

Density-dependence seedling mortality in Kadumane

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0.1 set up

```
library(tidyverse)
library(ggthemes)
library(knitr)
library(glmmTMB)
library(DHARMA)
library(broom.mixed)
library(ggeffects)
library(ggdist)
library(sjPlot)
library(patchwork)
```

```
theme_set(theme_tufte())
```

1 Data

Load data

```
sp_codes <- read_csv("data/sp_codes.csv")
```

```
## Rows: 26 Columns: 4
## -- Column specification -----
## Delimiter: ","
## chr (4): code, genus, species, family
##
## 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.
```

```
site_dat <- read_rds("data/kadumane_site_metadata.rds")
sdls <- read_rds("data/kadumane_seedlings.rds")
plot_dat <- read_rds("data/kadumane_plot_metadata.rds")
```

1. Join in site and plot meta-data.
2. Remove rows for species with no seedlings at start of the census in plot.
3. Select species that
 - Are recorded in at least 5 plots.
 - Vary in density among plots.
 - Are groups of many (unidentified) species with the same code.

```
sdls |> summarise(n_sdls = sum(census.start),
                 n_survs = sum(census.final),
                 n_species = n_distinct(species)) |> knitr::kable()
```

n_sdls	n_survs	n_species
7134	3054	102

```
sdls <- sdls |> left_join(site_dat) |> left_join(plot_dat) |>
  filter(census.start > 0)
```

```
## Joining with 'by = join_by(site)'
## Joining with 'by = join_by(site, location, group, plot)'
```

```
## find species with enough individuals and variation in density to allow
## analysis
sp_list <- group_by(sdls, species) |>
  summarise(abund = sum(census.start) , ## total abund
            n = sum(census.start > 0), ## number of plots with the species
            sd_dens = sd(census.start[census.start > 0])) |> ##var in density
  filter(n > 1) |> arrange(n)
## only lose 8 species by restricting to 5 or more occurrences (instead of 1)
## Seems reasonable. Also removing species that were unreliably identified.

sp_list <- filter(sp_list, n > 4, !(species %in% c("Palm", "Artoh", "SC")),
                 sd_dens > 0)
sdls <- filter(sdls, species %in% sp_list$species)
dim(sdls) ## 968 columns
```

```
## [1] 968 19
```

```
# Number of plots= 37 locs * 3 groups * 5 plots
n_plots <- 37*3*5
n_sites <- 21
```

Rename columns, add total seedling density, scale and centre data.

```
## shorten names
sdls <- rename(sdls,
  "trt_F" = "treatment.fungicide",
  "trt_I" = "treatment.insecticide",
  "Pr_m" = "proportion.mortality",
  "gr" = "group", ## group causes problems with some helper funcs
  "loc" = "location")
## categorical variable for treatment
sdls <- mutate(sdls, trt = case_when(
  trt_F == "0" & trt_I == "0" ~ "C",
  trt_F == "F" & trt_I == "0" ~ "F",
  trt_F == "0" & trt_I == "I" ~ "I",
  trt_F == "F" & trt_I == "I" ~ "FI"),
  trt = factor(trt, levels = c("C", "I", "F", "FI")))
## add total density
tot_dens <- sdls |> group_by(site, loc, gr, plot) |>
  summarise(tot_dens = sum(census.start))
```

*## 'summarise()' has grouped output by 'site', 'loc', 'gr'. You can override using
the '.groups' argument.*

```
## add species mean density
## divide by total number of plots
sp_mean_dens <- sdls |> group_by(species) |>
  summarise(sp_mean_condens = sum(census.start)/n_plots,
    sp_mean_surv = sum(census.final)/sum(census.start))

sdls <- left_join(sdls, tot_dens, by = c("site", "loc", "gr", "plot")) |>
  left_join(select(sp_mean_dens, - sp_mean_surv))
```

Joining with 'by = join_by(species)'

```
#scale density by mean, fix couple of NAs
sdls <- mutate(sdls,
  slope.degrees = replace_na(slope.degrees, 5),
  Pr_s = 1 - Pr_m,
  con_dens = census.start,
  con_dens_s = con_dens/sp_mean_condens,
  slope.degrees_s = as.vector(scale(slope.degrees)),
  trt_F = factor(trt_F, labels = c("0", "F")),
  trt_I = factor(trt_I, labels = c("0", "I"))
)
```

```
## calculate total scaled density. Note this is the sum of the scaled densities
## of all species in the plot. Remember that the total_density contrast only
## works when all conspecific densities sum to total density (replicating
## a sum-to-zero contrast for conspecific and heterospecific densities.
```

```
sdls <- left_join(sdls,
                  group_by(sdls, site, loc, gr, plot) |>
                  summarise(tot_dens_s = sum(con_dens_s)))
```

```
## 'summarise()' has grouped output by 'site', 'loc', 'gr'. You can override using
## the '.groups' argument.
```

```
## Joining with 'by = join_by(site, loc, gr, plot)'
```

```
summary(sdls)
```

```
##      site      loc      gr      plot      species      census.start
## S3       :119    L1:549   G1:283  1:185    SR       :172    Min.   : 1.000
## S1       :109    L2:225   G2:351  2:210    Symp      :122    1st Qu.: 1.000
## S12      : 77    L3:161   G3:334  5:183    Cinam     : 86    Median : 1.000
## S13      : 75    L4: 33           6:199    Climber1: 77    Mean   : 6.413
## S39      : 74           7:191    FLC      : 64    3rd Qu.: 3.000
## S5       : 63           Litsea  : 61    Max.   :300.000
## (Other):451           (Other) :386
##      census.mid      census.final      Pr_m      proportion.connectivity
## Min.   : 0.0000    Min.   : 0.0000    Min.   :0.0000    Min.   :0.0000
## 1st Qu.: 0.0000    1st Qu.: 0.0000    1st Qu.:0.0000    1st Qu.:0.0100
## Median : 1.0000    Median : 1.0000    Median :0.1667    Median :0.0200
## Mean   : 3.089     Mean   : 2.769     Mean   :0.3810    Mean   :0.1255
## 3rd Qu.: 2.000     3rd Qu.: 2.000     3rd Qu.:1.0000    3rd Qu.:0.1500
## Max.   :109.000    Max.   : 90.000    Max.   :1.0000    Max.   :0.6700
##
##      fragment.size      size.category      location.code      group.code
## Min.   : 1.10      Length:968      S14L1 : 54      S14L1G2: 23
## 1st Qu.: 9.00      Class :character      S1L2  : 49      S12L1G2: 18
## Median : 46.00      Mode  :character      S12L2 : 40      S14L1G3: 17
## Mean   : 51.15      S13L3 : 40      S1L1G3 : 17
## 3rd Qu.: 64.50      S12L1 : 37      S1L2G1 : 17
## Max.   :149.00      S3L3  : 37      S1L2G2 : 17
##                      (Other):711      (Other):859
##      proportion.rock      slope.degrees      treatment.control      trt_F      trt_I      trt
## Min.   :0.0000    Min.   : 0.000    Min.   :0.0000    0:594    0:578    C   :395
## 1st Qu.:0.0500    1st Qu.: 5.000    1st Qu.:0.0000    F:374    I:390    I   : 0
## Median :0.1000    Median : 5.000    Median :0.0000           F   : 0
## Mean   :0.1888    Mean   : 9.199    Mean   :0.4081           FI  : 0
## 3rd Qu.:0.3000    3rd Qu.:10.000    3rd Qu.:1.0000           NA's:573
## Max.   :0.9000    Max.   :40.000    Max.   :1.0000
## NA's   :3
##      tot_dens      sp_mean_condens      Pr_s      con_dens
## Min.   : 1.00    Min.   :0.01261    Min.   :0.0000    Min.   : 1.000
## 1st Qu.: 3.00    1st Qu.:0.12793    1st Qu.:0.0000    1st Qu.: 1.000
## Median : 6.00    Median :0.24685    Median :0.8333    Median : 1.000
## Mean   :15.79    Mean   :1.49738    Mean   :0.6190    Mean   : 6.413
## 3rd Qu.:14.00    3rd Qu.:1.14595    3rd Qu.:1.0000    3rd Qu.: 3.000
## Max.   :301.00    Max.   :6.48288    Max.   :1.0000    Max.   :300.000
```

```
##
##   con_dens_s      slope.degrees_s      tot_dens_s
##   Min.      : 0.1543   Min.      :-1.08744   Min.      : 0.1543
##   1st Qu.: 1.7732   1st Qu.: -0.49640   1st Qu.: 9.8715
##   Median : 6.8841   Median : -0.49640   Median : 23.5926
##   Mean   : 14.9070   Mean      : 0.00000   Mean      : 39.0650
##   3rd Qu.: 13.2143   3rd Qu.: 0.09464   3rd Qu.: 47.7227
##   Max.    :355.2000   Max.      : 3.64087   Max.      :357.8179
##
```

```
dim(sdls) ## 968 species x plot combinations
```

```
## [1] 968 27
```

2 Summary information for the paper

```
sdls |> summarise(n_sdls = sum(census.start),
                  n_survs = sum(census.final),
                  n_species = n_distinct(species)) |> knitr::kable()
```

n_sdls	n_survs	n_species
6208	2680	26

```
sdls <- droplevels(sdls)
table(sdls$species)[order(table(sdls$species))]
```

```
##
##   Here      SN      Humb  Crypto  Holi      Mac  Rattan  Toona
##   5         5         6         7         7         8         8         8
##   SP  Beilsch  Acacia Mallotus  Mel      Trich      Poly  UID20
##   9         12        15        16        19        21        26        31
##   Olea Climber Psyflav  Dimo  Litsea  FLC Climber1  Cinam
##   36        45        46        56        61        64        77        86
##   Symp      SR
##   122      172
```

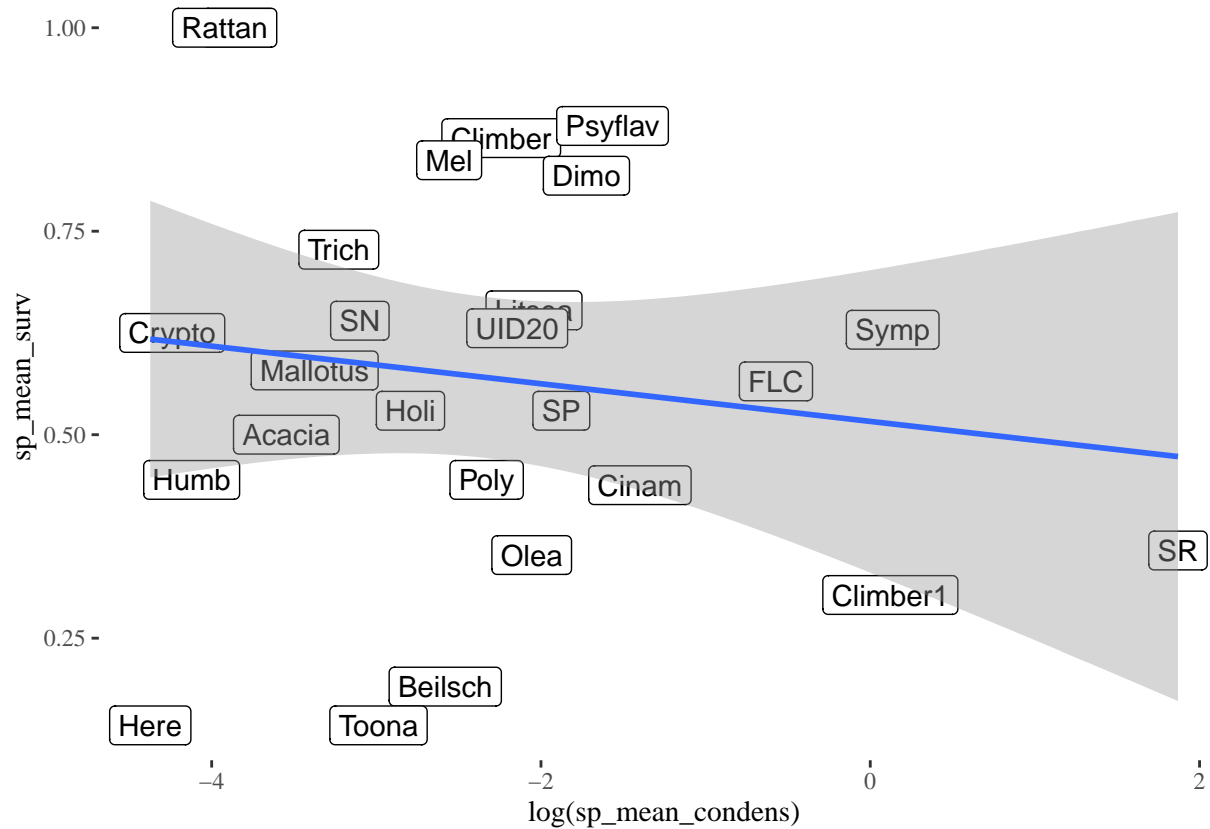
3 Models

3.1 Scaled conspecific density models

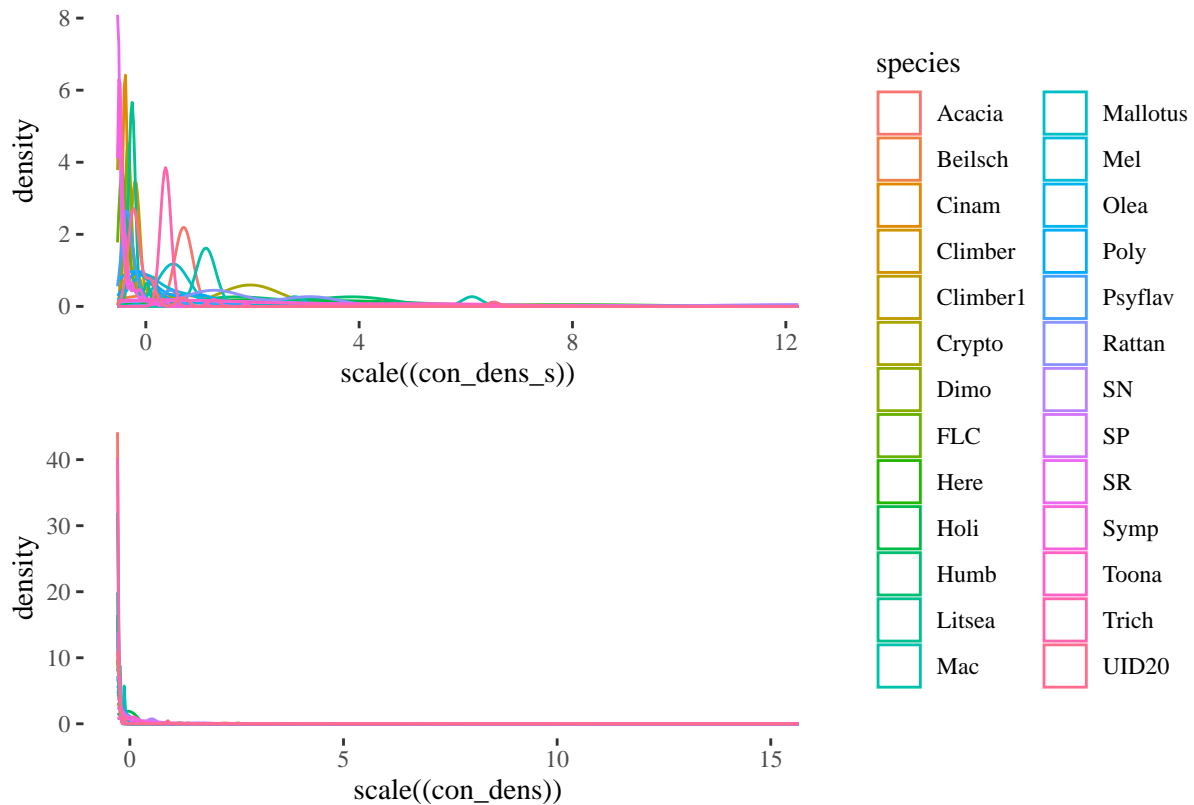
The most abundant species initially will often have lower survival (fecundity/ survival trade-off). This could generate what looks like a density-dependent relationship when looking across species, even without a relationship within species (i.e., Simpson's paradox).

```
ggplot(sp_mean_dens, aes(x = log(sp_mean_condens), y = sp_mean_surv)) +
  geom_label(aes(label= species)) + geom_smooth(method = "lm") + theme_tufte()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



```
## not the clearest pattern, but worth accounting for.
(ggplot(sdl, aes(x = scale((con_dens_s)), colour = species)) + geom_density())/
(ggplot(sdl, aes(x = scale((con_dens)), colour = species)) +
  geom_density() + plot_layout(guides = "collect"))
```



To account for this, we can scale conspecific density by dividing by mean density and refitting the models.

```
## Random intercept model
m_cdd_s_ri <- glmmTMB(Pr_s ~ slope.degrees_s +
  trt_I:trt_F +
  (scale(tot_dens_s) + scale(con_dens_s)) *
  (trt_I + trt_F) *
  scale(fragment.size) +
  (1|species) +
  (1|site/loc/gr/plot),
  weights = census.start, data = sdls,
  family=binomial)

## Random intercept and slope model for species specific effects
m_cdd_s_ris <- glmmTMB(Pr_s ~ slope.degrees_s +
  trt_I:trt_F +
  (scale(tot_dens_s) + scale(con_dens_s)) *
  (trt_I + trt_F) *
  scale(fragment.size) +
  (scale(con_dens_s) + scale(tot_dens_s)|species) +
  (1|site/loc/gr/plot),
  weights = census.start,
  data = sdls,
  family=binomial)

## note the slightly odd ordering of terms doesn't change the model structure,
## but does change the default ordering of terms in outputs and plots to a
```

```
## more convenient one for describing in paper (first CDD, then biocide effects
## then fragmentation effects).
```

```
anova(m_cdd_s_ri, m_cdd_s_ris) ## random slope *much* better
```

```
## Data: sdls
## Models:
## m_cdd_s_ri: Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) * , zi=~0
## m_cdd_s_ri:      (trt_I + trt_F) * scale(fragment.size) + (1 | species) + , zi=~0, disp=~1
## m_cdd_s_ri:      (1 | site/loc/gr/plot), zi=~0, disp=~1
## m_cdd_s_ris: Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) * , zi=~0
## m_cdd_s_ris:      (trt_I + trt_F) * scale(fragment.size) + (scale(con_dens_s) + , zi=~0, disp=~1
## m_cdd_s_ris:      scale(tot_dens_s) | species) + (1 | site/loc/gr/plot), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m_cdd_s_ri 25 2232.1 2353.9 -1091.0 2182.1
## m_cdd_s_ris 30 2215.1 2361.3 -1077.5 2155.1 27.02      5 5.654e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

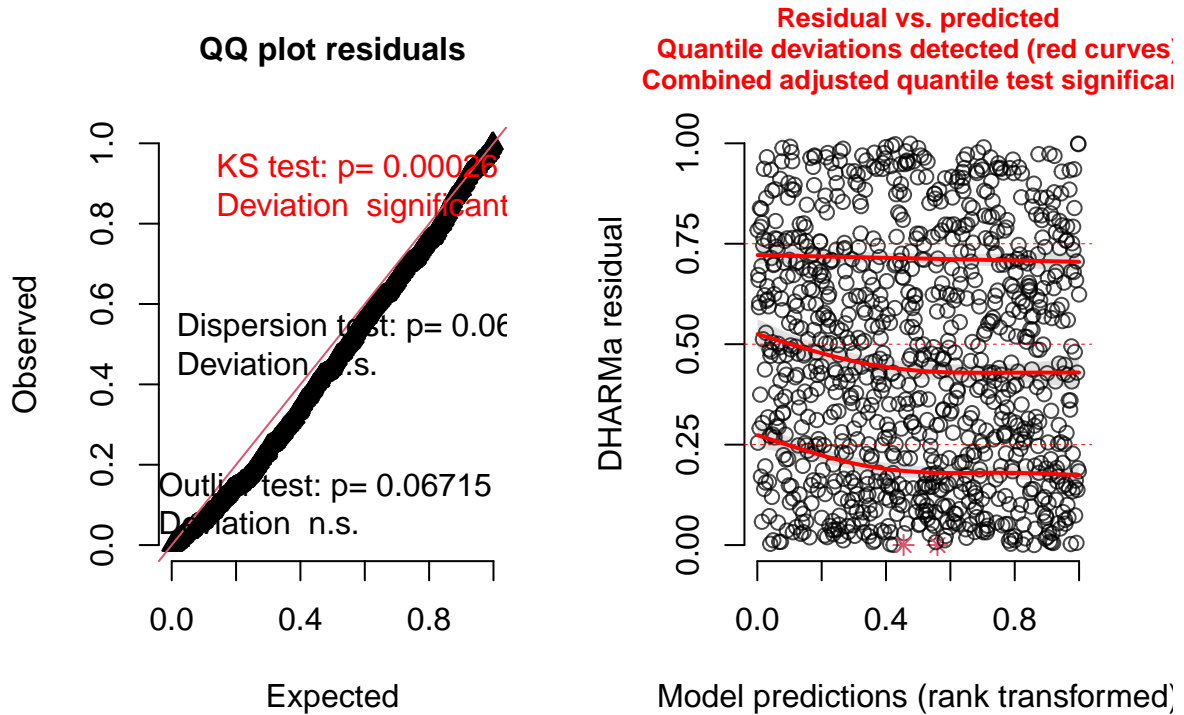
Models fit without issues, even with the correlation among density effects.

