

Beta diversity statistical analysis

Based on the workflow described here <https://github.com/nuorenarra/Analysing-dyadic-data-with-brms>

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A) 16S rRNA beta diversity statistical analysis

1. Bray-Curtis dissimilarities

```
#Load Packages

library(brms)
library(rstan)
library(parallel)
library(bayesplot)
library(ggplot2)

#Read in the data
data.dyad <- readRDS("data_dyad.rds")
```

Data-dyad is composed of 26,335 pairwise comparisons.

1.1 Scale predictors between 0-1

```
#scale all predictors to range between 0-1 if they are not already naturally on that scale

#define scaling function:

range.use <- function(x,min.use,max.use){ (x - min(x,na.rm=T)) / (max(x,na.rm=T)-min(x,na.rm=T)) * (max.use -
min.use) + min.use }

scalecols<-c("age_difference","bci_difference")

for(i in 1:ncol(data.dyad[,which(colnames(data.dyad)%in%scalecols)])){
  data.dyad[,which(colnames(data.dyad)%in%scalecols)][,i]<-
range.use(data.dyad[,which(colnames(data.dyad)%in%scalecols)][,i],0,1)
}

data.dyad$sex_sim <-factor(data.dyad$sex_sim, levels=c("0","1"))
data.dyad$nest_sim <-factor(data.dyad$nest_sim, levels=c("0","1"))
data.dyad$year_sim <-factor(data.dyad$year_sim, levels=c("0","1"))
data.dyad$lbinom_comp <-factor(data.dyad$lbinom_comp, levels=c("II","NiNi","NiI"))
data.dyad$habitat_sim<-factor(data.dyad$habitat_sim, levels=c("0","1"))
data.dyad$sampleA <-as.factor(data.dyad$sampleA)
data.dyad$sampleB <-as.factor(data.dyad$sampleB)
data.dyad$IDA <-as.factor(data.dyad$IDA)
data.dyad$IDB <-as.factor(data.dyad$IDB)
```

1.2 Model Bray-Curtis

```
ncores = detectCores()
options(mc.cores = parallel::detectCores())

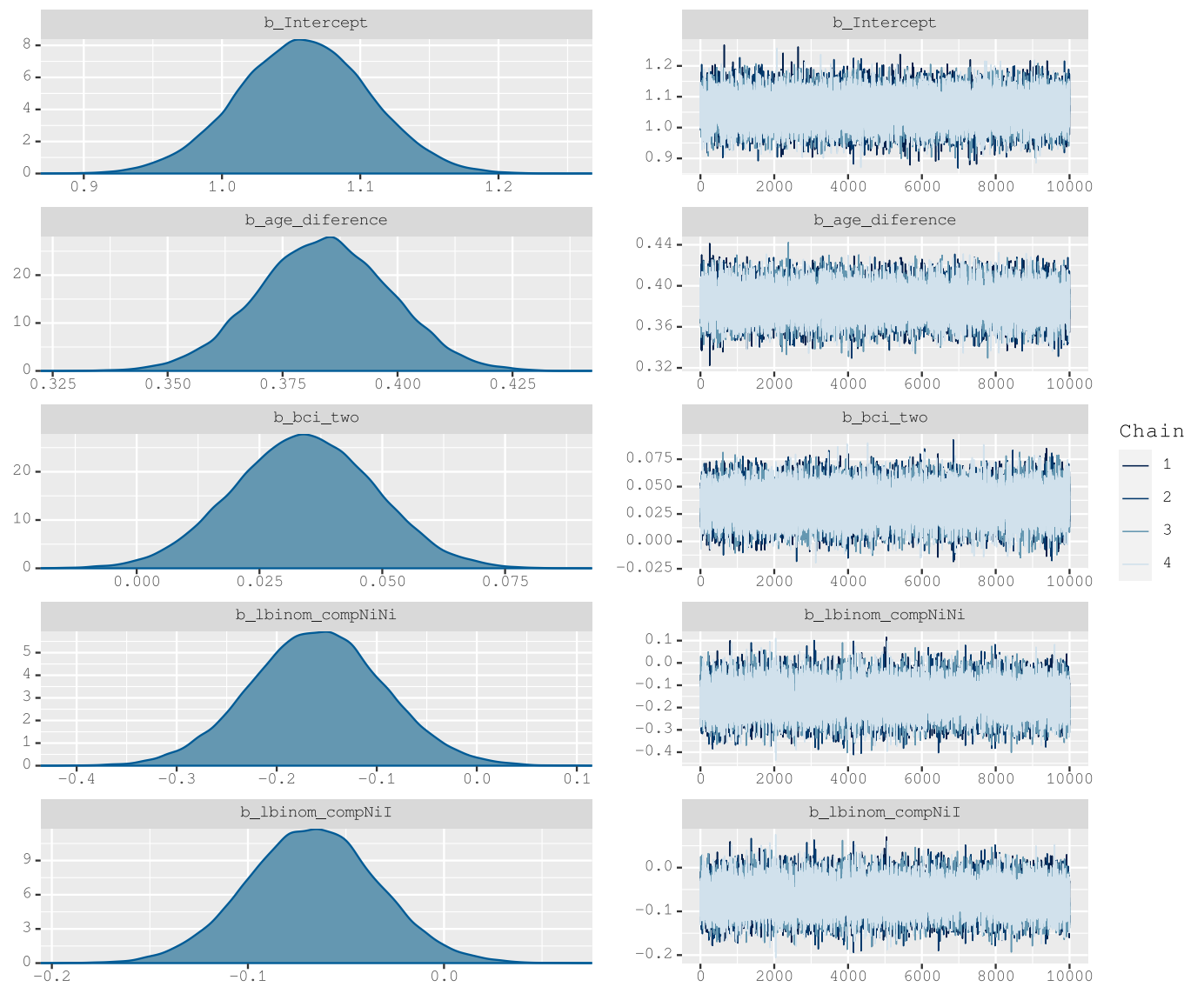
model_BC <- brm(BC_dissim~1+ age_difference + bci_difference + nest_sim + year_sim + sex_sim + habitat_sim +
lbinom_comp (1|mm(sampleA,sampleB)) + (1|mm(IDA,IDB)),
  data = data.dyad,
  family= "Beta",
  warmup = 10000, iter = 20000,
  cores = ncores, chains = 4,
  init=0)

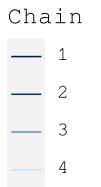
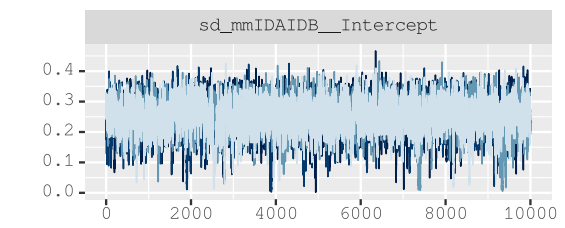
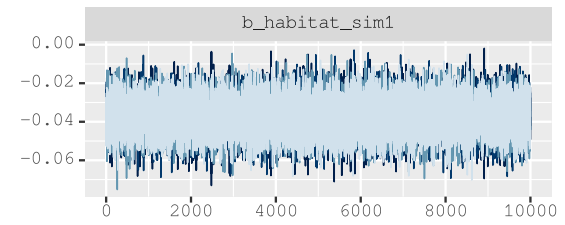
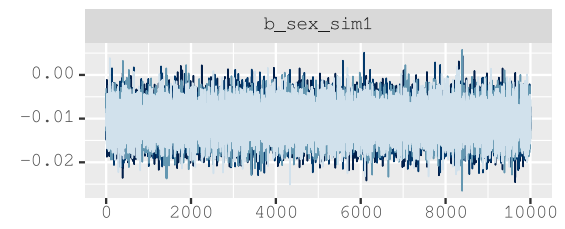
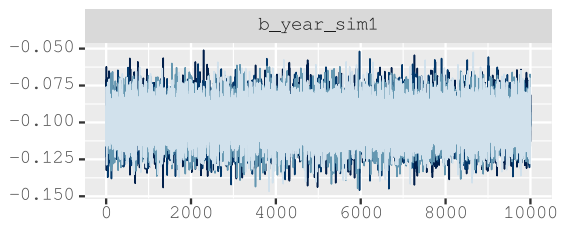
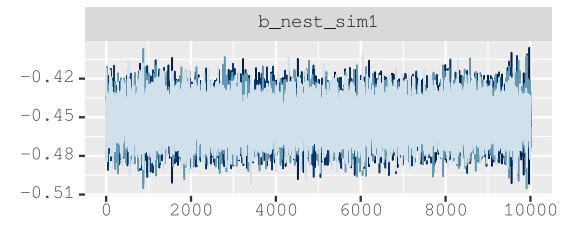
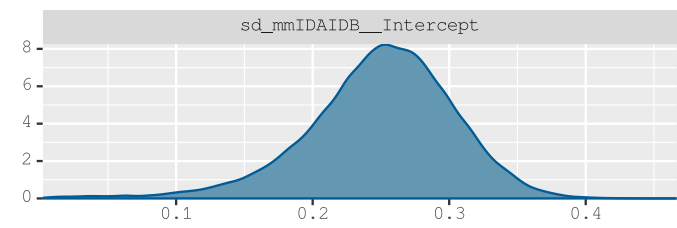
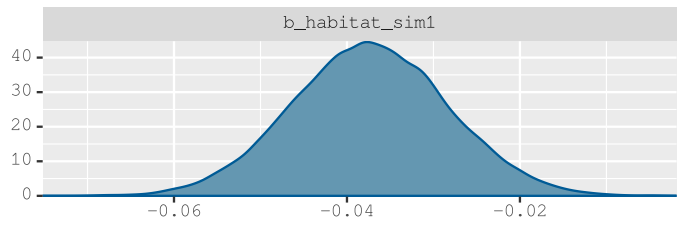
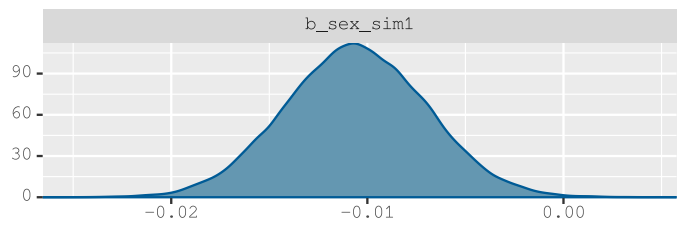
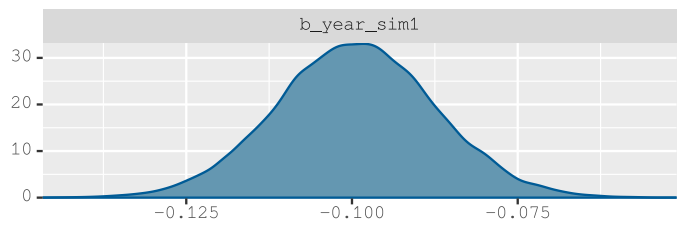
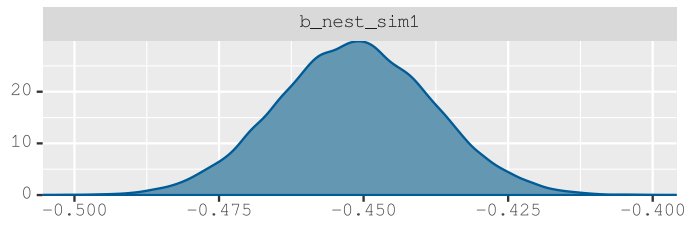
saveRDS(model_BC, "model_BC.rds")

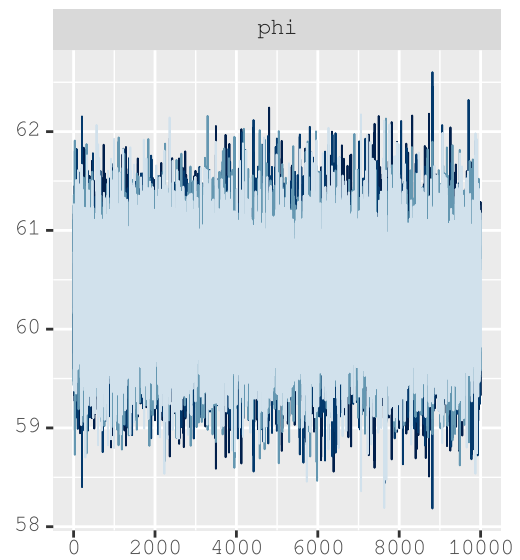
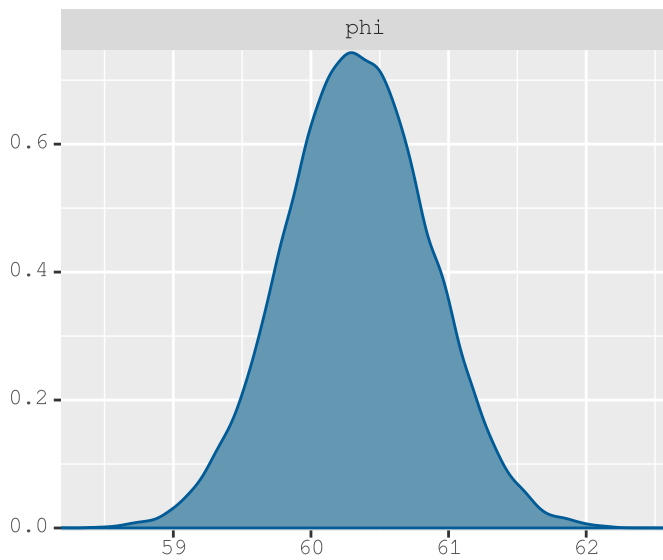
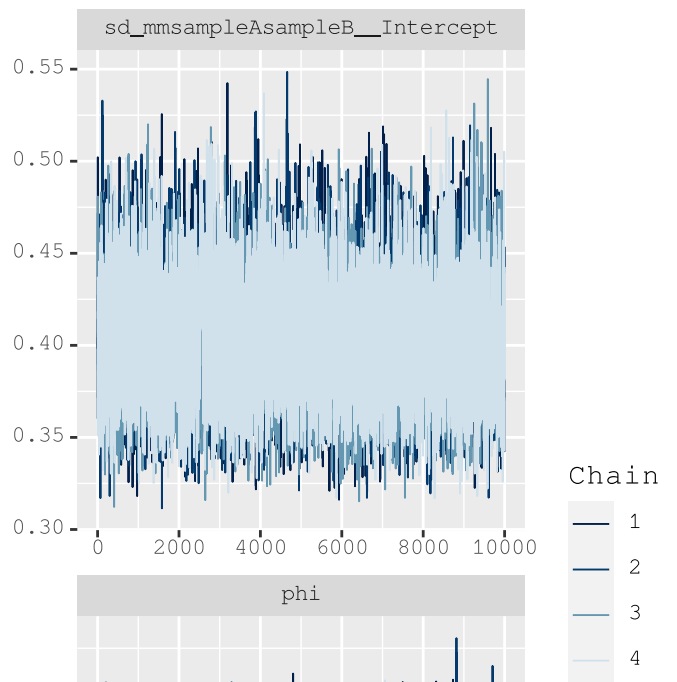
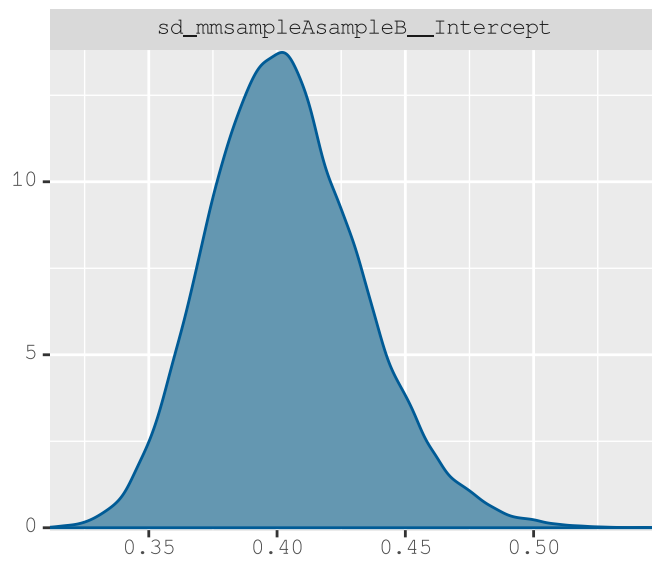
# Read in model
model_BC <- readRDS("model_final.rds")
```

