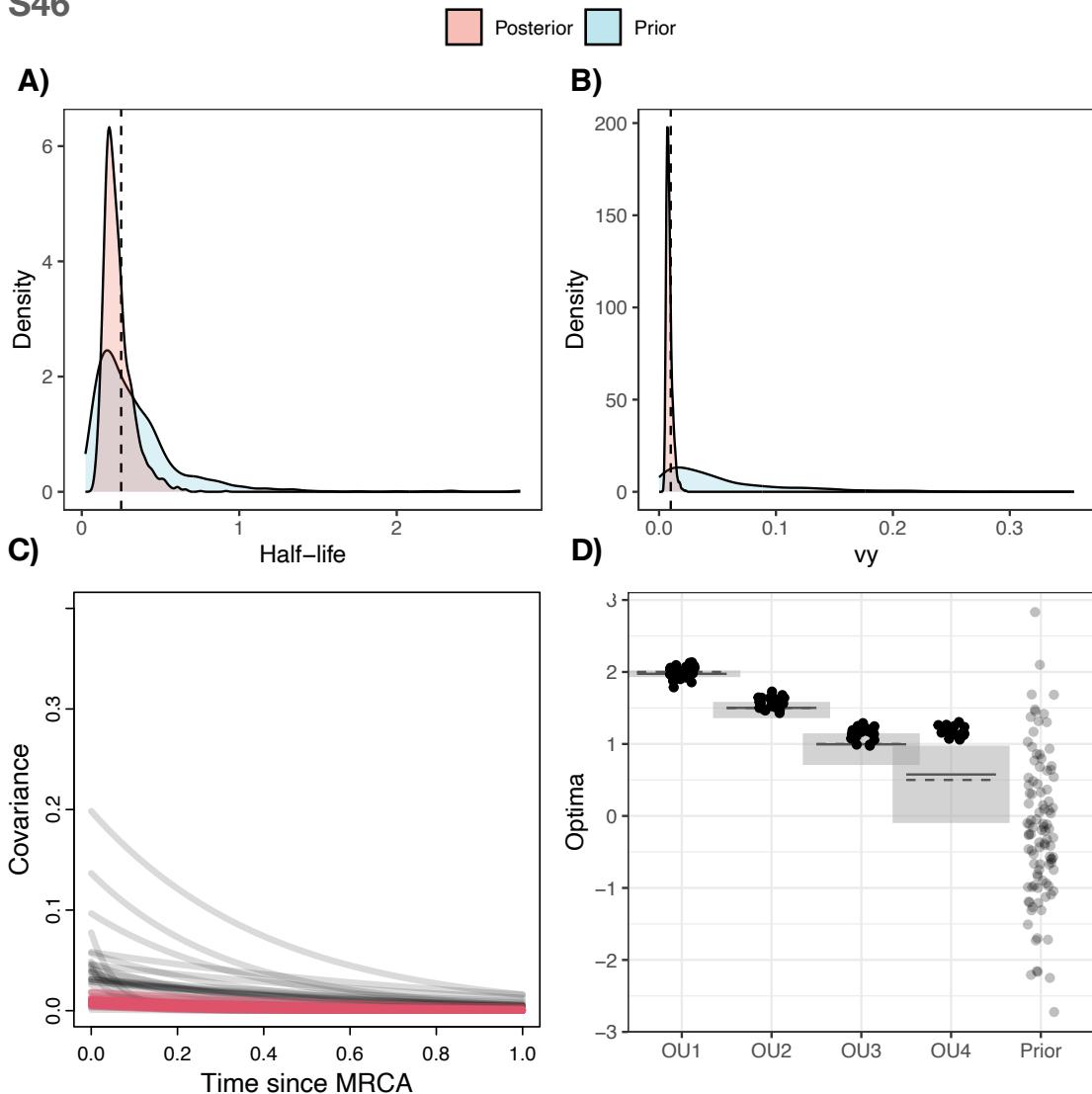


Fig. S46: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark grey and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: $hl=0.25$, $vy=0.01$, $optima=(2,1.5,1.0,0.5)$; Priors: $hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $optima_bar \sim \text{lognornam}(0, 0.5)$; $\sigma \sim \text{exponential}(5)$.

Table S46: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.23	0.01	0.09	0.11	0.17	0.21	0.27	0.47	228	1.00

vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	242	1.00
optima[1]	1.97	0.00	0.03	1.92	1.96	1.97	1.99	2.03	1164	1.00
optima[2]	1.50	0.00	0.08	1.30	1.48	1.52	1.55	1.60	342	1.00
optima[3]	0.99	0.01	0.15	0.57	0.94	1.04	1.09	1.16	245	1.00
optima[4]	0.58	0.02	0.37	-0.38	0.42	0.67	0.83	1.02	228	1.00
optima_bar	1.18	0.01	0.31	0.48	0.99	1.21	1.39	1.71	431	1.00
sigma	0.56	0.01	0.20	0.28	0.42	0.52	0.65	1.04	457	1.01

Long half-life (hl=0.75)

Fig. S47

Posterior Prior

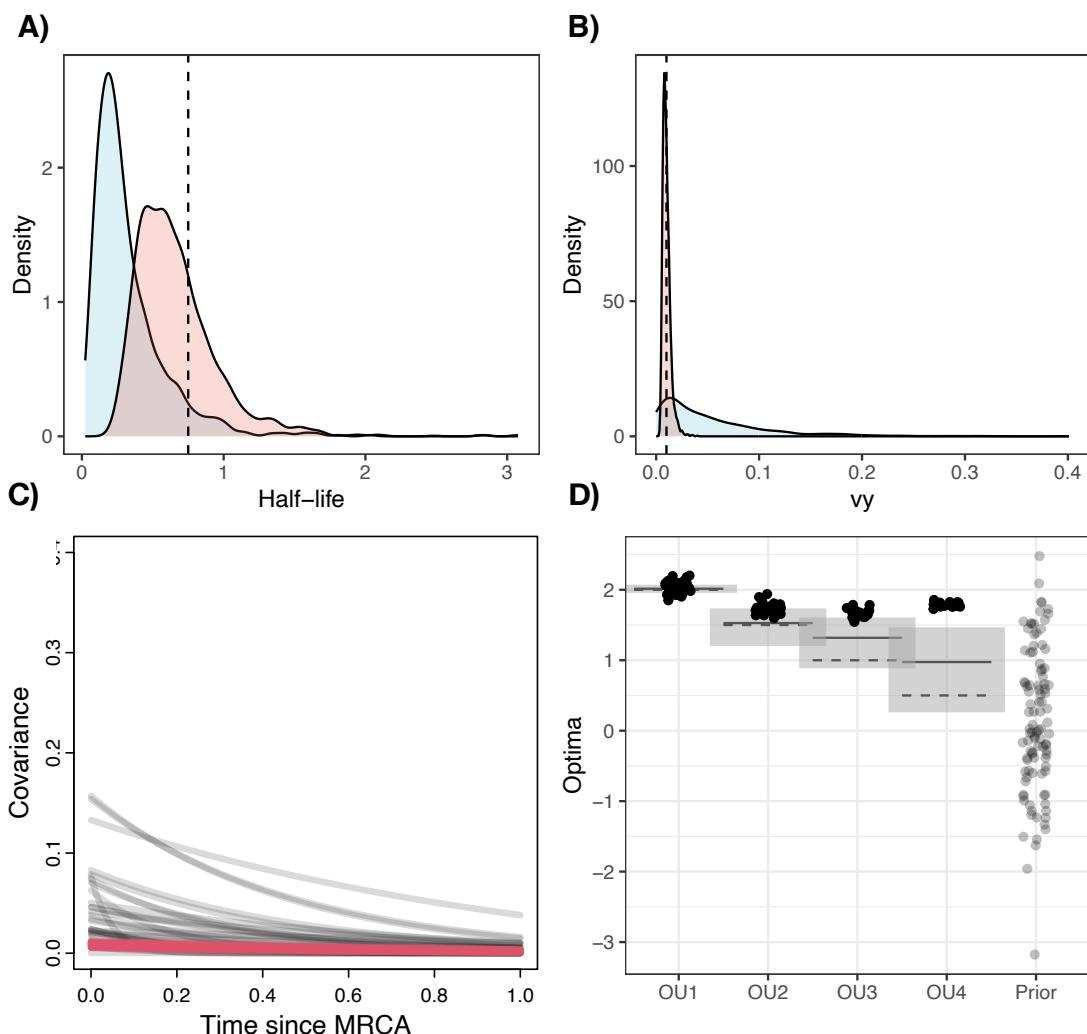


Fig. S47: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Mean predicted optima shown in solid lines and 89% compatibility interval for the means in shaded area, with simulated species values in dark great and priors in light grey circles. Dotted lines overlaying estimated optima are true values of the parameter. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2,1.5,1.0,0.5); Priors:

$hl \sim \text{lognormal}(\log(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $\text{optima_bar} \sim \text{lognorm}(0, 1)$;
 $\sigma \sim \text{exponential}(5)$.

Table S47: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.66	0.02	0.29	0.29	0.46	0.61	0.79	1.39	218	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	238	1.00
optima[1]	2.01	0.00	0.04	1.94	1.99	2.01	2.04	2.09	1162	1.00
optima[2]	1.53	0.01	0.18	1.04	1.44	1.56	1.66	1.76	237	1.00
optima[3]	1.32	0.02	0.25	0.68	1.21	1.37	1.49	1.63	239	1.00
optima[4]	0.97	0.03	0.41	0.01	0.76	1.05	1.26	1.54	263	1.00
optima_bar	1.38	0.02	0.31	0.65	1.21	1.44	1.59	1.86	357	1.00
sigma	0.43	0.01	0.19	0.18	0.30	0.40	0.52	0.92	504	1.00

Milestone 9: Multilevel Regime with Direct Effect Model with Measurement Error Short half-life ($hl=0.1$)

Fig. S48

Posterior Prior

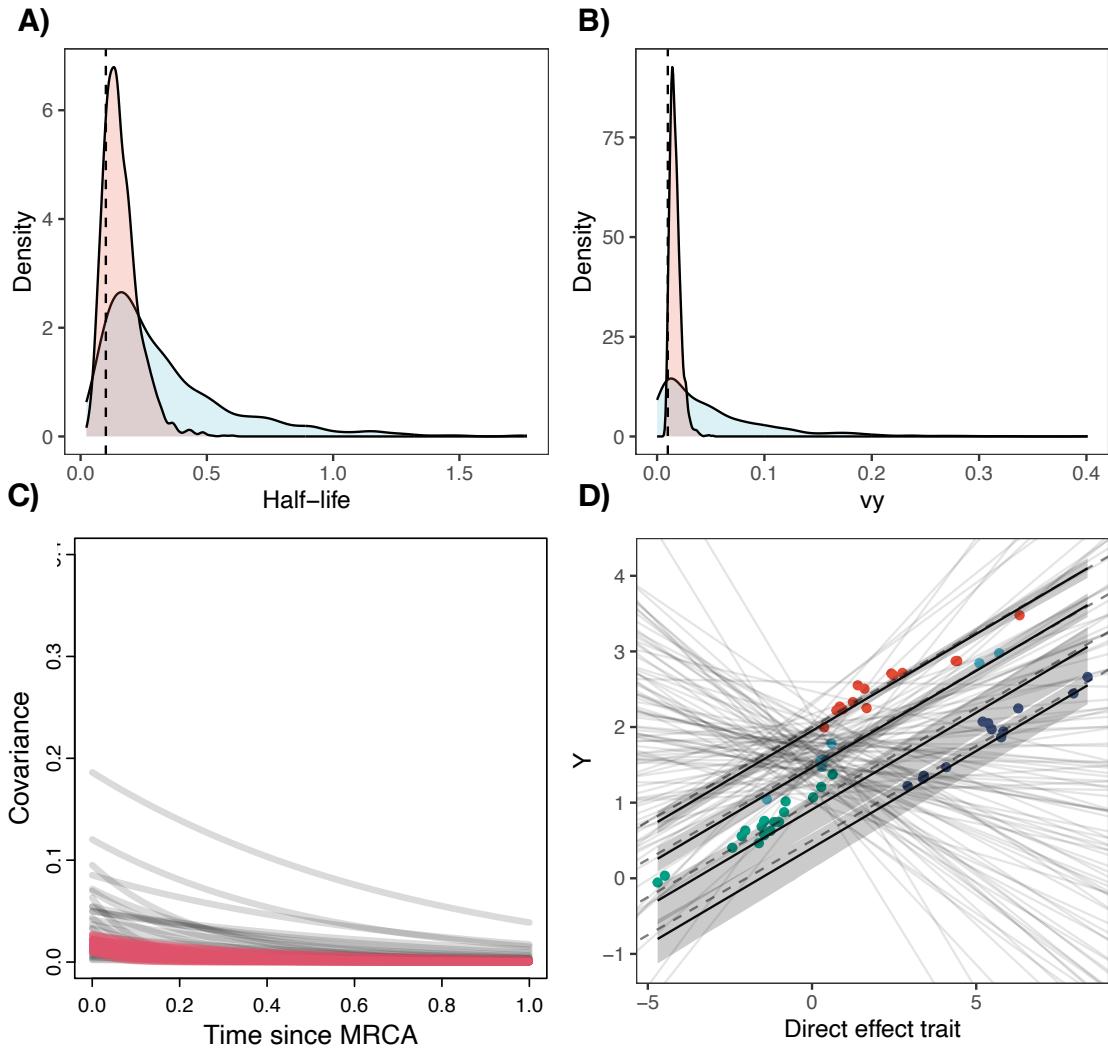


Fig. S48: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5,1.0,0.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S48: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.16	0.00	0.07	0.06	0.11	0.15	0.19	0.32	401	1.01
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.03	665	1.00
optima[1]	1.95	0.00	0.06	1.83	1.91	1.95	1.99	2.06	1564	1.00
optima[2]	1.46	0.00	0.08	1.29	1.42	1.47	1.51	1.60	1119	1.00
optima[3]	0.91	0.01	0.17	0.48	0.84	0.96	1.03	1.11	403	1.00
optima[4]	0.40	0.01	0.16	-0.01	0.33	0.43	0.51	0.63	411	1.01
optima_bar	1.45	0.00	0.19	1.09	1.31	1.44	1.59	1.84	2302	1.00
beta[1]	0.26	0.00	0.01	0.23	0.25	0.26	0.26	0.28	1389	1.00
sigma	0.60	0.01	0.19	0.35	0.47	0.57	0.70	1.06	1132	1.00

Medium half-life (hl=0.25)

Fig. S49

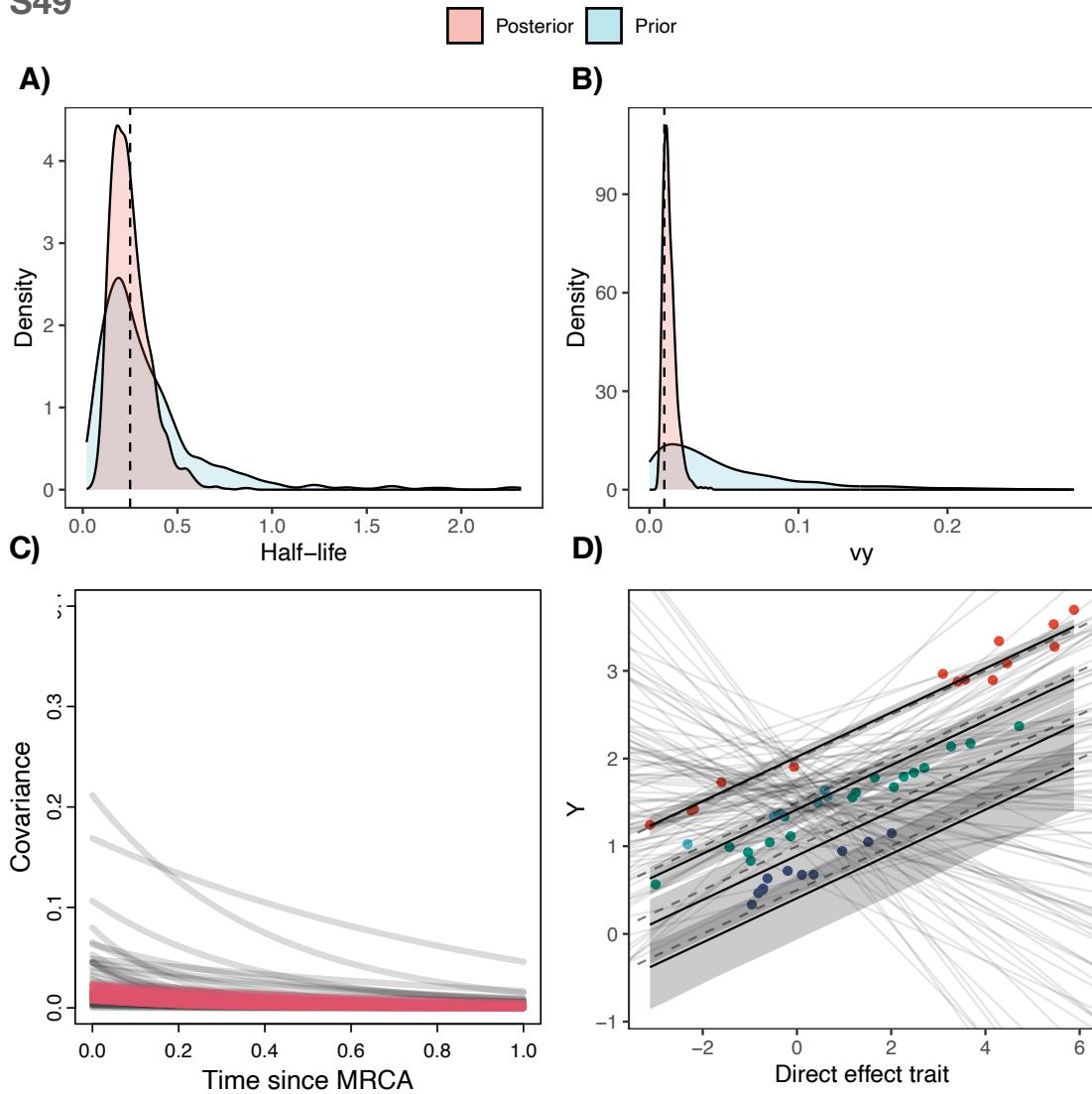


Fig. S49: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5,1.0,0.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S49: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.25	0.01	0.11	0.11	0.18	0.23	0.31	0.52	342	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.02	0.02	450	1.00
optima[1]	2.02	0.00	0.06	1.90	1.99	2.02	2.06	2.12	1357	1.00
optima[2]	1.42	0.00	0.10	1.16	1.37	1.44	1.49	1.57	562	1.00

optima[3]	0.89	0.01	0.25	0.31	0.78	0.95	1.07	1.20	365	1.00
optima[4]	0.41	0.01	0.24	-0.24	0.31	0.47	0.58	0.69	334	1.00
optima_bar	1.43	0.00	0.20	1.04	1.30	1.43	1.56	1.82	2147	1.00
beta[1]	0.25	0.00	0.01	0.24	0.25	0.25	0.26	0.27	2014	1.00
sigma	0.61	0.01	0.20	0.33	0.47	0.57	0.71	1.12	748	1.00

Long half-life (hl=0.75)

