

ManganetalGEIforrxiv.R

xbussl

2024-09-20

```
# This script was developed by Luc Bussière
# In collaboration with all the authors of the following MS

#
# Exploiting pathogen defence trade-offs to manage risks of crop pests
# evolving resistance to biocontrol.
#
#
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# Script originated May 1, 2023
# Last modified Aug 23, 2024

# The next line is to clear the memory, but it is annotated out
# to prevent accidental erasure of the big models that take a lot of time to find
rm(list = ls())

# load libraries ####
library(lme4)

## Loading required package: Matrix
library(brms)

## Loading required package: Rcpp
## Loading 'brms' package (version 2.21.0). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').
```

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## 
## Attaching package: 'brms'
## The following object is masked from 'package:lme4':
## 
##     ngrps
## 
## The following object is masked from 'package:stats':
## 
##     ar
library(lubridate)

## 
## Attaching package: 'lubridate'
## The following objects are masked from 'package:base':
## 
##     date, intersect, setdiff, union
library(graph4lg)

## Welcome to 'graph4lg' package. Let's do landscape genetics analysis with graphs
library(bayestestR)
library(performance)
library(reshape2)
library(data.table)

## 
## Attaching package: 'data.table'
## The following objects are masked from 'package:reshape2':
## 
##     dcast, melt
## The following objects are masked from 'package:lubridate':
## 
##     hour, isoweek, mday, minute, month, quarter, second, wday, week,
##     yday, year
library(coda)
library(ggpubr)

## Loading required package: ggplot2
library(Hmisc)

## 
## Attaching package: 'Hmisc'
## The following objects are masked from 'package:base':
## 
##     format.pval, units
library(png)
library(ggtext)
library(binom)
library(parallel)
library(ggridges)
library(pbkrtest)

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# library(QGglmm)
library(broom.mixed)
library(RColorBrewer)
library(tidybayes)

##
## Attaching package: 'tidybayes'

## The following objects are masked from 'package:ggridges':
##
##     scale_point_color_continuous, scale_point_color_discrete,
##     scale_point_colour_continuous, scale_point_colour_discrete,
##     scale_point_fill_continuous, scale_point_fill_discrete,
##     scale_point_size_continuous

## The following object is masked from 'package:bayestestR':
##
##     hdi

## The following objects are masked from 'package:brms':
##
##     dstudent_t, pstudent_t, qstudent_t, rstudent_t

# The script uses some functions from the rethinking package by McElreath,
# which can be downloaded using the annotated code below.
# install.packages("rethinking",
#                     repos=c(cran="https://cloud.r-project.org",
#                           rethinking="http://xcelab.net/R"))

# library(rethinking)
library(broom)
library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr    1.1.4      v stringr 1.5.1
## vforcats 1.0.0      v tibble   3.2.1
## v purrr   1.0.2      v tidyrr   1.3.1
## v readr   2.1.5

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::between()      masks data.table::between()
## x tidyrr::expand()       masks Matrix::expand()
## x dplyr::filter()        masks stats::filter()
## x dplyr::first()         masks data.table::first()
## x data.table::hour()      masks lubridate::hour()
## x data.table::isoweek()    masks lubridate::isoweek()
## x dplyr::lag()           masks stats::lag()
## x dplyr::last()          masks data.table::last()
## x data.table::mday()       masks lubridate::mday()
## x data.table::minute()     masks lubridate::minute()
## x data.table::month()      masks lubridate::month()
## x tidyrr::pack()          masks Matrix::pack()
## x data.table::quarter()    masks lubridate::quarter()
## x data.table::second()     masks lubridate::second()
## x dplyr::src()            masks Hmisc::src()
## x dplyr::summarize()      masks Hmisc::summarize()
## x purrr::transpose()      masks data.table::transpose()

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## x tidyR::unpack()      masks Matrix::unpack()
## x data.table::wday()   masks lubridate::wday()
## x data.table::week()   masks lubridate::week()
## x data.table::yday()   masks lubridate::yday()
## x data.table::year()   masks lubridate::year()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
# set the default ggplot theme for graphics
theme_set(theme_bw())

# preamble #####
## Import data #####
# read data in frame and examine it
df_qgen_pre<-read_csv2("data/Quan_Gene_APRI_12_2023_RM_LFB.csv")

## i Using "'","," as decimal and "'.'" as grouping mark. Use `read_delim()` for more control.
## Rows: 4344 Columns: 19-- Column specification -----
## Delimiter: ";"
## chr  (6): tubeID, plant, isolate, treatment, Pupal_sex, Notes
## dbl  (10): block, originl_rep, replicate, matingpair, damID, sireID, Days_to...
## date  (3): inoculationdate, Death_date, Pupation_date
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

names(df_qgen_pre)

## [1] "block"          "originl_rep"     "replicate"       "matingpair"
## [5] "damID"          "sireID"         "tubeID"         "plant"
## [9] "isolate"        "treatment"      "inoculationdate" "Death_date"
## [13] "Pupation_date"  "Days_to_pupation" "Days_to_death"   "Day_10_Mortality"
## [17] "Pupal_weight"   "Pupal_sex"       "Notes"

df_qgen_pre %>%
  filter(is.na(inoculationdate))

## # A tibble: 30 x 19
##   block originl_rep replicate matingpair damID sireID tubeID plant isolate
##   <dbl>      <dbl>      <dbl>      <dbl> <dbl> <dbl> <chr> <chr> <chr>
## 1 1          1          2791     2235      32  7495    149 32 _ 1 Soya  CON
## 2 2          1          2793     2237      32  7495    149 32 _ 3 Soya  CON
## 3 3          2          2959     2386      33  117     199 33_79 Maz   BB
## 4 4          2          2960     2387      33  117     199 33_80 Maz   BB
## 5 5          2          2969     2396      33  117     199 33_89 Maz   MT
## 6 6          2          2970     2397      33  117     199 33_90 Maz   MT
## 7 7          2          3514     2905      40  185     232 40_4  Soya  CON
## 8 8          2          3533     2924      40  185     232 40_23 Soya  MT
## 9 9          2          3534     2925      40  185     232 40_24 Soya  MT
## 10 10         2          3535     2926      40  185     232 40_25 Soya  MT
## # i 20 more rows
## # i 10 more variables: treatment <chr>, inoculationdate <date>,
## #   Death_date <date>, Pupation_date <date>, Days_to_pupation <dbl>,
## #   Days_to_death <dbl>, Day_10_Mortality <dbl>, Pupal_weight <dbl>,
## #   Pupal_sex <chr>, Notes <chr>

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## housekeeping ####

#remove NAs inoculation dates
df_qgen<-df_qgen_pre %>%
  filter(is.na(inoculationdate)==FALSE)

summary(df_qgen) #Summary of data

##      block      original_rep      replicate      matingpair      damID
##  Min.   :1.000   Min.   : 1   Min.   : 1   Min.   : 1.00   Min.   :  7.0
##  1st Qu.:1.000   1st Qu.:1240  1st Qu.:1079  1st Qu.:14.00  1st Qu.: 40.0
##  Median :1.000   Median :2688   Median :2158   Median :30.00   Median :117.0
##  Mean   :1.466   Mean   :2577   Mean   :2166   Mean   :29.13   Mean   :355.9
##  3rd Qu.:2.000   3rd Qu.:3879  3rd Qu.:3256  3rd Qu.:44.00  3rd Qu.:224.0
##  Max.   :2.000   Max.   :5130   Max.   :4344   Max.   :57.00   Max.   :7495.0
##
##      sireID      tubeID      plant      isolate
##  Min.   : 62.0   Length:4314   Length:4314   Length:4314
##  1st Qu.: 71.0   Class  :character  Class  :character  Class  :character
##  Median :199.0   Mode   :character  Mode   :character  Mode   :character
##  Mean   :299.7
##  3rd Qu.:257.0
##  Max.   :2000.0
##
##      treatment      inoculationdate      Death_date
##  Length:4314   Min.   :2018-11-21   Min.   :2018-11-23
##  Class  :character  1st Qu.:2018-11-23  1st Qu.:2018-12-02
##  Mode   :character  Median :2018-12-03  Median :2018-12-19
##                      Mean   :2019-03-05  Mean   :2019-02-13
##                      3rd Qu.:2019-06-29  3rd Qu.:2019-06-30
##                      Max.   :2019-07-09  Max.   :2019-07-18
##                      NA's   :1550
##
##      Pupation_date      Days_to_pupation      Days_to_death      Day_10_Mortality
##  Min.   :2018-12-08   Min.   :15.00   Min.   : 0.00   Min.   :0.0000
##  1st Qu.:2018-12-15   1st Qu.:23.00   1st Qu.: 3.00   1st Qu.:0.0000
##  Median :2018-12-20   Median :28.00   Median : 6.00   Median :0.0000
##  Mean   :2018-12-22   Mean   :28.55   Mean   :10.48   Mean   :0.4351
##  3rd Qu.:2018-12-28   3rd Qu.:34.00   3rd Qu.:17.00   3rd Qu.:1.0000
##  Max.   :2019-01-16   Max.   :46.00   Max.   :52.00   Max.   :1.0000
##  NA's   :3893       NA's   :3893   NA's   :1553   NA's   :2
##
##      Pupal_weight      Pupal_sex      Notes
##  Min.   :0.014   Length:4314   Length:4314
##  1st Qu.:0.099   Class  :character  Class  :character
##  Median :0.114   Mode   :character  Mode   :character
##  Mean   :0.114
##  3rd Qu.:0.131
##  Max.   :0.209
##  NA's   :3906

# CHANGE VARIABLES from num to factor
df_qgen$replicate<-as.factor(df_qgen$replicate)
df_qgen$matingpair<-as.factor(df_qgen$matingpair)

# MAKE NEW VARIABLES

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df_qgen<-df_qgen %>%
  mutate(mother = paste("D",damID,sep="_"),
         father = paste("S",sireID,sep="_"),
         id = paste("0",replicate,sep="_")) %>%
  mutate(animal=id) %>%
  select(-sireID,-damID)

df_qgen$mother<-as.factor(df_qgen$mother)
df_qgen$father<-as.factor(df_qgen$father)
df_qgen$animal<-as.factor(df_qgen$animal)

df_qgen$id<-as.factor(df_qgen$id)
df_qgen$plant<-as.factor(df_qgen$plant)
df_qgen$plant<-relevel(df_qgen$plant,ref="Tom")

df_qgen$isolate<-as.factor(df_qgen$isolate)
df_qgen$isolate<-relevel(df_qgen$isolate,ref="CON")

# can choose not to recode treatment as factor to suppress warnings later
df_qgen$treatment<-as.factor(df_qgen$treatment)
df_qgen$isolate<-relevel(df_qgen$isolate,ref="CON")

df_qgen$Pupal_sex<-as.factor(df_qgen$Pupal_sex)

names(df_qgen)

## [1] "block"           "originl_rep"      "replicate"       "matingpair"
## [5] "tubeID"          "plant"            "isolate"         "treatment"
## [9] "inoculationdate" "Death_date"        "Pupation_date"   "Days_to_pupation"
## [13] "Days_to_death"   "Day_10_Mortality" "Pupal_weight"    "Pupal_sex"
## [17] "Notes"           "mother"           "father"          "id"
## [21] "animal"

# MORTdayTENin the data file incorrectly does not include larvae that died on d10,
# and that all NAs not returned in ifelse statements,
# so these lines fix it and generate new mortality vars on several days (not just on d10)

## recreate death vars #####
df_qgen <- df_qgen %>%
  group_by(plant, isolate) %>%
  mutate(MORTdayFIVE = if_else(
    is.na(Days_to_death),
    0,
    if_else(Days_to_death < 6 & Days_to_death > 0,
           1,
           0))) %>%
  mutate(MORTdaySIX = if_else(
    is.na(Days_to_death),
    0,
    if_else(Days_to_death < 7 & Days_to_death > 0,
           1,
           0))) %>%
  mutate(MORTdaySEVEN = if_else(
    is.na(Days_to_death),

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0,
if_else(
  Days_to_death < 8 & Days_to_death > 0,
  1,
  0))) %>%
mutate(MORTdayEIGHT = if_else(
  is.na(Days_to_death),
  0,
  if_else(
    Days_to_death < 9 & Days_to_death > 0,
    1,
    0))) %>%
mutate(MORTdayNINE = if_else(
  is.na(Days_to_death),
  0,
  if_else(
    Days_to_death < 10 & Days_to_death > 0,
    1,
    0))) %>%
mutate(MORTdayTEN = if_else(
  is.na(Days_to_death),
  0,
  if_else(
    Days_to_death < 11 & Days_to_death > 0,
    1,
    0))) %>%
mutate(MORTday14 = if_else(
  is.na(Days_to_death),
  0,
  if_else(
    Days_to_death < 15 & Days_to_death > 0,
    1,
    0)))
## trim to essential cols #####
# variables plus exclude oil and early deaths
df_qgen_sub <- df_qgen %>%
  mutate(Exclude = if_else(
    Notes %in% c("oil death",
                "Oil death",
                "missing",
                "squashed",
                "Escaped"), 1, 0)) %>%
  filter(Exclude == 0) %>%
  filter(Days_to_death != 1 & Days_to_death != 2 | is.na(Days_to_death)) %>%
  select(animal, mother, father, plant, isolate, treatment, MORTday14)

df_qgen %>%
  mutate(oildeath = if_else(
    Notes %in% c("oil death",

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        "Oil death"), 1, 0)) %>%
group_by(oildeath) %>%
summarise(N = n())

## # A tibble: 2 x 2
##   oildeath     N
##       <dbl> <int>
## 1          0    4152
## 2          1     162

# check that this catches all?
df_qgen %>%
  mutate(oildeath = if_else(
    Notes %in% c("oil death",
                 "Oil death"), 1, 0)) %>%
  filter(oildeath == 0) %>%
  filter(Days_to_death != 1 & Days_to_death != 2 | is.na(Days_to_death)) %>%
group_by(oildeath) %>%
  summarise(N = n())

## # A tibble: 1 x 2
##   oildeath     N
##       <dbl> <int>
## 1          0    3813

df_qgen_wblock <- df_qgen %>%
  mutate(Exclude = if_else(
    Notes %in% c("oil death",
                 "Oil death",
                 "missing",
                 "squashed",
                 "Escaped"), 1, 0)) %>%
  filter(Exclude == 0) %>%
  filter(Days_to_death != 1 & Days_to_death != 2 | is.na(Days_to_death)) %>%
  select(animal,mother,father,plant,isolate,treatment,MORTday14, block)

# convert df to data.frame
df_qgen_sub_df <- as.data.frame(df_qgen_sub)

# write csv for records
# df_qgen_sub_df %>%
#   write_csv("outputs/ManganetalQG2023.csv")

## reorder levels in main df #####
names(df_qgen_sub_df)

## [1] "animal"      "mother"      "father"      "plant"       "isolate"      "treatment"
## [7] "MORTday14"

levels(factor(df_qgen_sub_df$plant))

## [1] "Tom" "Maz"  "Soya"
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levels(factor(df_qgen_sub_df$isolate))

## [1] "CON" "BB"   "MT"

levels(factor(df_qgen_sub_df$treatment))

## [1] "Maz_BB"   "Maz_CON"  "Maz_MT"   "Soya_BB"   "Soya_CON"  "Soya_MT"   "Tom_BB"
## [8] "Tom_CON"  "Tom_MT"

df_qgen_sub_df <- df_qgen_sub_df %>%
  mutate(plant = fct_relevel(plant, "Soya", "Maz", "Tom"),
        isolate = fct_relevel(isolate, "CON", "BB", "MT"),
        treatment = fct_relevel(treatment, "Soya_CON", "Soya_BB", "Soya_MT",
                                 "Maz_CON", "Maz_BB", "Maz_MT",
                                 "Tom_CON", "Tom_BB", "Tom_MT"))

names(df_qgen_wblock)

## [1] "animal"    "mother"    "father"    "plant"     "isolate"   "treatment"
## [7] "MORTday14" "block"

df_qgen_wblock <- df_qgen_wblock %>%
  mutate(plant = fct_relevel(plant, "Soya", "Maz", "Tom"),
        isolate = fct_relevel(isolate, "CON", "BB", "MT"),
        treatment = fct_relevel(treatment, "Soya_CON", "Soya_BB", "Soya_MT",
                                 "Maz_CON", "Maz_BB", "Maz_MT",
                                 "Tom_CON", "Tom_BB", "Tom_MT"))

names(df_qgen_wblock)

## [1] "animal"    "mother"    "father"    "plant"     "isolate"   "treatment"
## [7] "MORTday14" "block"

df_sum_qgfams <- df_qgen_wblock %>%
  group_by(mother,father, block) %>%
  summarise(N = n()) %>%
  arrange(block,father)

## `summarise()` has grouped output by 'mother', 'father'. You can override using
## the `.`groups` argument.

# model of plant and isolate ####

# fixed version of model to check overdispersion
glm_mortality_fixed <- glm(MORTday14 ~
                           plant *
                           isolate,
                           data = df_qgen_sub_df,
                           family = "binomial"
                           )

summary(glm_mortality_fixed)

## 
## Call:
## glm(formula = MORTday14 ~ plant * isolate, family = "binomial",
##      data = df_qgen_sub_df)
## 
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## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -2.1669    0.1464 -14.802 < 2e-16 ***
## plantMaz              1.8779    0.1745  10.762 < 2e-16 ***
## plantTom              1.5718    0.1896   8.292 < 2e-16 ***
## isolateBB             1.5809    0.1732   9.130 < 2e-16 ***
## isolateMT             1.2519    0.1763   7.100 1.24e-12 ***
## plantMaz:isolateBB  -0.7133    0.2194  -3.251  0.00115 **
## plantTom:isolateBB  -1.0926    0.2405  -4.543 5.56e-06 ***
## plantMaz:isolateMT  -0.8869    0.2215  -4.004 6.23e-05 ***
## plantTom:isolateMT  -0.6441    0.2417  -2.665  0.00770 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 5122.8 on 3810 degrees of freedom
## Residual deviance: 4704.3 on 3802 degrees of freedom
## AIC: 4722.3
##
## Number of Fisher Scoring iterations: 4
# no overdispersion in fixed model

```

```

# generalised mixed model
glm_mortality <- glmer(MORTday14 ~
                         plant *
                         isolate +
                         (1|mother) +
                         (1|father),
                         data = df_qgen_sub_df,
                         family = "binomial"
)

summary(glm_mortality)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: MORTday14 ~ plant * isolate + (1 | mother) + (1 | father)
## Data: df_qgen_sub_df
##
##      AIC      BIC      logLik deviance df.resid
## 4472.7  4541.4  -2225.3   4450.7     3800
##
## Scaled residuals:
##      Min      1Q Median      3Q      Max
## -2.6636 -0.7510 -0.3801  0.8287  4.8842
##
## Random effects:
## Groups Name        Variance Std.Dev.
## mother (Intercept) 0.2776   0.5269
## father (Intercept) 0.2198   0.4688

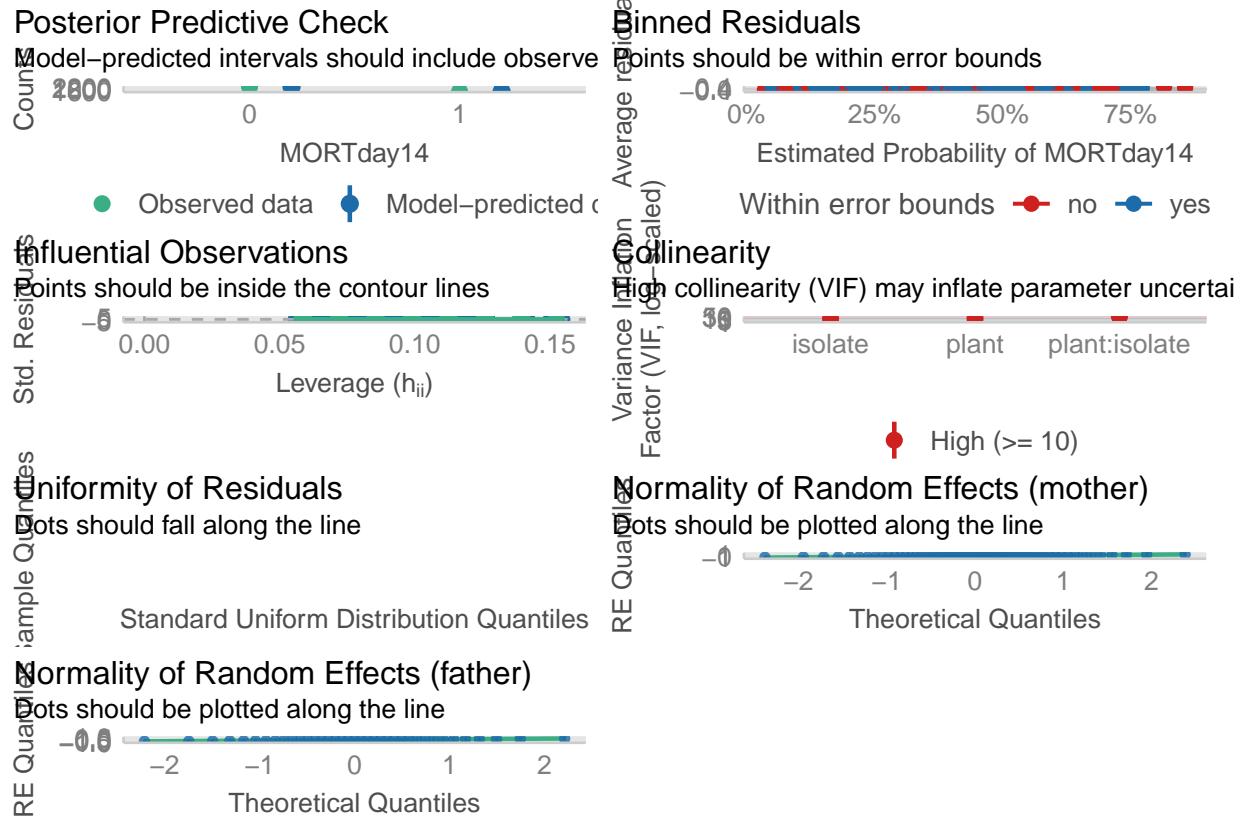
```

```

## Number of obs: 3811, groups: mother, 58; father, 37
##
## Fixed effects:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -2.3115    0.1862 -12.413 < 2e-16 ***
## plantMaz              2.0312    0.1822  11.149 < 2e-16 ***
## plantTom               1.7656    0.1996   8.844 < 2e-16 ***
## isolateBB              1.6882    0.1798   9.390 < 2e-16 ***
## isolateMT              1.3222    0.1827   7.236 4.63e-13 ***
## plantMaz:isolateBB   -0.7104    0.2286  -3.107  0.00189 **
## plantTom:isolateBB   -1.1348    0.2521  -4.501 6.75e-06 ***
## plantMaz:isolateMT   -0.9132    0.2310  -3.952 7.74e-05 ***
## plantTom:isolateMT   -0.6010    0.2533  -2.373  0.01764 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##                (Intr) plntMz plntTm isltBB isltMT plM:BB plT:BB plM:MT
## plantMaz     -0.682
## plantTom      -0.625  0.636
## isolateBB     -0.683  0.700  0.638
## isolateMT     -0.670  0.686  0.625  0.693
## plntMz:s1BB   0.533 -0.787 -0.498 -0.783 -0.543
## plntTm:s1BB   0.485 -0.497 -0.776 -0.711 -0.493  0.558
## plntMz:s1MT   0.529 -0.780 -0.492 -0.547 -0.790  0.620  0.390
## plntTm:s1MT   0.480 -0.492 -0.771 -0.497 -0.720  0.391  0.610  0.569
glm_mortality_noint <- update(glm_mortality,
                                ~. - plant:isolate)

check_model(glm_mortality)

```



```
# the following lines compute the probability associated with the interaction
# using parametric bootstrapping, but are annotated out to save processing time
# modcomp_glmint <- PBmodcomp(glm_mortality,
#                               glm_mortality_noint, nsim = 500)
# modcomp_glmint
```

```
# with 500 sims, p val is near minimum possible with 500 sims, 0.003
```

```
tidy_glm_mort <- tidy(glm_mortality) %>%
  mutate(across(where(is.numeric), round, 3))
```

```
## Warning: There was 1 warning in `mutate()` .
## i In argument: `across(where(is.numeric), round, 3)` .
## Caused by warning:
## ! The `...` argument of `across()` is deprecated as of dplyr 1.1.0.
## Supply arguments directly to `.fns` through an anonymous function instead.
##
##   # Previously
##   across(a:b, mean, na.rm = TRUE)
##
##   # Now
##   across(a:b, \((x) mean(x, na.rm = TRUE))
```

the next line saves the table as a csv

```
# write.csv(tidy_glm_mort, "outputs/glm_mort.csv")
```

```

# fig for mortalities by treatment ####

names(df_qgen_sub_df)

## [1] "animal"      "mother"       "father"       "plant"        "isolate"      "treatment"
## [7] "MORTday14"

df_qgen_sumbytreat <- df_qgen_sub_df %>%
  group_by(treatment) %>%
  summarise(Famsize = n(),
            Dead = sum(MORTday14,
                         na.rm = TRUE),
            Alive = Famsize - Dead,
            prop_mort = mean(MORTday14,
                              na.rm = TRUE))

df_qgen_trt_cis <- binom.confint(
  x = df_qgen_sumbytreat$Dead,
  n = df_qgen_sumbytreat$Famsize,
  methods = "exact") %>%
  rename(PropMort = mean,
         FamSize2 = n)

df_qgen_trt_data <- bind_cols(df_qgen_sumbytreat,
                                select(-method, -x, -PropMort, -FamSize2) %>%
                                  mutate(treatment2 = treatment) %>%
                                  separate(treatment2,
                                           into = c("Host_plant",
                                                   "Pathogen_trt")),

                                df_qgen_trt_cis) %>%

levels(factor(df_qgen_trt_data$treatment))

## [1] "Soya_CON"   "Soya_BB"    "Soya_MT"    "Maz_CON"    "Maz_BB"     "Maz_MT"     "Tom_CON"
## [8] "Tom_BB"     "Tom_MT"

df_qgen_trt_data$treatment <- factor(
  df_qgen_trt_data$treatment,
  levels = c("Soya_CON", "Soya_BB", "Soya_MT",
            "Maz_CON", "Maz_BB", "Maz_MT",
            "Tom_CON", "Tom_BB", "Tom_MT"))

levels(factor(df_qgen_trt_data$Host_plant))

## [1] "Maz"        "Soya"       "Tom"

df_qgen_trt_data$Host_plant <- factor(
  df_qgen_trt_data$Host_plant,
  levels = c("Soya", "Maz", "Tom"))

levels(factor(df_qgen_trt_data$Pathogen_trt))

```

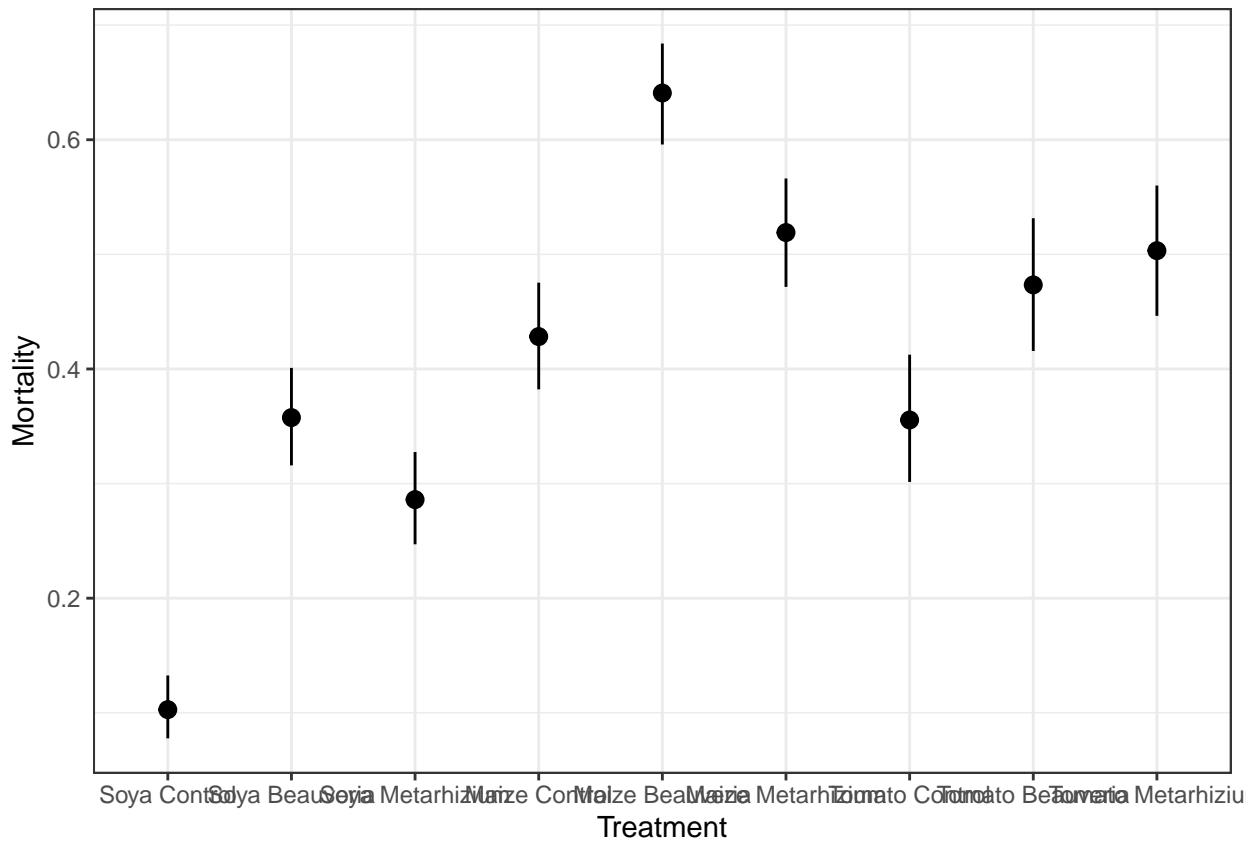
```

## [1] "BB"   "CON"  "MT"

df_qgen_trt_data$Pathogen_trt <- factor(
  df_qgen_trt_data$Pathogen_trt,
  levels = c("CON", "BB", "MT"))

df_qgen_trt_data %>%
  ggplot(aes(x = treatment, y = prop_mort)) +
  geom_pointrange(aes(ymax = lower,
                      ymin = upper)) +
  labs(y = "Mortality",
       x = "Treatment") +
  scale_x_discrete(labels = c(
    "Soya Control", "Soya Beauveria", "Soya Metarhizium",
    "Maize Control", "Maize Beauveria", "Maize Metarhizium",
    "Tomato Control", "Tomato Beauveria", "Tomato Metarhizium"))

```



```

Host_names <- c(
  Soya = "Soybean",
  Maz = "Maize",
  Tom = "Tomato")

