Varroa

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Varroa Analysis

This document outlines the code used for the analysis in O'Connell et al 2024 regarding the effects of various treatments on Varroa based on a literature search (see main manuscript for details). The analysis measures the effect of various treatments using the log ratio between the treatment and its associated control. This approach allows us to compared values from various sources and treatments from a wide general perspective.

Load up Packages

We will use the MCMCglmm package which allows us to run mixed effects models in a Bayesian framework.

```
library(MCMCglmm)
```

```
## Loading required package: Matrix
```

```
## Loading required package: coda
```

```
## Loading required package: ape
```

Data

The raw data set Varroa_treatment_database_2023.10.27.csv can be found in the supplementary of the manuscript. Once loaded we will also create a new variable which further splits the category Chemical into "Synthetic" and "Agriculturally_Organic".

```
varroa_data <- read.csv("Varroa_treatment_database_2023.10.27.csv",
                        sep = ",",
                        header = T)

#we will add a breakdown of synthetic versus non synthetic
chem_split <- as.vector(varroa_data$categoryTreatment)

#We will loop around and replace the the term Chemical with its entry in the
#SubCategory1Treatment variable
for(i in 1:length(chem_split)){

  if(chem_split[i] == "Chemical")
```

```
    {chem_split[i] <- varroa_data$SubCategory1Treatment[i]}
}

#Set it so Synthetic chemicals are the baseline.
chem_split <- factor(chem_split, levels = c("Synthetic",
                                            "Agriculturally_Organic",
                                            "Biological",
                                            "Physical",
                                            "Mixed"))

#Add this new chem_split variable to the data set.
varroa_data <-  data.frame(varroa_data,
                                      chem_split)
```

log ratio calculations

To calculate the log ratio vales we use a loop so that for every study we calculate the pairwise log ratio between the studies control and each of the treatment measures as log(treatment/control).

There are four different broad measurement types in the analysis. (1) HoneyBeeIncrease: Those that measure aspects of honey bees where an increase in the measure is a measure of the positive effects of the treatment. For example, if the number of bees increases in response to some treatment.

(2) HoneyBeeReduction Those that measure aspects of honey bees where a increase in the measure is a measure of the negative effects of the treatment. For example, if the mortality rate of bees increases in response to some treatment.

(3) VarroaReduction: Those that measure aspects of Varroa where an increase in the measure is a measure of the positive effects of the treatment. For example, if the Varroa mortality rate increases in response to some treatment.

(4) VarroaIncrease: Those that measure aspects of Varroa where an increase in the measure is a measure of the negative effects of the treatment. For example, if the Varroa population size increases in response to some treatment.

In order to include all 4 of these groups together in the main analysis we reversed the sign for the log ratio of HoneyBeeReduction and VarroaIncrease values so that positive values indicate positive outcomes for bee control.

We do not include any infinite ratios caused by either log(1/0) or log(0/1). We change log(0/0) values to zero as while it gives an NA a zero value of no change is comparable to values such as log(1/1).

First we will create a loop for each of the Response Variable Category types (HoneyBeeIncrease, HoneyBeeReduction, VarroaIncrease, VarroaReduction)

HoneyBeeIncrease

Loop matching up all the treatments and controls for measures where an increase is a positive outcome for bees. This loop only compares treatment values within studies and for the same response target (for example, within studies there may be several response targets such as adults, juveniles etc).

3 measures are dropped as the control and treatments have differnt signs leading to log(-t/c) which cannot be computed.

```r
#subset to just responses with HoneyBeeIncrease
HoneyBeeIncrease_data <- varroa_data[varroa_data$ResponseVariableCategory ==
                                       "HoneyBeeIncrease",]

#create a column that has unique treatment and response numbers
HoneyBeeIncrease_data$tre_resp <-  paste(HoneyBeeIncrease_data$Treatment_Group,
                                         "_",
                                         HoneyBeeIncrease_data$ResponseNo.,
                                         sep = "")

#empty list to put the final paired rows into
HoneyBeeIncrease_tret_group_temp <- list()

#Data for every study
for (i in 1:length(unique(HoneyBeeIncrease_data$StudyID))){

  hbi_stud <- HoneyBeeIncrease_data[HoneyBeeIncrease_data$StudyID ==
                                      unique(HoneyBeeIncrease_data$StudyID)[i],]
  #Data for every response target (juvinal. adult etc)
  for(z in 1:length(unique(hbi_stud$ResponseVariableTarget))){

    hbi_stud_res <- hbi_stud[hbi_stud$ResponseVariableTarget ==
                               unique(hbi_stud$ResponseVariableTarget)[z],]

     for(w in 1:length(unique(hbi_stud_res$tre_resp))){

       hbi_tret <- hbi_stud_res[hbi_stud_res$tre_resp ==
                                  unique(hbi_stud_res$tre_resp)[w],]

       #This given the median value across the responses
       median_res <- median(hbi_tret$specificResponseMean)

#HoneyBeeIncrease_tret_group_temp <- vector()

        for(t in 1:length(hbi_tret[hbi_tret$Status != "control",1])){

#we default to the first control for now.
hbi_control <- hbi_tret[hbi_tret$Status == "control", ][1,]

#rename the colunm names to _control
colnames(hbi_control) <- paste(names(hbi_control),"_control",sep = "")

#we default to the first control for now.
HoneyBeeIncrease_tret_group_temp[[length(HoneyBeeIncrease_tret_group_temp)+1]]<-
  cbind(hbi_tret[hbi_tret$Status != "control",][t,],
                  hbi_control, median_res)

        }
    }
  }
  }

#Now we just
```

```
HoneyBeeIncrease_paired <- do.call(rbind.data.frame,
                                   HoneyBeeIncrease_tret_group_temp)

#We can add a row of the log ratio of the response mean value
#(specificResponseMean) divided by the control (specificResponseMean_control)

HoneyBeeIncrease_paired$logratio <-
  log(c(HoneyBeeIncrease_paired$specificResponseMean +
          HoneyBeeIncrease_paired$median_res*0.01)/
        c(HoneyBeeIncrease_paired$specificResponseMean_control +
            HoneyBeeIncrease_paired$median_res*0.01))
```

```
## Warning in log(c(HoneyBeeIncrease_paired$specificResponseMean +
## HoneyBeeIncrease_paired$median_res * : NaNs produced
```

```
HoneyBeeIncrease_paired_fin <- HoneyBeeIncrease_paired

HoneyBeeIncrease_paired_fin <- HoneyBeeIncrease_paired[!(is.nan(HoneyBeeIncrease_paired$logratio)),]

#Lets just set Chemical as the baseline
HoneyBeeIncrease_paired_fin$categoryTreatment <-
  factor(HoneyBeeIncrease_paired_fin$categoryTreatment,
                                                      levels = c("Chemical",
                                                                 "Physical",
                                                                 "Biological",
                                                                 "Mixed")
                                                      )

#create a variable that gives a unique identify for nested country continent
HoneyBeeIncrease_paired_fin$Cont_Country <-
  paste0(HoneyBeeIncrease_paired_fin$Continent,
          HoneyBeeIncrease_paired_fin$Country)
```

HoneyBeeReduction

Loop matching up all the treatments and controls for measures where a decrease is a positive outcome for bees. This loop only compares treatment values within studies and for the same response target (for example, within studies there may be several response targets such as adults, juveniles etc).