Fig. S50

Posterior Prior

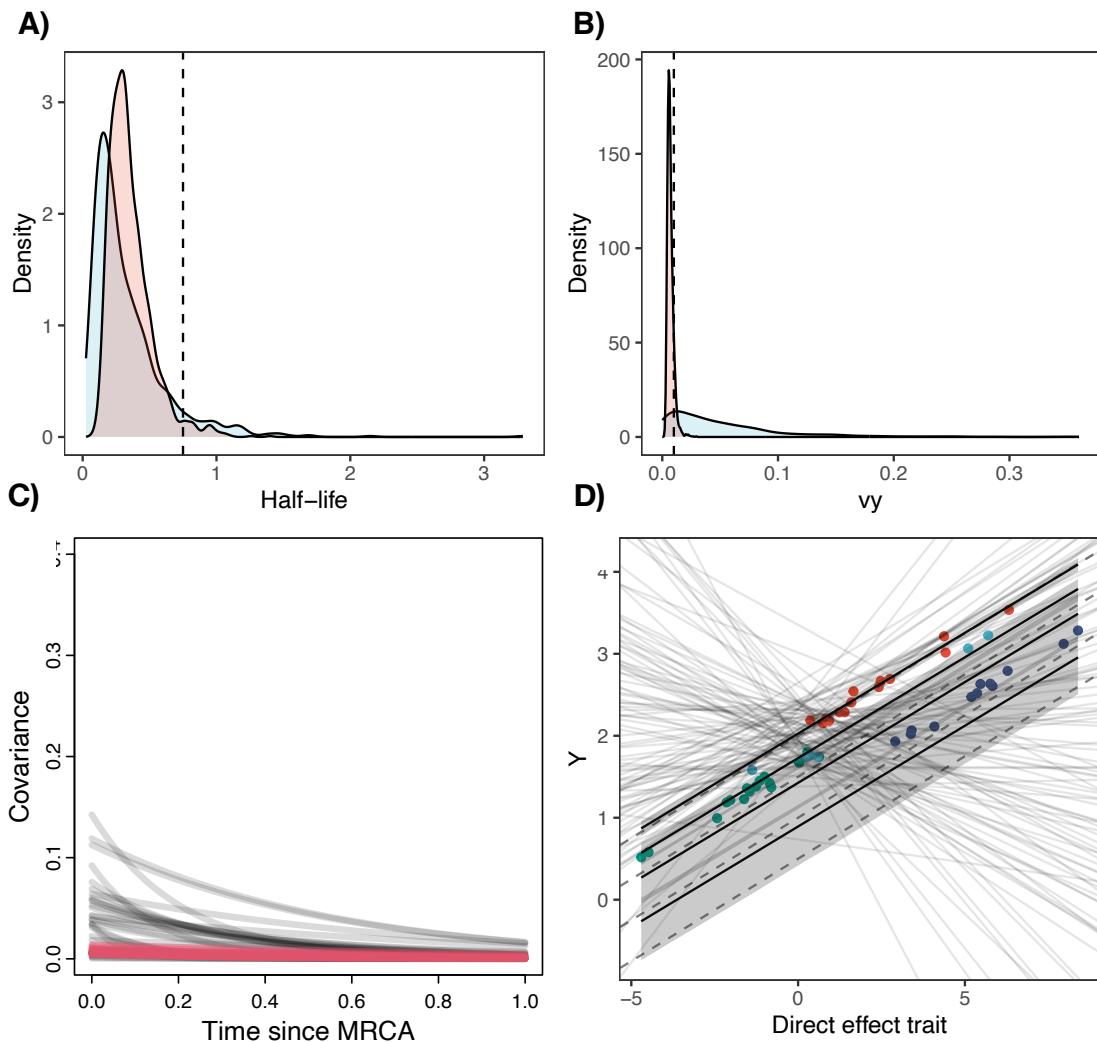


Fig. S50: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5,1.0,0.5,0.25), beta=0.25; Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S50: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.35	0.01	0.16	0.15	0.24	0.32	0.42	0.79	353	1.00
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.01	472	1.00
optima[1]	2.03	0.00	0.04	1.94	2.00	2.03	2.05	2.10	1398	1.00
optima[2]	1.73	0.00	0.08	1.53	1.69	1.74	1.78	1.85	873	1.00
optima[3]	1.43	0.01	0.18	0.98	1.34	1.46	1.55	1.65	431	1.00
optima[4]	0.89	0.01	0.25	0.22	0.79	0.95	1.06	1.19	403	1.00
optima_bar	1.78	0.00	0.19	1.42	1.65	1.77	1.90	2.17	1824	1.00
beta[1]	0.25	0.00	0.01	0.23	0.24	0.25	0.25	0.26	2340	1.00
sigma	0.49	0.01	0.19	0.23	0.36	0.46	0.59	0.96	763	1.00

Milestone 10: Multilevel Regime with Adaptive Model with Measurement Error

Fig. S51

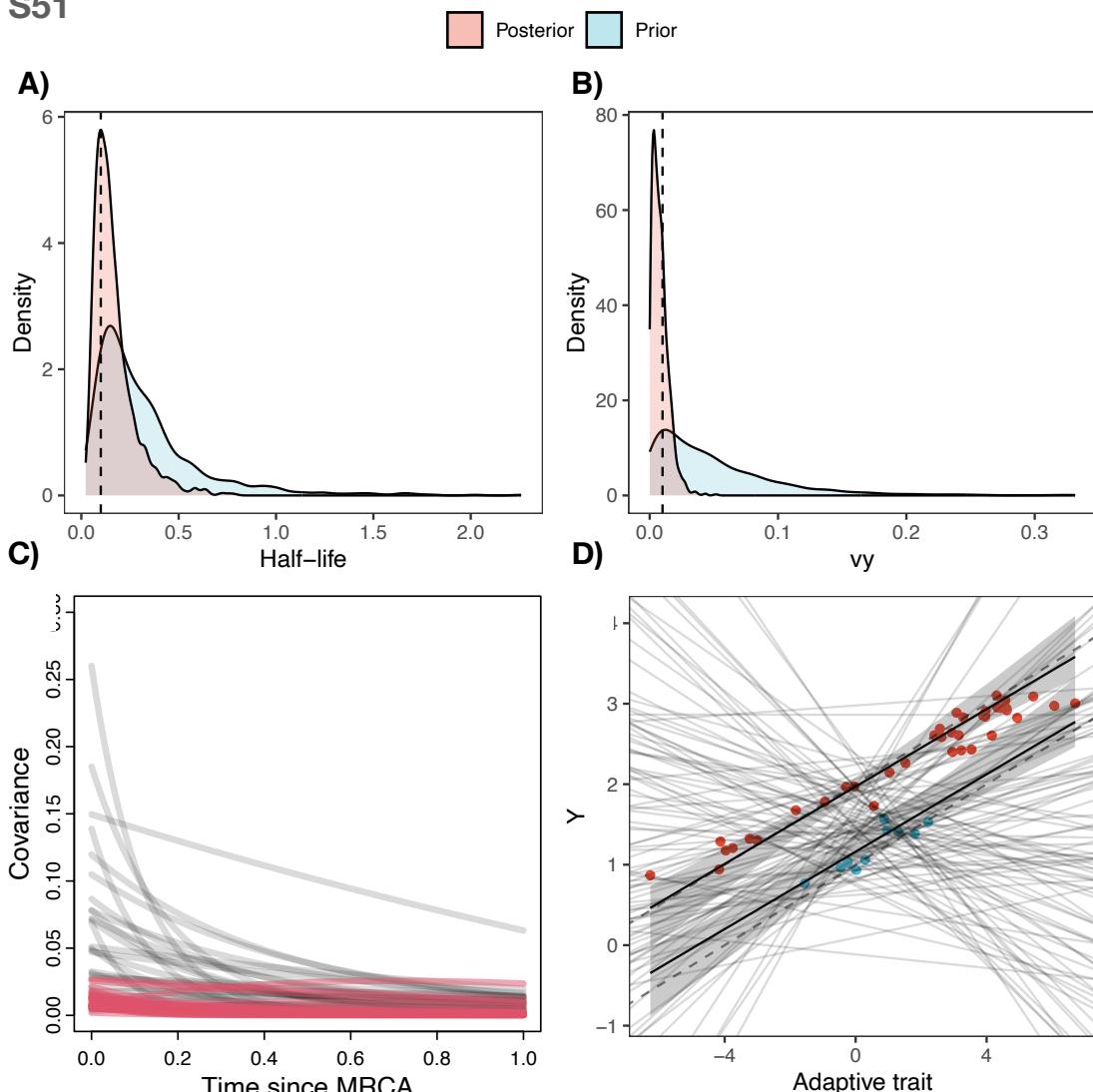


Fig. S51: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in

colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: $hl=0.1$, $vy=0.01$, $optima=(2.0,1.5)$. $\beta=(0.25,0.15)$; Priors: $hl \sim \text{lognormal}(\text{log}(0.25), 0.75)$; $vy \sim \text{exponential}(20)$; $\beta \sim \text{normal}(0, 0.25)$; $\sigma \sim \text{exponential}(5)$; $optima_bar \sim \text{normal}(\text{mean}(Y), 1)$; $optima \sim \text{normal}(optima_bar, \sigma)$

Table S51: Summary table for half-life = 0.1.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.17	0.00	0.11	0.05	0.09	0.14	0.20	0.47	483	1.00
vy	0.01	0.00	0.01	0.00	0.00	0.01	0.01	0.02	2690	1.00
optima[1]	1.97	0.00	0.07	1.81	1.93	1.97	2.02	2.12	2457	1.00
optima[2]	1.16	0.00	0.13	0.91	1.09	1.16	1.23	1.43	1682	1.00
optima_bar	1.88	0.00	0.21	1.50	1.73	1.87	2.04	2.32	2737	1.00
beta[1]	0.24	0.00	0.04	0.20	0.22	0.23	0.25	0.35	483	1.00
sigma	0.48	0.00	0.21	0.21	0.33	0.44	0.58	1.02	2136	1.00

Medium half-life ($hl=0.25$)

Fig. S52

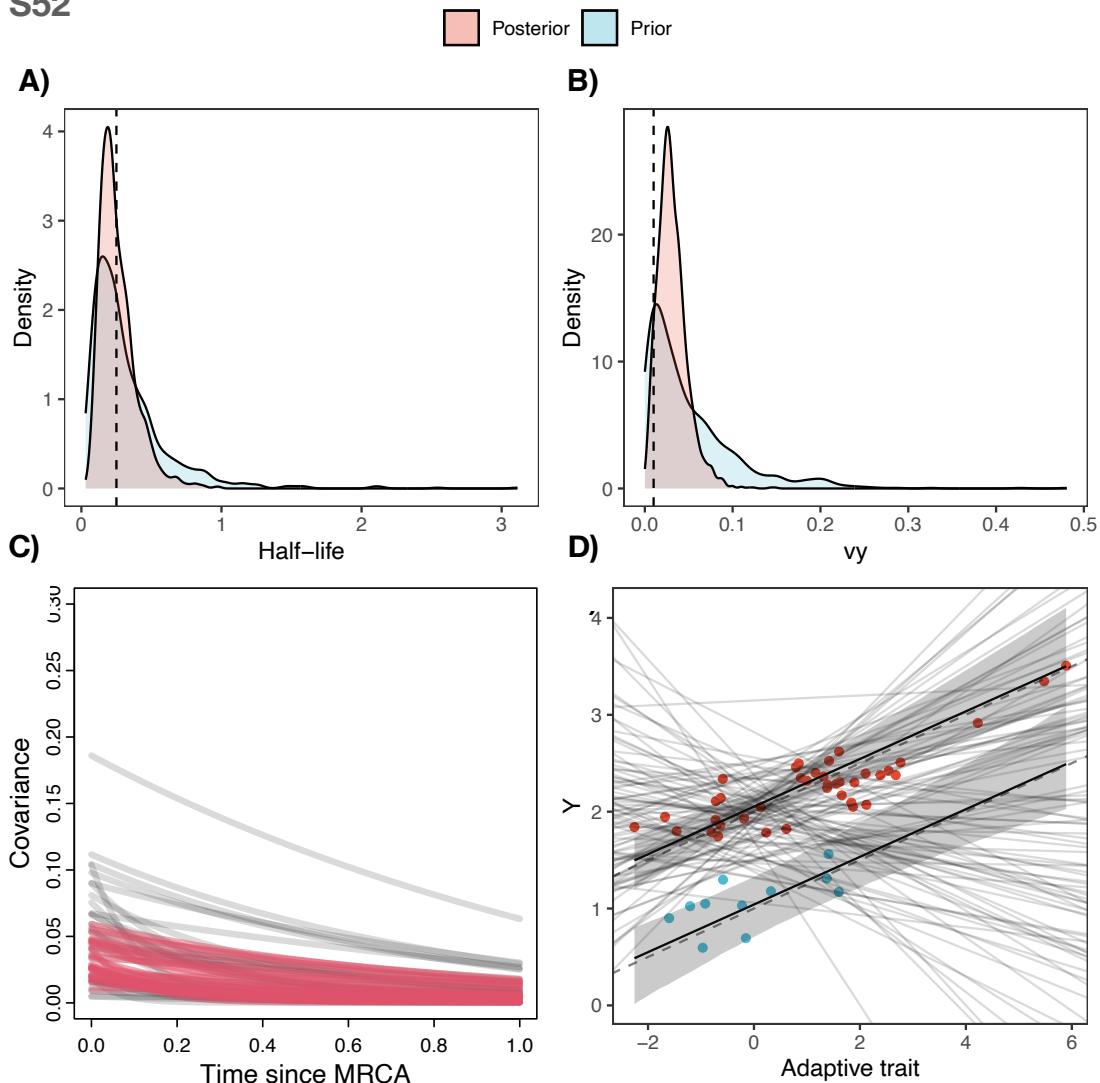


Fig. S52: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5). beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S52: Summary table for half-life = 0.25.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.26	0.00	0.13	0.09	0.17	0.23	0.32	0.60	821	1.00
vy	0.03	0.00	0.02	0.01	0.02	0.03	0.04	0.07	2218	1.00
optima[1]	2.05	0.00	0.10	1.85	1.98	2.06	2.12	2.26	2661	1.00
optima[2]	1.04	0.01	0.21	0.57	0.94	1.06	1.17	1.40	1157	1.00
optima_bar	1.84	0.00	0.22	1.42	1.69	1.83	1.98	2.28	4809	1.00
beta[1]	0.25	0.00	0.06	0.17	0.21	0.24	0.27	0.39	930	1.00
sigma	0.53	0.00	0.20	0.23	0.38	0.49	0.63	1.01	1897	1.00

Long half-life ($hl=0.75$)

Fig. S53

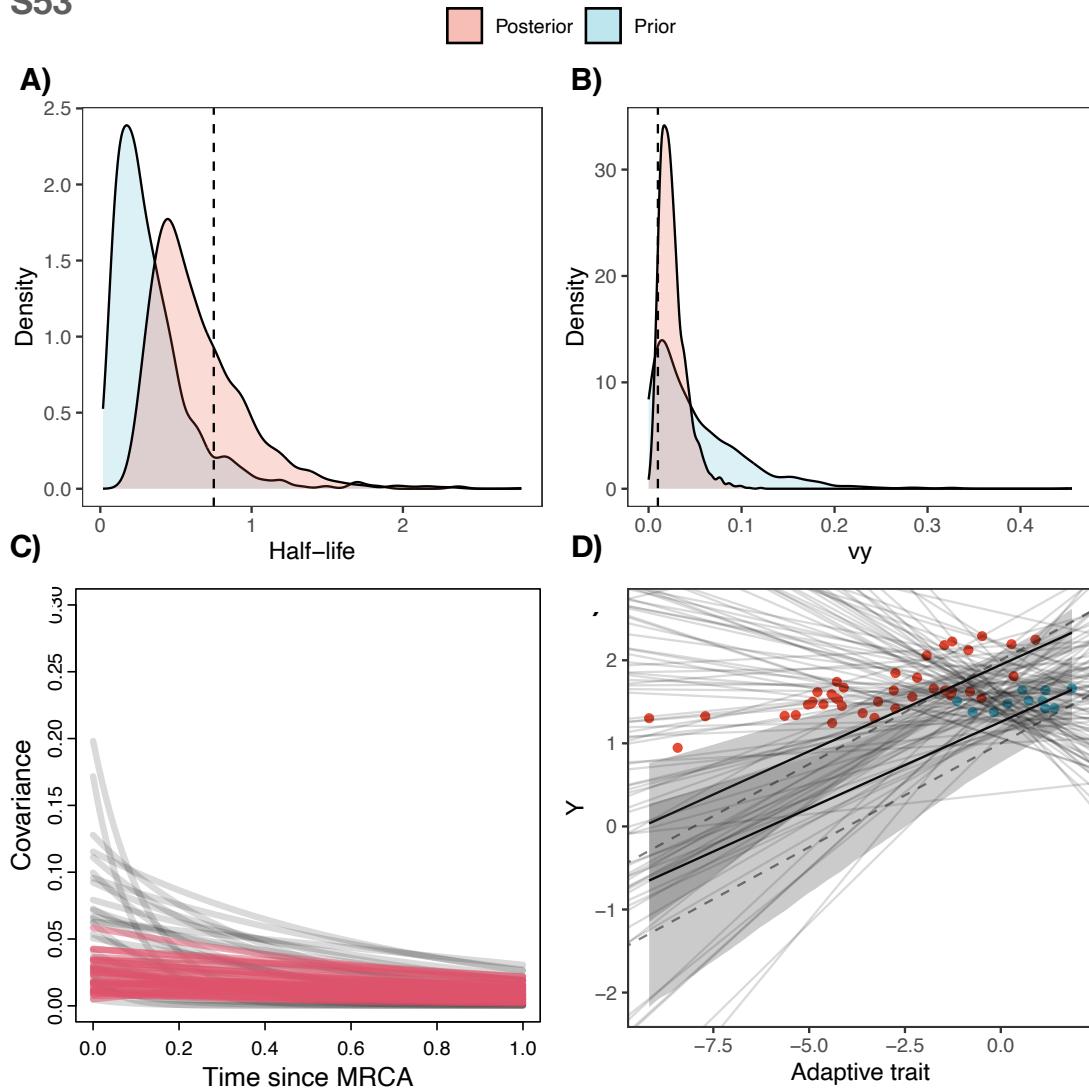


Fig. S53 MISSING

Table S53: Summary table for half-life = 0.75.