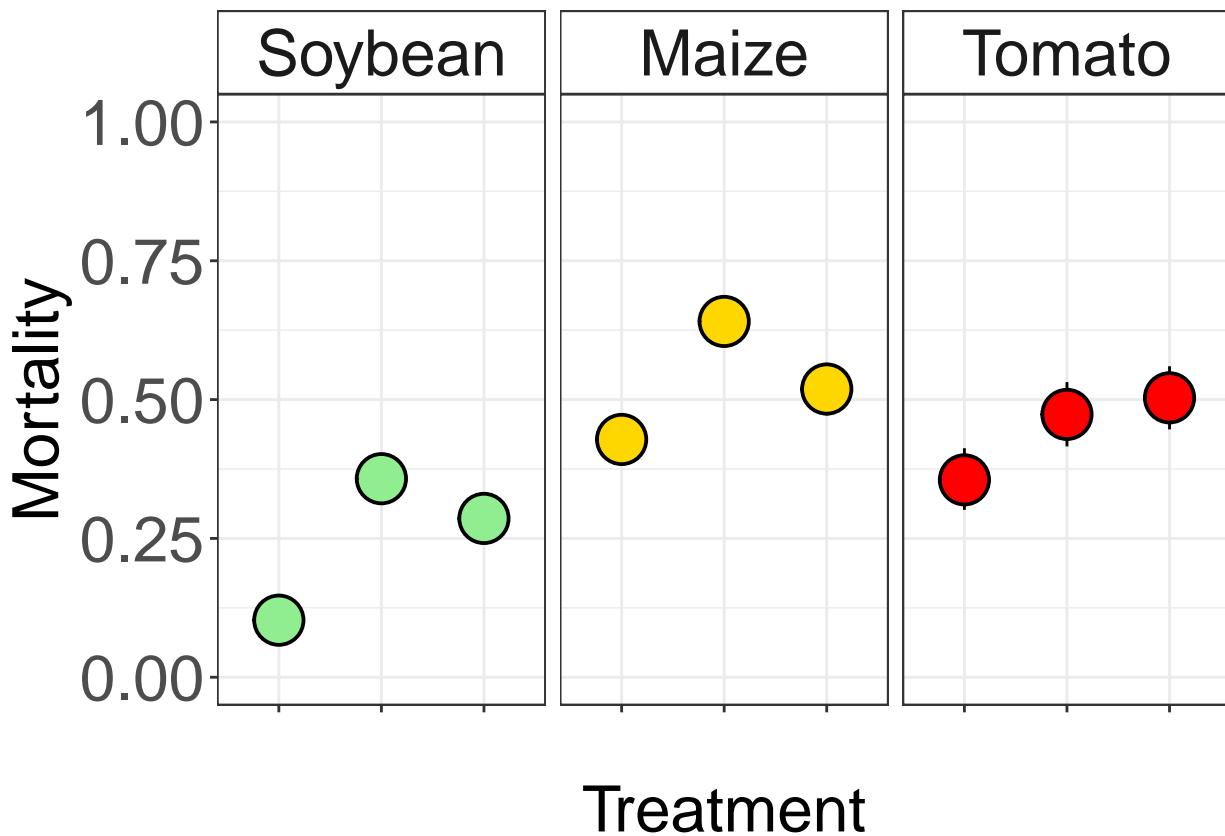
##### plot mortalities #####
df_qgen_trt_data %>%
  ggplot(aes(x = Pathogen_trt, y = prop_mort)) +

```

```

geom_pointrange(aes(ymin = lower,
                     ymax = upper,
                     fill = Host_plant),
                 pch = 21,
                 size = 2) +
  labs(y = "Mortality",
       x = "Treatment") +
  facet_wrap(~ Host_plant,
             labeller = labeller(Host_plant = Host_names)) +
  #scale_x_discrete(labels=expression(Control, italic(Beauveria), italic(Metarrhizium))) +
  scale_x_discrete(labels=c("","","")) +
  scale_fill_manual(values = c("lightgreen","gold","red")) +
  lims(y = c(0,1)) +
  theme(legend.position = "none",
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24),
        strip.text = element_text(size = 24),
        strip.background = element_rect(fill="white" ))

```



```

# ggsave("outputs/MortalityPhenotypes.png",
#        width = 20,
#        height = 20,
#        units = "cm")

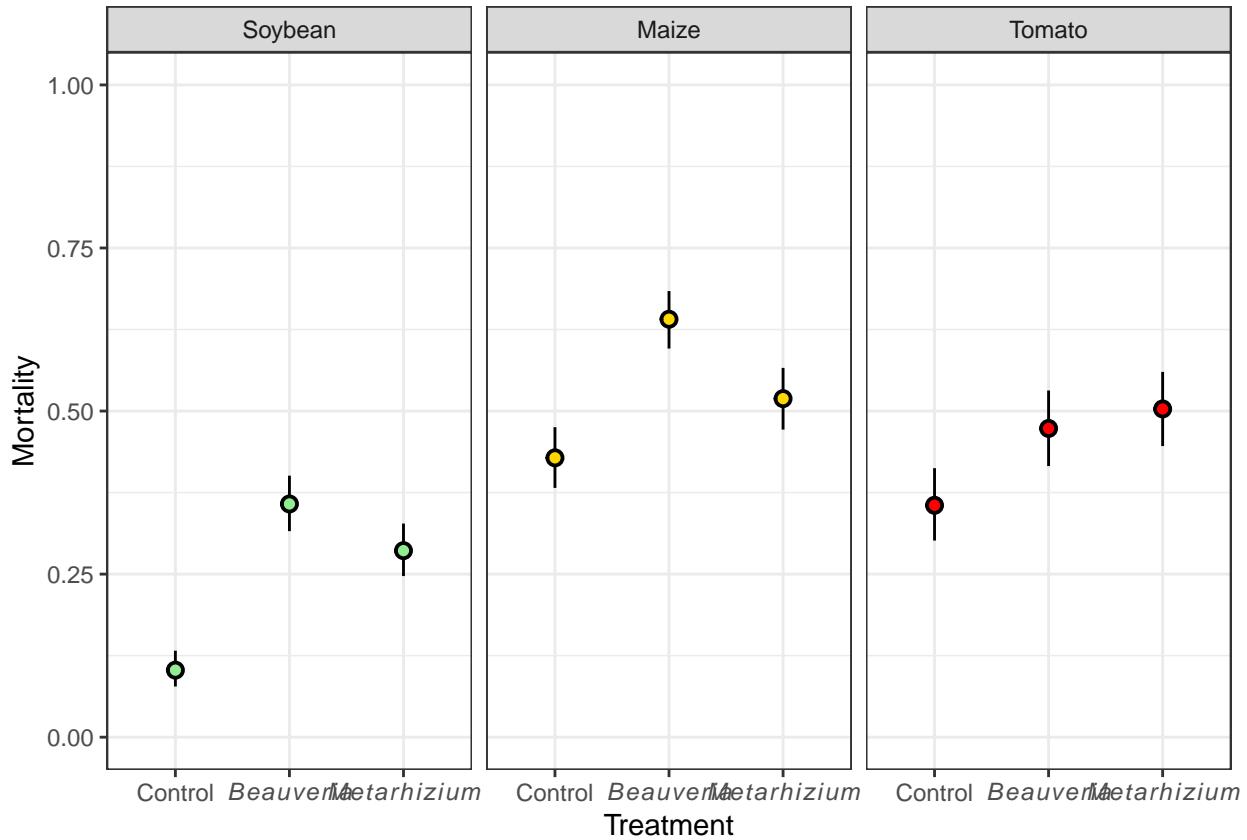
df_qgen_trt_data %>%
  ggplot(aes(x = Pathogen_trt, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,

```

```

        ymax = upper,
        fill = Host_plant),
      pch = 21) +
  labs(y = "Mortality",
       x = "Treatment") +
  facet_wrap(. ~ Host_plant,
             labeller = labeller(Host_plant = Host_names)) +
  scale_x_discrete(labels=expression(Control,italic(Beauveria),italic(Metarhizium))) +
  scale_fill_manual(values = c("lightgreen","gold","red")) +
  lims(y = c(0,1)) +
  theme(legend.position = "none")

```



```

# brms modelling

# these models take ages to run, so am providing a data object that includes the long chain models for
# can unannotate and run for a few iterations to verify that these work

# load data object containing models #####
# if you want to examine the Bayesian models quickly without running your computer for days,
# load the following data object
# load("ManganBigModels.RData")

# 9 trait brms model #####
# this is annotated out because it takes long to run
## long chain 9 trait model? #####

```

```

# to ensure that results are reproducible:
set.seed(1234)
model.9traits.brm.matnocov.long <-
  brm(MORTday14 ~ treatment +
    (treatment-1| p | gr(father)) +
    (1 | mother),
  data = df_qgen_sub_df,
  family = bernoulli(),
  chains = 8, cores = 8,
  iter = 8000,
  control = list(adapt_delta = 0.96))

## Compiling Stan program...
## Loading required package: adegenet
## Loading required package: ade4
##
##     /// adegenet 2.1.10 is loaded ///////////
##
##     > overview: '?adegenet'
##     > tutorials/doc/questions: 'adegenetWeb()'
##     > bug reports/feature requests: adegenetIssues()
##
## Start sampling
summary(model.9traits.brm.matnocov.long)

## Family: bernoulli
## Links: mu = logit
## Formula: MORTday14 ~ treatment + (treatment - 1 | p | gr(father)) + (1 | mother)
## Data: df_qgen_sub_df (Number of observations: 3811)
## Draws: 8 chains, each with iter = 8000; warmup = 4000; thin = 1;
##        total post-warmup draws = 32000
##
## Multilevel Hyperparameters:
## ~father (Number of levels: 37)
##                                         Estimate Est.Error l-95% CI u-95% CI
## sd(treatmentSoya_CON)                 1.36      0.37    0.72    2.18
## sd(treatmentSoya_BB)                  1.11      0.24    0.70    1.63
## sd(treatmentSoya_MT)                  1.03      0.22    0.64    1.51
## sd(treatmentMaz_CON)                  1.75      0.31    1.20    2.43
## sd(treatmentMaz_BB)                  1.57      0.30    1.05    2.24
## sd(treatmentMaz_MT)                  1.19      0.23    0.79    1.69
## sd(treatmentTom_CON)                  1.17      0.31    0.62    1.85
## sd(treatmentTom_BB)                  0.97      0.27    0.47    1.54
## sd(treatmentTom_MT)                  0.89      0.28    0.39    1.48
## cor(treatmentSoya_CON,treatmentSoya_BB) 0.25      0.21   -0.19    0.63
## cor(treatmentSoya_CON,treatmentSoya_MT) 0.36      0.21   -0.09    0.73
## cor(treatmentSoya_BB,treatmentSoya_MT) 0.59      0.17    0.21    0.86
## cor(treatmentSoya_CON,treatmentMaz_CON) 0.01      0.20   -0.39    0.40
## cor(treatmentSoya_BB,treatmentMaz_CON) -0.30      0.19   -0.65    0.08
## cor(treatmentSoya_MT,treatmentMaz_CON) -0.35      0.19   -0.70    0.03
## cor(treatmentSoya_CON,treatmentMaz_BB) -0.08      0.22   -0.50    0.33
## cor(treatmentSoya_BB,treatmentMaz_BB) -0.15      0.20   -0.53    0.25

```

## cor(treatmentSoya_MT,treatmentMaz_BB)	-0.25	0.20	-0.61	0.15
## cor(treatmentMaz_CON,treatmentMaz_BB)	0.64	0.13	0.33	0.85
## cor(treatmentSoya_CON,treatmentMaz_MT)	-0.23	0.21	-0.61	0.19
## cor(treatmentSoya_BB,treatmentMaz_MT)	-0.26	0.20	-0.64	0.14
## cor(treatmentSoya_MT,treatmentMaz_MT)	-0.48	0.18	-0.79	-0.10
## cor(treatmentMaz_CON,treatmentMaz_MT)	0.70	0.13	0.41	0.89
## cor(treatmentMaz_BB,treatmentMaz_MT)	0.69	0.13	0.38	0.89
## cor(treatmentSoya_CON,treatmentTom_CON)	-0.25	0.23	-0.68	0.21
## cor(treatmentSoya_BB,treatmentTom_CON)	-0.36	0.21	-0.73	0.08
## cor(treatmentSoya_MT,treatmentTom_CON)	-0.37	0.21	-0.75	0.07
## cor(treatmentMaz_CON,treatmentTom_CON)	0.15	0.19	-0.25	0.51
## cor(treatmentMaz_BB,treatmentTom_CON)	0.03	0.21	-0.39	0.43
## cor(treatmentMaz_MT,treatmentTom_CON)	0.16	0.21	-0.26	0.54
## cor(treatmentSoya_CON,treatmentTom_BB)	0.03	0.24	-0.45	0.48
## cor(treatmentSoya_BB,treatmentTom_BB)	-0.30	0.23	-0.72	0.15
## cor(treatmentSoya_MT,treatmentTom_BB)	-0.20	0.23	-0.64	0.25
## cor(treatmentMaz_CON,treatmentTom_BB)	0.38	0.19	-0.02	0.70
## cor(treatmentMaz_BB,treatmentTom_BB)	0.10	0.21	-0.33	0.50
## cor(treatmentMaz_MT,treatmentTom_BB)	0.20	0.21	-0.23	0.59
## cor(treatmentTom_CON,treatmentTom_BB)	0.27	0.22	-0.20	0.66
## cor(treatmentSoya_CON,treatmentTom_MT)	-0.11	0.25	-0.58	0.37
## cor(treatmentSoya_BB,treatmentTom_MT)	-0.26	0.23	-0.69	0.20
## cor(treatmentSoya_MT,treatmentTom_MT)	-0.22	0.23	-0.66	0.24
## cor(treatmentMaz_CON,treatmentTom_MT)	0.26	0.20	-0.16	0.62
## cor(treatmentMaz_BB,treatmentTom_MT)	0.06	0.22	-0.38	0.47
## cor(treatmentMaz_MT,treatmentTom_MT)	0.21	0.22	-0.23	0.61
## cor(treatmentTom_CON,treatmentTom_MT)	0.31	0.23	-0.18	0.71
## cor(treatmentTom_BB,treatmentTom_MT)	0.53	0.21	0.06	0.85
##	Rhat	Bulk_ESS	Tail_ESS	
## sd(treatmentSoya_CON)	1.00	9598	16625	
## sd(treatmentSoya_BB)	1.00	11973	20235	
## sd(treatmentSoya_MT)	1.00	14180	21361	
## sd(treatmentMaz_CON)	1.00	16890	22572	
## sd(treatmentMaz_BB)	1.00	18443	23434	
## sd(treatmentMaz_MT)	1.00	20074	24115	
## sd(treatmentTom_CON)	1.00	14874	19170	
## sd(treatmentTom_BB)	1.00	11149	13251	
## sd(treatmentTom_MT)	1.00	8693	9369	
## cor(treatmentSoya_CON,treatmentSoya_BB)	1.00	10822	17580	
## cor(treatmentSoya_CON,treatmentSoya_MT)	1.00	12435	19977	
## cor(treatmentSoya_BB,treatmentSoya_MT)	1.00	16726	22753	
## cor(treatmentSoya_CON,treatmentMaz_CON)	1.00	10059	16013	
## cor(treatmentSoya_BB,treatmentMaz_CON)	1.00	8675	16203	
## cor(treatmentSoya_MT,treatmentMaz_CON)	1.00	9838	18426	
## cor(treatmentSoya_CON,treatmentMaz_BB)	1.00	10113	15385	
## cor(treatmentSoya_BB,treatmentMaz_BB)	1.00	10045	17111	
## cor(treatmentSoya_MT,treatmentMaz_BB)	1.00	10785	18532	
## cor(treatmentMaz_CON,treatmentMaz_BB)	1.00	19341	26036	
## cor(treatmentSoya_CON,treatmentMaz_MT)	1.00	11813	18905	
## cor(treatmentSoya_BB,treatmentMaz_MT)	1.00	11319	16947	
## cor(treatmentSoya_MT,treatmentMaz_MT)	1.00	12235	20133	
## cor(treatmentMaz_CON,treatmentMaz_MT)	1.00	22534	26659	
## cor(treatmentMaz_BB,treatmentMaz_MT)	1.00	23312	26360	
## cor(treatmentSoya_CON,treatmentTom_CON)	1.00	15214	21417	

```

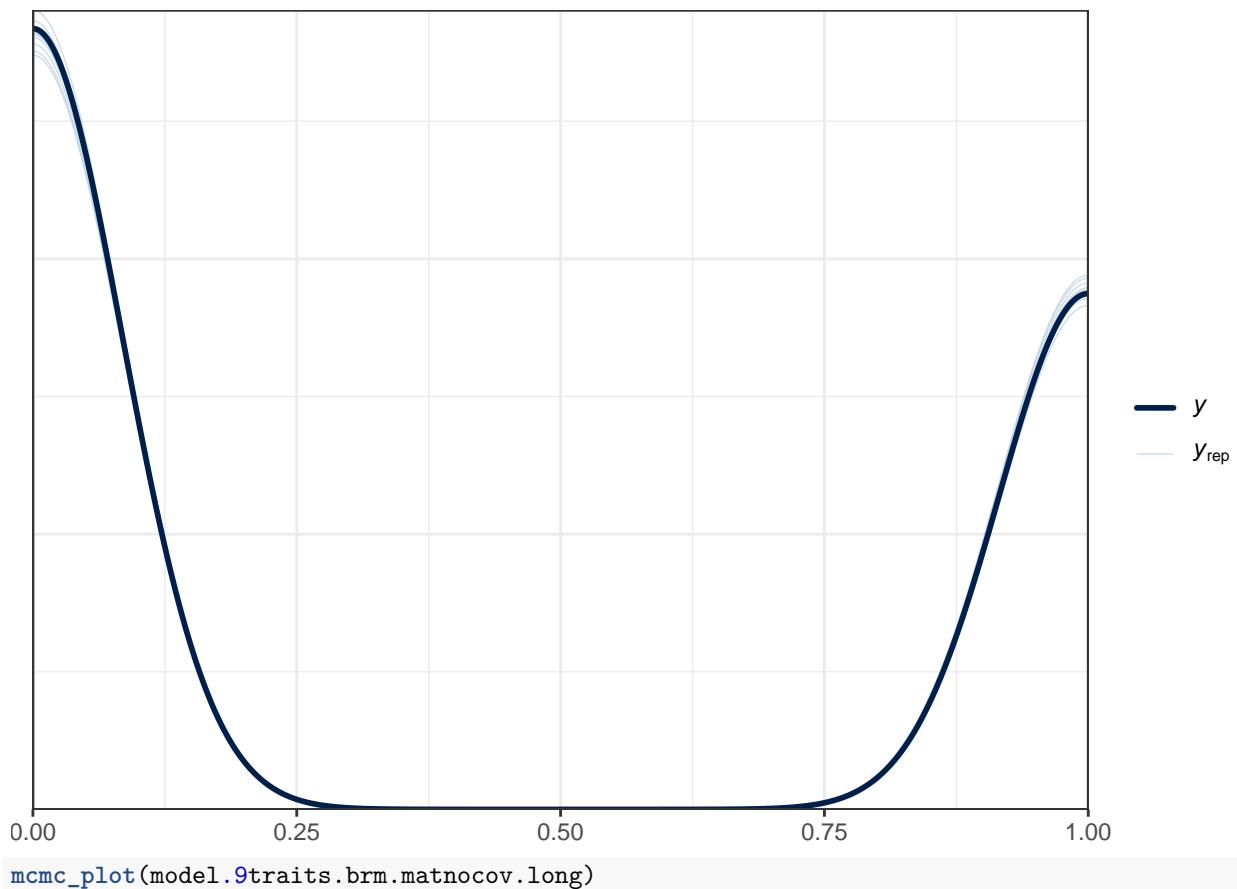
## cor(treatmentSoya_BB,treatmentTom_CON) 1.00 14586 20060
## cor(treatmentSoya_MT,treatmentTom_CON) 1.00 15120 22855
## cor(treatmentMaz_CON,treatmentTom_CON) 1.00 21067 25280
## cor(treatmentMaz_BB,treatmentTom_CON) 1.00 21694 26332
## cor(treatmentMaz_MT,treatmentTom_CON) 1.00 20956 25635
## cor(treatmentSoya_CON,treatmentTom_BB) 1.00 15773 19505
## cor(treatmentSoya_BB,treatmentTom_BB) 1.00 12043 18457
## cor(treatmentSoya_MT,treatmentTom_BB) 1.00 13971 20168
## cor(treatmentMaz_CON,treatmentTom_BB) 1.00 23254 24513
## cor(treatmentMaz_BB,treatmentTom_BB) 1.00 25219 28035
## cor(treatmentMaz_MT,treatmentTom_BB) 1.00 22963 25175
## cor(treatmentTom_CON,treatmentTom_BB) 1.00 19180 24033
## cor(treatmentSoya_CON,treatmentTom_MT) 1.00 16231 21704
## cor(treatmentSoya_BB,treatmentTom_MT) 1.00 12340 18431
## cor(treatmentSoya_MT,treatmentTom_MT) 1.00 13516 19128
## cor(treatmentMaz_CON,treatmentTom_MT) 1.00 21574 22126
## cor(treatmentMaz_BB,treatmentTom_MT) 1.00 25775 26185
## cor(treatmentMaz_MT,treatmentTom_MT) 1.00 21446 25467
## cor(treatmentTom_CON,treatmentTom_MT) 1.00 17780 22497
## cor(treatmentTom_BB,treatmentTom_MT) 1.00 14470 18292
##
## ~mother (Number of levels: 58)
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.60     0.12    0.38    0.83 1.00      6006     10627
##
## Regression Coefficients:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      -2.82     0.36   -3.60   -2.19 1.00      7276     9052
## treatmentSoya_BB 1.94     0.39    1.21    2.76 1.00      8498    10740
## treatmentSoya_MT 1.55     0.38    0.85    2.35 1.00      8990    11282
## treatmentMaz_CON 2.64     0.48    1.75    3.63 1.00      8261    11696
## treatmentMaz_BB 3.82     0.48    2.94    4.81 1.00      8303    11833
## treatmentMaz_MT 3.06     0.44    2.24    3.98 1.00      7767    10718
## treatmentTom_CON 2.15     0.45    1.30    3.09 1.00      8803    11145
## treatmentTom_BB 2.84     0.41    2.10    3.71 1.00      8102    11183
## treatmentTom_MT 3.02     0.42    2.25    3.89 1.00      7917    10161
##
## 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).
prior_summary(model.9traits.brm.matnucov.long)

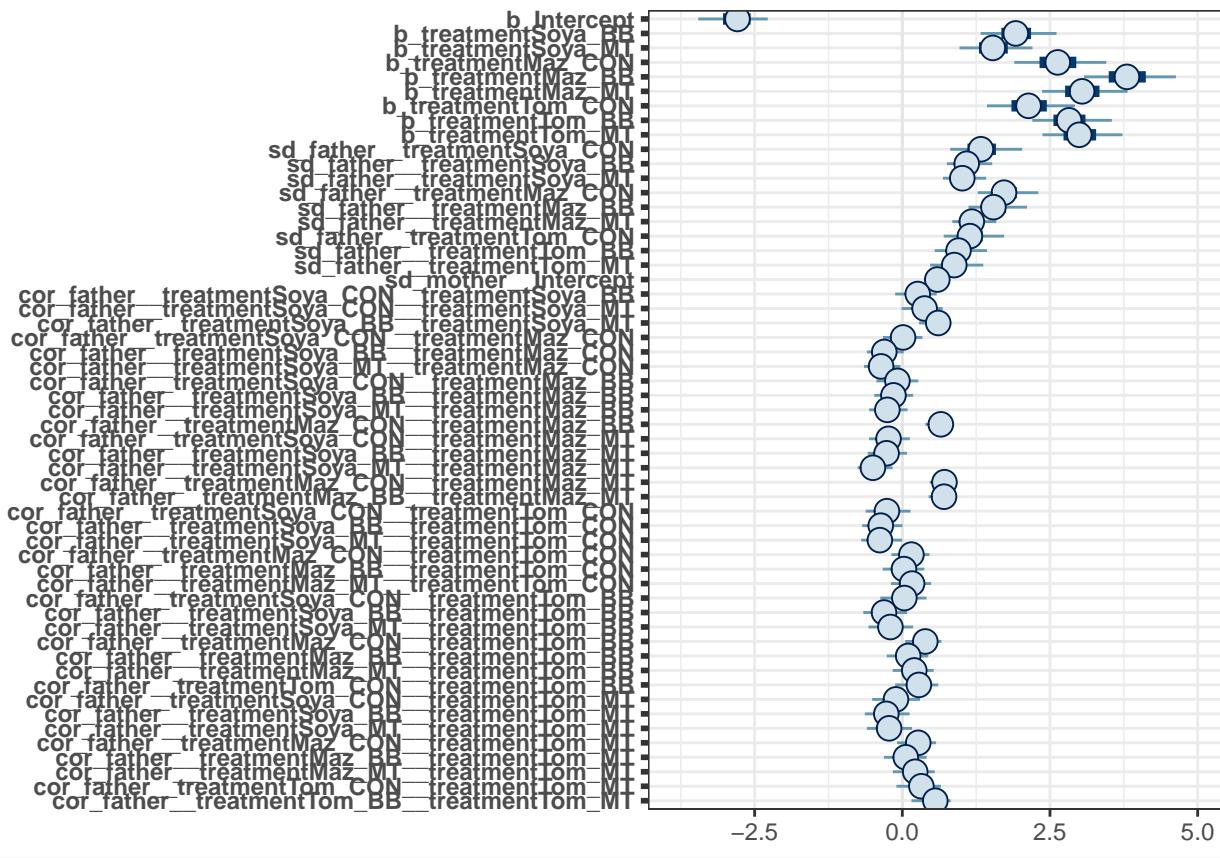
```

```

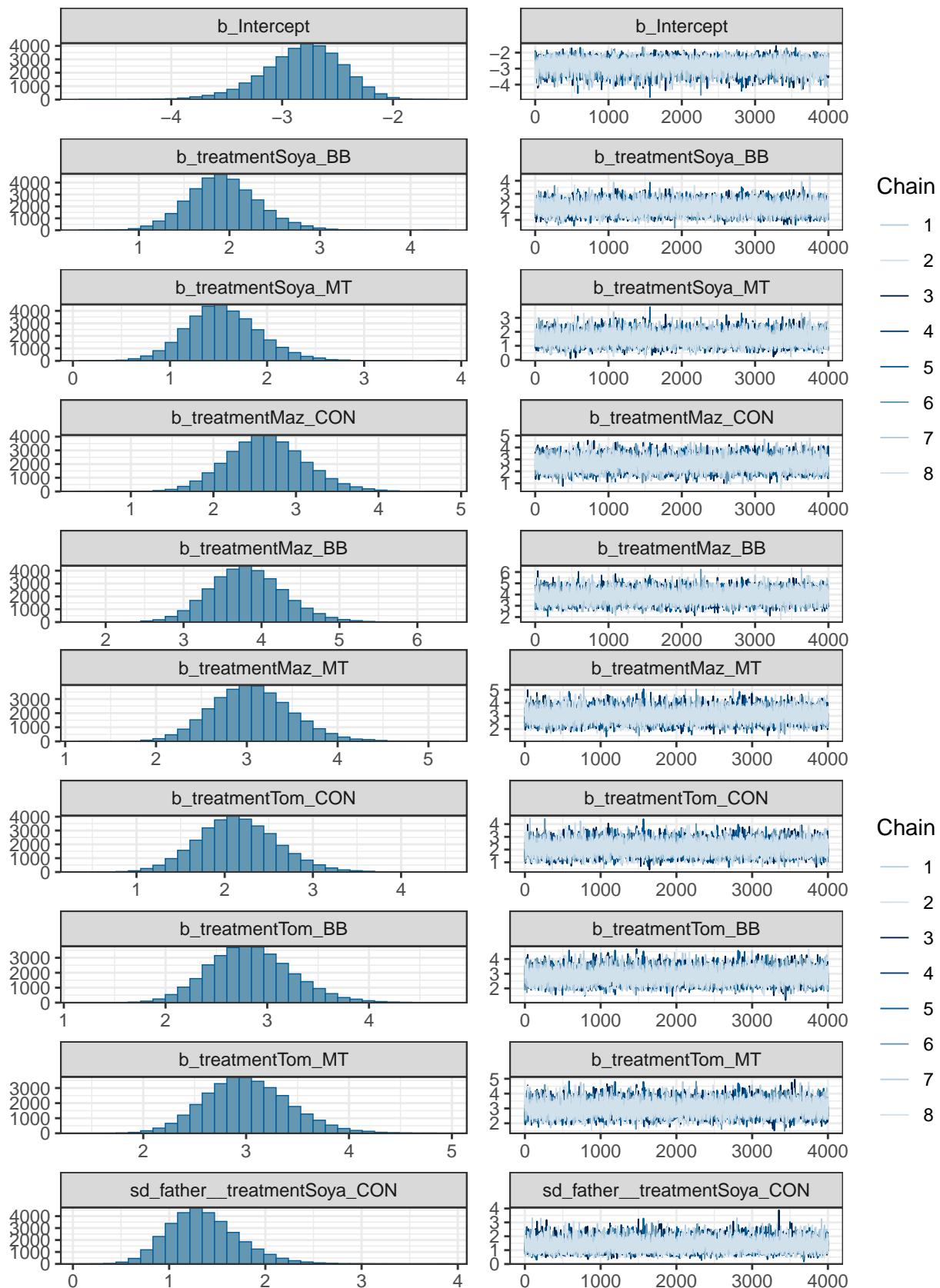
##          prior class       coef group resp dpar nlnpar lb ub
## (flat)      b
## (flat)      b  treatmentMaz_BB
## (flat)      b  treatmentMaz_CON
## (flat)      b  treatmentMaz_MT
## (flat)      b  treatmentSoya_BB
## (flat)      b  treatmentSoya_MT
## (flat)      b  treatmentTom_BB
## (flat)      b  treatmentTom_CON
## (flat)      b  treatmentTom_MT
## student_t(3, 0, 2.5) Intercept
## lkj_corr_cholesky(1)          L