After zero adjusting there are 3 NaN values which are caused by the control and treatment having differnt signs to thier values.

```
#subset to just responses with HoneyBeeIncrease
HoneyBeeReduction_data <- varroa_data[varroa_data$ResponseVariableCategory ==
                                      "HoneyBeeReduction",]

#create a column that has unique treatment and response numbers
HoneyBeeReduction_data$tre_resp <-  paste(HoneyBeeReduction_data$Treatment_Group,
                                          "_",
                                          HoneyBeeReduction_data$ResponseNo.,
                                          sep = "")
```

```r
#empty list to put the final paired rows into
HoneyBeeReduction_tret_group_temp <- list()

#Data for every study
for (i in 1:length(unique(HoneyBeeReduction_data$StudyID))){

  hbr_stud <- HoneyBeeReduction_data[HoneyBeeReduction_data$StudyID ==
                                       unique(HoneyBeeReduction_data$StudyID)[i],]
  #Data for every response target (juvinal. adult etc)
  for(z in 1:length(unique(hbr_stud$ResponseVariableTarget))){

    hbr_stud_res <- hbr_stud[hbr_stud$ResponseVariableTarget ==
                               unique(hbr_stud$ResponseVariableTarget)[z],]

     for(w in 1:length(unique(hbr_stud_res$tre_resp))){

hbr_tret <- hbr_stud_res[hbr_stud_res$tre_resp==unique(hbr_stud_res$tre_resp)[w],]

#HoneyBeeIncrease_tret_group_temp <- vector()

        for(t in 1:length(hbr_tret[hbr_tret$Status != "control",1])){

       #This given the median value across the responses
            median_hbr_tret_res <- median(hbr_tret$specificResponseMean)

#we default to the first control for now.
hbr_control <- hbr_tret[hbr_tret$Status == "control", ][1,]

#rename the colunm names to _control
colnames(hbr_control) <- paste(names(hbr_control),"_control",sep = "")

#we default to the first control for now.
HoneyBeeReduction_tret_group_temp[[length(HoneyBeeReduction_tret_group_temp)+1]]<-
  cbind(hbr_tret[hbr_tret$Status != "control",][t,],
                  hbr_control, median_hbr_tret_res)

        }
    }
  }
  }

#Now we just
HoneyBeeReduction_paired <- do.call(rbind.data.frame,
                                    HoneyBeeReduction_tret_group_temp)

#We can add a row of the log ratio of the response mean value
#(specificResponseMean) divided by the control (specificResponseMean_control)

HoneyBeeReduction_paired$logratio <-
  log(c(HoneyBeeReduction_paired$specificResponseMean +
          HoneyBeeReduction_paired$median_hbr_tret_res*0.01)/
        c(HoneyBeeReduction_paired$specificResponseMean_control +
            HoneyBeeReduction_paired$median_hbr_tret_res*0.01))
```

```
## Warning in log(c(HoneyBeeReduction_paired$specificResponseMean +
## HoneyBeeReduction_paired$median_hbr_tret_res * : NaNs produced
```

```
##From looking at the data values for 154,155,156 should have 0 values
#The loop does not work as the zero adjustment is also zero.
HoneyBeeReduction_paired$logratio[154:156] <- c(0)

#This give infinity due to the zero adjustment is also being zero
#So here we will adjust by 1% of the response varible
HoneyBeeReduction_paired$logratio[157] <- log(c(20+ 20*0.01)/c(20*0.01))

#Remove the NaN values that are caused by differnt signes between control and
#treatment
HoneyBeeReduction_paired_fin <- HoneyBeeReduction_paired[!(is.nan(HoneyBeeReduction_paired$logratio)),]

#Lets just set Chemical as the baseline
HoneyBeeReduction_paired_fin$categoryTreatment <-
  factor(HoneyBeeReduction_paired_fin$categoryTreatment,
                                                      levels = c("Chemical",
                                                                 "Physical",
                                                                 "Biological",
                                                                 "Mixed")
                                                      )

#create a variable that gives a unique identify for nested country continent
HoneyBeeReduction_paired_fin$Cont_Country <-
  paste0(HoneyBeeReduction_paired_fin$Continent,
         HoneyBeeReduction_paired_fin$Country)


#We can also create a version of the data set
#with the log ratio value flipped so that it can be read as a positive value

HoneyBeeReduction_paired_red_fin <- HoneyBeeReduction_paired_fin

HoneyBeeReduction_paired_red_fin$logratio <-
  -HoneyBeeReduction_paired_red_fin$logratio
```

VarroaIncrease

Loop matching up all the treatments and controls for measures where a decrease is a positive outcome for bees. This loop only compares treatment values within studies and for the same response target (for example, within studies there may be several response targets such as adults, juveniles etc).

No values where removed.

```
#subset to just responses with VarroaIncrease
VarroaIncrease_data <- varroa_data[varroa_data$ResponseVariableCategory ==
                                     "VarroaIncrease",]

#create a column that has unique treatment and response numbers
VarroaIncrease_data$tre_resp <-  paste(VarroaIncrease_data$Treatment_Group,
                                       "_",
```

```
                                        VarroaIncrease_data$ResponseNo.,
                                        sep = "")

#empty list to put the final paired rows into
VarroaIncrease_tret_group_temp <- list()

#Data for every study
for (i in 1:length(unique(VarroaIncrease_data$StudyID))){

  vi_stud <- VarroaIncrease_data[VarroaIncrease_data$StudyID ==
                                   unique(VarroaIncrease_data$StudyID)[i],]
  #Data for every response target (juvinal. adult etc)
  for(z in 1:length(unique(vi_stud$ResponseVariableTarget))){

    vi_stud_res <- vi_stud[vi_stud$ResponseVariableTarget ==
                             unique(vi_stud$ResponseVariableTarget)[z],]

     for(w in 1:length(unique(vi_stud_res$tre_resp))){

vi_tret <- vi_stud_res[vi_stud_res$tre_resp == unique(vi_stud_res$tre_resp)[w],]

       #This given the median value across the responses
            median_vi_tret_res <- median(vi_tret$specificResponseMean)

        for(t in 1:length(vi_tret[vi_tret$Status != "control",1])){

#we default to the first control for now.
vi_control <- vi_tret[vi_tret$Status == "control", ][1,]

#rename the colunm names to _control
colnames(vi_control) <- paste(names(vi_control),"_control",sep = "")

#we default to the first control for now.
VarroaIncrease_tret_group_temp[[length(VarroaIncrease_tret_group_temp) + 1]]  <-
  cbind(vi_tret[vi_tret$Status != "control",][t,],
                  vi_control, median_vi_tret_res)

        }
    }
  }
  }

#Now we just
VarroaIncrease_paired <- do.call(rbind.data.frame,
                                 VarroaIncrease_tret_group_temp)

#We can add a row of the log ratio of the response mean value
#(specificResponseMean) divided by the control (specificResponseMean_control)

VarroaIncrease_paired$logratio <-
  log(c(VarroaIncrease_paired$specificResponseMean +
          median_vi_tret_res*0.01)/
        c(VarroaIncrease_paired$specificResponseMean_control +
```

```
            median_vi_tret_res*0.01))

VarroaIncrease_paired_fin <- VarroaIncrease_paired

#lets recode the NaNs to 0 as they are caused by log(0/0)
#which for our purposes are the same as log(1/1)
#VarroaIncrease_paired[ is.nan(VarroaIncrease_paired$logratio), "logratio"] <- 0

#lets remove any pairs that are infinite.
#These are caused by zeros log(1/0) or log(0/1)
#VarroaIncrease_paired_fin <-
#  VarroaIncrease_paired[!(is.infinite(VarroaIncrease_paired$logratio)),]

#Lets just set Chemical as the baseline
VarroaIncrease_paired_fin$categoryTreatment <-
  factor(VarroaIncrease_paired_fin$categoryTreatment,
                                                    levels = c("Chemical",
                                                               "Physical",
                                                               "Biological",
                                                               "Mixed")
                                                    )

#create a variable that gives a unique identify for nested country continent
VarroaIncrease_paired_fin$Cont_Country <-
  paste0(VarroaIncrease_paired_fin$Continent,
         VarroaIncrease_paired_fin$Country)



#We can also create a version of the dataset
#with the log ratio value flipped so that it can be read as a positive value

VarroaIncrease_paired_red_fin <- VarroaIncrease_paired_fin
VarroaIncrease_paired_red_fin$logratio <- -VarroaIncrease_paired_red_fin$logratio
```

VarroaReduction

Loop matching up all the treatments and controls for measures where an increase is a positive outcome for bees. This loop only compares treatment values within studies and for the same response target (for example, within studies there may be several response targets such as adults, juveniles etc).

