

Fragmentation effects on Specialists

James Mickley & Robert Bagchi

June 05, 2024

Contents

Read in datasets	2
Data wrangling	2
Data summaries	5
Name homogenization	6
Calculate host density	7
Effects of fragment size on caterpillar density	9
Caterpillar abundance model	9
Figures presenting model results	16
Variation among species in fragmentation effects	18
Alternative measures of deer effects	23
Species richness and model	30
Host abundance model	34
Model of host abundance vs. fragment size.	34
Deer effects on host abundance	44
Plot of host abundance vs. fragment area and deer activity	49
Vegetation ordination	53
Ordination plot	56
Session Info	58

Read in datasets

Data wrangling

Steps:

1. Clean up species names of vegetation data.
2. Add information on which ring vegetation plots are from.
3. Calculate indices of deer pressure (deer captures, browse intensity and scat density).
4. Add in data on host leaf area examined

Note, I set the minimum abundance here as 3 because initial analyses suggested that the diagnostics get screwy with even rarer species.

```
## Set min number of records
min_N <- 3

## unique locations for points
vegdata %<>% mutate(PointLoc = str_split(PointID, "_")) %>%
  mutate(PointLoc = map_int(PointLoc, .f = function(.x) as.integer(.x[3])))

## Clean up species names
vegdata$TreeSpecies[is.na(vegdata$TreeSpecies)] <- "XX"
vegdata %<>% filter(!is.na(TreeGenus)) ## get rid of unidentified trees as
# we can't do anything with them

# Make unique 5 letter species names for trees
vegdata$HostID <- toupper(paste0(str_sub(vegdata$TreeGenus, 1, 3),
  str_sub(vegdata$TreeSpecies, 1, 2)))

vegdata_ord <- vegdata # a copy of the vegetation data without homogenization
# of taxonomy with caterpillar data for use in ordination

## Tidy up the deer data (make names same as other data sets)
deer_abund %<>% rename("SiteID" = "site", "DeerCaptures" = "Deer_captures")

## Make a data frame with per site summaries (means) of deer variables
## Scat was repeated for each plant per point - taking unique values
## and taking average per site.
deer_pres <- deer_browse %>% group_by(BlockID, SiteID, PointID, Year) %>%
  summarize(ScatPiles = unique(ScatPiles[!is.na(ScatPiles)])) %>%
  group_by(BlockID, SiteID) %>% summarize(ScatPiles = mean(ScatPiles))

## Building a model of deer browse vs site with plant species as a random effect
deer_browse_mod <- glmmTMB(Browsed/Plants ~ (1|BlockID) + (1|SiteID) + (1|PointID) +
  (1|PlantID), family = binomial,
  weights = Plants, data = deer_browse)

# use model to predict probability that a generic seedling is browsed by deer
deer_pres$BrowseProb <- plogis(fixef(deer_browse_mod)$cond +
```

```

                                ranef(deer_browse_mod)$cond$BlockID[deer_pres$BlockID,] +
                                ranef(deer_browse_mod)$cond$SiteID[deer_pres$SiteID,])
# add to data on deer capture from camera traps
deer_pres %<>% left_join(deer_abund)

## and integrate into site data
sites %<>% rename("BrowseProb_old" = "BrowseProb") %>%
  left_join(., deer_pres, by=c("BlockID", "SiteID")) %>%
  relocate(ScatPiles:DeerCaptures, .after = "Hunted")

# Add scaled versions of fragmentation and deer metrics to sites
sites %<>%
  # Scale variables for use in models
  mutate(
    # Add scaled fragment size, centered around 500 ha
    FragSize.c = as.vector(scale(FragSize, center = 500)),

    # Add scaled forest proportion, centered around 0.5
    ForestProp1km.c = as.vector(scale(ForestProp1km, center = 0.5)),

    # Add scaled fragmentation ratio, centered around 1
    FragRatio1km.c = as.vector(scale(FragRatio1km, center = 1)),

    # Log Fragment size, and scale, centered around 500 ha
    FragSize.Logc = as.vector(scale(log10(FragSize), center = log10(500))),

    # Deer metrics
    across(ScatPiles:ScatPredict, ~as.vector(scale(.x)), .names = "{.col}.c")
  )

## add number of plots at each site
sites <- vegdata %>% group_by(SiteID) %>%
  summarise(nplots = n_distinct(PointLoc)) %>%
  left_join(sites)

# Initial caterpillar data wrangling: add columns, filter rows
cat <- catdata %>%
  # Remove known bad host records
  filter(is.na(BadHost)) %>%
  # Add columns
  mutate(
    # Convert Year to a factor and set 2017 as the reference
    # 2015 last for sum contrasts
    Year = factor(Year, levels = c("2017", "2018", "2019", "2015")),
    # Some useful columns

    # Unique Branch ID
    BranchID = factor(paste(Year, PlotID, HostID, BranchNum, sep = "_")),

    # Make a binary specialist/generalist category based on wtMPD
    Diet = factor(ifelse(wtMPD < 100, "Specialist", "Generalist")),

    # Make a column showing whether a taxa is species-level or not

