**Bayes mosquito model summary- Virginia attempt**

Questions:

* Brms default family is linear gaussian. That works for my models, right?
* Not quite sure how to set the prior for a random effect
* I compared the model for larvae development with (brm1.m) and without (brm1) the interaction of state\* temp and the results appear the same?
  + And family (brm1.2) didn’t appear much different?
* Get prior error when I try to look at multivariate relationship between larvae, adult life and wing length

1. Looking at count (comparing dead vs alive)

> summary(brm0)

Family: gaussian

Links: mu = identity; sigma = identity

Formula: count ~ 1 + Temp\_num + State

Data: all.sum.nosex (Number of observations: 433)

Samples: 2 chains, each with iter = 3000; warmup = 1500; thin = 5;

total post-warmup samples = 600

ICs: LOO = NA; WAIC = NA; R2 = NA

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

Intercept 8.80 1.76 5.45 12.10 600 1.00

Temp\_num -0.05 0.07 -0.18 0.08 600 1.00

StateRondonia -0.05 0.45 -0.94 0.82 558 1.00

StateTocantins -0.49 0.56 -1.55 0.67 600 1.00

StateRiodeJaneiro -0.05 0.58 -1.12 1.16 500 1.01

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sigma 4.83 0.17 4.54 5.17 460 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample

is a crude measure of effective sample size, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

> fixef(brm0)

Estimate Est.Error 2.5%ile 97.5%ile

Intercept 8.79674756 1.75918978 5.4474335 12.09547200

Temp\_num -0.04921197 0.07164102 -0.1845052 0.07866465

StateRondonia -0.04983183 0.44707143 -0.9399359 0.81534700

StateTocantins -0.48669384 0.56363449 -1.5502070 0.67187771

StateRiodeJaneiro -0.05167428 0.57585804 -1.1244294 1.16062634

> bayes\_R2(brm0)

Estimate Est.Error 2.5%ile 97.5%ile

R2 0.008976939 0.00595602 0.001072126 0.02214511

* Tocantins had a larger difference than other states or temperature, but not on the same scale as the intercept. Can I conclude that there were not significant differences in dead or alive larvae by population or treatment?

1. Larvae development

> summary(brm1)

Family: gaussian

Links: mu = identity; sigma = identity

Formula: mean.sLL ~ 1 + Temp\_fac + State

Data: adult.sum.nosex (Number of observations: 232)

Samples: 2 chains, each with iter = 3000; warmup = 1500; thin = 5;

total post-warmup samples = 600

ICs: LOO = NA; WAIC = NA; R2 = NA

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

Intercept 31.04 0.57 29.90 32.10 457 1.01

Temp\_fac -0.63 0.02 -0.67 -0.58 455 1.00

StateRondonia 1.63 0.17 1.30 1.96 571 1.00

StateTocantins 3.25 0.23 2.76 3.70 600 1.00

StateRiodeJaneiro 3.68 0.24 3.17 4.13 593 1.00

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sigma 1.14 0.05 1.05 1.26 537 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample

is a crude measure of effective sample size, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

> bayes\_R2(brm1)

Estimate Est.Error 2.5%ile 97.5%ile

R2 0.8253442 0.01035892 0.8020984 0.84241

* Increasing temperature reduced larvae development time and increasing latitude and across biomes increased larvae development time. Tocantins (Cerrado) and Rio (Mata Atlantica) were not very different.

> summary(brm1.m)

 Family: gaussian

  Links: mu = identity; sigma = identity

Formula: mean.sLL ~ 1 + Temp\_fac \* State

   Data: adult.sum.nosex (Number of observations: 232)

Samples: 2 chains, each with iter = 3000; warmup = 1500; thin = 5;

         total post-warmup samples = 600

    ICs: LOO = NA; WAIC = NA; R2 = NA

Population-Level Effects:

                           Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

Intercept                 32.15      0.67    30.82    33.46        600 1.00

Temp\_fac                   -0.68      0.03    -0.73    -0.62        600 1.00

StateRondonia              0.84      0.78    -0.66     2.37        577 1.00

StateTocantins             -0.71      0.84    -2.33     0.94        600 1.00

StateRiodeJaneiro          2.30      0.87     0.54     4.09        600 1.01

Temp\_fac:StateRondonia      0.04      0.03    -0.02     0.10        587 1.00

Temp\_fac:StateTocantins    0.18      0.04     0.11     0.24        600 1.00

Temp\_fac:StateRiodeJaneiro  0.07      0.04    -0.01     0.14        600 1.01

Family Specific Parameters:

      Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sigma     1.13      0.05     1.04     1.24        478 1.00