1 NaN values were removed due to change in sign between control and main value

```
#subset to just responses with VarroaReduction
VarroaReduction_data <- varroa_data[varroa_data$ResponseVariableCategory ==
                                      "VarroaReduction",]

#create a column that has unique treatment and response numbers
VarroaReduction_data$tre_resp <-  paste(VarroaReduction_data$Treatment_Group,
                                        "_",
                                        VarroaReduction_data$ResponseNo.,
                                        sep = "")
```

```r
#empty list to put the final paired rows into
VarroaReduction_tret_group_temp <- list()

#Data for every study
for (i in 1:length(unique(VarroaReduction_data$StudyID))){

  vr_stud <- VarroaReduction_data[VarroaReduction_data$StudyID ==
                                    unique(VarroaReduction_data$StudyID)[i],]
  #Data for every response target (juvinal. adult etc)
  for(z in 1:length(unique(vr_stud$ResponseVariableTarget))){

    vr_stud_res <- vr_stud[vr_stud$ResponseVariableTarget ==
                             unique(vr_stud$ResponseVariableTarget)[z],]

     for(w in 1:length(unique(vr_stud_res$tre_resp))){

vr_tret <- vr_stud_res[vr_stud_res$tre_resp == unique(vr_stud_res$tre_resp)[w],]

            median_vr_tret_res <- median(vr_tret$specificResponseMean)


#HoneyBeeIncrease_tret_group_temp <- vector()

        for(t in 1:length(vr_tret[vr_tret$Status != "control",1])){

#we default to the first control for now.
vr_control <- vr_tret[vr_tret$Status == "control", ][1,]

#rename the colunm names to _control
colnames(vr_control) <- paste(names(vr_control),"_control",sep = "")

#we default to the first control for now.
VarroaReduction_tret_group_temp[[length(VarroaReduction_tret_group_temp) + 1]]<-
  cbind(vr_tret[vr_tret$Status != "control",][t,],
                  vr_control, median_vr_tret_res)

        }
    }
  }
  }

#Now we just
VarroaReduction_paired <- do.call(rbind.data.frame,
                                  VarroaReduction_tret_group_temp)

#We can add a row of the log ratio of the response mean value
#(specificResponseMean) divided by the control (specificResponseMean_control)

VarroaReduction_paired$logratio <-
  log(c(VarroaReduction_paired$specificResponseMean +
          VarroaReduction_paired$median_vr_tret_res*0.01)/
        c(VarroaReduction_paired$specificResponseMean_control +
          VarroaReduction_paired$median_vr_tret_res*0.01))
```

```
## Warning in log(c(VarroaReduction_paired$specificResponseMean +
## VarroaReduction_paired$median_vr_tret_res * : NaNs produced
```

```
#From looking at the data the values for 731,732,733,735,736,737,738
#should be zero as all values are zero
VarroaReduction_paired$logratio[c(731,732,733,735,736,737,738)] <- c(0)

VarroaReduction_paired$logratio[727] <- log(c(VarroaReduction_paired$specificResponseMean[727] +
                                                VarroaReduction_paired$specificResponseMean[727]*0.01)/
                                              c(VarroaReduction_paired$specificResponseMean[727]*0.01))

VarroaReduction_paired$logratio[728] <- log(c(VarroaReduction_paired$specificResponseMean[728] +
                                                VarroaReduction_paired$specificResponseMean[728]*0.01)/
                                              c(VarroaReduction_paired$specificResponseMean[728]*0.01))

VarroaReduction_paired$logratio[729] <- log(c(VarroaReduction_paired$specificResponseMean[729] +
                                                VarroaReduction_paired$specificResponseMean[729]*0.01)/
                                              c(VarroaReduction_paired$specificResponseMean[729]*0.01))

VarroaReduction_paired$logratio[730] <- log(c(VarroaReduction_paired$specificResponseMean[730] +
                                                VarroaReduction_paired$specificResponseMean[730]*0.01)/
                                              c(VarroaReduction_paired$specificResponseMean[730]*0.01))

VarroaReduction_paired$logratio[734] <- log(c(VarroaReduction_paired$specificResponseMean[734] +
                                                VarroaReduction_paired$specificResponseMean[734]*0.01)/
                                              c(VarroaReduction_paired$specificResponseMean[734]*0.01))


#lets recode the NaNs to 0 as they are caused by log(0/0)
#which for our purposes are the same as log(1/1)
VarroaReduction_paired_fin <-
  VarroaReduction_paired[!(is.nan(VarroaReduction_paired$logratio)),]

#lets remove any pairs that are infinite.
#These are caused by zeros log(1/0) or log(0/1)
VarroaReduction_paired_fin <-
  VarroaReduction_paired[!(is.infinite(VarroaReduction_paired$logratio)),]

#Lets just set Chemical as the baseline
VarroaReduction_paired_fin$categoryTreatment <-
  factor(VarroaReduction_paired_fin$categoryTreatment,
                                                        levels = c("Chemical",
                                                                   "Physical",
                                                                   "Biological",
                                                                   "Mixed"
                                                                   )
                                                        )

#create a variable that gives a unique identify for nested country continent
VarroaReduction_paired_fin$Cont_Country <-
  paste0(VarroaReduction_paired_fin$Continent,
         VarroaReduction_paired_fin$Country)
```

We can join all the studies together with the sign reversed so that a positive difference indicates postie

outcomes for control

```
#This just puts all the datasets together.
#Notice HoneyBeeReduction_paired_red_fin and VarroaIncrease_paired_red_fin
#have their signs reversed

#We need to rename the median response column to match
names(HoneyBeeReduction_paired_red_fin)[names(HoneyBeeReduction_paired_red_fin) == "median_hbr_tret_res
names(VarroaIncrease_paired_red_fin)[names(VarroaIncrease_paired_red_fin) == "median_vi_tret_res"] <- "
names(VarroaReduction_paired_fin)[names(VarroaReduction_paired_fin) == "median_vr_tret_res"] <- "median_

Full_comb_data <- rbind(HoneyBeeIncrease_paired_fin,
                        HoneyBeeReduction_paired_red_fin,
                        VarroaIncrease_paired_red_fin,
                        VarroaReduction_paired_fin)

#just bee data
Full_bees_data <- rbind(HoneyBeeIncrease_paired_fin,
                        HoneyBeeReduction_paired_red_fin)

#Reset the levels for bees so workers are the baseline
Full_bees_data$ResponseVariableTarget <-
  factor(Full_bees_data$ResponseVariableTarget,
                                              levels = c("Honey_bee_worker",
                                                         "Honey_bee_colony",
                                                         "Honey_bee_juvenile",
                                                         "Honey_bee_product",
                                                         "Honey_bee_queen"))

#just vorroa data
Full_varroa_data <- rbind(VarroaIncrease_paired_red_fin,
                          VarroaReduction_paired_fin)
```

MCMCglmm analysis

Prior and parameters

Now that we have a set of log ratios we can run some analysis. We first set up a non-informative prior for our our models, with a flat gamma distribution used as the non-informative prior for each for the random terms. For more info on priors see the Course notes (http://cran.nexr.com/web/packages/MCMCglmm/vignettes/CourseNotes.pdf).

```
prior_d <-list(R = list(V = 1, nu=0.002),
            G = list(G1=list(V = 1, nu=0.002, alpha.mu= 0, alpha.V= 10^3),
                     G2=list(V = 1, nu=0.002, alpha.mu= 0, alpha.V= 10^3),
                     G3=list(V = 1, nu=0.002, alpha.mu= 0, alpha.V= 10^3)
                     ))
```

We will also set the number of iterations (nitt), the burnin (burnin) and the thining (thining).

```
burnin <- c(10000)
nitt <- c(110000)
thining <- c(50)
```

Main model

The first model will include all studies with a positive values associated with a positive outcome for bee health.

We run three chains (mod_full, mod_full2 and mod_full3) so we can test if they converge.

