**Blouch Systematic Biology Revision Validation Results – 2023**

Mark Grabowski

I evaluated the model’s performance on data I simulated, with scripts to reproduce simulated data available in the Simulation Code folder on github.com. All plots were made using the Prior and Posterior Plots – Simulations.Rmd script in the XX folder.

Data was simulated mirroring the causal model that generated the data. All data was simulated on a randomly sampled set of 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:

1. Short, medium, and long half-lives
2. Presence of measurement error
3. 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:

1. Increasing number of regimes
2. Multilevel model for regimes -
3. Single SIMMAP tree with increasing number of regimes
4. Multiple simmap trees

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)

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~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 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)

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~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 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)

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~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 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)

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~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 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)

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. S 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~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 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)

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~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 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

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)

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)

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~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 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)

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

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Parameter | mean | se\_mean | sd | 2.50% | 25% | 50% | 75% | 97.50% | n\_eff | Rhat |
| 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)

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~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 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)

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~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 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)

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**

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)

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~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 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)

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~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 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)

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~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 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)

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).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 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)

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)

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~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 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: 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: 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=(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: 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~lognormal(log(0.25),0.75); vy~exponential(20); beta~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: 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=(2.0,1.5,1.0,0.5); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima~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: 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~lognormal(log(0.25),0.75); vy~exponential(20); optima~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: 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: 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: 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: 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~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~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 |

**Milestone 5: Combination Regime with Direct Effect Model with Measurement Error**

Short half-life (hl=0.1)

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~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~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 |

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 |
| 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 |

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: 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 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: 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~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~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: 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: 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 |

Medium half-life (hl=0.25)

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~lognormal(log(0.25),0.75); vy~exponential(20); optima~normal(1.5,0.5), beta~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: 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)

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)

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~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 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)

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~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 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 |
| beta\_e[1] | 0.07 | 0.00 | 0.05 | -0.03 | 0.03 | 0.07 | 0.10 | 0.17 | 1970 | 1.00 |

**Milestone 7: Combination Regime with Direct and Adaptive Predictor Model with Measurement Error**

Short half-life (hl=0.1)

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)

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)

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~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 S44: 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 | 0.32 | 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)

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 |

Medium half-life (hl=0.25)

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 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=(2,1.5,1.0,0.5); Priors: hl~lognormal(log(0.25),0.75); vy~exponential(20); optima\_bar~lognornam(0,0.5); sigma~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: 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~lognormal(log(0.25),0.75); vy~exponential(20); optima\_bar~lognornam(0,1); sigma~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: 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: 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: 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 |