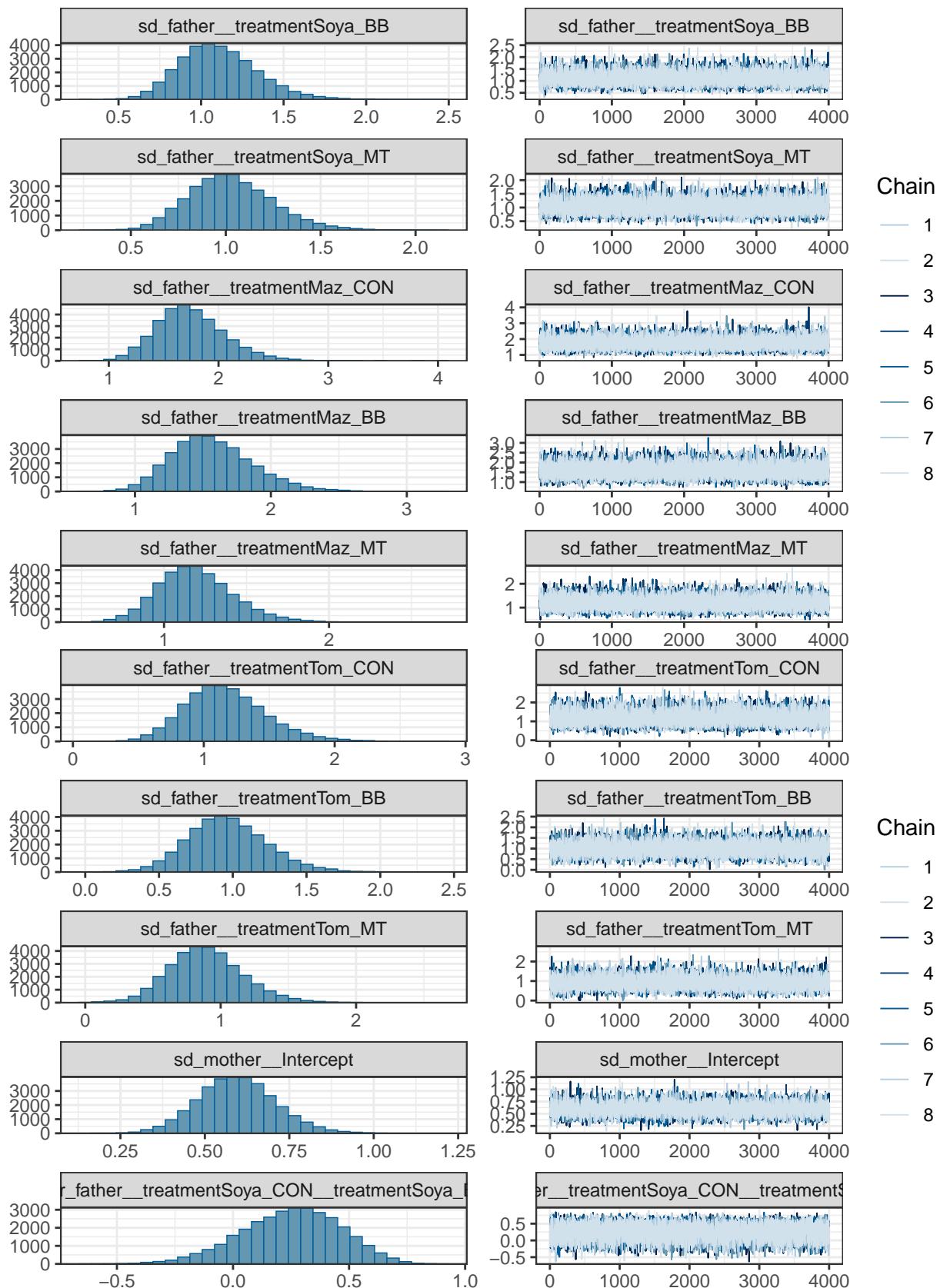
```

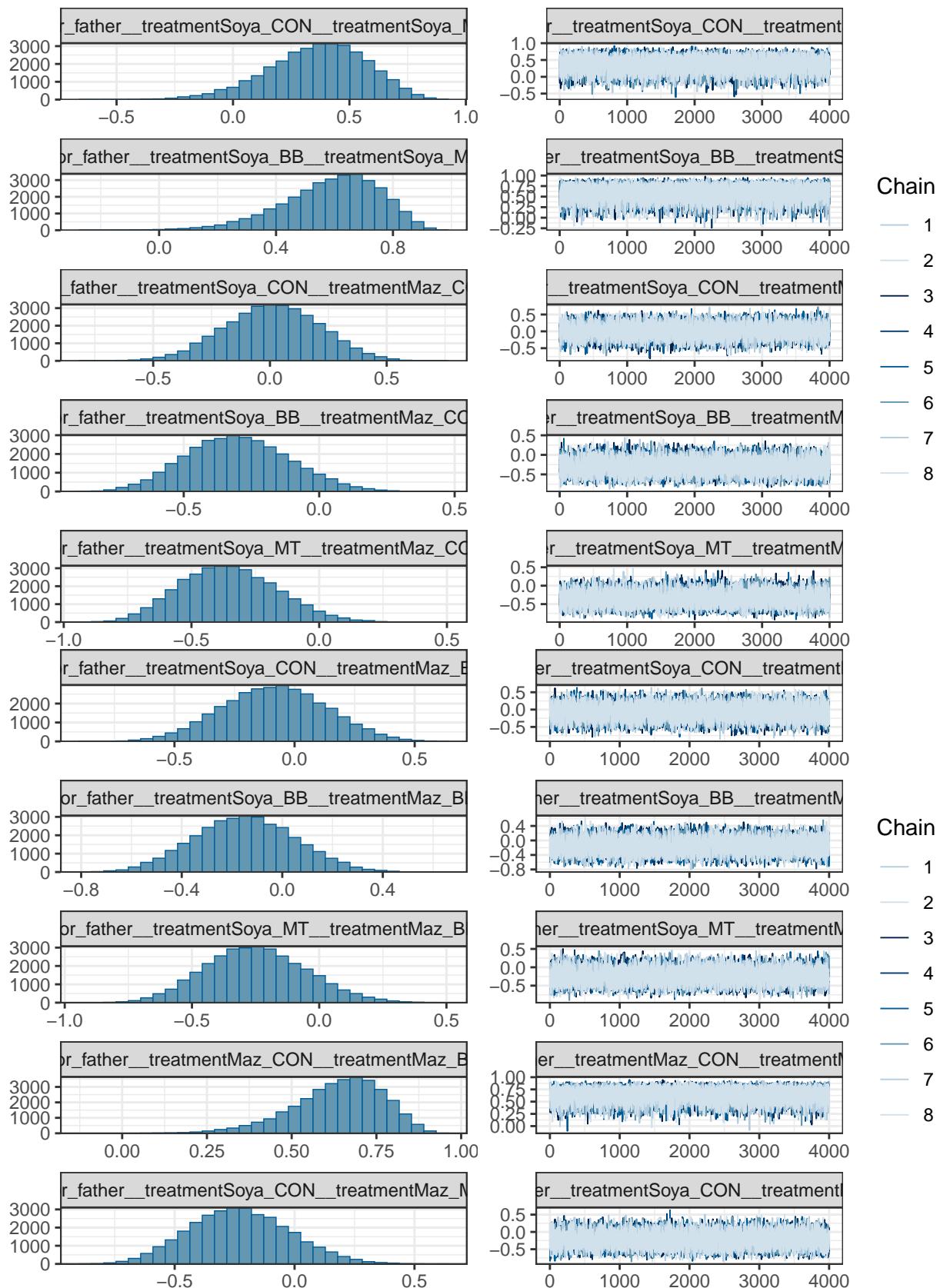



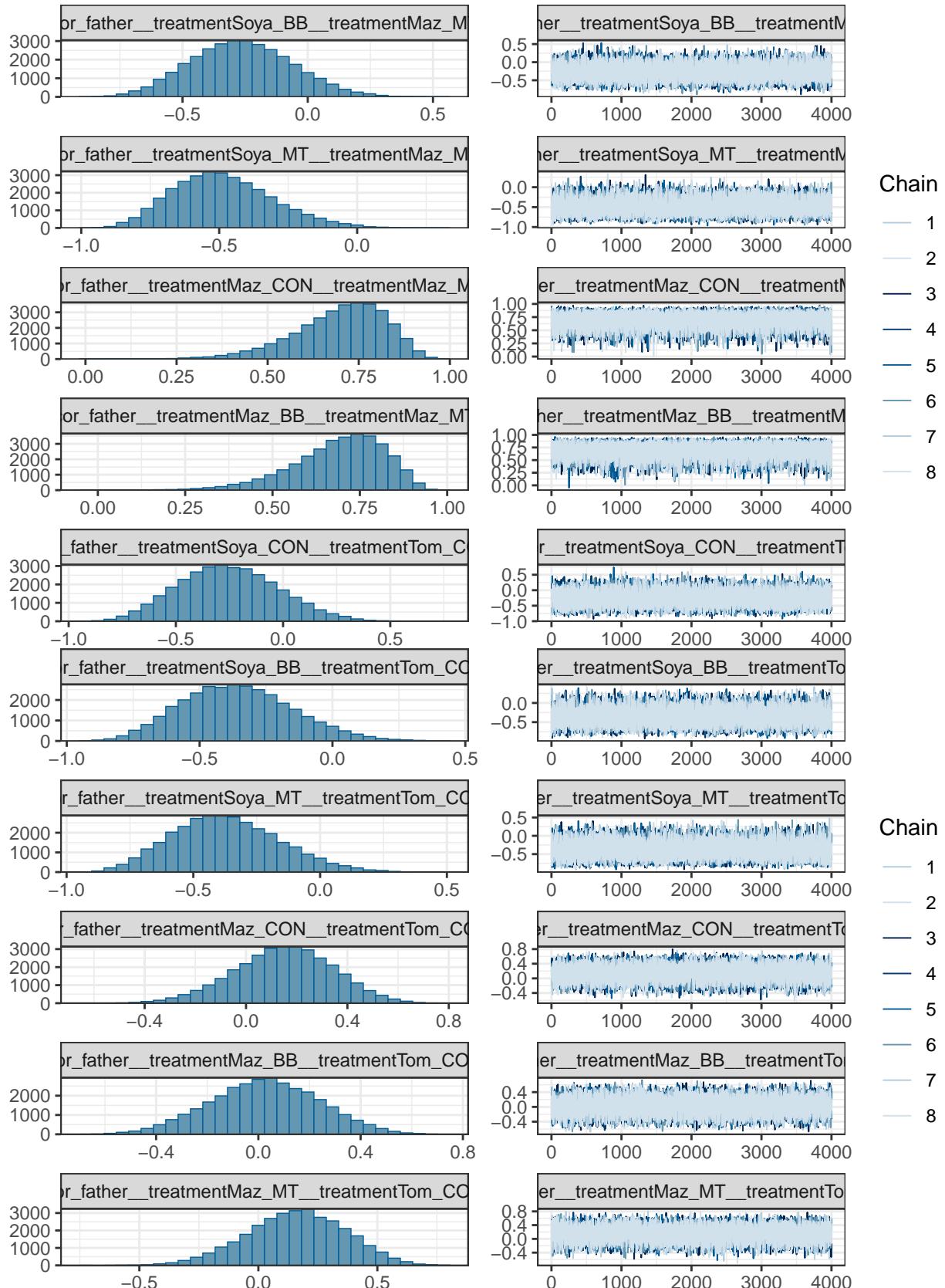


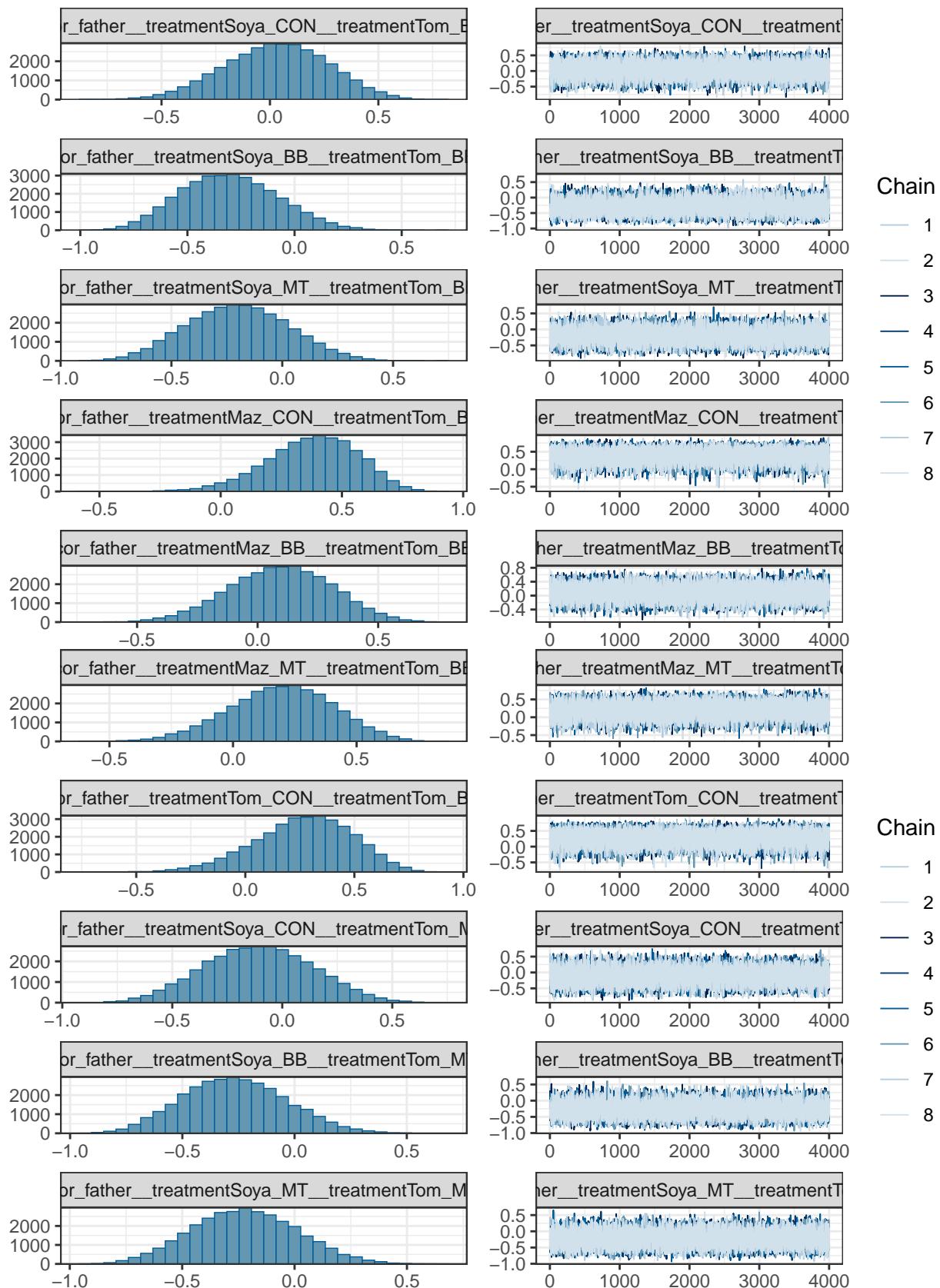
```
plot(model.9traits.brm.matnocov.long)
```

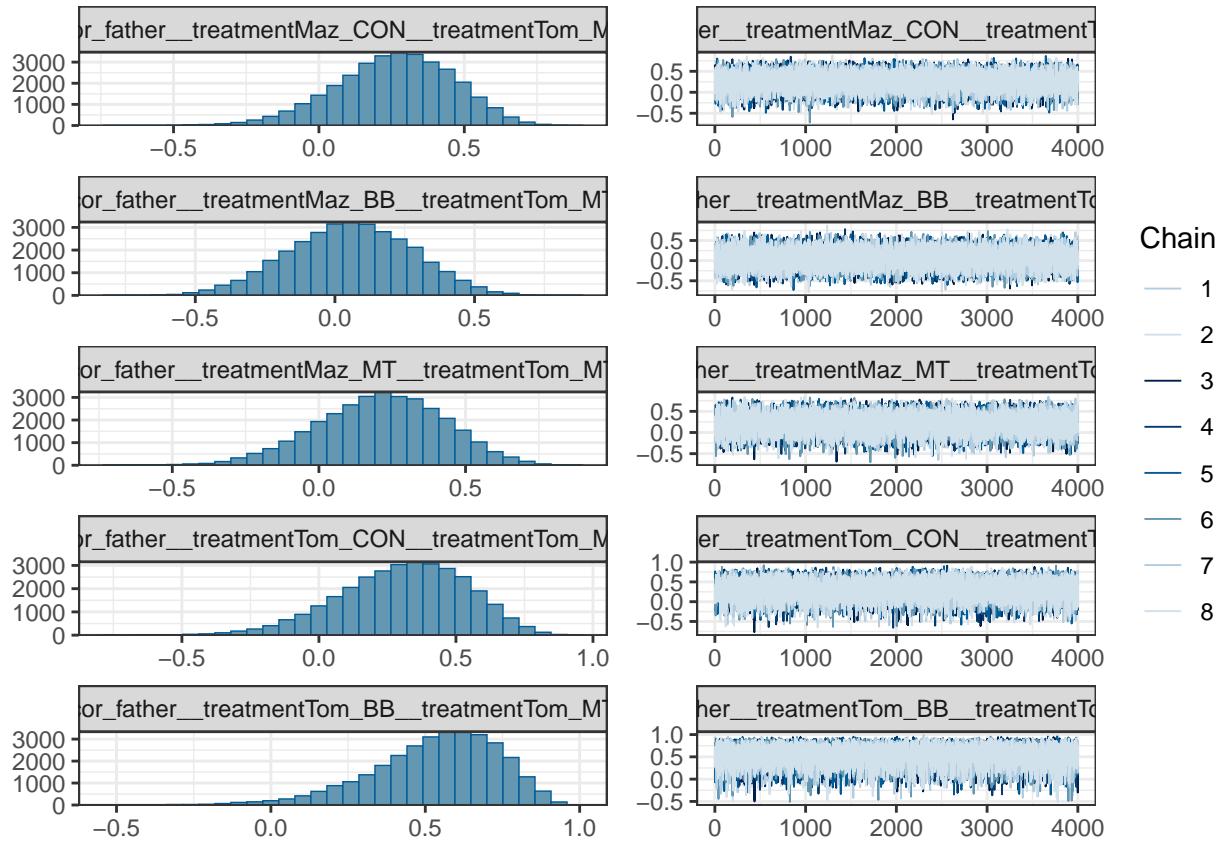












```
# Extract variances #####
# VCVarray9traits <- VarCorr(model.9traits.brm.matnocov.long)
```

```
VCVarray9traits <- VarCorr(model.9traits.brm.matnocov.long,
                           probs = c(0.11, 0.89))
```

```
## reorder levels #####
VCVarray9traits
```

```
## $father
## $father$sd
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 1.3619983 0.3724925 0.9301418 1.824557
## treatmentSoya_BB  1.1084698 0.2367510 0.8334786 1.401656
## treatmentSoya_MT 1.0300917 0.2241907 0.7662376 1.306006
## treatmentMaz_CON 1.7477107 0.3126154 1.3847238 2.137066
## treatmentMaz_BB  1.5709987 0.3043556 1.2189497 1.950404
## treatmentMaz_MT  1.1926679 0.2281678 0.9269706 1.477604
## treatmentTom_CON 1.1683871 0.3126210 0.8075579 1.554037
## treatmentTom_BB   0.9660868 0.2720391 0.6483763 1.299954
## treatmentTom_MT  0.8937435 0.2773698 0.5697214 1.232813
##
## $father$cor
## , , treatmentSoya_CON
##
##           Estimate Est.Error      Q11      Q89
```

```

## treatmentSoya_CON 1.00000000 0.0000000 1.00000000 1.00000000
## treatmentSoya_BB 0.24960793 0.2138051 -0.01938992 0.50827218
## treatmentSoya_MT 0.36176225 0.2111421 0.09345718 0.61414417
## treatmentMaz_CON 0.01023903 0.2032175 -0.24375768 0.26127676
## treatmentMaz_BB -0.08392726 0.2155860 -0.35301336 0.18448446
## treatmentMaz_MT -0.22751972 0.2079622 -0.48321167 0.03298769
## treatmentTom_CON -0.25300390 0.2311830 -0.53944673 0.03980738
## treatmentTom_BB 0.02907886 0.2377343 -0.27209615 0.32168091
## treatmentTom_MT -0.10691735 0.2464237 -0.41435247 0.20304664
##
## , , treatmentSoya_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.2496079 0.2138051 -0.01938992 0.50827218
## treatmentSoya_BB 1.0000000 0.0000000 1.00000000 1.00000000
## treatmentSoya_MT 0.5881188 0.1669264 0.37401519 0.78094588
## treatmentMaz_CON -0.2992638 0.1894279 -0.53144068 -0.05954919
## treatmentMaz_BB -0.1478591 0.1999846 -0.39738317 0.10196310
## treatmentMaz_MT -0.2627701 0.2015984 -0.51297651 -0.01007351
## treatmentTom_CON -0.3563290 0.2082216 -0.61059762 -0.09220973
## treatmentTom_BB -0.3030759 0.2256437 -0.58063671 -0.01552225
## treatmentTom_MT -0.2649264 0.2301124 -0.54929994 0.02827946
##
## , , treatmentSoya_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.3617623 0.2111421 0.09345718 0.614144167
## treatmentSoya_BB 0.5881188 0.1669264 0.37401519 0.780945878
## treatmentSoya_MT 1.0000000 0.0000000 1.00000000 1.00000000
## treatmentMaz_CON -0.3522722 0.1886244 -0.58283666 -0.113572005
## treatmentMaz_BB -0.2466624 0.1976510 -0.48922335 0.002202847
## treatmentMaz_MT -0.4846265 0.1799498 -0.69965747 -0.253625045
## treatmentTom_CON -0.3689684 0.2108118 -0.62586308 -0.100437036
## treatmentTom_BB -0.1999445 0.2291147 -0.48630534 0.087592185
## treatmentTom_MT -0.2204746 0.2325401 -0.51003925 0.071173588
##
## , , treatmentMaz_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.01023903 0.2032175 -0.243757677 0.26127676
## treatmentSoya_BB -0.29926382 0.1894279 -0.531440676 -0.05954919
## treatmentSoya_MT -0.35227216 0.1886244 -0.582836657 -0.11357201
## treatmentMaz_CON 1.00000000 0.0000000 1.00000000 1.00000000
## treatmentMaz_BB 0.63608991 0.1332859 0.467100913 0.78986058
## treatmentMaz_MT 0.69680462 0.1262295 0.534715299 0.83950056
## treatmentTom_CON 0.14873277 0.1943338 -0.094676762 0.38643629
## treatmentTom_BB 0.37707605 0.1879246 0.141618492 0.60125292
## treatmentTom_MT 0.25957509 0.2008477 0.007127548 0.50125430
##
## , , treatmentMaz_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.08392726 0.2155860 -0.3530134 0.184484459
## treatmentSoya_BB -0.14785909 0.1999846 -0.3973832 0.101963103

```

```

## treatmentSoya_MT -0.24666244 0.1976510 -0.4892234 0.002202847
## treatmentMaz_CON 0.63608991 0.1332859 0.4671009 0.789860576
## treatmentMaz_BB 1.00000000 0.0000000 1.0000000 1.000000000
## treatmentMaz_MT 0.68870501 0.1313029 0.5195323 0.837836812
## treatmentTom_CON 0.02527600 0.2128096 -0.2438687 0.289220967
## treatmentTom_BB 0.09527712 0.2129473 -0.1697080 0.356258963
## treatmentTom_MT 0.05515276 0.2197446 -0.2205008 0.326320339
##
## , , treatmentMaz_MT
##
## Estimate Est.Error Q11 Q89
## treatmentSoya_CON -0.2275197 0.2079622 -0.48321167 0.03298769
## treatmentSoya_BB -0.2627701 0.2015984 -0.51297651 -0.01007351
## treatmentSoya_MT -0.4846265 0.1799498 -0.69965747 -0.25362505
## treatmentMaz_CON 0.6968046 0.1262295 0.53471530 0.83950056
## treatmentMaz_BB 0.6887050 0.1313029 0.51953227 0.83783681
## treatmentMaz_MT 1.0000000 0.0000000 1.00000000 1.000000000
## treatmentTom_CON 0.1591878 0.2056926 -0.09970130 0.41291482
## treatmentTom_BB 0.1957683 0.2095573 -0.06832125 0.45198790
## treatmentTom_MT 0.2099224 0.2156261 -0.06100951 0.47256350
##
## , , treatmentTom_CON
##
## Estimate Est.Error Q11 Q89
## treatmentSoya_CON -0.2530039 0.2311830 -0.53944673 0.03980738
## treatmentSoya_BB -0.3563290 0.2082216 -0.61059762 -0.09220973
## treatmentSoya_MT -0.3689684 0.2108118 -0.62586308 -0.10043704
## treatmentMaz_CON 0.1487328 0.1943338 -0.09467676 0.38643629
## treatmentMaz_BB 0.0252760 0.2128096 -0.24386874 0.28922097
## treatmentMaz_MT 0.1591878 0.2056926 -0.09970130 0.41291482
## treatmentTom_CON 1.0000000 0.0000000 1.00000000 1.000000000
## treatmentTom_BB 0.2669217 0.2228346 -0.01752817 0.53496167
## treatmentTom_MT 0.3062881 0.2308417 0.01238175 0.58131447
##
## , , treatmentTom_BB
##
## Estimate Est.Error Q11 Q89
## treatmentSoya_CON 0.02907886 0.2377343 -0.27209615 0.32168091
## treatmentSoya_BB -0.30307590 0.2256437 -0.58063671 -0.01552225
## treatmentSoya_MT -0.19994454 0.2291147 -0.48630534 0.08759218
## treatmentMaz_CON 0.37707605 0.1879246 0.14161849 0.60125292
## treatmentMaz_BB 0.09527712 0.2129473 -0.16970800 0.35625896
## treatmentMaz_MT 0.19576825 0.2095573 -0.06832125 0.45198790
## treatmentTom_CON 0.26692169 0.2228346 -0.01752817 0.53496167
## treatmentTom_BB 1.00000000 0.0000000 1.00000000 1.000000000
## treatmentTom_MT 0.53208822 0.2065689 0.26849874 0.76611496
##
## , , treatmentTom_MT
##
## Estimate Est.Error Q11 Q89
## treatmentSoya_CON -0.10691735 0.2464237 -0.414352470 0.20304664
## treatmentSoya_BB -0.26492636 0.2301124 -0.549299938 0.02827946
## treatmentSoya_MT -0.22047461 0.2325401 -0.510039250 0.07117359
## treatmentMaz_CON 0.25957509 0.2008477 0.007127548 0.50125430

```

```

## treatmentMaz_BB    0.05515276 0.2197446 -0.220500831 0.32632034
## treatmentMaz_MT   0.20992243 0.2156261 -0.061009513 0.47256350
## treatmentTom_CON   0.30628812 0.2308417  0.012381750 0.58131447
## treatmentTom_BB    0.53208822 0.2065689  0.268498738 0.76611496
## treatmentTom_MT    1.00000000 0.0000000  1.000000000 1.00000000
##
##
## $father$cov
## , , treatmentSoya_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 1.99378560 1.1125225  0.86516378 3.32900967
## treatmentSoya_BB   0.39595334 0.3930833 -0.02281616 0.86675268
## treatmentSoya_MT   0.52330617 0.3881198  0.10375161 0.99246298
## treatmentMaz_CON   0.04890640 0.5143116 -0.52991895 0.65248168
## treatmentMaz_BB   -0.15379350 0.4847183 -0.70525601 0.39900381
## treatmentMaz_MT   -0.35999858 0.3708849 -0.79810525 0.05145167
## treatmentTom_CON  -0.38633207 0.4104512 -0.86542614 0.05864417
## treatmentTom_BB    0.05589562 0.3384706 -0.31959530 0.44529131
## treatmentTom_MT   -0.11652250 0.3228243 -0.48039781 0.24163776
##
## , , treatmentSoya_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.3959533 0.3930833 -0.02281616 0.86675268
## treatmentSoya_BB   1.2847547 0.5594397  0.69468665 1.96464090
## treatmentSoya_MT   0.6920906 0.3436490  0.32004446 1.11436691
## treatmentMaz_CON   -0.5626524 0.3962533 -1.03145048 -0.11310941
## treatmentMaz_BB   -0.2478231 0.3711212 -0.67989300 0.17478388
## treatmentMaz_MT   -0.3298306 0.2792732 -0.65635216 -0.01373665
## treatmentTom_CON  -0.4478187 0.3083062 -0.81338268 -0.10785815
## treatmentTom_BB   -0.3058008 0.2597254 -0.61117020 -0.01524303
## treatmentTom_MT   -0.2410211 0.2416544 -0.52259446 0.02594880
##
## , , treatmentSoya_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.5233062 0.3881198  0.1037516 0.992462978
## treatmentSoya_BB   0.6920906 0.3436490  0.3200445 1.114366907
## treatmentSoya_MT   1.1113489 0.4899571  0.5871200 1.705652526
## treatmentMaz_CON  -0.6202720 0.3792820 -1.0754176 -0.195504726
## treatmentMaz_BB   -0.3905211 0.3496597 -0.8016701 0.003403752
## treatmentMaz_MT   -0.5905648 0.2815019 -0.9362374 -0.274483981
## treatmentTom_CON  -0.4299022 0.2924460 -0.7748538 -0.109950975
## treatmentTom_BB   -0.1782904 0.2365936 -0.4478670 0.087940896
## treatmentTom_MT   -0.1827956 0.2231348 -0.4380830 0.064562700
##
## , , treatmentMaz_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.0489064 0.5143116 -0.529918953 0.6524817
## treatmentSoya_BB   -0.5626524 0.3962533 -1.031450479 -0.1131094
## treatmentSoya_MT   -0.6202720 0.3792820 -1.075417647 -0.1955047
## treatmentMaz_CON   3.1522180 1.1533496  1.917460079 4.5670515

```