100 studies of organic chemicals, 47 studies of synthetic chemicals, 18 studies biological, 7 of physical and 3 of mixed.

```
mod_full <- MCMCglmm(logratio ~ chem_split
                                + Context,
                                 rcov=~units,
                                 random =~StudyID_control
                                          + Continent
                                          + Cont_Country,
                                 family ="gaussian",
                                 data = Full_comb_data,
                                 nitt = nitt,
                                 thin = thining,
                                 burnin = burnin,
                                 prior = prior_d,
                                 verbose = F
                             )

#second model acts as second chain for convergence
#Add a 3rd later for final check
mod_full2 <- MCMCglmm(logratio ~ chem_split
                                  + Context,
                                 rcov=~units,
                                 random =~StudyID_control
                                          + Continent
                                          + Cont_Country,
                                 family ="gaussian",
                                 data = Full_comb_data,
                                 nitt = nitt,
                                 thin = thining,
                                 burnin = burnin,
                                 prior = prior_d,
                                 verbose = F
                             )

mod_full3 <- MCMCglmm(logratio ~ chem_split
                                  + Context,
                                 rcov=~units,
                                 random =~StudyID_control
                                          + Continent
                                          + Cont_Country,
                                 family ="gaussian",
```

```
                                data = Full_comb_data,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = F
                            )

summary(mod_full)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 9490.196
##
##  G-structure:  ~StudyID_control
##
##                  post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.073   0.7746    1.402     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.2299 2.917e-08    0.885     1824
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.05087 1.536e-08   0.2026     1858
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     2.631    2.481    2.776     2020
##
##  Location effects: logratio ~ chem_split + Context
##
##                                  post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)                        0.97349  0.40298  1.49565     2000  0.006
## chem_splitAgriculturally_Organic   0.02252 -0.19744  0.27826     2000  0.850
## chem_splitBiological              -0.56107 -1.05276 -0.04921     2000  0.028
## chem_splitPhysical                -0.49844 -1.48972  0.48493     2000  0.351
## chem_splitMixed                   -0.30235 -1.65429  1.27694     1627  0.682
## ContextLab                         0.66947  0.33630  0.99841     2000 <5e-04
##
## (Intercept)                       **
## chem_splitAgriculturally_Organic
## chem_splitBiological              *
## chem_splitPhysical
## chem_splitMixed
## ContextLab                        ***
```

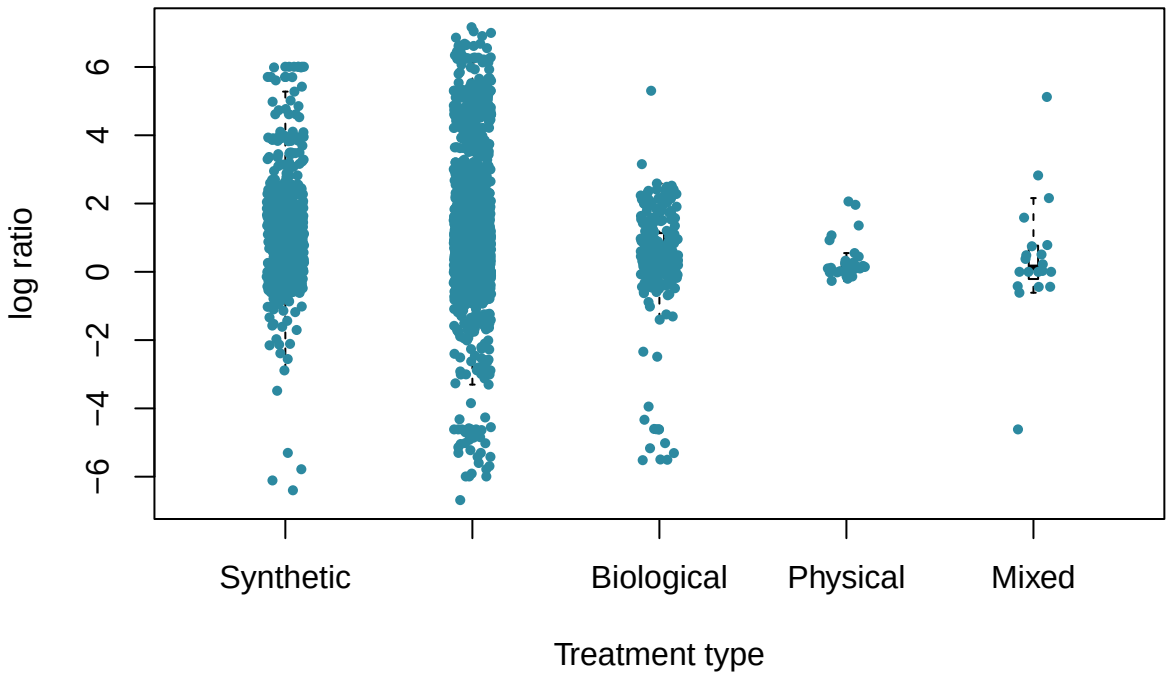
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can check for convergence using gelman.diag(). Values

We can do a simple plot of our results. I need to fix this graph up some more.

```
plot(Full_comb_data$logratio ~ Full_comb_data$chem_split,
     col ="white",
     bty = "n",
     boxwex = 0.05,
     ylab = "log ratio",
     xlab = "Treatment type",
     pch = 16,
     cex = 0)

#We can plot the points over the graph to show the distribution better
points(Full_comb_data$logratio ~ jitter(as.integer(Full_comb_data$chem_split),
                                        amount = 0.1),
       pch = 16,
       col = rgb(44,137,160, max=255),
       cex = 0.7)
```



Overall Synthetic chemicals have a significant overall positive outcome at a ratio of 2.7/1 when compared to the treatment compared to control. This is significantly higher when compared to biological controls which only have a positive outcome effect at a ratio of 1.5/1 when compared to the control.

There is no significant difference between organic chemicals and synthetic chemicals. (In the main model there was weak evidence that organic were not as effective)

Both Physical and Mixed treatments are found to have reduced effects on outcomes when compared to synthetic chemicals, however neither are significantly different.

Finally, there is significant support that treatments have higher positive outcomes when tested in lab based setting with an increase of 2/1 effect compared to non-lab settings.

Chemical sub analysis

We can also just look at the chemical treatments as a sub group.

100 studies of organic chemicals and 47 studies of synthetic chemicals

Organic treatments are significantly better than the Null at a ratio of about 2.3/1 when comparing the treatment to the control (exp(0.83240) gives you this). Synthetic have some evidence they are more effective compared to Organic but only a very minor increase of a ratio of 1.17/1.

#Biological

Lets look at the Biological sub category

5 studies of bee breeds and 13 studies of natural enemies.

Here bee bread has a significant effect compared to the null of about 1.8/1 with no significant difference of the effect of Natural enemies.

Breakdown on measurment type

Controls that increase bee pops

54 studies for this analysis. 33 studies of organic chemical, 9 studies of synthetic chemicals, 7 biological studies, 4 physical studies, 1 mixed study.

```
mod_HoneyBeeIncrease <- MCMCglmm(logratio ~ chem_split,
                                 rcov=~units,
                                 random =~StudyID_control
                                          + Continent
                                          + Cont_Country,
                                 family ="gaussian",
                                 data = HoneyBeeIncrease_paired_fin,
                                 nitt = nitt,
                                 thin = thining,
                                 burnin = burnin,
                                 prior = prior_d,
                                 verbose = FALSE
                               )

summary(mod_HoneyBeeIncrease)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 648.0173
##
##  G-structure:  ~StudyID_control
##
##                 post.mean l-95% CI u-95% CI eff.samp
## StudyID_control    0.1428   0.0361   0.2587     1733
##
```

```
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.3018 2.577e-07   0.9243     1255
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.05519 6.465e-08   0.1761     1791
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.2207   0.1929   0.2541     2000
##
##  Location effects: logratio ~ chem_split
##
##                                  post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                       -0.08233 -0.63097  0.42236     2000 0.690
## chem_splitAgriculturally_Organic   0.15808  0.02295  0.30151     2000 0.026 *
## chem_splitBiological               0.50273  0.18781  0.83228     2000 0.003 **
## chem_splitPhysical                 0.25980 -0.25327  0.80413     2000 0.346
## chem_splitMixed                   -0.04676 -1.17450  1.02455     2021 0.940
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Synthetic chemicals are not significantly different to controls regarding Honey Bee health, however organic chemical have a significantly positive effect compared to synthetic chemicals. Overall, this positive effect is very week with an effect ratio of 1.1/1 when compared to controls.

Biological treatments have a positive effect on bee pops at a ratio of 1.5/1 with no other significant effects.

Controls that decrease bee pops

This is with the original data so remember that a positive value here is something that decreases bee pops. There is 37 studies here. 6 biological studies, 25 with organic chemicals, 10 synthetic chemicals and 1 mixed study.