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.65	0.01	0.31	0.26	0.42	0.57	0.79	1.41	575	1.00
vy	0.03	0.00	0.02	0.01	0.02	0.02	0.03	0.06	769	1.00
optima[1]	1.94	0.00	0.10	1.73	1.88	1.95	2.01	2.13	1329	1.00
optima[2]	1.26	0.01	0.27	0.61	1.11	1.30	1.43	1.71	886	1.00
optima_bar	1.61	0.00	0.18	1.23	1.50	1.61	1.73	1.96	2416	1.00
beta[1]	0.21	0.00	0.07	0.12	0.16	0.19	0.24	0.39	633	1.00
sigma	0.38	0.01	0.19	0.11	0.25	0.35	0.48	0.84	1069	1.00

Milestone 11: Multilevel Regime with Direct Effect and Adaptive Model with Measurement Error

Fig. S54

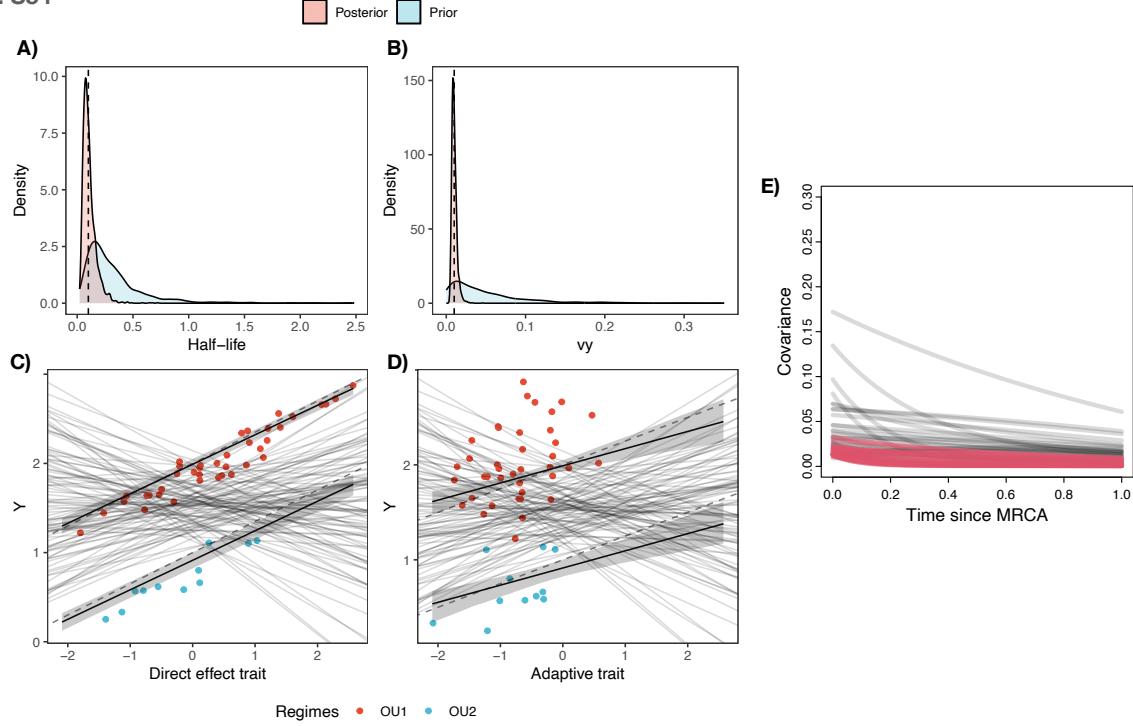


Fig. S54: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5). beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S54: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.11	0.00	0.06	0.04	0.07	0.09	0.13	0.27	581	1.00
vy	0.01	0.00	0.00	0.01	0.01	0.01	0.01	0.02	1131	1.00
optima[1]	1.99	0.00	0.04	1.92	1.97	1.99	2.01	2.07	2441	1.00
optima[2]	0.91	0.00	0.07	0.76	0.88	0.92	0.95	1.03	733	1.00
optima_bar	1.49	0.01	0.37	0.73	1.27	1.48	1.70	2.27	2063	1.00
beta[1]	0.33	0.00	0.01	0.30	0.32	0.33	0.34	0.36	3318	1.00
beta[2]	0.18	0.00	0.05	0.10	0.15	0.18	0.20	0.29	871	1.00
sigma	0.55	0.00	0.22	0.26	0.39	0.50	0.65	1.10	2230	1.00

Fig. S55

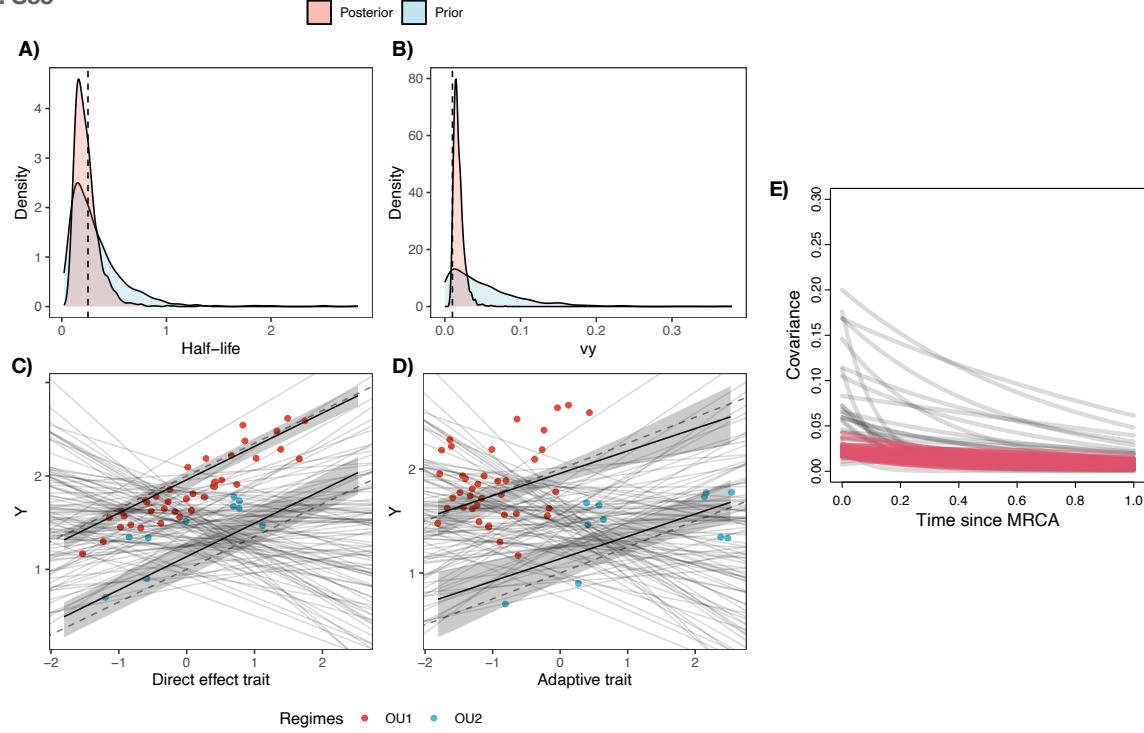


Fig. S55: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5). beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S55: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.24	0.00	0.12	0.09	0.15	0.21	0.28	0.53	815	1.00
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	1184	1.01
optima[1]	1.96	0.00	0.06	1.85	1.92	1.96	2.00	2.07	2718	1.00
optima[2]	1.14	0.00	0.13	0.81	1.09	1.16	1.21	1.31	1022	1.00
optima_bar	1.58	0.01	0.32	0.95	1.39	1.57	1.75	2.23	1768	1.00
beta[1]	0.36	0.00	0.02	0.33	0.35	0.36	0.37	0.39	4139	1.00
beta[2]	0.22	0.00	0.06	0.11	0.18	0.21	0.25	0.36	1401	1.00
sigma	0.46	0.00	0.18	0.22	0.33	0.41	0.54	0.92	1725	1.00

Fig. S56

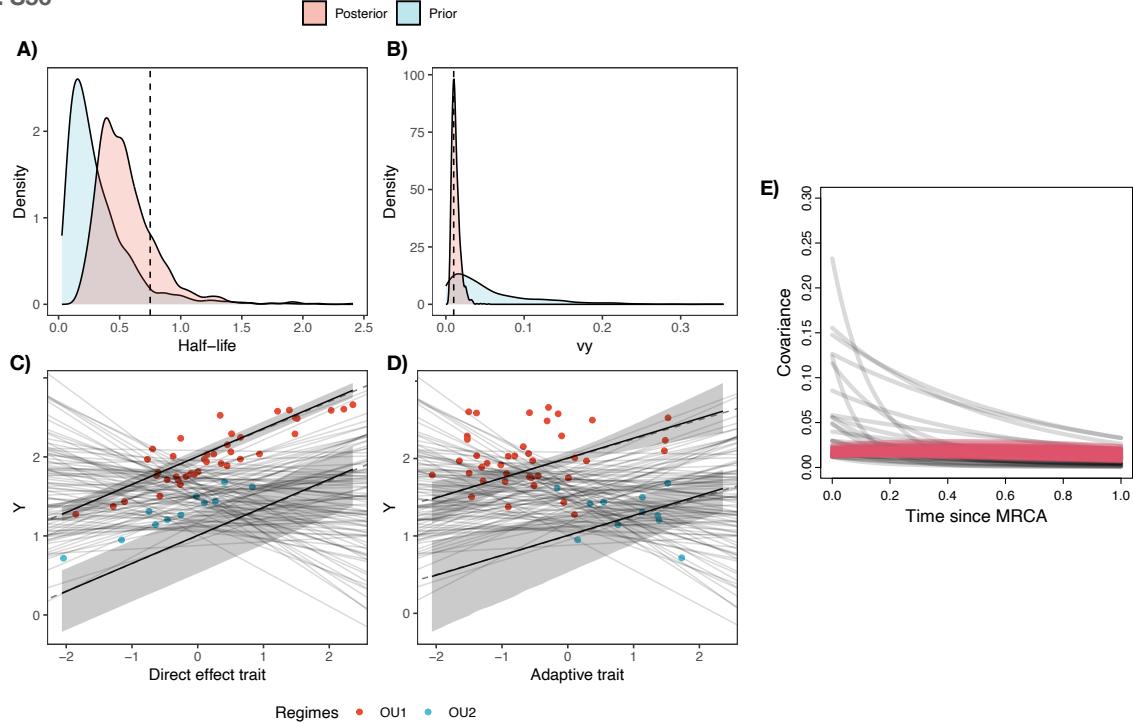


Fig. S56: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5). beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0,25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S56: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.55	0.01	0.24	0.24	0.38	0.51	0.67	1.19	515	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.03	745	1.00
optima[1]	2.01	0.00	0.05	1.90	1.97	2.01	2.04	2.11	2951	1.00
optima[2]	1.01	0.01	0.26	0.35	0.90	1.06	1.19	1.33	568	1.00
optima_bar	1.55	0.01	0.36	0.76	1.34	1.57	1.78	2.27	1715	1.00
beta[1]	0.35	0.00	0.01	0.34	0.35	0.35	0.36	0.37	3396	1.00
beta[2]	0.26	0.00	0.08	0.13	0.20	0.24	0.30	0.46	847	1.00
sigma	0.52	0.01	0.21	0.23	0.37	0.48	0.63	1.05	1390	1.00

Milestone 12: Combination of regime model with direct effect model with measurement error and varying effects

Fig. S57

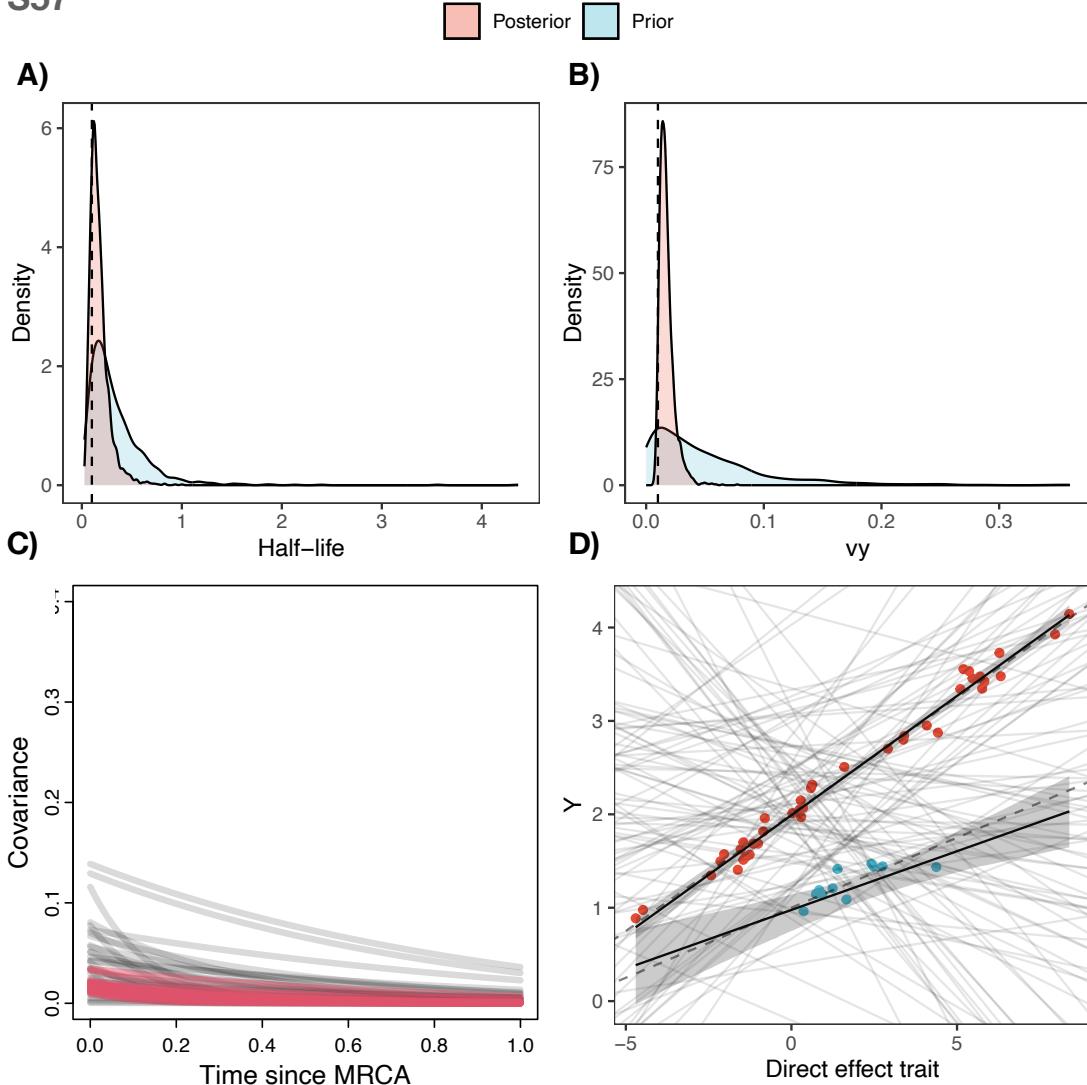


Fig. S57: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5). beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S57: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.17	0.00	0.09	0.06	0.11	0.15	0.20	0.40	952	1.00
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.03	1178	1.00
optima_beta[1]	1.99	0.00	0.04	1.91	1.97	2.00	2.02	2.07	1865	1.00
optima_beta[2]	0.98	0.00	0.11	0.70	0.92	1.00	1.06	1.17	1181	1.00
beta[1]	0.26	0.00	0.01	0.24	0.25	0.26	0.26	0.27	2658	1.00
beta[2]	0.13	0.00	0.03	0.06	0.10	0.13	0.15	0.19	2948	1.00

Fig. S58

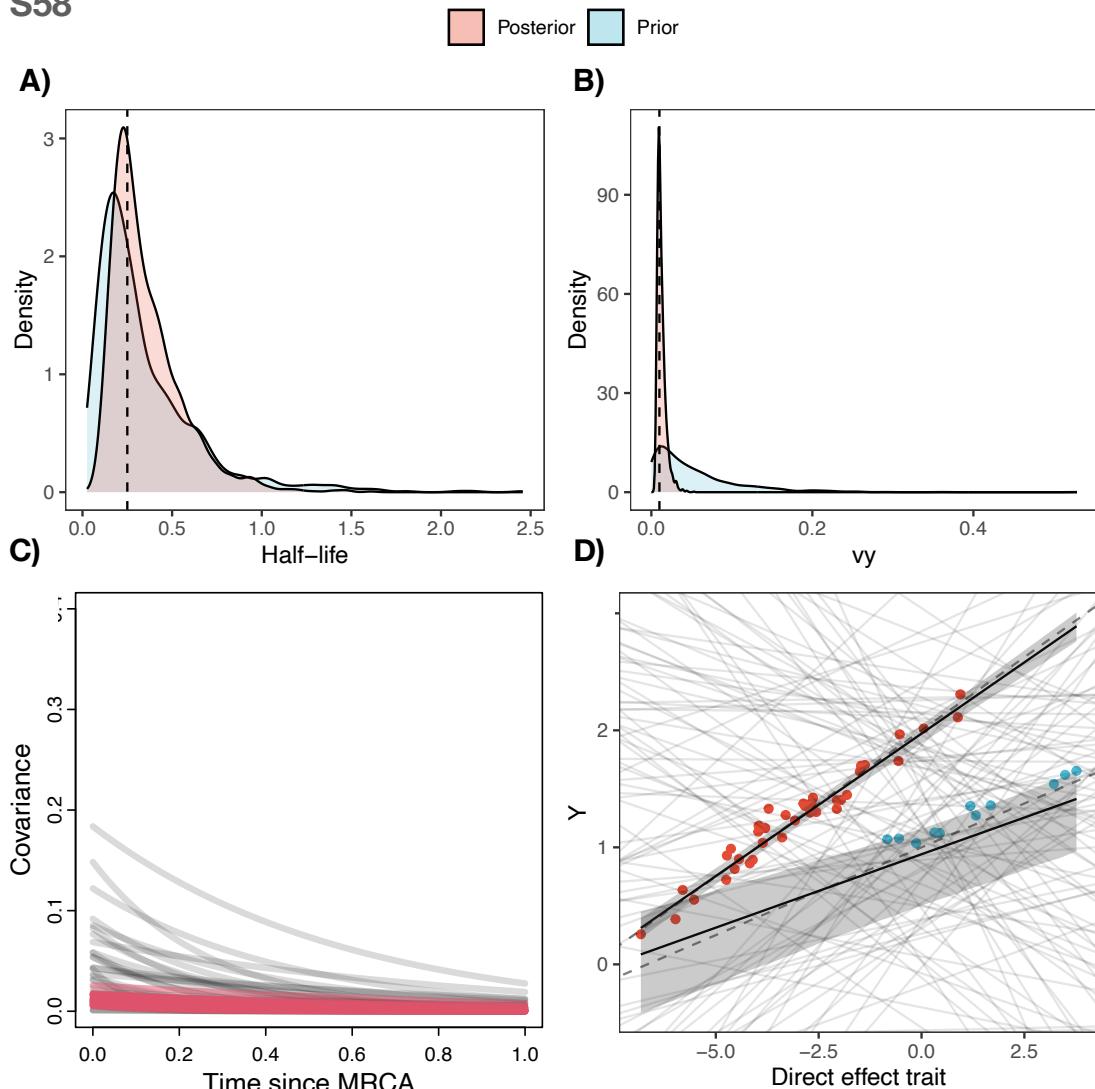


Fig. S58: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S58: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.35	0.01	0.20	0.12	0.22	0.30	0.44	0.87	958	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.03	968	1.00
optima_beta[1]	1.97	0.00	0.05	1.86	1.94	1.97	2.01	2.07	1943	1.00
optima_beta[2]	0.94	0.01	0.22	0.32	0.86	1.01	1.09	1.18	971	1.00

beta[1]	0.24	0.00	0.01	0.22	0.24	0.24	0.25	0.26	2267	1.00
beta[2]	0.13	0.00	0.02	0.09	0.11	0.13	0.14	0.17	2832	1.00