```

```

IsSpecies = ifelse(Species == "", FALSE, TRUE),

# Predict the number of leaves from branch length/diam/species
# Don't predict for 2015, data is not reliable
Leaves.fit = ifelse(Year == 2015, NA, predict(branch.model, newdata = .,
  allow.new.levels = TRUE, type = "response")),

# If leaves were counted, use that. Otherwise use the prediction
Leaves = ifelse(is.na(NumLeaves), Leaves.fit, NumLeaves),

# Predict leaf area per leaf
Area = ifelse(Year == 2015, NA, exp(predict(area.model, newdata = .,
  allow.new.levels = TRUE))),

# Calculate total leaf area
LeafArea.Log = log(Area * Leaves)

) %>%

# Join scaled fragmentation metrics from site data
left_join(sites %>% dplyr::select(SiteID, FragSize.c:ScatPredict.c), by = "SiteID") %>%

# Select columns to keep & reorder
dplyr::select(Year, BlockID, SiteID, PlotID, FragSize.c:ScatPredict.c,
  HostID, BranchID, LeafArea.Log, CatID, IsSpecies, Diet, wtMPD,
  Records, Count)

## summary of number of records per species
abund <- cat %>% group_by(CatID) %>% summarize(n_records = sum(Count)) %>%
  filter(!is.na(CatID))

cat %<>% left_join(abund, by = "CatID") ## add n_records column

```

Clean up diet classification using Mike and Dave's expertise

```

cat_diets <- dplyr::select(cat, CatID, Diet) %>% group_by(CatID) %>%
  summarize(Diet = unique(Diet))
expert_diets <- dplyr::select(species_expert, SpeciesID, Specialist) %>%
  mutate(CatID = SpeciesID)

## replace diet column with expert confirmed values
diet_c <- left_join(cat_diets, expert_diets) %>%
  left_join(abund) %>% filter(!is.na(CatID))

table(diet_c$Specialist, diet_c$Diet, diet_c$n_records > 4, useNA = "ifany")
## , , = FALSE
##
##
##      Generalist Specialist <NA>
## no           15          36    0
## yes           3          40    0
## <NA>          2          14    4
##

```

```
## , , = TRUE
##
##
##      Generalist Specialist <NA>
##   no          42          5    0
##   yes          4          13   0
##   <NA>         5           1    6

## When both agree, doesn't matter (110 species)
## When experts and observed diet disagree (48)
## if < 5 records, go with expert opinion (39)

## So all species with > 4 records go with data; all < 5 go with experts;
## If < 5 and no expert opinion, NA

diet_c <- mutate(diet_c,
  Diet2 = case_when(
    n_records >= 5 ~ Diet,
    n_records < 5 & Specialist == "yes" ~ "Specialist",
    n_records < 5 & Specialist == "no" ~ "Generalist",
    .default = NA_character_)

#diet_c$Diet[is.na(diet_c$Diet2)] <- NA
diet_c$agree <- ifelse(diet_c$Diet == diet_c$Diet2 |
  (is.na(diet_c$Diet) & is.na(diet_c$Diet2)), 1, 0)

table(diet_c$agree, cut(diet_c$n_records, c(1:10,10000)), useNA = "ifany")
##
##      (1,2] (2,3] (3,4] (4,5] (5,6] (6,7] (7,8] (8,9] (9,10] (10,1e+04] <NA>
##   0         6      4      1      0      0      0      0      0      0      0      28
##   1        16      6     10      8      5      4      1      1      1      56     27
##   <NA>       2      1      0      0      0      0      0      0      0      0     13

## most disagreements are 1 or 2 records (> 4 is made to agree anyway)
cat$Diet <- as.factor(diet_c$Diet2[match(as.character(cat$CatID), diet_c$CatID)])
cat <- mutate(cat, Diet = relevel(Diet, "Specialist"))
```

