RESULTS BRMS OBJECTIVE 1

> summary(model2)

Family: beta

Links: mu = logit; phi = identity

Formula: Perlocation ~ Host\_Status

Data: dados4 (Number of observations: 667)

Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;

total post-warmup samples = 4000

Population-Level Effects:

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

Intercept -4.64 0.11 -4.86 -4.43 1.00 1326 1885

Host\_StatusPM -0.04 0.18 -0.42 0.31 1.00 2086 2700

Host\_StatusR 0.09 0.11 -0.12 0.32 1.00 1459 2130

Host\_StatusR\_M 0.88 0.15 0.58 1.17 1.00 1598 2323

Host\_StatusR\_PM 0.76 0.14 0.50 1.02 1.00 1760 2564

Host\_StatusR\_PM\_M 1.56 0.17 1.22 1.88 1.00 1991 2447

Family Specific Parameters:

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

phi 194.77 11.39 173.44 217.48 1.00 3036 3314

Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

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

> parameters::p\_value(model2)

Parameter p

1 b\_Intercept 0.000

2 b\_Host\_StatusPM 0.817

3 b\_Host\_StatusR 0.421

4 b\_Host\_StatusR\_M 0.000

5 b\_Host\_StatusR\_PM 0.000

6 b\_Host\_StatusR\_PM\_M 0.000

> plot$Host\_Status$data$estimate\_\_

[1] 0.009657210 0.009325139 0.010532317 0.023004869 0.020317839 0.044498106

> plot$Host\_Status$data$lower\_\_

[1] 0.007804603 0.006865527 0.009947991 0.018748621 0.017284341 0.034454136

> plot$Host\_Status$data$upper\_\_

[1] 0.01173459 0.01209398 0.01112132 0.02755341 0.02357926 0.05524896

plot$Host\_Status$data$se\_\_

[1] 0.0009968639 0.0013496914 0.0003038824 0.0022848043 0.0016260828 0.0053705089

**PLASMODIUM**

> summary(model4)

Family: beta

Links: mu = logit; phi = identity

Formula: Perlocation ~ Host\_Status

Data: dados6 (Number of observations: 410)

Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;

total post-warmup samples = 4000

Population-Level Effects:

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

Intercept -4.77 0.20 -5.18 -4.41 1.00 1110 1565

Host\_StatusPM 0.08 0.28 -0.47 0.65 1.00 1658 1851

Host\_StatusR 0.24 0.20 -0.13 0.65 1.00 1133 1385

Host\_StatusR\_M 1.03 0.25 0.54 1.54 1.00 1316 1877

Host\_StatusR\_PM 1.02 0.23 0.60 1.48 1.00 1239 1582

Host\_StatusR\_PM\_M 2.83 0.23 2.41 3.29 1.00 1215 1454

Family Specific Parameters:

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

phi 204.84 14.77 176.72 235.01 1.00 2635 2686

Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

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

> parameters::p\_value(model4)

Parameter p

1 b\_Intercept 0.0000

2 b\_Host\_StatusPM 0.7625

3 b\_Host\_StatusR 0.2370

4 b\_Host\_StatusR\_M 0.0000

5 b\_Host\_StatusR\_PM 0.0000

6 b\_Host\_StatusR\_PM\_M 0.0000

> plot2 <- plot(conditional\_effects(model4), points = FALSE, theme = a)

> plot2$Host\_Status$data$estimate\_\_

[1] 0.008515367 0.009251122 0.010661664 0.023455197 0.023130909 0.126235238

> plot2$Host\_Status$data$lower\_\_

[1] 0.005611104 0.006002381 0.009989841 0.016996693 0.018603496 0.103914951

> plot2$Host\_Status$data$upper\_\_

[1] 0.01205595 0.01324077 0.01140572 0.03095470 0.02837997 0.14864661

plot2$Host\_Status$data$se\_\_

[1] 0.0016797096 0.0018670094 0.0003706215 0.0035488382 0.0025002969 0.0115883490

**HAEMOPROTEUS**

> summary(model5)

Family: beta

Links: mu = logit; phi = identity

Formula: Perlocation ~ Host\_Status

Data: dados7 (Number of observations: 226)

Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;

total post-warmup samples = 4000

Population-Level Effects:

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

Intercept -4.68 0.15 -5.00 -4.40 1.00 1528 1499

Host\_StatusPM -0.10 0.24 -0.59 0.38 1.00 2197 2018

Host\_StatusR 0.04 0.16 -0.25 0.37 1.00 1550 1446

Host\_StatusR\_M 1.07 0.19 0.70 1.45 1.00 1849 1870

Host\_StatusR\_PM 0.61 0.18 0.27 0.99 1.00 1809 1818

Host\_StatusR\_PM\_M 0.09 0.37 -0.72 0.74 1.00 2681 2122

Family Specific Parameters:

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

phi 279.73 26.85 228.75 334.68 1.00 2802 3080

Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

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

> parameters::p\_value(model5)

Parameter p

1 b\_Intercept 0.0000

2 b\_Host\_StatusPM 0.6995

3 b\_Host\_StatusR 0.8585

4 b\_Host\_StatusR\_M 0.0000

5 b\_Host\_StatusR\_PM 0.0005

6 b\_Host\_StatusR\_PM\_M 0.7525

> plot3 <- plot(conditional\_effects(model5), points = FALSE, theme = a)

> plot3$Host\_Status$data$estimate\_\_

[1] 0.009288978 0.008440480 0.009532098 0.026297956 0.016909072 0.010376862

> plot3$Host\_Status$data$lower\_\_

[1] 0.006692834 0.005469153 0.008737242 0.020953967 0.013675278 0.004640532

> plot3$Host\_Status$data$upper\_\_

[1] 0.01211053 0.01186251 0.01045085 0.03184453 0.02048814 0.01782792

plot3$Host\_Status$data$se\_\_

[1] 0.0013645069 0.0015770338 0.0004473936 0.0027519610 0.0018224898 0.0032770908