Fig. S59

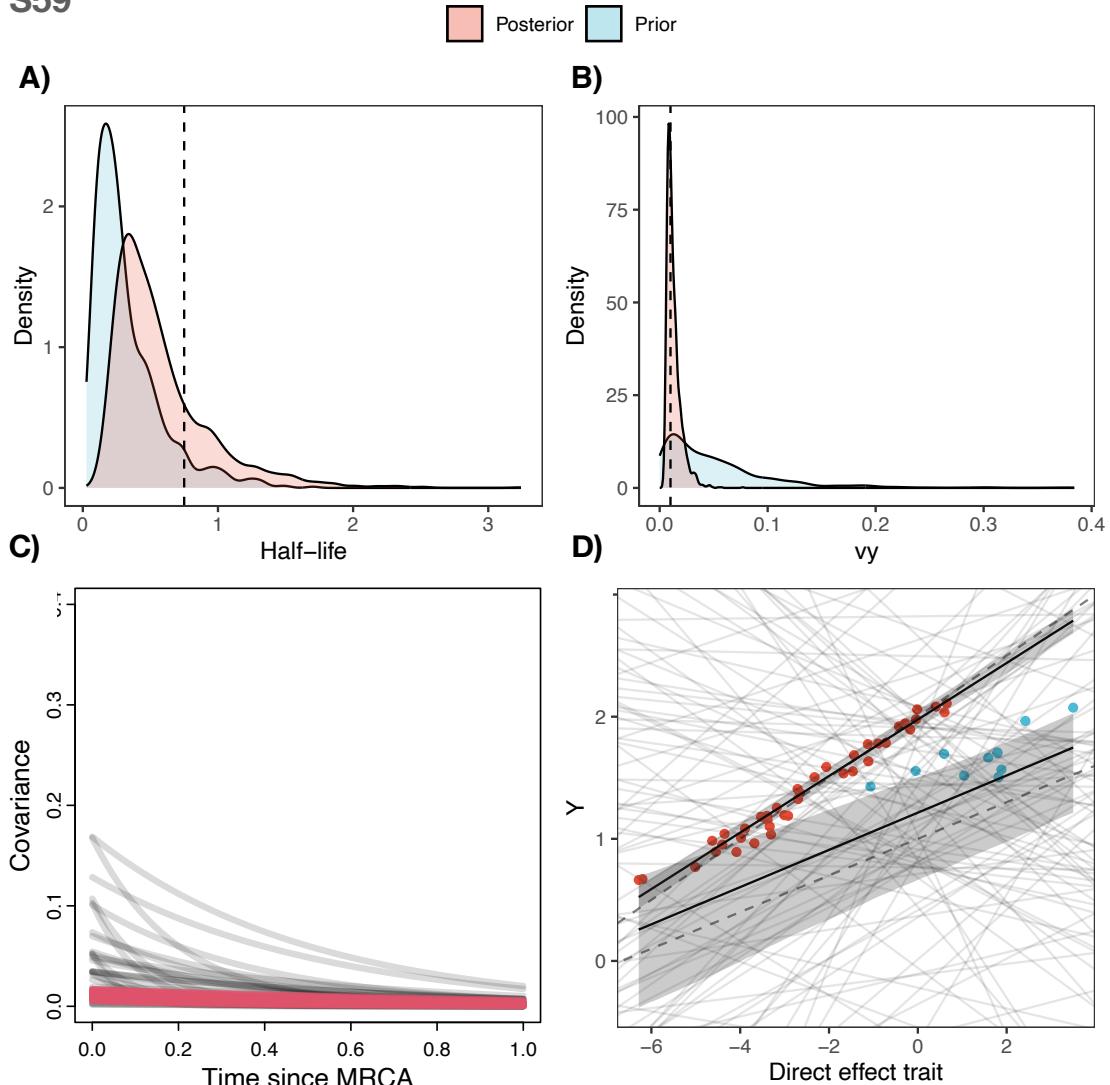


Fig. S59: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S59: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.58	0.02	0.36	0.19	0.33	0.48	0.71	1.55	337	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.02	0.03	375	1.00
optima_beta[1]	1.98	0.00	0.05	1.88	1.95	1.98	2.01	2.07	1601	1.00

optima_beta[2]	1.21	0.02	0.30	0.42	1.11	1.30	1.41	1.53	345	1.00
beta[1]	0.23	0.00	0.01	0.21	0.23	0.23	0.24	0.25	2601	1.00
beta[2]	0.15	0.00	0.02	0.11	0.14	0.15	0.17	0.19	3041	1.00

Milestone 13: Combination of regime model with direct effect model with measurement error and varying effects

Fig. S60

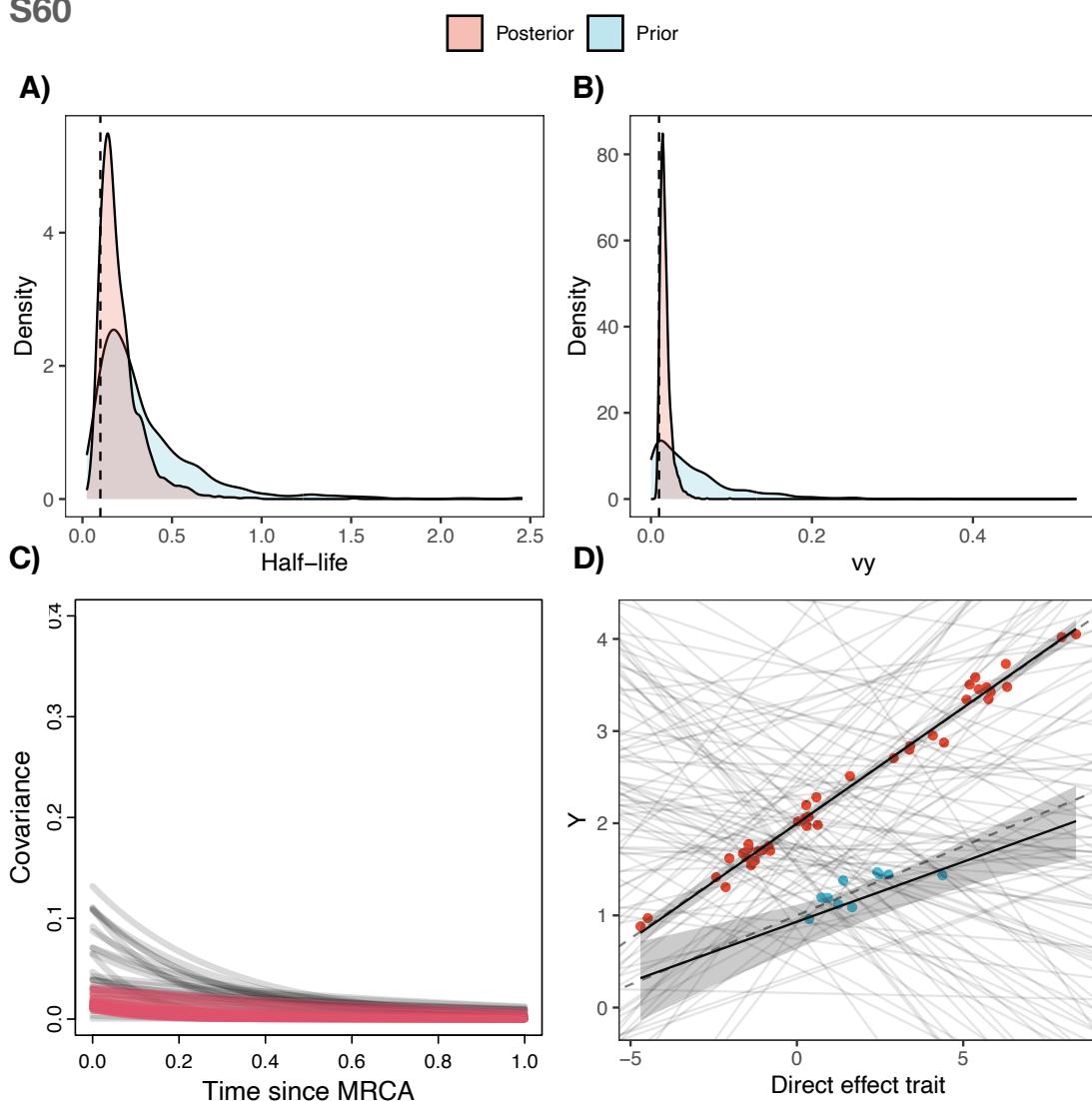


Fig. S60: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S60: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
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hl	0.20	0.01	0.11	0.07	0.12	0.17	0.25	0.50	354	1.01
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	422	1.01
optima_bar	1.69	0.02	0.56	0.65	1.34	1.64	2.01	2.92	1264	1.00
beta_bar[1]	0.14	0.00	0.15	-0.21	0.07	0.17	0.22	0.39	1149	1.00
optima[1]	2.00	0.00	0.04	1.90	1.97	2.00	2.02	2.08	1113	1.00
optima[2]	0.93	0.01	0.16	0.52	0.87	0.97	1.04	1.15	343	1.01
beta[1,1]	0.25	0.00	0.01	0.23	0.25	0.25	0.26	0.27	1842	1.00
beta[2,1]	0.13	0.00	0.03	0.07	0.11	0.13	0.15	0.19	1470	1.00

Fig. S61

Posterior Prior

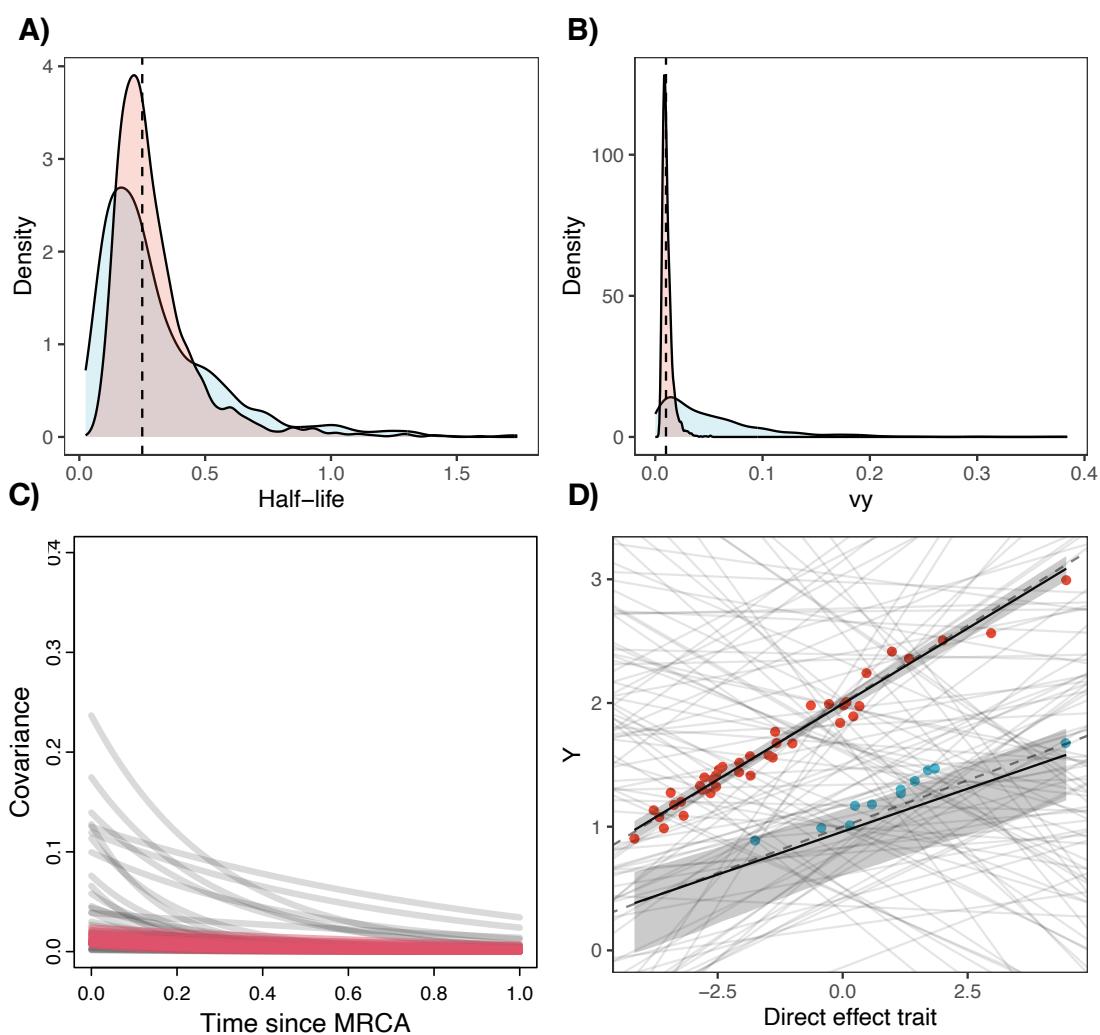


Fig. S61: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20);

$\text{beta} \sim \text{normal}(0, 0.25)$; $\sigma \sim \text{exponential}(5)$; $\text{optima_bar} \sim \text{normal}(\text{mean}(Y), 1)$;
 $\text{optima} \sim \text{normal}(\text{optima_bar}, \sigma)$

Table S61: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.30	0.01	0.18	0.11	0.19	0.25	0.35	0.83	275	1.01
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.02	336	1.00
optima_bar	1.51	0.01	0.54	0.35	1.20	1.51	1.81	2.60	1956	1.00
beta_bar[1]	0.13	0.01	0.15	-0.24	0.07	0.16	0.22	0.38	866	1.00
optima[1]	1.99	0.00	0.04	1.91	1.97	1.99	2.02	2.07	1003	1.00
optima[2]	0.96	0.01	0.22	0.32	0.92	1.02	1.09	1.16	257	1.01
beta[1,1]	0.24	0.00	0.01	0.23	0.24	0.24	0.25	0.26	2716	1.00
beta[2,1]	0.14	0.00	0.02	0.10	0.13	0.14	0.15	0.18	2432	1.00

Fig. S62

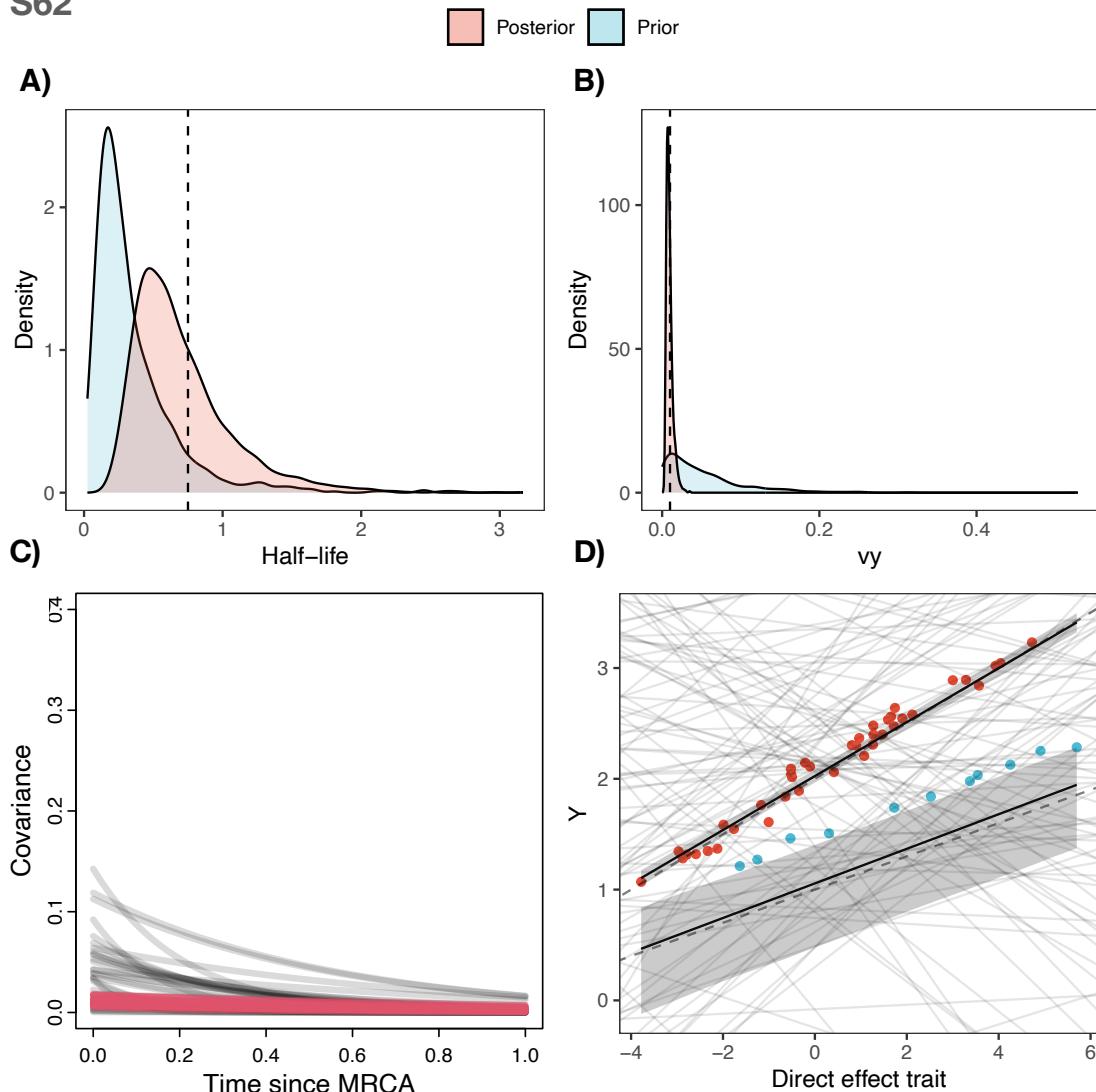


Fig. S62: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D)

Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S62: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.66	0.01	0.33	0.24	0.43	0.58	0.80	1.53	798	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.03	838	1.00
optima_bar	1.75	0.01	0.56	0.71	1.44	1.71	2.04	3.01	1545	1.00
beta_bar[1]	0.14	0.00	0.14	-0.23	0.08	0.17	0.23	0.39	1079	1.00
optima[1]	1.98	0.00	0.05	1.89	1.95	1.98	2.01	2.08	2302	1.00
optima[2]	1.14	0.01	0.28	0.44	1.02	1.21	1.34	1.48	855	1.00
beta[1,1]	0.24	0.00	0.01	0.23	0.24	0.24	0.25	0.26	2440	1.00
beta[2,1]	0.15	0.00	0.02	0.11	0.14	0.15	0.16	0.19	2497	1.00

Milestone 14: Combination of regime model with direct effect model with measurement error and varying effects – non-centered

Fig. S63

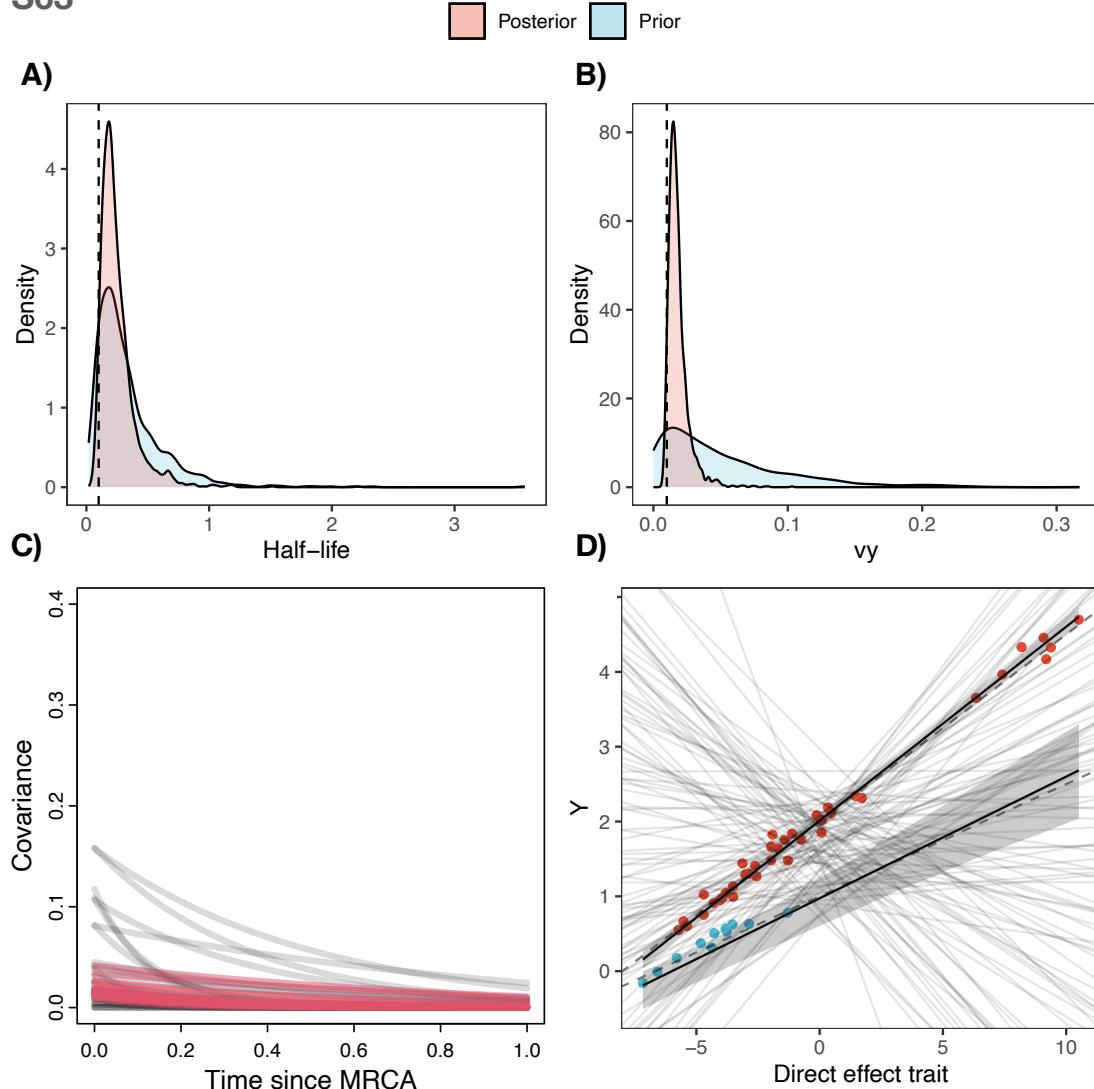


Fig. S63: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S63: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.25	0.01	0.15	0.09	0.16	0.21	0.30	0.66	558	1.00
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	599	1.00
optima_bar	1.55	0.02	0.55	0.40	1.23	1.54	1.86	2.71	595	1.01
beta_bar	0.15	0.01	0.15	-0.23	0.09	0.18	0.23	0.39	157	1.02
optima[1]	2.01	0.00	0.05	1.91	1.99	2.01	2.04	2.10	1934	1.00
optima[2]	0.97	0.01	0.23	0.42	0.89	1.01	1.11	1.28	805	1.00

beta[1,1]	0.26	0.00	0.01	0.24	0.25	0.26	0.26	0.27	2157	1.00
beta[2,1]	0.16	0.00	0.02	0.12	0.15	0.16	0.18	0.21	1797	1.00