The improvement with the random slopes model suggests we need to look at individual species. Proceeding with the random intercept and slope model from here on.

3.1.1 Diagnostics

```
res_s <- simulateResiduals(m_cdd_s_ris)
plot(res_s) ## ok - some deviation from ideal residual distribution, but
```


DHARMA residual



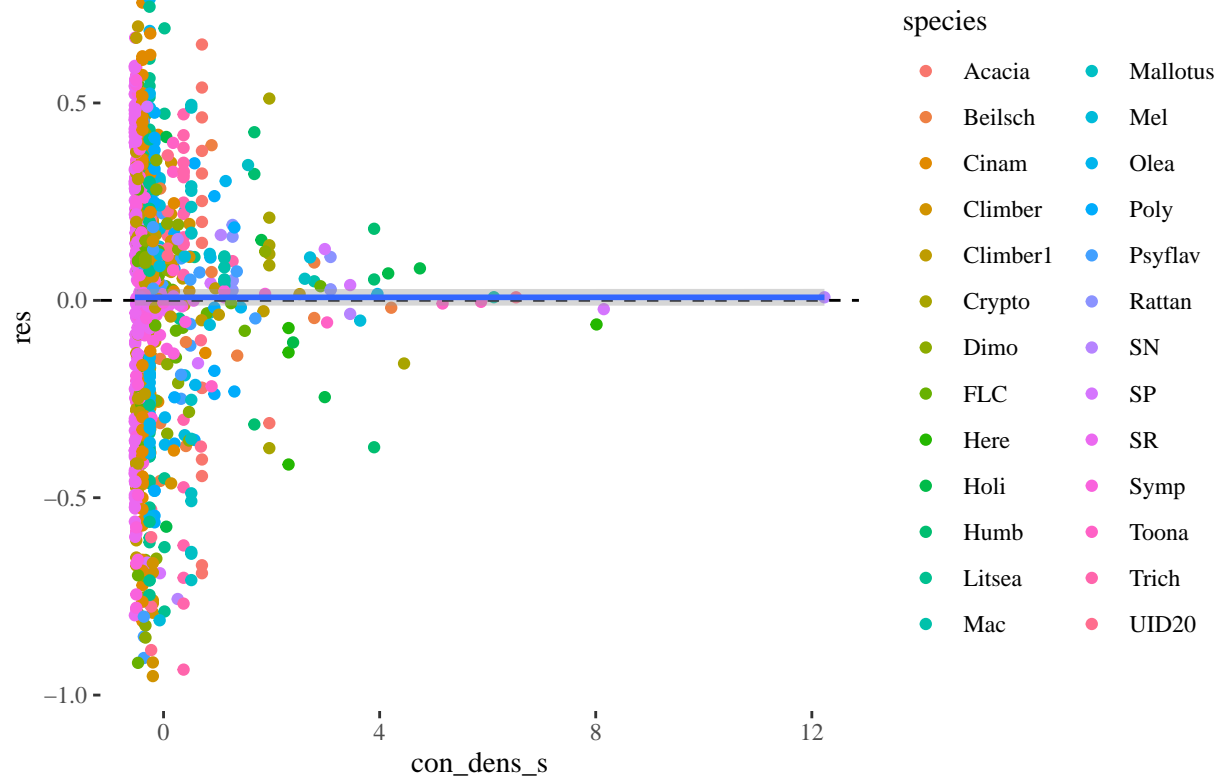
```
## acceptable.

## look at relationship with covariates
diag_dat <- data.frame(m_cdd_s_ris$frame, res = res_s$fittedResiduals)

diag_dat <- rename_with(diag_dat, ~ str_replace(.x, "scale\\.", "")) |>
  rename_with(~str_replace(.x, "\\.$", ""))

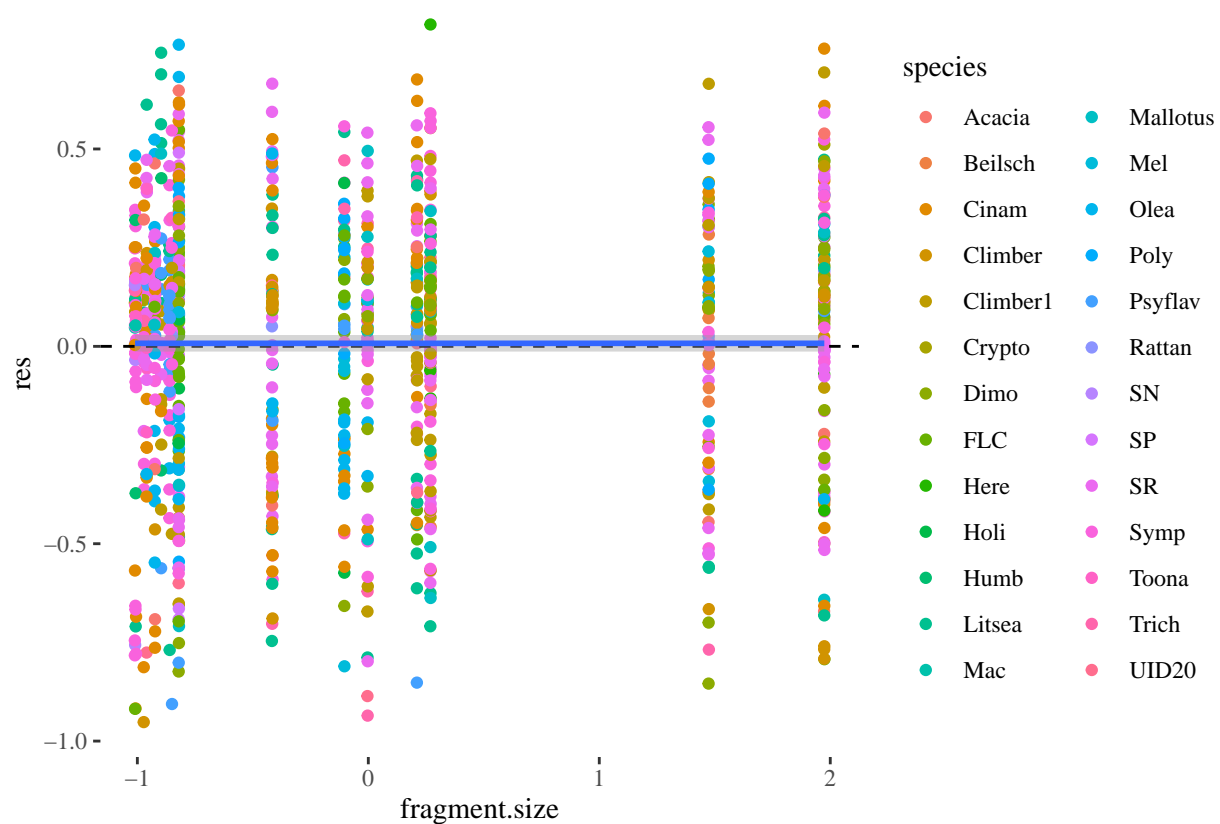
ggplot(diag_dat, aes(x = con_dens_s, y = res)) +
  geom_point(aes(colour = species)) +
  geom_hline(yintercept=0, linetype = "dashed") +
  geom_smooth(method="gam") ## no trend.

## 'geom_smooth()' using formula = 'y ~ s(x, bs = "cs")'
```



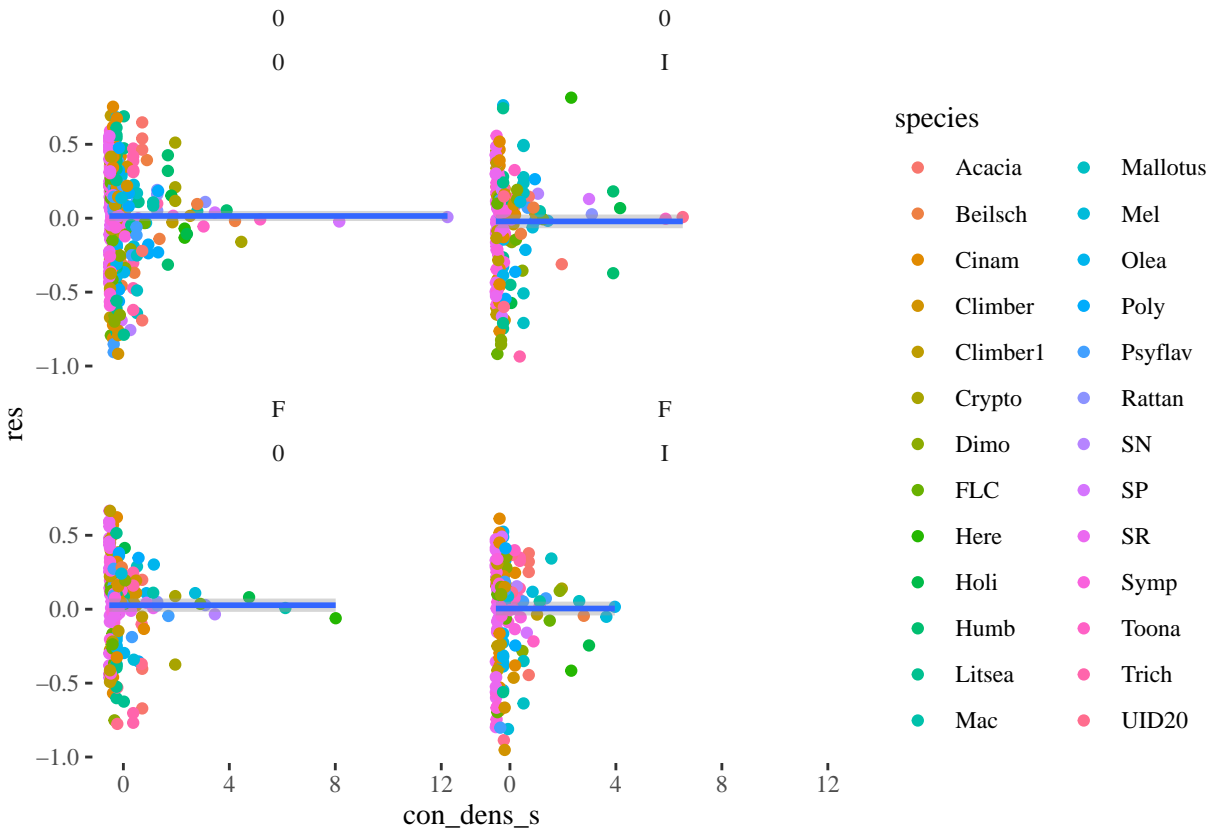
```
ggplot(diag_dat, aes(x = fragment.size, y = res)) +
  geom_point(aes(colour = species), position = "jitter") +
  geom_hline(yintercept=0, linetype = "dashed") +
  geom_smooth(method="gam") ## no trend.
```

```
## 'geom_smooth()' using formula = 'y ~ s(x, bs = "cs")'
```



```
ggplot(diag_dat, aes(x = con_dens_s, y = res)) +
  facet_wrap(~trt_F + trt_I ) +
  geom_point(aes(colour = species)) +
  geom_smooth(method="gam") ## no trend with treatment
```

```
## 'geom_smooth()' using formula = 'y ~ s(x, bs = "cs")'
```



The diagnostics aren't perfect, but not particularly unusual for a binomial model. None of the big problems (e.g., overdispersion, trends with covariates) seem to apply here.

3.1.2 Model inference

```
summary(m_cdd_s_ris)
```

```
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) *
## (trt_I + trt_F) * scale(fragment.size) + (scale(con_dens_s) +
## scale(tot_dens_s) | species) + (1 | site/loc/gr/plot)
## Data: sdls
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##  2215.0   2361.3  -1077.5   2155.0     938
##
## Random effects:
##
## Conditional model:
## Groups      Name                Variance Std.Dev.  Corr
## species      (Intercept)         1.027e+00 1.0131846
##              scale(con_dens_s)  3.887e-01 0.6234621  0.56
```

```

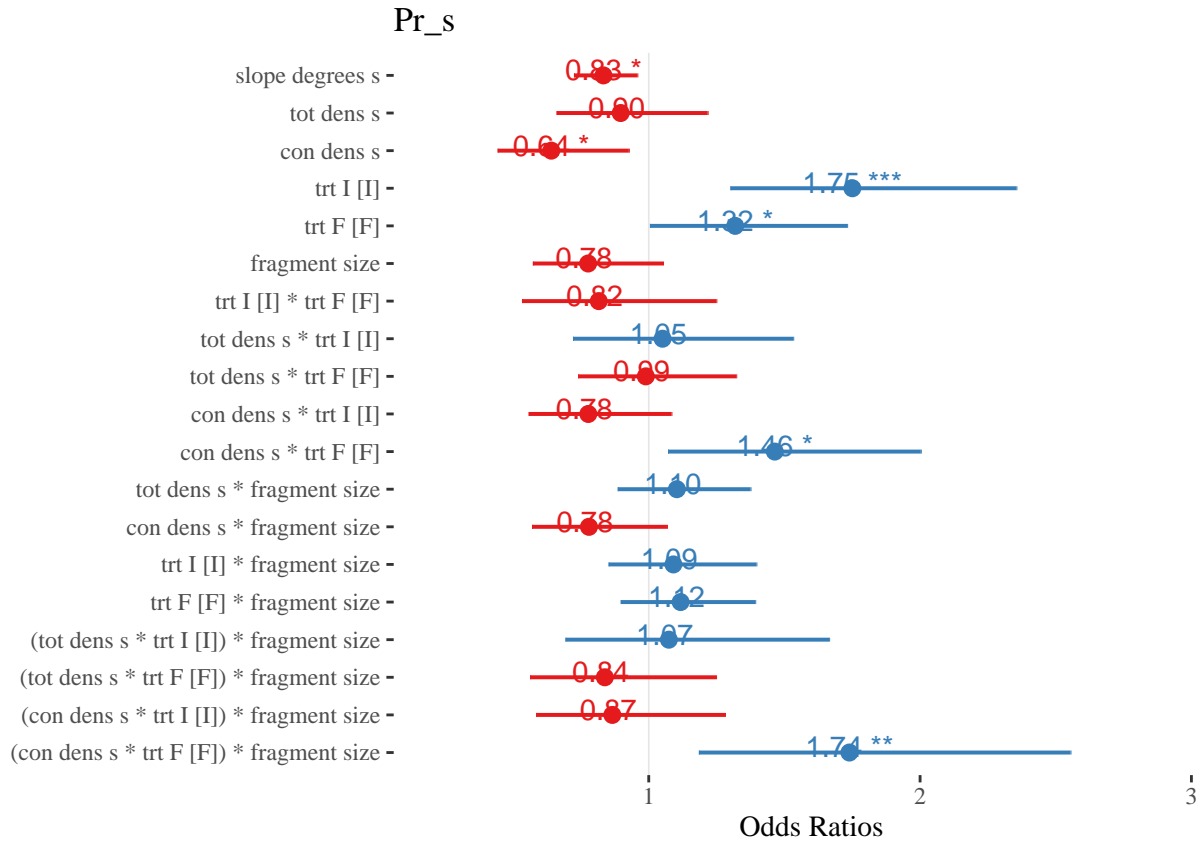
##               scale(tot_dens_s) 3.738e-02 0.1933384 -0.47 -0.71
## plot:gr:loc:site (Intercept)    2.788e-01 0.5280003
## gr:loc:site      (Intercept)    2.057e-01 0.4535170
## loc:site         (Intercept)    4.782e-01 0.6915250
## site             (Intercept)    2.188e-08 0.0001479
## Number of obs: 968, groups:
## species, 26; plot:gr:loc:site, 474; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##
##               Estimate Std. Error z value
## (Intercept)      0.66723    0.27771   2.403
## slope.degrees_s  -0.18268    0.07133  -2.561
## scale(tot_dens_s) -0.10921    0.15595  -0.700
## scale(con_dens_s) -0.44496    0.18820  -2.364
## trt_II            0.55988    0.15137   3.699
## trt_FF            0.27661    0.13886   1.992
## scale(fragment.size) -0.25279    0.15514  -1.629
## trt_II:trt_FF      -0.20355    0.21738  -0.936
## scale(tot_dens_s):trt_II  0.04971    0.19245   0.258
## scale(tot_dens_s):trt_FF -0.01093    0.14816  -0.074
## scale(con_dens_s):trt_II -0.25189    0.16952  -1.486
## scale(con_dens_s):trt_FF  0.38152    0.15970   2.389
## scale(tot_dens_s):scale(fragment.size) 0.09861    0.11221   0.879
## scale(con_dens_s):scale(fragment.size) -0.24883    0.16012  -1.554
## trt_II:scale(fragment.size) 0.08701    0.12608   0.690
## trt_FF:scale(fragment.size) 0.11108    0.11225   0.990
## scale(tot_dens_s):trt_II:scale(fragment.size) 0.07160    0.22351   0.320
## scale(tot_dens_s):trt_FF:scale(fragment.size) -0.17654    0.20314  -0.869
## scale(con_dens_s):trt_II:scale(fragment.size) -0.14412    0.19987  -0.721
## scale(con_dens_s):trt_FF:scale(fragment.size) 0.55367    0.19600   2.825
##
##               Pr(>|z|)
## (Intercept)      0.016277 *
## slope.degrees_s  0.010437 *
## scale(tot_dens_s) 0.483771
## scale(con_dens_s) 0.018061 *
## trt_II           0.000217 ***
## trt_FF           0.046363 *
## scale(fragment.size) 0.103231
## trt_II:trt_FF     0.349094
## scale(tot_dens_s):trt_II 0.796159
## scale(tot_dens_s):trt_FF 0.941199
## scale(con_dens_s):trt_II 0.137312
## scale(con_dens_s):trt_FF 0.016894 *
## scale(tot_dens_s):scale(fragment.size) 0.379537
## scale(con_dens_s):scale(fragment.size) 0.120172
## trt_II:scale(fragment.size) 0.490132
## trt_FF:scale(fragment.size) 0.322352
## scale(tot_dens_s):trt_II:scale(fragment.size) 0.748722
## scale(tot_dens_s):trt_FF:scale(fragment.size) 0.384811
## scale(con_dens_s):trt_II:scale(fragment.size) 0.470860
## scale(con_dens_s):trt_FF:scale(fragment.size) 0.004731 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
plot_model(m_cdd_s_ris, show.values=TRUE) + ylim(c(0.2, 3))
```

Scale for y is already present.

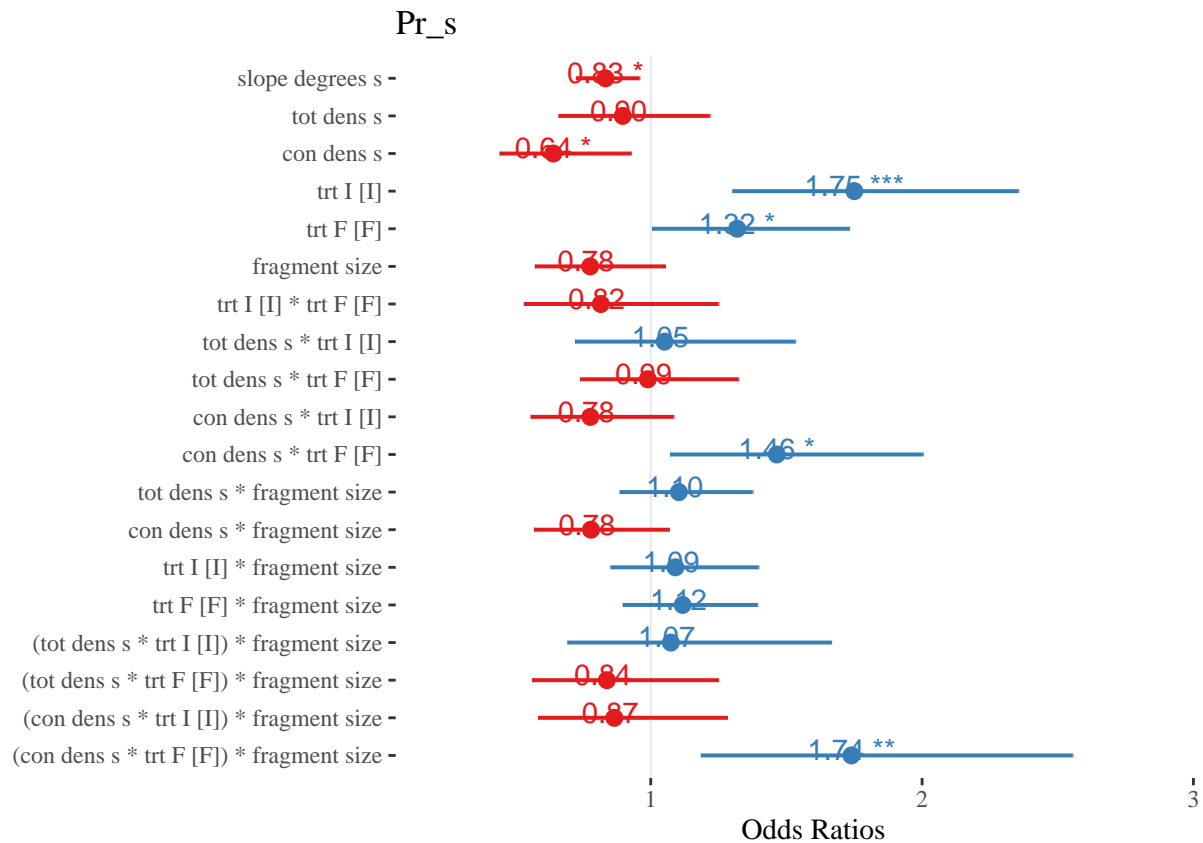
Adding another scale for y, which will replace the existing scale.



```
plot_model(m_cdd_s_ris, show.values=TRUE) + ylim(c(0.2, 3))
```

Scale for y is already present.