```
mod_HoneyBeeReduction <- MCMCglmm(logratio ~ chem_split,
                                  rcov=~units,
                                  random =~StudyID_control
                                           + Continent
                                           + Cont_Country,
                                  family ="gaussian",
                                  data = HoneyBeeReduction_paired_fin,
                                  nitt = nitt,
                                  thin = thining,
                                  burnin = burnin,
                                  prior = prior_d,
                                  verbose = FALSE
                              )
```

```
## Warning in MCMCglmm(logratio ~ chem_split, rcov = ~units, random =
```

```
## ~StudyID_control + : some fixed effects are not estimable and have been
## removed. Use singular.ok=TRUE to sample these effects, but use an informative
## prior!
```

```
summary(mod_HoneyBeeReduction)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 1271.884
##
##  G-structure:  ~StudyID_control
##
##                 post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.913   0.8325    3.347     2000
##
##                ~Continent
##
##           post.mean l-95% CI u-95% CI eff.samp
## Continent    0.9558 1.68e-06    3.698     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country    0.4901 1.803e-08    1.834     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     2.831     2.39    3.301     2000
##
##  Location effects: logratio ~ chem_split
##
##                                  post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                         1.6113   0.1700   3.0257     2382 0.030 *
## chem_splitAgriculturally_Organic   -0.7387  -1.8160   0.2495     1901 0.161
## chem_splitBiological               -0.4416  -2.1863   1.1870     2000 0.595
## chem_splitMixed                    -1.8506  -4.9309   1.2708     2000 0.221
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Chemical studies are found to significantly decrease bee pops when compared to the Null at a ratio of about 4.9/1 when comparing the treatment to the control. While there is no significant difference with all other effects they all have reduced effects on the reduction of bee populations. In effect, all

Controls that include both increase and decrease of bee pops

This is with both increases and decreases combined but with the decreases pop data sign flipped so now any positive value is good for the bees. The first model is with the chemical category split into organic/synthetic.

There are 52 studies using organic chemicals, 18 studies using synthethic chemicals, 10 biological studies, 2 mixed and 4 physical

```
All_bees_data <- rbind(HoneyBeeReduction_paired_red_fin,
                       HoneyBeeIncrease_paired_fin)

mod_all_bees <- MCMCglmm(logratio ~ chem_split,
                                 rcov=~units,
                                 random =~StudyID_control
                                          + Continent
                                          + Cont_Country,
                                 family ="gaussian",
                                 data = All_bees_data,
                                 nitt = nitt,
                                 thin = thining,
                                 burnin = burnin,
                                 prior = prior_d,
                                 verbose = FALSE
                             )

summary(mod_all_bees)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 2505.109
##
##  G-structure:  ~StudyID_control
##
##                  post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.266   0.8076    1.797     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.1773 1.847e-09   0.6499     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.06408 3.822e-09   0.2666     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.346    1.213    1.489     2182
##
##  Location effects: logratio ~ chem_split
##
##                                  post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                       -0.66243 -1.17363 -0.09840     2000 0.027 *
## chem_splitAgriculturally_Organic   0.28778 -0.01322  0.62940     2164 0.076 .
```

```
## chem_splitBiological                0.44862 -0.23839  1.17335     2000 0.201
## chem_splitPhysical                  0.61454 -0.72531  1.98780     2727 0.378
## chem_splitMixed                     0.74929 -1.00376  2.62352     2167 0.394
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Synthetic chemical are found to significantly negatively affect bee pops when compared to the Null (i.e. controls), at a ratio of 1.9/1. Synthetic chemicals have a less negative effect, but still an effect of 1.45.

While all other treatments are not significantly different the effect sizes indicate that these effects on bee health are neutral. The non significance is likely due to the lack of these types of studies.

```
All_bees_data <- rbind(HoneyBeeReduction_paired_red_fin,
                       HoneyBeeIncrease_paired_fin)

mod_all_bees_no_split <- MCMCglmm(logratio ~ categoryTreatment,
                                  rcov=~units,
                                  random =~StudyID_control
                                           + Continent
                                           + Cont_Country,
                                  family ="gaussian",
                                  data = All_bees_data,
                                  nitt = nitt,
                                  thin = thining,
                                  burnin = burnin,
                                  prior = prior_d,
                                  verbose = FALSE
                              )

summary(mod_all_bees_no_split)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 2507.972
##
##  G-structure:  ~StudyID_control
##
##                 post.mean l-95% CI u-95% CI eff.samp
## StudyID_control      1.25   0.8206    1.792     2000
##
##                ~Continent
##
##           post.mean l-95% CI u-95% CI eff.samp
## Continent    0.1947 1.21e-08   0.7984     1529
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.06236 5.352e-08    0.249     2000
##
##  R-structure:  ~units
```

```
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.353    1.212     1.49     2292
##
##  Location effects: logratio ~ categoryTreatment
##
##                              post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                   -0.44172 -0.94993  0.01603     2201 0.074 .
## categoryTreatmentPhysical      0.36593 -1.02599  1.68327     2000 0.580
## categoryTreatmentBiological    0.24441 -0.39197  0.94240     2000 0.442
## categoryTreatmentMixed         0.44295 -1.33254  2.10454     2000 0.621
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Similar to the analysis where the chemicals are split into organic and synthetic.

Controls that measure decreases varroa pops

There is 101 studies here.

```
mod_VarroaReduction_paired_fin <- MCMCglmm(logratio ~ chem_split,
                                rcov=~units,
                                random =~StudyID_control
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = VarroaReduction_paired_fin,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE

                              )

summary(mod_VarroaReduction_paired_fin)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 4399.47
##
##  G-structure:  ~StudyID_control
##
##                 post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.264   0.8654    1.687     1854
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
```

```
## Continent    0.1623 5.466e-08   0.6667     1695
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.06025 1.718e-09   0.2447     1646
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.735    1.598    1.877     2000
##
##  Location effects: logratio ~ chem_split
##
##                                  post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)                         1.9819   1.5037   2.5052     2000 <5e-04
## chem_splitAgriculturally_Organic   -0.1814  -0.5394   0.1742     2000  0.317
## chem_splitBiological               -0.7707  -1.4532  -0.0755     2000  0.033
## chem_splitPhysical                 -1.2685  -2.9054   0.3832     2339  0.149
## chem_splitMixed                     0.2795  -2.6881   3.2588     2000  0.853
##
## (Intercept)                        ***
## chem_splitAgriculturally_Organic
## chem_splitBiological               *
## chem_splitPhysical
## chem_splitMixed
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Chemical studies are found to reduce Varroa at a ratio of about 7 to 1 when comparing treatment to controls (exp(1.9798) which is the baseline). Organic chemicals are not significantly different at reducing varroa compared to synthetic.

Biological treatments are significantly less effective at reducing varroa, with a ratio of 3.4/1. There is no sigificant differnce for the other groups.

Controls that measure increases in varroa pops

There is 38 studies here.