Fig. S64

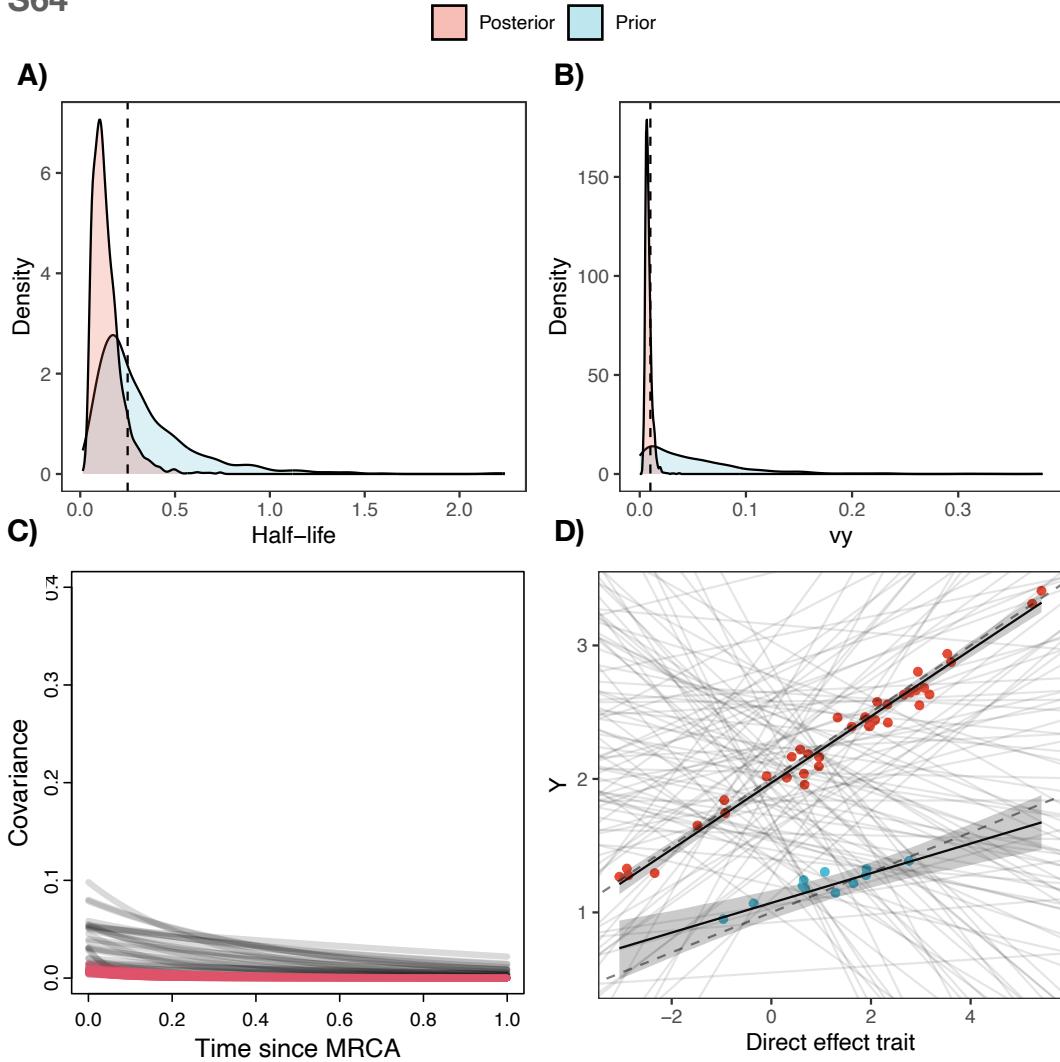


Fig. S64: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S64: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.14	0.01	0.08	0.05	0.09	0.12	0.17	0.36	191	1.02
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.02	190	1.01

optima_bar	1.72	0.02	0.51	0.76	1.41	1.70	1.98	2.89	701	1.01
beta_bar	0.13	0.01	0.15	-0.22	0.05	0.15	0.23	0.38	107	1.03
optima[1]	1.97	0.00	0.03	1.92	1.96	1.97	1.99	2.02	2070	1.00
optima[2]	1.07	0.00	0.08	0.87	1.04	1.08	1.12	1.18	796	1.00
beta[1,1]	0.25	0.00	0.01	0.23	0.24	0.25	0.26	0.27	1517	1.00
beta[2,1]	0.11	0.00	0.03	0.06	0.09	0.11	0.13	0.17	1553	1.00

Fig. S65

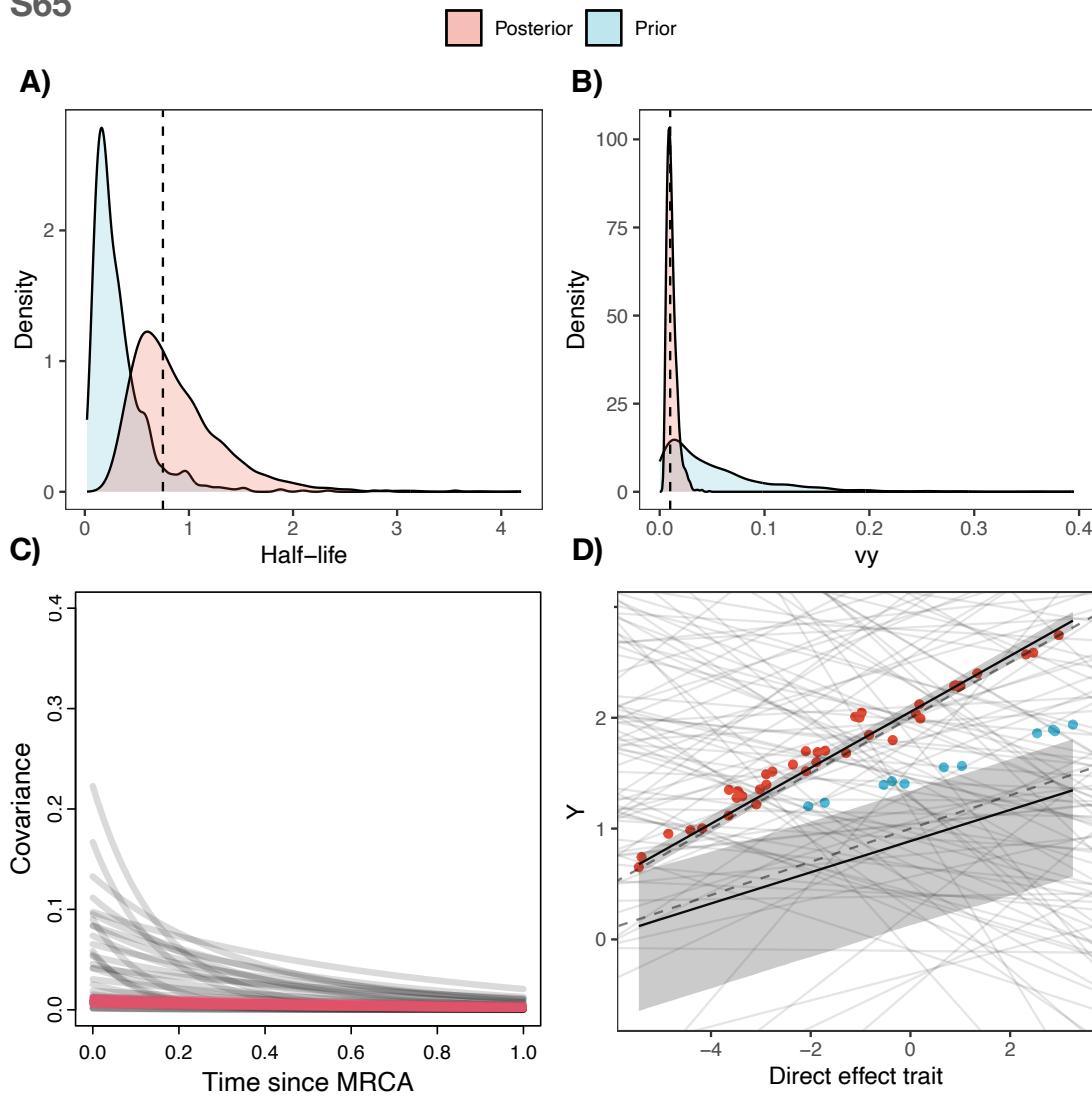


Fig. S65: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for direct effect model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S65: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.88	0.01	0.44	0.33	0.57	0.78	1.08	1.97	1079	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.03	1150	1.00
optima_bar	1.52	0.02	0.58	0.38	1.19	1.54	1.86	2.74	908	1.00
beta_bar	0.15	0.01	0.13	-0.17	0.09	0.17	0.23	0.37	474	1.00
optima[1]	2.05	0.00	0.04	1.96	2.03	2.05	2.08	2.14	1827	1.00
optima[2]	0.89	0.01	0.42	-0.15	0.72	1.00	1.18	1.38	1158	1.00
beta[1,1]	0.25	0.00	0.01	0.24	0.25	0.25	0.26	0.26	2106	1.00
beta[2,1]	0.14	0.00	0.01	0.12	0.13	0.14	0.15	0.17	1992	1.00

Milestone 15: Combination of Regime model with Adaptive Varying Slopes and Measurement Error

Fig. S66

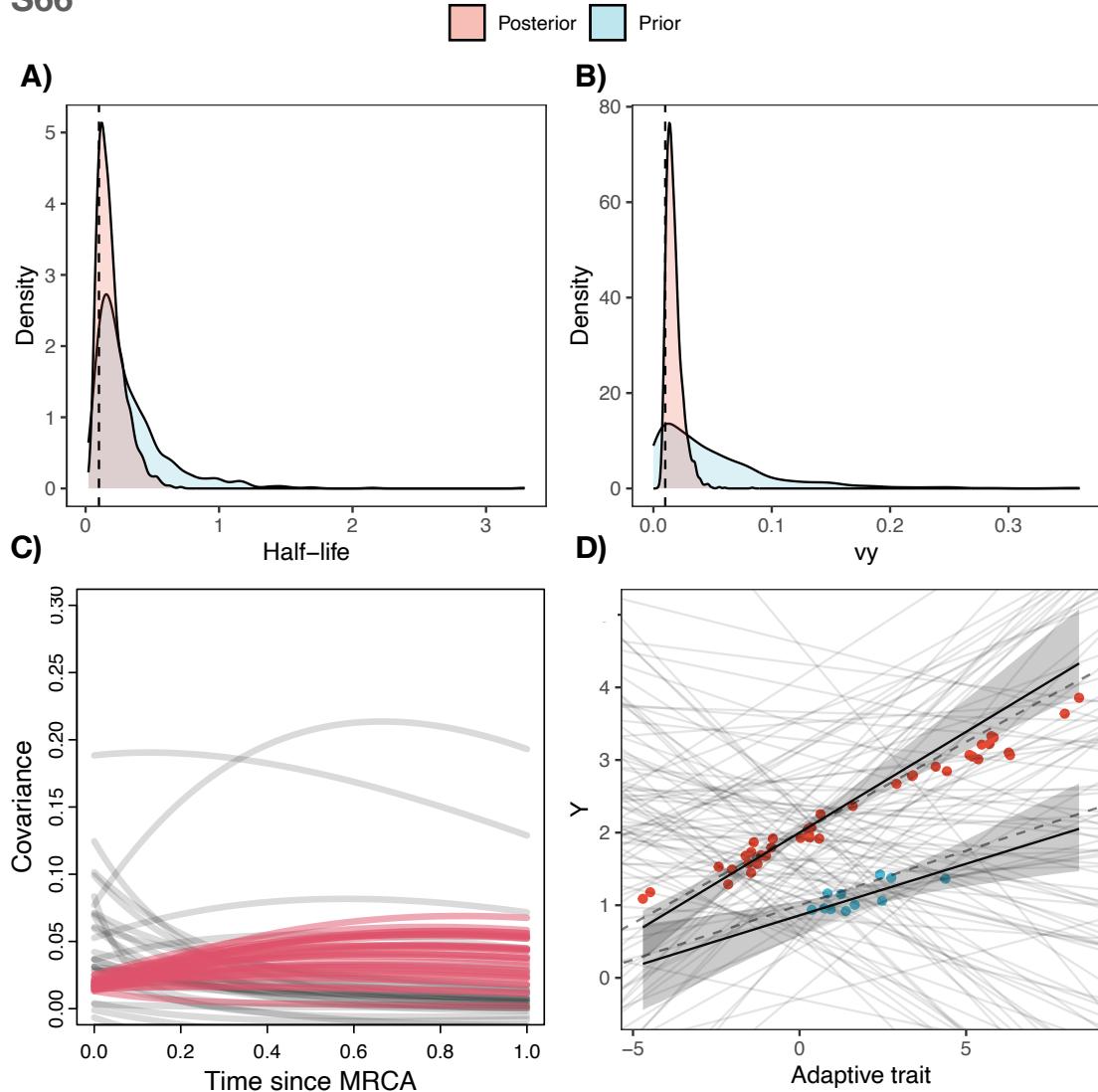


Fig. S66: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for

adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S66: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.09	0.00	0.05	0.03	0.05	0.08	0.11	0.21	700	1.00
vy	0.02	0.00	0.00	0.01	0.01	0.02	0.02	0.03	1689	1.00
optima[1]	1.93	0.00	0.04	1.85	1.91	1.93	1.95	2.00	2045	1.00
optima[2]	1.03	0.00	0.12	0.78	0.96	1.04	1.11	1.25	1236	1.00
beta[1,1]	0.25	0.00	0.03	0.21	0.23	0.24	0.26	0.31	761	1.00
beta[2,1]	0.12	0.00	0.04	0.06	0.10	0.12	0.15	0.21	1019	1.00
beta_e[1,1]	0.21	0.00	0.01	0.19	0.20	0.21	0.22	0.24	2357	1.00
beta_e[2,1]	0.11	0.00	0.03	0.05	0.09	0.11	0.13	0.17	1475	1.00

Fig. S67

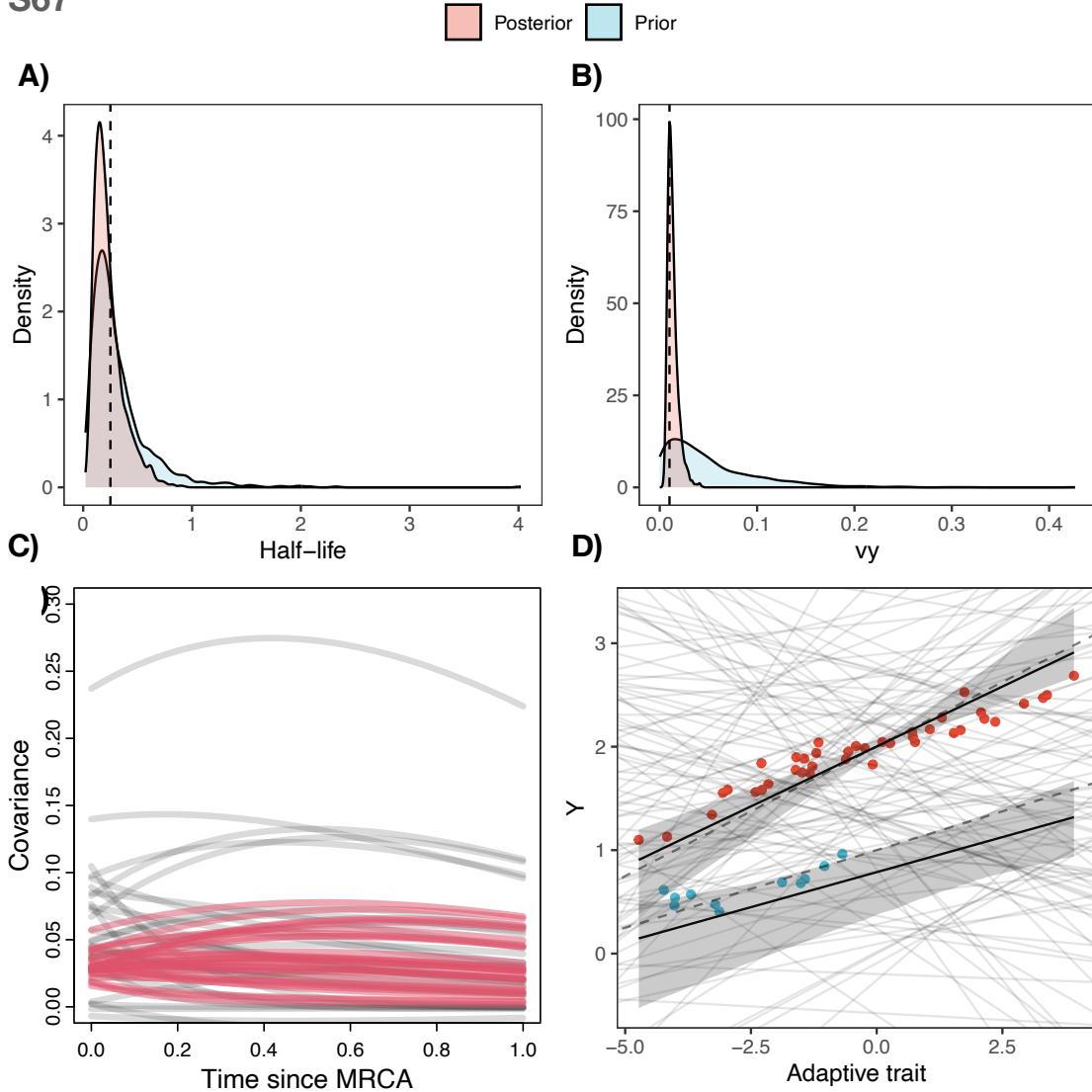


Fig. S67: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S67: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.35	0.01	0.17	0.13	0.23	0.32	0.44	0.74	459	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.02	0.03	790	1.00
optima[1]	1.98	0.00	0.06	1.86	1.95	1.98	2.02	2.10	1597	1.00
optima[2]	1.04	0.01	0.20	0.55	0.94	1.08	1.17	1.31	723	1.00
beta[1,1]	0.29	0.00	0.07	0.19	0.23	0.27	0.32	0.46	511	1.00
beta[2,1]	0.21	0.00	0.07	0.10	0.16	0.19	0.25	0.37	828	1.00
beta_e[1,1]	0.16	0.00	0.01	0.13	0.15	0.16	0.17	0.19	2240	1.00