> bayes\_R2(brm1.m)

    Estimate   Est.Error   2.5%ile  97.5%ile

R2 0.8350492 0.008225556 0.8168905 0.8500667

summary(brm1.2)

 Family: gaussian

  Links: mu = identity; sigma = identity

Formula: mean.sLL ~ 1 + Temp\_num + State + (1 | Fam\_new)

   Data: all.sum.nosex (Number of observations: 232)

Samples: 2 chains, each with iter = 3000; warmup = 1500; thin = 5;

         total post-warmup samples = 600

    ICs: LOO = NA; WAIC = NA; R2 = NA

Group-Level Effects:

~Fam\_new (Number of levels: 78)

              Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sd(Intercept)     0.42      0.15     0.06     0.67        261 1.01

Population-Level Effects:

                  Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

Intercept            31.06      0.54    30.07    32.16        600 1.00

Temp\_num             -0.63      0.02    -0.67    -0.59        600 1.00

StateRondonia         1.59      0.21     1.16     1.97        476 1.00

StateTocantins        3.17      0.25     2.68     3.63        600 1.00

StateRiodeJaneiro     3.61      0.28     3.01     4.14        600 1.00

Family Specific Parameters:

      Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sigma     1.07      0.06     0.96     1.19        547 1.01

1. Adult lifespan

> summary(brm2)

Family: gaussian

Links: mu = identity; sigma = identity

Formula: mean.AL ~ 1 + Temp\_fac + State

Data: adult.sum.nosex (Number of observations: 232)

Samples: 2 chains, each with iter = 3000; warmup = 1500; thin = 5;

total post-warmup samples = 600

ICs: LOO = NA; WAIC = NA; R2 = NA

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

Intercept 10.57 0.21 10.16 11.00 584 1.00

Temp\_fac -0.31 0.01 -0.32 -0.29 578 1.00

StateRondonia -0.32 0.06 -0.44 -0.20 565 1.00

StateTocantins -0.62 0.09 -0.79 -0.46 600 1.00

StateRiodeJaneiro -0.16 0.09 -0.34 0.01 600 1.00

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sigma 0.43 0.02 0.39 0.47 410 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample

is a crude measure of effective sample size, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

> fixef(brm2)

Estimate Est.Error 2.5%ile 97.5%ile

Intercept 10.5708132 0.212701402 10.1582339 10.996699448

Temp\_fac -0.3063994 0.008609926 -0.3239842 -0.290082259

StateRondonia -0.3174390 0.063702008 -0.4417309 -0.199209437

StateTocantins -0.6237952 0.087278257 -0.7910687 -0.461440918

StateRiodeJaneiro -0.1586125 0.090349462 -0.3406958 0.005918647

> bayes\_R2(brm2)

Estimate Est.Error 2.5%ile 97.5%ile

R2 0.8528954 0.007002762 0.8370509 0.8647286

* Increasing temperature increased adult life. Differences by state were complex, with differences within Amazon biome but Rio is more similar to Amazonas than Amazonas is to Rondonia? Tocantins and Rio are more distinct than they were by larvae development

> summary(brm3)

Family: gaussian

Links: mu = identity; sigma = identity

Formula: mean.wing ~ 1 + Temp\_fac + State

Data: adult.sum.nosex (Number of observations: 232)

Samples: 2 chains, each with iter = 3000; warmup = 1500; thin = 5;

total post-warmup samples = 600

ICs: LOO = NA; WAIC = NA; R2 = NA

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

Intercept 3.45 0.03 3.39 3.52 539 1.00

Temp\_fac -0.03 0.00 -0.04 -0.03 459 1.00

StateRondonia 0.01 0.01 -0.01 0.04 514 1.00

StateTocantins 0.08 0.01 0.05 0.10 600 1.00

StateRiodeJaneiro 0.18 0.01 0.15 0.21 513 1.01

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat

sigma 0.07 0.00 0.06 0.07 600 1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample

is a crude measure of effective sample size, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

> fixef(brm3)

Estimate Est.Error 2.5%ile 97.5%ile

Intercept 3.45378493 0.034008906 3.392262890 3.51608879

Temp\_fac -0.03413711 0.001398454 -0.036684565 -0.03144715

StateRondonia 0.01411588 0.011306204 -0.006312604 0.03631874

StateTocantins 0.07687021 0.013101485 0.051879697 0.10277863

StateRiodeJaneiro 0.17999728 0.014190970 0.153484677 0.20974411

> bayes\_R2(brm3)

Estimate Est.Error 2.5%ile 97.5%ile

R2 0.7868082 0.01192175 0.7595281 0.8059609