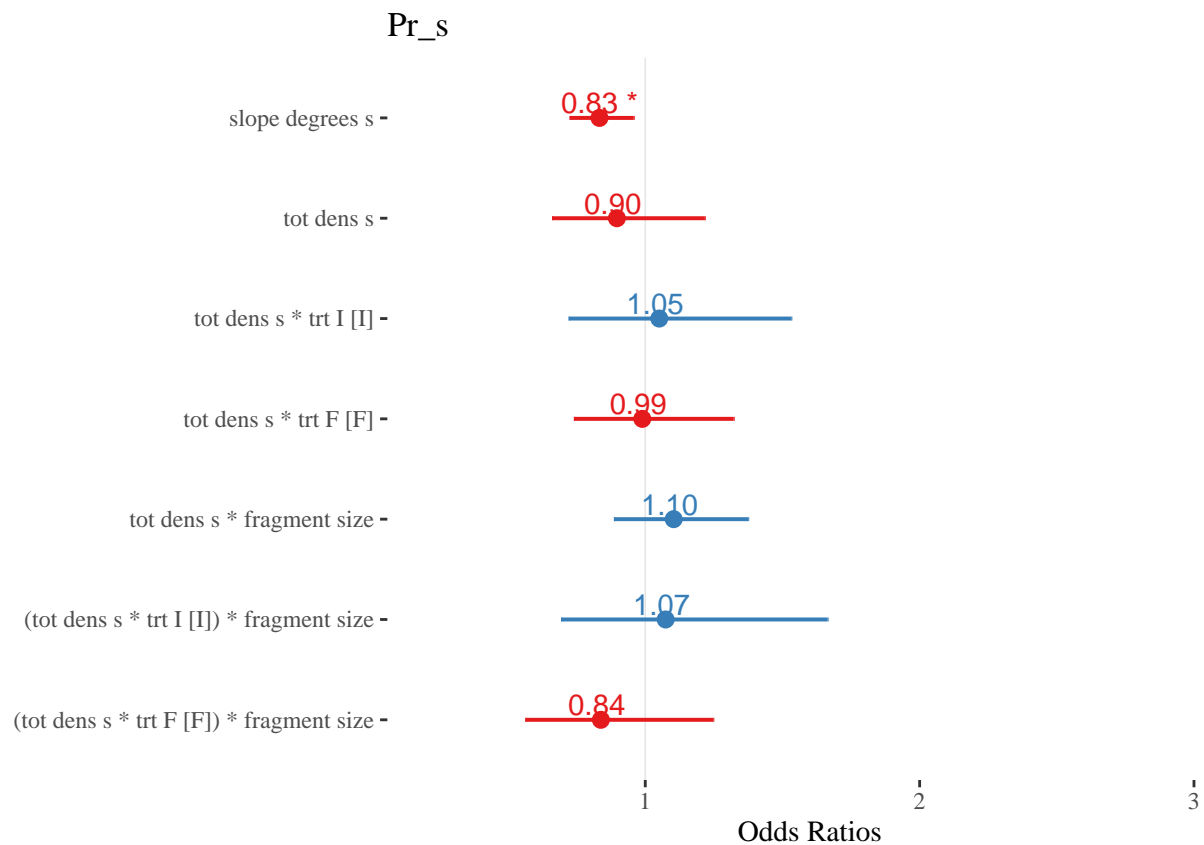
Adding another scale for y, which will replace the existing scale.



```
## total density is never very important, so separating out it's effects
rmvars <- names(fixef(m_cdd_s_ris)$cond)
rmvars <- c(rmvars[grepl("tot_dens_s", rmvars)], "slope.degrees_s")

## First confirm it isn't influential
plot_model(m_cdd_s_ris, show.values=TRUE, terms=rmvars) + ylim(c(0.2, 3))
```

```
## Scale for y is already present.
## Adding another scale for y, which will replace the existing scale.
```



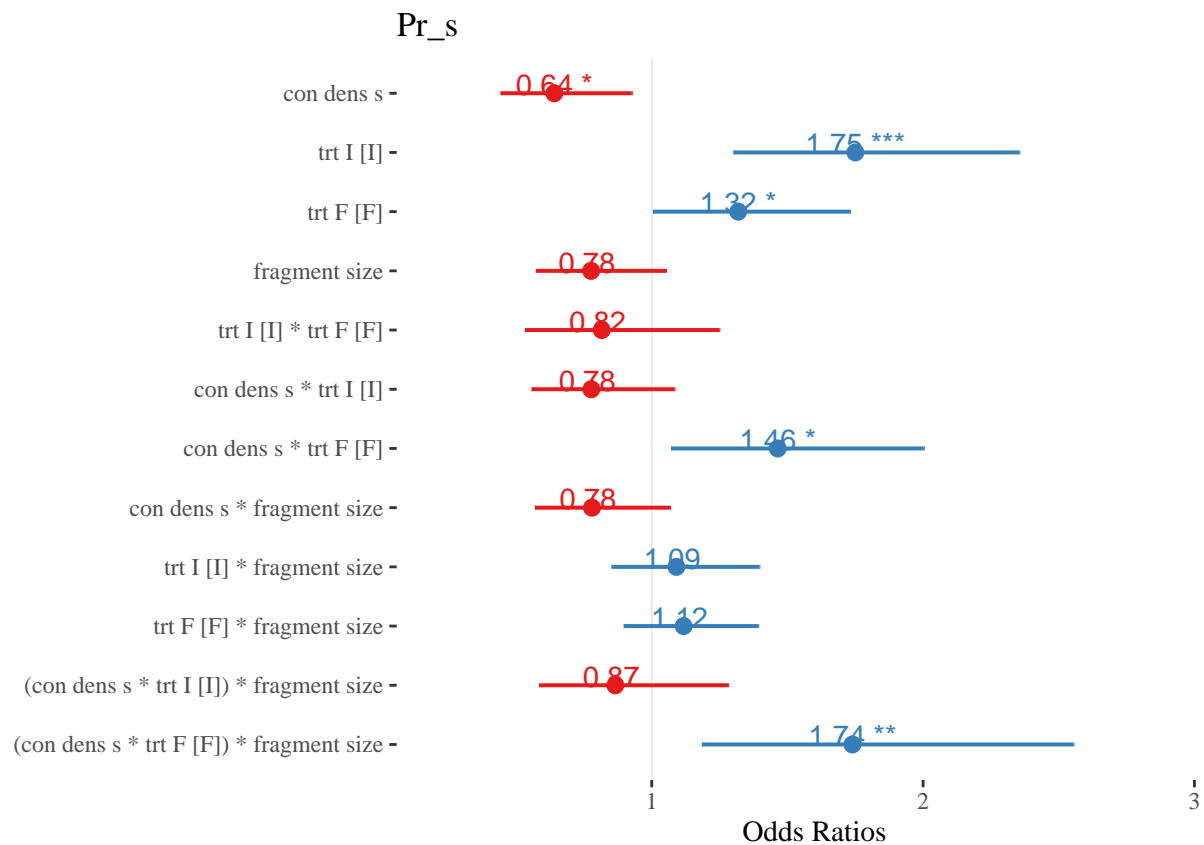
```
# basically what we thought
```

```
## now decluttered version
```

```
plot_model(m_cdd_s_ris, show.values=TRUE, rm.terms=rmvars) + ylim(c(0.2, 3))
```

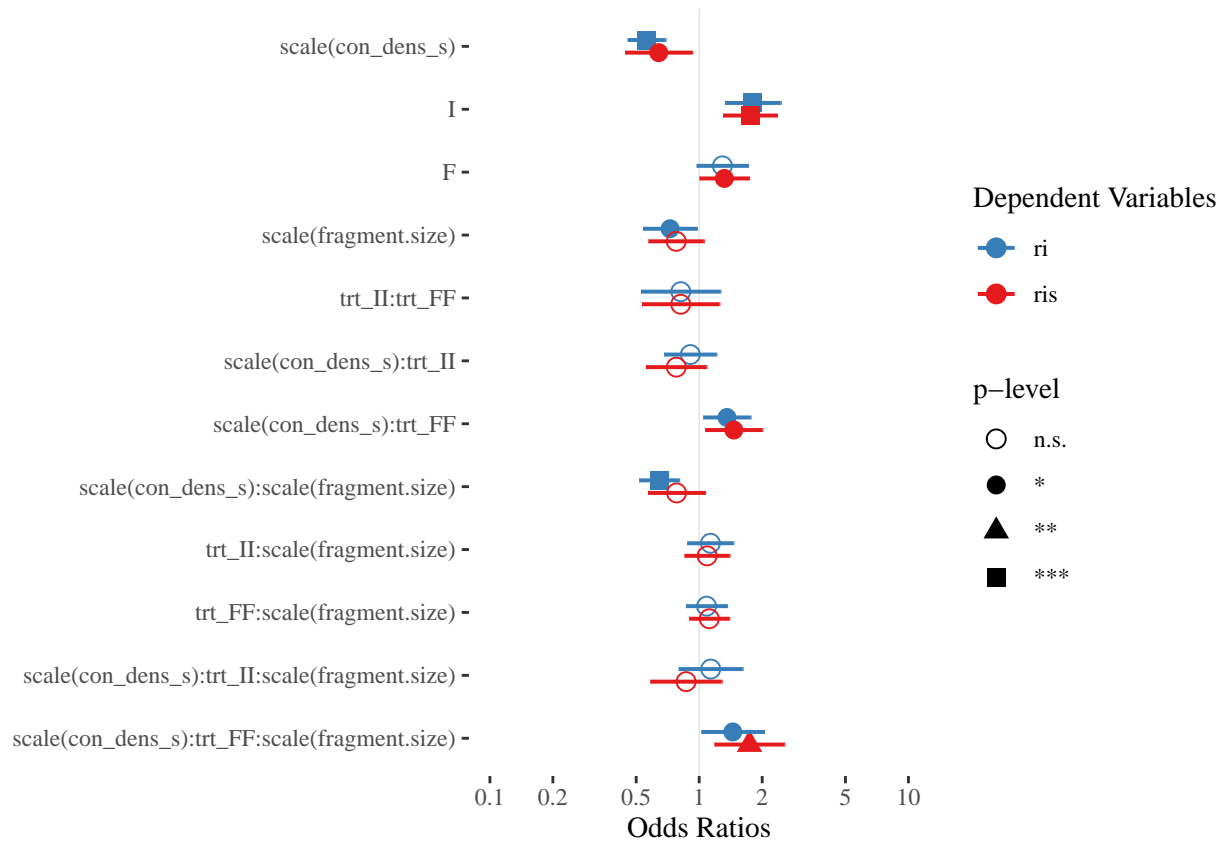
```
## Scale for y is already present.
```

```
## Adding another scale for y, which will replace the existing scale.
```

```
## compare to random intercept model
```

```
plot_models(m_cdd_s_ri, m_cdd_s_ris, rm.terms=rmvars, m.labels=c("ri", "ris"),
            p.shape = TRUE)
```



```
summary(m_cdd_s_ri)
```

```
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) *
##      (trt_I + trt_F) * scale(fragment.size) + (1 | species) +
##      (1 | site/loc/gr/plot)
## Data: sdls
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##  2232.1   2353.9  -1091.0   2182.1     943
##
## Random effects:
##
## Conditional model:
## Groups      Name          Variance Std.Dev.
## species      (Intercept)  1.496e+00 1.2230929
## plot:gr:loc:site (Intercept) 3.554e-01 0.5961589
## gr:loc:site    (Intercept) 2.921e-01 0.5404754
## loc:site       (Intercept) 4.210e-01 0.6488833
## site          (Intercept) 1.522e-08 0.0001234
## Number of obs: 968, groups:
## species, 26; plot:gr:loc:site, 474; gr:loc:site, 110; loc:site, 37; site, 21
##
```

```

## Conditional model:
##
## Estimate Std. Error z value
## (Intercept) 0.81111 0.30834 2.631
## slope.degrees_s -0.18928 0.07399 -2.558
## scale(tot_dens_s) 0.06247 0.11818 0.529
## scale(con_dens_s) -0.57768 0.10619 -5.440
## trt_II 0.59141 0.15620 3.786
## trt_FF 0.25563 0.14449 1.769
## scale(fragment.size) -0.32059 0.15085 -2.125
## trt_II:trt_FF -0.20244 0.22300 -0.908
## scale(tot_dens_s):trt_II 0.04069 0.19865 0.205
## scale(tot_dens_s):trt_FF -0.07806 0.15129 -0.516
## scale(con_dens_s):trt_II -0.09714 0.14638 -0.664
## scale(con_dens_s):trt_FF 0.30573 0.13274 2.303
## scale(tot_dens_s):scale(fragment.size) 0.04495 0.11292 0.398
## scale(con_dens_s):scale(fragment.size) -0.43936 0.11188 -3.927
## trt_II:scale(fragment.size) 0.12382 0.12955 0.956
## trt_FF:scale(fragment.size) 0.08116 0.11529 0.704
## scale(tot_dens_s):trt_II:scale(fragment.size) 0.01694 0.22765 0.074
## scale(tot_dens_s):trt_FF:scale(fragment.size) -0.07885 0.19887 -0.396
## scale(con_dens_s):trt_II:scale(fragment.size) 0.12721 0.17947 0.709
## scale(con_dens_s):trt_FF:scale(fragment.size) 0.36934 0.17565 2.103
## Pr(>|z|)
## (Intercept) 0.008524 **
## slope.degrees_s 0.010518 *
## scale(tot_dens_s) 0.597063
## scale(con_dens_s) 5.33e-08 ***
## trt_II 0.000153 ***
## trt_FF 0.076857 .
## scale(fragment.size) 0.033566 *
## trt_II:trt_FF 0.363984
## scale(tot_dens_s):trt_II 0.837712
## scale(tot_dens_s):trt_FF 0.605885
## scale(con_dens_s):trt_II 0.506951
## scale(con_dens_s):trt_FF 0.021267 *
## scale(tot_dens_s):scale(fragment.size) 0.690614
## scale(con_dens_s):scale(fragment.size) 8.60e-05 ***
## trt_II:scale(fragment.size) 0.339178
## trt_FF:scale(fragment.size) 0.481443
## scale(tot_dens_s):trt_II:scale(fragment.size) 0.940699
## scale(tot_dens_s):trt_FF:scale(fragment.size) 0.691760
## scale(con_dens_s):trt_II:scale(fragment.size) 0.478457
## scale(con_dens_s):trt_FF:scale(fragment.size) 0.035493 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

3.1.3 Take-homes:

- Survival is negatively conspecific density dependent. This result is consistent across all permutations of the model tried.
- Insecticide and fungicide (to a lesser extent) increase survival significantly.
- Fungicide removes the CDD, and that effect strengthens with fragment area. However, that effect

needs more exploration (see below).

- The interaction between CDD and fragment size is complex, but perhaps explained by species turnover. The CDD effect strengthens with fragment area, but not significantly (or even close) in the (better) random slope model. In the random intercept model, the relationship is significant. This is probably because of species turnover - perhaps species that prefer larger fragments happen to be ones that show stronger density dependence?
- Effects of fragment area and any interactions with density need more probing as the effects are sensitive to model structure.

3.1.4 Models split by categorical fragment size

The effect of fragment

```
# Using 3 categories
sdls <- mutate(sdls,
               frag_sizeclass3 = cut(fragment.size,
                                     round(quantile(site_dat$fragment.size,
                                                    c(0, 0.33, 0.66, 1))),
                                     include.lowest=TRUE))

## quick look at how many fragments and seedlings within each
## fragment size category

sdls |> group_by(frag_sizeclass3) |> summarise(n_frag = n_distinct(site),
                                             n_sdl = n())

## # A tibble: 3 x 3
##   frag_sizeclass3 n_frag n_sdl
##   <fct>          <int> <int>
## 1 [1,5]           6    124
## 2 (5,31]         9    342
## 3 (31,149]       6    502

m_cdd_s_ris_frag3 <- lapply(split(sdls, f= sdls$frag_sizeclass3), function(d){
  var_d <- d |> group_by(species) |>
    summarise(var_dens = var(con_dens_s)) |>
    filter(!is.na(var_dens) & var_dens > 0)

  glmmTMB(Pr_s ~ slope.degrees_s +
          trt_I:trt_F +
          (scale(tot_dens_s) + scale(con_dens_s)) *
          (trt_I + trt_F) +
          (scale(con_dens_s) + scale(tot_dens_s)||species) +
          (1|site/loc/gr/plot),
          weights = census.start,
          data = filter(d, species %in% var_d$species),
          family=binomial))})

## Warning in finalizeTMB(TMBStruc, obj, fit, h, data.tmb.old): Model convergence
## problem; singular convergence (7). See vignette('troubleshooting'),
## help('diagnose')
```

```

## can probably ignore the warning, which comes from the random
## effect structure and tiny variances. We don't want to remove it because
## that would hamper comparison.