```

## treatmentMaz_BB    1.7775362 0.7000727  0.999035897  2.6419712
## treatmentMaz_MT   1.4747179 0.5474020  0.871785306  2.1446849
## treatmentTom_CON   0.3119198 0.4375464 -0.176314013  0.8272130
## treatmentTom_BB    0.6493163 0.4146496  0.190846012  1.1535791
## treatmentTom_MT    0.4218772 0.3796450  0.009021686  0.8843290
##
## , , treatmentMaz_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.15379350 0.4847183 -0.7052560 0.399003813
## treatmentSoya_BB   -0.24782309 0.3711212 -0.6798930 0.174783875
## treatmentSoya_MT   -0.39052115 0.3496597 -0.8016701 0.003403752
## treatmentMaz_CON   1.77753617 0.7000727  0.9990359 2.641971225
## treatmentMaz_BB    2.56066625 1.0154366  1.4858384 3.804074730
## treatmentMaz_MT    1.31928528 0.5294519  0.7347358 1.968740541
## treatmentTom_CON   0.04824825 0.4168820 -0.4283615 0.529303931
## treatmentTom_BB    0.14647265 0.3473098 -0.2392336 0.551162942
## treatmentTom_MT    0.07723459 0.3263917 -0.2964368 0.460336126
##
## , , treatmentMaz_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.3599986 0.3708849 -0.79810525 0.05145167
## treatmentSoya_BB   -0.3298306 0.2792732 -0.65635216 -0.01373665
## treatmentSoya_MT   -0.5905648 0.2815019 -0.93623736 -0.27448398
## treatmentMaz_CON   1.4747179 0.5474020  0.87178531 2.14468486
## treatmentMaz_BB    1.3192853 0.5294519  0.73473579 1.96874054
## treatmentMaz_MT    1.4745157 0.5728256  0.85927443 2.18331326
## treatmentTom_CON   0.2222896 0.3134847 -0.12627618 0.59607972
## treatmentTom_BB    0.2256769 0.2660349 -0.07057674 0.54388053
## treatmentTom_MT    0.2251845 0.2584114 -0.05601325 0.53142922
##
## , , treatmentTom_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.38633207 0.4104512 -0.865426138 0.05864417
## treatmentSoya_BB   -0.44781872 0.3083062 -0.813382682 -0.10785815
## treatmentSoya_MT   -0.42990222 0.2924460 -0.774853753 -0.10995097
## treatmentMaz_CON   0.31191978 0.4375464 -0.176314013 0.82721301
## treatmentMaz_BB    0.04824825 0.4168820 -0.428361489 0.52930393
## treatmentMaz_MT    0.22228957 0.3134847 -0.126276181 0.59607972
## treatmentTom_CON   1.46285718 0.7933583  0.652149834 2.41502984
## treatmentTom_BB    0.32001675 0.3155653 -0.015339592 0.69674104
## treatmentTom_MT    0.34370790 0.3225550  0.008862167 0.73512979
##
## , , treatmentTom_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON  0.05589562 0.3384706 -0.31959530 0.44529131
## treatmentSoya_BB   -0.30580081 0.2597254 -0.61117020 -0.01524303
## treatmentSoya_MT   -0.17829045 0.2365936 -0.44786696 0.08794090
## treatmentMaz_CON   0.64931625 0.4146496  0.19084601 1.15357910
## treatmentMaz_BB    0.14647265 0.3473098 -0.23923360 0.55116294
## treatmentMaz_MT    0.22567693 0.2660349 -0.07057674 0.54388053

```

```

## treatmentTom_CON  0.32001675 0.3155653 -0.01533959  0.69674104
## treatmentTom_BB   1.00732673 0.5615369  0.42039188  1.68987963
## treatmentTom_MT   0.49154843 0.3248218  0.14377166  0.88897042
##
## , , treatmentTom_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.11652250 0.3228243 -0.480397814 0.2416378
## treatmentSoya_BB   -0.24102113 0.2416544 -0.522594458 0.0259488
## treatmentSoya_MT   -0.18279556 0.2231348 -0.438082996 0.0645627
## treatmentMaz_CON   0.42187722 0.3796450  0.009021686 0.8843290
## treatmentMaz_BB    0.07723459 0.3263917 -0.296436835 0.4603361
## treatmentMaz_MT    0.22518447 0.2584114 -0.056013247 0.5314292
## treatmentTom_CON   0.34370790 0.3225550  0.008862167 0.7351298
## treatmentTom_BB    0.49154843 0.3248218  0.143771658 0.8889704
## treatmentTom_MT    0.87570901 0.5360039  0.324582491 1.5198276
##
## 
## $mother
## $mother$sd
##           Estimate Est.Error      Q11      Q89
## Intercept 0.5955149 0.1155592 0.4569561 0.7364939
names(VCVarray9traits$father)

## [1] "sd"  "cor" "cov"
VCVarray9traits$father$cor

## , , treatmentSoya_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 1.00000000 0.0000000 1.00000000 1.00000000
## treatmentSoya_BB   0.24960793 0.2138051 -0.01938992 0.50827218
## treatmentSoya_MT   0.36176225 0.2111421  0.09345718 0.61414417
## treatmentMaz_CON   0.01023903 0.2032175 -0.24375768 0.26127676
## treatmentMaz_BB    -0.08392726 0.2155860 -0.35301336 0.18448446
## treatmentMaz_MT    -0.22751972 0.2079622 -0.48321167 0.03298769
## treatmentTom_CON   -0.25300390 0.2311830 -0.53944673 0.03980738
## treatmentTom_BB    0.02907886 0.2377343 -0.27209615 0.32168091
## treatmentTom_MT    -0.10691735 0.2464237 -0.41435247 0.20304664
##
## , , treatmentSoya_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.2496079 0.2138051 -0.01938992 0.50827218
## treatmentSoya_BB   1.0000000 0.0000000 1.00000000 1.00000000
## treatmentSoya_MT   0.5881188 0.1669264  0.37401519 0.78094588
## treatmentMaz_CON   -0.2992638 0.1894279 -0.53144068 -0.05954919
## treatmentMaz_BB    -0.1478591 0.1999846 -0.39738317 0.10196310
## treatmentMaz_MT    -0.2627701 0.2015984 -0.51297651 -0.01007351
## treatmentTom_CON   -0.3563290 0.2082216 -0.61059762 -0.09220973
## treatmentTom_BB    -0.3030759 0.2256437 -0.58063671 -0.01552225
## treatmentTom_MT    -0.2649264 0.2301124 -0.54929994 0.02827946

```

```

##
## , , treatmentSoya_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.3617623 0.2111421 0.09345718 0.614144167
## treatmentSoya_BB   0.5881188 0.1669264 0.37401519 0.780945878
## treatmentSoya_MT  1.0000000 0.0000000 1.000000000 1.000000000
## treatmentMaz_CON -0.3522722 0.1886244 -0.58283666 -0.113572005
## treatmentMaz_BB   -0.2466624 0.1976510 -0.48922335 0.002202847
## treatmentMaz_MT   -0.4846265 0.1799498 -0.69965747 -0.253625045
## treatmentTom_CON -0.3689684 0.2108118 -0.62586308 -0.100437036
## treatmentTom_BB   -0.1999445 0.2291147 -0.48630534 0.087592185
## treatmentTom_MT   -0.2204746 0.2325401 -0.51003925 0.071173588
##
## , , treatmentMaz_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.01023903 0.2032175 -0.243757677 0.26127676
## treatmentSoya_BB   -0.29926382 0.1894279 -0.531440676 -0.05954919
## treatmentSoya_MT   -0.35227216 0.1886244 -0.582836657 -0.11357201
## treatmentMaz_CON  1.00000000 0.0000000 1.000000000 1.000000000
## treatmentMaz_BB   0.63608991 0.1332859 0.467100913 0.78986058
## treatmentMaz_MT   0.69680462 0.1262295 0.534715299 0.83950056
## treatmentTom_CON  0.14873277 0.1943338 -0.094676762 0.38643629
## treatmentTom_BB   0.37707605 0.1879246 0.141618492 0.60125292
## treatmentTom_MT   0.25957509 0.2008477 0.007127548 0.50125430
##
## , , treatmentMaz_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.08392726 0.2155860 -0.3530134 0.184484459
## treatmentSoya_BB   -0.14785909 0.1999846 -0.3973832 0.101963103
## treatmentSoya_MT   -0.24666244 0.1976510 -0.4892234 0.002202847
## treatmentMaz_CON  0.63608991 0.1332859 0.4671009 0.789860576
## treatmentMaz_BB   1.00000000 0.0000000 1.0000000 1.000000000
## treatmentMaz_MT   0.68870501 0.1313029 0.5195323 0.837836812
## treatmentTom_CON  0.02527600 0.2128096 -0.2438687 0.289220967
## treatmentTom_BB   0.09527712 0.2129473 -0.1697080 0.356258963
## treatmentTom_MT   0.05515276 0.2197446 -0.2205008 0.326320339
##
## , , treatmentMaz_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.2275197 0.2079622 -0.48321167 0.03298769
## treatmentSoya_BB   -0.2627701 0.2015984 -0.51297651 -0.01007351
## treatmentSoya_MT   -0.4846265 0.1799498 -0.69965747 -0.25362505
## treatmentMaz_CON  0.6968046 0.1262295 0.53471530 0.83950056
## treatmentMaz_BB   0.6887050 0.1313029 0.51953227 0.83783681
## treatmentMaz_MT   1.0000000 0.0000000 1.0000000 1.000000000
## treatmentTom_CON  0.1591878 0.2056926 -0.09970130 0.41291482
## treatmentTom_BB   0.1957683 0.2095573 -0.06832125 0.45198790
## treatmentTom_MT   0.2099224 0.2156261 -0.06100951 0.47256350
##
## , , treatmentTom_CON

```

```

##                                     Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.2530039 0.2311830 -0.53944673 0.03980738
## treatmentSoya_BB  -0.3563290 0.2082216 -0.61059762 -0.09220973
## treatmentSoya_MT -0.3689684 0.2108118 -0.62586308 -0.10043704
## treatmentMaz_CON  0.1487328 0.1943338 -0.09467676 0.38643629
## treatmentMaz_BB   0.0252760 0.2128096 -0.24386874 0.28922097
## treatmentMaz_MT   0.1591878 0.2056926 -0.09970130 0.41291482
## treatmentTom_CON  1.0000000 0.0000000 1.00000000 1.00000000
## treatmentTom_BB   0.2669217 0.2228346 -0.01752817 0.53496167
## treatmentTom_MT   0.3062881 0.2308417  0.01238175 0.58131447
##
## , , treatmentTom_BB
##
##                                     Estimate Est.Error      Q11      Q89
## treatmentSoya_CON  0.02907886 0.2377343 -0.27209615 0.32168091
## treatmentSoya_BB   -0.30307590 0.2256437 -0.58063671 -0.01552225
## treatmentSoya_MT   -0.19994454 0.2291147 -0.48630534 0.08759218
## treatmentMaz_CON   0.37707605 0.1879246  0.14161849 0.60125292
## treatmentMaz_BB    0.09527712 0.2129473 -0.16970800 0.35625896
## treatmentMaz_MT    0.19576825 0.2095573 -0.06832125 0.45198790
## treatmentTom_CON   0.26692169 0.2228346 -0.01752817 0.53496167
## treatmentTom_BB    1.0000000 0.0000000 1.00000000 1.00000000
## treatmentTom_MT   0.53208822 0.2065689  0.26849874 0.76611496
##
## , , treatmentTom_MT
##
##                                     Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.10691735 0.2464237 -0.414352470 0.20304664
## treatmentSoya_BB   -0.26492636 0.2301124 -0.549299938 0.02827946
## treatmentSoya_MT   -0.22047461 0.2325401 -0.510039250 0.07117359
## treatmentMaz_CON   0.25957509 0.2008477  0.007127548 0.50125430
## treatmentMaz_BB    0.05515276 0.2197446 -0.220500831 0.32632034
## treatmentMaz_MT    0.20992243 0.2156261 -0.061009513 0.47256350
## treatmentTom_CON   0.30628812 0.2308417  0.012381750 0.58131447
## treatmentTom_BB    0.53208822 0.2065689  0.268498738 0.76611496
## treatmentTom_MT   1.0000000 0.0000000 1.000000000 1.000000000
VCVaray9traits$father$cov

## , , treatmentSoya_CON
##
##                                     Estimate Est.Error      Q11      Q89
## treatmentSoya_CON  1.99378560 1.1125225  0.86516378 3.32900967
## treatmentSoya_BB   0.39595334 0.3930833 -0.02281616 0.86675268
## treatmentSoya_MT   0.52330617 0.3881198  0.10375161 0.99246298
## treatmentMaz_CON   0.04890640 0.5143116 -0.52991895 0.65248168
## treatmentMaz_BB   -0.15379350 0.4847183 -0.70525601 0.39900381
## treatmentMaz_MT   -0.35999858 0.3708849 -0.79810525 0.05145167
## treatmentTom_CON   -0.38633207 0.4104512 -0.86542614 0.05864417
## treatmentTom_BB    0.05589562 0.3384706 -0.31959530 0.44529131
## treatmentTom_MT   -0.11652250 0.3228243 -0.48039781 0.24163776
##
## , , treatmentSoya_BB
##

```

```

##                               Estimate Est.Error      Q11      Q89
## treatmentSoya_CON  0.3959533 0.3930833 -0.02281616  0.86675268
## treatmentSoya_BB   1.2847547 0.5594397  0.69468665  1.96464090
## treatmentSoya_MT   0.6920906 0.3436490  0.32004446  1.11436691
## treatmentMaz_CON  -0.5626524 0.3962533 -1.03145048 -0.11310941
## treatmentMaz_BB   -0.2478231 0.3711212 -0.67989300  0.17478388
## treatmentMaz_MT   -0.3298306 0.2792732 -0.65635216 -0.01373665
## treatmentTom_CON  -0.4478187 0.3083062 -0.81338268 -0.10785815
## treatmentTom_BB   -0.3058008 0.2597254 -0.61117020 -0.01524303
## treatmentTom_MT   -0.2410211 0.2416544 -0.52259446  0.02594880
##
## , , treatmentSoya_MT
##
##                               Estimate Est.Error      Q11      Q89
## treatmentSoya_CON  0.5233062 0.3881198  0.1037516  0.992462978
## treatmentSoya_BB   0.6920906 0.3436490  0.3200445  1.114366907
## treatmentSoya_MT   1.1113489 0.4899571  0.5871200  1.705652526
## treatmentMaz_CON  -0.6202720 0.3792820 -1.0754176 -0.195504726
## treatmentMaz_BB   -0.3905211 0.3496597 -0.8016701  0.003403752
## treatmentMaz_MT   -0.5905648 0.2815019 -0.9362374 -0.274483981
## treatmentTom_CON  -0.4299022 0.2924460 -0.7748538 -0.109950975
## treatmentTom_BB   -0.1782904 0.2365936 -0.4478670  0.087940896
## treatmentTom_MT   -0.1827956 0.2231348 -0.4380830  0.064562700
##
## , , treatmentMaz_CON
##
##                               Estimate Est.Error      Q11      Q89
## treatmentSoya_CON  0.0489064 0.5143116 -0.529918953  0.6524817
## treatmentSoya_BB   -0.5626524 0.3962533 -1.031450479 -0.1131094
## treatmentSoya_MT  -0.6202720 0.3792820 -1.075417647 -0.1955047
## treatmentMaz_CON   3.1522180 1.1533496  1.917460079  4.5670515
## treatmentMaz_BB    1.7775362 0.7000727  0.999035897  2.6419712
## treatmentMaz_MT    1.4747179 0.5474020  0.871785306  2.1446849
## treatmentTom_CON   0.3119198 0.4375464 -0.176314013  0.8272130
## treatmentTom_BB    0.6493163 0.4146496  0.190846012  1.1535791
## treatmentTom_MT    0.4218772 0.3796450  0.009021686  0.8843290
##
## , , treatmentMaz_BB
##
##                               Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.15379350 0.4847183 -0.7052560  0.399003813
## treatmentSoya_BB   -0.24782309 0.3711212 -0.6798930  0.174783875
## treatmentSoya_MT   -0.39052115 0.3496597 -0.8016701  0.003403752
## treatmentMaz_CON   1.77753617 0.7000727  0.9990359  2.641971225
## treatmentMaz_BB    2.56066625 1.0154366  1.4858384  3.804074730
## treatmentMaz_MT    1.31928528 0.5294519  0.7347358  1.968740541
## treatmentTom_CON   0.04824825 0.4168820 -0.4283615  0.529303931
## treatmentTom_BB    0.14647265 0.3473098 -0.2392336  0.551162942
## treatmentTom_MT    0.07723459 0.3263917 -0.2964368  0.460336126
##
## , , treatmentMaz_MT
##
##                               Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.3599986 0.3708849 -0.79810525  0.05145167

```

```

## treatmentSoya_BB -0.3298306 0.2792732 -0.65635216 -0.01373665
## treatmentSoya_MT -0.5905648 0.2815019 -0.93623736 -0.27448398
## treatmentMaz_CON 1.4747179 0.5474020 0.87178531 2.14468486
## treatmentMaz_BB 1.3192853 0.5294519 0.73473579 1.96874054
## treatmentMaz_MT 1.4745157 0.5728256 0.85927443 2.18331326
## treatmentTom_CON 0.2222896 0.3134847 -0.12627618 0.59607972
## treatmentTom_BB 0.2256769 0.2660349 -0.07057674 0.54388053
## treatmentTom_MT 0.2251845 0.2584114 -0.05601325 0.53142922
##
## , , treatmentTom_CON
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.38633207 0.4104512 -0.865426138 0.05864417
## treatmentSoya_BB -0.44781872 0.3083062 -0.813382682 -0.10785815
## treatmentSoya_MT -0.42990222 0.2924460 -0.774853753 -0.10995097
## treatmentMaz_CON 0.31191978 0.4375464 -0.176314013 0.82721301
## treatmentMaz_BB 0.04824825 0.4168820 -0.428361489 0.52930393
## treatmentMaz_MT 0.22228957 0.3134847 -0.126276181 0.59607972
## treatmentTom_CON 1.46285718 0.7933583 0.652149834 2.41502984
## treatmentTom_BB 0.32001675 0.3155653 -0.015339592 0.69674104
## treatmentTom_MT 0.34370790 0.3225550 0.008862167 0.73512979
##
## , , treatmentTom_BB
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON 0.05589562 0.3384706 -0.31959530 0.44529131
## treatmentSoya_BB -0.30580081 0.2597254 -0.61117020 -0.01524303
## treatmentSoya_MT -0.17829045 0.2365936 -0.44786696 0.08794090
## treatmentMaz_CON 0.64931625 0.4146496 0.19084601 1.15357910
## treatmentMaz_BB 0.14647265 0.3473098 -0.23923360 0.55116294
## treatmentMaz_MT 0.22567693 0.2660349 -0.07057674 0.54388053
## treatmentTom_CON 0.32001675 0.3155653 -0.01533959 0.69674104
## treatmentTom_BB 1.00732673 0.5615369 0.42039188 1.68987963
## treatmentTom_MT 0.49154843 0.3248218 0.14377166 0.88897042
##
## , , treatmentTom_MT
##
##           Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.11652250 0.3228243 -0.480397814 0.2416378
## treatmentSoya_BB -0.24102113 0.2416544 -0.522594458 0.0259488
## treatmentSoya_MT -0.18279556 0.2231348 -0.438082996 0.0645627
## treatmentMaz_CON 0.42187722 0.3796450 0.009021686 0.8843290
## treatmentMaz_BB 0.07723459 0.3263917 -0.296436835 0.4603361
## treatmentMaz_MT 0.22518447 0.2584114 -0.056013247 0.5314292
## treatmentTom_CON 0.34370790 0.3225550 0.008862167 0.7351298
## treatmentTom_BB 0.49154843 0.3248218 0.143771658 0.8889704
## treatmentTom_MT 0.87570901 0.5360039 0.324582491 1.5198276

GCovs9traits <- melt(VCVarray9traits) %>%
  filter(L2 == "cov",
         Var2 == "Estimate") %>%
  rename(Cov = Var3,
         Trait1 = Var1) %>%
  pivot_wider(,

```

```

        names_from = Cov,
        values_from = value) %>%
select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVararray9traits). In the next version, this warning will become
## an error.

Q11Covs9traitswide <- melt(VCVararray9traits) %>%
  filter(L2 == "cov",
         Var2 == "Q11") %>%
  rename(Q11 = Var3,
         Trait1 = Var1) %>%
  pivot_wider.,
    names_from = Q11,
    values_from = value) %>%
select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVararray9traits). In the next version, this warning will become
## an error.

Q89Covs9traitswide <- melt(VCVararray9traits) %>%
  filter(L2 == "cov",
         Var2 == "Q89") %>%
  rename(Q89 = Var3,
         Trait1 = Var1) %>%
  pivot_wider.,
    names_from = Q89,
    values_from = value) %>%
select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVararray9traits). In the next version, this warning will become
## an error.

UpperHalfCovmat9traitswide <- GCovs9traits %>%
  column_to_rownames(var = "Trait1") %>%
  as.matrix()

UpperHalfCovmat9traitswide[lower.tri(UpperHalfCovmat9traitswide)] <- NA

```

```

## Create VCV matrix ####
VCVarray9traits$father$cor[,,"treatmentTom_MT"]

##                                     Estimate Est.Error      Q11      Q89
## treatmentSoya_CON -0.10691735 0.2464237 -0.414352470 0.20304664
## treatmentSoya_BB  -0.26492636 0.2301124 -0.549299938 0.02827946
## treatmentSoya_MT -0.22047461 0.2325401 -0.510039250 0.07117359
## treatmentMaz_CON  0.25957509 0.2008477  0.007127548 0.50125430
## treatmentMaz_BB   0.05515276 0.2197446 -0.220500831 0.32632034
## treatmentMaz_MT   0.20992243 0.2156261 -0.061009513 0.47256350
## treatmentTom_CON  0.30628812 0.2308417  0.012381750 0.58131447
## treatmentTom_BB   0.53208822 0.2065689  0.268498738 0.76611496
## treatmentTom_MT   1.00000000 0.0000000  1.000000000 1.000000000

Gmat9traitswide <- melt(VCVarray9traits) %>%
  filter(L2 == "cor",
         Var2 == "Estimate") %>%
  rename(Cor = Var3,
         Trait1 = Var1) %>%
  pivot_wider(.,
              names_from = Cor,
              values_from = value) %>%
  select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVarray9traits). In the next version, this warning will become
## an error.

order_levels <- c("treatmentSoya_CON",
                  "treatmentSoya_BB",
                  "treatmentSoya_MT",
                  "treatmentMaz_CON",
                  "treatmentMaz_BB",
                  "treatmentMaz_MT",
                  "treatmentTom_CON",
                  "treatmentTom_BB",
                  "treatmentTom_MT" )

# convert to a matrix with row and column names

Gmat9traitswide_mat <- Gmat9traitswide %>%
  column_to_rownames(var = "Trait1") %>%
  as.matrix(.)

Gvar9traitswide <- melt(VCVarray9traits) %>%
  filter(L2 == "sd",
         Var2 == "Estimate") %>%
  rename(Cor = Var3,

```

```

Trait1 = Var1) %>%
pivot_wider(.,
             names_from = Cor,
             values_from = value) %>%
select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVarray9traits). In the next version, this warning will become
## an error.

Gmat9traitswide <- Gmat9traitswide %>%
  mutate(Trait1 = factor(Trait1,
                        levels = c("treatmentSoya_CON",
                                  "treatmentSoya_BB",
                                  "treatmentSoya_MT",
                                  "treatmentMaz_CON",
                                  "treatmentMaz_BB",
                                  "treatmentMaz_MT",
                                  "treatmentTom_CON",
                                  "treatmentTom_BB",
                                  "treatmentTom_MT" )))

# convert to half of the matrix
LowerHalfGmat9traitswide <- Gmat9traitswide_mat

# remove half of the matrix
LowerHalfGmat9traitswide[upper.tri(LowerHalfGmat9traitswide)] <- NA

diag(LowerHalfGmat9traitswide) <- NA

FullTableGMat <- UpperHalfCovmat9traitswide
FullTableGMat[lower.tri(FullTableGMat)] <- LowerHalfGmat9traitswide[lower.tri(LowerHalfGmat9traitswide)]

# rounding
FullTableGMat <- round(FullTableGMat, digits = 3)
# write out file
# write.csv(FullTableGMat, "outputs/FullGTable.csv")

# work with posteriors #####
# Extract sds for each trait for father and mother

```

```

## create new labels for treatments #####
newcroplabs <- c("Maize", "Soybean",
                 "Tomato")
names(newcroplabs) <- c("Maz", "Soya",
                           "Tom")

newfunglabs <- c("Beauveria", "Control",
                  "Metarhizium")
names(newfunglabs) <- c("BB", "CON",
                           "MT")

## wrangle data #####
summary(model.9traits.brm.matnocov.long)

## Family: bernoulli
## Links: mu = logit
## Formula: MORTday14 ~ treatment + (treatment - 1 | p | gr(father)) + (1 | mother)
## Data: df_qgen_sub_df (Number of observations: 3811)
## Draws: 8 chains, each with iter = 8000; warmup = 4000; thin = 1;
##         total post-warmup draws = 32000
##
## Multilevel Hyperparameters:
## ~father (Number of levels: 37)
##                                         Estimate Est.Error 1-95% CI u-95% CI
## sd(treatmentSoya_CON)                1.36     0.37    0.72    2.18
## sd(treatmentSoya_BB)                 1.11     0.24    0.70    1.63
## sd(treatmentSoya_MT)                 1.03     0.22    0.64    1.51
## sd(treatmentMaz_CON)                1.75     0.31    1.20    2.43
## sd(treatmentMaz_BB)                 1.57     0.30    1.05    2.24
## sd(treatmentMaz_MT)                 1.19     0.23    0.79    1.69
## sd(treatmentTom_CON)                1.17     0.31    0.62    1.85
## sd(treatmentTom_BB)                 0.97     0.27    0.47    1.54
## sd(treatmentTom_MT)                 0.89     0.28    0.39    1.48
## cor(treatmentSoya_CON,treatmentSoya_BB) 0.25     0.21   -0.19    0.63
## cor(treatmentSoya_CON,treatmentSoya_MT) 0.36     0.21   -0.09    0.73
## cor(treatmentSoya_BB,treatmentSoya_MT) 0.59     0.17    0.21    0.86
## cor(treatmentSoya_CON,treatmentMaz_CON) 0.01     0.20   -0.39    0.40
## cor(treatmentSoya_BB,treatmentMaz_CON) -0.30     0.19   -0.65    0.08
## cor(treatmentSoya_MT,treatmentMaz_CON) -0.35     0.19   -0.70    0.03
## cor(treatmentSoya_CON,treatmentMaz_BB) -0.08     0.22   -0.50    0.33
## cor(treatmentSoya_BB,treatmentMaz_BB) -0.15     0.20   -0.53    0.25
## cor(treatmentSoya_MT,treatmentMaz_BB) -0.25     0.20   -0.61    0.15
## cor(treatmentMaz_CON,treatmentMaz_BB)  0.64     0.13    0.33    0.85
## cor(treatmentSoya_CON,treatmentMaz_MT) -0.23     0.21   -0.61    0.19
## cor(treatmentSoya_BB,treatmentMaz_MT) -0.26     0.20   -0.64    0.14
## cor(treatmentSoya_MT,treatmentMaz_MT) -0.48     0.18   -0.79   -0.10
## cor(treatmentMaz_CON,treatmentMaz_MT)  0.70     0.13    0.41    0.89
## cor(treatmentMaz_BB,treatmentMaz_MT)  0.69     0.13    0.38    0.89
## cor(treatmentSoya_CON,treatmentTom_CON) -0.25     0.23   -0.68    0.21
## cor(treatmentSoya_BB,treatmentTom_CON) -0.36     0.21   -0.73    0.08
## cor(treatmentSoya_MT,treatmentTom_CON) -0.37     0.21   -0.75    0.07
## cor(treatmentMaz_CON,treatmentTom_CON)  0.15     0.19   -0.25    0.51
## cor(treatmentMaz_BB,treatmentTom_CON)  0.03     0.21   -0.39    0.43
## cor(treatmentMaz_MT,treatmentTom_CON)  0.16     0.21   -0.26    0.54
## cor(treatmentSoya_CON,treatmentTom_BB)  0.03     0.24   -0.45    0.48

```

## cor(treatmentSoya_BB,treatmentTom_BB)	-0.30	0.23	-0.72	0.15
## cor(treatmentSoya_MT,treatmentTom_BB)	-0.20	0.23	-0.64	0.25
## cor(treatmentMaz_CON,treatmentTom_BB)	0.38	0.19	-0.02	0.70
## cor(treatmentMaz_BB,treatmentTom_BB)	0.10	0.21	-0.33	0.50
## cor(treatmentMaz_MT,treatmentTom_BB)	0.20	0.21	-0.23	0.59
## cor(treatmentTom_CON,treatmentTom_BB)	0.27	0.22	-0.20	0.66
## cor(treatmentSoya_CON,treatmentTom_MT)	-0.11	0.25	-0.58	0.37
## cor(treatmentSoya_BB,treatmentTom_MT)	-0.26	0.23	-0.69	0.20
## cor(treatmentSoya_MT,treatmentTom_MT)	-0.22	0.23	-0.66	0.24
## cor(treatmentMaz_CON,treatmentTom_MT)	0.26	0.20	-0.16	0.62
## cor(treatmentMaz_BB,treatmentTom_MT)	0.06	0.22	-0.38	0.47
## cor(treatmentMaz_MT,treatmentTom_MT)	0.21	0.22	-0.23	0.61
## cor(treatmentTom_CON,treatmentTom_MT)	0.31	0.23	-0.18	0.71
## cor(treatmentTom_BB,treatmentTom_MT)	0.53	0.21	0.06	0.85
##	Rhat	Bulk_ESS	Tail_ESS	
## sd(treatmentSoya_CON)	1.00	9598	16625	
## sd(treatmentSoya_BB)	1.00	11973	20235	
## sd(treatmentSoya_MT)	1.00	14180	21361	
## sd(treatmentMaz_CON)	1.00	16890	22572	
## sd(treatmentMaz_BB)	1.00	18443	23434	
## sd(treatmentMaz_MT)	1.00	20074	24115	
## sd(treatmentTom_CON)	1.00	14874	19170	
## sd(treatmentTom_BB)	1.00	11149	13251	
## sd(treatmentTom_MT)	1.00	8693	9369	
## cor(treatmentSoya_CON,treatmentSoya_BB)	1.00	10822	17580	
## cor(treatmentSoya_CON,treatmentSoya_MT)	1.00	12435	19977	
## cor(treatmentSoya_BB,treatmentSoya_MT)	1.00	16726	22753	
## cor(treatmentSoya_CON,treatmentMaz_CON)	1.00	10059	16013	
## cor(treatmentSoya_BB,treatmentMaz_CON)	1.00	8675	16203	
## cor(treatmentSoya_MT,treatmentMaz_CON)	1.00	9838	18426	
## cor(treatmentSoya_CON,treatmentMaz_BB)	1.00	10113	15385	
## cor(treatmentSoya_BB,treatmentMaz_BB)	1.00	10045	17111	
## cor(treatmentSoya_MT,treatmentMaz_BB)	1.00	10785	18532	
## cor(treatmentMaz_CON,treatmentMaz_BB)	1.00	19341	26036	
## cor(treatmentSoya_CON,treatmentMaz_MT)	1.00	11813	18905	
## cor(treatmentSoya_BB,treatmentMaz_MT)	1.00	11319	16947	
## cor(treatmentSoya_MT,treatmentMaz_MT)	1.00	12235	20133	
## cor(treatmentMaz_CON,treatmentMaz_MT)	1.00	22534	26659	
## cor(treatmentMaz_BB,treatmentMaz_MT)	1.00	23312	26360	
## cor(treatmentSoya_CON,treatmentTom_CON)	1.00	15214	21417	
## cor(treatmentSoya_BB,treatmentTom_CON)	1.00	14586	20060	
## cor(treatmentSoya_MT,treatmentTom_CON)	1.00	15120	22855	
## cor(treatmentMaz_CON,treatmentTom_CON)	1.00	21067	25280	
## cor(treatmentMaz_BB,treatmentTom_CON)	1.00	21694	26332	
## cor(treatmentMaz_MT,treatmentTom_CON)	1.00	20956	25635	
## cor(treatmentSoya_CON,treatmentTom_BB)	1.00	15773	19505	
## cor(treatmentSoya_BB,treatmentTom_BB)	1.00	12043	18457	
## cor(treatmentSoya_MT,treatmentTom_BB)	1.00	13971	20168	
## cor(treatmentMaz_CON,treatmentTom_BB)	1.00	23254	24513	
## cor(treatmentMaz_BB,treatmentTom_BB)	1.00	25219	28035	
## cor(treatmentMaz_MT,treatmentTom_BB)	1.00	22963	25175	
## cor(treatmentTom_CON,treatmentTom_BB)	1.00	19180	24033	
## cor(treatmentSoya_CON,treatmentTom_MT)	1.00	16231	21704	
## cor(treatmentSoya_BB,treatmentTom_MT)	1.00	12340	18431	