<u>beta_e[2,1]</u>	0.11	0.00	0.03	0.06	0.10	0.11	0.13	0.17	2290	1.00
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Fig. S68

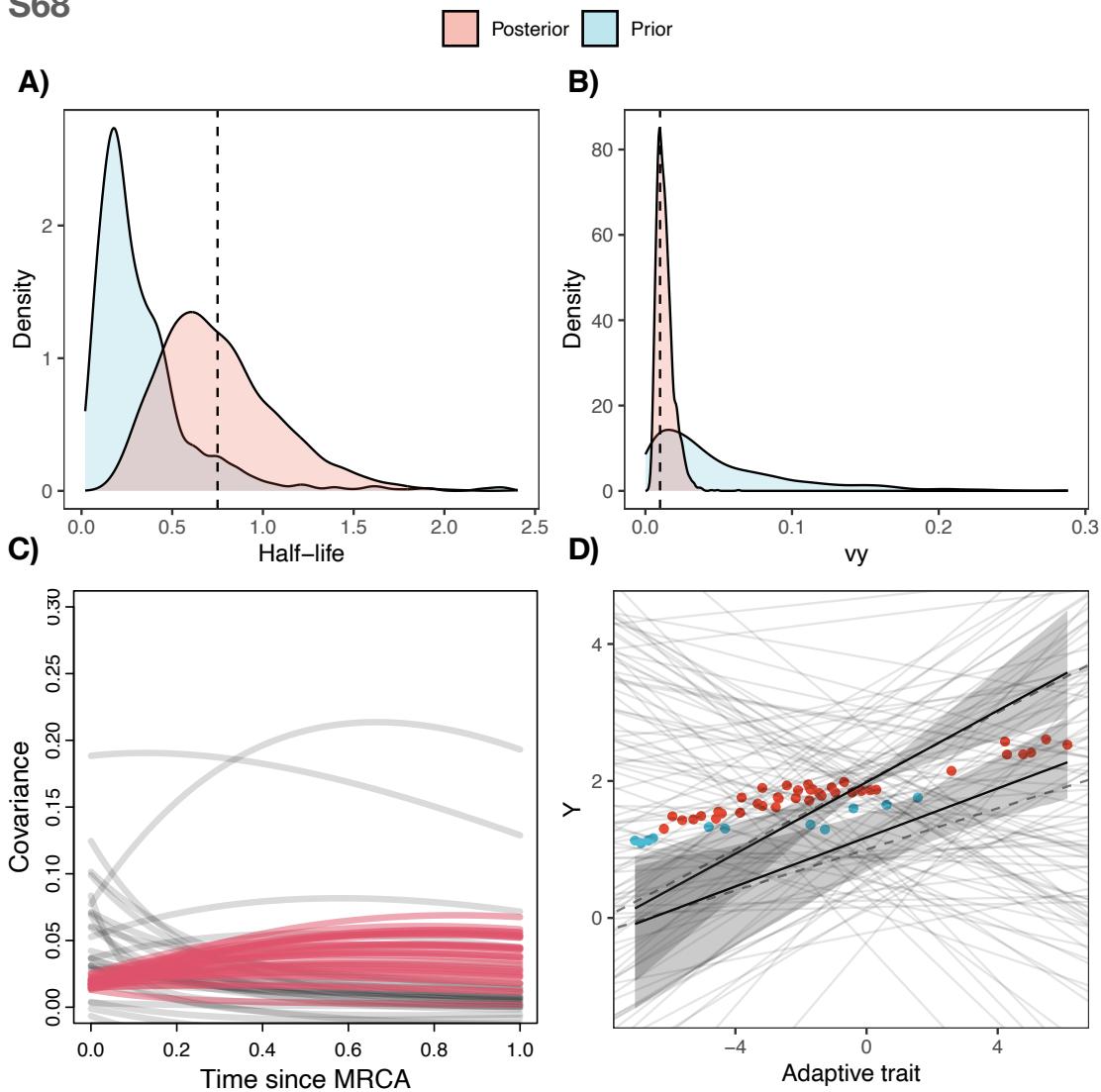


Fig. S68: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S68: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.76	0.01	0.32	0.27	0.52	0.70	0.94	1.52	743	1.00
vy	0.01	0.00	0.01	0.01	0.01	0.01	0.02	0.03	1043	1.00
optima[1]	1.98	0.00	0.05	1.88	1.95	1.98	2.02	2.09	4356	1.00
optima[2]	1.18	0.01	0.28	0.52	1.03	1.22	1.38	1.58	1050	1.00

beta[1,1]	0.26	0.00	0.08	0.14	0.20	0.25	0.31	0.45	768	1.00
beta[2,1]	0.18	0.00	0.07	0.08	0.13	0.17	0.22	0.34	988	1.00
beta_e[1,1]	0.09	0.00	0.01	0.08	0.08	0.09	0.10	0.11	1811	1.00
beta_e[2,1]	0.06	0.00	0.01	0.04	0.05	0.06	0.07	0.09	2375	1.00

Note the number of iterations is decreased to 1000 for the remaining validations.

Milestone 16: Combination of regime model with Adaptive Varying Effects and Measurement Error

blouchOU_reg_multiadaptive_ME_VarEff.stan

Fig. S69

Posterior Prior

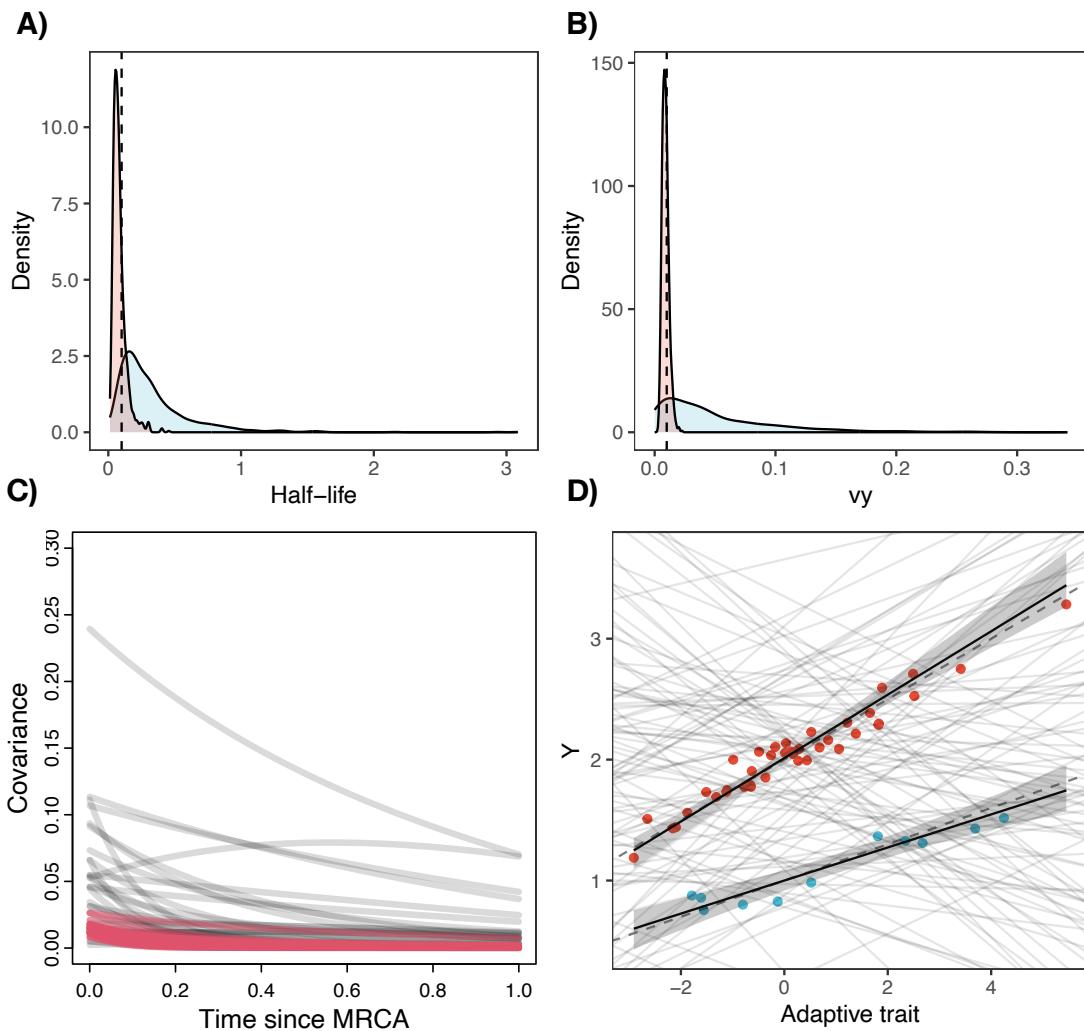


Fig. S69: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S69: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.08	0.00	0.05	0.03	0.05	0.07	0.10	0.23	141	1.01
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.02	866	1.00
optima_bar	1.64	0.02	0.54	0.60	1.31	1.60	1.95	2.82	721	1.00
beta_bar[1]	0.14	0.01	0.14	-0.24	0.07	0.16	0.22	0.36	620	1.00
optima[1]	2.01	0.00	0.03	1.95	1.99	2.01	2.03	2.07	921	1.00
optima[2]	1.00	0.00	0.06	0.87	0.97	1.00	1.04	1.11	290	1.00
beta[1,1]	0.26	0.00	0.03	0.22	0.24	0.26	0.27	0.34	146	1.01
beta[2,1]	0.14	0.00	0.02	0.09	0.12	0.13	0.15	0.20	388	1.00
beta_e[1,1]	0.23	0.00	0.01	0.20	0.22	0.23	0.24	0.25	925	1.00
beta_e[2,1]	0.12	0.00	0.02	0.08	0.11	0.12	0.13	0.16	1595	1.00

Fig. S70

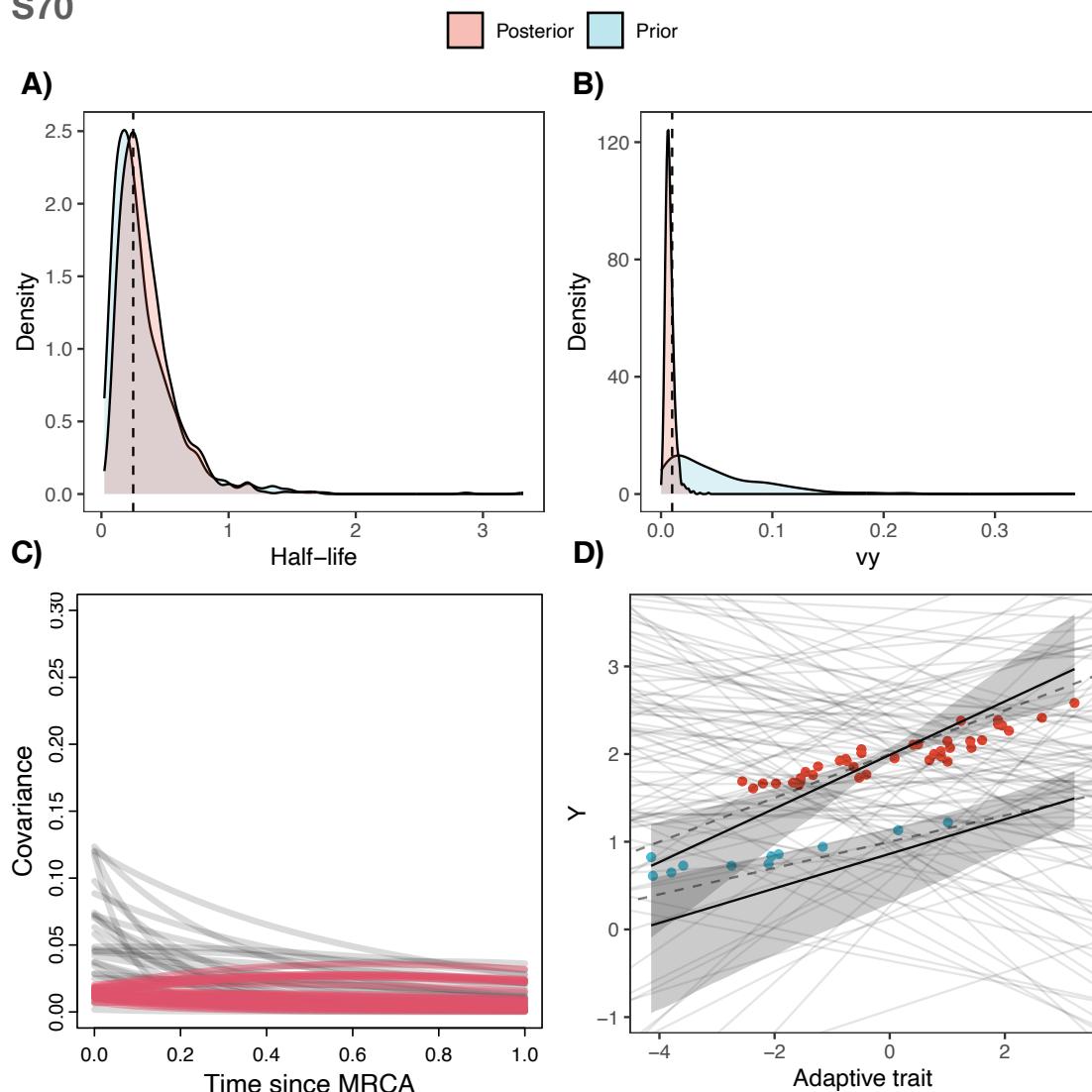


Fig. S70: Prior vs. posterior for A) Half-life; B) vy ; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for

adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S70: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.36	0.01	0.22	0.09	0.21	0.30	0.45	0.91	273	1.00
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.02	764	1.00
optima_bar	1.55	0.02	0.59	0.44	1.22	1.54	1.85	2.92	971	1.00
beta_bar[1]	0.17	0.01	0.15	-0.19	0.10	0.19	0.26	0.43	579	1.00
optima[1]	1.99	0.00	0.05	1.88	1.96	1.99	2.02	2.10	1159	1.00
optima[2]	0.86	0.02	0.30	0.07	0.76	0.96	1.05	1.18	275	1.00
beta[1,1]	0.31	0.01	0.11	0.18	0.23	0.28	0.35	0.58	280	1.00
beta[2,1]	0.20	0.00	0.08	0.10	0.14	0.18	0.23	0.39	324	1.00
beta_e[1,1]	0.17	0.00	0.01	0.14	0.16	0.17	0.18	0.20	984	1.00
beta_e[2,1]	0.11	0.00	0.02	0.07	0.10	0.11	0.12	0.15	944	1.00

Fig. S71

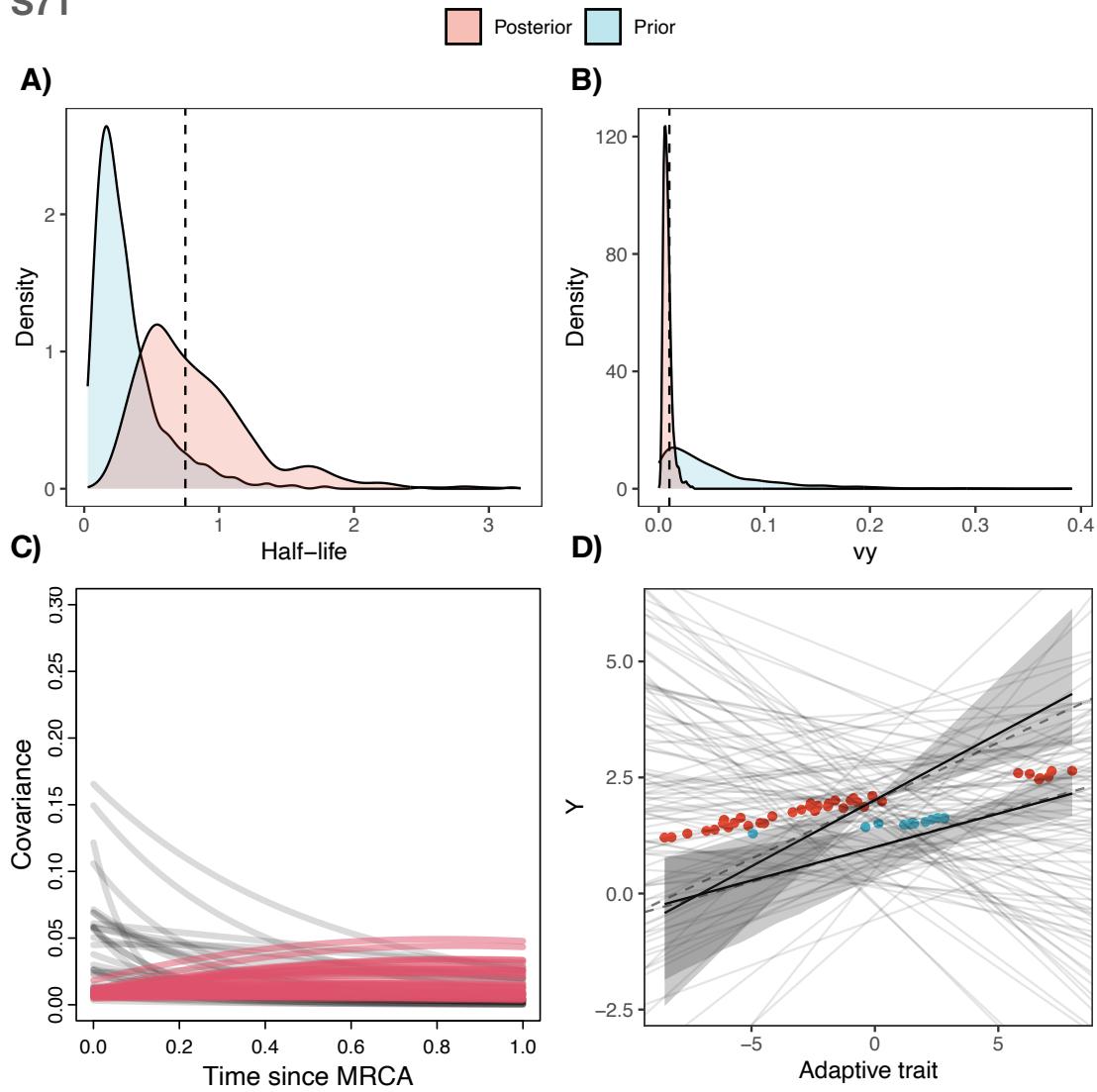


Fig. S71: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S71: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.83	0.04	0.45	0.27	0.52	0.74	1.03	1.95	141	1.01
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.02	235	1.00
optima_bar	1.56	0.02	0.55	0.42	1.26	1.57	1.85	2.71	660	1.00
beta_bar[1]	0.13	0.01	0.17	-0.26	0.04	0.15	0.23	0.43	431	1.00
optima[1]	2.01	0.00	0.05	1.92	1.99	2.01	2.04	2.11	1335	1.00
optima[2]	1.00	0.03	0.38	-0.01	0.83	1.10	1.27	1.43	152	1.01
beta[1,1]	0.29	0.01	0.12	0.14	0.20	0.26	0.34	0.60	141	1.01

beta[2,1]	0.14	0.01	0.07	0.05	0.09	0.13	0.18	0.31	184	1.00
beta_e[1,1]	0.09	0.00	0.01	0.08	0.09	0.09	0.09	0.10	742	1.00
beta_e[2,1]	0.05	0.00	0.01	0.03	0.04	0.05	0.05	0.07	1473	1.00

Milestone 17: Regime model with adaptive predictor and varying effects and measurement error – non-centered reparameterization
blouchOU_reg_multiadaptive_ME_VarEff_nc.stan