#diagnose(m_cdd_s_ris_frag3[[2]])

term_nms <- names(fixef(m_cdd_s_ris_frag3[[1]])$cond)
names(m_cdd_s_ris_frag3) <- c("1 - 4", "5 - 32", "33 - 150") ## renaming to

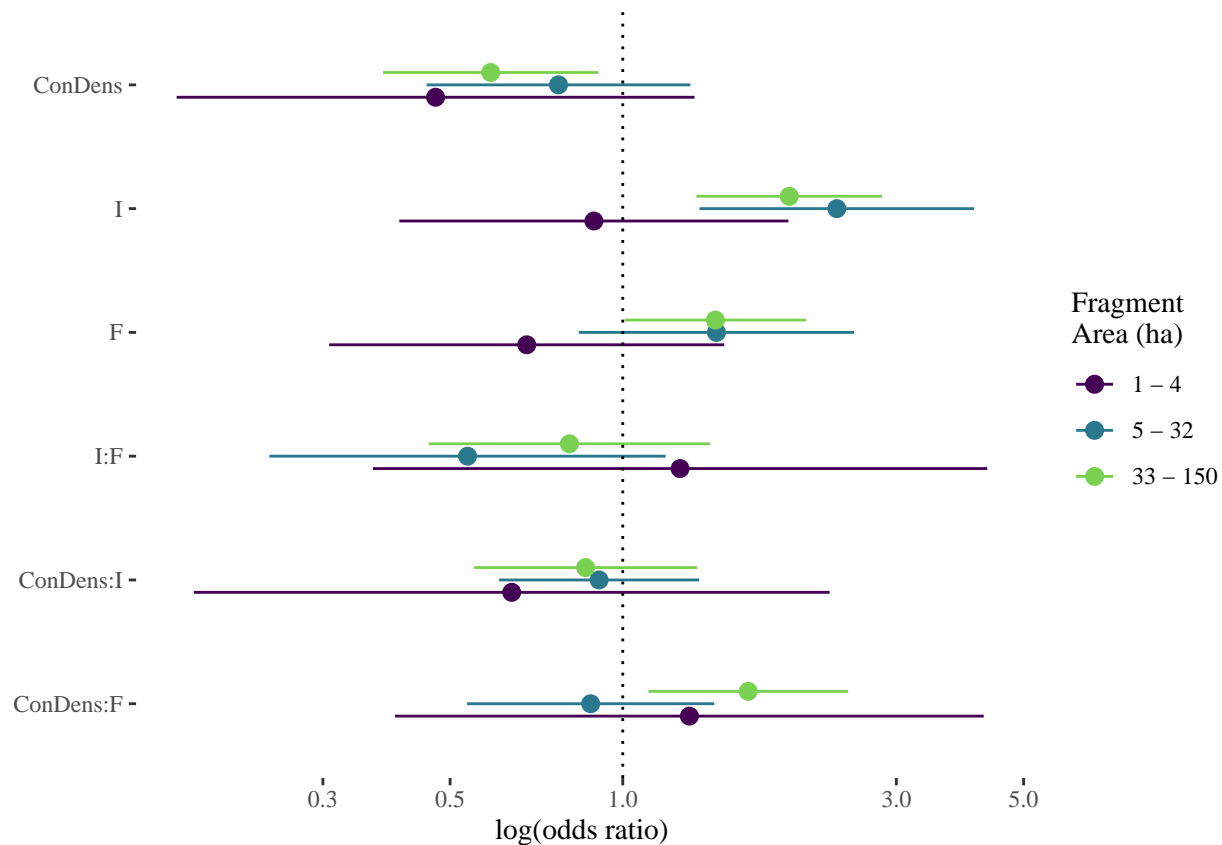
## be clearer and correct (from looking at observed boundaries)
plot_discrete <- plot_models(m_cdd_s_ris_frag3,
  rm.terms=c("slope.degrees_s",
    term_nms[str_detect(term_nms, "tot")]), ## declutter
  m.labels=names(m_cdd_s_ris_frag3), p.shape=TRUE,
  show.values = TRUE) +
  labs(colour = "Fragment Area")

pl_discrete <- plot_discrete$data |>
  mutate(term = str_replace_all(term, fixed("scale(con_dens_s)"), "ConDens"),
    term = str_replace_all(term, "trt_[FI]", ""),
    term = factor(term, levels = rev(unique(term))),
    FragArea = factor(group, levels = c("1 - 4", "5 - 32", "33 - 150")))

pl_discrete <- ggplot(pl_discrete, aes(x = estimate, xmin = conf.low, xmax = conf.high,
  y = term, colour = FragArea)) +
  geom_pointrange(position = position_dodge2(width = 0.3)) +
  geom_vline(xintercept=1, linetype = "dotted") +
  scale_x_continuous(trans = "log10", n.breaks = 7) +
  scale_colour_viridis_d(option="D", end=0.8) +
  labs(x = "log(odds ratio)", y = NULL, colour = "Fragment\nArea (ha)")

pl_discrete

```



```
ggsave(pl_discrete, file = "figures/CatFragPlot.png", height = 5, width = 5)
```

```
map(m_cdd_s_ris_frag3, summary)
```

```
## $'1 - 4'
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) *
## (trt_I + trt_F) + (scale(con_dens_s) + scale(tot_dens_s) ||
## species) + (1 | site/loc/gr/plot)
## Data: filter(d, species %in% var_d$species)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##    319.9    368.2  -142.0    283.9      90
##
## Random effects:
##
## Conditional model:
## Groups      Name                Variance Std.Dev. Corr
## species      (Intercept)         0.20970  0.4579
##              scale(con_dens_s)  0.21980  0.4688  0.00
##              scale(tot_dens_s)  0.09292  0.3048  0.00 0.00
## plot:gr:loc:site (Intercept)     0.26650  0.5162
## gr:loc:site      (Intercept)     0.32066  0.5663
```

```

## loc:site      (Intercept)      0.22937  0.4789
## site          (Intercept)      0.22937  0.4789
## Number of obs: 108, groups:
## species, 8; plot:gr:loc:site, 68; gr:loc:site, 17; loc:site, 6; site, 6
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.96258    0.48338   1.991   0.0464 *
## slope.degrees_s  -0.09686    0.23156  -0.418   0.6757
## scale(tot_dens_s) -0.09204    0.34452  -0.267   0.7893
## scale(con_dens_s) -0.75158    0.53049  -1.417   0.1566
## trt_II           -0.11596    0.39854  -0.291   0.7711
## trt_FF           -0.38553    0.40475  -0.953   0.3408
## trt_II:trt_FF      0.23016    0.62914   0.366   0.7145
## scale(tot_dens_s):trt_II 0.44546    0.40368   1.103   0.2698
## scale(tot_dens_s):trt_FF -0.23049    0.71206  -0.324   0.7462
## scale(con_dens_s):trt_II -0.44574    0.65129  -0.684   0.4937
## scale(con_dens_s):trt_FF 0.26750    0.60297   0.444   0.6573
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $'5 - 32'
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) *
##       (trt_I + trt_F) + (scale(con_dens_s) + scale(tot_dens_s) ||
##       species) + (1 | site/loc/gr/plot)
## Data: filter(d, species %in% var_d$species)
## Weights: census.start
##
##      AIC      BIC    logLik deviance df.resid
##    717.0    784.3   -340.5    681.0     293
##
## Random effects:
##
## Conditional model:
## Groups      Name              Variance Std.Dev.  Corr
## species      (Intercept)      1.344e+00 1.159e+00
##               scale(con_dens_s) 1.527e-01 3.907e-01 0.00
##               scale(tot_dens_s) 8.330e-71 9.127e-36 0.00 0.00
## plot:gr:loc:site (Intercept)  3.356e-01 5.793e-01
## gr:loc:site      (Intercept)  3.435e-01 5.861e-01
## loc:site         (Intercept)  5.088e-01 7.133e-01
## site             (Intercept)  1.248e-06 1.117e-03
## Number of obs: 311, groups:
## species, 19; plot:gr:loc:site, 153; gr:loc:site, 36; loc:site, 12; site, 9
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.39506    0.42938   0.920   0.35754
## slope.degrees_s  -0.35259    0.12759  -2.764   0.00572 **
## scale(tot_dens_s) -0.04612    0.25566  -0.180   0.85684
## scale(con_dens_s) -0.25801    0.27010  -0.955   0.33947
## trt_II           0.85949    0.28140   3.054   0.00226 **

```

```

## trt_FF          0.37630    0.28207    1.334    0.18219
## trt_II:trt_FF   -0.62306    0.40586   -1.535    0.12474
## scale(tot_dens_s):trt_II -0.25100    0.24672   -1.017    0.30899
## scale(tot_dens_s):trt_FF  0.17258    0.26432    0.653    0.51379
## scale(con_dens_s):trt_II -0.09498    0.20487   -0.464    0.64292
## scale(con_dens_s):trt_FF -0.12890    0.25318   -0.509    0.61066
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $'33 - 150'
## Family: binomial (logit)
## Formula:
## Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) *
##      (trt_I + trt_F) + (scale(con_dens_s) + scale(tot_dens_s) | |
##      species) + (1 | site/loc/gr/plot)
## Data: filter(d, species %in% var_d$species)
## Weights: census.start
##
##      AIC      BIC    logLik deviance df.resid
##  1123.1   1197.8   -543.6   1087.1     449
##
## Random effects:
##
## Conditional model:
## Groups      Name              Variance Std.Dev.  Corr
## species      (Intercept)       8.871e-01 9.418e-01
##               scale(con_dens_s) 2.247e-01 4.741e-01 0.00
##               scale(tot_dens_s) 7.522e-11 8.673e-06 0.00 0.00
## plot:gr:loc:site (Intercept)    2.416e-01 4.915e-01
## gr:loc:site      (Intercept)    2.724e-01 5.219e-01
## loc:site         (Intercept)    3.565e-01 5.970e-01
## site             (Intercept)    1.271e-08 1.127e-04
## Number of obs: 467, groups:
## species, 17; plot:gr:loc:site, 236; gr:loc:site, 56; loc:site, 19; site, 6
##
## Conditional model:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.65966    0.33804   1.951 0.051006 .
## slope.degrees_s -0.09605    0.10450  -0.919 0.358013
## scale(tot_dens_s) -0.03133    0.15311  -0.205 0.837843
## scale(con_dens_s) -0.53039    0.22085  -2.402 0.016325 *
## trt_II          0.66851    0.19030   3.513 0.000443 ***
## trt_FF          0.37203    0.18583   2.002 0.045281 *
## trt_II:trt_FF   -0.21407    0.28842  -0.742 0.457956
## scale(tot_dens_s):trt_II 0.04324    0.26389   0.164 0.869845
## scale(tot_dens_s):trt_FF 0.01724    0.17809   0.097 0.922882
## scale(con_dens_s):trt_II -0.14922    0.22863  -0.653 0.513979
## scale(con_dens_s):trt_FF 0.50369    0.20459   2.462 0.013819 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```


3.1.5 Take-homes

The model gets a bit complex when split like this, but it serves as a useful exploration of what's going on.

- Conspecific density reduces survival most clearly in the larger fragments.
- The results of fungicide:cdens make a bit more sense when the data are broken up like this. Fungicide only interacts with cdens in the largest fragments, which makes sense, because these are the fragments where cdens has an effect.
- insects seem to only reduce plant survival in the medium and large fragments

3.1.6 Graphics

```
## refitting model to control order of coefficients
m_cdd_s_ris <- glmmTMB(Pr_s ~ slope.degrees_s +
  (scale(tot_dens_s) + scale(con_dens_s)) +
  scale(fragment.size) +
  trt_I*trt_F +
  (scale(tot_dens_s) + scale(con_dens_s)) *
  (trt_I + trt_F) *
  scale(fragment.size) +
  (scale(con_dens_s) + scale(tot_dens_s)|species) +
  ## setting cor to 0 to converge
  (1|site/loc/gr/plot),
  weights = census.start,
  data = sdls,
  family=binomial)
fixef(m_cdd_s_ris)
```

```
##
## Conditional model:
##               (Intercept)
##               0.66723
##               slope.degrees_s
##               -0.18268
##               scale(tot_dens_s)
##               -0.10921
##               scale(con_dens_s)
##               -0.44496
##               scale(fragment.size)
##               -0.25279
##               trt_II
##               0.55988
##               trt_FF
##               0.27661
##               trt_II:trt_FF
##               -0.20355
##               scale(tot_dens_s):trt_II
##               0.04971
##               scale(tot_dens_s):trt_FF
##               -0.01093
```

```

##          scale(con_dens_s):trt_II
##          -0.25189
##          scale(con_dens_s):trt_FF
##          0.38152
##          scale(tot_dens_s):scale(fragment.size)
##          0.09861
##          scale(con_dens_s):scale(fragment.size)
##          -0.24883
##          scale(fragment.size):trt_II
##          0.08701
##          scale(fragment.size):trt_FF
##          0.11108
## scale(tot_dens_s):scale(fragment.size):trt_II
##          0.07160
## scale(tot_dens_s):scale(fragment.size):trt_FF
##          -0.17654
## scale(con_dens_s):scale(fragment.size):trt_II
##          -0.14412
## scale(con_dens_s):scale(fragment.size):trt_FF
##          0.55367

labs <- c("ConDens", "FragArea", "I", "F", "I:F",
          "ConDens:I", "ConDens:F", "FragArea:\n ConDens",
          "FragArea:I", "FragArea:F",
          "FragArea:\n (ConDens:I)", "FragArea:\n (ConDens:F)")

tp_cdd_s_ris <-
  tidy(m_cdd_s_ris, conf.int = TRUE) |>
  filter(effect == "fixed",
         !str_detect(term, "tot_dens"),
         !term %in% c("(Intercept)", "slope.degrees_s")) |>
  mutate(labels = factor(labs, levels = rev(labs)),
         Biocide = case_when(
           str_detect(term, "trt_II") ~ "Insecticide",
           str_detect(term, "trt_FF") ~ "Fungicide",
           .default = "Control"),
         Biocide = factor(ifelse(str_detect(term, "trt_II:trt_FF"),
                                "Both", Biocide),
                          levels = c("Control", "Insecticide",
                                      "Fungicide", "Both"))) |>
  ggplot(aes(y = labels, x = estimate, xmin = conf.low, xmax = conf.high,
             colour = Biocide)) +
  geom_pointrange(aes(shape = p.value < 0.05 )) +
  geom_vline(xintercept=0, linetype = "dotted") +
  scale_colour_brewer(palette="Set2") +
  scale_shape_manual(values=c(1, 16), guide = "none" ) +
  labs(y = NULL, x = "log(odds ratio)" ) +
  guides(colour = guide_legend(title= "Biocide:", position = "top",
                              direction = "horizontal",
                              title.position = "left", title.hjust = 0.5)) +
  theme(
    legend.margin = margin(0, 0, 0, 0),
    legend.justification.top = "left",
    legend.location = "plot",

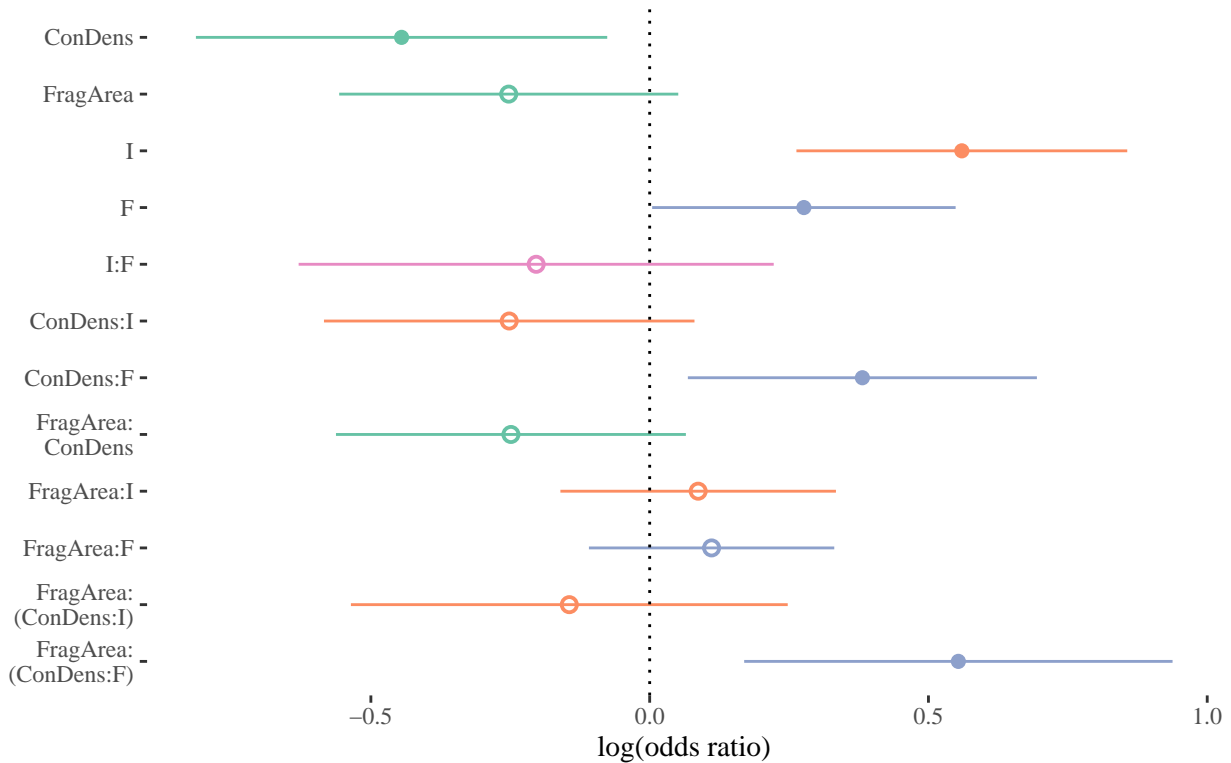
```

```

  plot.title.position = "plot"
)
tp_cdd_s_ris

```

Biocide: ● Control ● Insecticide ● Fungicide ● Both



```

p_cdd_s_ris <- predict_response(m_cdd_s_ris,
                                terms=c("con_dens_s[1:80, by = 1]",
                                          "trt_I", "trt_F",
                                          "fragment.size[5, 65, 125]"))

pr_cdd_s_ris <- residualize_over_grid(p_cdd_s_ris, m_cdd_s_ris) |>
  bind_cols(species = sdds$species) |>
  mutate(trt = factor(
    case_when(
      group == "0" & facet == "0" ~ "Control",
      group == "0" & facet == "F" ~ "Fungicide",
      group == "I" & facet == "0" ~ "Insecticide",
      group == "I" & facet == "F" ~ "Both"),
    levels = c("Control", "Insecticide", "Fungicide", "Both")),
  facet_lab = "Fragment Area (ha)") |>
  rename("con_dens" = "x", "frag_area" = "panel") |>
  group_by(con_dens, trt, frag_area, facet_lab, species) |>
  summarise(predicted = mean(predicted), n = n())

```

'summarise()' has grouped output by 'con_dens', 'trt', 'frag_area',
'facet_lab'. You can override using the '.groups' argument.

```

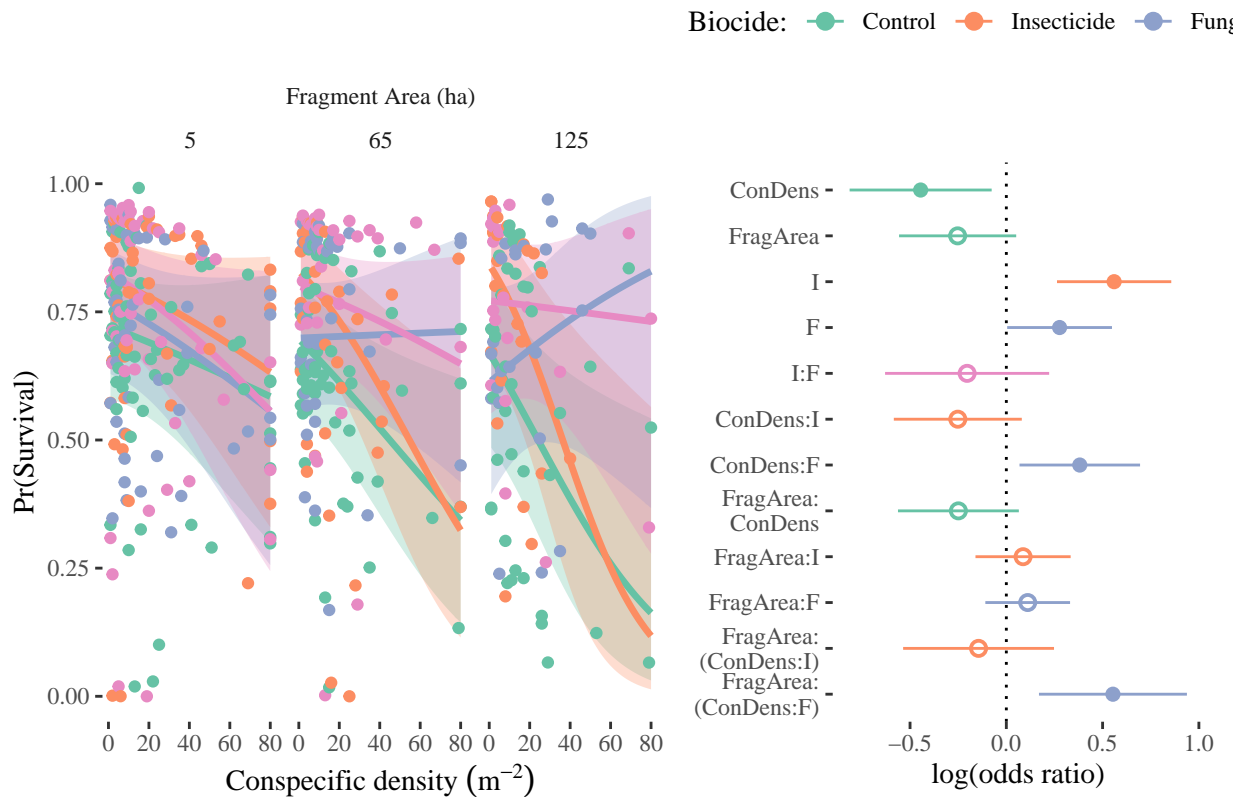
p_cdd_s_ris <- as.data.frame(p_cdd_s_ris) |>
  mutate(trt = factor(
    case_when(
      group == "0" & facet == "0" ~ "Control",
      group == "0" & facet == "F" ~ "Fungicide",
      group == "I" & facet == "0" ~ "Insecticide",
      group == "I" & facet == "F" ~ "Both"),
    levels = c("Control", "Insecticide", "Fungicide", "Both")),
  facet_lab = "Fragment Area (ha)" |>
  rename("con_dens" = "x", "frag_area" = "panel")

# summary(p_cdd_s_ris)
# summary(pr_cdd_s_ris)

pl_cdd_s <- ggplot(p_cdd_s_ris,
  aes(x=con_dens, y = predicted, colour = trt)) +
  ggh4x::facet_nested(~facet_lab + frag_area) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = trt),
    colour = NA, alpha = 0.3) +
  geom_line(linewidth = 1.2) +
  geom_point(data = pr_cdd_s_ris) +
  scale_colour_brewer(palette="Set2") +
  scale_fill_brewer(palette="Set2", guide = "none") +
  labs(x = expression(Conspecific~density~(m^-2)), y = "Pr(Survival)",
    colour = "Treatment") + theme(legend.position="none")

mod_plot <- (pl_cdd_s | tp_cdd_s_ris ) +
  plot_layout(widths=c(0.6, 0.4))
mod_plot