Data summaries

Summary data for beginning of results

```
cat %>% filter(Year != 2015) %>%
  summarize(n_branches = length(unique(BranchID)),
    n_plantspecies = length(unique(HostID[!is.na(HostID)])),
    n_cats = sum(Count),
    n_catspecies = length(unique(CatID[!is.na(CatID)]))
  ) %>% kable()
```

n_branches	n_plantspecies	n_cats	n_catspecies
9616	53	11165	176

```
cat %>% filter(Year != 2015) %>% group_by(Diet) %>%
  summarize(n_cats = sum(Count),
            n_catspecies = length(unique(CatID[!is.na(CatID)])))
  ) %>% kable()
```

Diet	n_cats	n_catspecies
Specialist	810	57
Generalist	10140	97
NA	215	22

```
cat %>% filter(Year != 2015 & CatID == "LYMADI") %>% group_by(Year) %>%
  summarize(n_cats = sum(Count)) %>% kable()
```

Year	n_cats
2017	6461
2018	729
2019	690

```
cat %>% filter(n_records >= min_N & Year != 2015 &
              !(CatID == "LYMADI" & Year == 2017)) %>%
  group_by(Diet) %>%
  summarize(n_cats = sum(Count),
            n_catspecies = length(unique(CatID[!is.na(CatID)])))
  ) %>% kable()
```

Diet	n_cats	n_catspecies
Specialist	772	27
Generalist	3634	63
NA	198	8

```
min_N ## min number of records for inclusion
## [1] 3
```

```
sp_list <- species %>% filter(Taxon == "Lepidoptera") %>%
  dplyr::select(-SPID, -Infraspecific) %>%
  filter(!is.na(Records)) %>% arrange(Family, Genus, Species)
```

Name homogenization

Homogenize the species ID codes and taxonomic resolution of the caterpillar and tree datasets.

```

# 1. lump together similar tree species that can't be unambiguously identified
# 2. homogenize nomenclature for all data sets

# this table defines the conversions
treeGroups <- bind_rows(
  data.frame(HostID = c('ACESA', 'ACENI'), HostID_c = "ACEBL"), # combine sugar and black maple
  data.frame(HostID = c('BETAL', 'BETLE'), HostID_c = "BETBL"), # combine black and yellow birch
  data.frame(HostID = c('CARGL', 'CARTO', 'CARXX', 'CAROV'), HostID_c = "CARYA"), #combine hickories
  data.frame(HostID = c('CORCO', 'CORAM'), HostID_c = "CORYL"), # combine hazels
  #data.frame(HostID = c('FRAAM'), HostID_c = "FRAXX"), # set white ash to unknown
  data.frame(HostID = c('GAYBA', 'GAYXX'), HostID_c = "GAYLU"), # combine Huckleberries
  data.frame(HostID = c('PRUVI', 'PRUXX'), HostID_c = "PRUSE"), # set all cherries to black cherry
  data.frame(HostID = c('QUERU', 'QUEVE', 'QUECO'), HostID_c = "QUERE") # combine red oaks
  #data.frame(HostID = c('RUBAL'), HostID_c = "RUBXX")
)

## convert names
vegdata <- vegdata %>% mutate(
  HostID = case_when(
    HostID %in% treeGroups$HostID ~
      plyr::mapvalues(HostID, treeGroups$HostID, treeGroups$HostID_c),
    TRUE ~ HostID)
)

cat2 <- cat %>% mutate(
  HostID = case_when(
    HostID %in% treeGroups$HostID ~
      plyr::mapvalues(HostID, treeGroups$HostID, treeGroups$HostID_c),
    TRUE ~ HostID)
)

```

Calculate host density

We now calculate the total density of hosts for each caterpillar species.

First we document the hosts that lep species are found on at least twice. Then we find the abundance of each of these hosts in each site, before adding the abundances of all host species within a caterpillars diet. Thus, if a species eats all maples, we compute the abundance of maples at each site and use that as the density of possible hosts of the species in the fragment.

These densities can then be modeled as a function of fragmentation metrics to assess whether there are fewer hosts for specialist, but not generalist, caterpillars in small forest fragments.