1.3 Model Diagnostics

```
plot(model_BC)
```

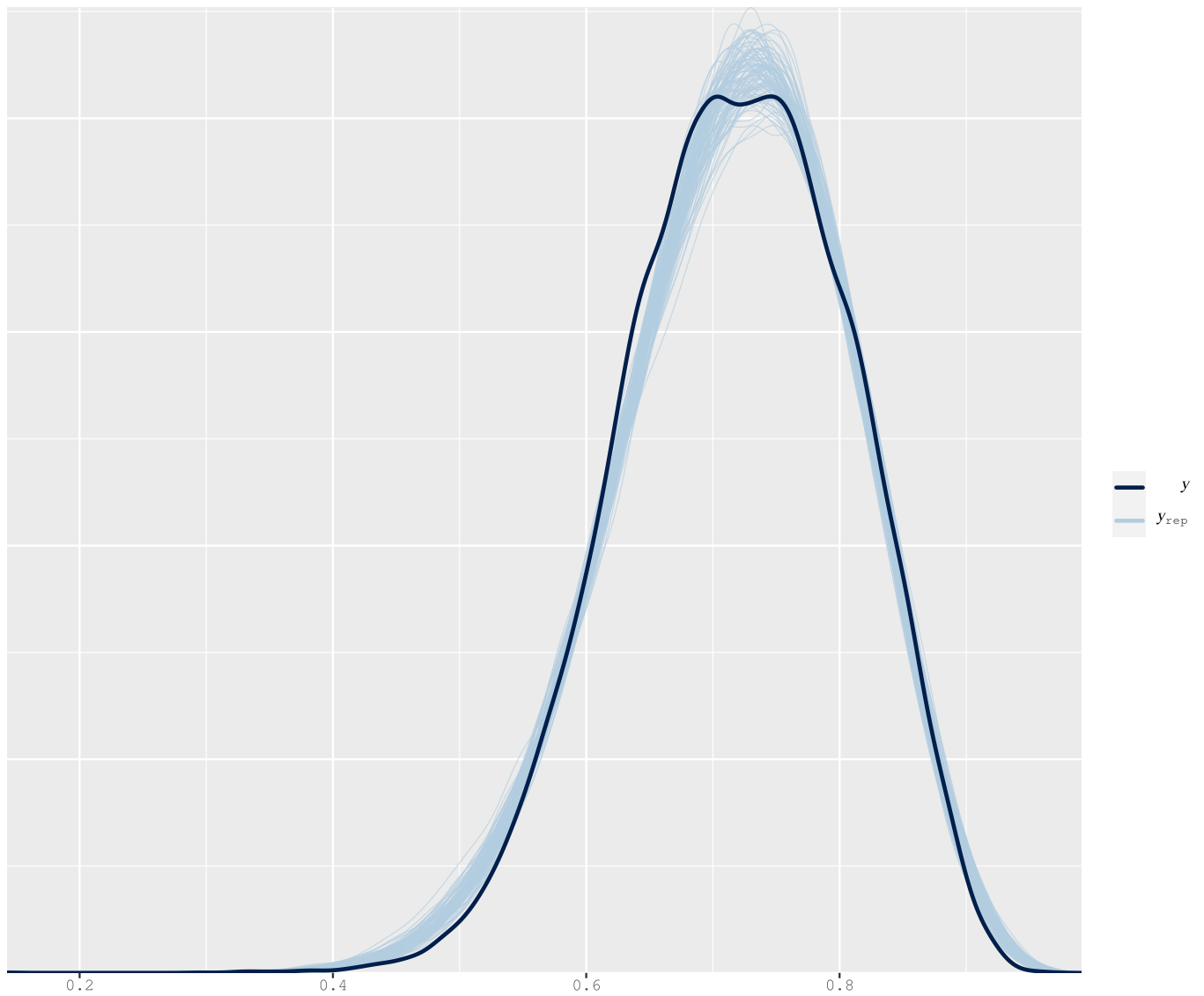






1.3.1 Compare distribution of response variable to distributions of predicted response variable values

```
pp_model_BC <- pp_check(model_BC, ndraws = 100)
pp_model_final
```



1.5 Model Summary

```
summary(model_BC)
```

Family: beta
 Links: mu = logit; phi = identity
 Formula: BC_dissim ~ 1 + age_diference + bci_diference + lbinom_comp + nest_sim + year_sim + sex_sim + habitat_sim + (1 | mm(sampleA, sampleB)) + (1 | mm(IDA, IDB))
 Data: data.dyad (Number of observations: 25425)
 Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
 total post-warmup draws = 40000

Group-Level Effects:

~mmIDAIDB (Number of levels: 117)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.25	0.05	0.13	0.34	1.00	2990	2652

~mmsampleAsampleB (Number of levels: 226)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.40	0.03	0.35	0.47	1.00	5918	8058

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	1.06	0.05	0.97	1.15	1.00	35066	30616

age_difference	0.38	0.01	0.36	0.41	1.00	58577	25412
bci_difference	0.03	0.01	0.01	0.06	1.00	59493	25555
lbinom_compNiNi	-0.16	0.07	-0.29	-0.03	1.00	21670	26641
lbinom_compNiI	-0.07	0.03	-0.13	-0.00	1.00	21753	26841
nest_sim1	-0.45	0.01	-0.48	-0.43	1.00	59044	27921
year_sim1	-0.10	0.01	-0.12	-0.08	1.00	59803	26444
sex_sim1	-0.01	0.00	-0.02	-0.00	1.00	58233	26359
habitat_sim1	-0.04	0.01	-0.05	-0.02	1.00	55160	26715

Family Specific Parameters:

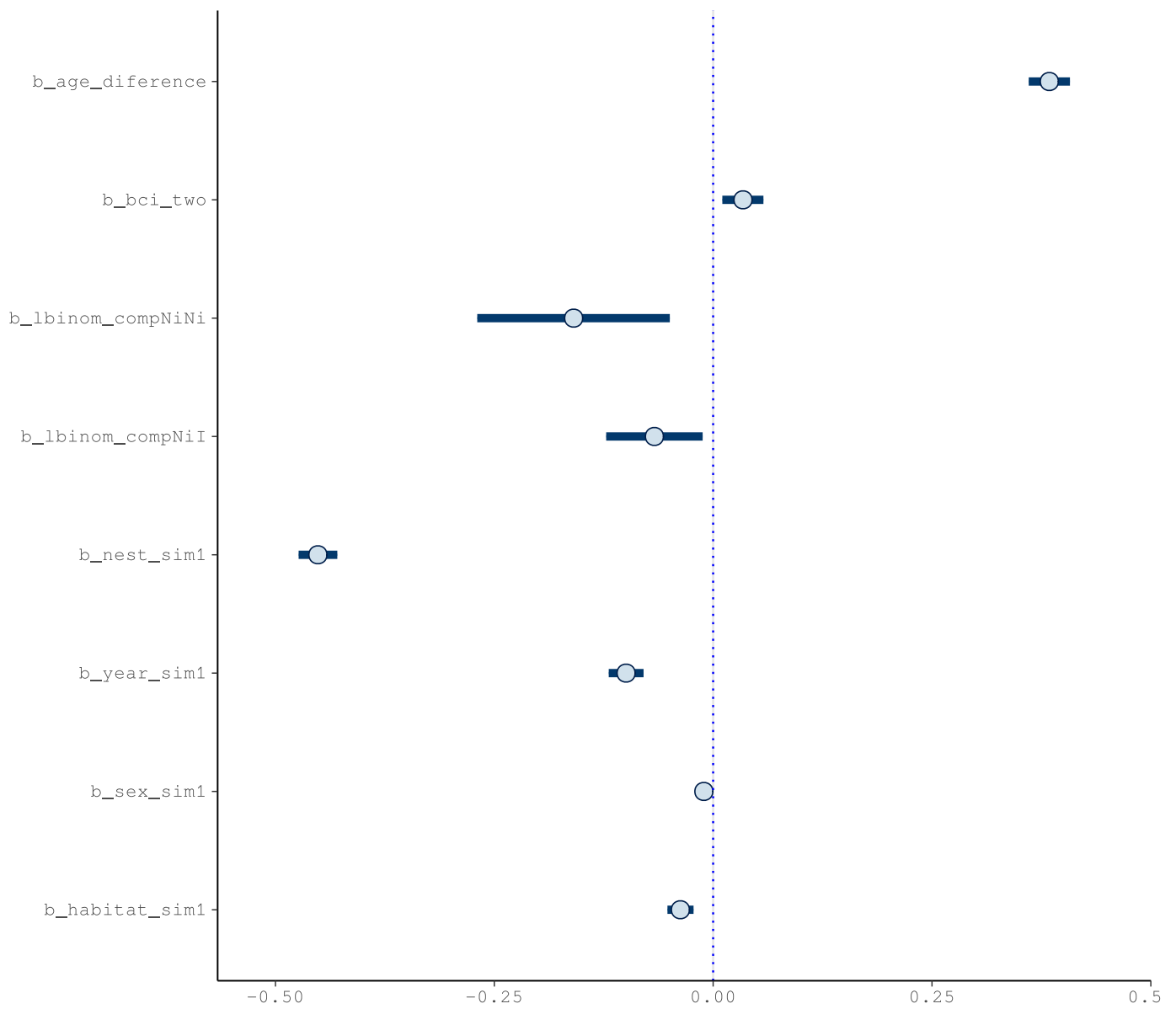
	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
phi	60.34	0.53	59.30	61.37	1.00	55129	25683

Draws were sampled 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).

1.4 Plot model posterior and credible intervals

```
plot1 <-mcmc_plot(model_final_lbinom, type = "intervals", prob = 0.90,
  variable = c("b_age_difference", "b_bci_difference", "b_lbinom_compNiNi", "b_lbinom_compNiI",
    "b_nest_sim1", "b_year_sim1", "b_sex_sim1", "b_habitat_sim1"))

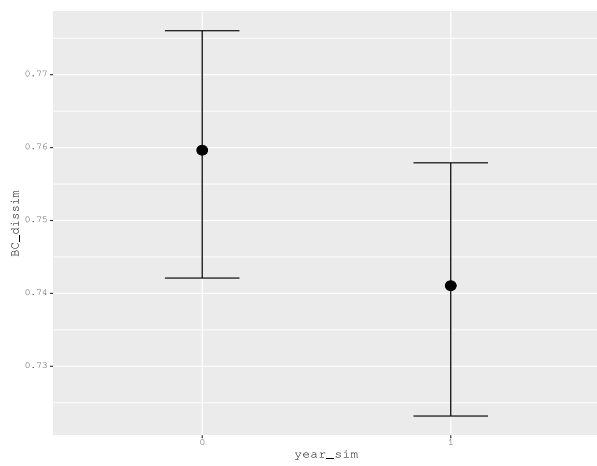
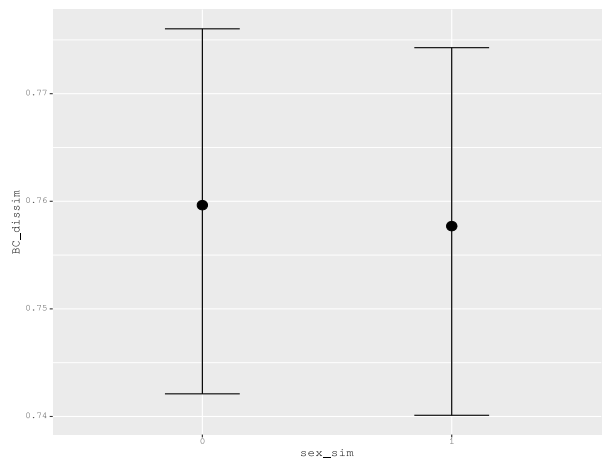
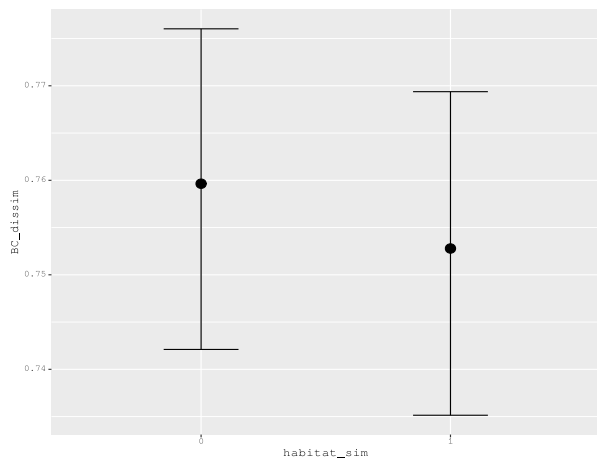
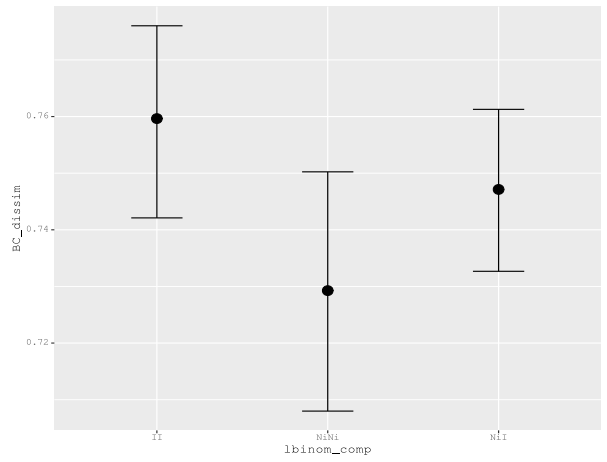
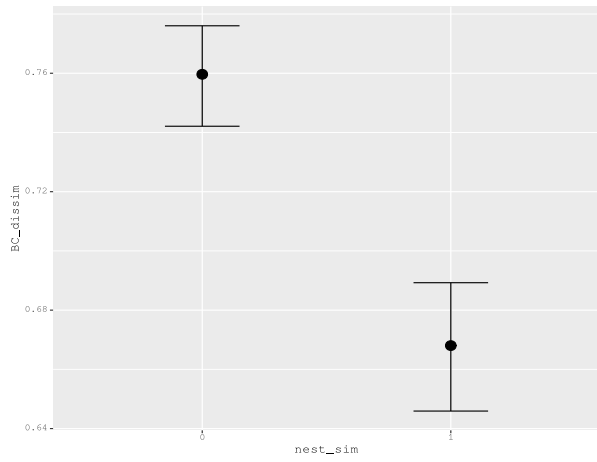
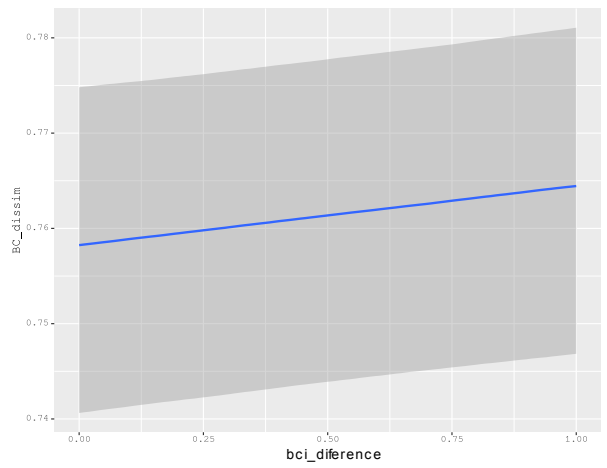
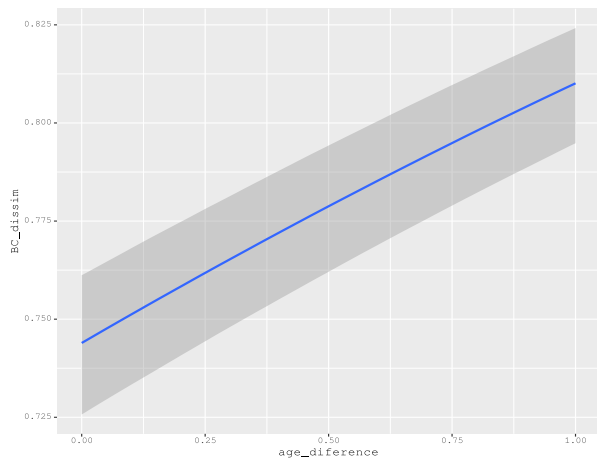
plot1 + theme_minimal() + geom_vline(xintercept = 0, linetype="dotted", color="blue")
```