```

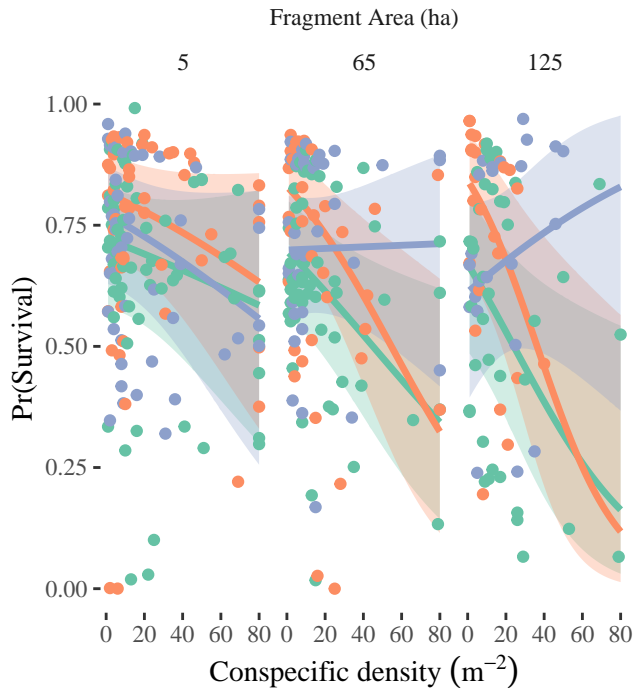


the predictions with the "both" treatment get really busy. Given the
lack of an interaction, trying without both

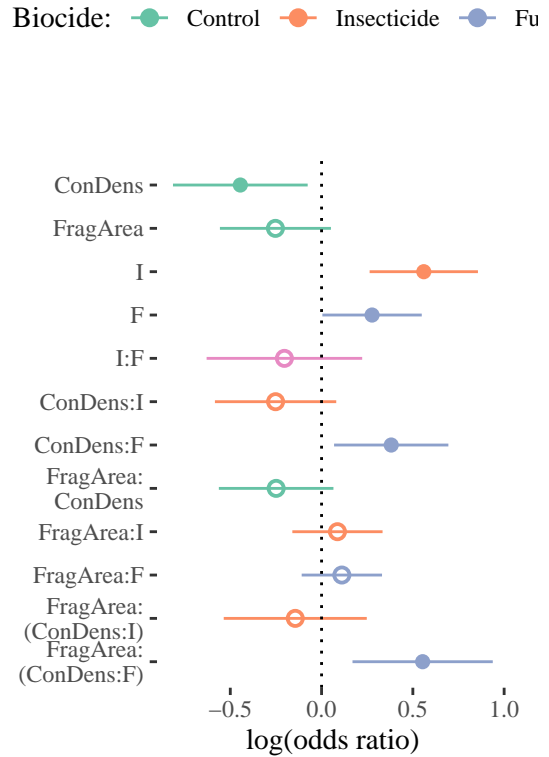
```
pl_cdd_s_2 <- ggplot(filter(p_cdd_s_ris, trt != "Both"),
  aes(x=con_dens, y = predicted, colour = trt)) +
  ggh4x::facet_nested(~facet_lab + frag_area) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = trt),
    colour = NA, alpha = 0.3) +
  geom_line(linewidth = 1.2) +
  geom_point(data = filter(pr_cdd_s_ris, trt != "Both")) +
  scale_colour_brewer(palette="Set2") +
  scale_fill_brewer(palette="Set2", guide = "none") +
  labs(x = expression(Conspecific-density~(m^-2)), y = "Pr(Survival)",
    colour = "Treatment") + theme(legend.position="none")

mod_plot2 <- (pl_cdd_s_2 | tp_cdd_s_ris ) +
  plot_layout(widths=c(0.6, 0.4)) + plot_annotation(tag_level = "A") ## better
mod_plot2
```

A



B



```
ggsave(mod_plot2, file = "figures/model_results.png", height = 5.5, width = 7.5)
```

3.1.7 Plotting effects of fragment area

The effects are complex and hinge on a non-significant interaction between fragment area and the fungicide effect. To interrogate them more, here are some plots (basically Neyman-Johnson interaction plots)

```
## plot the effect of density over fragment size
## helps to scale and log data outside the model formula to set this up
int_data <- sdls |>
  mutate(con_dens_ss = scale(con_dens_s),
         tot_dens_ss = scale(tot_dens_s),
         fragsize_s = scale(fragment.size))

int_mod <- glmmTMB(Pr_s ~ slope.degrees_s +
  trt_I:trt_F +
  (tot_dens_ss + con_dens_ss) *
  (trt_I + trt_F) * fragsize_s +
  (1 + tot_dens_ss + con_dens_ss | species) +
  (1 | site/loc/gr/plot),
  weights = census.start, family = binomial,
  data = int_data)

preddat <- expand.grid(
  trt_F = levels(int_data$trt_F),
```

```

trt_I = levels(int_data$trt_I),
con_dens_ss = 1,
fragsize_s = seq(-1, 2.1, length = 20)) |>
filter(!(trt_F == "F" & trt_I == "I"))

xmat <- model.matrix(~ con_dens_ss + con_dens_ss:(trt_F + trt_I + fragsize_s) +
                     con_dens_ss:trt_F:fragsize_s +
                     con_dens_ss:trt_I:fragsize_s,
                     preddat)[ , -1]

preddat$int_hat <- as.vector(xmat %*% fixef(int_mod)$cond[colnames(xmat)])
vmat <- (vcov(int_mod)$cond[colnames(xmat), colnames(xmat)])
preddat$int_se <- sqrt(diag(xmat %*% vmat %*% t(xmat)))

preddat <- preddat |> mutate(.lower = int_hat - 1.96*int_se,
                           .upper = int_hat + 1.96*int_se,
                           frag_area = fragsize_s*
                             sd(sdls$fragment.size) +
                             mean(sdls$fragment.size),
                           trt = factor(case_when(
                             trt_F == "0" & trt_I == "0" ~ "Control",
                             trt_F == "F" & trt_I == "0" ~ "Fungicide",
                             trt_F == "0" & trt_I == "I" ~ "Insecticide")))

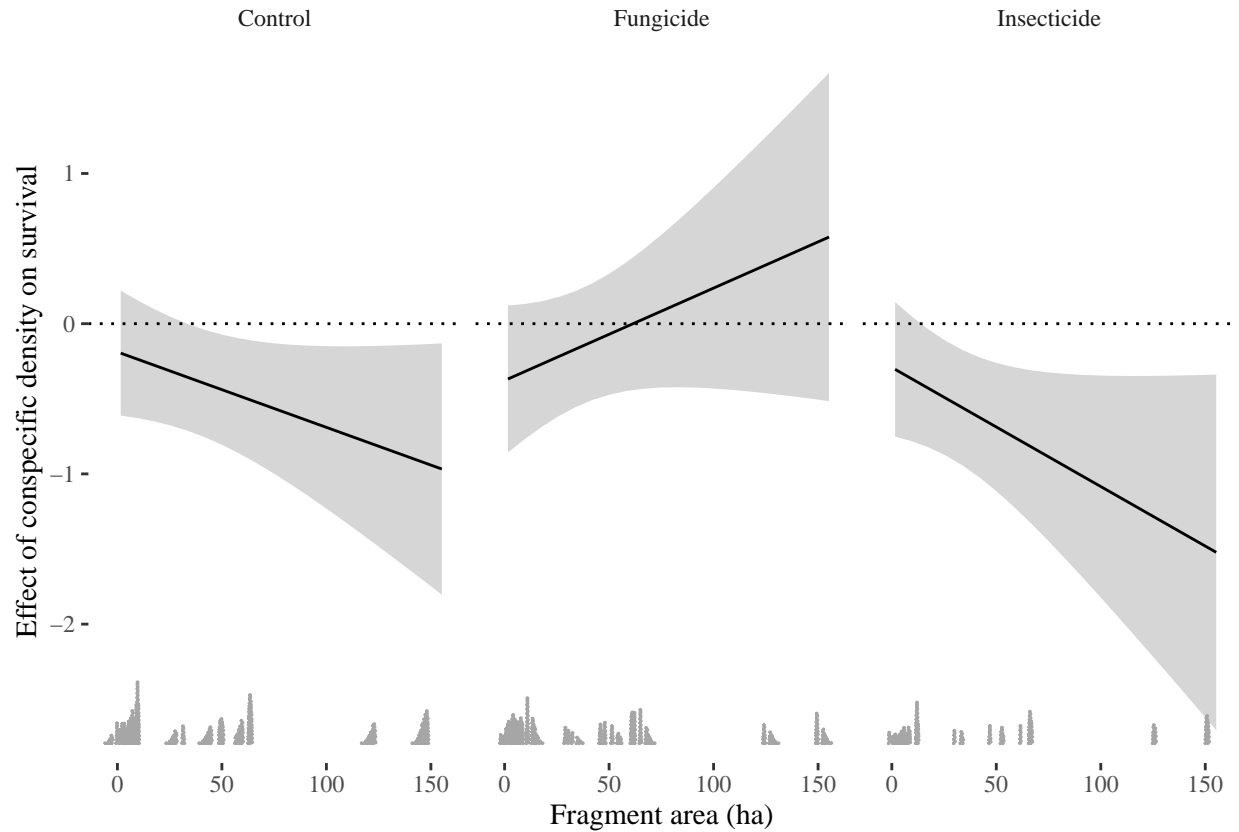
int_plot <- ggplot(preddat, aes(x = frag_area)) + facet_wrap( ~ trt) +
  geom_ribbon(aes(y = int_hat, ymin = .lower, ymax = .upper),
            alpha = 0.2, colour = NA) +
  geom_line(aes(y = int_hat)) + geom_hline(yintercept=0, linetype = "dotted") +
  labs(x = "Fragment area (ha)",
       y = "Effect of conspecific density on survival")

sdls <- mutate(sdls, trt = case_when(
  trt_F == "F" ~ "F",
  trt_I == "I" ~ "I",
  .default = "C"),
  trt = factor(trt, labels = c("Control", "Fungicide", "Insecticide")))

int_plot <- int_plot +
  ggdist::geom_dots(data = sdls, aes(x = fragment.size), y = -2.8,
                    smooth = ggdist::smooth_unbounded(), layout = "swarm",
                    side = "top", binwidth = 1, # alpha = 0.7,
                    overflow = "compress")

int_plot

```



```
ggsave(int_plot, file = "figures/interaction_plot.png", width=6.6, height = 4)
```

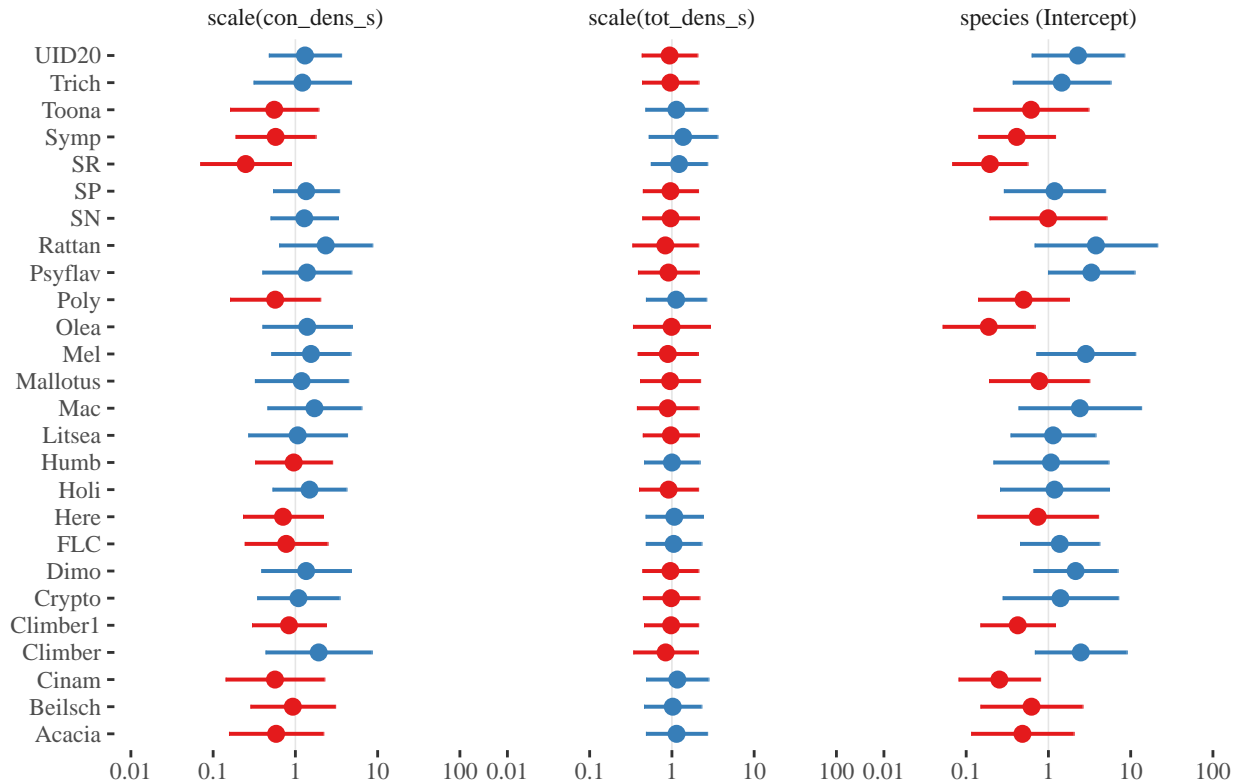
3.2 Species specific inferences.

Initial analyses suggested that some species were heavily influencing the results.

The random slope should partly account for that.

```
sjPlot::plot_model(m_cdd_s_ris, type = "re", terms = "species", ri.nr = 1)
```


Random effects



```
## observable variation among species in CDD slopes, but not in tot_dens_s
sp_eff <- as.data.frame(ranef(m_cdd_s_ris, condVar = T)$cond$species)
```

```
sp_eff <- bind_cols(sp_eff,
  t(apply(attr(sp_eff, "condVar"), 3, function(x)
    sqrt(diag(x))))))
```

```
## New names:
## * ' ' -> '...4'
## * ' ' -> '...5'
## * ' ' -> '...6'
```

```
names(sp_eff) <- c("Intercept", "con_dens", "tot_dens",
  "Intercept_se", "con_dens_se", "tot_dens_se")
```

```
## extract total effects
```

```
sp_eff <- mutate(sp_eff, sp_names = row.names(sp_eff),
  Intercept = Intercept + fixef(m_cdd_s_ris)$cond[1],
  con_dens = con_dens +
    fixef(m_cdd_s_ris)$cond["scale(con_dens_s)"],
  tot_dens = tot_dens +
    fixef(m_cdd_s_ris)$cond["scale(tot_dens)"])
```

```
sp_eff <- left_join(sp_eff, sp_codes, by = c("sp_names" = "code"))
## wrangle species names
```

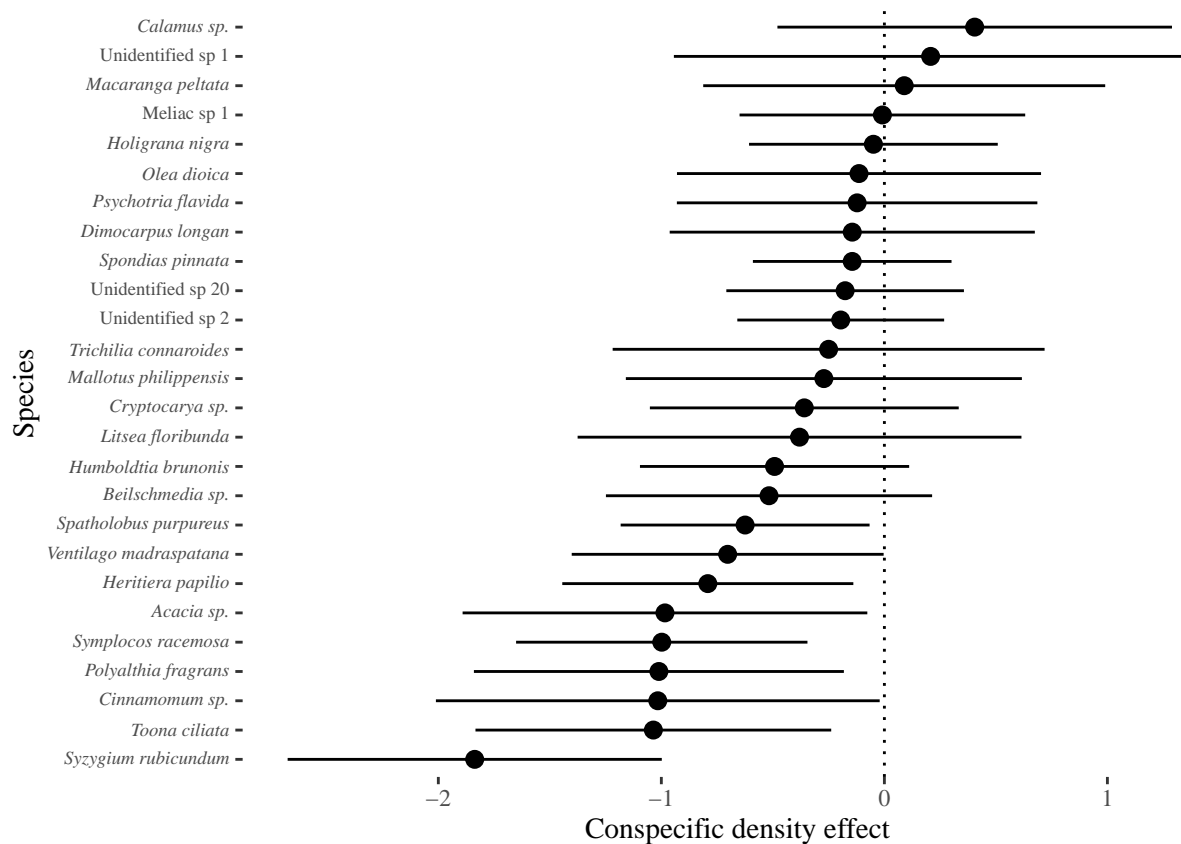
```

sp_eff <- sp_eff |> mutate(spbins = case_when(
  genus %in% c("Unidentified", "Meliac") ~ paste(genus, species, sep = "~"),
  genus != "Unidentified" & str_starts("sp", species) ~
    paste(paste0("italic('", genus, "'"), species, sep = "~"),
    paste0("italic('", paste(genus, species, sep = " "), "'"))))

blup_plot <- sp_eff |> arrange(con_dens) |>
  ggplot(aes(y = reorder(spbins, con_dens), x = con_dens,
    xmin = con_dens - 2*con_dens_se,
    xmax = con_dens + 2*con_dens_se)) +
  geom_vline(xintercept=0, linetype = "dotted") +
  geom_pointrange() +
  scale_y_discrete(labels = scales::label_parse()) +
  labs(x = "Conspecific density effect", y = "Species")

blup_plot <- blup_plot + theme(axis.text.y = element_text(size = 7))
blup_plot

```



```

# ggsave(blup_plot, file = "figures/cdd_blups.png", width = 4, height = 5)

anova(m_cdd_s_ris, m_cdd_s_ri)

```

```
## Data: sdfs
```

```
## Models:
```

```
## m_cdd_s_ri: Pr_s ~ slope.degrees_s + trt_I:trt_F + (scale(tot_dens_s) + scale(con_dens_s)) * , zi=~0
```

```
## m_cdd_s_ri:      (trt_I + trt_F) * scale(fragment.size) + (1 | species) + , zi=~0, disp=~1
## m_cdd_s_ri:      (1 | site/loc/gr/plot), zi=~0, disp=~1
## m_cdd_s_ris: Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) + , zi=~0, disp=~1
## m_cdd_s_ris:      scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) + , zi=~0, disp=~1
## m_cdd_s_ris:      scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) + , zi=~0, disp=~1
## m_cdd_s_ris:      (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 | , zi=~0, disp=~1
## m_cdd_s_ris:      site/loc/gr/plot), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## m_cdd_s_ri 25 2232.1 2353.9 -1091.0 2182.1
## m_cdd_s_ris 30 2215.1 2361.3 -1077.5 2155.1 27.02      5 5.654e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Substantial variation in cdd among species -

Perhaps remove most abundant species to check if patterns are robust.