We do this at the scale of the nearest caterpillar plots

```

## matrix of who eats who
HostCatMat <- cat2 %>% filter(CatID != "") %>% count(CatID, HostID) %>%
  mutate(n = ifelse(n > 1, 1, 0)) %>% # don't count single records
  spread(key = CatID, value = n, fill = 0)

## abundance of each host species in vegetation plots
HostAbund <- vegdata %>% group_by(BlockID, SiteID, HostID) %>%
  filter(is.na(Dead) | Dead == "no" & PointLoc < 5) %>%

```

```

count(.drop = FALSE)

## Basal area of each species in adjacent vegetation plots
HostBA <- vegdata %>% group_by(BlockID, SiteID, HostID) %>%
  filter(is.na(Dead) | Dead == "no" & PointLoc < 5) %>%
  mutate(basal_area = ifelse(!is.na(DBH), pi*(0.5*DBH)^2, pi*0.05^2)) %>%
  summarise(BA = sum(basal_area))

# Get rid of plants that aren't known hosts of any sampled caterpillars
# and that never occurred in the plots
HostCatMat <- HostCatMat[HostCatMat$HostID %in% unique(HostAbund$HostID),]
HostAbund %<>% filter(HostID %in% HostCatMat$HostID)
HostBA <- HostBA %>% filter(HostID %in% HostCatMat$HostID)

all(HostCatMat$HostID %in% HostAbund$HostID) # check all hosts names are listed
## [1] TRUE

all(HostAbund$HostID %in% HostCatMat$HostID ) # check all hosts names are listed
## [1] TRUE

all(HostBA$HostID %in% HostCatMat$HostID ) # check all hosts names are listed
## [1] TRUE

all(HostCatMat$HostID %in% HostBA$HostID ) # check all hosts names are listed
## [1] TRUE

## function to efficiently calculate the number of host plants for each moth species
# uses matrix multiplication
hostDensCalc <- function(host_abund, host_cat_mat){
  site_host_mat <- host_abund %>% ungroup() %>%
    dplyr::select(c(SiteID, HostID, n)) %>%
    pivot_wider(names_from = HostID, values_from = n, values_fill = 0)
  ## make sure host-cat matrix and site-host matrices have hosts in same order
  host_cat_mat %<>% arrange(as.character(HostID))
  site_host_mat %<>% dplyr::select(SiteID, as.character(host_cat_mat$HostID))

  stopifnot(all.equal(colnames(site_host_mat)[-1],
    as.character(host_cat_mat$HostID)))

  site_cat_mat <- as.matrix(dplyr::select(site_host_mat, -SiteID)) %*%
    as.matrix(dplyr::select(host_cat_mat, -HostID))
  site_cat_mat <- bind_cols(SiteID = site_host_mat$SiteID, site_cat_mat)
  site_cat_mat %<>% group_by(SiteID) %>%
    pivot_longer(cols = -SiteID, names_to = "CatID", values_to = "N")
  return(site_cat_mat)
}

##
host_abund <- left_join(hostDensCalc(HostAbund, HostCatMat), sites) %>%
  mutate(nplots = 3) # all sites have 3 plots in inner ring

host_BA <- left_join(hostDensCalc(

```



```

rename(HostBA, "n" = "BA"), HostCatMat),
sites) %>%
mutate(nplots = 3)      # all sites have 3 plots in inner ring

## get diet data for each moth species and merge it into host density data sets
#cat_diet <- cat %>% group_by(CatID) %>% summarise(Diet = unique(Diet))

# merge in diet info to the host abundance and basal area data
host_abund$Diet <- diet_c$Diet2[match(host_abund$CatID, diet_c$CatID)]
host_BA$Diet <- diet_c$Diet2[match(host_BA$CatID, diet_c$CatID)]

```

Effects of fragment size on caterpillar density

The central question of the paper is whether specialist abundance respond more strongly to fragment area. Testing that here

First step is calculating the sampled leaf area per plot

```

## Total leaf area per site
# Need to calculate leaf area carefully - take data for unique branch ids, then
# transform to data scale, add them and transform back to log scale.
LeafArea <- cat %>% filter(Year != 2015) %>% mutate(Year = droplevels(Year)) %>%
  group_by(Year, BlockID, SiteID, BranchID) %>%
  summarize(LeafArea = mean(unique(LeafArea.Log), na.rm=TRUE)) %>% ## use mean for 3 cases with 2 (all
  group_by(Year, BlockID, SiteID) %>%
  summarise(LeafArea.Log = log(sum(exp(LeafArea), na.rm = TRUE)))

# total leaf area of each branch - average across cat species because each
# branch may be repeated, but always the same value (barring typos and rounding
# errors - hence the mean)
LeafArea_branch <- cat %>% filter(Year != 2015) %>% mutate(Year = droplevels(Year)) %>%
  group_by(Year, BlockID, SiteID, PlotID, BranchID) %>%
  summarize(LeafArea.Log = mean(unique(LeafArea.Log), na.rm=TRUE))

```

Caterpillar abundance model

Now we have the data for the model, we can start fitting it.