```

## cor(treatmentSoya_MT,treatmentTom_MT) 1.00 13516 19128
## cor(treatmentMaz_CON,treatmentTom_MT) 1.00 21574 22126
## cor(treatmentMaz_BB,treatmentTom_MT) 1.00 25775 26185
## cor(treatmentMaz_MT,treatmentTom_MT) 1.00 21446 25467
## cor(treatmentTom_CON,treatmentTom_MT) 1.00 17780 22497
## cor(treatmentTom_BB,treatmentTom_MT) 1.00 14470 18292
##
## ~mother (Number of levels: 58)
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.60 0.12 0.38 0.83 1.00 6006 10627
##
## Regression Coefficients:
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept -2.82 0.36 -3.60 -2.19 1.00 7276 9052
## treatmentSoya_BB 1.94 0.39 1.21 2.76 1.00 8498 10740
## treatmentSoya_MT 1.55 0.38 0.85 2.35 1.00 8990 11282
## treatmentMaz_CON 2.64 0.48 1.75 3.63 1.00 8261 11696
## treatmentMaz_BB 3.82 0.48 2.94 4.81 1.00 8303 11833
## treatmentMaz_MT 3.06 0.44 2.24 3.98 1.00 7767 10718
## treatmentTom_CON 2.15 0.45 1.30 3.09 1.00 8803 11145
## treatmentTom_BB 2.84 0.41 2.10 3.71 1.00 8102 11183
## treatmentTom_MT 3.02 0.42 2.25 3.89 1.00 7917 10161
##
## 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).
Posterior9Traits_lc <- as_tibble(as_draws_df(model.9traits.brm.matnocov.long))
names(Posterior9Traits_lc)
```

```

## [1] "b_Intercept"
## [2] "b_treatmentSoya_BB"
## [3] "b_treatmentSoya_MT"
## [4] "b_treatmentMaz_CON"
## [5] "b_treatmentMaz_BB"
## [6] "b_treatmentMaz_MT"
## [7] "b_treatmentTom_CON"
## [8] "b_treatmentTom_BB"
## [9] "b_treatmentTom_MT"
## [10] "sd_father__treatmentSoya_CON"
## [11] "sd_father__treatmentSoya_BB"
## [12] "sd_father__treatmentSoya_MT"
## [13] "sd_father__treatmentMaz_CON"
## [14] "sd_father__treatmentMaz_BB"
## [15] "sd_father__treatmentMaz_MT"
## [16] "sd_father__treatmentTom_CON"
## [17] "sd_father__treatmentTom_BB"
## [18] "sd_father__treatmentTom_MT"
## [19] "sd_mother__Intercept"
## [20] "cor_father__treatmentSoya_CON__treatmentSoya_BB"
## [21] "cor_father__treatmentSoya_CON__treatmentSoya_MT"
## [22] "cor_father__treatmentSoya_BB__treatmentSoya_MT"
## [23] "cor_father__treatmentSoya_CON__treatmentMaz_CON"
## [24] "cor_father__treatmentSoya_BB__treatmentMaz_CON"
## [25] "cor_father__treatmentSoya_MT__treatmentMaz_CON"
```

```

## [26] "cor_father__treatmentSoya_CON__treatmentMaz_BB"
## [27] "cor_father__treatmentSoya_BB__treatmentMaz_BB"
## [28] "cor_father__treatmentSoya_MT__treatmentMaz_BB"
## [29] "cor_father__treatmentMaz_CON__treatmentMaz_BB"
## [30] "cor_father__treatmentSoya_CON__treatmentMaz_MT"
## [31] "cor_father__treatmentSoya_BB__treatmentMaz_MT"
## [32] "cor_father__treatmentSoya_MT__treatmentMaz_MT"
## [33] "cor_father__treatmentMaz_CON__treatmentMaz_MT"
## [34] "cor_father__treatmentMaz_BB__treatmentMaz_MT"
## [35] "cor_father__treatmentSoya_CON__treatmentTom_CON"
## [36] "cor_father__treatmentSoya_BB__treatmentTom_CON"
## [37] "cor_father__treatmentSoya_MT__treatmentTom_CON"
## [38] "cor_father__treatmentMaz_CON__treatmentTom_CON"
## [39] "cor_father__treatmentMaz_BB__treatmentTom_CON"
## [40] "cor_father__treatmentMaz_MT__treatmentTom_CON"
## [41] "cor_father__treatmentSoya_CON__treatmentTom_BB"
## [42] "cor_father__treatmentSoya_BB__treatmentTom_BB"
## [43] "cor_father__treatmentSoya_MT__treatmentTom_BB"
## [44] "cor_father__treatmentMaz_CON__treatmentTom_BB"
## [45] "cor_father__treatmentMaz_BB__treatmentTom_BB"
## [46] "cor_father__treatmentMaz_MT__treatmentTom_BB"
## [47] "cor_father__treatmentTom_CON__treatmentTom_BB"
## [48] "cor_father__treatmentSoya_CON__treatmentTom_MT"
## [49] "cor_father__treatmentSoya_BB__treatmentTom_MT"
## [50] "cor_father__treatmentSoya_MT__treatmentTom_MT"
## [51] "cor_father__treatmentMaz_CON__treatmentTom_MT"
## [52] "cor_father__treatmentMaz_BB__treatmentTom_MT"
## [53] "cor_father__treatmentMaz_MT__treatmentTom_MT"
## [54] "cor_father__treatmentTom_CON__treatmentTom_MT"
## [55] "cor_father__treatmentTom_BB__treatmentTom_MT"
## [56] "Intercept"
## [57] "r_father[S_1000,treatmentSoya_CON]"
## [58] "r_father[S_128,treatmentSoya_CON]"
## [59] "r_father[S_1330,treatmentSoya_CON]"
## [60] "r_father[S_1335,treatmentSoya_CON]"
## [61] "r_father[S_141,treatmentSoya_CON]"
## [62] "r_father[S_148,treatmentSoya_CON]"
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Posterior9Traits_lc %>%
  rownames_to_column()

## # A tibble: 32,000 x 453
##       rowname b_Intercept b_treatmentSoya_BB b_treatmentSoya_MT b_treatmentMaz_CON

```

```

##      <chr>      <dbl>      <dbl>      <dbl>      <dbl>
## 1 1          -2.98       2.37      1.59      2.88
## 2 2          -2.81       2.35      1.70      2.50
## 3 3          -2.93       2.22      1.83      2.56
## 4 4          -2.79       2.10      1.60      2.17
## 5 5          -2.98       2.10      1.60      2.49
## 6 6          -2.55       2.00      1.56      2.31
## 7 7          -2.58       1.96      1.38      2.44
## 8 8          -3.10       1.72      1.71      2.86
## 9 9          -3.49       2.57      1.83      3.56
## 10 10        -3.25       2.17      2.03      2.67
## # i 31,990 more rows
## # i 448 more variables: b_treatmentMaz_BB <dbl>, b_treatmentMaz_MT <dbl>,
## #   b_treatmentTom_CON <dbl>, b_treatmentTom_BB <dbl>, b_treatmentTom_MT <dbl>,
## #   sd_father__treatmentSoya_CON <dbl>, sd_father__treatmentSoya_BB <dbl>,
## #   sd_father__treatmentSoya_MT <dbl>, sd_father__treatmentMaz_CON <dbl>,
## #   sd_father__treatmentMaz_BB <dbl>, sd_father__treatmentMaz_MT <dbl>,
## #   sd_father__treatmentTom_CON <dbl>, sd_father__treatmentTom_BB <dbl>, ...
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## [3] "b_treatmentSoya_MT"
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## [27] "cor_father__treatmentSoya_BB__treatmentMaz_BB"
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## [377] "r_father[S_292,treatmentTom_MT]"
## [378] "r_father[S_295,treatmentTom_MT]"
## [379] "r_father[S_297,treatmentTom_MT]"
## [380] "r_father[S_62,treatmentTom_MT]"
## [381] "r_father[S_63,treatmentTom_MT]"
## [382] "r_father[S_64,treatmentTom_MT]"
## [383] "r_father[S_65,treatmentTom_MT]"
## [384] "r_father[S_67,treatmentTom_MT]"
## [385] "r_father[S_69,treatmentTom_MT]"
## [386] "r_father[S_71,treatmentTom_MT]"
## [387] "r_father[S_74,treatmentTom_MT]"
## [388] "r_father[S_75,treatmentTom_MT]"
## [389] "r_father[S_76,treatmentTom_MT]"
## [390] "r_mother[D_117,Intercept]"
## [391] "r_mother[D_12,Intercept]"
## [392] "r_mother[D_13,Intercept]"
## [393] "r_mother[D_1332,Intercept]"
## [394] "r_mother[D_1337,Intercept]"
## [395] "r_mother[D_14,Intercept]"
## [396] "r_mother[D_157,Intercept]"
## [397] "r_mother[D_164,Intercept]"
## [398] "r_mother[D_165,Intercept]"
## [399] "r_mother[D_166,Intercept]"
## [400] "r_mother[D_167,Intercept]"
## [401] "r_mother[D_171,Intercept]"
## [402] "r_mother[D_173,Intercept]"
## [403] "r_mother[D_185,Intercept]"
## [404] "r_mother[D_198,Intercept]"
## [405] "r_mother[D_199,Intercept]"
## [406] "r_mother[D_20,Intercept]"
## [407] "r_mother[D_207,Intercept]"
## [408] "r_mother[D_216,Intercept]"
## [409] "r_mother[D_22,Intercept]"
## [410] "r_mother[D_224,Intercept]"
## [411] "r_mother[D_225,Intercept]"
## [412] "r_mother[D_228,Intercept]"

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## [413] "r_mother[D_230,Intercept]"
## [414] "r_mother[D_234,Intercept]"
## [415] "r_mother[D_235,Intercept]"
## [416] "r_mother[D_236,Intercept]"
## [417] "r_mother[D_242,Intercept]"
## [418] "r_mother[D_25,Intercept]"
## [419] "r_mother[D_261,Intercept]"
## [420] "r_mother[D_267,Intercept]"
## [421] "r_mother[D_276,Intercept]"
## [422] "r_mother[D_279,Intercept]"
## [423] "r_mother[D_28,Intercept]"
## [424] "r_mother[D_288,Intercept]"
## [425] "r_mother[D_29,Intercept]"
## [426] "r_mother[D_30,Intercept]"
## [427] "r_mother[D_31,Intercept]"
## [428] "r_mother[D_33,Intercept]"
## [429] "r_mother[D_34,Intercept]"
## [430] "r_mother[D_40,Intercept]"
## [431] "r_mother[D_42,Intercept]"
## [432] "r_mother[D_45,Intercept]"
## [433] "r_mother[D_48,Intercept]"
## [434] "r_mother[D_49,Intercept]"
## [435] "r_mother[D_50,Intercept]"
## [436] "r_mother[D_51,Intercept]"
## [437] "r_mother[D_52,Intercept]"
## [438] "r_mother[D_56,Intercept]"
## [439] "r_mother[D_58,Intercept]"
## [440] "r_mother[D_60,Intercept]"
## [441] "r_mother[D_61,Intercept]"
## [442] "r_mother[D_62,Intercept]"
## [443] "r_mother[D_66,Intercept]"
## [444] "r_mother[D_7,Intercept]"
## [445] "r_mother[D_71,Intercept]"
## [446] "r_mother[D_7490,Intercept]"
## [447] "r_mother[D_7495,Intercept]"
## [448] "lprior"
## [449] "lp__"
## [450] ".chain"
## [451] ".iteration"
## [452] ".draw"

Posterior9Traits_sds_lc <- Posterior9Traits_lc %>%
  rownames_to_column() %>%
  select(rownames, sd_father__treatmentSoya_CON:
         sd_mother__Intercept) %>%
  pivot_longer(sd_father__treatmentSoya_CON:
               sd_father__treatmentTom_MT,
               names_to = "traits",
               values_to = "SD") %>%
  mutate(treat = traits) %>%
  separate(traits, into = c("junk", "junk2", "crop",
                           "fungus")) %>%
  select(-junk, -junk2) %>%
  separate(crop,

```

```

      into = c("junk3", "crop"),
      sep = 9) %>%
  select(-junk3) %>%
  separate(treat, into = c("junk4", "treat"), sep = 20) %>%
  select(-junk4)

# in following line compute heritability within treatments considering residual variance set to 1,
# and square of iteration-level maternal variance
## extract sample-level maternal variance #####
Posterior9Traits_sds_lc <- Posterior9Traits_sds_lc %>%
  mutate(herit = SD*SD / ((SD * SD) + 1 + (sd_mother_Intercept * sd_mother_Intercept)))

# extract 89%HDI for heritability
Posterior9Traits_sds_lc %>%
  group_by(treat) %>%
  summarise(HDI_herit = hdi(herit, ci = 0.89))

## # A tibble: 9 x 2
##   treat    HDI_herit[,1] [,2]
##   <chr>        <dbl>  <dbl>
## 1 Maz_BB       0.447   0.800
## 2 Maz_CON      0.512   0.829
## 3 Maz_MT       0.312   0.692
## 4 Soya_BB      0.259   0.665
## 5 Soya_CON     0.296   0.801
## 6 Soya_MT      0.226   0.629
## 7 Tom_BB       0.135   0.651
## 8 Tom_CON      0.231   0.733
## 9 Tom_MT       0.0895  0.624

# Posterior9Traits_sds_lc %>%
#   select(treat, herit) %>%
#   group_by(treat) %>%
#   summarise(HDI_MAP = map_estimate(herit))

map_estimate(model.9traits.brm.matnocov.long, effects = "random")

## MAP Estimate
##
## Parameter | MAP_Estimate
## -----
## r_father[S_1000,treatmentSoya_CON] | -0.45
## r_father[S_128,treatmentSoya_CON] | -0.59
## r_father[S_1330,treatmentSoya_CON] | 0.77
## r_father[S_1335,treatmentSoya_CON] | -0.50
## r_father[S_141,treatmentSoya_CON] | -0.19
## r_father[S_148,treatmentSoya_CON] | 1.16
## r_father[S_149,treatmentSoya_CON] | 0.07
## r_father[S_150,treatmentSoya_CON] | -0.50
## r_father[S_152,treatmentSoya_CON] | 1.05

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## r_father[S_199,treatmentSoya_CON]		1.10
## r_father[S_2000,treatmentSoya_CON]		1.85
## r_father[S_209,treatmentSoya_CON]		-0.76
## r_father[S_212,treatmentSoya_CON]		-1.05
## r_father[S_214,treatmentSoya_CON]		-0.02
## r_father[S_224,treatmentSoya_CON]		-0.15
## r_father[S_225,treatmentSoya_CON]		-0.50
## r_father[S_232,treatmentSoya_CON]		0.48
## r_father[S_245,treatmentSoya_CON]		-0.36
## r_father[S_250,treatmentSoya_CON]		-0.59
## r_father[S_254,treatmentSoya_CON]		0.20
## r_father[S_257,treatmentSoya_CON]		-0.79
## r_father[S_282,treatmentSoya_CON]		-0.59
## r_father[S_288,treatmentSoya_CON]		0.18
## r_father[S_290,treatmentSoya_CON]		-0.35
## r_father[S_292,treatmentSoya_CON]		2.05
## r_father[S_295,treatmentSoya_CON]		2.41
## r_father[S_297,treatmentSoya_CON]		-1.05
## r_father[S_62,treatmentSoya_CON]		0.55
## r_father[S_63,treatmentSoya_CON]		-0.27
## r_father[S_64,treatmentSoya_CON]		-0.65
## r_father[S_65,treatmentSoya_CON]		0.82
## r_father[S_67,treatmentSoya_CON]		-0.09
## r_father[S_69,treatmentSoya_CON]		-0.36
## r_father[S_71,treatmentSoya_CON]		0.63
## r_father[S_74,treatmentSoya_CON]		0.91
## r_father[S_75,treatmentSoya_CON]		-0.30
## r_father[S_76,treatmentSoya_CON]		0.24
## r_father[S_1000,treatmentSoya_BB]		-1.57
## r_father[S_128,treatmentSoya_BB]		-0.40
## r_father[S_1330,treatmentSoya_BB]		1.29
## r_father[S_1335,treatmentSoya_BB]		0.47
## r_father[S_141,treatmentSoya_BB]		1.14
## r_father[S_148,treatmentSoya_BB]		1.47
## r_father[S_149,treatmentSoya_BB]		-0.43
## r_father[S_150,treatmentSoya_BB]		-0.68
## r_father[S_152,treatmentSoya_BB]		-0.01
## r_father[S_199,treatmentSoya_BB]		1.03
## r_father[S_2000,treatmentSoya_BB]		-0.20
## r_father[S_209,treatmentSoya_BB]		-0.54
## r_father[S_212,treatmentSoya_BB]		-1.44
## r_father[S_214,treatmentSoya_BB]		0.13
## r_father[S_224,treatmentSoya_BB]		0.54
## r_father[S_225,treatmentSoya_BB]		-1.14
## r_father[S_232,treatmentSoya_BB]		0.21
## r_father[S_245,treatmentSoya_BB]		-2.98e-05
## r_father[S_250,treatmentSoya_BB]		-1.11
## r_father[S_254,treatmentSoya_BB]		-0.40
## r_father[S_257,treatmentSoya_BB]		-0.18
## r_father[S_282,treatmentSoya_BB]		-1.04
## r_father[S_288,treatmentSoya_BB]		-1.10
## r_father[S_290,treatmentSoya_BB]		-0.69
## r_father[S_292,treatmentSoya_BB]		0.90
## r_father[S_295,treatmentSoya_BB]		0.12

## r_father[S_297,treatmentSoya_BB]		-1.33
## r_father[S_62,treatmentSoya_BB]		0.83
## r_father[S_63,treatmentSoya_BB]		0.44
## r_father[S_64,treatmentSoya_BB]		-0.50
## r_father[S_65,treatmentSoya_BB]		1.38
## r_father[S_67,treatmentSoya_BB]		1.22
## r_father[S_69,treatmentSoya_BB]		0.99
## r_father[S_71,treatmentSoya_BB]		0.74
## r_father[S_74,treatmentSoya_BB]		0.13
## r_father[S_75,treatmentSoya_BB]		0.55
## r_father[S_76,treatmentSoya_BB]		0.20
## r_father[S_1000,treatmentSoya_MT]		-1.35
## r_father[S_128,treatmentSoya_MT]		0.32
## r_father[S_1330,treatmentSoya_MT]		1.56
## r_father[S_1335,treatmentSoya_MT]		-0.41
## r_father[S_141,treatmentSoya_MT]		0.97
## r_father[S_148,treatmentSoya_MT]		0.74
## r_father[S_149,treatmentSoya_MT]		-0.44
## r_father[S_150,treatmentSoya_MT]		-0.32
## r_father[S_152,treatmentSoya_MT]		0.26
## r_father[S_199,treatmentSoya_MT]		0.99
## r_father[S_2000,treatmentSoya_MT]		-0.08
## r_father[S_209,treatmentSoya_MT]		-0.44
## r_father[S_212,treatmentSoya_MT]		-1.24
## r_father[S_214,treatmentSoya_MT]		-0.45
## r_father[S_224,treatmentSoya_MT]		-0.20
## r_father[S_225,treatmentSoya_MT]		-1.63
## r_father[S_232,treatmentSoya_MT]		0.16
## r_father[S_245,treatmentSoya_MT]		-0.36
## r_father[S_250,treatmentSoya_MT]		-0.69
## r_father[S_254,treatmentSoya_MT]		-0.18
## r_father[S_257,treatmentSoya_MT]		-0.30
## r_father[S_282,treatmentSoya_MT]		-0.75
## r_father[S_288,treatmentSoya_MT]		-1.10
## r_father[S_290,treatmentSoya_MT]		-0.48
## r_father[S_292,treatmentSoya_MT]		1.48
## r_father[S_295,treatmentSoya_MT]		1.17
## r_father[S_297,treatmentSoya_MT]		-1.58
## r_father[S_62,treatmentSoya_MT]		1.17
## r_father[S_63,treatmentSoya_MT]		0.43
## r_father[S_64,treatmentSoya_MT]		-0.61
## r_father[S_65,treatmentSoya_MT]		1.05
## r_father[S_67,treatmentSoya_MT]		0.45
## r_father[S_69,treatmentSoya_MT]		1.15
## r_father[S_71,treatmentSoya_MT]		0.12
## r_father[S_74,treatmentSoya_MT]		0.51
## r_father[S_75,treatmentSoya_MT]		0.41
## r_father[S_76,treatmentSoya_MT]		0.28
## r_father[S_1000,treatmentMaz_CON]		3.68
## r_father[S_128,treatmentMaz_CON]		-0.52
## r_father[S_1330,treatmentMaz_CON]		-0.39
## r_father[S_1335,treatmentMaz_CON]		0.15
## r_father[S_141,treatmentMaz_CON]		-1.37
## r_father[S_148,treatmentMaz_CON]		0.22

## r_father[S_149,treatmentMaz_CON]		0.19
## r_father[S_150,treatmentMaz_CON]		1.26
## r_father[S_152,treatmentMaz_CON]		0.05
## r_father[S_199,treatmentMaz_CON]		-1.31
## r_father[S_2000,treatmentMaz_CON]		1.75
## r_father[S_209,treatmentMaz_CON]		-1.56
## r_father[S_212,treatmentMaz_CON]		2.44
## r_father[S_214,treatmentMaz_CON]		1.47
## r_father[S_224,treatmentMaz_CON]		1.74
## r_father[S_225,treatmentMaz_CON]		2.41
## r_father[S_232,treatmentMaz_CON]		-1.45
## r_father[S_245,treatmentMaz_CON]		0.83
## r_father[S_250,treatmentMaz_CON]		-0.89
## r_father[S_254,treatmentMaz_CON]		-1.41
## r_father[S_257,treatmentMaz_CON]		-1.72
## r_father[S_282,treatmentMaz_CON]		2.87e-03
## r_father[S_288,treatmentMaz_CON]		3.21
## r_father[S_290,treatmentMaz_CON]		0.16
## r_father[S_292,treatmentMaz_CON]		-1.84
## r_father[S_295,treatmentMaz_CON]		-0.68
## r_father[S_297,treatmentMaz_CON]		2.62
## r_father[S_62,treatmentMaz_CON]		-2.87
## r_father[S_63,treatmentMaz_CON]		-0.03
## r_father[S_64,treatmentMaz_CON]		0.15
## r_father[S_65,treatmentMaz_CON]		-1.34
## r_father[S_67,treatmentMaz_CON]		-1.47
## r_father[S_69,treatmentMaz_CON]		-1.73
## r_father[S_71,treatmentMaz_CON]		-0.53
## r_father[S_74,treatmentMaz_CON]		0.84
## r_father[S_75,treatmentMaz_CON]		-0.72
## r_father[S_76,treatmentMaz_CON]		-0.93
## r_father[S_1000,treatmentMaz_BB]		2.58
## r_father[S_128,treatmentMaz_BB]		-0.16
## r_father[S_1330,treatmentMaz_BB]		1.05
## r_father[S_1335,treatmentMaz_BB]		0.91
## r_father[S_141,treatmentMaz_BB]		-0.26
## r_father[S_148,treatmentMaz_BB]		-1.06
## r_father[S_149,treatmentMaz_BB]		0.74
## r_father[S_150,treatmentMaz_BB]		0.48
## r_father[S_152,treatmentMaz_BB]		-0.78
## r_father[S_199,treatmentMaz_BB]		-0.55
## r_father[S_2000,treatmentMaz_BB]		0.97
## r_father[S_209,treatmentMaz_BB]		-1.42
## r_father[S_212,treatmentMaz_BB]		1.68
## r_father[S_214,treatmentMaz_BB]		1.20
## r_father[S_224,treatmentMaz_BB]		0.84
## r_father[S_225,treatmentMaz_BB]		1.66
## r_father[S_232,treatmentMaz_BB]		-0.41
## r_father[S_245,treatmentMaz_BB]		0.04
## r_father[S_250,treatmentMaz_BB]		-3.06
## r_father[S_254,treatmentMaz_BB]		-0.71
## r_father[S_257,treatmentMaz_BB]		-1.35
## r_father[S_282,treatmentMaz_BB]		-0.74
## r_father[S_288,treatmentMaz_BB]		2.63

## r_father[S_290,treatmentMaz_BB]		-0.08
## r_father[S_292,treatmentMaz_BB]		-2.55
## r_father[S_295,treatmentMaz_BB]		-0.87
## r_father[S_297,treatmentMaz_BB]		2.55
## r_father[S_62,treatmentMaz_BB]		-2.30
## r_father[S_63,treatmentMaz_BB]		0.62
## r_father[S_64,treatmentMaz_BB]		0.25
## r_father[S_65,treatmentMaz_BB]		-0.94
## r_father[S_67,treatmentMaz_BB]		-0.28
## r_father[S_69,treatmentMaz_BB]		-0.82
## r_father[S_71,treatmentMaz_BB]		-0.16
## r_father[S_74,treatmentMaz_BB]		-0.01
## r_father[S_75,treatmentMaz_BB]		-0.64
## r_father[S_76,treatmentMaz_BB]		-0.77
## r_father[S_1000,treatmentMaz_MT]		2.17
## r_father[S_128,treatmentMaz_MT]		0.02
## r_father[S_1330,treatmentMaz_MT]		-0.73
## r_father[S_1335,treatmentMaz_MT]		0.96
## r_father[S_141,treatmentMaz_MT]		-0.59
## r_father[S_148,treatmentMaz_MT]		-0.47
## r_father[S_149,treatmentMaz_MT]		0.64
## r_father[S_150,treatmentMaz_MT]		0.35
## r_father[S_152,treatmentMaz_MT]		-0.39
## r_father[S_199,treatmentMaz_MT]		-0.91
## r_father[S_2000,treatmentMaz_MT]		0.69
## r_father[S_209,treatmentMaz_MT]		-0.54
## r_father[S_212,treatmentMaz_MT]		1.44
## r_father[S_214,treatmentMaz_MT]		1.15
## r_father[S_224,treatmentMaz_MT]		1.21
## r_father[S_225,treatmentMaz_MT]		1.62
## r_father[S_232,treatmentMaz_MT]		-1.08
## r_father[S_245,treatmentMaz_MT]		0.54
## r_father[S_250,treatmentMaz_MT]		-1.17
## r_father[S_254,treatmentMaz_MT]		-1.01
## r_father[S_257,treatmentMaz_MT]		-0.34
## r_father[S_282,treatmentMaz_MT]		-0.03
## r_father[S_288,treatmentMaz_MT]		2.01
## r_father[S_290,treatmentMaz_MT]		0.25
## r_father[S_292,treatmentMaz_MT]		-2.09
## r_father[S_295,treatmentMaz_MT]		-1.14
## r_father[S_297,treatmentMaz_MT]		2.24
## r_father[S_62,treatmentMaz_MT]		-1.74
## r_father[S_63,treatmentMaz_MT]		0.03
## r_father[S_64,treatmentMaz_MT]		0.34
## r_father[S_65,treatmentMaz_MT]		-1.06
## r_father[S_67,treatmentMaz_MT]		-0.47
## r_father[S_69,treatmentMaz_MT]		-0.92
## r_father[S_71,treatmentMaz_MT]		-0.14
## r_father[S_74,treatmentMaz_MT]		-0.40
## r_father[S_75,treatmentMaz_MT]		-0.53
## r_father[S_76,treatmentMaz_MT]		-0.69
## r_father[S_1000,treatmentTom_CON]		0.35
## r_father[S_128,treatmentTom_CON]		0.23
## r_father[S_1330,treatmentTom_CON]		-1.24

## r_father[S_1335,treatmentTom_CON]		-0.28
## r_father[S_141,treatmentTom_CON]		-0.50
## r_father[S_148,treatmentTom_CON]		-0.82
## r_father[S_149,treatmentTom_CON]		0.21
## r_father[S_150,treatmentTom_CON]		0.59
## r_father[S_152,treatmentTom_CON]		-0.08
## r_father[S_199,treatmentTom_CON]		-0.94
## r_father[S_2000,treatmentTom_CON]		-0.84
## r_father[S_209,treatmentTom_CON]		0.11
## r_father[S_212,treatmentTom_CON]		1.57
## r_father[S_214,treatmentTom_CON]		0.70
## r_father[S_224,treatmentTom_CON]		-0.43
## r_father[S_225,treatmentTom_CON]		1.69
## r_father[S_232,treatmentTom_CON]		0.41
## r_father[S_245,treatmentTom_CON]		0.24
## r_father[S_250,treatmentTom_CON]		2.16
## r_father[S_254,treatmentTom_CON]		0.42
## r_father[S_257,treatmentTom_CON]		0.02
## r_father[S_282,treatmentTom_CON]		0.74
## r_father[S_288,treatmentTom_CON]		-0.08
## r_father[S_290,treatmentTom_CON]		-9.89e-03
## r_father[S_292,treatmentTom_CON]		-0.46
## r_father[S_295,treatmentTom_CON]		-0.39
## r_father[S_297,treatmentTom_CON]		0.75
## r_father[S_62,treatmentTom_CON]		-0.46
## r_father[S_63,treatmentTom_CON]		-0.53
## r_father[S_64,treatmentTom_CON]		0.54
## r_father[S_65,treatmentTom_CON]		-1.70
## r_father[S_67,treatmentTom_CON]		-0.08
## r_father[S_69,treatmentTom_CON]		-0.34
## r_father[S_71,treatmentTom_CON]		-0.14
## r_father[S_74,treatmentTom_CON]		-0.53
## r_father[S_75,treatmentTom_CON]		-0.06
## r_father[S_76,treatmentTom_CON]		-0.10
## r_father[S_1000,treatmentTom_BB]		1.52
## r_father[S_128,treatmentTom_BB]		-0.31
## r_father[S_1330,treatmentTom_BB]		-0.52
## r_father[S_1335,treatmentTom_BB]		-0.51
## r_father[S_141,treatmentTom_BB]		-0.49
## r_father[S_148,treatmentTom_BB]		-0.34
## r_father[S_149,treatmentTom_BB]		-0.11
## r_father[S_150,treatmentTom_BB]		0.65
## r_father[S_152,treatmentTom_BB]		0.49
## r_father[S_199,treatmentTom_BB]		-0.82
## r_father[S_2000,treatmentTom_BB]		0.61
## r_father[S_209,treatmentTom_BB]		-0.24
## r_father[S_212,treatmentTom_BB]		0.76
## r_father[S_214,treatmentTom_BB]		0.49
## r_father[S_224,treatmentTom_BB]		0.29
## r_father[S_225,treatmentTom_BB]		0.54
## r_father[S_232,treatmentTom_BB]		-0.65
## r_father[S_245,treatmentTom_BB]		0.05
## r_father[S_250,treatmentTom_BB]		1.30
## r_father[S_254,treatmentTom_BB]		0.22