```
sdl$ |> group_by(species) |> summarise(n = sum(census.start)) |>
  arrange(desc(n)) |> print(n = 26)
```

```
## # A tibble: 26 x 2
##   species      n
##   <fct>    <int>
## 1 SR        3598
## 2 Symp       636
## 3 Climber1   627
## 4 FLC        313
## 5 Cinam      137
## 6 Psyflav    116
## 7 Dimo        99
## 8 SP          85
## 9 Litsea      72
## 10 Olea       71
## 11 UID20       65
## 12 Climber     59
## 13 Poly        54
## 14 Mel         43
## 15 Beilsch     42
## 16 Holi        34
## 17 Toona       28
## 18 SN          25
## 19 Trich       22
## 20 Mallotus    19
## 21 Acacia      16
## 22 Mac         12
## 23 Rattan      11
## 24 Humb        9
## 25 Crypto       8
## 26 Here        7
```

```
sp_common <- sdl$ |> group_by(species) |> summarise(n = sum(census.start)) |>
  arrange(desc(n)) |> pull(species)
sp_mods <- lapply(c("none", as.character(sp_common[1:5])), function(i) {
  update(m_cdd_s_ris, data = filter(sdl$, !species == i))})
```

```

## Warning in (function (start, objective, gradient = NULL, hessian = NULL, :
## NA/NaN function evaluation
## Warning in (function (start, objective, gradient = NULL, hessian = NULL, :
## NA/NaN function evaluation
## Warning in (function (start, objective, gradient = NULL, hessian = NULL, :
## NA/NaN function evaluation

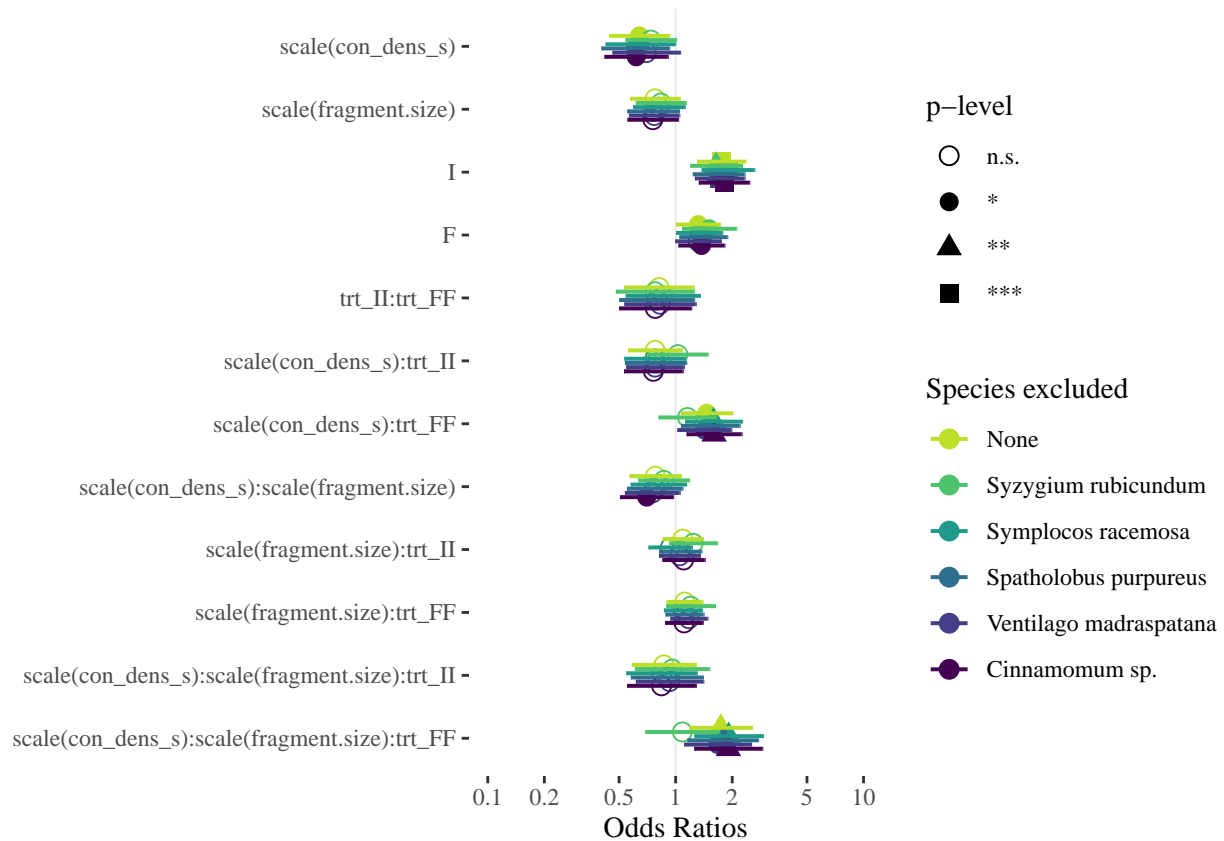
## Warning in finalizeTMB(TMBStruc, obj, fit, h, data.tmb.old): Model convergence
## problem; non-positive-definite Hessian matrix. See vignette('troubleshooting')

## Warning in finalizeTMB(TMBStruc, obj, fit, h, data.tmb.old): Model convergence
## problem; singular convergence (7). See vignette('troubleshooting'),
## help('diagnose')

sp_codes <- mutate(sp_codes, spbin = paste(genus, species))
term_nms <- names(fixef(sp_mods[[1]])$cond)
names(sp_mods) <- c("None", as.character(sp_common[1:5]))
plot_models(sp_mods,
  rm.terms = c("slope.degrees_s",
    term_nms[str_detect(term_nms, "tot")] ),
  m.labels = c("None",
    sp_codes$spbin[match(sp_common[1:5], sp_codes$code)] ),
  p.shape=TRUE) + labs(colour = "Species excluded") +
  scale_color_viridis_d(end=0.9) ## getting rid of the awful yellow.

## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.

```



```
map(sp_mods, summary)
```

```
## $None
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
##       site/loc/gr/plot)
## Data: filter(sdls, !species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##  2215.0   2361.3 -1077.5   2155.0     938
##
## Random effects:
##
## Conditional model:
## Groups      Name                Variance Std.Dev.  Corr
## species      (Intercept)         1.027e+00 1.0131846
##               scale(con_dens_s)  3.887e-01 0.6234621  0.56
##               scale(tot_dens_s)  3.738e-02 0.1933384 -0.47 -0.71
## plot:gr:loc:site (Intercept)     2.788e-01 0.5280003
## gr:loc:site      (Intercept)     2.057e-01 0.4535170
```

```

## loc:site      (Intercept)      4.782e-01 0.6915250
## site          (Intercept)      2.188e-08 0.0001479
## Number of obs: 968, groups:
## species, 26; plot:gr:loc:site, 474; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)      0.66723    0.27771   2.403
## slope.degrees_s  -0.18268    0.07133  -2.561
## scale(tot_dens_s) -0.10921    0.15595  -0.700
## scale(con_dens_s) -0.44496    0.18820  -2.364
## scale(fragment.size) -0.25279    0.15514  -1.629
## trt_II            0.55988    0.15137   3.699
## trt_FF            0.27661    0.13886   1.992
## trt_II:trt_FF     -0.20355    0.21738  -0.936
## scale(tot_dens_s):trt_II 0.04971    0.19245   0.258
## scale(tot_dens_s):trt_FF -0.01093    0.14816  -0.074
## scale(con_dens_s):trt_II -0.25189    0.16952  -1.486
## scale(con_dens_s):trt_FF 0.38152    0.15970   2.389
## scale(tot_dens_s):scale(fragment.size) 0.09861    0.11221   0.879
## scale(con_dens_s):scale(fragment.size) -0.24883    0.16012  -1.554
## scale(fragment.size):trt_II 0.08701    0.12608   0.690
## scale(fragment.size):trt_FF 0.11108    0.11225   0.990
## scale(tot_dens_s):scale(fragment.size):trt_II 0.07160    0.22351   0.320
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.17654    0.20314  -0.869
## scale(con_dens_s):scale(fragment.size):trt_II -0.14412    0.19987  -0.721
## scale(con_dens_s):scale(fragment.size):trt_FF 0.55367    0.19600   2.825
##
##              Pr(>|z|)
## (Intercept)      0.016277 *
## slope.degrees_s  0.010437 *
## scale(tot_dens_s) 0.483771
## scale(con_dens_s) 0.018061 *
## scale(fragment.size) 0.103231
## trt_II            0.000217 ***
## trt_FF            0.046363 *
## trt_II:trt_FF     0.349094
## scale(tot_dens_s):trt_II 0.796159
## scale(tot_dens_s):trt_FF 0.941199
## scale(con_dens_s):trt_II 0.137312
## scale(con_dens_s):trt_FF 0.016894 *
## scale(tot_dens_s):scale(fragment.size) 0.379537
## scale(con_dens_s):scale(fragment.size) 0.120172
## scale(fragment.size):trt_II 0.490132
## scale(fragment.size):trt_FF 0.322352
## scale(tot_dens_s):scale(fragment.size):trt_II 0.748722
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.384811
## scale(con_dens_s):scale(fragment.size):trt_II 0.470860
## scale(con_dens_s):scale(fragment.size):trt_FF 0.004731 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $SR
## Family: binomial ( logit )
## Formula:

```

```

## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##   scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##   scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##   (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
##   site/loc/gr/plot)
## Data: filter(sdls, !species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##  1538.8   1679.2   -739.4   1478.8     766
##
## Random effects:
##
## Conditional model:
##   Groups      Name              Variance Std.Dev. Corr
##   species      (Intercept)       9.948e-01 0.997383
##               scale(con_dens_s)  1.666e-01 0.408201  0.49
##               scale(tot_dens_s)  5.029e-02 0.224248 -0.68 -0.95
##   plot:gr:loc:site (Intercept)   9.819e-02 0.313348
##   gr:loc:site      (Intercept)   1.978e-01 0.444692
##   loc:site         (Intercept)   4.018e-01 0.633879
##   site             (Intercept)   1.277e-08 0.000113
## Number of obs: 796, groups:
## species, 25; plot:gr:loc:site, 436; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##                                     Estimate Std. Error z value
## (Intercept)                        0.63850    0.27529   2.319
## slope.degrees_s                    -0.02056    0.08536  -0.241
## scale(tot_dens_s)                  -0.17944    0.16530  -1.085
## scale(con_dens_s)                  -0.30396    0.15773  -1.927
## scale(fragment.size)               -0.18107    0.15650  -1.157
## trt_II                             0.49663    0.16145   3.076
## trt_FF                             0.41105    0.16944   2.426
## trt_II:trt_FF                     -0.25253    0.24472  -1.032
## scale(tot_dens_s):trt_II           -0.08794    0.22453  -0.392
## scale(tot_dens_s):trt_FF           -0.03447    0.19921  -0.173
## scale(con_dens_s):trt_II           0.02762    0.18700   0.148
## scale(con_dens_s):trt_FF           0.14500    0.18050   0.803
## scale(tot_dens_s):scale(fragment.size) -0.06969    0.14652  -0.476
## scale(con_dens_s):scale(fragment.size) -0.14534    0.15883  -0.915
## scale(fragment.size):trt_II        0.21404    0.14875   1.439
## scale(fragment.size):trt_FF        0.18394    0.15205   1.210
## scale(tot_dens_s):scale(fragment.size):trt_II 0.11592    0.27765   0.418
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.10503    0.25202  -0.417
## scale(con_dens_s):scale(fragment.size):trt_II -0.04202    0.23315  -0.180
## scale(con_dens_s):scale(fragment.size):trt_FF 0.08224    0.23157   0.355
##                                     Pr(>|z|)
## (Intercept)                        0.0204 *
## slope.degrees_s                    0.8096
## scale(tot_dens_s)                   0.2777
## scale(con_dens_s)                   0.0540 .
## scale(fragment.size)                0.2473
## trt_II                              0.0021 **

```

```

## trt_FF                                0.0153 *
## trt_II:trt_FF                        0.3021
## scale(tot_dens_s):trt_II             0.6953
## scale(tot_dens_s):trt_FF             0.8626
## scale(con_dens_s):trt_II             0.8826
## scale(con_dens_s):trt_FF             0.4218
## scale(tot_dens_s):scale(fragment.size) 0.6343
## scale(con_dens_s):scale(fragment.size) 0.3601
## scale(fragment.size):trt_II          0.1502
## scale(fragment.size):trt_FF          0.2264
## scale(tot_dens_s):scale(fragment.size):trt_II 0.6763
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.6769
## scale(con_dens_s):scale(fragment.size):trt_II 0.8570
## scale(con_dens_s):scale(fragment.size):trt_FF 0.7225
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $Symp
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
##       site/loc/gr/plot)
## Data: filter(sdls, !species == i)
## Weights: census.start
##
##      AIC      BIC    logLik deviance df.resid
##      NA       NA      NA      NA      816
##
## Random effects:
##
## Conditional model:
## Groups      Name              Variance Std.Dev.  Corr
## species      (Intercept)      1.197e+00 1.094e+00
##              scale(con_dens_s) 5.227e-01 7.230e-01 0.47
##              scale(tot_dens_s) 1.641e-02 1.281e-01 -0.36 -0.99
## plot:gr:loc:site (Intercept)  2.593e-01 5.093e-01
## gr:loc:site      (Intercept)  2.719e-01 5.214e-01
## loc:site         (Intercept)  4.625e-01 6.801e-01
## site             (Intercept)  1.189e-295 3.449e-148
## Number of obs: 846, groups:
## species, 25; plot:gr:loc:site, 443; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)    0.623087  0.299655  2.079
## slope.degrees_s -0.238159  0.078978 -3.016
## scale(tot_dens_s) -0.172296  0.157359 -1.095
## scale(con_dens_s) -0.431181  0.217797 -1.980
## scale(fragment.size) -0.204384  0.161807 -1.263
## trt_II          0.642882  0.164703  3.903
## trt_FF          0.288345  0.145095  1.987

```



```

## trt_II:trt_FF -0.156364 0.231996 -0.674
## scale(tot_dens_s):trt_II -0.045501 0.201656 -0.226
## scale(tot_dens_s):trt_FF -0.003621 0.155956 -0.023
## scale(con_dens_s):trt_II -0.254715 0.190675 -1.336
## scale(con_dens_s):trt_FF 0.465605 0.178066 2.615
## scale(tot_dens_s):scale(fragment.size) 0.098487 0.117733 0.837
## scale(con_dens_s):scale(fragment.size) -0.211136 0.172688 -1.223
## scale(fragment.size):trt_II -0.065994 0.135574 -0.487
## scale(fragment.size):trt_FF 0.090493 0.119279 0.759
## scale(tot_dens_s):scale(fragment.size):trt_II 0.108954 0.228006 0.478
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.251520 0.211014 -1.192
## scale(con_dens_s):scale(fragment.size):trt_II -0.171561 0.220288 -0.779
## scale(con_dens_s):scale(fragment.size):trt_FF 0.650795 0.214434 3.035
## Pr(>|z|)
## (Intercept) 0.03759 *
## slope.degrees_s 0.00257 **
## scale(tot_dens_s) 0.27355
## scale(con_dens_s) 0.04773 *
## scale(fragment.size) 0.20654
## trt_II 9.49e-05 ***
## trt_FF 0.04689 *
## trt_II:trt_FF 0.50032
## scale(tot_dens_s):trt_II 0.82149
## scale(tot_dens_s):trt_FF 0.98148
## scale(con_dens_s):trt_II 0.18160
## scale(con_dens_s):trt_FF 0.00893 **
## scale(tot_dens_s):scale(fragment.size) 0.40286
## scale(con_dens_s):scale(fragment.size) 0.22146
## scale(fragment.size):trt_II 0.62642
## scale(fragment.size):trt_FF 0.44805
## scale(tot_dens_s):scale(fragment.size):trt_II 0.63275
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.23328
## scale(con_dens_s):scale(fragment.size):trt_II 0.43610
## scale(con_dens_s):scale(fragment.size):trt_FF 0.00241 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $Climber1
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
## scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
## scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
## (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
## site/loc/gr/plot)
## Data: filter(sdls, !species == i)
## Weights: census.start
##
## AIC BIC logLik deviance df.resid
## 2004.3 2148.1 -972.1 1944.3 861
##
## Random effects:
##
## Conditional model:

```

```

## Groups          Name          Variance Std.Dev.  Corr
## species         (Intercept)    1.110e+00 1.0536851
##                  scale(con_dens_s) 4.279e-01 0.6541436 0.58
##                  scale(tot_dens_s) 3.649e-02 0.1910162 -0.54 -0.62
## plot:gr:loc:site (Intercept)    3.125e-01 0.5589869
## gr:loc:site      (Intercept)    2.224e-01 0.4716092
## loc:site         (Intercept)    4.840e-01 0.6957357
## site            (Intercept)    1.601e-08 0.0001265
## Number of obs: 891, groups:
## species, 25; plot:gr:loc:site, 468; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##
##                  Estimate Std. Error z value
## (Intercept)      0.72418    0.29263   2.475
## slope.degrees_s  -0.18938    0.07488  -2.529
## scale(tot_dens_s) -0.05951    0.17064  -0.349
## scale(con_dens_s) -0.49321    0.21218  -2.325
## scale(fragment.size) -0.27528    0.16120  -1.708
## trt_II            0.52847    0.16187   3.265
## trt_FF            0.33985    0.14975   2.269
## trt_II:trt_FF     -0.23080    0.23385  -0.987
## scale(tot_dens_s):trt_II 0.02794    0.19797   0.141
## scale(tot_dens_s):trt_FF -0.02253    0.15547  -0.145
## scale(con_dens_s):trt_II -0.24455    0.19155  -1.277
## scale(con_dens_s):trt_FF 0.42565    0.18361   2.318
## scale(tot_dens_s):scale(fragment.size) 0.13497    0.11919   1.132
## scale(con_dens_s):scale(fragment.size) -0.25574    0.17360  -1.473
## scale(fragment.size):trt_II 0.05831    0.13213   0.441
## scale(fragment.size):trt_FF 0.10946    0.11909   0.919
## scale(tot_dens_s):scale(fragment.size):trt_II 0.01717    0.23536   0.073
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.16414    0.22013  -0.746
## scale(con_dens_s):scale(fragment.size):trt_II -0.10702    0.22543  -0.475
## scale(con_dens_s):scale(fragment.size):trt_FF 0.57845    0.22089   2.619
##
##                  Pr(>|z|)
## (Intercept)      0.01333 *
## slope.degrees_s  0.01144 *
## scale(tot_dens_s) 0.72728
## scale(con_dens_s) 0.02010 *
## scale(fragment.size) 0.08770 .
## trt_II           0.00110 **
## trt_FF           0.02324 *
## trt_II:trt_FF    0.32367
## scale(tot_dens_s):trt_II 0.88777
## scale(tot_dens_s):trt_FF 0.88479
## scale(con_dens_s):trt_II 0.20171
## scale(con_dens_s):trt_FF 0.02044 *
## scale(tot_dens_s):scale(fragment.size) 0.25748
## scale(con_dens_s):scale(fragment.size) 0.14071
## scale(fragment.size):trt_II 0.65901
## scale(fragment.size):trt_FF 0.35802
## scale(tot_dens_s):scale(fragment.size):trt_II 0.94184
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.45590
## scale(con_dens_s):scale(fragment.size):trt_II 0.63498
## scale(con_dens_s):scale(fragment.size):trt_FF 0.00882 **

```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $FLC
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
##       site/loc/gr/plot)
## Data: filter(sdls, !species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
## 2081.8   2226.0 -1010.9   2021.8      874
##
## Random effects:
##
## Conditional model:
## Groups          Name              Variance Std.Dev.  Corr
## species          (Intercept)       1.054e+00 1.0267284
##                  scale(con_dens_s)  5.047e-01 0.7104215  0.55
##                  scale(tot_dens_s)  8.428e-02 0.2903098 -0.44 -0.72
## plot:gr:loc:site (Intercept)       2.697e-01 0.5193591
## gr:loc:site      (Intercept)       1.919e-01 0.4380878
## loc:site         (Intercept)       4.780e-01 0.6913691
## site             (Intercept)       2.726e-08 0.0001651
## Number of obs: 904, groups:
## species, 25; plot:gr:loc:site, 466; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)      0.60130    0.28614   2.101
## slope.degrees_s  -0.19046    0.07263  -2.622
## scale(tot_dens_s) -0.24177    0.17930  -1.348
## scale(con_dens_s) -0.35898    0.21142  -1.698
## scale(fragment.size) -0.26189    0.15705  -1.668
## trt_II           0.54049    0.15528   3.481
## trt_FF           0.27584    0.14241   1.937
## trt_II:trt_FF    -0.19031    0.22314  -0.853
## scale(tot_dens_s):trt_II  0.10583    0.20414   0.518
## scale(tot_dens_s):trt_FF  0.04725    0.15841   0.298
## scale(con_dens_s):trt_II -0.25219    0.18033  -1.398
## scale(con_dens_s):trt_FF  0.35289    0.16866   2.092
## scale(tot_dens_s):scale(fragment.size)  0.17530    0.11231   1.561
## scale(con_dens_s):scale(fragment.size) -0.28594    0.17139  -1.668
## scale(fragment.size):trt_II  0.04834    0.12808   0.377
## scale(fragment.size):trt_FF  0.16345    0.11585   1.411
## scale(tot_dens_s):scale(fragment.size):trt_II -0.05304    0.23021  -0.230
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.13798    0.21737  -0.635
## scale(con_dens_s):scale(fragment.size):trt_II -0.07390    0.21099  -0.350
## scale(con_dens_s):scale(fragment.size):trt_FF  0.51571    0.20874   2.471
##
##              Pr(>|z|)