1.5 Plot model effects

Depicts the range of predicted Bray-Curtis dissimilarity values, does not depict confidence intervals.

```
conditional_effects(model_BC) # all effect plots for BC_dissimilarity
```



2. Weighted UniFrac distances

2.1 Model WU distances

```
ncores = detectCores()
options(mc.cores = parallel::detectCores())

# In order to enhance model convergence, a uniform prior was applied
prior1 <- c(set_prior("normal(0,1)", class = "b", coef = "age_difference"),
            set_prior("normal(0,1)", class = "b", coef = "bci_difference"),
            set_prior("normal(0,1)", class = "b", coef = "nest_sim1"),
            set_prior("normal(0,1)", class = "b", coef = "year_sim1"),
            set_prior("normal(0,1)", class = "b", coef = "sex_sim1"),
            set_prior("normal(0,1)", class = "b", coef = "habitat_sim"),
            set_prior("normal(0,1)", class = "b", coef = "lbinom_compNiI"),
            set_prior("normal(0,1)", class = "b", coef = "lbinom_compNiNi"))

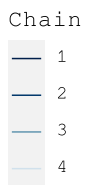
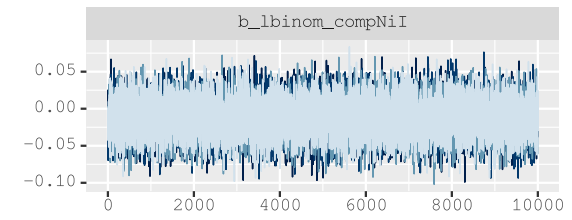
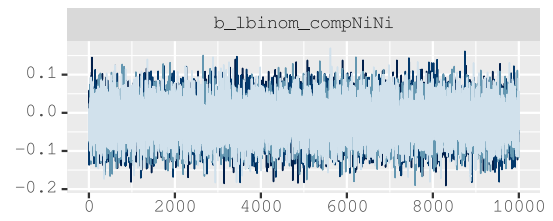
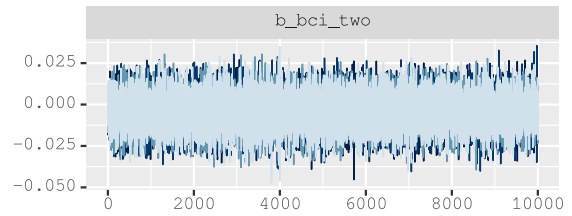
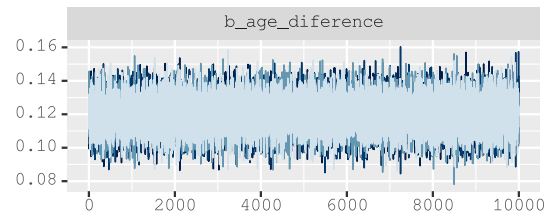
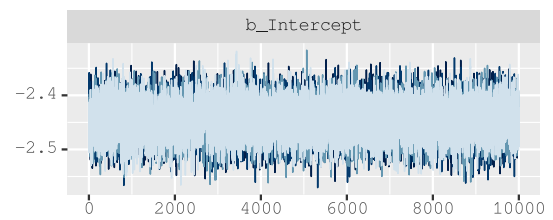
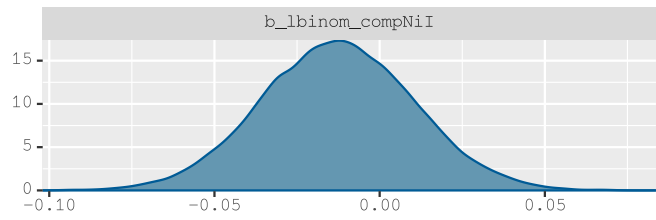
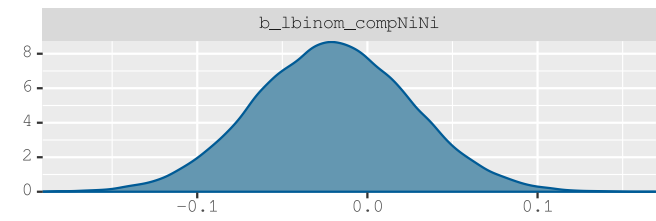
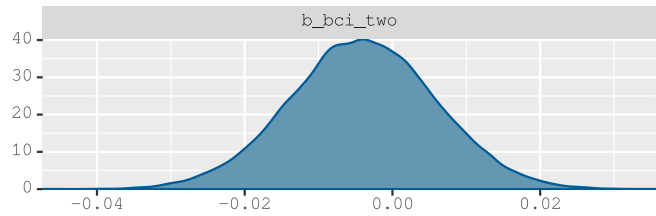
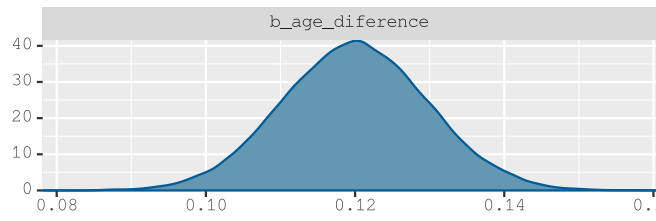
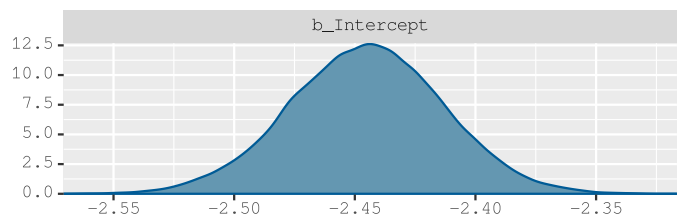
model_WU <- brm(WU_distance~1+ age_difference + bci_difference + nest_sim + year_sim + sex_sim + habitat_sim +
  (1|mm(sampleA,sampleB)) + (1|mm(IDA,IDB)),
  data = data.dyad,
  family= "Beta",
  prior = prior1,
  warmup = 10000, iter = 20000,
  control = list(adapt_delta = 0.99, max_treedepth = 15),
  cores = ncores, chains = 4, init=0)

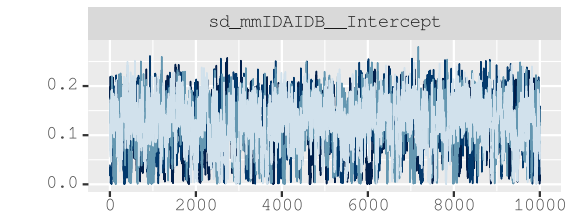
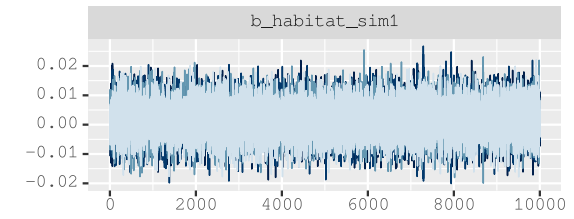
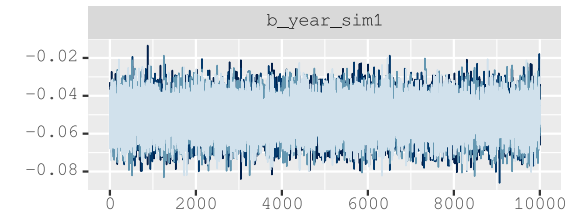
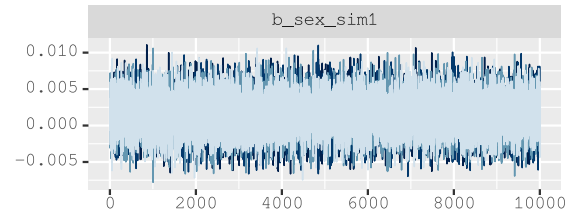
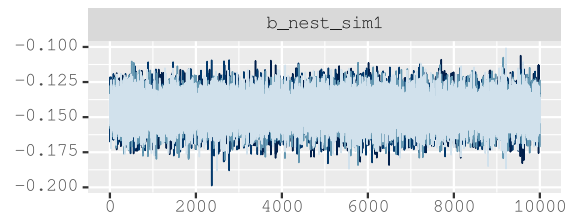
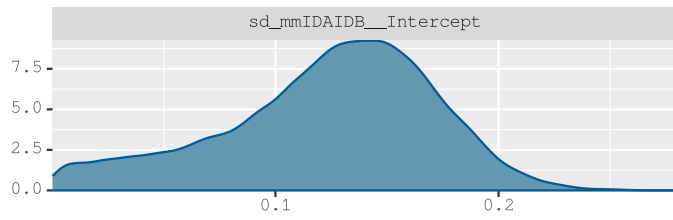
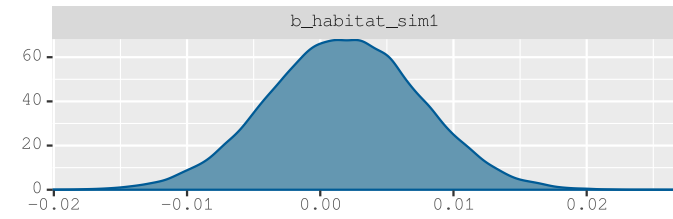
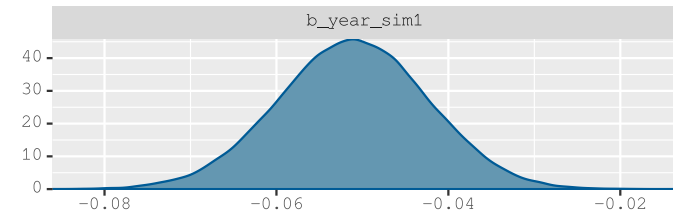
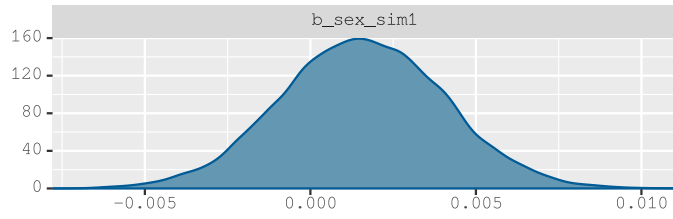
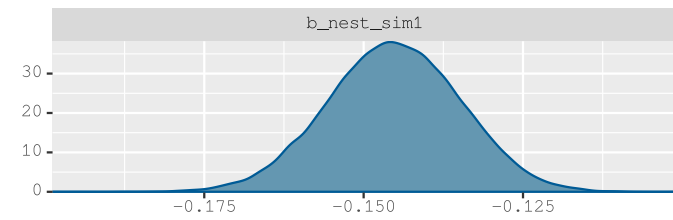
saveRDS(model_WU, "model_WU.rds")

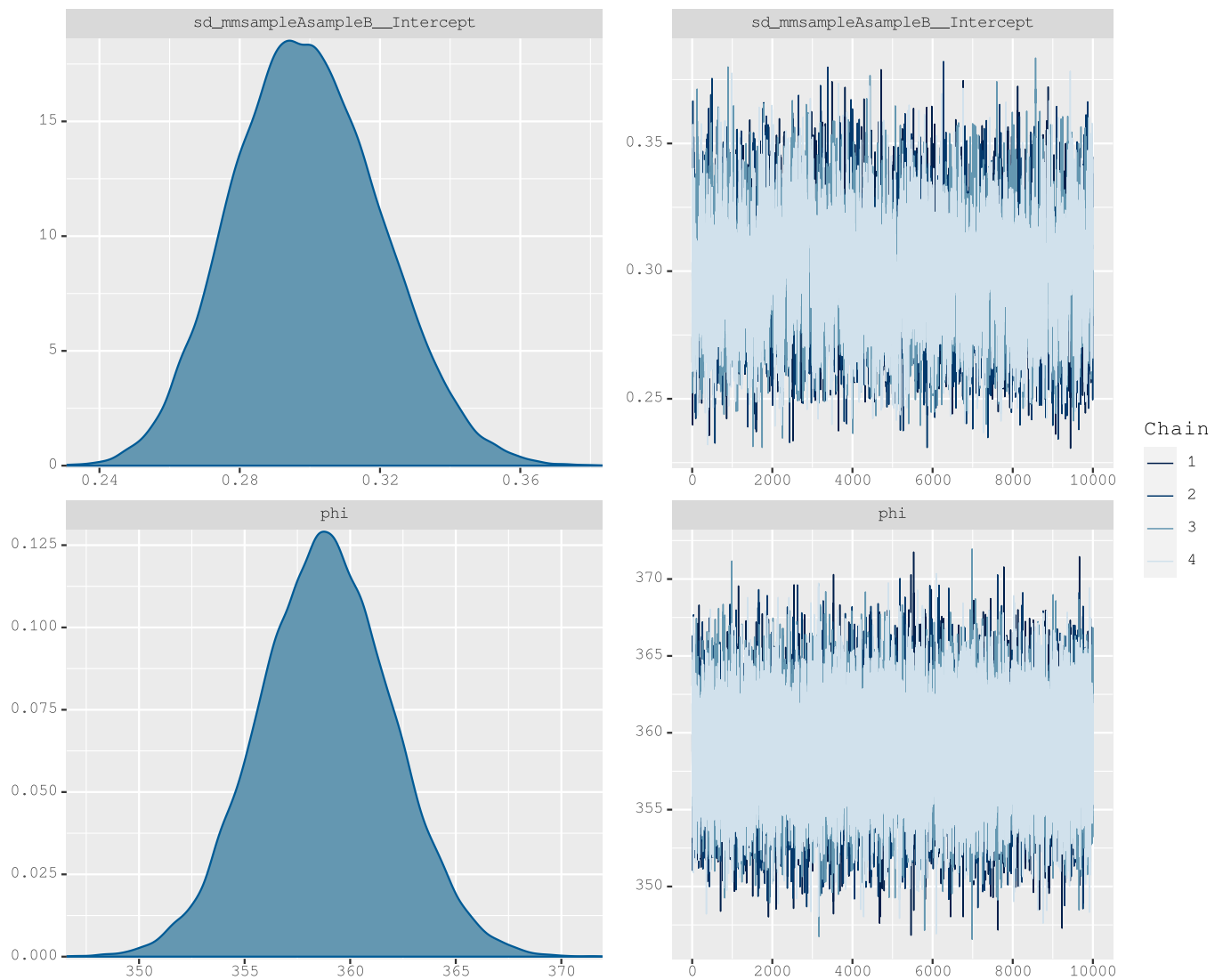
# Read in the model
model_WU <- readRDS("model_WU.rds")
```