## r_father[S_257,treatmentTom_BB]		-0.24
## r_father[S_282,treatmentTom_BB]		-0.07
## r_father[S_288,treatmentTom_BB]		0.10
## r_father[S_290,treatmentTom_BB]		0.73
## r_father[S_292,treatmentTom_BB]		-0.32
## r_father[S_295,treatmentTom_BB]		0.04
## r_father[S_297,treatmentTom_BB]		0.15
## r_father[S_62,treatmentTom_BB]		-0.75
## r_father[S_63,treatmentTom_BB]		-0.31
## r_father[S_64,treatmentTom_BB]		0.11
## r_father[S_65,treatmentTom_BB]		-0.86
## r_father[S_67,treatmentTom_BB]		-1.12
## r_father[S_69,treatmentTom_BB]		-0.79
## r_father[S_71,treatmentTom_BB]		-0.71
## r_father[S_74,treatmentTom_BB]		0.04
## r_father[S_75,treatmentTom_BB]		-0.29
## r_father[S_76,treatmentTom_BB]		0.77
## r_father[S_1000,treatmentTom_MT]		0.96
## r_father[S_128,treatmentTom_MT]		-0.07
## r_father[S_1330,treatmentTom_MT]		-0.36
## r_father[S_1335,treatmentTom_MT]		-0.22
## r_father[S_141,treatmentTom_MT]		-0.56
## r_father[S_148,treatmentTom_MT]		-0.35
## r_father[S_149,treatmentTom_MT]		-0.01
## r_father[S_150,treatmentTom_MT]		0.46
## r_father[S_152,treatmentTom_MT]		0.42
## r_father[S_199,treatmentTom_MT]		-0.82
## r_father[S_2000,treatmentTom_MT]		0.28
## r_father[S_209,treatmentTom_MT]		0.28
## r_father[S_212,treatmentTom_MT]		0.72
## r_father[S_214,treatmentTom_MT]		0.09
## r_father[S_224,treatmentTom_MT]		0.41
## r_father[S_225,treatmentTom_MT]		0.90
## r_father[S_232,treatmentTom_MT]		-0.56
## r_father[S_245,treatmentTom_MT]		-0.22
## r_father[S_250,treatmentTom_MT]		1.18
## r_father[S_254,treatmentTom_MT]		-0.02
## r_father[S_257,treatmentTom_MT]		0.43
## r_father[S_282,treatmentTom_MT]		-0.03
## r_father[S_288,treatmentTom_MT]		-0.05
## r_father[S_290,treatmentTom_MT]		0.44
## r_father[S_292,treatmentTom_MT]		-0.35
## r_father[S_295,treatmentTom_MT]		-0.23
## r_father[S_297,treatmentTom_MT]		-0.04
## r_father[S_62,treatmentTom_MT]		-0.64
## r_father[S_63,treatmentTom_MT]		-0.11
## r_father[S_64,treatmentTom_MT]		-0.04
## r_father[S_65,treatmentTom_MT]		-1.16
## r_father[S_67,treatmentTom_MT]		-0.40
## r_father[S_69,treatmentTom_MT]		-0.43
## r_father[S_71,treatmentTom_MT]		-0.65
## r_father[S_74,treatmentTom_MT]		-0.22
## r_father[S_75,treatmentTom_MT]		-0.06
## r_father[S_76,treatmentTom_MT]		0.60

## r_mother[D_117,Intercept]		-0.28
## r_mother[D_12,Intercept]		-0.55
## r_mother[D_13,Intercept]		-0.03
## r_mother[D_1332,Intercept]		-0.10
## r_mother[D_1337,Intercept]		0.03
## r_mother[D_14,Intercept]		-0.03
## r_mother[D_157,Intercept]		-0.47
## r_mother[D_164,Intercept]		-0.13
## r_mother[D_165,Intercept]		0.56
## r_mother[D_166,Intercept]		-0.46
## r_mother[D_167,Intercept]		1.00
## r_mother[D_171,Intercept]		0.63
## r_mother[D_173,Intercept]		1.19
## r_mother[D_185,Intercept]		-0.10
## r_mother[D_198,Intercept]		-0.59
## r_mother[D_199,Intercept]		-0.55
## r_mother[D_20,Intercept]		0.07
## r_mother[D_207,Intercept]		-0.86
## r_mother[D_216,Intercept]		-0.54
## r_mother[D_22,Intercept]		0.26
## r_mother[D_224,Intercept]		0.13
## r_mother[D_225,Intercept]		0.04
## r_mother[D_228,Intercept]		0.47
## r_mother[D_230,Intercept]		-0.37
## r_mother[D_234,Intercept]		-0.37
## r_mother[D_235,Intercept]		-0.19
## r_mother[D_236,Intercept]		0.19
## r_mother[D_242,Intercept]		-0.26
## r_mother[D_25,Intercept]		0.12
## r_mother[D_261,Intercept]		-0.16
## r_mother[D_267,Intercept]		0.53
## r_mother[D_276,Intercept]		0.67
## r_mother[D_279,Intercept]		-0.08
## r_mother[D_28,Intercept]		-0.27
## r_mother[D_288,Intercept]		-0.04
## r_mother[D_29,Intercept]		-0.16
## r_mother[D_30,Intercept]		-0.23
## r_mother[D_31,Intercept]		0.32
## r_mother[D_33,Intercept]		-0.05
## r_mother[D_34,Intercept]		0.31
## r_mother[D_40,Intercept]		-0.52
## r_mother[D_42,Intercept]		0.21
## r_mother[D_45,Intercept]		-0.09
## r_mother[D_48,Intercept]		0.48
## r_mother[D_49,Intercept]		-0.55
## r_mother[D_50,Intercept]		-0.13
## r_mother[D_51,Intercept]		-0.56
## r_mother[D_52,Intercept]		0.41
## r_mother[D_56,Intercept]		-0.11
## r_mother[D_58,Intercept]		0.54
## r_mother[D_60,Intercept]		-0.35
## r_mother[D_61,Intercept]		-0.30
## r_mother[D_62,Intercept]		0.20
## r_mother[D_66,Intercept]		0.55

```

## r_mother[D_7,Intercept] | -0.23
## r_mother[D_71,Intercept] | 0.36
## r_mother[D_7490,Intercept] | 0.67
## r_mother[D_7495,Intercept] | -0.01
## sd_father__treatmentSoya_CON | 1.26
## sd_father__treatmentSoya_BB | 1.04
## sd_father__treatmentSoya_MT | 1.01
## sd_father__treatmentMaz_CON | 1.67
## sd_father__treatmentMaz_BB | 1.50
## sd_father__treatmentMaz_MT | 1.16
## sd_father__treatmentTom_CON | 1.09
## sd_father__treatmentTom_BB | 0.94
## sd_father__treatmentTom_MT | 0.85
## sd_mother__Intercept | 0.60
## cor_father__treatmentSoya_CON__treatmentSoya_BB | 0.28
## cor_father__treatmentSoya_CON__treatmentSoya_MT | 0.40
## cor_father__treatmentSoya_BB__treatmentSoya_MT | 0.67
## cor_father__treatmentSoya_CON__treatmentMaz_CON | -4.45e-03
## cor_father__treatmentSoya_BB__treatmentMaz_CON | -0.31
## cor_father__treatmentSoya_MT__treatmentMaz_CON | -0.37
## cor_father__treatmentSoya_CON__treatmentMaz_BB | -0.06
## cor_father__treatmentSoya_BB__treatmentMaz_BB | -0.14
## cor_father__treatmentSoya_MT__treatmentMaz_BB | -0.26
## cor_father__treatmentMaz_CON__treatmentMaz_BB | 0.69
## cor_father__treatmentSoya_CON__treatmentMaz_MT | -0.25
## cor_father__treatmentSoya_BB__treatmentMaz_MT | -0.27
## cor_father__treatmentSoya_MT__treatmentMaz_MT | -0.52
## cor_father__treatmentMaz_CON__treatmentMaz_MT | 0.74
## cor_father__treatmentMaz_BB__treatmentMaz_MT | 0.74
## cor_father__treatmentSoya_CON__treatmentTom_CON | -0.30
## cor_father__treatmentSoya_BB__treatmentTom_CON | -0.36
## cor_father__treatmentSoya_MT__treatmentTom_CON | -0.40
## cor_father__treatmentMaz_CON__treatmentTom_CON | 0.17
## cor_father__treatmentMaz_BB__treatmentTom_CON | 0.03
## cor_father__treatmentMaz_MT__treatmentTom_CON | 0.19
## cor_father__treatmentSoya_CON__treatmentTom_BB | 0.03
## cor_father__treatmentSoya_BB__treatmentTom_BB | -0.30
## cor_father__treatmentSoya_MT__treatmentTom_BB | -0.20
## cor_father__treatmentMaz_CON__treatmentTom_BB | 0.41
## cor_father__treatmentMaz_BB__treatmentTom_BB | 0.09
## cor_father__treatmentMaz_MT__treatmentTom_BB | 0.22
## cor_father__treatmentTom_CON__treatmentTom_BB | 0.33
## cor_father__treatmentSoya_CON__treatmentTom_MT | -0.09
## cor_father__treatmentSoya_BB__treatmentTom_MT | -0.27
## cor_father__treatmentSoya_MT__treatmentTom_MT | -0.21
## cor_father__treatmentMaz_CON__treatmentTom_MT | 0.29
## cor_father__treatmentMaz_BB__treatmentTom_MT | 0.06
## cor_father__treatmentMaz_MT__treatmentTom_MT | 0.22
## cor_father__treatmentTom_CON__treatmentTom_MT | 0.36
## cor_father__treatmentTom_BB__treatmentTom_MT | 0.59

model.9traitslongRC <- model.9traits.brm.matnocov.long %>%
  recover_types()

```

```

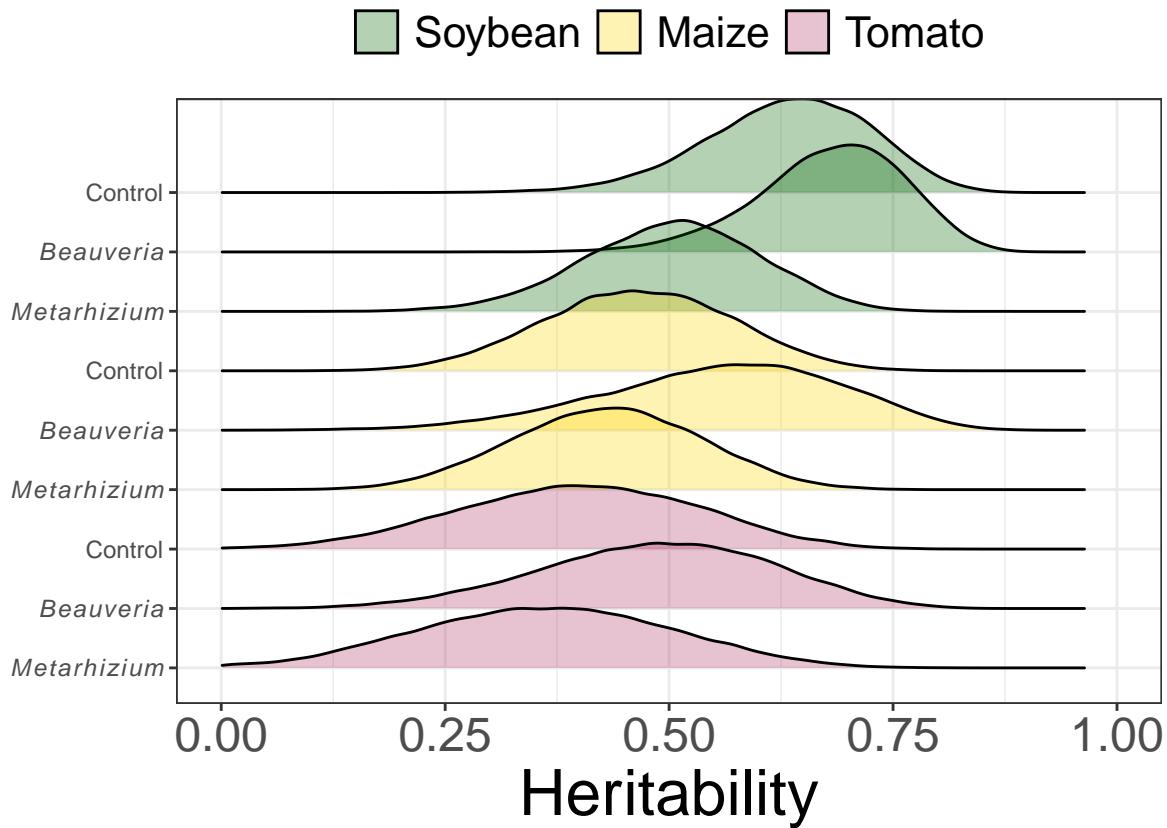
model.9traitslongRC %>%
  summarise_draws()

## # A tibble: 449 x 10
##   variable      mean median    sd    mad     q5    q95 rhat ess_bulk ess_tail
##   <chr>        <dbl>  <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl>    <dbl>
## 1 b_Intercept -2.82  -2.79  0.358 0.344 -3.45 -2.28  1.00  7276.   9052.
## 2 b_treatmentSoy~ 1.94   1.92  0.390 0.373  1.33  2.61  1.00  8498.  10740.
## 3 b_treatmentSoy~ 1.55   1.53  0.377 0.362  0.968 2.20  1.00  8990.  11282.
## 4 b_treatmentMaz~ 2.64   2.63  0.475 0.461  1.90  3.45  1.00  8261.  11696.
## 5 b_treatmentMaz~ 3.82   3.80  0.476 0.466  3.08  4.63  1.00  8303.  11833.
## 6 b_treatmentMaz~ 3.06   3.04  0.442 0.431  2.37  3.81  1.00  7767.  10718.
## 7 b_treatmentTom~ 2.15   2.14  0.454 0.442  1.43  2.92  1.00  8803.  11145.
## 8 b_treatmentTom~ 2.84   2.82  0.410 0.402  2.20  3.55  1.00  8102.  11183.
## 9 b_treatmentTom~ 3.02   3.00  0.416 0.409  2.37  3.73  1.00  7917.  10161.
## 10 sd_father__tre~ 1.36   1.33  0.372 0.357  0.811 2.03  1.00  9598.  16625.
## # i 439 more rows

## heritability ridge plot #####
Posterior9Traits_sds_lc %>%
  ggplot(aes(x = herit,
             y = fct_rev(treat),
             # group = treat,
             fill = crop)) +
  geom_density_ridges(alpha = 0.3) +
  # facet_wrap(crop~fungus, nrow = 3,
  #             labeller = labeller(fungus = newfunglabs)) +
  lims(x = c(0,1)) +
  labs(x = "Heritability",
       y = "") +
  scale_fill_manual(labels = c("Soybean", "Maize", "Tomato"),
                    values = c("darkgreen", "gold", "maroon")) +
  scale_y_discrete(labels=expression(italic(Metarhizium), italic(Beauveria), Control, italic(Metarhizium)),
                    theme(legend.position = "top",
                          legend.title=element_blank(),
                          axis.text.x = element_text(size = 18),
                          axis.title = element_text(size = 24),
                          legend.text = element_text(size = 16)))

## Picking joint bandwidth of 0.0127

```



```

ggsave("outputs/Heritability_ridges.png",
       height = 20,
       width = 12,
       units = "cm")

## Picking joint bandwidth of 0.0127
# Extract sds for each trait for father and mother
Gmat9traitslong <- Gmat9traitswide %>%
  pivot_longer(treatmentMaz_BB:treatmentTom_MT,
               names_to = "Trait2",
               values_to = "Rg") %>%
  separate(Trait1,
           into = c("crop1","fungus1")) %>%
  separate(crop1,
           into = c("junk1","crop1"),
           sep = 9) %>%
  separate(Trait2,
           into = c("crop2","fungus2")) %>%
  separate(crop2,
           into = c("junk2","crop2"),
           sep = 9) %>%
  select(-junk1,-junk2) %>%
  distinct(Rg,
           .keep_all = TRUE) %>%
  filter(Rg != 1) %>%
  mutate(cropdiff = if_else(crop1 == crop2, 0, 1),
        fungdiff = if_else(fungus1 == fungus2, 0, 1),
        )

```

```

    diff_dims = cropdiff+fungdiff,
    funguscontrol = if_else(fungus1 == "CON" | fungus2 == "CON", "control", "2 fungi")) %>%
  mutate(diff_desc = if_else(diff_dims == 2, "both different",
                             if_else(cropdiff == 1, "crop different", "infection treatment different")))
# maybe plot differences in estimates for indiv correlations in mcmcglmm vs brms

# plot correlations 9-trait model long chains ####

Posteriors9Traits_lc <- as_tibble(as_draws_df(model.9traits.brm.matnocov.long))
names(Posteriors9Traits_lc)

## [1] "b_Intercept"
## [2] "b_treatmentSoya_BB"
## [3] "b_treatmentSoya_MT"
## [4] "b_treatmentMaz_CON"
## [5] "b_treatmentMaz_BB"
## [6] "b_treatmentMaz_MT"
## [7] "b_treatmentTom_CON"
## [8] "b_treatmentTom_BB"
## [9] "b_treatmentTom_MT"
## [10] "sd_father__treatmentSoya_CON"
## [11] "sd_father__treatmentSoya_BB"
## [12] "sd_father__treatmentSoya_MT"
## [13] "sd_father__treatmentMaz_CON"
## [14] "sd_father__treatmentMaz_BB"
## [15] "sd_father__treatmentMaz_MT"
## [16] "sd_father__treatmentTom_CON"
## [17] "sd_father__treatmentTom_BB"
## [18] "sd_father__treatmentTom_MT"
## [19] "sd_mother__Intercept"
## [20] "cor_father__treatmentSoya_CON__treatmentSoya_BB"
## [21] "cor_father__treatmentSoya_CON__treatmentSoya_MT"
## [22] "cor_father__treatmentSoya_BB__treatmentSoya_MT"
## [23] "cor_father__treatmentSoya_CON__treatmentMaz_CON"
## [24] "cor_father__treatmentSoya_BB__treatmentMaz_CON"
## [25] "cor_father__treatmentSoya_MT__treatmentMaz_CON"
## [26] "cor_father__treatmentSoya_CON__treatmentMaz_BB"
## [27] "cor_father__treatmentSoya_BB__treatmentMaz_BB"
## [28] "cor_father__treatmentSoya_MT__treatmentMaz_BB"
## [29] "cor_father__treatmentMaz_CON__treatmentMaz_BB"
## [30] "cor_father__treatmentSoya_CON__treatmentMaz_MT"
## [31] "cor_father__treatmentSoya_BB__treatmentMaz_MT"
## [32] "cor_father__treatmentSoya_MT__treatmentMaz_MT"
## [33] "cor_father__treatmentMaz_CON__treatmentMaz_MT"
## [34] "cor_father__treatmentMaz_BB__treatmentMaz_MT"
## [35] "cor_father__treatmentSoya_CON__treatmentTom_CON"
## [36] "cor_father__treatmentSoya_BB__treatmentTom_CON"
## [37] "cor_father__treatmentSoya_MT__treatmentTom_CON"
## [38] "cor_father__treatmentMaz_CON__treatmentTom_CON"
## [39] "cor_father__treatmentMaz_BB__treatmentTom_CON"
## [40] "cor_father__treatmentMaz_MT__treatmentTom_CON"
## [41] "cor_father__treatmentSoya_CON__treatmentTom_BB"

```

```

## [42] "cor_father__treatmentSoya_BB__treatmentTom_BB"
## [43] "cor_father__treatmentSoya_MT__treatmentTom_BB"
## [44] "cor_father__treatmentMaz_CON__treatmentTom_BB"
## [45] "cor_father__treatmentMaz_BB__treatmentTom_BB"
## [46] "cor_father__treatmentMaz_MT__treatmentTom_BB"
## [47] "cor_father__treatmentTom_CON__treatmentTom_BB"
## [48] "cor_father__treatmentSoya_CON__treatmentTom_MT"
## [49] "cor_father__treatmentSoya_BB__treatmentTom_MT"
## [50] "cor_father__treatmentSoya_MT__treatmentTom_MT"
## [51] "cor_father__treatmentMaz_CON__treatmentTom_MT"
## [52] "cor_father__treatmentMaz_BB__treatmentTom_MT"
## [53] "cor_father__treatmentMaz_MT__treatmentTom_MT"
## [54] "cor_father__treatmentTom_CON__treatmentTom_MT"
## [55] "cor_father__treatmentTom_BB__treatmentTom_MT"
## [56] "Intercept"
## [57] "r_father[S_1000,treatmentSoya_CON]"
## [58] "r_father[S_128,treatmentSoya_CON]"
## [59] "r_father[S_1330,treatmentSoya_CON]"
## [60] "r_father[S_1335,treatmentSoya_CON]"
## [61] "r_father[S_141,treatmentSoya_CON]"
## [62] "r_father[S_148,treatmentSoya_CON]"
## [63] "r_father[S_149,treatmentSoya_CON]"
## [64] "r_father[S_150,treatmentSoya_CON]"
## [65] "r_father[S_152,treatmentSoya_CON]"
## [66] "r_father[S_199,treatmentSoya_CON]"
## [67] "r_father[S_2000,treatmentSoya_CON]"
## [68] "r_father[S_209,treatmentSoya_CON]"
## [69] "r_father[S_212,treatmentSoya_CON]"
## [70] "r_father[S_214,treatmentSoya_CON]"
## [71] "r_father[S_224,treatmentSoya_CON]"
## [72] "r_father[S_225,treatmentSoya_CON]"
## [73] "r_father[S_232,treatmentSoya_CON]"
## [74] "r_father[S_245,treatmentSoya_CON]"
## [75] "r_father[S_250,treatmentSoya_CON]"
## [76] "r_father[S_254,treatmentSoya_CON]"
## [77] "r_father[S_257,treatmentSoya_CON]"
## [78] "r_father[S_282,treatmentSoya_CON]"
## [79] "r_father[S_288,treatmentSoya_CON]"
## [80] "r_father[S_290,treatmentSoya_CON]"
## [81] "r_father[S_292,treatmentSoya_CON]"
## [82] "r_father[S_295,treatmentSoya_CON]"
## [83] "r_father[S_297,treatmentSoya_CON]"
## [84] "r_father[S_62,treatmentSoya_CON]"
## [85] "r_father[S_63,treatmentSoya_CON]"
## [86] "r_father[S_64,treatmentSoya_CON]"
## [87] "r_father[S_65,treatmentSoya_CON]"
## [88] "r_father[S_67,treatmentSoya_CON]"
## [89] "r_father[S_69,treatmentSoya_CON]"
## [90] "r_father[S_71,treatmentSoya_CON]"
## [91] "r_father[S_74,treatmentSoya_CON]"
## [92] "r_father[S_75,treatmentSoya_CON]"
## [93] "r_father[S_76,treatmentSoya_CON]"
## [94] "r_father[S_1000,treatmentSoya_BB]"
## [95] "r_father[S_128,treatmentSoya_BB]"

```

```

## [96] "r_father[S_1330,treatmentSoya_BB]"
## [97] "r_father[S_1335,treatmentSoya_BB]"
## [98] "r_father[S_141,treatmentSoya_BB]"
## [99] "r_father[S_148,treatmentSoya_BB]"
## [100] "r_father[S_149,treatmentSoya_BB]"
## [101] "r_father[S_150,treatmentSoya_BB]"
## [102] "r_father[S_152,treatmentSoya_BB]"
## [103] "r_father[S_199,treatmentSoya_BB]"
## [104] "r_father[S_2000,treatmentSoya_BB]"
## [105] "r_father[S_209,treatmentSoya_BB]"
## [106] "r_father[S_212,treatmentSoya_BB]"
## [107] "r_father[S_214,treatmentSoya_BB]"
## [108] "r_father[S_224,treatmentSoya_BB]"
## [109] "r_father[S_225,treatmentSoya_BB]"
## [110] "r_father[S_232,treatmentSoya_BB]"
## [111] "r_father[S_245,treatmentSoya_BB]"
## [112] "r_father[S_250,treatmentSoya_BB]"
## [113] "r_father[S_254,treatmentSoya_BB]"
## [114] "r_father[S_257,treatmentSoya_BB]"
## [115] "r_father[S_282,treatmentSoya_BB]"
## [116] "r_father[S_288,treatmentSoya_BB]"
## [117] "r_father[S_290,treatmentSoya_BB]"
## [118] "r_father[S_292,treatmentSoya_BB]"
## [119] "r_father[S_295,treatmentSoya_BB]"
## [120] "r_father[S_297,treatmentSoya_BB]"
## [121] "r_father[S_62,treatmentSoya_BB]"
## [122] "r_father[S_63,treatmentSoya_BB]"
## [123] "r_father[S_64,treatmentSoya_BB]"
## [124] "r_father[S_65,treatmentSoya_BB]"
## [125] "r_father[S_67,treatmentSoya_BB]"
## [126] "r_father[S_69,treatmentSoya_BB]"
## [127] "r_father[S_71,treatmentSoya_BB]"
## [128] "r_father[S_74,treatmentSoya_BB]"
## [129] "r_father[S_75,treatmentSoya_BB]"
## [130] "r_father[S_76,treatmentSoya_BB]"
## [131] "r_father[S_1000,treatmentSoya_MT]"
## [132] "r_father[S_128,treatmentSoya_MT]"
## [133] "r_father[S_1330,treatmentSoya_MT]"
## [134] "r_father[S_1335,treatmentSoya_MT]"
## [135] "r_father[S_141,treatmentSoya_MT]"
## [136] "r_father[S_148,treatmentSoya_MT]"
## [137] "r_father[S_149,treatmentSoya_MT]"
## [138] "r_father[S_150,treatmentSoya_MT]"
## [139] "r_father[S_152,treatmentSoya_MT]"
## [140] "r_father[S_199,treatmentSoya_MT]"
## [141] "r_father[S_2000,treatmentSoya_MT]"
## [142] "r_father[S_209,treatmentSoya_MT]"
## [143] "r_father[S_212,treatmentSoya_MT]"
## [144] "r_father[S_214,treatmentSoya_MT]"
## [145] "r_father[S_224,treatmentSoya_MT]"
## [146] "r_father[S_225,treatmentSoya_MT]"
## [147] "r_father[S_232,treatmentSoya_MT]"
## [148] "r_father[S_245,treatmentSoya_MT]"
## [149] "r_father[S_250,treatmentSoya_MT]"