```

```

## (Intercept) 0.03560 *
## slope.degrees_s 0.00873 **
## scale(tot_dens_s) 0.17753
## scale(con_dens_s) 0.08951 .
## scale(fragment.size) 0.09540 .
## trt_II 0.00050 ***
## trt_FF 0.05274 .
## trt_II:trt_FF 0.39374
## scale(tot_dens_s):trt_II 0.60416
## scale(tot_dens_s):trt_FF 0.76549
## scale(con_dens_s):trt_II 0.16196
## scale(con_dens_s):trt_FF 0.03641 *
## scale(tot_dens_s):scale(fragment.size) 0.11854
## scale(con_dens_s):scale(fragment.size) 0.09525 .
## scale(fragment.size):trt_II 0.70588
## scale(fragment.size):trt_FF 0.15828
## scale(tot_dens_s):scale(fragment.size):trt_II 0.81778
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.52559
## scale(con_dens_s):scale(fragment.size):trt_II 0.72616
## scale(con_dens_s):scale(fragment.size):trt_FF 0.01349 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $Cinam
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
##       site/loc/gr/plot)
## Data: filter(sdls, !species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##  2059.4   2202.9   -999.7   1999.4      852
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.  Corr
##   species      (Intercept)  9.639e-01 0.9817926
##              scale(con_dens_s) 4.032e-01 0.6349760  0.45
##              scale(tot_dens_s) 4.948e-02 0.2224359 -0.38 -0.79
##   plot:gr:loc:site (Intercept)  2.906e-01 0.5390979
##   gr:loc:site      (Intercept)  2.685e-01 0.5181503
##   loc:site         (Intercept)  4.422e-01 0.6649552
##   site             (Intercept)  2.109e-08 0.0001452
## Number of obs: 882, groups:
## species, 25; plot:gr:loc:site, 461; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##
##                                     Estimate Std. Error z value
## (Intercept)                        0.70050    0.27933   2.508

```

```
## slope.degrees_s          -0.19170    0.07382   -2.597
## scale(tot_dens_s)        -0.13076    0.16765   -0.780
## scale(con_dens_s)        -0.48358    0.19780   -2.445
## scale(fragment.size)     -0.27909    0.15808   -1.765
## trt_II                   0.59369    0.15775    3.763
## trt_FF                   0.31667    0.14362    2.205
## trt_II:trt_FF            -0.24942    0.22545   -1.106
## scale(tot_dens_s):trt_II  0.05476    0.20594    0.266
## scale(tot_dens_s):trt_FF -0.03671    0.15834   -0.232
## scale(con_dens_s):trt_II -0.27294    0.18369   -1.486
## scale(con_dens_s):trt_FF  0.47156    0.17190    2.743
## scale(tot_dens_s):scale(fragment.size) 0.11020    0.12150    0.907
## scale(con_dens_s):scale(fragment.size) -0.35449    0.16559   -2.141
## scale(fragment.size):trt_II 0.09773    0.13213    0.740
## scale(fragment.size):trt_FF 0.10274    0.11743    0.875
## scale(tot_dens_s):scale(fragment.size):trt_II 0.09621    0.23656    0.407
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.23337    0.21662   -1.077
## scale(con_dens_s):scale(fragment.size):trt_II -0.17272    0.21472   -0.804
## scale(con_dens_s):scale(fragment.size):trt_FF 0.64615    0.21256    3.040
##                           Pr(>|z|)
## (Intercept)              0.012149 *
## slope.degrees_s          0.009406 **
## scale(tot_dens_s)         0.435430
## scale(con_dens_s)         0.014492 *
## scale(fragment.size)      0.077487 .
## trt_II                   0.000168 ***
## trt_FF                   0.027460 *
## trt_II:trt_FF            0.268580
## scale(tot_dens_s):trt_II  0.790319
## scale(tot_dens_s):trt_FF  0.816674
## scale(con_dens_s):trt_II  0.137320
## scale(con_dens_s):trt_FF  0.006083 **
## scale(tot_dens_s):scale(fragment.size) 0.364392
## scale(con_dens_s):scale(fragment.size) 0.032297 *
## scale(fragment.size):trt_II 0.459497
## scale(fragment.size):trt_FF 0.381631
## scale(tot_dens_s):scale(fragment.size):trt_II 0.684220
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.281345
## scale(con_dens_s):scale(fragment.size):trt_II 0.421187
## scale(con_dens_s):scale(fragment.size):trt_FF 0.002366 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Only species that makes a difference is *S. rubicundum* - removing it dampens interaction between density and fungicide (it is still there, but marginally non-significant)

what about single species models?

```
## base model.
## remove species random effect
names(sp_common) <- sp_common
single_sp_mods <- map(sp_common[1:5], function(i) {
  glmmTMB(Pr_s ~ slope.degrees_s +
    (scale(tot_dens_s) + scale(con_dens_s)) +
```

```

    scale(fragment.size) +
    trt_I*trt_F +
    (scale(tot_dens_s) + scale(con_dens_s)) *
    (trt_I + trt_F) *
    scale(fragment.size) +
    ## setting cor to 0 to converge
    (1|site/loc/gr/plot),
  weights = census.start,
  data = filter(sdls, species == i),
  family=binomial)})

names(single_sp_mods) <-
  sp_codes$spbin[match(names(single_sp_mods), sp_codes$code)]
single_sp_mods$All <- m_cdd_s_ris

map(single_sp_mods, summary)

## '$Syzygium rubicundum'
## Family: binomial (logit)
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (1 | site/loc/gr/plot)
## Data: filter(sdls, species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##    664.8    740.4   -308.4    616.8     148
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## plot:gr:loc:site (Intercept) 2.103e-01 0.4586119
## gr:loc:site      (Intercept) 1.693e-01 0.4114793
## loc:site         (Intercept) 6.510e-01 0.8068493
## site             (Intercept) 1.922e-07 0.0004384
## Number of obs: 172, groups:
## plot:gr:loc:site, 172; gr:loc:site, 61; loc:site, 30; site, 16
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)   -0.14989    0.23065  -0.650
## slope.degrees_s -0.31491    0.10682  -2.948
## scale(tot_dens_s)  0.04320    0.14091   0.307
## scale(con_dens_s) -0.65441    0.16022  -4.084
## scale(fragment.size) -0.19506    0.23153  -0.842
## trt_II          0.69260    0.25888   2.675
## trt_FF          -0.01042    0.20949  -0.050
## trt_II:trt_FF    -0.24727    0.33821  -0.731
## scale(tot_dens_s):trt_II -0.04539    0.34754  -0.131
## scale(tot_dens_s):trt_FF -0.05204    0.18634  -0.279

```

```

## scale(con_dens_s):trt_II          0.06969    0.24165    0.288
## scale(con_dens_s):trt_FF          0.07628    0.21351    0.357
## scale(tot_dens_s):scale(fragment.size) 0.32513    0.12538    2.593
## scale(con_dens_s):scale(fragment.size) -0.08381    0.11571   -0.724
## scale(fragment.size):trt_II       -0.07710    0.24413   -0.316
## scale(fragment.size):trt_FF       -0.28855    0.20967   -1.376
## scale(tot_dens_s):scale(fragment.size):trt_II -0.42050    0.33640   -1.250
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.26047    0.33499   -0.778
## scale(con_dens_s):scale(fragment.size):trt_II -0.01368    0.17338   -0.079
## scale(con_dens_s):scale(fragment.size):trt_FF  0.37473    0.15094    2.483
##                                     Pr(>|z|)
## (Intercept)                        0.51578
## slope.degrees_s                    0.00320 **
## scale(tot_dens_s)                  0.75919
## scale(con_dens_s)                  4.42e-05 ***
## scale(fragment.size)               0.39952
## trt_II                             0.00746 **
## trt_FF                             0.96033
## trt_II:trt_FF                     0.46470
## scale(tot_dens_s):trt_II           0.89608
## scale(tot_dens_s):trt_FF           0.78005
## scale(con_dens_s):trt_II           0.77306
## scale(con_dens_s):trt_FF           0.72090
## scale(tot_dens_s):scale(fragment.size) 0.00951 **
## scale(con_dens_s):scale(fragment.size) 0.46888
## scale(fragment.size):trt_II        0.75214
## scale(fragment.size):trt_FF        0.16877
## scale(tot_dens_s):scale(fragment.size):trt_II 0.21130
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.43684
## scale(con_dens_s):scale(fragment.size):trt_II 0.93710
## scale(con_dens_s):scale(fragment.size):trt_FF 0.01304 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $'Symplocos racemosa'
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (1 | site/loc/gr/plot)
## Data: filter(sdls, species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##    328.1    395.4   -140.0    280.1      98
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
## plot:gr:loc:site (Intercept) 1.625e-01 0.4030853
## gr:loc:site      (Intercept) 2.503e-02 0.1582100
## loc:site         (Intercept) 5.766e-01 0.7593371

```

```

## site (Intercept) 1.487e-08 0.0001219
## Number of obs: 122, groups:
## plot:gr:loc:site, 122; gr:loc:site, 53; loc:site, 24; site, 17
##
## Conditional model:
##
## Estimate Std. Error z value
## (Intercept) 0.71220 0.34523 2.063
## slope.degrees_s 0.19652 0.15944 1.233
## scale(tot_dens_s) 0.30384 0.33337 0.911
## scale(con_dens_s) 0.25698 0.61914 0.415
## scale(fragment.size) -0.22861 0.43806 -0.522
## trt_II -0.26647 0.48631 -0.548
## trt_FF 1.60922 0.79724 2.018
## trt_II:trt_FF -1.12097 0.69201 -1.620
## scale(tot_dens_s):trt_II -0.04651 0.73245 -0.064
## scale(tot_dens_s):trt_FF 1.53285 1.47131 1.042
## scale(con_dens_s):trt_II -1.73483 1.47049 -1.180
## scale(con_dens_s):trt_FF 0.89298 2.64710 0.337
## scale(tot_dens_s):scale(fragment.size) 0.10147 0.39163 0.259
## scale(con_dens_s):scale(fragment.size) 0.69530 0.85389 0.814
## scale(fragment.size):trt_II -0.33443 0.63470 -0.527
## scale(fragment.size):trt_FF 1.42770 0.91043 1.568
## scale(tot_dens_s):scale(fragment.size):trt_II -0.79311 0.95984 -0.826
## scale(tot_dens_s):scale(fragment.size):trt_FF 2.43647 2.06836 1.178
## scale(con_dens_s):scale(fragment.size):trt_II -2.56759 1.99589 -1.286
## scale(con_dens_s):scale(fragment.size):trt_FF 1.12732 3.66319 0.308
## Pr(>|z|)
## (Intercept) 0.0391 *
## slope.degrees_s 0.2177
## scale(tot_dens_s) 0.3621
## scale(con_dens_s) 0.6781
## scale(fragment.size) 0.6018
## trt_II 0.5837
## trt_FF 0.0435 *
## trt_II:trt_FF 0.1053
## scale(tot_dens_s):trt_II 0.9494
## scale(tot_dens_s):trt_FF 0.2975
## scale(con_dens_s):trt_II 0.2381
## scale(con_dens_s):trt_FF 0.7359
## scale(tot_dens_s):scale(fragment.size) 0.7956
## scale(con_dens_s):scale(fragment.size) 0.4155
## scale(fragment.size):trt_II 0.5983
## scale(fragment.size):trt_FF 0.1168
## scale(tot_dens_s):scale(fragment.size):trt_II 0.4086
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.2388
## scale(con_dens_s):scale(fragment.size):trt_II 0.1983
## scale(con_dens_s):scale(fragment.size):trt_FF 0.7583
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $'Spatholobus purpureus'
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +

```



```

##      scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##      scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##      (1 | site/loc/gr/plot)
## Data: filter(sdls, species == i)
## Weights: census.start
##
##      AIC      BIC    logLik deviance df.resid
##      221.1    277.4    -86.6    173.1      53
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
## plot:gr:loc:site (Intercept) 3.501e-11 5.917e-06
## gr:loc:site      (Intercept) 6.978e-12 2.642e-06
## loc:site         (Intercept) 1.120e-10 1.058e-05
## site             (Intercept) 3.560e-11 5.967e-06
## Number of obs: 77, groups:
## plot:gr:loc:site, 77; gr:loc:site, 30; loc:site, 15; site, 10
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)    -0.88691    0.24982  -3.550
## slope.degrees_s -0.40153    0.12585  -3.191
## scale(tot_dens_s) -1.01314    0.52171  -1.942
## scale(con_dens_s) -0.03815    0.13710  -0.278
## scale(fragment.size) -0.36087    0.24130  -1.496
## trt_II           1.22403    0.48781   2.509
## trt_FF           0.41325    0.37907   1.090
## trt_II:trt_FF    -0.31901    0.42278  -0.755
## scale(tot_dens_s):trt_II 0.17701    0.88399   0.200
## scale(tot_dens_s):trt_FF 0.78859    0.65603   1.202
## scale(con_dens_s):trt_II -0.20655    0.26658  -0.775
## scale(con_dens_s):trt_FF -0.18489    0.22084  -0.837
## scale(tot_dens_s):scale(fragment.size) -0.77759    0.50864  -1.529
## scale(con_dens_s):scale(fragment.size) -1.55347    0.86887  -1.788
## scale(fragment.size):trt_II -1.70031    1.44116  -1.180
## scale(fragment.size):trt_FF 1.48540    0.63381   2.344
## scale(tot_dens_s):scale(fragment.size):trt_II 0.42592    0.79637   0.535
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.40897    0.63428   0.645
## scale(con_dens_s):scale(fragment.size):trt_II -5.94422    4.07890  -1.457
## scale(con_dens_s):scale(fragment.size):trt_FF 3.21763    1.72268   1.868
##
##              Pr(>|z|)
## (Intercept)    0.000385 ***
## slope.degrees_s 0.001420 **
## scale(tot_dens_s) 0.052141 .
## scale(con_dens_s) 0.780831
## scale(fragment.size) 0.134775
## trt_II          0.012099 *
## trt_FF          0.275639
## trt_II:trt_FF    0.450521
## scale(tot_dens_s):trt_II 0.841293
## scale(tot_dens_s):trt_FF 0.229340
## scale(con_dens_s):trt_II 0.438433

```

```

## scale(con_dens_s):trt_FF                                0.402457
## scale(tot_dens_s):scale(fragment.size)                 0.126322
## scale(con_dens_s):scale(fragment.size)                 0.073789 .
## scale(fragment.size):trt_II                             0.238070
## scale(fragment.size):trt_FF                             0.019098 *
## scale(tot_dens_s):scale(fragment.size):trt_II 0.592770
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.519066
## scale(con_dens_s):scale(fragment.size):trt_II 0.145030
## scale(con_dens_s):scale(fragment.size):trt_FF 0.061790 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $'Ventilago madraspatana'
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (1 | site/loc/gr/plot)
## Data: filter(sdls, species == i)
## Weights: census.start
##
##      AIC      BIC    logLik deviance df.resid
##    140.5    192.4    -46.3     92.5      40
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## plot:gr:loc:site (Intercept) 1.595e-10 1.263e-05
## gr:loc:site      (Intercept) 3.794e-17 6.159e-09
## loc:site         (Intercept) 3.726e-13 6.104e-07
## site             (Intercept) 2.325e-13 4.821e-07
## Number of obs: 64, groups:
## plot:gr:loc:site, 64; gr:loc:site, 27; loc:site, 16; site, 10
##
## Conditional model:
##
## Estimate Std. Error z value
## (Intercept)          1.08195    0.43536   2.485
## slope.degrees_s      -0.33295    0.25156  -1.324
## scale(tot_dens_s)      0.77152    0.99666   0.774
## scale(con_dens_s)     -1.10041    0.66212  -1.662
## scale(fragment.size)   0.32157    0.41979   0.766
## trt_II                5.03424    2.00733   2.508
## trt_FF                0.01163    0.61168   0.019
## trt_II:trt_FF         -2.26606    1.09780  -2.064
## scale(tot_dens_s):trt_II -3.30626    3.59749  -0.919
## scale(tot_dens_s):trt_FF -0.16767    0.93832  -0.179
## scale(con_dens_s):trt_II -7.36897    3.06914  -2.401
## scale(con_dens_s):trt_FF  1.17060    1.27183   0.920
## scale(tot_dens_s):scale(fragment.size) -1.60292    0.90233  -1.776
## scale(con_dens_s):scale(fragment.size)  1.32854    1.18201   1.124
## scale(fragment.size):trt_II  4.12978    2.49481   1.655
## scale(fragment.size):trt_FF -1.07212    0.74249  -1.444

```

```

## scale(tot_dens_s):scale(fragment.size):trt_II -3.00156    5.18441   -0.579
## scale(tot_dens_s):scale(fragment.size):trt_FF  0.20736    1.29481    0.160
## scale(con_dens_s):scale(fragment.size):trt_II -10.58223    4.14115   -2.555
## scale(con_dens_s):scale(fragment.size):trt_FF  0.54595    1.81312    0.301
##
##                                     Pr(>|z|)
## (Intercept)                                0.0129 *
## slope.degrees_s                            0.1856
## scale(tot_dens_s)                          0.4389
## scale(con_dens_s)                          0.0965 .
## scale(fragment.size)                      0.4437
## trt_II                                     0.0121 *
## trt_FF                                     0.9848
## trt_II:trt_FF                             0.0390 *
## scale(tot_dens_s):trt_II                   0.3581
## scale(tot_dens_s):trt_FF                   0.8582
## scale(con_dens_s):trt_II                   0.0164 *
## scale(con_dens_s):trt_FF                   0.3574
## scale(tot_dens_s):scale(fragment.size)     0.0757 .
## scale(con_dens_s):scale(fragment.size)     0.2610
## scale(fragment.size):trt_II                0.0979 .
## scale(fragment.size):trt_FF                0.1488
## scale(tot_dens_s):scale(fragment.size):trt_II 0.5626
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.8728
## scale(con_dens_s):scale(fragment.size):trt_II 0.0106 *
## scale(con_dens_s):scale(fragment.size):trt_FF 0.7633
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $'Cinnamomum sp.'
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
##       scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
##       scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
##       (1 | site/loc/gr/plot)
## Data: filter(sdls, species == i)
## Weights: census.start
##
##      AIC      BIC   logLik deviance df.resid
##    158.7    217.6   -55.3    110.7      62
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## plot:gr:loc:site (Intercept) 2.994e-09 5.472e-05
## gr:loc:site      (Intercept) 9.293e-01 9.640e-01
## loc:site         (Intercept) 3.086e-09 5.555e-05
## site            (Intercept) 7.390e-01 8.597e-01
## Number of obs: 86, groups:
## plot:gr:loc:site, 86; gr:loc:site, 42; loc:site, 23; site, 17
##
## Conditional model:
##
##                                     Estimate Std. Error z value

```

```

## (Intercept) -0.71081 0.57847 -1.229
## slope.degrees_s -0.21513 0.49865 -0.431
## scale(tot_dens_s) -0.82516 0.59356 -1.390
## scale(con_dens_s) 0.37420 0.50413 0.742
## scale(fragment.size) -0.40154 0.59974 -0.669
## trt_II 0.41253 0.82832 0.498
## trt_FF 1.92466 1.11891 1.720
## trt_II:trt_FF -1.35961 1.49140 -0.912
## scale(tot_dens_s):trt_II -0.18009 1.13034 -0.159
## scale(tot_dens_s):trt_FF 3.47128 1.77665 1.954
## scale(con_dens_s):trt_II -0.38512 1.64299 -0.234
## scale(con_dens_s):trt_FF -0.33156 1.60517 -0.207
## scale(tot_dens_s):scale(fragment.size) 0.59999 0.40618 1.477
## scale(con_dens_s):scale(fragment.size) 0.36357 0.58390 0.623
## scale(fragment.size):trt_II -1.45627 1.03267 -1.410
## scale(fragment.size):trt_FF 1.92983 1.33244 1.448
## scale(tot_dens_s):scale(fragment.size):trt_II -1.81786 1.65778 -1.097
## scale(tot_dens_s):scale(fragment.size):trt_FF 3.45466 2.25046 1.535
## scale(con_dens_s):scale(fragment.size):trt_II 0.07232 2.04916 0.035
## scale(con_dens_s):scale(fragment.size):trt_FF 0.98437 2.05481 0.479
## Pr(>|z|)
## (Intercept) 0.2192
## slope.degrees_s 0.6662
## scale(tot_dens_s) 0.1645
## scale(con_dens_s) 0.4579
## scale(fragment.size) 0.5032
## trt_II 0.6185
## trt_FF 0.0854 .
## trt_II:trt_FF 0.3620
## scale(tot_dens_s):trt_II 0.8734
## scale(tot_dens_s):trt_FF 0.0507 .
## scale(con_dens_s):trt_II 0.8147
## scale(con_dens_s):trt_FF 0.8364
## scale(tot_dens_s):scale(fragment.size) 0.1396
## scale(con_dens_s):scale(fragment.size) 0.5335
## scale(fragment.size):trt_II 0.1585
## scale(fragment.size):trt_FF 0.1475
## scale(tot_dens_s):scale(fragment.size):trt_II 0.2728
## scale(tot_dens_s):scale(fragment.size):trt_FF 0.1248
## scale(con_dens_s):scale(fragment.size):trt_II 0.9718
## scale(con_dens_s):scale(fragment.size):trt_FF 0.6319
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $All
## Family: binomial ( logit )
## Formula:
## Pr_s ~ slope.degrees_s + (scale(tot_dens_s) + scale(con_dens_s)) +
## scale(fragment.size) + trt_I * trt_F + (scale(tot_dens_s) +
## scale(con_dens_s)) * (trt_I + trt_F) * scale(fragment.size) +
## (scale(con_dens_s) + scale(tot_dens_s) | species) + (1 |
## site/loc/gr/plot)
## Data: sdls
## Weights: census.start

```