1.3 Model Diagnostics

```
plot(model_WU)
```

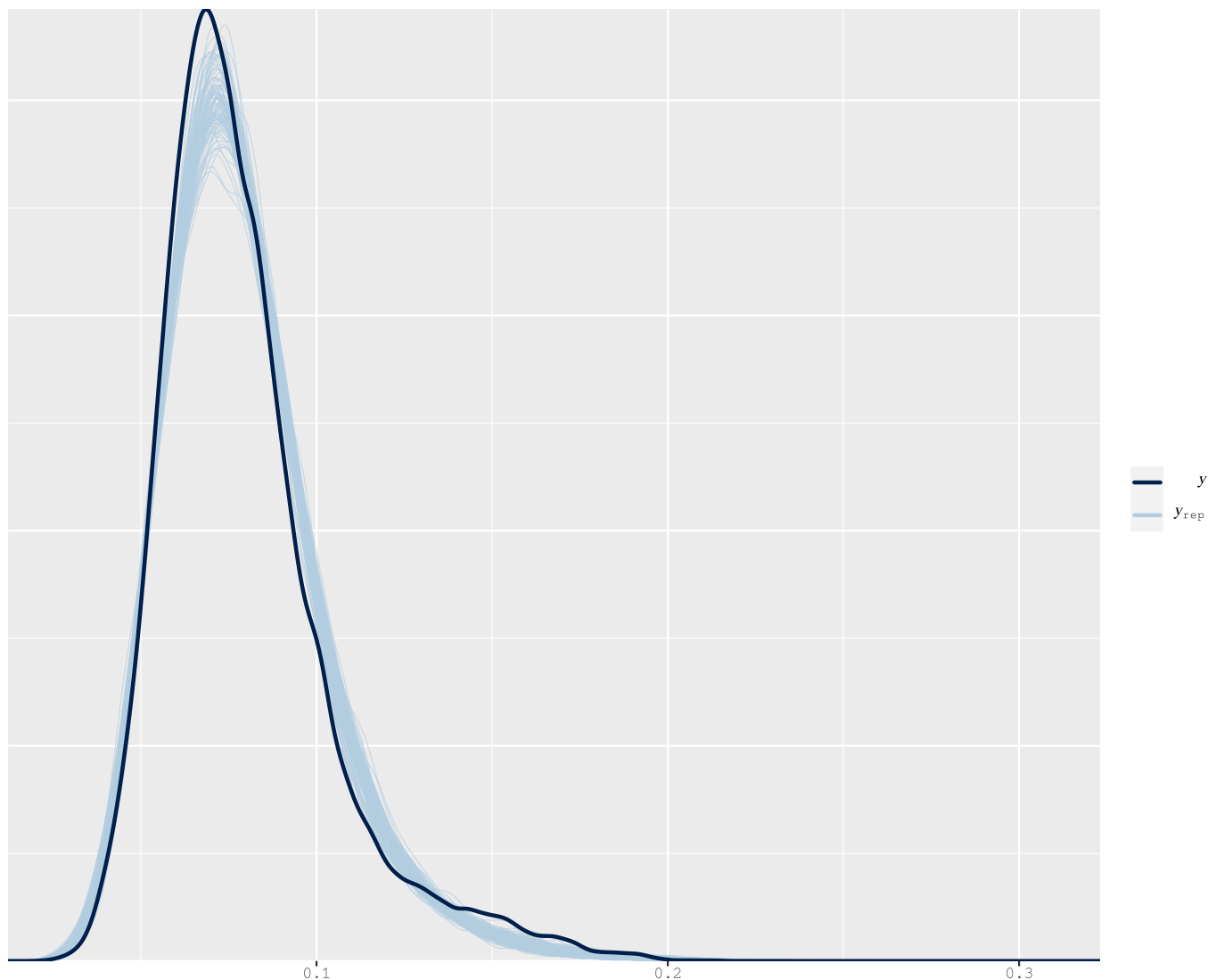






1.3.1 Compare distribution of response variable to distributions of predicted response variable values

```
pp_model_BC <- pp_check(model_WU, ndraws = 100)
pp_model_WU
```



1.5 Model Summary

```
summary(model_WU)
```

Family: beta

Links: mu = logit; phi = identity

Formula: WU_distance ~ 1 + age_difference + bci_difference + lbinom_comp + nest_sim + sex_sim + year_sim + habitat_sim + (1 | mm(sampleA, sampleB)) + (1 | mm(IDA, IDB))

Data: data.dyad (Number of observations: 25425)

Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
total post-warmup draws = 40000

Group-Level Effects:

~mmIDAIDB (Number of levels: 117)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.12	0.05	0.01	0.20	1.00	1090	1738

~mmsampleAsampleB (Number of levels: 226)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.30	0.02	0.26	0.34	1.00	2450	7741

Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	-2.45	0.03	-2.51	-2.38	1.00	17900	25545
age_difference	0.12	0.01	0.10	0.14	1.00	67396	27034
bci_difference	-0.00	0.01	-0.02	0.02	1.00	66325	26781
lbinom_compNiNi	-0.02	0.05	-0.11	0.07	1.00	10353	17451
lbinom_compNiI	-0.01	0.02	-0.06	0.03	1.00	10461	17112
nest_sim1	-0.15	0.01	-0.17	-0.13	1.00	66733	28983

sex_sim1	0.00	0.00	-0.00	0.01	1.00	60472	27160
year_sim1	-0.05	0.01	-0.07	-0.03	1.00	69858	29156
habitat_sim1	0.00	0.01	-0.01	0.01	1.00	66748	28899

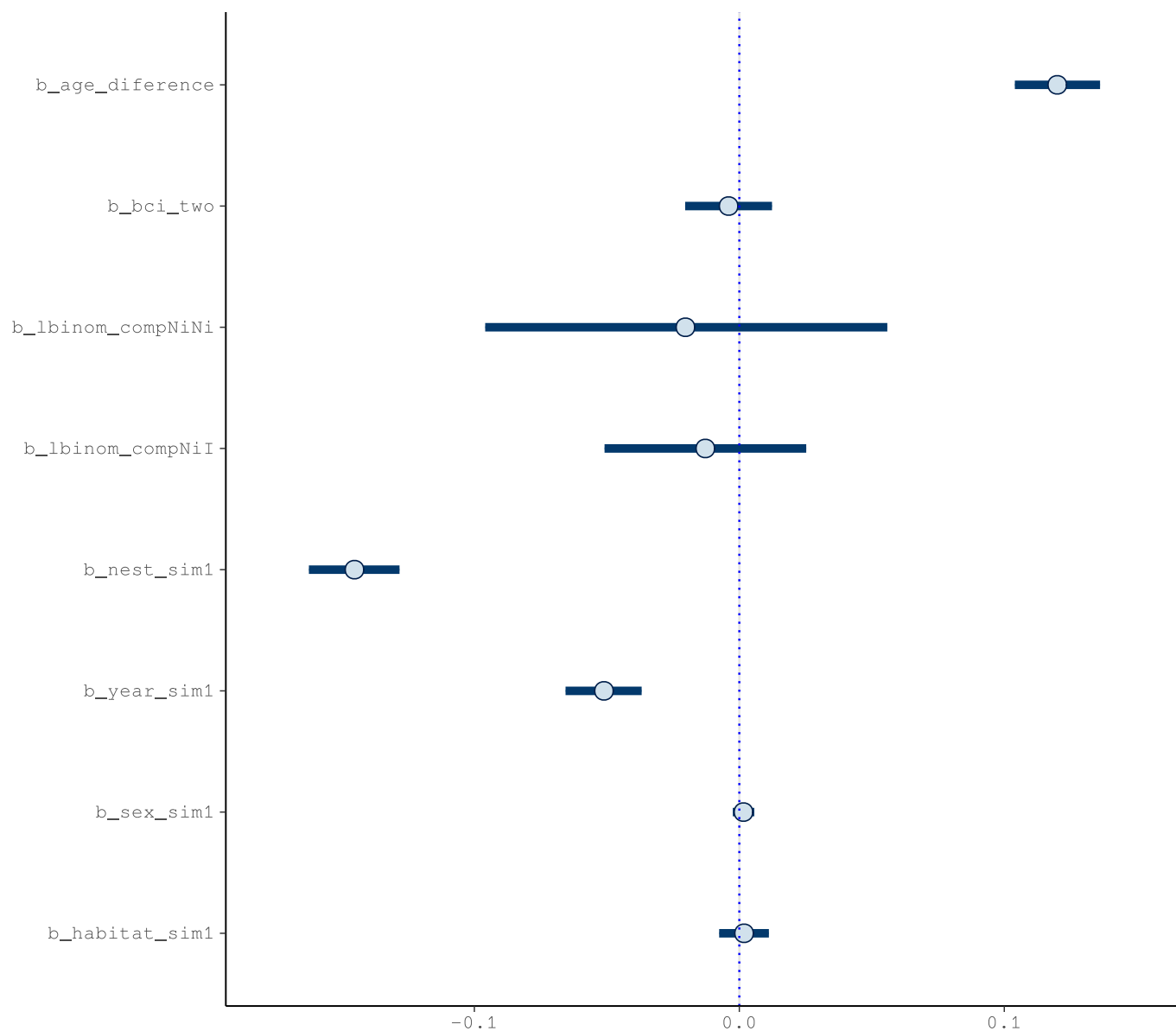
Family Specific Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
phi	358.85	3.16	352.67	365.09	1.00	64829	27654

Draws were sampled 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).

1.4 Plot model posterior and credible intervals

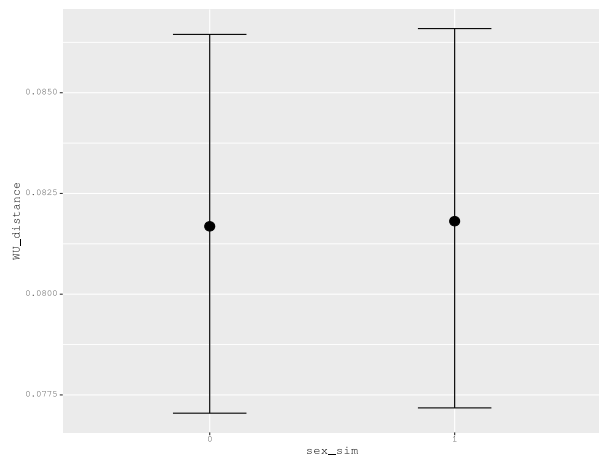
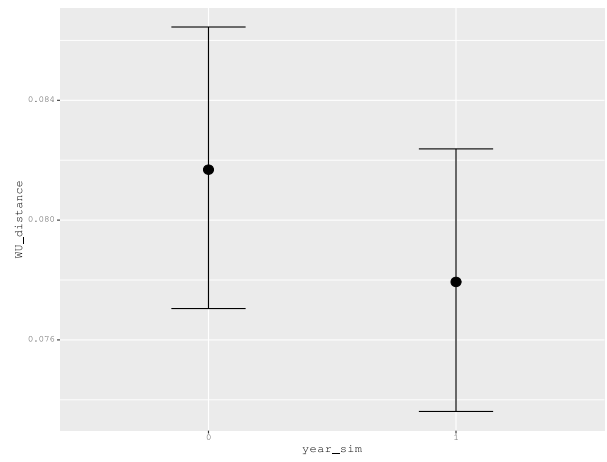
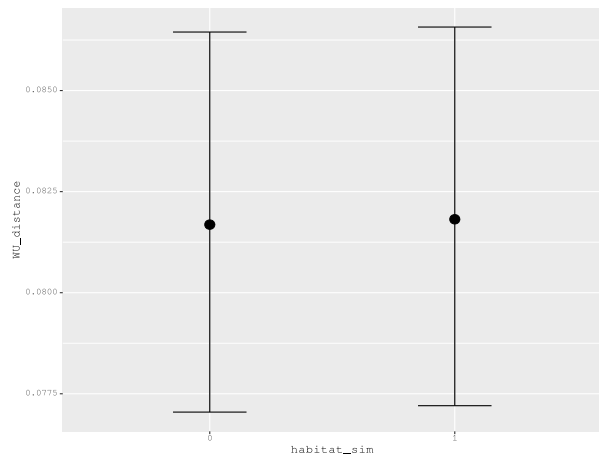
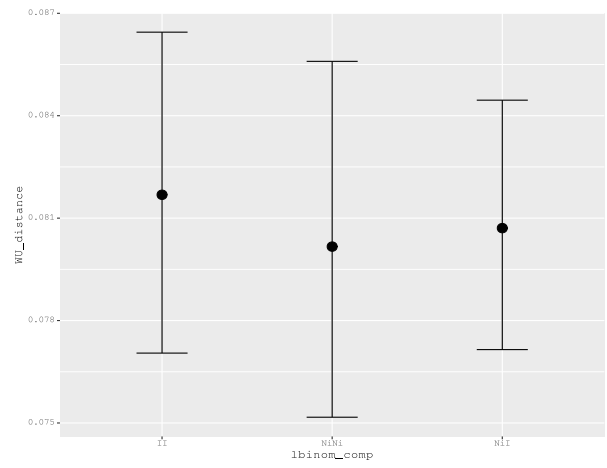
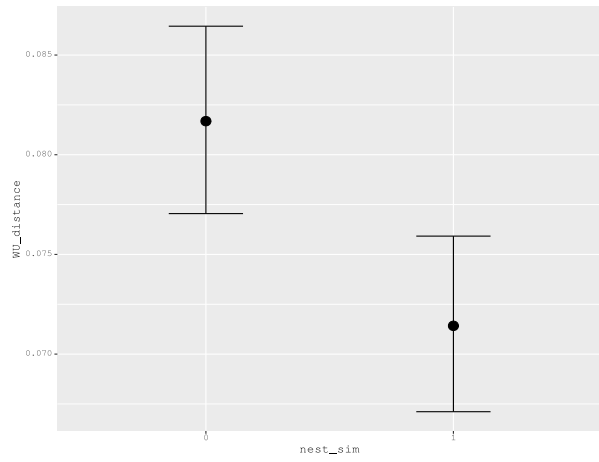
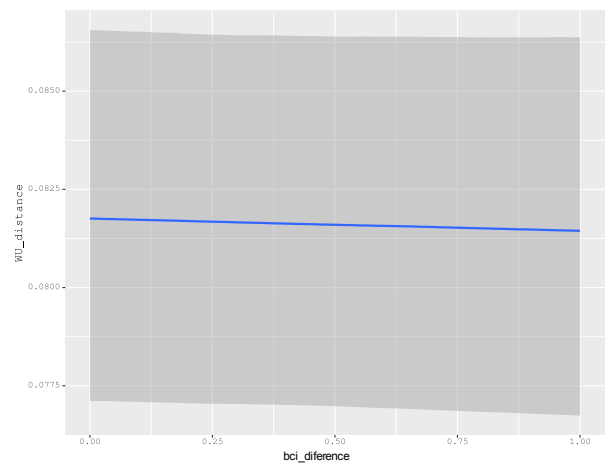
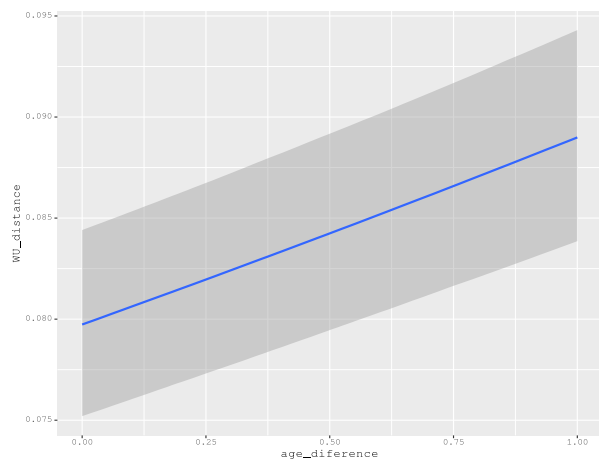
```
plot1 <- mcmc_plot(model_WU, type = "intervals", prob = 0.95, pars = rownames(fixef(model_final))
[2:nrow(fixef(model_final))])
plot1 + theme_minimal() + geom_vline(xintercept = 0, linetype="dotted", color="blue")
```