Fig. S72

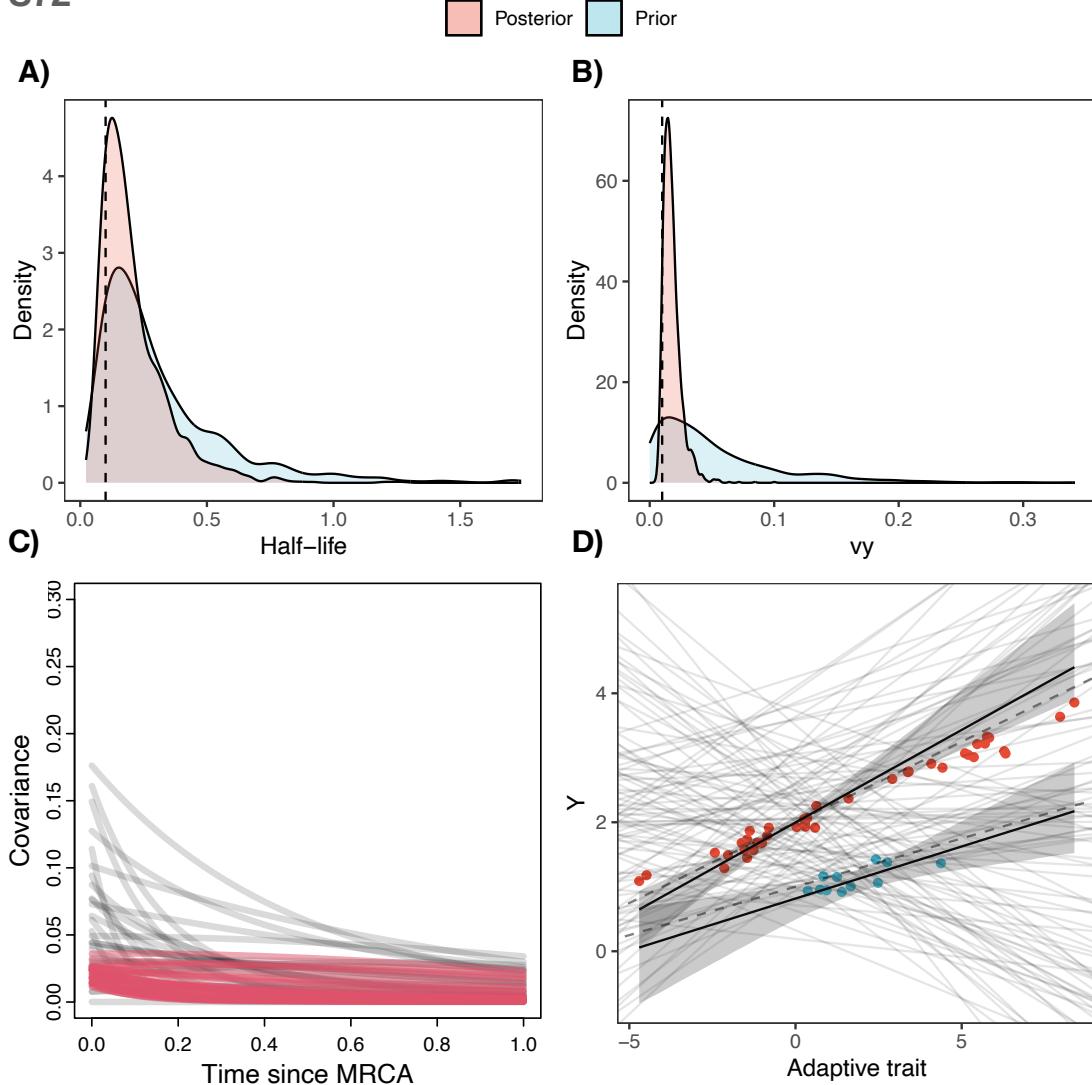


Fig. S72: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S72: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.21	0.00	0.13	0.06	0.12	0.17	0.26	0.56	1140	1.00
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	1198	1.00
optima_bar	1.62	0.02	0.58	0.52	1.25	1.60	1.95	2.87	1089	1.00
beta_bar	0.16	0.01	0.14	-0.17	0.09	0.19	0.25	0.40	731	1.00
optima[1]	2.00	0.00	0.06	1.89	1.96	1.99	2.03	2.12	2007	1.00
optima[2]	0.82	0.01	0.21	0.31	0.75	0.86	0.94	1.07	1404	1.00
beta[1,1]	0.29	0.00	0.07	0.22	0.25	0.27	0.31	0.46	1138	1.00
beta[2,1]	0.16	0.00	0.07	0.05	0.11	0.15	0.20	0.31	1656	1.00
beta_e[1,1]	0.20	0.00	0.01	0.18	0.20	0.20	0.21	0.22	1832	1.00
beta_e[2,1]	0.11	0.00	0.04	0.04	0.09	0.11	0.14	0.19	1635	1.00

Fig. S73

Posterior Prior

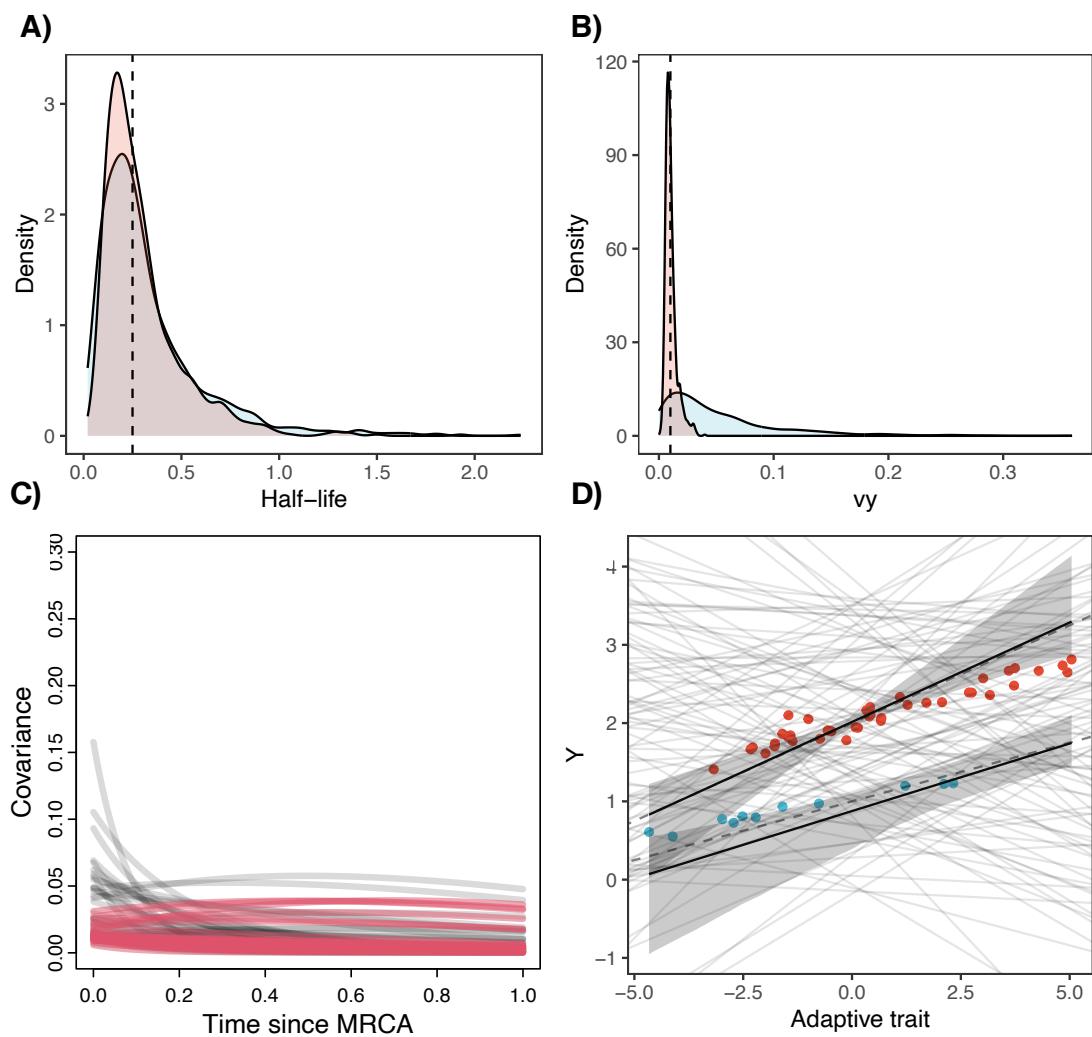


Fig. S73: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma).

Table S73: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.30	0.01	0.21	0.08	0.16	0.24	0.36	0.83	341	1.01
vy	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.03	412	1.01
optima_bar	1.59	0.03	0.57	0.52	1.25	1.57	1.91	2.88	407	1.00
beta_bar	0.17	0.01	0.13	-0.16	0.12	0.18	0.23	0.42	307	1.01
optima[1]	2.01	0.00	0.05	1.92	1.99	2.01	2.04	2.11	962	1.00
optima[2]	0.88	0.02	0.28	0.19	0.81	0.96	1.04	1.13	340	1.01
beta[1,1]	0.25	0.00	0.09	0.16	0.19	0.23	0.28	0.49	358	1.01
beta[2,1]	0.17	0.00	0.07	0.09	0.13	0.15	0.19	0.35	420	1.00
beta_e[1,1]	0.15	0.00	0.01	0.13	0.15	0.15	0.16	0.17	861	1.01
beta_e[2,1]	0.10	0.00	0.02	0.07	0.09	0.10	0.12	0.14	932	1.00

Fig. S74

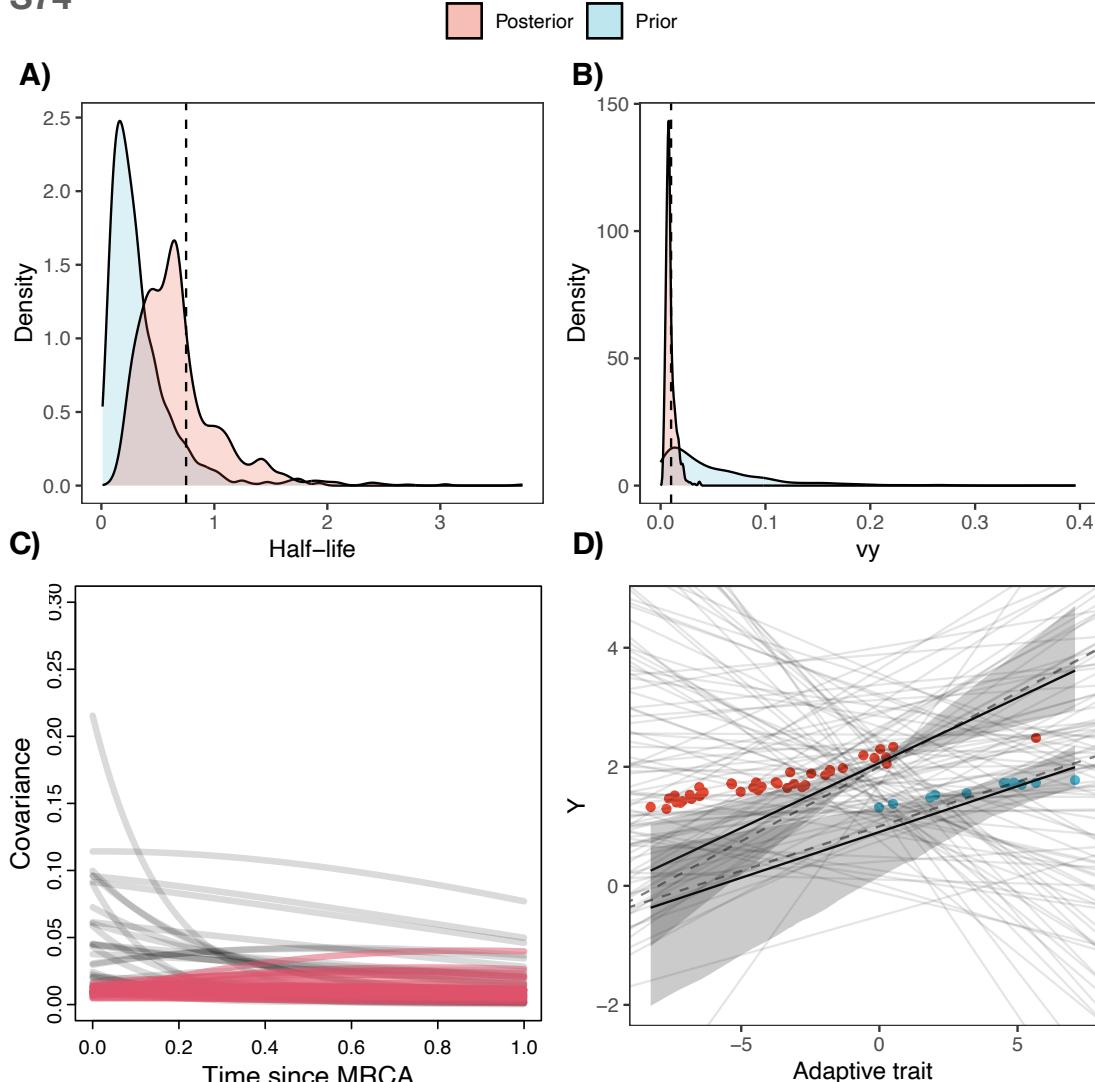


Fig. S74: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma).

Table S74: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.67	0.02	0.37	0.23	0.43	0.62	0.79	1.59	462	1.00
vy	0.01	0.00	0.00	0.00	0.01	0.01	0.01	0.02	432	1.00
optima_bar	1.51	0.04	0.65	0.08	1.24	1.50	1.84	2.74	212	1.01
beta_bar	0.14	0.01	0.13	-0.18	0.09	0.14	0.21	0.39	377	1.00
optima[1]	2.07	0.00	0.05	1.97	2.03	2.07	2.10	2.15	733	1.00
optima[2]	0.90	0.02	0.41	-0.24	0.79	1.00	1.17	1.37	494	1.00

beta[1,1]	0.22	0.00	0.08	0.12	0.16	0.20	0.25	0.44	464	1.00
beta[2,1]	0.15	0.00	0.07	0.07	0.11	0.14	0.18	0.32	574	1.00
beta_e[1,1]	0.08	0.00	0.01	0.07	0.08	0.08	0.09	0.09	845	1.00
beta_e[2,1]	0.06	0.00	0.01	0.03	0.05	0.06	0.07	0.08	555	1.00

Milestone 18: Regime model with direct and adaptive predictors with varying effects and measurement error

blouchOU_reg_multidirectadaptive_ME_VarEff.stan

Fig. S75

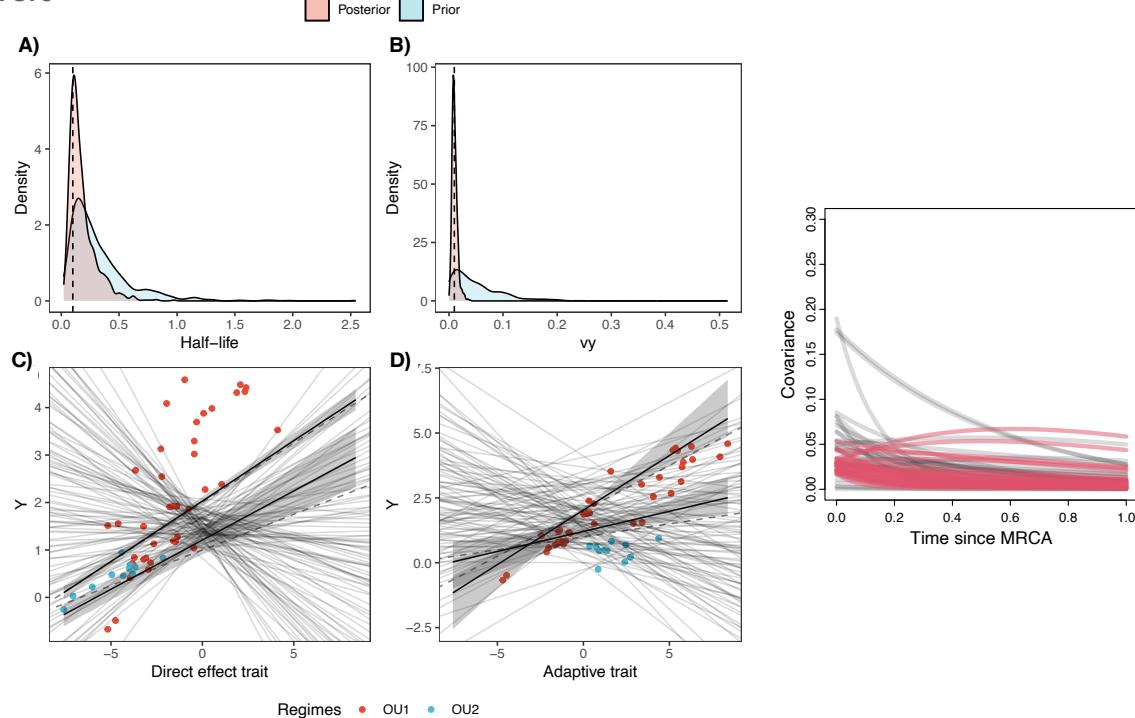


Fig. S75: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S75: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.18	0.01	0.12	0.05	0.10	0.14	0.22	0.50	163	1.02
vy	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.02	744	1.00
optima_bar	1.63	0.02	0.47	0.59	1.39	1.65	1.93	2.56	599	1.00
beta_bar[1]	0.18	0.01	0.13	-0.18	0.14	0.21	0.25	0.35	268	1.00
beta_bar[2]	0.15	0.01	0.19	-0.31	0.05	0.18	0.27	0.46	398	1.02
optima[1]	2.03	0.00	0.06	1.90	1.99	2.03	2.07	2.14	595	1.00

optima[2]	1.21	0.01	0.19	0.80	1.09	1.21	1.34	1.55	355	1.00
beta[1,1]	0.25	0.00	0.01	0.23	0.25	0.25	0.26	0.28	729	1.01
beta[1,2]	0.42	0.01	0.09	0.33	0.36	0.39	0.45	0.68	149	1.02
beta[2,1]	0.21	0.00	0.03	0.15	0.19	0.21	0.23	0.26	651	1.00
beta[2,2]	0.15	0.00	0.06	0.05	0.12	0.15	0.18	0.29	352	1.00
beta_e[1,1]	0.31	0.00	0.01	0.29	0.30	0.31	0.32	0.33	796	1.00
beta_e[2,1]	0.11	0.00	0.04	0.04	0.09	0.11	0.14	0.19	1020	1.00