```
mod_VarroaIncrease_paired_fin <- MCMCglmm(logratio ~ categoryTreatment,
                                  rcov=~units,
                                  random =~StudyID_control
                                           + Continent
                                           + Cont_Country,
                                  family ="gaussian",
                                  data = VarroaIncrease_paired_fin,
                                  nitt = nitt,
                                  thin = thining,
                                  burnin = burnin,
                                  prior = prior_d,
                                  verbose = FALSE
                                )
```

```
summary(mod_VarroaIncrease_paired_fin)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 1321.894
##
##  G-structure:  ~StudyID_control
##
##                 post.mean l-95% CI u-95% CI eff.samp
## StudyID_control    0.7166   0.3098    1.206     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.2526 1.968e-09    1.046     2000
##
##                ~Cont_Country
##
##              post.mean l-95% CI u-95% CI eff.samp
## Cont_Country    0.1295 4.11e-08   0.5348     1305
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.328     1.16     1.53     2000
##
##  Location effects: logratio ~ categoryTreatment
##
##                              post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                    -1.3285  -1.9389  -0.7135     2259 0.001 ***
## categoryTreatmentPhysical       0.6021  -0.4270   1.7977     2000 0.274
## categoryTreatmentBiological     0.9023   0.3777   1.4694     2000 0.001 ***
## categoryTreatmentMixed          0.8228  -0.6011   2.1240     2000 0.229
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Model with chemicals not split) Similar to the results above, but in reverse,chemical studies are found to have a negative effect on Varroa at a ratio of about 3.7 to 1 when comparing treatment to controls (exp(-1.3129) which is the baseline). These are also significantly more effective than Biological controls at reducing Varroa, which reduce at about 1.5/1.

```
mod_VarroaIncrease_paired_fin_split <- MCMCglmm(logratio ~ chem_split,
                                rcov=~units,
                                random =~StudyID_control
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = VarroaIncrease_paired_fin,
                                nitt = nitt,
```

```
                                  thin = thining,
                                  burnin = burnin,
                                  prior = prior_d,
                                  verbose = FALSE
                              )

summary(mod_VarroaIncrease_paired_fin_split)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 1322.508
##
##  G-structure:  ~StudyID_control
##
##                  post.mean l-95% CI u-95% CI eff.samp
## StudyID_control    0.7402   0.3468    1.247     1824
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.3121 4.242e-07    1.289     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country    0.1391 2.588e-07   0.5383     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.331    1.145    1.527     2000
##
##  Location effects: logratio ~ chem_split
##
##                                    post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                          -1.2585  -1.9197  -0.5511     2000 0.008 **
## chem_splitAgriculturally_Organic     -0.1151  -0.4711   0.2259     2000 0.515
## chem_splitBiological                  0.8495   0.2607   1.3865     2000 0.003 **
## chem_splitPhysical                    0.5259  -0.6795   1.5797     2221 0.366
## chem_splitMixed                       0.7343  -0.6065   2.0614     1792 0.277
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Splitting the chemicals has no real change here, synthetic chemicals have a significant negative effect and there is no difference between organic and synthetic)

Controls that measure both increases/decrease in varroa pops

```
All_varroa_data <- rbind(VarroaReduction_paired_fin,
                         VarroaIncrease_paired_red_fin)

All_varroa_data_mod <- MCMCglmm(logratio ~ categoryTreatment,
                                rcov=~units,
                                random =~StudyID_control
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = All_varroa_data,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                              )

summary(All_varroa_data_mod)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 5746.15
##
##  G-structure:  ~StudyID_control
##
##                  post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.105   0.7651    1.436     1741
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.1278 1.011e-10   0.5034     1585
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.06137 4.025e-09   0.2379     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.665    1.556    1.776     2000
##
##  Location effects: logratio ~ categoryTreatment
##
##                             post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)                   1.78087  1.40461  2.23810     2000 <5e-04 ***
```

```
## categoryTreatmentPhysical    -0.91757 -1.87746  0.09112     2000  0.067 .
## categoryTreatmentBiological  -0.81026 -1.27373 -0.36871     2000 <5e-04 ***
## categoryTreatmentMixed       -0.64246 -2.00434  0.70963     2000  0.379
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Same as before chemicals are the best at a ratio of 6/1, biological significantly less effective at a ratio of 2.7/1 with physical 2.4/1 and haivng some support.

```
All_varroa_data <- rbind(VarroaReduction_paired_fin,
                         VarroaIncrease_paired_red_fin)

All_varroa_data_mod_split <- MCMCglmm(logratio ~ chem_split,
                                      rcov=~units,
                                      random =~StudyID_control
                                               + Continent
                                               + Cont_Country,
                                      family ="gaussian",
                                      data = All_varroa_data,
                                      nitt = nitt,
                                      thin = thining,
                                      burnin = burnin,
                                      prior = prior_d,
                                      verbose = FALSE
                                )

summary(All_varroa_data_mod_split)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 5748.071
##
##  G-structure:  ~StudyID_control
##
##                  post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.104   0.7827    1.428     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.1319 1.163e-08   0.4602     1796
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.05758 7.991e-08   0.2223     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
```

```
## units     1.665    1.556    1.781     2000
##
##  Location effects: logratio ~ chem_split
##
##                                  post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                        1.76448  1.31569  2.21199     1848 0.001 ***
## chem_splitAgriculturally_Organic   0.02276 -0.23788  0.25298     2000 0.869
## chem_splitBiological              -0.78574 -1.25200 -0.31336     2387 0.002 **
## chem_splitPhysical                -0.88661 -1.90173  0.15516     2000 0.098 .
## chem_splitMixed                   -0.63202 -2.10847  0.72837     1853 0.364
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Same as above, there is no difference between chemical types.

Models of life stage target

We will look at life stage separately for bees and Varroa.

Bees life stage

First lets do it for bees, which have 71 studies

Just look at interaction term between worker/juvenile versus treatment type.

```
mod_bees_life <- MCMCglmm(logratio ~ categoryTreatment
                                   + ResponseVariableTarget,
                                rcov=~units,
                                random =~StudyID_control
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = Full_bees_data,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                            )

summary(mod_bees_life)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 2505.405
##
##  G-structure:  ~StudyID_control
##
```

```
##                 post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.159   0.6783    1.618     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.1709 6.324e-10   0.7206     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country    0.0572 4.737e-10   0.2353     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.345    1.205    1.492     3069
##
##  Location effects: logratio ~ categoryTreatment + ResponseVariableTarget
##
##                                         post.mean l-95% CI u-95% CI eff.samp
## (Intercept)                              -0.61596 -1.10328 -0.08509     2000
## categoryTreatmentPhysical                 0.31474 -0.98173  1.65119     2174
## categoryTreatmentBiological               0.26218 -0.36209  0.93744     2000
## categoryTreatmentMixed                    0.27769 -1.42701  2.12819     2000
## ResponseVariableTargetHoney_bee_colony    0.57361 -0.15222  1.24072     1953
## ResponseVariableTargetHoney_bee_juvenile  0.51001  0.23206  0.79582     2000
## ResponseVariableTargetHoney_bee_product   0.37949 -0.09867  0.83629     2151
## ResponseVariableTargetHoney_bee_queen     0.37147 -0.43328  1.12417     2264
##                                          pMCMC
## (Intercept)                              0.035 *
## categoryTreatmentPhysical                0.642
## categoryTreatmentBiological              0.438
## categoryTreatmentMixed                   0.748
## ResponseVariableTargetHoney_bee_colony   0.121
## ResponseVariableTargetHoney_bee_juvenile <5e-04 ***
## ResponseVariableTargetHoney_bee_product  0.113
## ResponseVariableTargetHoney_bee_queen    0.336
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Overall, worked bees respond negatively to chemical treatment, with no significant difference regarding treatment type. Juvenile bees (1.1/1) have a significantly larger positive repose to treatment compared to worker bees (effectively neutral) with some support for a similar differnce for colony and bee products. Overall, it seems like worker bees have the worst response to treatments.

Varroa life stage

```
mod_varroa_life <- MCMCglmm(logratio ~ categoryTreatment
                                    + ResponseVariableTarget,
                                rcov=~units,
                                random =~StudyID_control
```

```
                                        + Continent
                                        + Cont_Country,
                                    family ="gaussian",
                                    data = Full_varroa_data,
                                    nitt = nitt,
                                    thin = thining,
                                    burnin = burnin,
                                    prior = prior_d,
                                    verbose = FALSE
                                )

summary(mod_varroa_life)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 5748.008
##
##  G-structure:  ~StudyID_control
##
##                  post.mean l-95% CI u-95% CI eff.samp
## StudyID_control     1.091   0.7713    1.421     1780
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.1694 2.394e-07    0.535     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.05671 4.553e-10   0.2139     1778
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.667    1.567     1.79     2222
##
##  Location effects: logratio ~ categoryTreatment + ResponseVariableTarget
##
##                                       post.mean l-95% CI u-95% CI eff.samp
## (Intercept)                              1.7779   1.3922   2.2220     2000
## categoryTreatmentPhysical               -0.9337  -1.8778   0.1098     2458
## categoryTreatmentBiological             -0.8047  -1.2493  -0.3897     1870
## categoryTreatmentMixed                  -0.6583  -2.0547   0.7424     2000
## ResponseVariableTargetVarroa_juvenile   -0.3310  -1.2017   0.5396     2000
##                                        pMCMC
## (Intercept)                            0.001 ***
## categoryTreatmentPhysical              0.061 .
## categoryTreatmentBiological           <5e-04 ***
## categoryTreatmentMixed                 0.325
```

```
## ResponseVariableTargetVarroa_juvenile  0.464
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

No difference between life stages in varroa

Dosage dependance

Taking from the Full_comb_data, which has the signs flipped so any positive number is a positive effect for bees (i.e. decreased bee mortality is now a positive number).