1.5 Plot model effects

Depicts the range of predicted Bray-Curtis dissimilarity values, does not depict confidence intervals.

```
conditional_effects(model_WU) # all effect plots for BC_dissimilarity
```



B) 28S rRNA beta diversity statistical analysis

1. Bray-Curtis dissimilarities

```
#Load Packages

library(brms)
library(rstan)
library(parallel)
library(bayesplot)
library(ggplot2)

#Read in the data
data.dyad <- readRDS("data_dyad.rds")
```

1.1. Scale predictors between 0-1

```
#scale all predictors to range between 0-1 if they are not already naturally on that scale

#define scaling function:

range.use <- function(x,min.use,max.use){ (x - min(x,na.rm=T)) / (max(x,na.rm=T)-min(x,na.rm=T)) * (max.use - min.use) + min.use }

scalecols<-c("age_difference","bci_difference")

for(i in 1:ncol(data.dyad[,which(colnames(data.dyad)%in%scalecols)])){
  data.dyad[,which(colnames(data.dyad)%in%scalecols)][,i]<-
range.use(data.dyad[,which(colnames(data.dyad)%in%scalecols)][,i],0,1)
}

data.dyad$sex_sim <-factor(data.dyad$sex_sim, levels=c("0","1"))
data.dyad$nest_sim <-factor(data.dyad$nest_sim, levels=c("0","1"))
data.dyad$year_sim <-factor(data.dyad$year_sim, levels=c("0","1"))
data.dyad$lbinom_comp <-factor(data.dyad$lbinom_comp, levels=c("II","NiNi","NiI"))
data.dyad$habitat_sim<-factor(data.dyad$habitat_sim, levels=c("0","1"))
data.dyad$sampleA <-as.factor(data.dyad$sampleA)
data.dyad$sampleB <-as.factor(data.dyad$sampleB)
data.dyad$IDA <-as.factor(data.dyad$IDA)
data.dyad$IDB <-as.factor(data.dyad$IDB)
```

1.2. Model Bray-Curtis

```
ncores = detectCores()
options(mc.cores = parallel::detectCores())

prior1 <- c(set_prior("normal(0,1)", class = "b", coef = "age_difference"),
  set_prior("normal(0,1)", class = "b", coef = "bci_difference"),
  set_prior("normal(0,1)", class = "b", coef = "nest_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "year_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "sex_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "habitat_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "lbinom_compNiI"),
```

```

set_prior("normal(0,1)", class = "b", coef = "lbinom_compNiNi")

model_final <- brm(BC_dissim~1+ age_difference + bci_difference + nest_sim + year_sim + sex_sim + habitat_sim +
  lbinom_comp + (1|mm(sampleA,sampleB)) + (1|mm(IDA,IDB)),
  data = data.dyad,
  family= "zero_one_inflated_beta",
  prior = prior1,
  warmup = 10000, iter = 20000,
  control = list(adapt_delta = 0.99, max_tredepth = 15),
  cores = ncores, chains = 4, init=0)

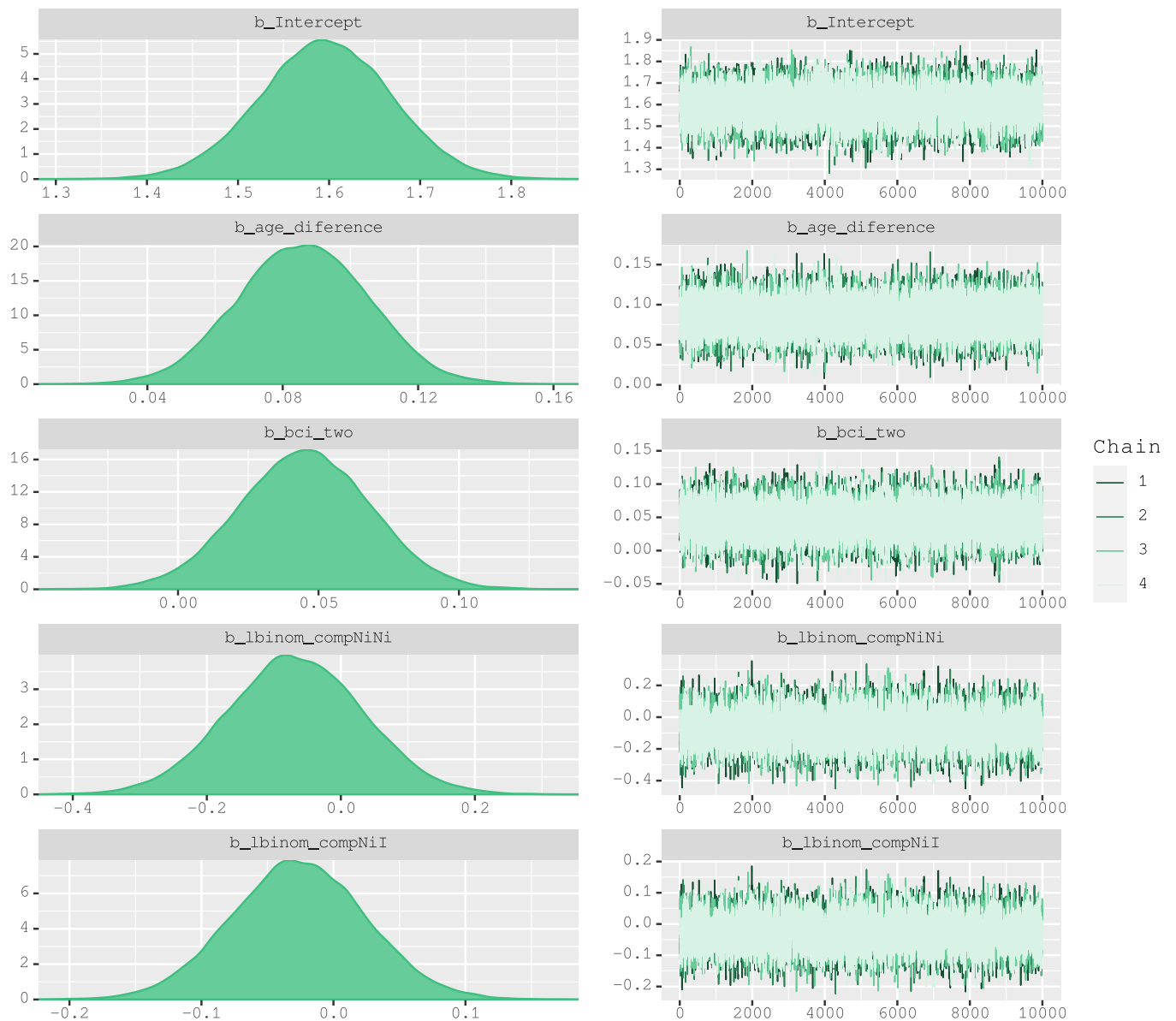
saveRDS(model_final, "model_final.rds")

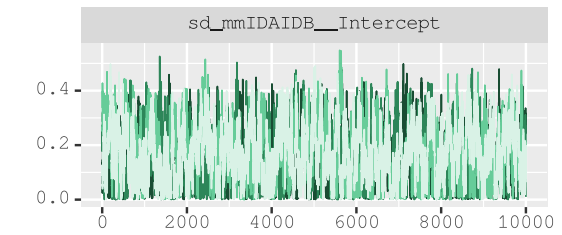
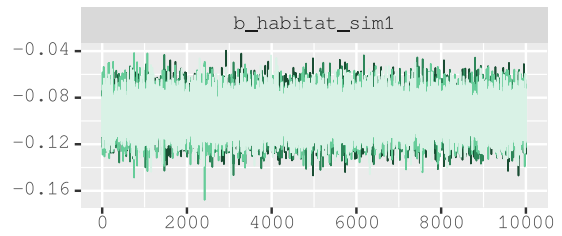
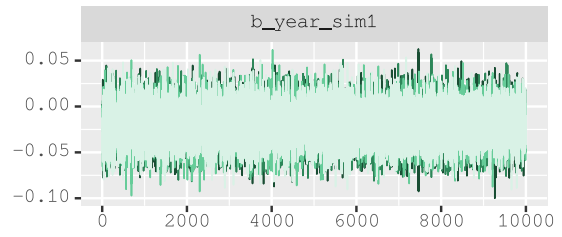
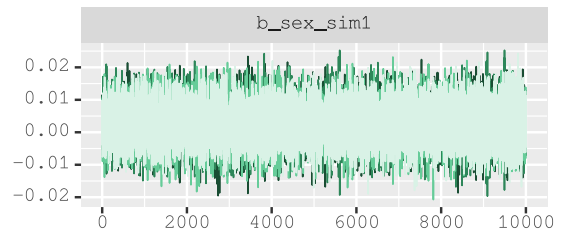
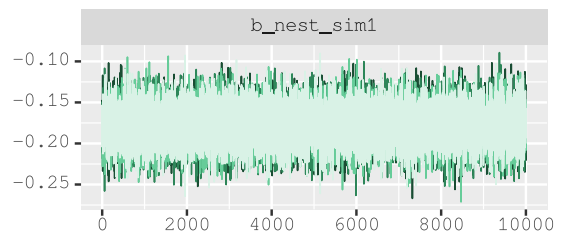
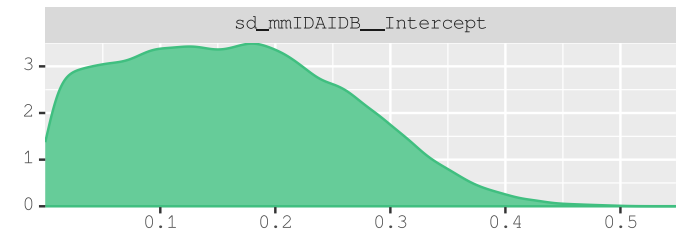
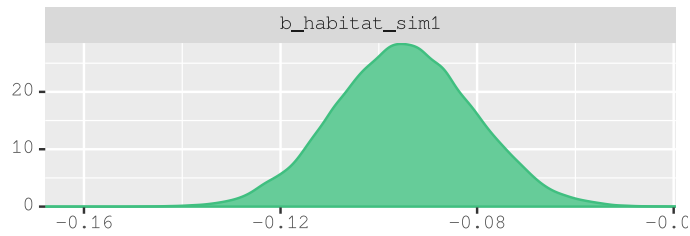
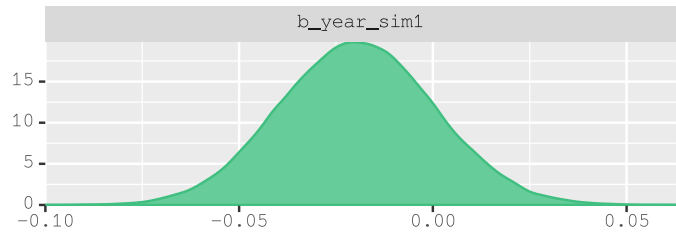
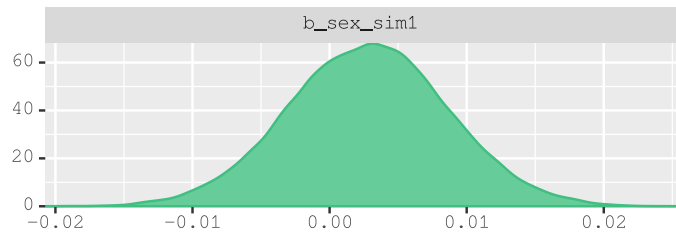
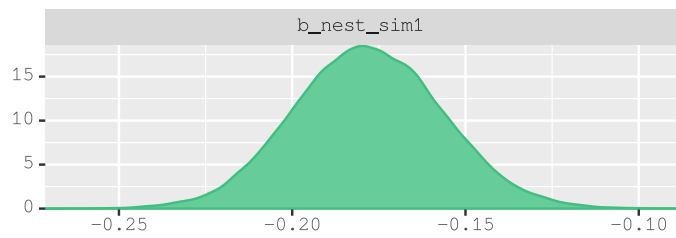
#Read in the model
model_final <- readRDS("model_final.rds")