Fig. S76

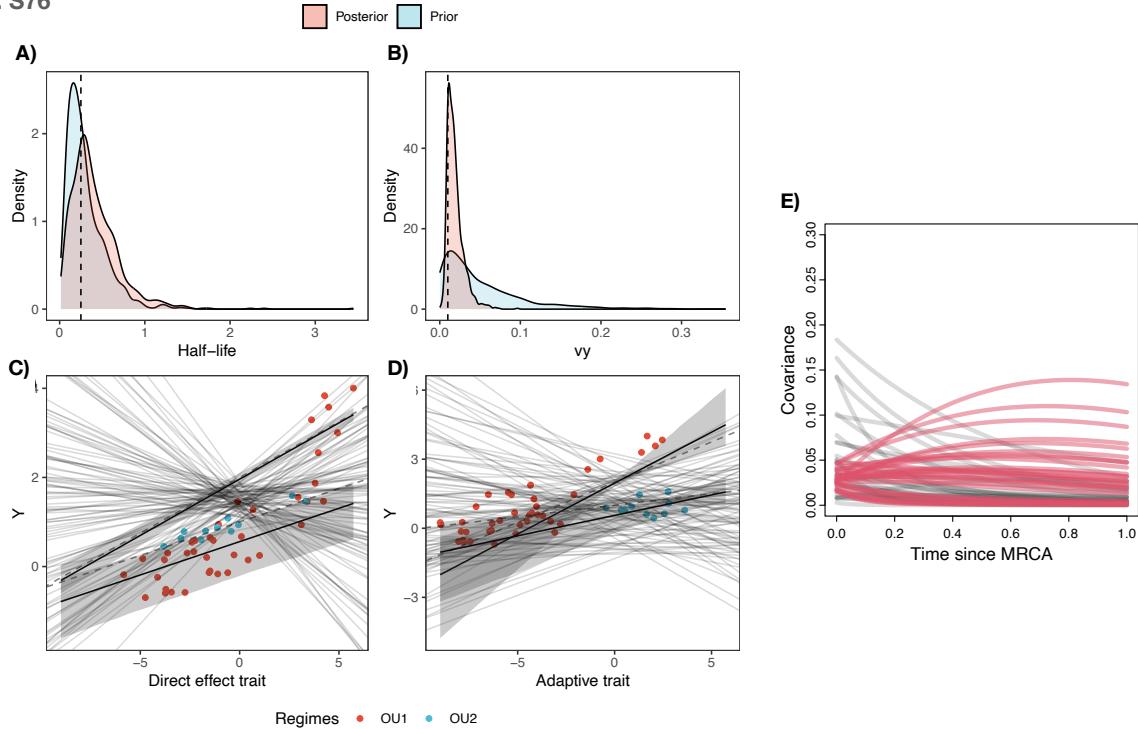


Fig. S76: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S76: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.41	0.03	0.26	0.07	0.23	0.35	0.54	1.10	65	1.03
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.05	207	1.01
optima_bar	1.07	0.02	0.60	-0.22	0.72	1.09	1.45	2.24	762	1.00
beta_bar[1]	0.14	0.01	0.15	-0.23	0.08	0.17	0.23	0.36	147	1.03
beta_bar[2]	0.16	0.01	0.19	-0.26	0.03	0.17	0.28	0.51	256	1.00
optima[1]	1.96	0.01	0.10	1.74	1.90	1.97	2.04	2.14	202	1.02
optima[2]	0.56	0.04	0.42	-0.60	0.39	0.68	0.86	1.03	113	1.01

beta[1,1]	0.25	0.00	0.01	0.22	0.24	0.25	0.26	0.28	34	1.06
beta[1,2]	0.44	0.02	0.16	0.27	0.33	0.40	0.51	0.89	100	1.02
beta[2,1]	0.15	0.00	0.02	0.11	0.14	0.15	0.16	0.19	399	1.01
beta[2,2]	0.18	0.01	0.09	0.05	0.11	0.16	0.22	0.43	156	1.01
beta_e[1,1]	0.23	0.00	0.01	0.20	0.22	0.23	0.24	0.25	93	1.03
beta_e[2,1]	0.09	0.00	0.03	0.03	0.07	0.09	0.11	0.16	948	1.00

Fig. S77

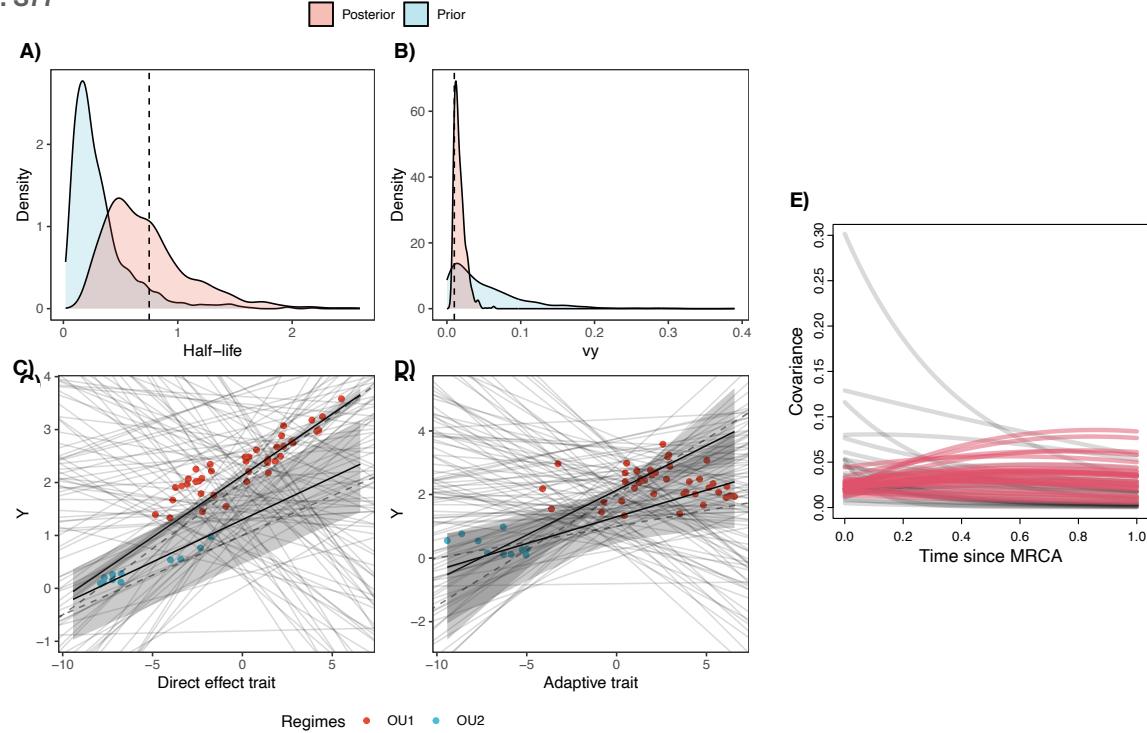


Fig. S77: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S77: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.73	0.03	0.38	0.25	0.45	0.65	0.89	1.72	164	1.02
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	211	1.01
optima_bar	1.81	0.03	0.55	0.61	1.51	1.84	2.12	2.98	463	1.00
beta_bar[1]	0.15	0.01	0.13	-0.15	0.09	0.17	0.22	0.39	447	1.01
beta_bar[2]	0.15	0.01	0.16	-0.21	0.07	0.16	0.25	0.44	569	1.00
optima[1]	2.13	0.00	0.06	2.01	2.10	2.13	2.17	2.24	873	1.00
optima[2]	1.30	0.03	0.50	0.25	1.00	1.34	1.67	2.10	337	1.00
beta[1,1]	0.23	0.00	0.01	0.22	0.23	0.23	0.24	0.25	167	1.01

beta[1,2]	0.28	0.01	0.11	0.13	0.20	0.26	0.33	0.57	156	1.02
beta[2,1]	0.16	0.00	0.02	0.13	0.15	0.16	0.17	0.19	450	1.00
beta[2,2]	0.17	0.01	0.11	0.02	0.10	0.14	0.22	0.44	241	1.01
beta_e[1,1]	0.10	0.00	0.01	0.08	0.09	0.10	0.11	0.12	214	1.02
beta_e[2,1]	0.06	0.00	0.03	0.01	0.04	0.06	0.08	0.11	453	1.00

Milestone 19: Regime model with direct and adaptive predictors with varying effects and measurement error – non-centered

blouchOU_reg_multidirectadaptive_ME_VarEff_nc.stan

Fig. S78

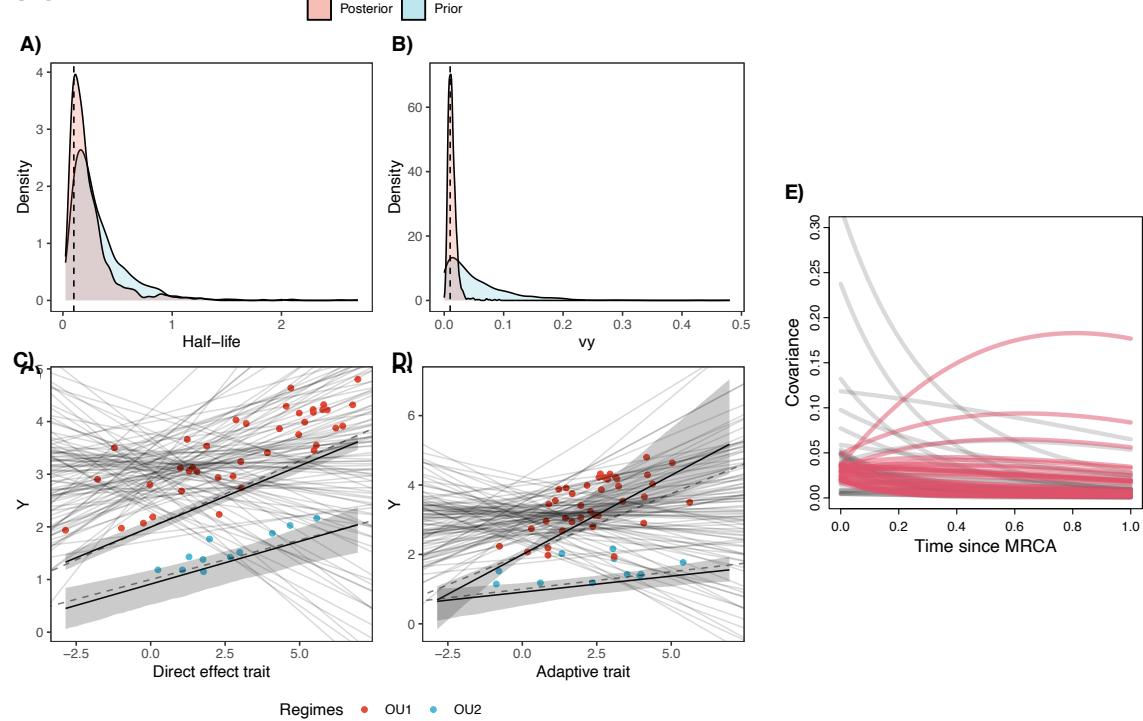


Fig. S78: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters. For this simulation parameter values were set to: hl=0.1, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S78: Summary table for half-life = 0.1

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.24	0.01	0.21	0.06	0.11	0.18	0.29	0.89	379	1.00
vy	0.01	0.00	0.01	0.00	0.01	0.01	0.02	0.03	355	1.00
optima_bar	2.62	0.02	0.47	1.74	2.28	2.64	2.91	3.62	464	1.00
beta_bar	0.18	0.01	0.08	-0.02	0.14	0.19	0.23	0.35	252	1.00
optima[1]	2.00	0.00	0.08	1.84	1.95	1.99	2.05	2.15	992	1.00
optima[2]	0.91	0.01	0.25	0.22	0.85	0.95	1.05	1.22	457	1.01

beta[1,1]	0.23	0.00	0.01	0.21	0.23	0.23	0.24	0.26	890	1.00
beta[1,2]	0.46	0.01	0.17	0.32	0.37	0.41	0.48	0.98	425	1.00
beta[2,1]	0.16	0.00	0.03	0.09	0.14	0.16	0.19	0.22	225	1.01
beta[2,2]	0.09	0.00	0.05	0.03	0.06	0.09	0.11	0.20	665	1.00
beta_e[1,1]	0.46	0.01	0.17	0.32	0.37	0.41	0.48	0.98	425	1.00
beta_e[2,1]	0.09	0.00	0.05	0.03	0.06	0.09	0.11	0.20	665	1.00

Fig. S79

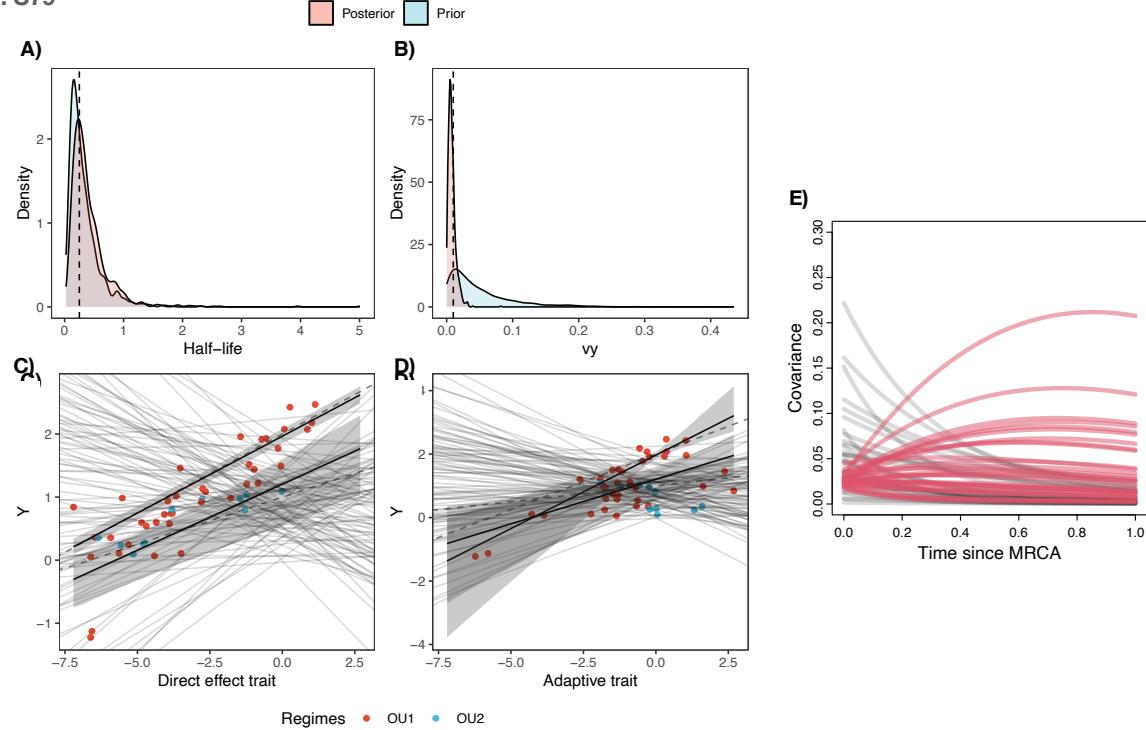


Fig. S79: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters.

For this simulation parameter values were set to: hl=0.25, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15);

Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S79: Summary table for half-life = 0.25

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.41	0.01	0.31	0.09	0.21	0.32	0.51	1.14	564	1.00
vy	0.01	0.00	0.01	0.00	0.00	0.01	0.01	0.02	599	1.00
optima_bar	1.21	0.02	0.45	0.27	0.93	1.27	1.53	1.94	477	1.00
beta_bar	0.24	0.01	0.08	0.05	0.20	0.24	0.27	0.41	238	1.00
optima[1]	1.97	0.00	0.07	1.80	1.92	1.97	2.01	2.10	1023	1.00
optima[2]	1.20	0.02	0.36	0.33	1.05	1.30	1.44	1.64	554	1.00

beta[1,1]	0.24	0.00	0.01	0.22	0.24	0.24	0.25	0.26	866	1.00
beta[1,2]	0.46	0.01	0.21	0.27	0.33	0.40	0.53	0.97	534	1.00
beta[2,1]	0.21	0.00	0.04	0.13	0.18	0.21	0.24	0.27	526	1.00
beta[2,2]	0.28	0.01	0.14	0.07	0.20	0.26	0.33	0.58	783	1.00
beta_e[1,1]	0.46	0.01	0.21	0.27	0.33	0.40	0.53	0.97	534	1.00
beta_e[2,1]	0.28	0.01	0.14	0.07	0.20	0.26	0.33	0.58	783	1.00

Fig. S80

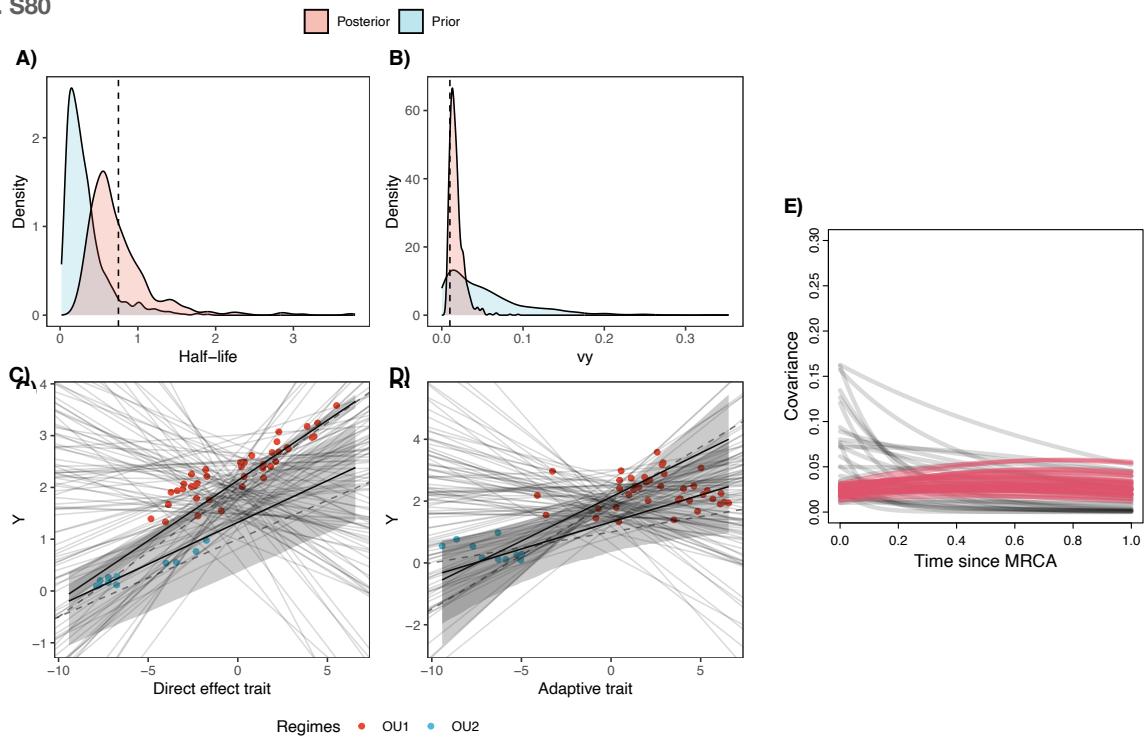


Fig. S80: Prior vs. posterior for A) Half-life; B) vy; C) Phylogenetic covariance as a reflection of time since MRCA with priors (grey lines) and posterior (light red line); and D) Posterior prediction means (black line) and 89% compatibility intervals (light grey region) for adaptive model with estimated optima, with priors in light grey. Species values are shown in colored circles. Dotted lines overlaying are true values of the parameters.

For this simulation parameter values were set to: hl=0.75, vy=0.01, optima=(2.0,1.5), beta=(0.25,0.15);

Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); beta~normal(0,0.25); sigma ~exponential(5); optima_bar ~normal(mean(Y),1); optima~normal(optima_bar,sigma)

Table S80: Summary table for half-life = 0.75

Parameter	mean	se_mean	sd	2.50%	25%	50%	75%	97.50%	n_eff	Rhat
hl	0.75	0.04	0.44	0.28	0.48	0.63	0.88	1.89	145	1.01
vy	0.02	0.00	0.01	0.01	0.01	0.02	0.02	0.04	181	1.01
optima_bar	1.75	0.04	0.54	0.60	1.47	1.80	2.06	2.73	230	1.01
beta_bar	0.20	0.01	0.08	0.07	0.16	0.19	0.23	0.36	99	1.01
optima[1]	2.13	0.00	0.06	2.02	2.09	2.13	2.18	2.25	960	1.00
optima[2]	1.32	0.03	0.58	0.04	1.06	1.41	1.71	2.11	347	1.00

beta[1,1]	0.23	0.00	0.01	0.22	0.23	0.23	0.24	0.25	913	1.00
beta[1,2]	0.28	0.01	0.13	0.15	0.21	0.25	0.33	0.63	154	1.01
beta[2,1]	0.16	0.00	0.02	0.13	0.15	0.16	0.17	0.19	472	1.01
beta[2,2]	0.17	0.01	0.11	0.02	0.11	0.16	0.22	0.41	249	1.01
beta_e[1,1]	0.28	0.01	0.13	0.15	0.21	0.25	0.33	0.63	154	1.01
beta_e[2,1]	0.17	0.01	0.11	0.02	0.11	0.16	0.22	0.41	249	1.01