```

```

## [150] "r_father[S_254,treatmentSoya_MT]"
## [151] "r_father[S_257,treatmentSoya_MT]"
## [152] "r_father[S_282,treatmentSoya_MT]"
## [153] "r_father[S_288,treatmentSoya_MT]"
## [154] "r_father[S_290,treatmentSoya_MT]"
## [155] "r_father[S_292,treatmentSoya_MT]"
## [156] "r_father[S_295,treatmentSoya_MT]"
## [157] "r_father[S_297,treatmentSoya_MT]"
## [158] "r_father[S_62,treatmentSoya_MT]"
## [159] "r_father[S_63,treatmentSoya_MT]"
## [160] "r_father[S_64,treatmentSoya_MT]"
## [161] "r_father[S_65,treatmentSoya_MT]"
## [162] "r_father[S_67,treatmentSoya_MT]"
## [163] "r_father[S_69,treatmentSoya_MT]"
## [164] "r_father[S_71,treatmentSoya_MT]"
## [165] "r_father[S_74,treatmentSoya_MT]"
## [166] "r_father[S_75,treatmentSoya_MT]"
## [167] "r_father[S_76,treatmentSoya_MT]"
## [168] "r_father[S_1000,treatmentMaz_CON]"
## [169] "r_father[S_128,treatmentMaz_CON]"
## [170] "r_father[S_1330,treatmentMaz_CON]"
## [171] "r_father[S_1335,treatmentMaz_CON]"
## [172] "r_father[S_141,treatmentMaz_CON]"
## [173] "r_father[S_148,treatmentMaz_CON]"
## [174] "r_father[S_149,treatmentMaz_CON]"
## [175] "r_father[S_150,treatmentMaz_CON]"
## [176] "r_father[S_152,treatmentMaz_CON]"
## [177] "r_father[S_199,treatmentMaz_CON]"
## [178] "r_father[S_2000,treatmentMaz_CON]"
## [179] "r_father[S_209,treatmentMaz_CON]"
## [180] "r_father[S_212,treatmentMaz_CON]"
## [181] "r_father[S_214,treatmentMaz_CON]"
## [182] "r_father[S_224,treatmentMaz_CON]"
## [183] "r_father[S_225,treatmentMaz_CON]"
## [184] "r_father[S_232,treatmentMaz_CON]"
## [185] "r_father[S_245,treatmentMaz_CON]"
## [186] "r_father[S_250,treatmentMaz_CON]"
## [187] "r_father[S_254,treatmentMaz_CON]"
## [188] "r_father[S_257,treatmentMaz_CON]"
## [189] "r_father[S_282,treatmentMaz_CON]"
## [190] "r_father[S_288,treatmentMaz_CON]"
## [191] "r_father[S_290,treatmentMaz_CON]"
## [192] "r_father[S_292,treatmentMaz_CON]"
## [193] "r_father[S_295,treatmentMaz_CON]"
## [194] "r_father[S_297,treatmentMaz_CON]"
## [195] "r_father[S_62,treatmentMaz_CON]"
## [196] "r_father[S_63,treatmentMaz_CON]"
## [197] "r_father[S_64,treatmentMaz_CON]"
## [198] "r_father[S_65,treatmentMaz_CON]"
## [199] "r_father[S_67,treatmentMaz_CON]"
## [200] "r_father[S_69,treatmentMaz_CON]"
## [201] "r_father[S_71,treatmentMaz_CON]"
## [202] "r_father[S_74,treatmentMaz_CON]"
## [203] "r_father[S_75,treatmentMaz_CON]"

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## [204] "r_father[S_76,treatmentMaz_CON]"
## [205] "r_father[S_1000,treatmentMaz_BB]"
## [206] "r_father[S_128,treatmentMaz_BB]"
## [207] "r_father[S_1330,treatmentMaz_BB]"
## [208] "r_father[S_1335,treatmentMaz_BB]"
## [209] "r_father[S_141,treatmentMaz_BB]"
## [210] "r_father[S_148,treatmentMaz_BB]"
## [211] "r_father[S_149,treatmentMaz_BB]"
## [212] "r_father[S_150,treatmentMaz_BB]"
## [213] "r_father[S_152,treatmentMaz_BB]"
## [214] "r_father[S_199,treatmentMaz_BB]"
## [215] "r_father[S_2000,treatmentMaz_BB]"
## [216] "r_father[S_209,treatmentMaz_BB]"
## [217] "r_father[S_212,treatmentMaz_BB]"
## [218] "r_father[S_214,treatmentMaz_BB]"
## [219] "r_father[S_224,treatmentMaz_BB]"
## [220] "r_father[S_225,treatmentMaz_BB]"
## [221] "r_father[S_232,treatmentMaz_BB]"
## [222] "r_father[S_245,treatmentMaz_BB]"
## [223] "r_father[S_250,treatmentMaz_BB]"
## [224] "r_father[S_254,treatmentMaz_BB]"
## [225] "r_father[S_257,treatmentMaz_BB]"
## [226] "r_father[S_282,treatmentMaz_BB]"
## [227] "r_father[S_288,treatmentMaz_BB]"
## [228] "r_father[S_290,treatmentMaz_BB]"
## [229] "r_father[S_292,treatmentMaz_BB]"
## [230] "r_father[S_295,treatmentMaz_BB]"
## [231] "r_father[S_297,treatmentMaz_BB]"
## [232] "r_father[S_62,treatmentMaz_BB]"
## [233] "r_father[S_63,treatmentMaz_BB]"
## [234] "r_father[S_64,treatmentMaz_BB]"
## [235] "r_father[S_65,treatmentMaz_BB]"
## [236] "r_father[S_67,treatmentMaz_BB]"
## [237] "r_father[S_69,treatmentMaz_BB]"
## [238] "r_father[S_71,treatmentMaz_BB]"
## [239] "r_father[S_74,treatmentMaz_BB]"
## [240] "r_father[S_75,treatmentMaz_BB]"
## [241] "r_father[S_76,treatmentMaz_BB]"
## [242] "r_father[S_1000,treatmentMaz_MT]"
## [243] "r_father[S_128,treatmentMaz_MT]"
## [244] "r_father[S_1330,treatmentMaz_MT]"
## [245] "r_father[S_1335,treatmentMaz_MT]"
## [246] "r_father[S_141,treatmentMaz_MT]"
## [247] "r_father[S_148,treatmentMaz_MT]"
## [248] "r_father[S_149,treatmentMaz_MT]"
## [249] "r_father[S_150,treatmentMaz_MT]"
## [250] "r_father[S_152,treatmentMaz_MT]"
## [251] "r_father[S_199,treatmentMaz_MT]"
## [252] "r_father[S_2000,treatmentMaz_MT]"
## [253] "r_father[S_209,treatmentMaz_MT]"
## [254] "r_father[S_212,treatmentMaz_MT]"
## [255] "r_father[S_214,treatmentMaz_MT]"
## [256] "r_father[S_224,treatmentMaz_MT]"
## [257] "r_father[S_225,treatmentMaz_MT]"

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## [258] "r_father[S_232,treatmentMaz_MT]"
## [259] "r_father[S_245,treatmentMaz_MT]"
## [260] "r_father[S_250,treatmentMaz_MT]"
## [261] "r_father[S_254,treatmentMaz_MT]"
## [262] "r_father[S_257,treatmentMaz_MT]"
## [263] "r_father[S_282,treatmentMaz_MT]"
## [264] "r_father[S_288,treatmentMaz_MT]"
## [265] "r_father[S_290,treatmentMaz_MT]"
## [266] "r_father[S_292,treatmentMaz_MT]"
## [267] "r_father[S_295,treatmentMaz_MT]"
## [268] "r_father[S_297,treatmentMaz_MT]"
## [269] "r_father[S_62,treatmentMaz_MT]"
## [270] "r_father[S_63,treatmentMaz_MT]"
## [271] "r_father[S_64,treatmentMaz_MT]"
## [272] "r_father[S_65,treatmentMaz_MT]"
## [273] "r_father[S_67,treatmentMaz_MT]"
## [274] "r_father[S_69,treatmentMaz_MT]"
## [275] "r_father[S_71,treatmentMaz_MT]"
## [276] "r_father[S_74,treatmentMaz_MT]"
## [277] "r_father[S_75,treatmentMaz_MT]"
## [278] "r_father[S_76,treatmentMaz_MT]"
## [279] "r_father[S_1000,treatmentTom_CON]"
## [280] "r_father[S_128,treatmentTom_CON]"
## [281] "r_father[S_1330,treatmentTom_CON]"
## [282] "r_father[S_1335,treatmentTom_CON]"
## [283] "r_father[S_141,treatmentTom_CON]"
## [284] "r_father[S_148,treatmentTom_CON]"
## [285] "r_father[S_149,treatmentTom_CON]"
## [286] "r_father[S_150,treatmentTom_CON]"
## [287] "r_father[S_152,treatmentTom_CON]"
## [288] "r_father[S_199,treatmentTom_CON]"
## [289] "r_father[S_2000,treatmentTom_CON]"
## [290] "r_father[S_209,treatmentTom_CON]"
## [291] "r_father[S_212,treatmentTom_CON]"
## [292] "r_father[S_214,treatmentTom_CON]"
## [293] "r_father[S_224,treatmentTom_CON]"
## [294] "r_father[S_225,treatmentTom_CON]"
## [295] "r_father[S_232,treatmentTom_CON]"
## [296] "r_father[S_245,treatmentTom_CON]"
## [297] "r_father[S_250,treatmentTom_CON]"
## [298] "r_father[S_254,treatmentTom_CON]"
## [299] "r_father[S_257,treatmentTom_CON]"
## [300] "r_father[S_282,treatmentTom_CON]"
## [301] "r_father[S_288,treatmentTom_CON]"
## [302] "r_father[S_290,treatmentTom_CON]"
## [303] "r_father[S_292,treatmentTom_CON]"
## [304] "r_father[S_295,treatmentTom_CON]"
## [305] "r_father[S_297,treatmentTom_CON]"
## [306] "r_father[S_62,treatmentTom_CON]"
## [307] "r_father[S_63,treatmentTom_CON]"
## [308] "r_father[S_64,treatmentTom_CON]"
## [309] "r_father[S_65,treatmentTom_CON]"
## [310] "r_father[S_67,treatmentTom_CON]"
## [311] "r_father[S_69,treatmentTom_CON]"

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## [312] "r_father[S_71,treatmentTom_CON]"
## [313] "r_father[S_74,treatmentTom_CON]"
## [314] "r_father[S_75,treatmentTom_CON]"
## [315] "r_father[S_76,treatmentTom_CON]"
## [316] "r_father[S_1000,treatmentTom_BB]"
## [317] "r_father[S_128,treatmentTom_BB]"
## [318] "r_father[S_1330,treatmentTom_BB]"
## [319] "r_father[S_1335,treatmentTom_BB]"
## [320] "r_father[S_141,treatmentTom_BB]"
## [321] "r_father[S_148,treatmentTom_BB]"
## [322] "r_father[S_149,treatmentTom_BB]"
## [323] "r_father[S_150,treatmentTom_BB]"
## [324] "r_father[S_152,treatmentTom_BB]"
## [325] "r_father[S_199,treatmentTom_BB]"
## [326] "r_father[S_2000,treatmentTom_BB]"
## [327] "r_father[S_209,treatmentTom_BB]"
## [328] "r_father[S_212,treatmentTom_BB]"
## [329] "r_father[S_214,treatmentTom_BB]"
## [330] "r_father[S_224,treatmentTom_BB]"
## [331] "r_father[S_225,treatmentTom_BB]"
## [332] "r_father[S_232,treatmentTom_BB]"
## [333] "r_father[S_245,treatmentTom_BB]"
## [334] "r_father[S_250,treatmentTom_BB]"
## [335] "r_father[S_254,treatmentTom_BB]"
## [336] "r_father[S_257,treatmentTom_BB]"
## [337] "r_father[S_282,treatmentTom_BB]"
## [338] "r_father[S_288,treatmentTom_BB]"
## [339] "r_father[S_290,treatmentTom_BB]"
## [340] "r_father[S_292,treatmentTom_BB]"
## [341] "r_father[S_295,treatmentTom_BB]"
## [342] "r_father[S_297,treatmentTom_BB]"
## [343] "r_father[S_62,treatmentTom_BB]"
## [344] "r_father[S_63,treatmentTom_BB]"
## [345] "r_father[S_64,treatmentTom_BB]"
## [346] "r_father[S_65,treatmentTom_BB]"
## [347] "r_father[S_67,treatmentTom_BB]"
## [348] "r_father[S_69,treatmentTom_BB]"
## [349] "r_father[S_71,treatmentTom_BB]"
## [350] "r_father[S_74,treatmentTom_BB]"
## [351] "r_father[S_75,treatmentTom_BB]"
## [352] "r_father[S_76,treatmentTom_BB]"
## [353] "r_father[S_1000,treatmentTom_MT]"
## [354] "r_father[S_128,treatmentTom_MT]"
## [355] "r_father[S_1330,treatmentTom_MT]"
## [356] "r_father[S_1335,treatmentTom_MT]"
## [357] "r_father[S_141,treatmentTom_MT]"
## [358] "r_father[S_148,treatmentTom_MT]"
## [359] "r_father[S_149,treatmentTom_MT]"
## [360] "r_father[S_150,treatmentTom_MT]"
## [361] "r_father[S_152,treatmentTom_MT]"
## [362] "r_father[S_199,treatmentTom_MT]"
## [363] "r_father[S_2000,treatmentTom_MT]"
## [364] "r_father[S_209,treatmentTom_MT]"
## [365] "r_father[S_212,treatmentTom_MT]"

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## [366] "r_father[S_214,treatmentTom_MT]"
## [367] "r_father[S_224,treatmentTom_MT]"
## [368] "r_father[S_225,treatmentTom_MT]"
## [369] "r_father[S_232,treatmentTom_MT]"
## [370] "r_father[S_245,treatmentTom_MT]"
## [371] "r_father[S_250,treatmentTom_MT]"
## [372] "r_father[S_254,treatmentTom_MT]"
## [373] "r_father[S_257,treatmentTom_MT]"
## [374] "r_father[S_282,treatmentTom_MT]"
## [375] "r_father[S_288,treatmentTom_MT]"
## [376] "r_father[S_290,treatmentTom_MT]"
## [377] "r_father[S_292,treatmentTom_MT]"
## [378] "r_father[S_295,treatmentTom_MT]"
## [379] "r_father[S_297,treatmentTom_MT]"
## [380] "r_father[S_62,treatmentTom_MT]"
## [381] "r_father[S_63,treatmentTom_MT]"
## [382] "r_father[S_64,treatmentTom_MT]"
## [383] "r_father[S_65,treatmentTom_MT]"
## [384] "r_father[S_67,treatmentTom_MT]"
## [385] "r_father[S_69,treatmentTom_MT]"
## [386] "r_father[S_71,treatmentTom_MT]"
## [387] "r_father[S_74,treatmentTom_MT]"
## [388] "r_father[S_75,treatmentTom_MT]"
## [389] "r_father[S_76,treatmentTom_MT]"
## [390] "r_mother[D_117,Intercept]"
## [391] "r_mother[D_12,Intercept]"
## [392] "r_mother[D_13,Intercept]"
## [393] "r_mother[D_1332,Intercept]"
## [394] "r_mother[D_1337,Intercept]"
## [395] "r_mother[D_14,Intercept]"
## [396] "r_mother[D_157,Intercept]"
## [397] "r_mother[D_164,Intercept]"
## [398] "r_mother[D_165,Intercept]"
## [399] "r_mother[D_166,Intercept]"
## [400] "r_mother[D_167,Intercept]"
## [401] "r_mother[D_171,Intercept]"
## [402] "r_mother[D_173,Intercept]"
## [403] "r_mother[D_185,Intercept]"
## [404] "r_mother[D_198,Intercept]"
## [405] "r_mother[D_199,Intercept]"
## [406] "r_mother[D_20,Intercept]"
## [407] "r_mother[D_207,Intercept]"
## [408] "r_mother[D_216,Intercept]"
## [409] "r_mother[D_22,Intercept]"
## [410] "r_mother[D_224,Intercept]"
## [411] "r_mother[D_225,Intercept]"
## [412] "r_mother[D_228,Intercept]"
## [413] "r_mother[D_230,Intercept]"
## [414] "r_mother[D_234,Intercept]"
## [415] "r_mother[D_235,Intercept]"
## [416] "r_mother[D_236,Intercept]"
## [417] "r_mother[D_242,Intercept]"
## [418] "r_mother[D_25,Intercept]"
## [419] "r_mother[D_261,Intercept]"

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## [420] "r_mother[D_267,Intercept]"
## [421] "r_mother[D_276,Intercept]"
## [422] "r_mother[D_279,Intercept]"
## [423] "r_mother[D_28,Intercept]"
## [424] "r_mother[D_288,Intercept]"
## [425] "r_mother[D_29,Intercept]"
## [426] "r_mother[D_30,Intercept]"
## [427] "r_mother[D_31,Intercept]"
## [428] "r_mother[D_33,Intercept]"
## [429] "r_mother[D_34,Intercept]"
## [430] "r_mother[D_40,Intercept]"
## [431] "r_mother[D_42,Intercept]"
## [432] "r_mother[D_45,Intercept]"
## [433] "r_mother[D_48,Intercept]"
## [434] "r_mother[D_49,Intercept]"
## [435] "r_mother[D_50,Intercept]"
## [436] "r_mother[D_51,Intercept]"
## [437] "r_mother[D_52,Intercept]"
## [438] "r_mother[D_56,Intercept]"
## [439] "r_mother[D_58,Intercept]"
## [440] "r_mother[D_60,Intercept]"
## [441] "r_mother[D_61,Intercept]"
## [442] "r_mother[D_62,Intercept]"
## [443] "r_mother[D_66,Intercept]"
## [444] "r_mother[D_7,Intercept]"
## [445] "r_mother[D_71,Intercept]"
## [446] "r_mother[D_7490,Intercept]"
## [447] "r_mother[D_7495,Intercept]"
## [448] "lprior"
## [449] "lp_"
## [450] ".chain"
## [451] ".iteration"
## [452] ".draw"

Posterior9Traits_long_lc <- Posteriors9Traits_lc %>%
  select(cor_father__treatmentSoya_CON__treatmentSoya_BB:
         cor_father__treatmentTom_BB__treatmentTom_MT) %>%
  pivot_longer(cor_father__treatmentSoya_CON__treatmentSoya_BB:
               cor_father__treatmentTom_BB__treatmentTom_MT,
               names_to = "traits",
               values_to = "Rg") %>%
  mutate(treat = traits) %>%
  separate(traits, into = c("junk", "junk2", "crop1",
                           "fungus1", "crop2", "fungus2")) %>%
  select(-junk, -junk2) %>%
  separate(crop1,
           into = c("junk3", "crop1"),
           sep = 9) %>%
  separate(crop2,
           into = c("junk4", "crop2"),
           sep = 9) %>%
  select(-junk3, -junk4) %>%
  mutate(cropdiff = if_else(crop1 == crop2, 0, 1),
        fungdiff = if_else(fungus1 == fungus2, 0, 1),

```

```

diff_dims = cropdiff+fungdiff,
funguscontrol = if_else(fungus1 == "CON" | fungus2 == "CON", "control", "2 fungi")) %>%
mutate(diff_desc = if_else(diff_dims == 2, "both different",
                           if_else(cropdiff == 1, "crop different", "infection treatment different")))
mutate(treat1 = paste(crop1,fungus1, sep = "_"),
       treat2 = paste(crop2,fungus2, sep = "_"))

# change order of levels
levels(factor(Posterior9Traits_long_lc$treat1))

## [1] "Maz_BB"    "Maz_CON"   "Maz_MT"    "Soya_BB"   "Soya_CON"  "Soya_MT"   "Tom_BB"
## [8] "Tom_CON"

names(Posterior9Traits_long_lc)

## [1] "crop1"           "fungus1"         "crop2"           "fungus2"
## [5] "Rg"              "treat"            "cropdiff"        "fungdiff"
## [9] "diff_dims"       "funguscontrol"  "diff_desc"       "treat1"
## [13] "treat2"

Posterior9Traits_long_lc <- Posterior9Traits_long_lc %>%
  mutate(crop1 = fct_relevel(crop1, "Soya", "Maz", "Tom"),
         fungus1 = fct_relevel(fungus1, "CON", "BB", "MT"),
         treat1 = fct_relevel(treat1, "Soya_CON", "Soya_BB", "Soya_MT",
                               "Maz_CON", "Maz_BB", "Maz_MT",
                               "Tom_CON", "Tom_BB"),
         crop2 = fct_relevel(crop2, "Soya", "Maz", "Tom"),
         fungus2 = fct_relevel(fungus2, "CON", "BB", "MT"),
         diff_desc = fct_relevel(diff_desc, "crop different", "infection treatment different", "both di",
         treat2 = fct_relevel(treat2, "Soya_BB", "Soya_MT",
                               "Maz_CON", "Maz_BB", "Maz_MT",
                               "Tom_CON", "Tom_BB", "Tom_MT"),
         treatshort = paste(treat1,treat2),
         treatshort = fct_relevel(treatshort,
                                   "Soya_CON Soya_BB",
                                   "Soya_CON Soya_MT",
                                   "Soya_CON Maz_CON",
                                   "Soya_CON Maz_BB",
                                   "Soya_CON Maz_MT",
                                   "Soya_CON Tom_CON",
                                   "Soya_CON Tom_BB",
                                   "Soya_CON Tom_MT",
                                   "Soya_BB Soya_MT",
                                   "Soya_BB Maz_CON",
                                   "Soya_BB Maz_BB",
                                   "Soya_BB Maz_MT",
                                   "Soya_BB Tom_CON",
                                   "Soya_BB Tom_BB",
                                   "Soya_BB Tom_MT",
                                   "Soya_MT Maz_CON",
                                   "Soya_MT Maz_BB",
                                   "Soya_MT Maz_MT",
                                   "Soya_MT Tom_CON",
                                   "Soya_MT Tom_BB")

```

```

    "Soya_MT Tom_MT" ,
    "Maz_CON Maz_BB" ,
    "Maz_CON Maz_MT" ,
    "Maz_CON Tom_CON" ,
    "Maz_CON Tom_BB" ,
    "Maz_CON Tom_MT" ,
    "Maz_BB Maz_MT" ,
    "Maz_BB Tom_CON" ,
    "Maz_BB Tom_BB" ,
    "Maz_BB Tom_MT" ,
    "Maz_MT Tom_CON" ,
    "Maz_MT Tom_BB" ,
    "Maz_MT Tom_MT" ,
    "Tom_CON Tom_BB" ,
    "Tom_CON Tom_MT" ,
    "Tom_BB Tom_MT"))
}

levels(factor(Posterior9Traits_long_lc$treatshort))

## [1] "Soya_CON Soya_BB" "Soya_CON Soya_MT" "Soya_CON Maz_CON" "Soya_CON Maz_BB"
## [5] "Soya_CON Maz_MT" "Soya_CON Tom_CON" "Soya_CON Tom_BB" "Soya_CON Tom_MT"
## [9] "Soya_BB Soya_MT" "Soya_BB Maz_CON" "Soya_BB Maz_BB" "Soya_BB Maz_MT"
## [13] "Soya_BB Tom_CON" "Soya_BB Tom_BB" "Soya_BB Tom_MT" "Soya_MT Maz_CON"
## [17] "Soya_MT Maz_BB" "Soya_MT Maz_MT" "Soya_MT Tom_CON" "Soya_MT Tom_BB"
## [21] "Soya_MT Tom_MT" "Maz_CON Maz_BB" "Maz_CON Maz_MT" "Maz_CON Tom_CON"
## [25] "Maz_CON Tom_BB" "Maz_CON Tom_MT" "Maz_BB Maz_MT" "Maz_BB Tom_CON"
## [29] "Maz_BB Tom_BB" "Maz_BB Tom_MT" "Maz_MT Tom_CON" "Maz_MT Tom_BB"
## [33] "Maz_MT Tom_MT" "Tom_CON Tom_BB" "Tom_CON Tom_MT" "Tom_BB Tom_MT"

## create new labels for treatments ####

newcroplabs <- c("Maize", "Soybean",
                  "Tomato")
names(newcroplabs) <- c("Maz", "Soya",
                           "Tom")

newfunglabs <- c("Beauveria", "Control",
                  "Metarhizium")
names(newfunglabs) <- c("BB", "CON",
                           "MT")

## Genetic correlation ridges ####

facet_names <- as_labeller(c(`1` = "1D difference",
                             `2` = "2D difference"))

names(Posterior9Traits_long_lc)

## [1] "crop1"          "fungus1"        "crop2"          "fungus2"
## [5] "Rg"             "treat"          "cropdiff"       "fungdiff"
## [9] "diff_dims"      "funguscontrol" "diff_desc"      "treat1"

```

```

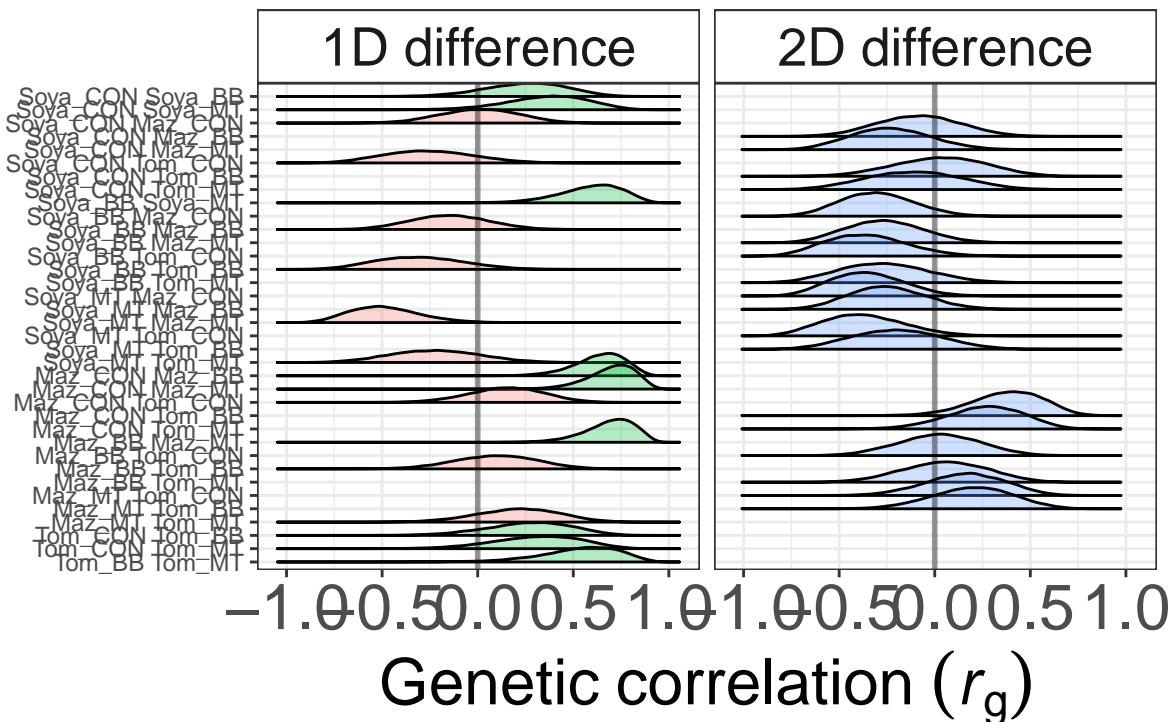
## [13] "treat2"           "treatshort"
Posterior9Traits_long_lc %>%
  ggplot(aes(x = Rg,
             y = fct_rev(treatshort),
             group = treatshort,
             fill = factor(diff_desc))) +
  geom_density_ridges2(alpha = 0.3) +
  facet_wrap(~ diff_dims,
             labeller = facet_names) +
  geom_vline(xintercept = 0,
             linetype = 1,
             size = 1,
             alpha = 0.4) +
  labs(x = expression(Genetic~correlation~italic(r)[g])),
  y = "") +
  theme(legend.position = "top",
        legend.title=element_blank(),
        axis.text.x = element_text(size = 24),
        axis.title = element_text(size = 24),
        legend.text = element_text(size = 18),
        strip.text = element_text(size = 20),
        strip.background = element_rect(fill="white" ))

```

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
This warning is displayed once every 8 hours.
Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
generated.

Picking joint bandwidth of 0.0222
Picking joint bandwidth of 0.0239

crop different infection treatment different bot

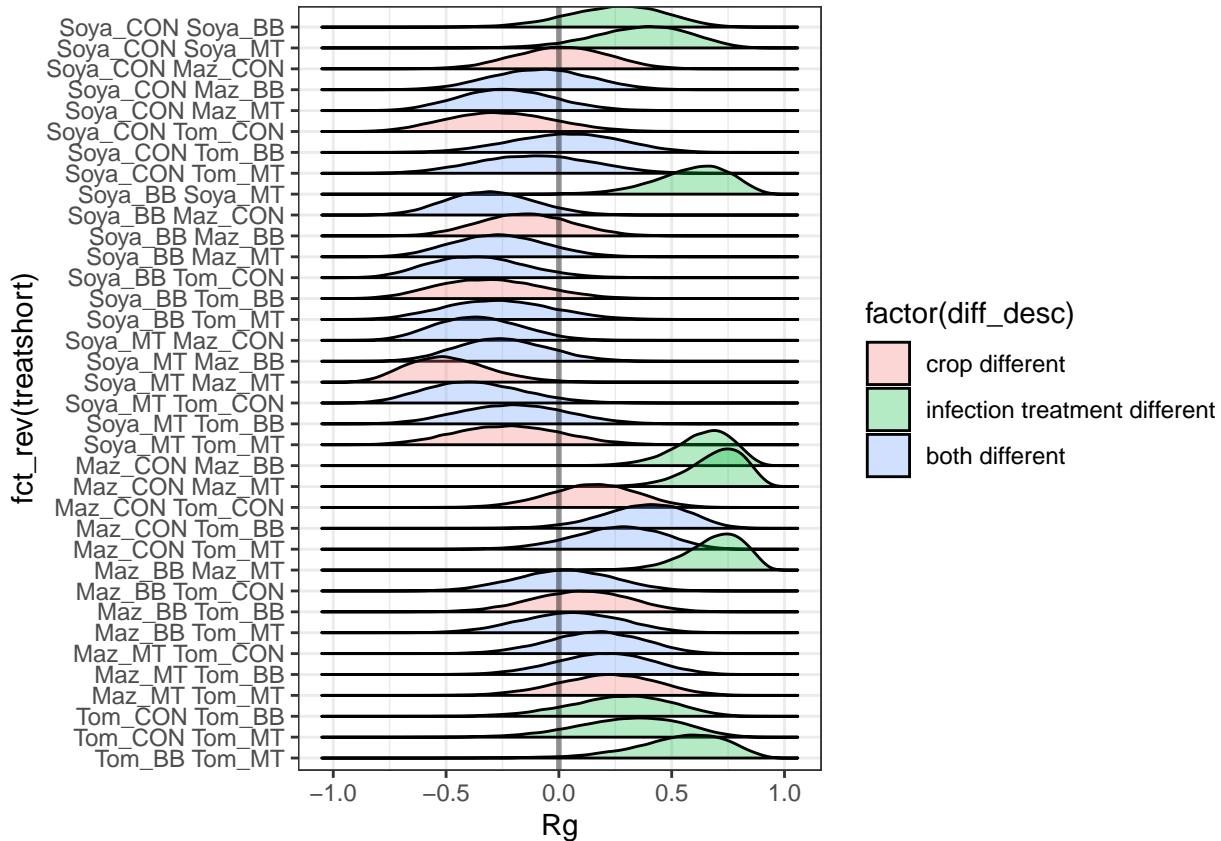


```
ggsave("outputs/RGsRidgeFacetDiffDesc.png",
       height = 30,
       width = 25,
       units = "cm",
       bg = "white")
```

```
## Picking joint bandwidth of 0.0222
## Picking joint bandwidth of 0.0239

Posterior9Traits_long_lc %>%
  ggplot(aes(x = Rg,
             y = fct_rev(treatshort),
             group = treatshort,
             fill = factor(diff_desc))) +
  geom_density_ridges2(alpha = 0.3) +
  geom_vline(xintercept = 0,
             linetype = 1,
             size = 1,
             alpha = 0.4)
```

```
## Picking joint bandwidth of 0.023
```

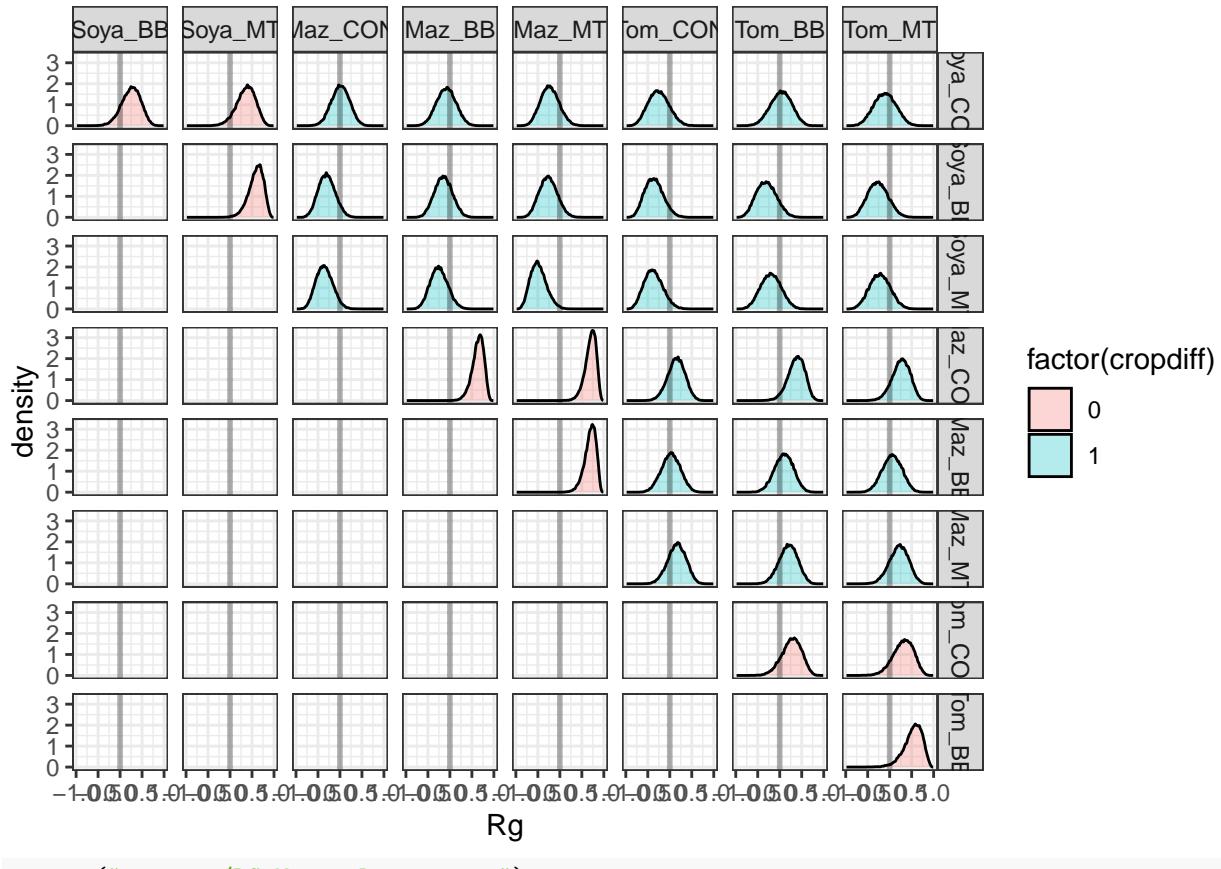


```
ggsave("outputs/RGsRidgeSingleDiffDesc.png")
```

```
## Saving 6.5 x 4.5 in image
## Picking joint bandwidth of 0.023

Posterior9Traits_long_lc %>%
  ggplot(aes(x = Rg,
             y = ..density..,
             group = treat,
             fill = factor(cropdiff))) +
  geom_density(adjust = 1/2,
               alpha = 0.3,
               bw = 0.02) +
  facet_grid(treat1~treat2) +
  geom_vline(xintercept = 0,
             linetype = 1,
             size = 1,
             alpha = 0.3)

## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