```

1.3. Model Diagnostics

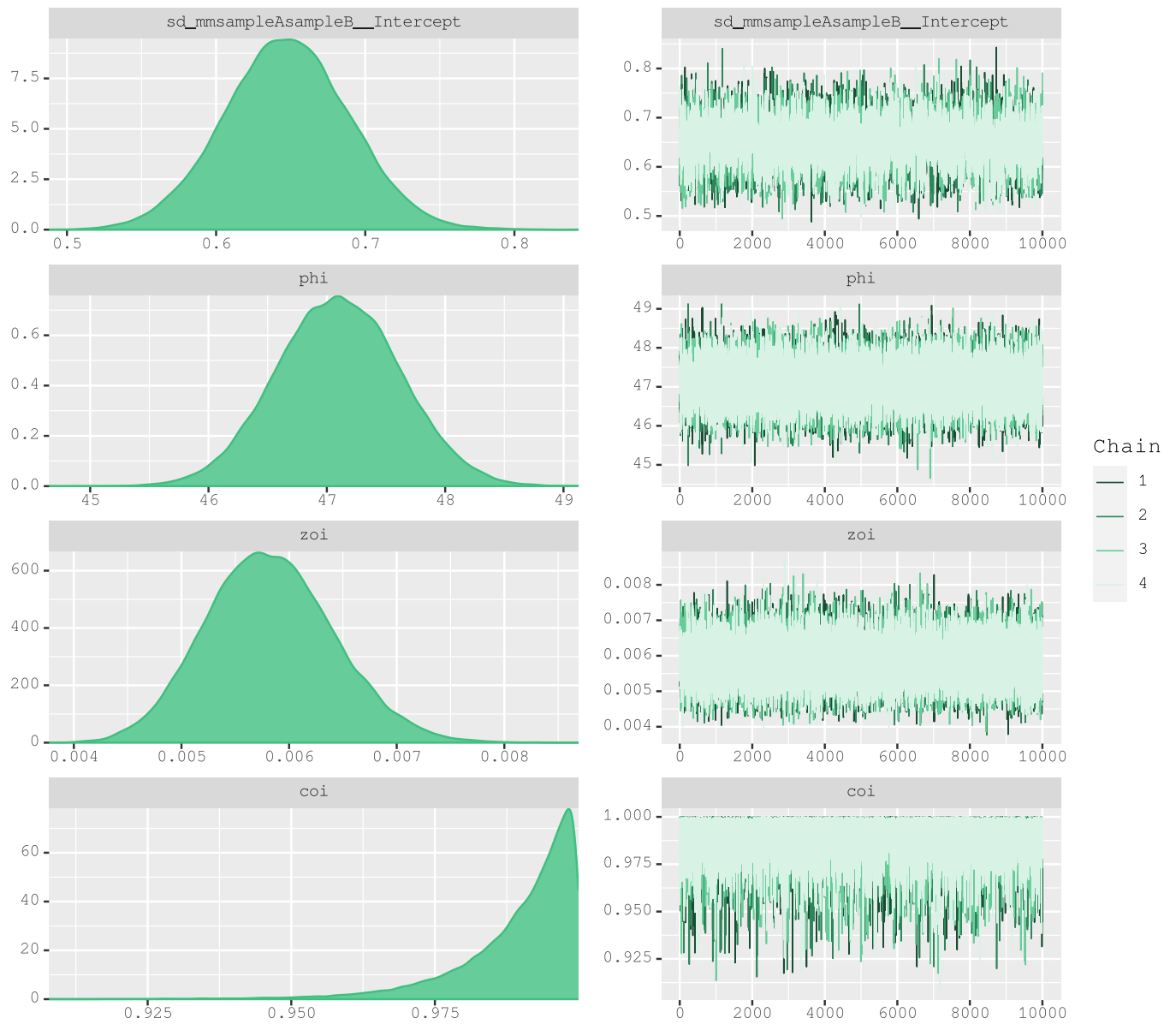
```
plot(model_BC)
```





Chain

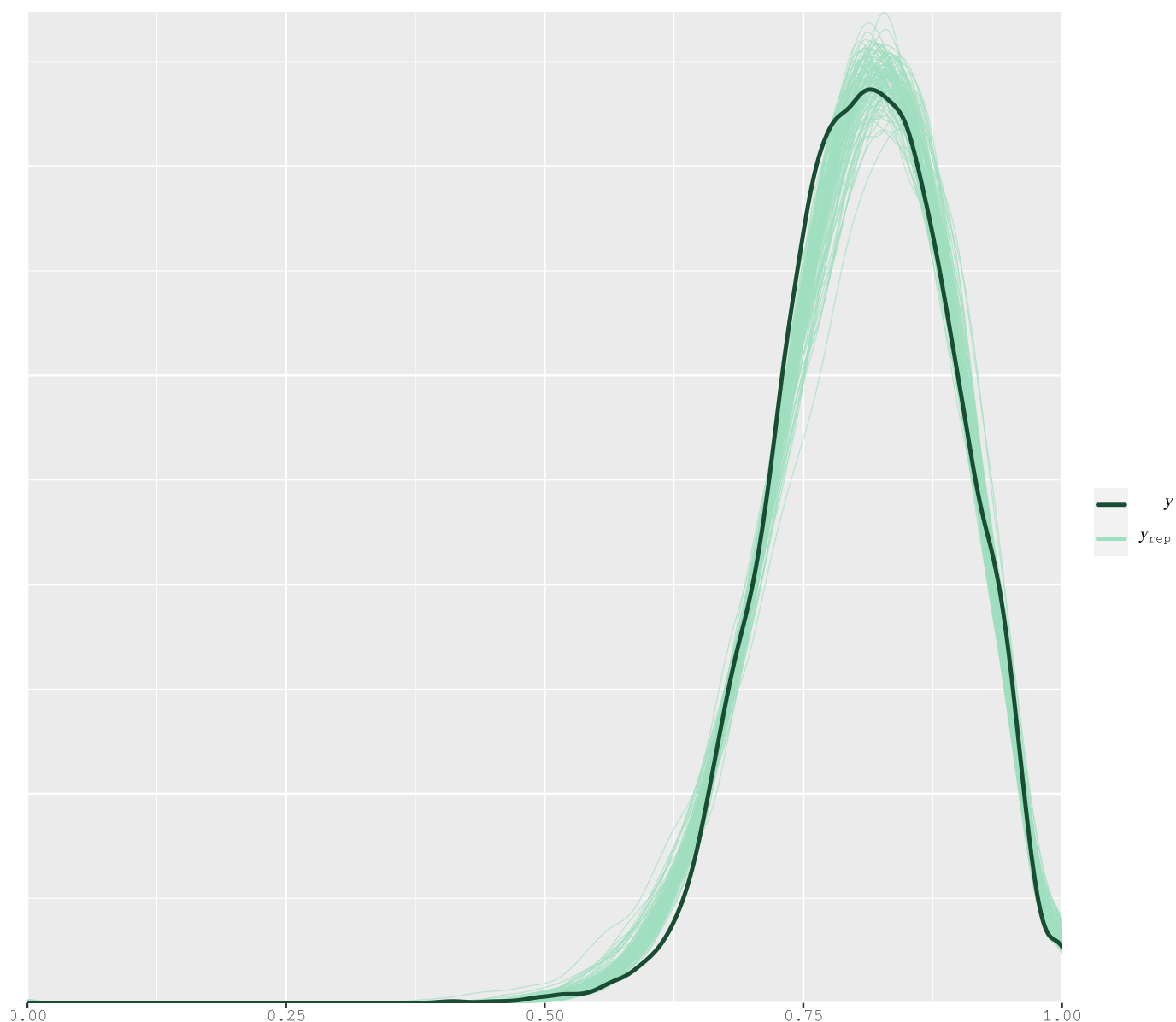




1.3.1. Compare distribution of response variable to distributions of predicted response variable values

```
pp_model_BC <- pp_check(model_BC, ndraws = 50)

pp_model_final
```



1.4. Model Summary

```
summary(model_BC)
```

Family: zero_one_inflated_beta

Links: mu = logit; phi = identity; zoi = identity; coi = identity

Formula: BC_dissim ~ 1 + age_diference + bci_diference + lbinom_comp + nest_sim + sex_sim + year_sim + habitat_sim + (1 | mm(sampleA, sampleB)) + (1 | mm(IDA, IDB))

Data: data.dyad (Number of observations: 16471)

Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
total post-warmup draws = 40000

Group-Level Effects:

~mmIDAIDB (Number of levels: 110)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.16	0.10	0.01	0.36	1.01	783	2381

~mmsampleAsampleB (Number of levels: 182)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.65	0.04	0.57	0.73	1.00	3000	6849

Population-Level Effects:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	1.60	0.07	1.45	1.74	1.00	10560	19316

age_diference	0.09	0.02	0.05	0.12	1.00	80195	27859
bci_two	0.05	0.02	-0.00	0.09	1.00	85005	26947
lbinom_compNiNi	-0.07	0.10	-0.27	0.13	1.00	8718	15364
lbinom_compNiI	-0.03	0.05	-0.13	0.07	1.00	8771	15815
nest_sim1	-0.18	0.02	-0.22	-0.14	1.00	79725	29045
sex_sim1	0.00	0.01	-0.01	0.01	1.00	78734	26540
year_sim1	-0.02	0.02	-0.06	0.02	1.00	72869	31147
habitat_sim1	-0.09	0.01	-0.12	-0.07	1.00	71270	28517

Family Specific Parameters:

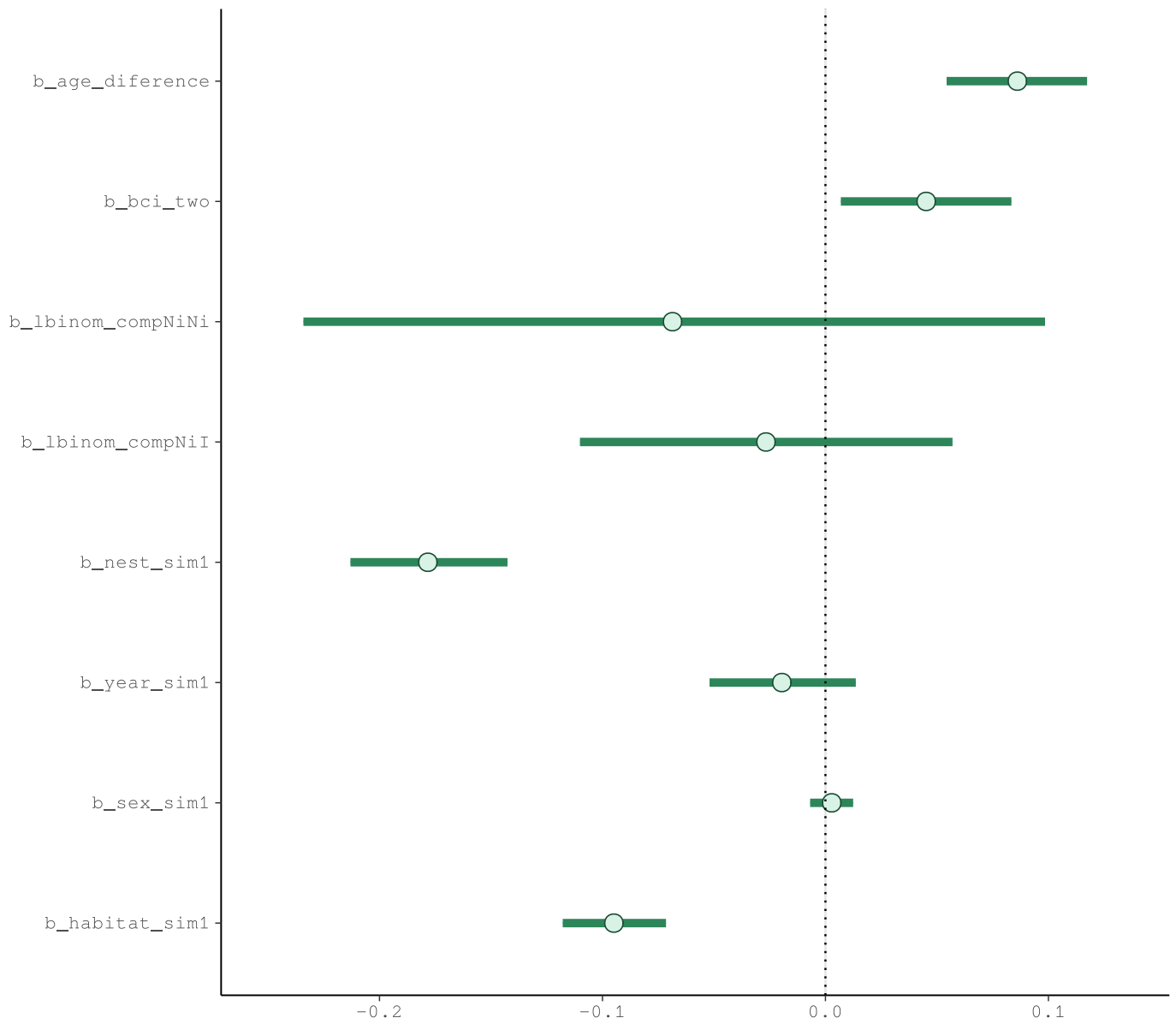
	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
phi	47.10	0.52	46.09	48.12	1.00	81005	27166
zoi	0.01	0.00	0.00	0.01	1.00	74765	26599
coi	0.99	0.01	0.96	1.00	1.00	46936	21236

Draws were sampled 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).