```
Full_dosage <- data.frame(logratio = Full_comb_data$logratio,
                          StudyID = Full_comb_data$StudyID,
                          SubCa2Treat = Full_comb_data$SubCategory2Treatment,
                          Dosage_level = Full_comb_data$Dosage_level,
                          Continent = Full_comb_data$Continent,
                          Country = Full_comb_data$Country,
                          Cont_Country = Full_comb_data$Cont_Country)

Full_dosage <- na.omit(Full_dosage)
```

Ordinal dosage analysis.

```
mod_dos <- MCMCglmm(logratio ~ Dosage_level,
                                rcov=~units,
                                random =~StudyID
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = Full_dosage,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                            )

summary(mod_dos)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 854.6568
##
##  G-structure:  ~StudyID
##
##         post.mean  l-95% CI u-95% CI eff.samp
## StudyID    0.3232 3.203e-09   0.8399     2000
##
```

```
##                ~Continent
##
##           post.mean l-95% CI u-95% CI eff.samp
## Continent    0.7327 2.16e-07    2.592     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country    0.3869 1.399e-06    1.232     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.659    1.368    1.989     2000
##
##  Location effects: logratio ~ Dosage_level
##
##                     post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)            1.1299   0.3014   2.1190     2736 0.030 *
## Dosage_levelLOW       -0.2026  -0.5664   0.1281     1767 0.266
## Dosage_levelMEDIUM     0.1229  -0.4095   0.6044     2232 0.631
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is no strong support for any doage dependence here. Note that there are only 24 studies in this analysis so it cannot really be broken down more.

break down each of the chemicals

```
temp_Sub_chem <- Full_comb_data

#combine Flumethrin and Fluvalinate and call them Pyrethroid
temp_Sub_chem[temp_Sub_chem$broadTreatment %in% c("Flumethrin",
                                                  "Fluvalinate"),
              "broadTreatment"] <- "Pyrethroid"

Sub_chem <- temp_Sub_chem[temp_Sub_chem$broadTreatment %in%
c("Amitraz",
  "Coumaphos",
  "Thymol",
  "Oxalic_acid",
  "Formic_acid",
  "Pyrethroid"), ]
```

Currently I just run a model with one as a contrast but we can change this. We need to have some expectation of what drives what.

```
mod_spec_chem <- MCMCglmm(logratio ~ broadTreatment,
                                  rcov=~units,
                                  random =~StudyID
                                           + Continent
```

```
                                        + Cont_Country,
                                    family ="gaussian",
                                    data = Sub_chem,
                                    nitt = nitt,
                                    thin = thining,
                                    burnin = burnin,
                                    prior = prior_d,
                                    verbose = FALSE
                                )

summary(mod_spec_chem)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 3510.74
##
##  G-structure:  ~StudyID
##
##         post.mean l-95% CI u-95% CI eff.samp
## StudyID    0.4764   0.2435   0.7647     2181
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.8049 2.634e-07    2.898     1733
##
##                ~Cont_Country
##
##              post.mean l-95% CI u-95% CI eff.samp
## Cont_Country    0.1735 5.14e-07   0.5407     1875
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     1.959     1.79    2.144     2000
##
##  Location effects: logratio ~ broadTreatment
##
##                             post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)                   1.48411  0.68599  2.53735     2000  0.012 *
## broadTreatmentCoumaphos      -0.99548 -1.45295 -0.52676     2000 <5e-04 ***
## broadTreatmentFormic_acid    -0.35274 -0.76167  0.03697     2172  0.077 .
## broadTreatmentOxalic_acid    -0.29385 -0.73657  0.19314     2000  0.228
## broadTreatmentPyrethroid     -0.30324 -0.66475  0.04278     1738  0.098 .
## broadTreatmentThymol         -0.15162 -0.49536  0.23445     1717  0.397
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Amitraz as the baseline has an effect of 4.4/1. Coumaphos is significantly less effective compared to Amitraz with a ratio of 1.7/1 while there is some support that Formic Acid is also less effective at a ratio of 3/1.

Chem specific effect on bee increases

Model checking each chemical on bee pops

```
temp_Sub_chem_HI <- HoneyBeeIncrease_paired_fin


#combine Flumethrin and Fluvalinate and call them Pyrethroid
temp_Sub_chem_HI[temp_Sub_chem_HI$broadTreatment %in% c("Flumethrin","Fluvalinate"),
                 "broadTreatment"] <- "Pyrethroid"

Sub_chem_HI <- temp_Sub_chem_HI[temp_Sub_chem_HI$broadTreatment %in%
c("Amitraz",
  "Coumaphos",
  "Thymol",
  "Oxalic_acid",
  "Formic_acid",
  "Pyrethroid"), ]
```

```
mod_spec_chem_HI <- MCMCglmm(logratio ~ broadTreatment,
                                rcov=~units,
                                random =~StudyID
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = Sub_chem_HI,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                             )

summary(mod_spec_chem_HI)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 486.6577
##
##  G-structure:  ~StudyID
##
##         post.mean  l-95% CI u-95% CI eff.samp
## StudyID   0.09568 3.136e-07   0.2487     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.3537 1.051e-07    1.211     1717
##
##                ~Cont_Country
```

```
##
##               post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country     0.0686 1.188e-08   0.2298     1815
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.2866    0.235   0.3402     1737
##
##  Location effects: logratio ~ broadTreatment
##
##                             post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                  -0.01666 -0.62056  0.65482     2000 0.907
## broadTreatmentCoumaphos      -0.11153 -0.53972  0.27380     2000 0.588
## broadTreatmentFormic_acid    -0.07512 -0.33389  0.16497     1798 0.554
## broadTreatmentOxalic_acid     0.32373 -0.04367  0.66440     2000 0.068 .
## broadTreatmentPyrethroid     -0.03276 -0.27203  0.25577     2000 0.792
## broadTreatmentThymol          0.11208 -0.11081  0.32397     2000 0.316
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As the baseline Amitraz is not significantly differnt when compared to the control. Some evidence that Oxalic_acid is better with regards to bee pop increases at a ratio of 1.4/1

Chem specific effect on bee decreases

Model checking each chemical on bee decreases

Only 15 studies here so not enough studies.

```
temp_Sub_chem_HR <- HoneyBeeReduction_paired_fin

#combine Flumethrin and Fluvalinate and call them Pyrethroid
temp_Sub_chem_HR[temp_Sub_chem_HR$broadTreatment %in% c("Flumethrin","Fluvalinate"),"broadTreatment"] <-

Sub_chem_HR <- temp_Sub_chem_HR[temp_Sub_chem_HR$broadTreatment %in%
c("Amitraz",
  "Coumaphos",
  "Thymol",
  "Oxalic_acid",
  "Formic_acid",
  "Pyrethroid"), ]
```

```
mod_spec_chem_HR <- MCMCglmm(logratio ~ broadTreatment,
                             rcov=~units,
                             random =~StudyID
                                      + Continent
                                      + Cont_Country,
                             family ="gaussian",
                             data = Sub_chem_HR,
                             nitt = nitt,
                             thin = thining,
```

```
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                            )

summary(mod_spec_chem_HR)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 352.0154
##
##  G-structure:  ~StudyID
##
##         post.mean  l-95% CI u-95% CI eff.samp
## StudyID     1.251 2.324e-06    3.079     1948
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent     4.524 2.547e-06     12.5     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country     1.049 1.849e-06    4.137     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     2.419    1.609    3.225     2000
##
##  Location effects: logratio ~ broadTreatment
##
##                             post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                    1.0133  -2.8266   4.8647     2000 0.597
## broadTreatmentCoumaphos        0.1345  -3.2940   3.5493     1593 0.913
## broadTreatmentFormic_acid     -0.5237  -3.7936   2.9697     2000 0.764
## broadTreatmentOxalic_acid     -0.3447  -3.8157   3.1354     2000 0.845
## broadTreatmentPyrethroid       1.6052  -2.0897   4.8902     2000 0.364
## broadTreatmentThymol          -0.1975  -3.5896   3.2864     2000 0.917
```

Nothing here but not enough data really.