```
ggsave("outputs/RGsMatrixLayout.png")
```

```
## Saving 6.5 x 4.5 in image
```

```
# reaction norm plots #####
```

```
## calc sire level survival by treat comb #####
df_qgen_sub_sirecols <- df_qgen_sub_df %>%
  group_by(father, treatment) %>%
  summarise(Famsize = n(),
            Dead = sum(MORTday14,
                        na.rm = TRUE),
            Alive = Famsize - Dead,
            prop_mort = mean(MORTday14,
                              na.rm = TRUE)) %>%
  ungroup()
```

```
## `summarise()` has grouped output by 'father'. You can override using the
## `.groups` argument.
```

```
# compute CIs for mortality
df_qgen_sire_cis <- binom.confint(
  x = df_qgen_sub_sirecols$Dead,
  n = df_qgen_sub_sirecols$Famsize,
  methods = "exact") %>%
  rename(PropMort = mean,
        FamSize2 = n)
```

```

df_qgen_sire_data <- bind_cols(df_qgen_sub_sirecols,
                                df_qgen_sire_cis) %>%
  select(-method, -x, -PropMort, -FamSize2)

## compute spearman correlations #####
names(df_qgen_sire_data)

## [1] "father"      "treatment"   "Famsize"     "Dead"        "Alive"       "prop_mort"
## [7] "lower"        "upper"

df_qgen_sire_morts_wide <- df_qgen_sire_data %>%
  select(father, prop_mort, treatment) %>%
  pivot_wider(names_from = treatment,
              values_from = prop_mort)

df_qgen_sire_morts_wide <- as.matrix(df_qgen_sire_morts_wide)

rcorr(df_qgen_sire_morts_wide[,2:10],
      type = "spearman")

##          Soya_CON Soya_BB Soya_MT Maz_CON Maz_BB Maz_MT Tom_CON Tom_BB Tom_MT
## Soya_CON    1.00    0.36    0.32    0.02   -0.04   -0.17   -0.19    0.04    0.08
## Soya_BB     0.36    1.00    0.62   -0.18   -0.11   -0.17   -0.33   -0.18   -0.12
## Soya_MT     0.32    0.62    1.00   -0.19   -0.22   -0.33   -0.20   -0.05   -0.02
## Maz_CON     0.02   -0.18   -0.19    1.00    0.74    0.78    0.26    0.42    0.44
## Maz_BB     -0.04   -0.11   -0.22    0.74    1.00    0.77    0.19    0.28    0.21
## Maz_MT     -0.17   -0.17   -0.33    0.78    0.77    1.00    0.24    0.25    0.27
## Tom_CON    -0.19   -0.33   -0.20    0.26    0.19    0.24    1.00    0.45    0.35
## Tom_BB      0.04   -0.18   -0.05    0.42    0.28    0.25    0.45    1.00    0.59
## Tom_MT      0.08   -0.12   -0.02    0.44    0.21    0.27    0.35    0.59    1.00
##
## n
##          Soya_CON Soya_BB Soya_MT Maz_CON Maz_BB Maz_MT Tom_CON Tom_BB Tom_MT
## Soya_CON     37      37      37      37      37      37      36      37      37
## Soya_BB      37      37      37      37      37      37      36      37      37
## Soya_MT      37      37      37      37      37      37      36      37      37
## Maz_CON      37      37      37      37      37      37      36      37      37
## Maz_BB       37      37      37      37      37      37      36      37      37
## Maz_MT       37      37      37      37      37      37      36      37      37
## Tom_CON      36      36      36      36      36      36      36      36      36
## Tom_BB       37      37      37      37      37      37      36      37      37
## Tom_MT       37      37      37      37      37      37      36      37      37
##
## P
##          Soya_CON Soya_BB Soya_MT Maz_CON Maz_BB Maz_MT Tom_CON Tom_BB Tom_MT
## Soya_CON     0.0294  0.0543  0.9117  0.8292  0.3053  0.2762  0.7927  0.6235
## Soya_BB      0.0294           0.0000  0.2872  0.5020  0.3241  0.0460  0.2993  0.4697
## Soya_MT      0.0543  0.0000           0.2718  0.2001  0.0448  0.2466  0.7723  0.9067
## Maz_CON      0.9117  0.2872  0.2718           0.0000  0.0000  0.1308  0.0088  0.0064
## Maz_BB       0.8292  0.5020  0.2001  0.0000           0.0000  0.2674  0.0885  0.2133
## Maz_MT       0.3053  0.3241  0.0448  0.0000  0.0000           0.1666  0.1283  0.1034
## Tom_CON      0.2762  0.0460  0.2466  0.1308  0.2674  0.1666           0.0060  0.0387
## Tom_BB       0.7927  0.2993  0.7723  0.0088  0.0885  0.1283  0.0060           0.0001

```

```

## Tom_MT 0.6235 0.4697 0.9067 0.0064 0.2133 0.1034 0.0387 0.0001
# create subset and arrange by soyaBB
df_qgen_sire_data_soyBB <- df_qgen_sire_data %>%
  filter(treatment == "Soya_BB") %>%
  arrange(prop_mort)

df_qgen_sire_data$father <- factor(df_qgen_sire_data$father, levels = df_qgen_sire_data_soyBB$father[order(levels(df_qgen_sire_data_soyBB$father))])

## [1] "S_1000"  "S_128"   "S_1330"  "S_1335"  "S_141"   "S_148"   "S_149"   "S_150"
## [9] "S_152"   "S_199"   "S_2000"  "S_209"   "S_212"   "S_214"   "S_224"   "S_225"
## [17] "S_232"   "S_245"   "S_250"   "S_254"   "S_257"   "S_282"   "S_288"   "S_290"
## [25] "S_292"   "S_295"   "S_297"   "S_62"    "S_63"    "S_64"    "S_65"    "S_67"
## [33] "S_69"    "S_71"    "S_74"    "S_75"    "S_76"

# colour fathers to highlight a few
df_qgen_sire_data <- df_qgen_sire_data %>%
  mutate(father_colour = if_else(
    father == "S_288", "2",
    if_else(father == "S_250", "3",
           if_else(father == "S_1335", "4",
                  if_else(father == "S_214", "5",
                         "1"))))

cbbPalette <- c("gray40", "#E69F00", "#0072B2", "#CC79A7", "#009E73", "#F0E442", "#56B4E9", "#D55E00" )

colnames(df_qgen_sire_data)

## [1] "father"        "treatment"      "Famsize"       "Dead"
## [5] "Alive"         "prop_mort"      "lower"         "upper"
## [9] "father_colour"

## individual panels #####
SoyaBB_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Soya_BB") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  labs(x="Sire Identity",
       y="Beauveria",
       title = "Soybean") +
  lims(y = c(0,1)) +
  guides(colour="none") +
  scale_colour_manual(values=cbbPalette) +
  theme(axis.text.x = element_blank(),
        # axis.text.y = element_blank(),
        axis.title.y=element_text(face="italic"),
        # axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        plot.title = element_text(hjust = 0.5,
                                  vjust = 0,

```

```

            size = 24),
axis.text = element_text(size = 24),
axis.title = element_text(size = 24)
)

SoyaMT_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Soya_MT") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  labs(x="Sire Identity",
       y="Metarhizium") +
  lims(y = c(0,1)) +
  scale_colour_manual(values=cbbPalette) +
  guides(colour="none") +
  theme(axis.text.x = element_blank(),
        # axis.text.y = element_blank(),
        axis.title.y=element_text(face="italic"),
        # axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24)
  )

SoyaCON_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Soya_CON") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  labs(x="Sire Identity",
       y="Control") +
  lims(y = c(0,1)) +
  scale_colour_manual(values=cbbPalette) +
  guides(colour="none") +
  theme(axis.text.x = element_blank(),
        # axis.text.y = element_blank(),
        # axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24)
  )

MaizeBB_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Maz_BB") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  labs(x="Sire Identity",

```

```

y="Mortality",
  title = "Maize")+
scale_colour_manual(values=cbbPalette) +
lims(y = c(0,1)) +
guides(colour="none") +
theme(axis.text.x = element_blank(),
      #axis.text.y = element_blank(),
      axis.title.y=element_blank(),
      axis.title.x=element_blank(),
      plot.title = element_text(hjust = 0.5,
                                 vjust = 0,
                                 size = 24),
      axis.text = element_text(size = 24),
      axis.title = element_text(size = 24)
)

MaizeMT_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Maz_MT") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  labs(x="Sire Identity",
       y="") +
  scale_colour_manual(values=cbbPalette) +
  lims(y = c(0,1)) +
  guides(colour="none") +
  theme(axis.text.x = element_blank(),
        #axis.text.y = element_blank(),
        axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24)
)

MaizeCON_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Maz_CON") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  labs(x="Sire Identity",
       y="") +
  scale_colour_manual(values=cbbPalette) +
  lims(y = c(0,1)) +
  guides(colour="none") +
  theme(axis.text.x = element_blank(),
        #axis.text.y = element_blank(),
        axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24)
)

```

```

TomBB_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Tom_BB") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  scale_colour_manual(values=cbbPalette) +
  labs(x="Sire Identity",
       y="Mortality",
       title = "Tomato")+
  lims(y = c(0,1)) +
  guides(colour="none") +
  theme(axis.text.x = element_blank(),
        #axis.text.y = element_blank(),
        axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        plot.title = element_text(hjust = 0.5,
                                  vjust = 0,
                                  size = 24),
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24)
  )

TomMT_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Tom_MT") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  scale_colour_manual(values=cbbPalette) +
  labs(x="Sire Identity",
       y="")+
  lims(y = c(0,1)) +
  guides(colour="none") +
  theme(axis.text.x = element_blank(),
        #axis.text.y = element_blank(),
        axis.title.y=element_blank(),
        axis.title.x=element_blank(),
        axis.text = element_text(size = 24),
        axis.title = element_text(size = 24)
  )

TomCON_SireMort <- df_qgen_sire_data %>%
  filter(treatment == "Tom_CON") %>%
  ggplot(aes(x = father, y = prop_mort)) +
  geom_pointrange(aes(ymin = lower,
                       ymax = upper,
                       colour = father_colour)) +
  scale_colour_manual(values=cbbPalette) +
  labs(x="Sire Identity",
       y="")+

```

```

lims(y = c(0,1)) +
guides(colour="none") +
theme(axis.text.x = element_blank(),
      #axis.text.y = element_blank(),
      axis.title.y=element_blank(),
      axis.title.x=element_blank(),
      axis.text = element_text(size = 24),
      axis.title = element_text(size = 24)
)

## ggarrange 9 panels #####
rxnnorms9panel <- ggarrange(SoyaBB_SireMort, MaizeBB_SireMort,
                             TomBB_SireMort, SoyaMT_SireMort,
                             MaizeMT_SireMort, TomMT_SireMort,
                             SoyaCON_SireMort, MaizeCON_SireMort,
                             TomCON_SireMort,
                             labels = c("1.00",
                                       "-0.04",
                                       "0.01",
                                       "0.68",
                                       "-0.04",
                                       "0.01",
                                       "0.54",
                                       "-0.13",
                                       "-0.02"),
                             label.x = c(0.3,0.8,0.18,
                                       0.3,0.8,0.18,
                                       0.3,0.8,0.16),
                             label.y = c(0.83,0.16,0.16,
                                       0.95,0.16,0.16,
                                       0.95,0.16,0.16),
                             # hjust = c(-6,-2,-2,-4,-4,-4,-4,-4,-4),
                             # vjust = 3,
                             widths = c(1,0.92,0.92),
                             heights = c(1,0.9,0.9),
                             nrow = 3,
                             ncol = 3
)

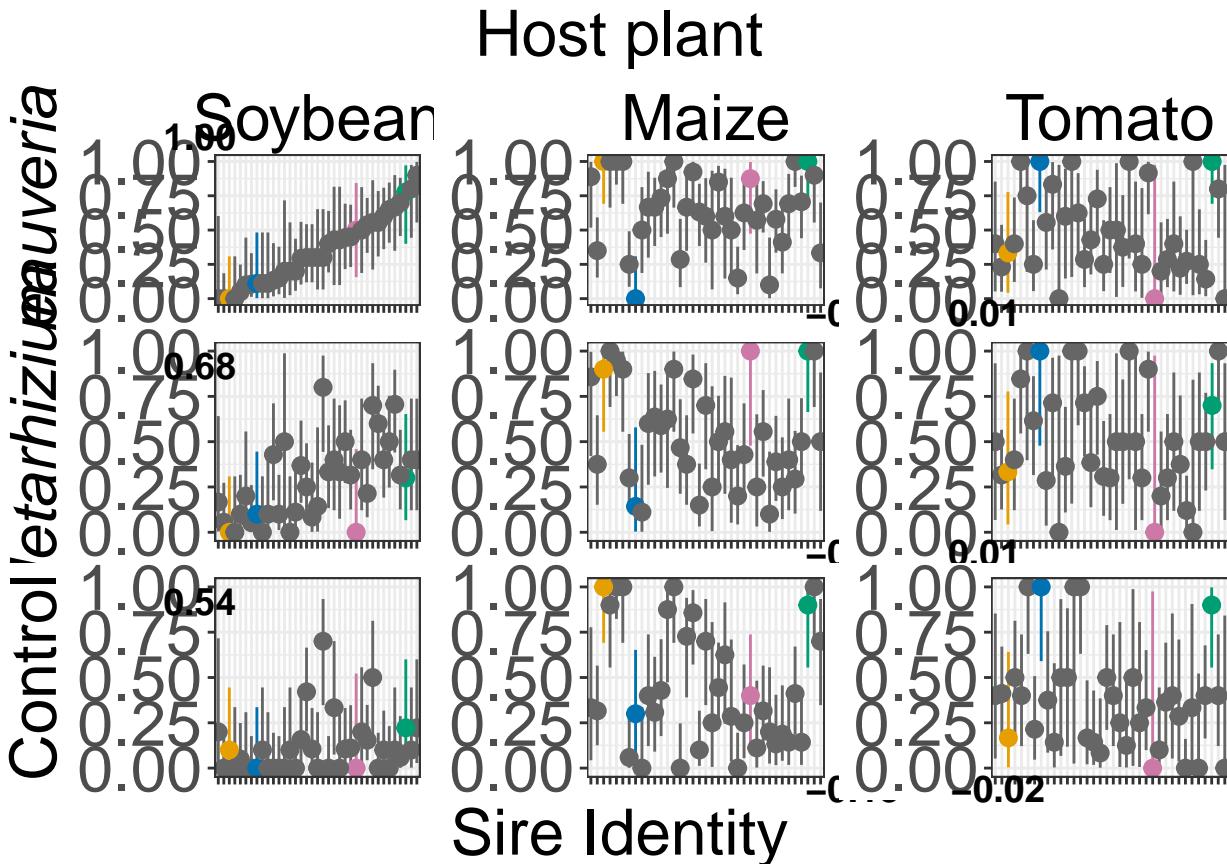
# Annotate the figure by adding a common labels
annotate_figure(rxnnorms9panel,
               top = text_grob("Host plant",
                               # color = "red",
                               size = 24),
               bottom = text_grob("Sire Identity",
                                  # color = "blue",
                                  # hjust = 1,
                                  # x = 1,
                                  # face = "italic",
                                  size = 24),

```

```

# left = text_grob("Pathogen treatment",
#                   # color = "green",
#                   rot = 90),
# right = "I'm done, thanks :-)!",
# fig.lab = "Figure 1", fig.lab.face = "bold"
)

```



```

ggsave("outputs/NewReactionNorms3x3.png",
       height = 20,
       width = 30,
       units = "cm",
       bg = "white")

```

```

## ggarrange no corr numbers 9 panels #####
rxnnorms9panel <- ggarrange(SoyaBB_SireMort, MaizeBB_SireMort,
                             TomBB_SireMort, SoyaMT_SireMort,
                             MaizeMT_SireMort, TomMT_SireMort,
                             SoyaCON_SireMort, MaizeCON_SireMort,
                             TomCON_SireMort,
                             # labels = c("1.00",
                             #           "-0.04",
                             #           "0.01",
                             #           "0.68",

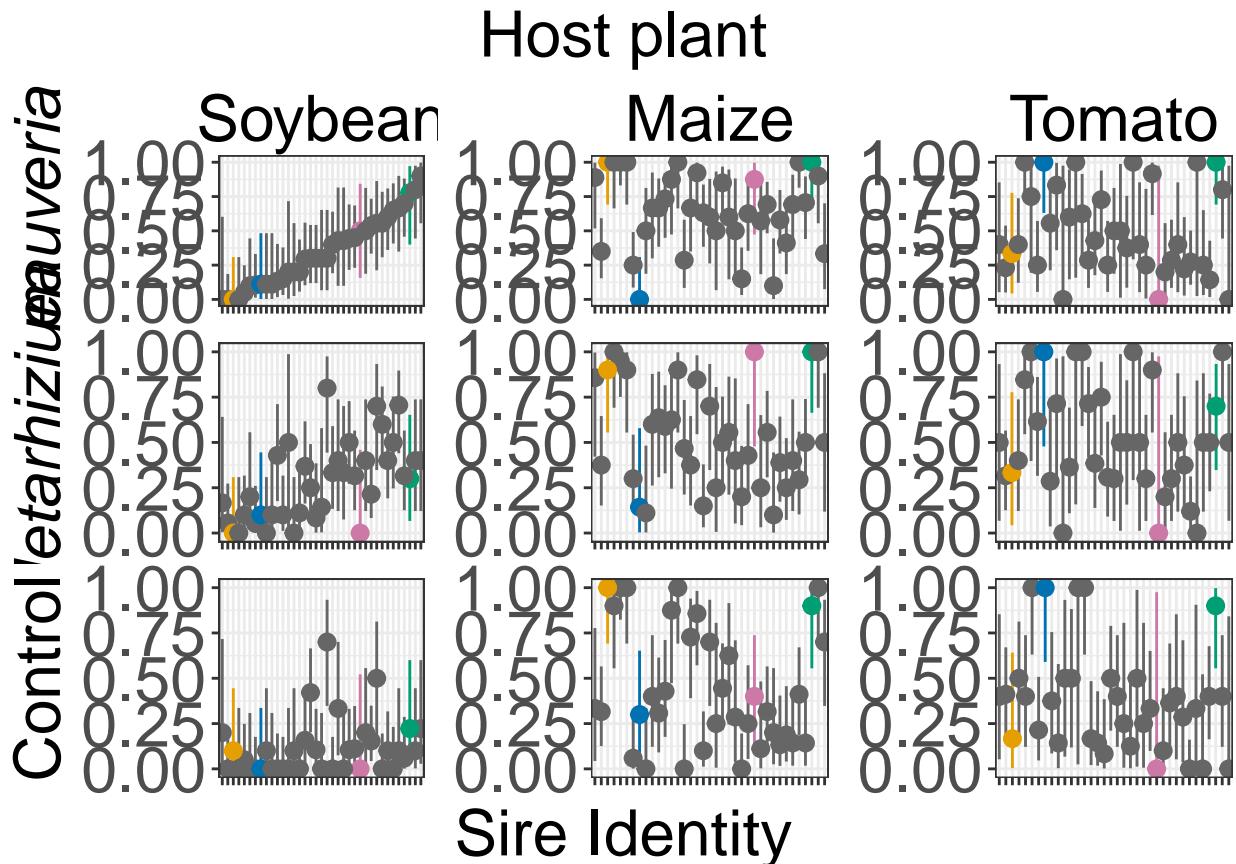
```

```

#           "-0.04",
#           "0.01",
#           "0.54",
#           "-0.13",
#           "-0.02"),
# label.x = c(0.3,0.8,0.18,
#           0.3,0.8,0.18,
#           0.3,0.8,0.16),
# label.y = c(0.83,0.16,0.16,
#           0.95,0.16,0.16,
#           0.95,0.16,0.16),
# hjust = c(-6,-2,-2,-4,-4,-4,-4,-4,-4),
# vjust = 3,
widths = c(1,0.92,0.92),
heights = c(1,0.9,0.9),
nrow = 3,
ncol = 3
)

# Annotate the figure by adding a common labels
annotate_figure(rxnnorms9panel,
    top = text_grob("Host plant",
                    # color = "red",
                    size = 24),
    bottom = text_grob("Sire Identity",
                      # color = "blue",
                      # hjust = 1,
                      # x = 1,
                      # face = "italic",
                      size = 24),
    # left = text_grob("Pathogen treatment",
    #                   # color = "green",
    #                   rot = 90),
    # right = "I'm done, thanks :-)!",
    # fig.lab = "Figure 1", fig.lab.face = "bold"
)

```



```

ggsave("outputs/NoCorrs_NewReactionNorms3x3.png",
       height = 20,
       width = 30,
       units = "cm",
       bg = "white")

# get summary stats on genetic corrs #####
VCVaray9traits_werr <- VarCorr(model.9traits.brm.matnocov.long,
                                  probs = c(0.11,0.89))

names(VCVaray9traits_werr)

## [1] "father" "mother"

Q11Cors9traitswide <- melt(VCVaray9traits_werr) %>%
  filter(L2 == "cor",
         Var2 == "Q11") %>%
  rename(Q11 = Var3,
         Trait1 = Var1) %>%
  pivot_wider(.,
              names_from = Q11,
              values_from = value) %>%
  select(-Var2,-L2,-L1)

```

```

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVararray9traits_werr). In the next version, this warning will
## become an error.

Q89Cors9traitswide <- melt(VCVararray9traits_werr) %>%
  filter(L2 == "cor",
         Var2 == "Q89") %>%
  rename(Q89 = Var3,
         Trait1 = Var1) %>%
  pivot_wider(.,
              names_from = Q89,
              values_from = value) %>%
  select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVararray9traits_werr). In the next version, this warning will
## become an error.

Gcor9traitswide <- melt(VCVararray9traits_werr) %>%
  filter(L2 == "cor",
         Var2 == "Estimate") %>%
  rename(Cor = Var3,
         Trait1 = Var1) %>%
  pivot_wider(.,
              names_from = Cor,
              values_from = value) %>%
  select(-Var2,-L2,-L1)

## Warning: The melt generic in data.table has been passed a list and will attempt
## to redirect to the relevant reshape2 method; please note that reshape2 is
## superseded and is no longer actively developed, and this redirection is now
## deprecated. To continue using melt methods from reshape2 while both libraries
## are attached, e.g. melt.list, you can prepend the namespace, i.e.
## reshape2::melt(VCVararray9traits_werr). In the next version, this warning will
## become an error.

#
# order_levels <- c("treatmentSoya_CON",
#                   "treatmentSoya_BB",
#                   "treatmentSoya_MT",
#                   "treatmentMaz_CON",
#                   "treatmentMaz_BB",
#                   "treatmentMaz_MT",
#                   "treatmentTom_CON",
#                   "treatmentTom_BB",
#                   "treatmentTom_MT" )

```

```

Gcors9traitslong <- Gcor9traitswide %>%
  pivot_longer(treatmentSoya_CON:treatmentTom_MT,
               names_to = "Trait2",
               values_to = "Rg") %>%
  separate(Trait1,
           into = c("crop1","fungus1")) %>%
  separate(crop1,
           into = c("junk1","crop1"),
           sep = 9) %>%
  separate(Trait2,
           into = c("crop2","fungus2")) %>%
  separate(crop2,
           into = c("junk2","crop2"),
           sep = 9) %>%
  select(-junk1,-junk2) %>%
  distinct(Rg,
           .keep_all = TRUE) %>%
  filter(Rg != 1) %>%
  mutate(cropdiff = if_else(crop1 == crop2, 0, 1),
         fungdiff = if_else(fungus1 == fungus2, 0, 1),
         diff_dims = cropdiff+fungdiff,
         funguscontrol = if_else(fungus1 == "CON" | fungus2 == "CON", "control", "2 fungi")) %>%
  mutate(diff_desc = if_else(diff_dims == 2, "both different",
                             if_else(cropdiff == 1, "crop different", "infection treatment different")))

```

Gcors9traitslong

```

## # A tibble: 36 x 10
##   crop1 fungus1 crop2 fungus2     Rg cropdiff fungdiff diff_dims funguscontrol
##   <chr> <chr>   <chr> <chr>    <dbl>    <dbl>    <dbl>    <dbl> <chr>
## 1 Soya  CON     Soya  BB      0.250     0       1       1 control
## 2 Soya  CON     Soya  MT      0.362     0       1       1 control
## 3 Soya  CON     Maz   CON     0.0102    1       0       1 control
## 4 Soya  CON     Maz   BB     -0.0839    1       1       2 control
## 5 Soya  CON     Maz   MT     -0.228     1       1       2 control
## 6 Soya  CON     Tom   CON    -0.253     1       0       1 control
## 7 Soya  CON     Tom   BB     0.0291    1       1       2 control
## 8 Soya  CON     Tom   MT     -0.107     1       1       2 control
## 9 Soya  BB      Soya  MT     0.588     0       1       1 2 fungi
## 10 Soya BB     Maz   CON    -0.299     1       1       2 control
## # i 26 more rows
## # i 1 more variable: diff_desc <chr>
# relevel categories
Gcors9traitslong$diff_desc <- factor(Gcors9traitslong$diff_desc,
                                         levels = c("infection treatment different","crop different","both d
levels(Gcors9traitslong$diff_desc)

```

```

## [1] "infection treatment different" "crop different"
## [3] "both different"
## extract Q11 #####
Q11Gcors9traitslong <- Q11Cors9traitswide %>%
  pivot_longer(treatmentSoya_CON:treatmentTom_MT,

```

```

        names_to = "Trait2",
        values_to = "Rg") %>%
separate(Trait1,
         into = c("crop1", "fungus1")) %>%
separate(crop1,
         into = c("junk1", "crop1"),
         sep = 9) %>%
separate(Trait2,
         into = c("crop2", "fungus2")) %>%
separate(crop2,
         into = c("junk2", "crop2"),
         sep = 9) %>%
select(-junk1, -junk2) %>%
distinct(Rg,
         .keep_all = TRUE) %>%
filter(Rg != 1) %>%
mutate(cropdiff = if_else(crop1 == crop2, 0, 1),
       fungdiff = if_else(fungus1 == fungus2, 0, 1),
       diff_dims = cropdiff+fungdiff,
       funguscontrol = if_else(fungus1 == "CON" | fungus2 == "CON", "control", "2 fungi")) %>%
mutate(diff_desc = if_else(diff_dims == 2, "both different",
                            if_else(cropdiff == 1, "crop different", "infection treatment different")))
## extract Q89 #####
Q89Cors9traitsLong <- Q89Cors9traitswide %>%
  pivot_longer(treatmentSoya_CON:treatmentTom_MT,
               names_to = "Trait2",
               values_to = "Q89") %>%
separate(Trait1,
         into = c("crop1", "fungus1")) %>%
separate(crop1,
         into = c("junk1", "crop1"),
         sep = 9) %>%
separate(Trait2,
         into = c("crop2", "fungus2")) %>%
separate(crop2,
         into = c("junk2", "crop2"),
         sep = 9) %>%
select(-junk1, -junk2) %>%
distinct(Q89,
         .keep_all = TRUE) %>%
filter(Q89 != 1)

## joins frames #####
GmatwErrors <- left_join(Gcors9traitslong, Q11Gcors9traitslong) %>%
  left_join(., Q89Cors9traitsLong)

## Joining with `by = join_by(crop1, fungus1, crop2, fungus2, Rg, cropdiff,
## fungdiff, diff_dims, funguscontrol, diff_desc)`#
## Joining with `by = join_by(crop1, fungus1, crop2, fungus2)`#

```

```

GmatwErrors <- GmatwErrors %>%
  mutate(diff_desc_2 = if_else(fungdiff == 0,
                               if_else(fungus1 == "CON",
                                       "uninfected",
                                       "infected"),
                               if_else(fungus1 == "CON" |
                                       fungus2 == "CON",
                                       "control-infected",
                                       "isolate genus")),
         fung_diff_2 = if_else(fungdiff == 0,
                               if_else(fungus1 == "CON",
                                       "both control",
                                       "same isolate"),
                               if_else(fungus1 == "CON" |
                                       fungus2 == "CON",
                                       "control-infected",
                                       "different isolate")))

names(GmatwErrors)

## [1] "crop1"           "fungus1"        "crop2"          "fungus2"
## [5] "Rg"              "cropdiff"       "fungdiff"       "diff_dims"
## [9] "funguscontrol"  "diff_desc"      "Q89"           "diff_desc_2"
## [13] "fung_diff_2"

# compute bootstrapped CIs #####
GmatwErrors %>%
  group_by(diff_desc) %>%
  summarise(meanRg = mean_cl_boot(Rg))

## # A tibble: 3 x 2
##   diff_desc               meanRg$y  $ymin   $ymax
##   <chr>                  <dbl>    <dbl>    <dbl>
## 1 both different          -0.0927 -0.190  0.00716
## 2 crop different          -0.105   -0.246  0.0374
## 3 infection treatment different  0.481   0.357  0.589

# make a plot of genetic correlations by diff
GmatwBootsPlot <- GmatwErrors %>%
  ggplot(aes(x = diff_desc, y = Rg)) +
  geom_violin(alpha = 0.2,
              fill = "gray20",
              trim = FALSE) +
  stat_summary(fun.data = "mean_cl_boot", colour = "black",
              linewidth = 1.2, size = 1.5,
              alpha = 0.5) +
  geom_jitter(height = 0,
              width = 0.04,
              alpha = 0.6,
              aes(color = diff_desc_2))

```