1.5. Plot model posterior and credible intervals

```
plot1 <-mcmc_plot(model_WU, type = "intervals", prob = 0.90, variable = c("b_age_diference", "b_bci_diference",
"b_lbinom_compNiNi",
"b_lbinom_compNiI", "b_nest_sim1", "b_year_sim1",
"b_sex_sim1", "b_habitat_sim1"))

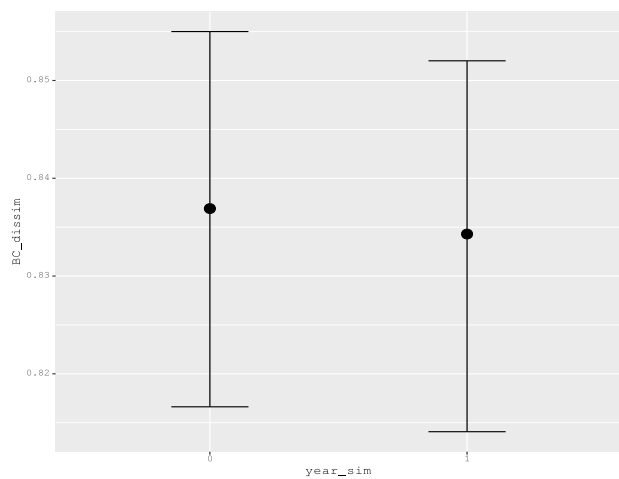
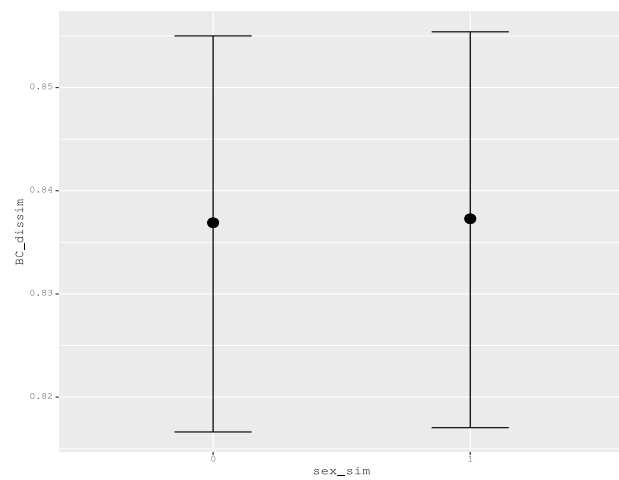
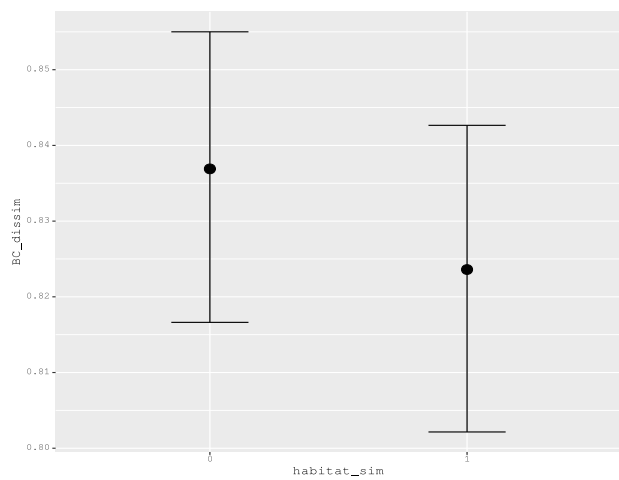
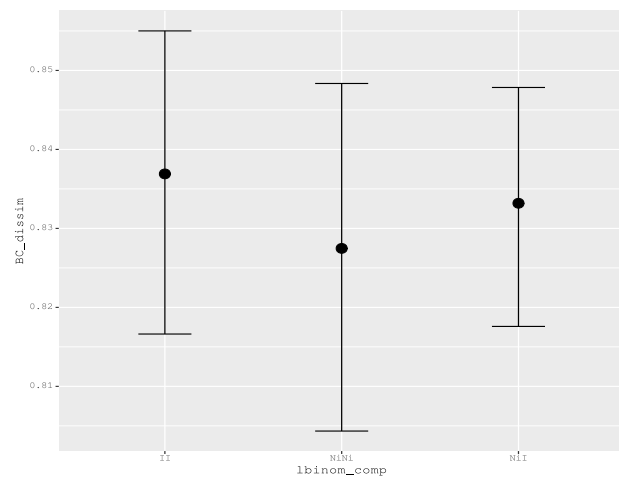
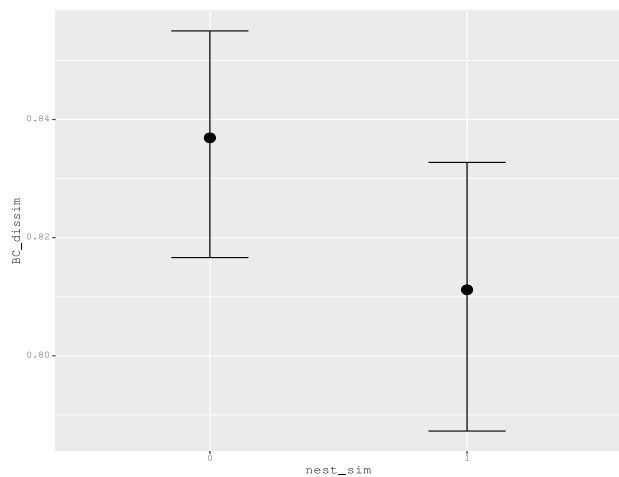
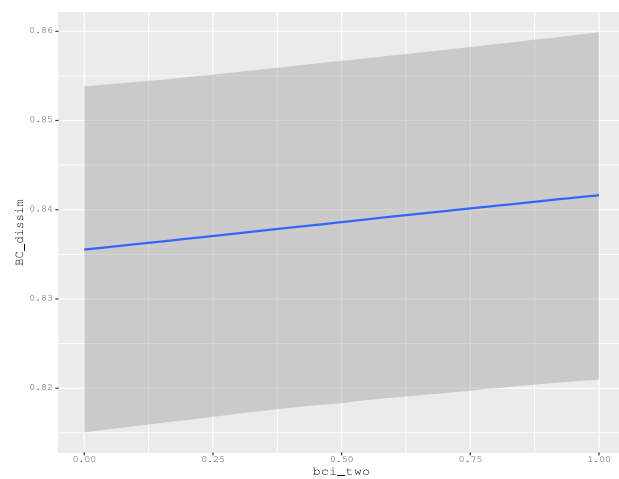
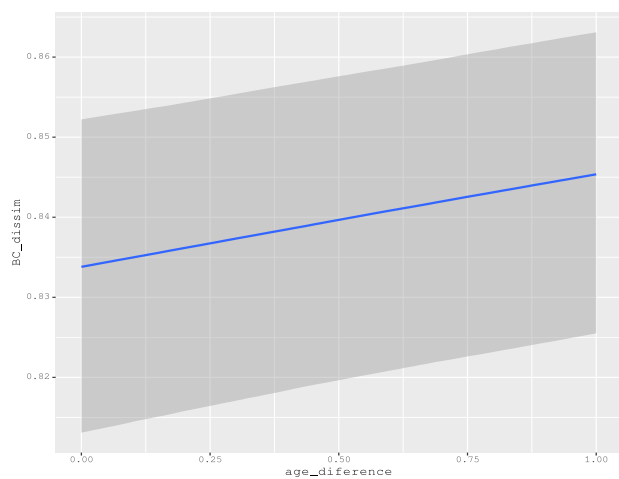
plot1 + theme_default() + geom_vline(xintercept = 0, linetype="dotted", color="black")
```



1.6. Plot model effects

Depicts the range of predicted Bray-Curtis dissimilarity values, does not depict confidence intervals.

```
conditional_effects(model_BC)
```



2. Weighted UniFrac distances

```
#Load Packages

library(brms)
library(rstan)
library(parallel)
library(bayesplot)
library(ggplot2)

#Read in the data
data.dyad <- readRDS("data_dyad.rds")
```

Data dyad composed of 17,020 pairwise comparisons.

2.1. Scale predictors between 0-1

```
#scale all predictors to range between 0-1 if they are not already naturally on that scale

#define scaling function:

range.use <- function(x,min.use,max.use){ (x - min(x,na.rm=T)) / (max(x,na.rm=T)-min(x,na.rm=T)) * (max.use - min.use) + min.use }

scalecols<-c("age_difference","bci_difference","sampling_time")

for(i in 1:ncol(data.dyad[,which(colnames(data.dyad)%in%scalecols)])){
  data.dyad[,which(colnames(data.dyad)%in%scalecols)][,i]<-
range.use(data.dyad[,which(colnames(data.dyad)%in%scalecols)][,i],0,1)
}

data.dyad$sex_sim <-factor(data.dyad$sex_sim, levels=c("0","1"))
data.dyad$nest_sim <-factor(data.dyad$nest_sim, levels=c("0","1"))
data.dyad$year_sim <-factor(data.dyad$year_sim, levels=c("0","1"))
data.dyad$lbinom_comp <-factor(data.dyad$lbinom_comp, levels=c("II","NiNi","NiI"))
data.dyad$habitat_sim<-factor(data.dyad$habitat_sim, levels=c("0","1"))
data.dyad$sampleA <-as.factor(data.dyad$sampleA)
data.dyad$sampleB <-as.factor(data.dyad$sampleB)
data.dyad$IDA <-as.factor(data.dyad$IDA)
data.dyad$IDB <-as.factor(data.dyad$IDB)
```

2.2. Model WU distances

```
ncores = detectCores()
options(mc.cores = parallel::detectCores())

# In order to enhance model convergence, a uniform prior was applied
prior1 <- c(set_prior("normal(0,1)", class = "b", coef = "age_difference"),
  set_prior("normal(0,1)", class = "b", coef = "bci_difference"),
  set_prior("normal(0,1)", class = "b", coef = "nest_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "year_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "sex_sim1"),
  set_prior("normal(0,1)", class = "b", coef = "habitat_sim"),
  set_prior("normal(0,1)", class = "b", coef = "lbinom_compNiI"),
  set_prior("normal(0,1)", class = "b", coef = "lbinom_compNiNi"))
```

```

model_final <- brm(WU_distance~1+ age_diference + bci_diference + nest_sim + year_sim + sex_sim + habitat_sim
+lbinom_comp (1|mm(sampleA,sampleB)) + (1|mm(IDA,IDB)),
  data = data.dyad,
  family= "Beta",
  prior = prior1,
  warmup = 10000, iter = 20000,
  control = list(adapt_delta = 0.99, max_tredepth = 15),
  cores = ncores, chains = 4, init=0)

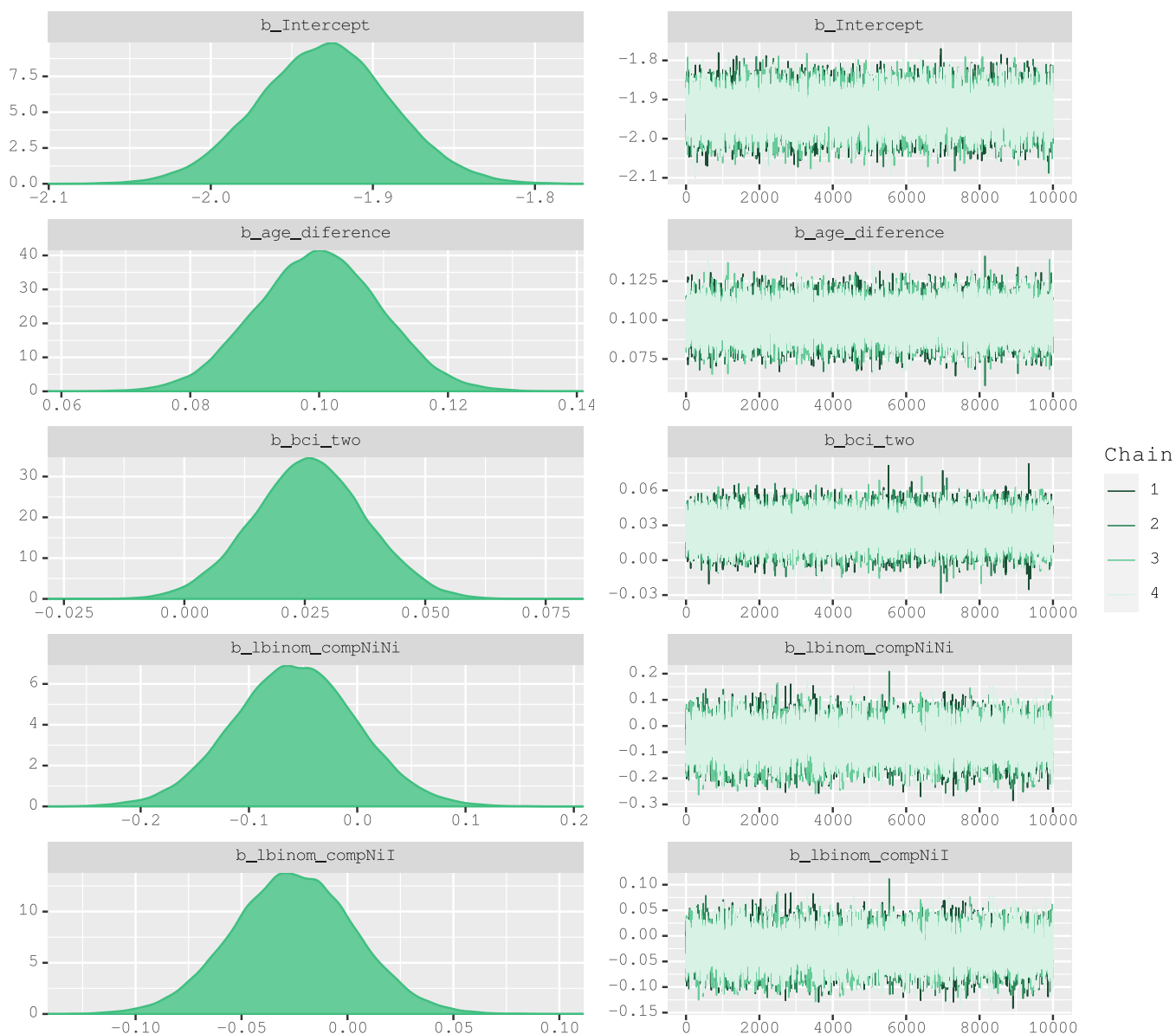
saveRDS(model_WU, "model_WU.rds")

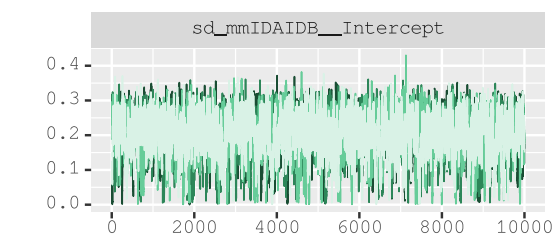
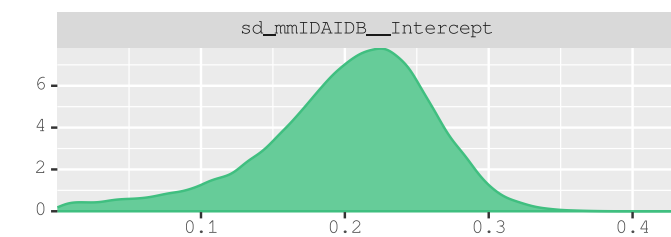
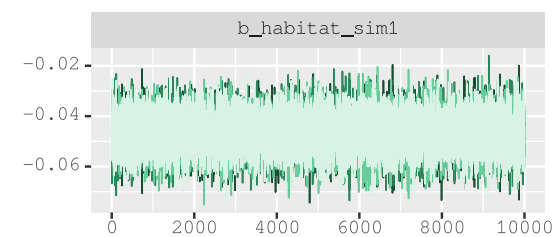
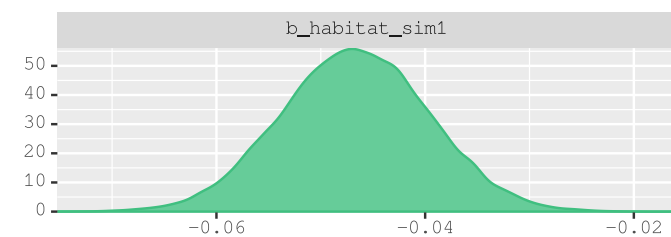
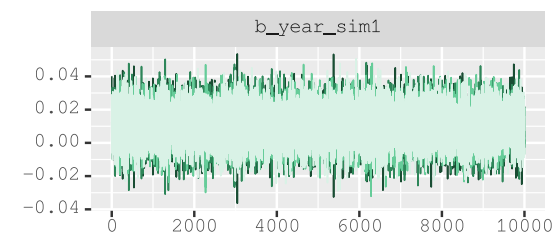
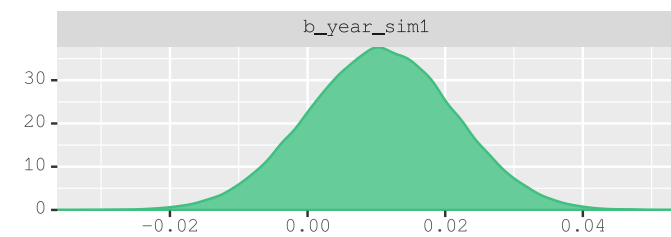
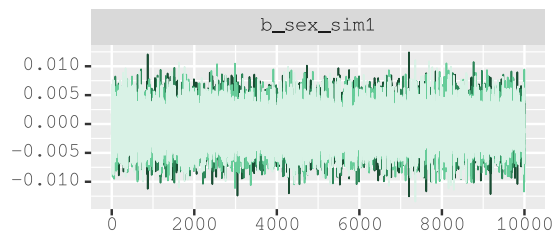
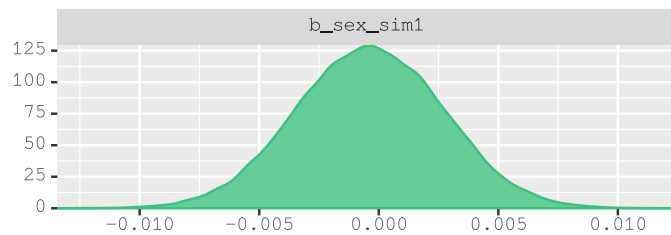
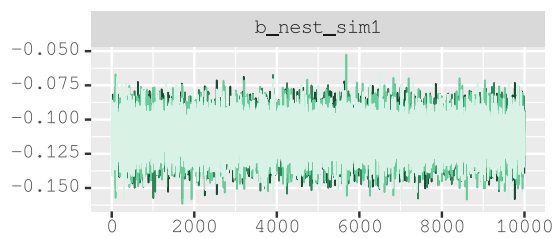
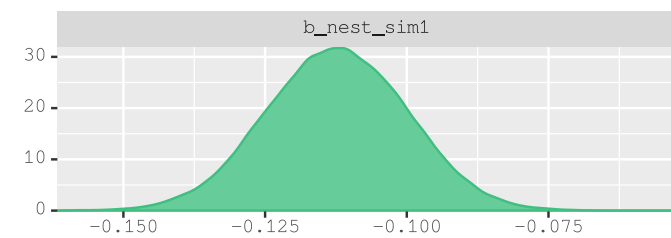
# Read in the model
model_WU <- readRDS("model_WU.rds")

