1. **Means**

**Contrast-based with complete dataset (higher temps = numerator)**

> # Fit model with phylogeny-ROM

> model1\_phylo <- rma.mv(yi ~ delta\_t + log(body\_mass\_g), V = vi, random = list(~1|study\_ID, ~1|species\_rotl, ~1|obs), R = list(species\_rotl = PhyloA), data = data\_verts\_ROM)

> model1\_phylo

Multivariate Meta-Analysis Model (k = 55; method: REML)

Variance Components:

estim sqrt nlvls fixed factor R

sigma^2.1 0.3111 0.5578 15 no study\_ID no

sigma^2.2 0.2172 0.4661 16 no species\_rotl yes

sigma^2.3 0.0542 0.2329 55 no obs no

Test for Residual Heterogeneity:

QE(df = 52) = 883.3388, p-val < .0001

Test of Moderators (coefficients 2:3):

QM(df = 2) = 59.1939, p-val < .0001

Model Results:

estimate se zval pval ci.lb ci.ub

intrcpt -2.0795 2.3854 -0.8718 0.3833 -6.7548 2.5957

delta\_t 0.1144 0.0151 7.5938 <.0001 0.0849 0.1439 \*\*\*

log(body\_mass\_g) 0.6050 0.6652 0.9094 0.3631 -0.6988 1.9088

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**Arm-based model**

model1 <- MCMCglmm(log(mean) ~ log(body\_mass\_g) + T, mev = data2$mean\_sv, random = ~us(1):study\_ID + us(1+T):species\_list, ginverse = list(species\_list = A), data = data2, prior = prior\_slope, nitt = 50000, burnin = 10000, thin = 30)

> summary(model1)

Iterations = 10001:49991

Thinning interval = 30

Sample size = 1334

DIC: -49.84003

G-structure: ~us(1):study\_ID

post.mean l-95% CI u-95% CI eff.samp

(Intercept):(Intercept).study\_ID 0.5485 0.03979 1.491 1334

~us(1 + T):species\_list

post.mean l-95% CI u-95% CI eff.samp

(Intercept):(Intercept).species\_list 8.4645 1.11263 19.0654 1334

T:(Intercept).species\_list -0.2249 -1.15587 0.4198 1553

(Intercept):T.species\_list -0.2249 -1.15587 0.4198 1553

T:T.species\_list 0.1965 0.07432 0.3822 1334

R-structure: ~units

post.mean l-95% CI u-95% CI eff.samp

units 0.01644 0.0009747 0.0418 496.3

Location effects: log(mean) ~ log(body\_mass\_g) + T

post.mean l-95% CI u-95% CI eff.samp pMCMC

(Intercept) 6.25832 2.46405 10.67176 1334 0.006 \*\*

log(body\_mass\_g) -0.13435 -0.35128 0.08492 1334 0.216

T -0.09578 -0.66080 0.45839 1334 0.747

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

1. **SD**

**Contrast-based with complete dataset**

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| > model1\_CVR <- rma.mv(yi ~ delta\_t + log(body\_mass\_g), V = vi, random =  list(~1|study\_ID, ~1|species\_rotl, ~1|obs), R = list(species\_rotl = PhyloA),  data = data\_verts\_CVR)  > model1\_CVR  Multivariate Meta-Analysis Model (k = 55; method: REML)  Variance Components:  estim sqrt nlvls fixed factor R  sigma^2.1 0.0788 0.2807 15 no study\_ID no  sigma^2.2 0.0582 0.2412 16 no species\_rotl yes  sigma^2.3 0.1234 0.3512 55 no obs no  Test for Residual Heterogeneity:  QE(df = 52) = 140.7016, p-val < .0001  Test of Moderators (coefficients 2:3):  QM(df = 2) = 3.7492, p-val = 0.1534  Model Results:  estimate se zval pval ci.lb ci.ub  intrcpt 3.4736 2.2354 1.5539 0.1202 -0.9077 7.8548  delta\_t -0.0243 0.0231 -1.0493 0.2940 -0.0696 0.0211  log(body\_mass\_g) -0.9223 0.6312 -1.4611 0.1440 -2.1596 0.3149  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  **Arm-based model**  model2 <- MCMCglmm(log(sd) ~ log(mean) + log(body\_mass\_g) + T,  mev = data2$sd\_sv, random = ~us(1):study\_ID + us(1+T):species\_list,  ginverse = list(species\_list = A), data = data2, prior = prior\_slope,  nitt = 50000, burnin = 10000, thin = 30)  > summary(model2)  Iterations = 10001:49991  Thinning interval = 30  Sample size = 1334  DIC: -111.8982  G-structure: ~us(1):study\_ID  post.mean l-95% CI u-95% CI eff.samp  (Intercept):(Intercept).study\_ID 0.3714 0.002252 1.516 1231  ~us(1 + T):species\_list  post.mean l-95% CI u-95% CI eff.samp  (Intercept):(Intercept).species\_list 2.43756 0.12513 8.0572 874.2  T:(Intercept).species\_list -0.07947 -0.67195 0.3446 1334.0  (Intercept):T.species\_list -0.07947 -0.67195 0.3446 1334.0  T:T.species\_list 0.22048 0.07726 0.4211 1334.0  R-structure: ~units  post.mean l-95% CI u-95% CI eff.samp  units 0.05113 8.941e-05 0.235 348.1  Location effects: log(sd) ~ log(mean) + log(body\_mass\_g) + T  post.mean l-95% CI u-95% CI eff.samp pMCMC  (Intercept) -3.98396 -14.83781 5.92891 1334 0.4378  log(mean) 1.40868 0.29539 2.67213 1334 0.0225 \*  log(body\_mass\_g) 0.07204 -0.64621 0.76033 1334 0.8231  T 0.06361 -0.54236 0.65502 1334 0.8126  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 |
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