Chem specific effect on Verrora increase

Model checking each chemical on Varroa Increase only 24 studies.

```r
temp_Sub_chem_VI <- VarroaIncrease_paired_red_fin

#combine Flumethrin and Fluvalinate and call them Pyrethroid
temp_Sub_chem_VI[temp_Sub_chem_VI$broadTreatment %in% c("Flumethrin","Fluvalinate"),"broadTreatment"] <-

Sub_chem_VI <- temp_Sub_chem_VI[temp_Sub_chem_VI$broadTreatment %in%
c("Amitraz",
  "Coumaphos",
  "Thymol",
  "Oxalic_acid",
  "Formic_acid",
  "Pyrethroid"), ]
```

```r
mod_spec_chem_VI <- MCMCglmm(logratio ~ broadTreatment,
                                rcov=~units,
                                random =~StudyID
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = Sub_chem_VI,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                             )

summary(mod_spec_chem_VI)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 820.5317
##
##  G-structure:  ~StudyID
##
##         post.mean l-95% CI u-95% CI eff.samp
## StudyID     1.124    0.329    2.063     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent     1.423 2.103e-06    5.424     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country    0.3632 3.437e-11     1.51     2000
##
##  R-structure:  ~units
##
```

```
##       post.mean l-95% CI u-95% CI eff.samp
## units      1.72    1.427    2.076     2000
##
##  Location effects: logratio ~ broadTreatment
##
##                             post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)                    1.9226   0.4687   3.2008     2000  0.016 *
## broadTreatmentCoumaphos       -3.2092  -4.2019  -2.0750     2000 <5e-04 ***
## broadTreatmentFormic_acid     -0.1002  -0.8173   0.6204     1870  0.786
## broadTreatmentOxalic_acid     -0.7038  -1.7716   0.3490     2000  0.184
## broadTreatmentPyrethroid      -0.7045  -1.2926  -0.1486     2000  0.023 *
## broadTreatmentThymol           0.3669  -0.3038   0.9583     2000  0.256
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As the baseline Amitraz is significantly different when compared to the control, with a ratio of 6.4/1. Coumaphos is significantly less effective, performing worse than the control at a ratio of 1/3.9. Pyrethroid was also significantly worse when compared to the Amitraz with a ratio of 3.2/1 when compared to the control.

Chem specific effect on Verrora decreases

Model checking each chemical on Varroa decreases 72 studies.

```
temp_Sub_chem_VR <- VarroaReduction_paired_fin

#combine Flumethrin and Fluvalinate and call them Pyrethroid
temp_Sub_chem_VR[temp_Sub_chem_VR$broadTreatment %in% c("Flumethrin","Fluvalinate"),"broadTreatment"] <-

Sub_chem_VR <- temp_Sub_chem_VR[temp_Sub_chem_VR$broadTreatment %in%
c("Amitraz",
  "Coumaphos",
  "Thymol",
  "Oxalic_acid",
  "Formic_acid",
  "Pyrethroid"), ]
```

```
mod_spec_chem_VR <- MCMCglmm(logratio ~ broadTreatment,
                             rcov=~units,
                             random =~StudyID
                                      + Continent
                                      + Cont_Country,
                             family ="gaussian",
                             data = Sub_chem_VR,
                             nitt = nitt,
                             thin = thining,
                             burnin = burnin,
                             prior = prior_d,
                             verbose = FALSE
                            )

summary(mod_spec_chem_VR)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 1064.027
##
##  G-structure:  ~StudyID
##
##         post.mean l-95% CI u-95% CI eff.samp
## StudyID    0.7904   0.4454    1.193     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.5763 4.434e-10     1.01     2000
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.06395 2.137e-09   0.2407     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.9171   0.7802    1.071     2000
##
##  Location effects: logratio ~ broadTreatment
##
##                             post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)                   1.93875  1.33988  2.66401     2000 0.001 ***
## broadTreatmentCoumaphos      -0.43251 -0.99197  0.07984     2000 0.110
## broadTreatmentFormic_acid    -0.40538 -0.97518  0.17680     2380 0.159
## broadTreatmentOxalic_acid    -0.25191 -0.81894  0.39451     2000 0.424
## broadTreatmentPyrethroid      0.09610 -0.39140  0.59095     2000 0.709
## broadTreatmentThymol         -0.31604 -0.84784  0.26553     2000 0.278
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As the baseline Amitraz is significantly different when compared to the control, with a ratio of 6.9/1. Some evidence that Coumaphos is less effective, with a ratio of 4.5/1. Some evidence that Formic_acid is less effective, with a ratio of 4.6/1

```
temp_Sub_chem_Vb <- rbind(VarroaReduction_paired_fin,
                          VarroaIncrease_paired_red_fin)

#combine Flumethrin and Fluvalinate and call them Pyrethroid
temp_Sub_chem_Vb[temp_Sub_chem_Vb$broadTreatment %in% c("Flumethrin",
                                                        "Fluvalinate"),
                 "broadTreatment"] <- "Pyrethroid"

Sub_chem_Vb <- temp_Sub_chem_Vb[temp_Sub_chem_Vb$broadTreatment %in%
c("Amitraz",
  "Coumaphos",
```

```
  "Thymol",
  "Oxalic_acid",
  "Formic_acid",
  "Pyrethroid"), ]
```

```
mod_spec_chem_Vb <- MCMCglmm(logratio ~ broadTreatment,
                                rcov=~units,
                                random =~StudyID
                                         + Continent
                                         + Cont_Country,
                                family ="gaussian",
                                data = Sub_chem_Vb,
                                nitt = nitt,
                                thin = thining,
                                burnin = burnin,
                                prior = prior_d,
                                verbose = FALSE
                            )

summary(mod_spec_chem_Vb)
```

```
##
##  Iterations = 10001:109951
##  Thinning interval  = 50
##  Sample size  = 2000
##
##  DIC: 1972.831
##
##  G-structure:  ~StudyID
##
##         post.mean l-95% CI u-95% CI eff.samp
## StudyID    0.6995   0.3856    1.066     2000
##
##                ~Continent
##
##           post.mean  l-95% CI u-95% CI eff.samp
## Continent    0.5974 6.916e-08     2.09     1811
##
##                ~Cont_Country
##
##              post.mean  l-95% CI u-95% CI eff.samp
## Cont_Country   0.07207 6.275e-10    0.291     2000
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units       1.4     1.23     1.57     2000
##
##  Location effects: logratio ~ broadTreatment
##
##                            post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)                  2.05970  1.25085  2.79966     2000  0.001 ***
## broadTreatmentCoumaphos     -1.13229 -1.62438 -0.60630     2000 <5e-04 ***
```

```
## broadTreatmentFormic_acid  -0.32819 -0.77679  0.10409     2000  0.159
## broadTreatmentOxalic_acid  -0.37821 -0.88246  0.15621     1840  0.170
## broadTreatmentPyrethroid   -0.32030 -0.65582  0.09908     2000  0.105
## broadTreatmentThymol       -0.07740 -0.49985  0.32683     1855  0.742
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Overall, as the baseline Amitraz is significantly different when compared to the control, with a ratio of 7.9/1. Coumaphos is significantly less effective, with a ratio of 2.55/1. Some weak evidence that Formic_acid and Pyrethroid are also less effective, with ratios of 5.6/1 and 5.7/1 when compared to their controls.