```

2.3. Model Diagnostics

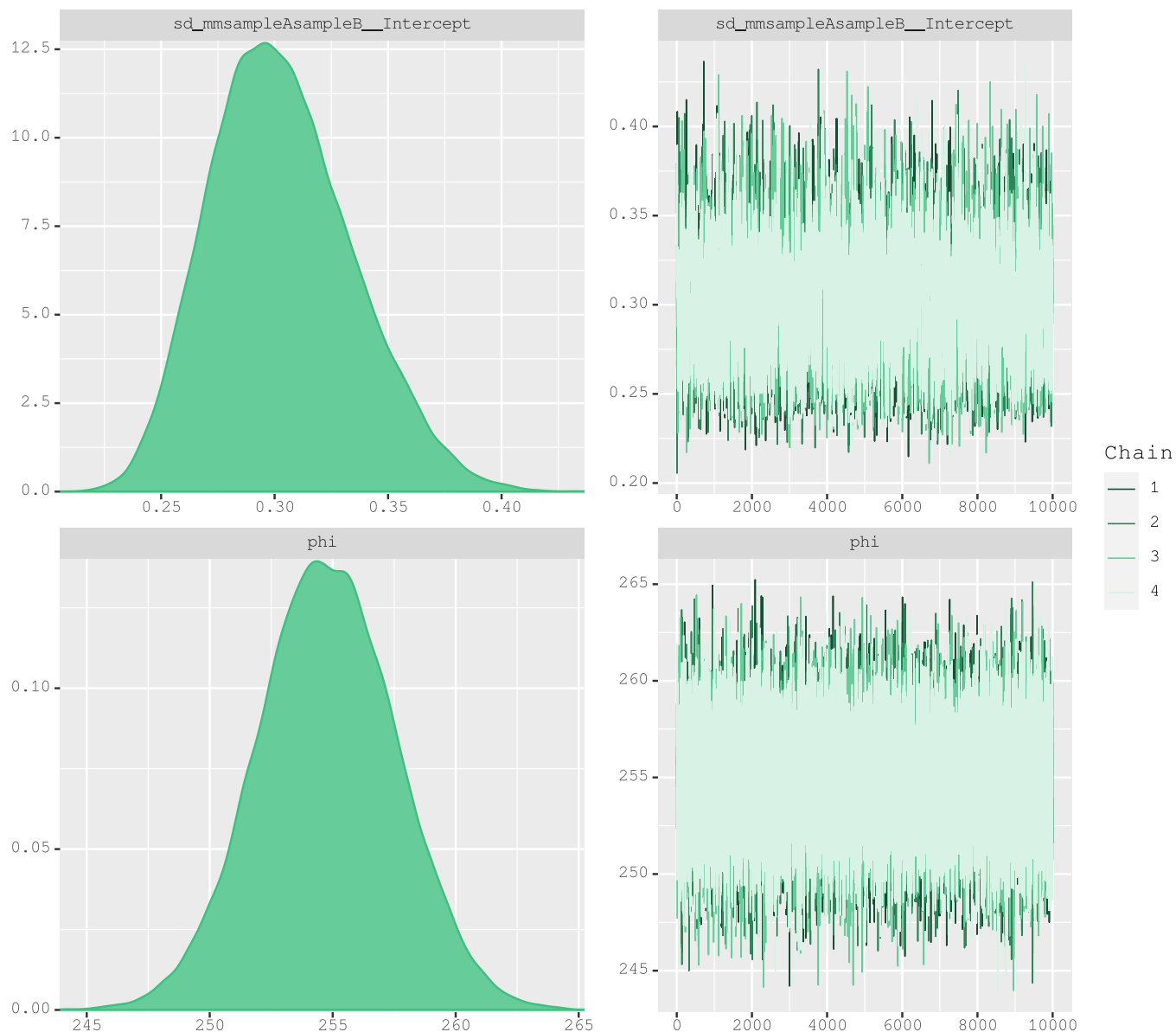
```
plot(model_WU)
```





Chain

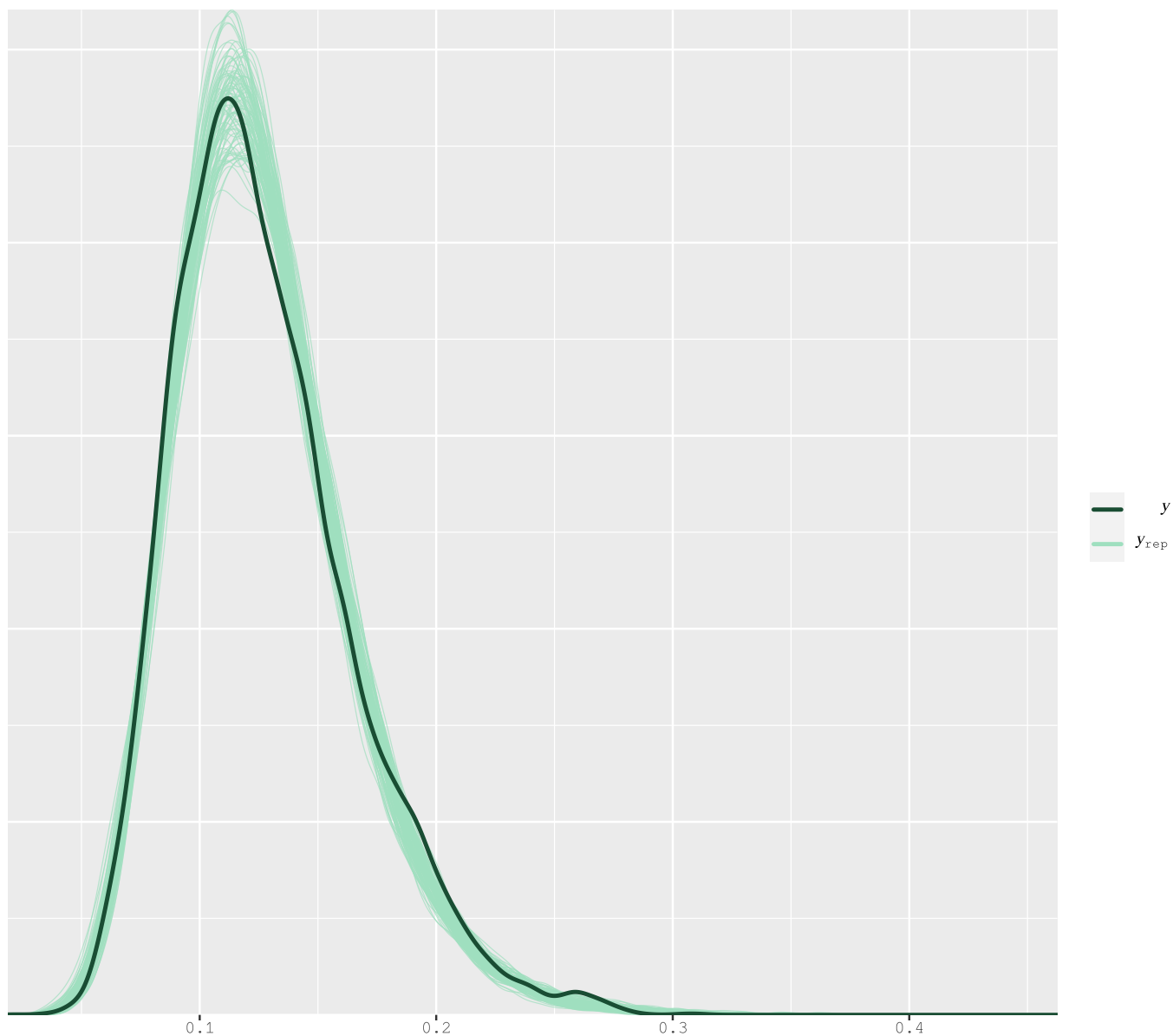




2.3.1. Compare distribution of response variable to distributions of predicted response variable values

```
pp_model_BC <- pp_check(model_WU, ndraws = 50)
```

```
pp_model_WU
```



2.4. Model Summary

```
summary(model_WU)
```

Family: beta

Links: $\mu = \text{logit}$; $\phi = \text{identity}$

Formula: $\text{WU_distance} \sim 1 + \text{age_difference} + \text{bci_difference} + \text{lbinom_comp} + \text{nest_sim} + \text{sex_sim} + \text{year_sim} + \text{habitat_sim} + (1 \mid \text{mm}(\text{sampleA}, \text{sampleB})) + (1 \mid \text{mm}(\text{IDA}, \text{IDB}))$

Data: data.dyad (Number of observations: 16471)

Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
total post-warmup draws = 40000

Group-Level Effects:

~mmIDAIDB (Number of levels: 110)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.20	0.06	0.05	0.30	1.00	2473	2493

~mmsampleAsampleB (Number of levels: 182)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	0.30	0.03	0.25	0.37	1.00	3590	5450

Population-Level Effects:

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

Intercept	-1.93	0.04	-2.01	-1.85	1.00	22627	27001
age_diference	0.10	0.01	0.08	0.12	1.00	94893	27585
bci_diference	0.03	0.01	0.00	0.05	1.00	93067	26189
lbinom_compNiNi	-0.06	0.06	-0.17	0.05	1.00	11669	20499
lbinom_compNiI	-0.03	0.03	-0.08	0.03	1.00	11780	21192
nest_sim1	-0.11	0.01	-0.14	-0.09	1.00	88616	27856
sex_sim1	-0.00	0.00	-0.01	0.01	1.00	89743	26096
year_sim1	0.01	0.01	-0.01	0.03	1.00	90232	28801
habitat_sim1	-0.05	0.01	-0.06	-0.03	1.00	92715	27700

Family Specific Parameters:

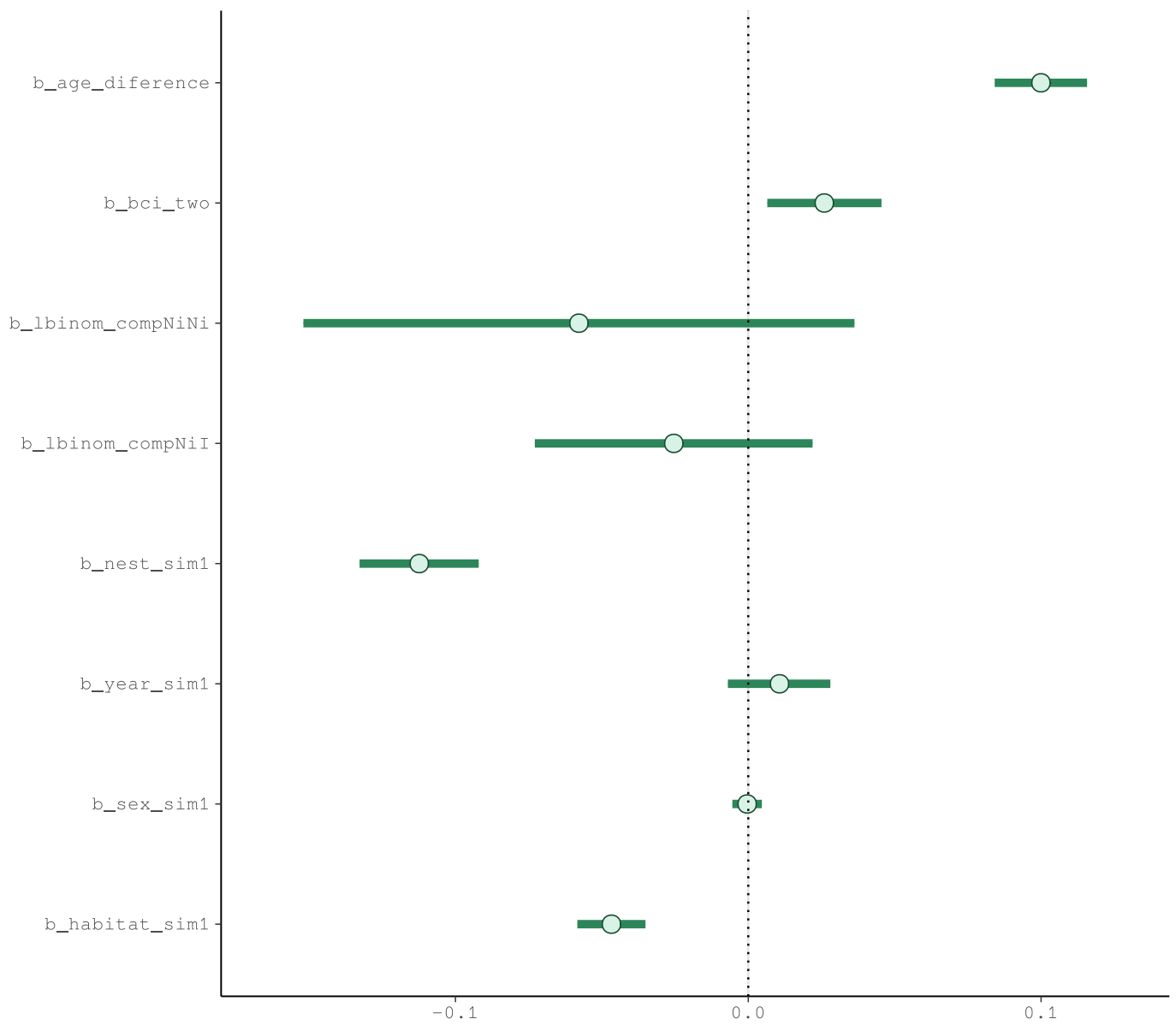
	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
phi	254.78	2.81	249.27	260.30	1.00	86114	27141

Draws were sampled 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).

2.5. Plot model posterior and credible intervals

```
plot1 <-mcmc_plot(model_WU, type = "intervals", prob = 0.90, variable = c("b_age_diference", "b_bci_diference",
"b_lbinom_compNiNi",
"b_lbinom_compNiI", "b_nest_sim1", "b_year_sim1",
"b_sex_sim1", "b_habitat_sim1"))

plot1 + theme_default() + geom_vline(xintercept = 0, linetype="dotted", color="black")
```



2.6. Plot model effects

Depicts the range of predicted Bray-Curtis dissimilarity values, does not depict confidence intervals.

```
conditional_effects(model_WU)
```