```

##
##      AIC      BIC    logLik deviance df.resid
##    2215.0    2361.3 -1077.5   2155.0     938
##
## Random effects:
##
## Conditional model:
##   Groups      Name              Variance Std.Dev.  Corr
##   species      (Intercept)        1.027e+00 1.0131846
##               scale(con_dens_s)  3.887e-01 0.6234621  0.56
##               scale(tot_dens_s)  3.738e-02 0.1933384 -0.47 -0.71
##   plot:gr:loc:site (Intercept)        2.788e-01 0.5280003
##   gr:loc:site      (Intercept)        2.057e-01 0.4535170
##   loc:site         (Intercept)        4.782e-01 0.6915250
##   site             (Intercept)        2.188e-08 0.0001479
## Number of obs: 968, groups:
## species, 26; plot:gr:loc:site, 474; gr:loc:site, 110; loc:site, 37; site, 21
##
## Conditional model:
##                                     Estimate Std. Error z value
## (Intercept)                        0.66723    0.27771    2.403
## slope.degrees_s                    -0.18268    0.07133   -2.561
## scale(tot_dens_s)                  -0.10921    0.15595   -0.700
## scale(con_dens_s)                  -0.44496    0.18820   -2.364
## scale(fragment.size)               -0.25279    0.15514   -1.629
## trt_II                             0.55988    0.15137    3.699
## trt_FF                             0.27661    0.13886    1.992
## trt_II:trt_FF                     -0.20355    0.21738   -0.936
## scale(tot_dens_s):trt_II           0.04971    0.19245    0.258
## scale(tot_dens_s):trt_FF           -0.01093    0.14816   -0.074
## scale(con_dens_s):trt_II           -0.25189    0.16952   -1.486
## scale(con_dens_s):trt_FF           0.38152    0.15970    2.389
## scale(tot_dens_s):scale(fragment.size) 0.09861    0.11221    0.879
## scale(con_dens_s):scale(fragment.size) -0.24883    0.16012   -1.554
## scale(fragment.size):trt_II        0.08701    0.12608    0.690
## scale(fragment.size):trt_FF        0.11108    0.11225    0.990
## scale(tot_dens_s):scale(fragment.size):trt_II 0.07160    0.22351    0.320
## scale(tot_dens_s):scale(fragment.size):trt_FF -0.17654    0.20314   -0.869
## scale(con_dens_s):scale(fragment.size):trt_II -0.14412    0.19987   -0.721
## scale(con_dens_s):scale(fragment.size):trt_FF 0.55367    0.19600    2.825
##                                     Pr(>|z|)
## (Intercept)                        0.016277 *
## slope.degrees_s                    0.010437 *
## scale(tot_dens_s)                  0.483771
## scale(con_dens_s)                  0.018061 *
## scale(fragment.size)              0.103231
## trt_II                             0.000217 ***
## trt_FF                             0.046363 *
## trt_II:trt_FF                     0.349094
## scale(tot_dens_s):trt_II           0.796159
## scale(tot_dens_s):trt_FF           0.941199
## scale(con_dens_s):trt_II           0.137312
## scale(con_dens_s):trt_FF           0.016894 *
## scale(tot_dens_s):scale(fragment.size) 0.379537

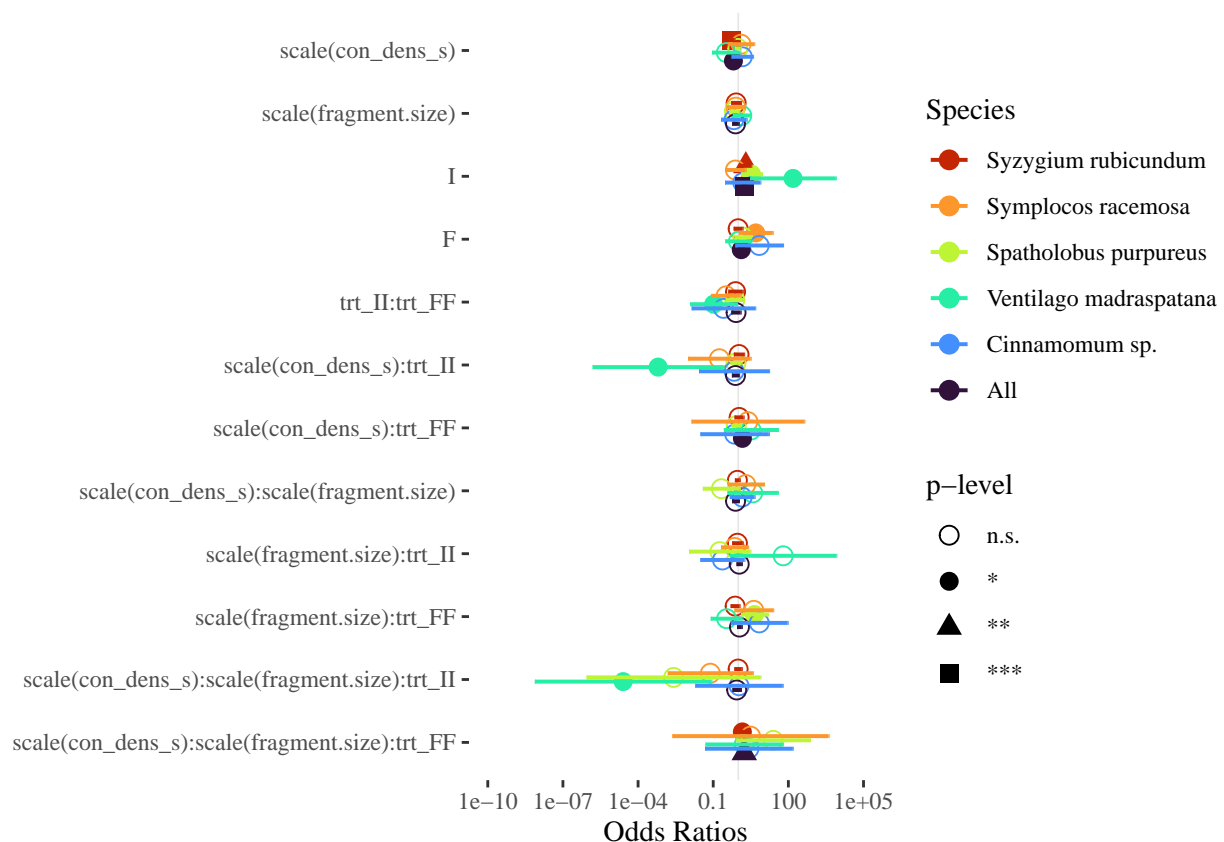
```

```
## scale(con_dens_s):scale(fragment.size)          0.120172
## scale(fragment.size):trt_II                      0.490132
## scale(fragment.size):trt_FF                      0.322352
## scale(tot_dens_s):scale(fragment.size):trt_II    0.748722
## scale(tot_dens_s):scale(fragment.size):trt_FF    0.384811
## scale(con_dens_s):scale(fragment.size):trt_II    0.470860
## scale(con_dens_s):scale(fragment.size):trt_FF    0.004731 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
term_nms <- names(fixef(single_sp_mods[[1]])$cond)

plot_models(single_sp_mods, m.labels=names(single_sp_mods), p.shape=TRUE,
            rm.terms = c("slope.degrees_s",
                        term_nms[str_detect(term_nms, "tot")])) +
  scale_colour_viridis_d(end=0.9, name="Species", option="H")
```

```
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```

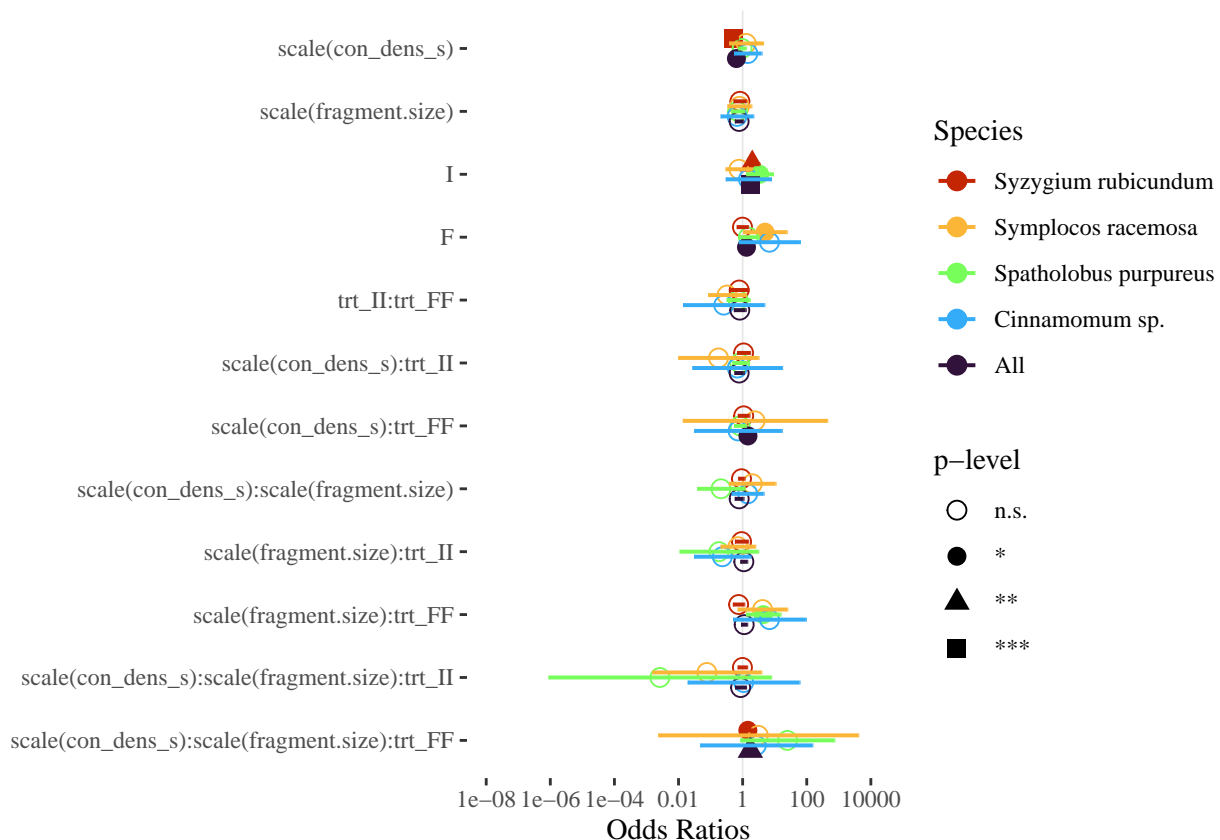


```
## Ventilago distorts scale, so dropping it
plot_models(single_sp_mods[-4], m.labels=names(single_sp_mods)[-4],
            p.shape=TRUE,
            rm.terms = c("slope.degrees_s",
```

```
term_nms[str_detect(term_nms, "tot")))) +
scale_colour_viridis_d(end=0.9, name="Species", option="H")
```

Scale for colour is already present.

Adding another scale for colour, which will replace the existing scale.



As convenient as the plot_models function is, it would be nice to
plot different species on different scales and simplify the
p-values

```
sp_effects <- map(single_sp_mods, \(d) {
  tidy(d, conf.int = TRUE) |>
  filter(effect == "fixed", str_detect(term, "tot", negate=TRUE),
    !(term %in% c("(Intercept)", "slope.degrees_s")))
}) |> bind_rows(.id = "Species")

labs <- data.frame(par = c("ConDens", "FragArea", "I", "F", "I:F",
  "ConDens:I", "ConDens:F", "FragArea:\n ConDens",
  "FragArea:I", "FragArea:F",
  "FragArea:\n (ConDens:I)", "FragArea:\n (ConDens:F)"),
  term = unique(sp_effects$term)) |>
  mutate(par = factor(par, levels = rev(par)))
```

```

sp_effects <- left_join(sp_effects, labs, by = "term")

sp_effects <- mutate(sp_effects,
  Biocide = case_when(
    str_detect(term, "trt_II") ~ "Insecticide",
    str_detect(term, "trt_FF") ~ "Fungicide",
    .default = "Control"),
  Biocide = factor(
    ifelse(str_detect(term, "trt_II:trt_FF"),
      "Both", Biocide),
    levels = c("Control", "Insecticide",
      "Fungicide", "Both")))

sp_effects <- sp_effects |> mutate(sp_effects,
  Species = ifelse(Species == "All", "All",
    paste0("italic('", Species, "')"))))

pl_species <-
  filter(sp_effects, Species != "All", par != "I:F") |>
  ggplot(aes(x = estimate, xmin = conf.low, xmax = conf.high,
    y = par, colour = Biocide)) +
  facet_wrap(~Species, scales = "free_x", labeller = label_parsed) +
  geom_pointrange(aes(shape = p.value < 0.05 )) +
  geom_vline(xintercept=0, linetype = "dotted") +
  scale_colour_brewer(palette="Set2") +
  scale_shape_manual(values=c(21, 16), guide = "none" ) +
  labs(y = NULL, x = "log(odds ratio)")

# lemon::reposition_legend(pl_species, position = 'top right',
#                           panel='panel-3-2')

# ggsave(lemon::reposition_legend(pl_species, position = 'top right',
#                                 panel='panel-3-2'),
#         file = "figures/species_plot.png", height = 7, width = 7)

pl_species <- ((blup_plot) |
  (pl_species + theme(legend.position = c(0.95, 0.05),
    legend.justification=c(1, 0)))) +
  plot_layout(widths=c(0.35, 0.65)) + plot_annotation(tag_levels = "A")

```

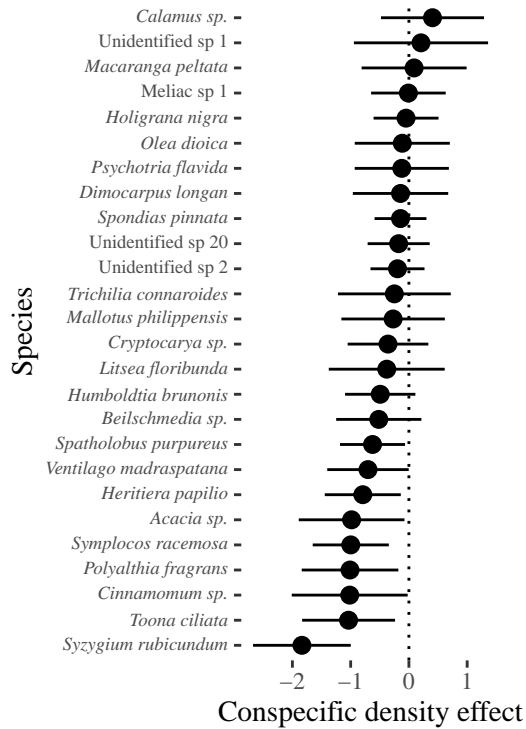
```

## Warning: A numeric 'legend.position' argument in 'theme()' was deprecated in ggplot2
## 3.5.0.
## i Please use the 'legend.position.inside' argument of 'theme()' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

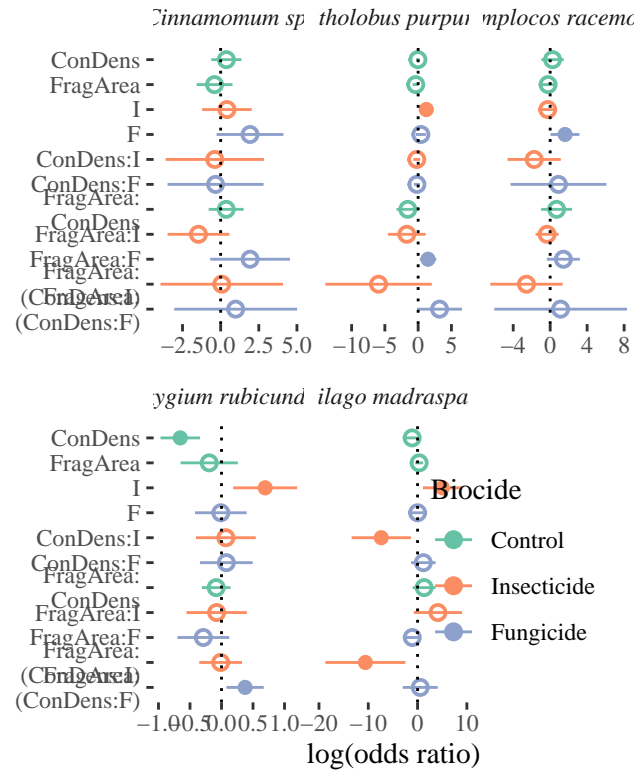
```

```
pl_species
```


A



B



```
ggsave(pl_species,
  file = "figures/species_plot.png", height = 7, width = 9)
```

4 Session Information

```
sessionInfo()
```

```
## R version 4.4.0 (2024-04-24 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 10 x64 (build 17763)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## time zone: America/New_York
```

```

## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] patchwork_1.2.0      sjPlot_2.8.16      ggdist_3.3.2
## [4] ggeffects_1.6.0.2    broom.mixed_0.2.9.5 DHARMA_0.4.6
## [7] glmmTMB_1.1.9        knitr_1.47          ggthemes_5.1.0
## [10] lubridate_1.9.3      forcats_1.0.0      stringr_1.5.1
## [13] dplyr_1.1.4          purrr_1.0.2         readr_2.1.5
## [16] tidyr_1.3.1          tibble_3.2.1        ggplot2_3.5.1
## [19] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] RColorBrewer_1.1-3    rstudioapi_0.16.0    datawizard_0.10.0
## [4] magrittr_2.0.3        estimability_1.5.1   farver_2.1.2
## [7] nloptr_2.0.3          rmarkdown_2.27       ragg_1.3.2
## [10] vctrs_0.6.5           minqa_1.2.7          effectsize_0.8.8
## [13] htmltools_0.5.8.1     distributional_0.4.0 haven_2.5.4
## [16] broom_1.0.6           sjmisc_2.8.10        parallelly_1.37.1
## [19] StanHeaders_2.32.9    plyr_1.8.9           emmeans_1.10.2
## [22] TMB_1.9.11            mime_0.12            lifecycle_1.0.4
## [25] iterators_1.0.14      pkgconfig_2.0.3      gap_1.5-3
## [28] sjlabelled_1.2.0      Matrix_1.7-0         R6_2.5.1
## [31] fastmap_1.2.0         rbibutils_2.2.16     future_1.33.2
## [34] shiny_1.8.1.1         digest_0.6.35        numDeriv_2016.8-1.1
## [37] colorspace_2.1-0      frrrr_0.3.1          textshaping_0.4.0
## [40] qgam_1.3.4            labeling_0.4.3        fansi_1.0.6
## [43] timechange_0.3.0      mgcv_1.9-1           compiler_4.4.0
## [46] bit64_4.0.5           withr_3.0.0          doParallel_1.0.17
## [49] backports_1.5.0       inline_0.3.19        performance_0.11.0
## [52] QuickJSR_1.2.0        pkgbuild_1.4.4       highr_0.11
## [55] MASS_7.3-60.2         sjstats_0.19.0       loo_2.7.0
## [58] tools_4.4.0           beeswarm_0.4.0       httpuv_1.6.15
## [61] glue_1.7.0            nlme_3.1-164         promises_1.3.0
## [64] grid_4.4.0            generics_0.1.3       gtable_0.3.5
## [67] tzdb_0.4.0            hms_1.1.3            utf8_1.2.4
## [70] foreach_1.5.2         pillar_1.9.0         vroom_1.6.5
## [73] later_1.3.2           splines_4.4.0        lattice_0.22-6
## [76] bit_4.0.5             tidyselect_1.2.1     gridExtra_2.3
## [79] stats4_4.4.0          xfun_0.44            matrixStats_1.3.0
## [82] rstan_2.32.6          stringi_1.8.4        yaml_2.3.8
## [85] boot_1.3-30           evaluate_0.23        codetools_0.2-20
## [88] cli_3.6.2            RcppParallel_5.1.7   xtable_1.8-4
## [91] parameters_0.21.7     systemfonts_1.1.0    Rdpack_2.6
## [94] munsell_0.5.1         Rcpp_1.0.12          globals_0.16.3
## [97] coda_0.19-4.1         parallel_4.4.0       ggh4x_0.2.8
## [100] bayestestR_0.13.2     gap.datasets_0.0.6   lme4_1.1-35.3
## [103] listenv_0.9.1         viridisLite_0.4.2    mvtnorm_1.2-5
## [106] scales_1.3.0          insight_0.19.11      crayon_1.5.2
## [109] rlang_1.1.3

```