> summary(mbrm)

Family: poisson

Links: mu = log

Formula: count ~ mixed + (1 | species) + (1 | leafID)

Data: df1 (Number of observations: 951)

Samples: 3 chains, each with iter = 2000; warmup = 1000; thin = 1;

 total post-warmup samples = 3000

Group-Level Effects:

~leafID (Number of levels: 317)

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

sd(Intercept) 1.18 0.06 1.07 1.31 1.00

Bulk\_ESS Tail\_ESS

sd(Intercept) 447 1079

~species (Number of levels: 10)

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

sd(Intercept) 1.19 0.39 0.68 2.22 1.00

Bulk\_ESS Tail\_ESS

sd(Intercept) 929 1351

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS

Intercept -0.72 0.80 -2.34 0.89 1.00 695

mixed 0.02 0.01 -0.01 0.04 1.00 812

Tail\_ESS

Intercept 1131

mixed 1260

> mbrm %>%

+ gather\_draws(b\_Intercept, b\_mixed, sd\_leafID\_\_Intercept, sd\_species\_\_Intercept) %>%

+ median\_qi(.width=c(.9, .95))

# A tibble: 8 x 7

.variable .value .lower .upper .width .point .interval

<chr> <dbl> <dbl> <dbl> <dbl> <chr> <chr>

1 b\_Intercept -0.707 -2.06 0.557 0.9 median qi

2 b\_mixed 0.0161 -0.00364 0.0357 0.9 median qi

3 sd\_leafID\_… 1.17 1.08 1.29 0.9 median qi

4 sd\_species… 1.11 0.728 1.90 0.9 median qi

5 b\_Intercept -0.707 -2.34 0.890 0.95 median qi

6 b\_mixed 0.0161 -0.00917 0.0411 0.95 median qi

7 sd\_leafID\_… 1.17 1.07 1.31 0.95 median qi

8 sd\_species… 1.11 0.678 2.22 0.95 median qi

> summary(m1)

Family: poisson

Links: mu = log

Formula: count ~ -1 + species + (1 | leafID) + offset(log(prop))

Data: df2 (Number of observations: 159)

Samples: 3 chains, each with iter = 4000; warmup = 2000; thin = 1;

total post-warmup samples = 6000

Group-Level Effects:

~leafID (Number of levels: 159)

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

sd(Intercept) 2.33 0.18 2.00 2.71 1.00 1004 2206

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

speciesACMA 7.41 0.42 6.61 8.20 1.01 449 1055

speciesARME 2.98 0.42 2.17 3.75 1.00 466 929

speciesCEOL 6.54 0.42 5.69 7.37 1.01 467 894

speciesLIDE -1.68 0.60 -2.92 -0.56 1.00 1537 2820

speciesTODI 0.87 0.48 -0.14 1.76 1.00 1459 2459

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).

>

> m1 %>%

+ gather\_draws(b\_speciesACMA, b\_speciesARME, b\_speciesCEOL, b\_speciesLIDE, b\_speciesTODI, sd\_leafID\_\_Intercept) %>%

+ median\_qi(.width=c(.9, .95))

# A tibble: 12 x 7

.variable .value .lower .upper .width .point .interval

<chr> <dbl> <dbl> <dbl> <dbl> <chr> <chr>

1 b\_speciesACMA 7.42 6.74 8.09 0.9 median qi

2 b\_speciesARME 2.99 2.28 3.64 0.9 median qi

3 b\_speciesCEOL 6.54 5.85 7.21 0.9 median qi

4 b\_speciesLIDE -1.66 -2.70 -0.734 0.9 median qi

5 b\_speciesTODI 0.883 0.0540 1.63 0.9 median qi

6 sd\_leafID\_\_Intercept 2.32 2.05 2.65 0.9 median qi

7 b\_speciesACMA 7.42 6.61 8.20 0.95 median qi

8 b\_speciesARME 2.99 2.17 3.75 0.95 median qi

9 b\_speciesCEOL 6.54 5.69 7.37 0.95 median qi

10 b\_speciesLIDE -1.66 -2.92 -0.558 0.95 median qi

11 b\_speciesTODI 0.883 -0.138 1.76 0.95 median qi

12 sd\_leafID\_\_Intercept 2.32 2.00 2.71 0.95 median qi

> pr %>% median\_qi(.width=c(.9, .95))

# A tibble: 10 x 9

# Groups: species, prop [5]

species prop .row .value .lower .upper .width .point

<fct> <dbl> <int> <dbl> <dbl> <dbl> <dbl> <chr>

1 ACMA 1 1 1.68e+3 8.46e+2 3.26e+3 0.9 median

2 ARME 1 2 1.99e+1 9.80e+0 3.82e+1 0.9 median

3 CEOL 1 3 6.95e+2 3.48e+2 1.35e+3 0.9 median

4 LIDE 1 4 1.91e-1 6.73e-2 4.80e-1 0.9 median

5 TODI 1 5 2.42e+0 1.06e+0 5.12e+0 0.9 median

6 ACMA 1 1 1.68e+3 7.39e+2 3.64e+3 0.95 median

7 ARME 1 2 1.99e+1 8.74e+0 4.26e+1 0.95 median

8 CEOL 1 3 6.95e+2 2.95e+2 1.59e+3 0.95 median

9 LIDE 1 4 1.91e-1 5.39e-2 5.72e-1 0.95 median

10 TODI 1 5 2.42e+0 8.71e-1 5.82e+0 0. 95 median