After playing around with the data a bunch, it seems like the model fits a lot faster (unsurprisingly) and with better diagnostics, when we sum caterpillars per site x species combination rather than at a per branch level

```

# number of caterpillars per species per site, per year.
cat.pois_ag <- cat %>% filter(Year != 2015) %>% mutate(Year = droplevels(Year)) %>%
  group_by(Year, BlockID, SiteID, CatID, Diet) %>%
  summarize(Count = sum(Count)) %>%
  filter(!is.na(Diet)) %>% mutate(CatID = droplevels(CatID)) # drop NA

## Need to add zeros - otherwise bias relationships by removing absences
cat.pois_ag %<>% ungroup() %>%
  complete(Year, nesting(BlockID, SiteID),
           nesting(CatID, Diet),

```

```

fill = list(Count = 0))

# Add leaf area data
cat.pois_ag %<>% left_join(LeafArea, by = c("Year", "BlockID", "SiteID"))

## Add site level covariates and abundance data
cat.pois_ag <- left_join(cat.pois_ag,
  dplyr::select(sites, SiteID, FragSize:ScatPredict, FragSize.c:ScatPredict.c),
  by = c("SiteID")) %>% left_join(abund, by = "CatID")

## Calculate DeerActivity Using the average of all types (after standardization)
cat.pois_ag <- rowwise(cat.pois_ag) %>%
  mutate(DeerPressure.c = mean(c(ScatPiles.c, BrowseProb.c, DeerCaptures.c)))

## Fit model

## Lymantria seems to cause issues with diagnostics as do rare species (see below).
## Running a model without LYMADI and without species with n_records < 3 (other
## cut-offs give similar results.
nb.abund_frag_deer <- glmmTMB::glmmTMB(
  Count ~ offset(LeafArea.Log) +
    Year + Diet * (FragSize.c + DeerPressure.c) +
    (1|BlockID/SiteID) + (1|CatID),
  family = glmmTMB::nbinom2,
  contrasts = list(Year = "contr.sum"),
  control=glmmTMB::glmmTMBControl(parallel = parallel::detectCores(),
    collect = FALSE),
  data = subset(cat.pois_ag, n_records >= min_N &
    !(CatID == "LYMADI" & Year == 2017 )))

summary(nb.abund_frag_deer)
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + DeerPressure.c) +
## (1 | BlockID/SiteID) + (1 | CatID)
## Data: subset(cat.pois_ag, n_records >= min_N & !(CatID == "LYMADI" &
## Year == 2017))
##
##      AIC      BIC   logLik deviance df.resid
##  9235.8   9320.5  -4605.9   9211.8     8596
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.1406   0.3749
## BlockID      (Intercept) 0.1682   0.4102
## CatID        (Intercept) 1.9718   1.4042
## Number of obs: 8608, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 90
##
## Dispersion parameter for nbinom2 family (): 0.282
##
## Conditional model:

```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.71085    0.32635  -45.08  <2e-16 ***
## Year1          -0.50828    0.05551   -9.16  <2e-16 ***
## Year2           0.06990    0.05101    1.37   0.1706
## DietGeneralist  0.11708    0.34560    0.34   0.7348
## FragSize.c      0.34076    0.14183    2.40   0.0163 *
## DeerPressure.c  0.04151    0.15106    0.27   0.7835
## DietGeneralist:FragSize.c -0.27685    0.11508   -2.41   0.0161 *
## DietGeneralist:DeerPressure.c 0.03460    0.11610    0.30   0.7657
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Initial analyses suggested some variation in effects of fragmentation
## among years
nb.abund_frag_year <- glmmTMB::glmmTMB(
  Count ~ offset(LeafArea.Log) +
    Year * Diet * (FragSize.c + DeerPressure.c) +
    (1|BlockID/SiteID) + (1|CatID),
  family = glmmTMB::nbinom2,
  contrasts = list(Year = "contr.sum"),
  control=glmmTMB::glmmTMBControl(parallel = parallel::detectCores(),
    collect = FALSE),
  data = subset(cat.pois_ag, n_records >= min_N & !(CatID == "LYMADI" & Year ==2017) ))

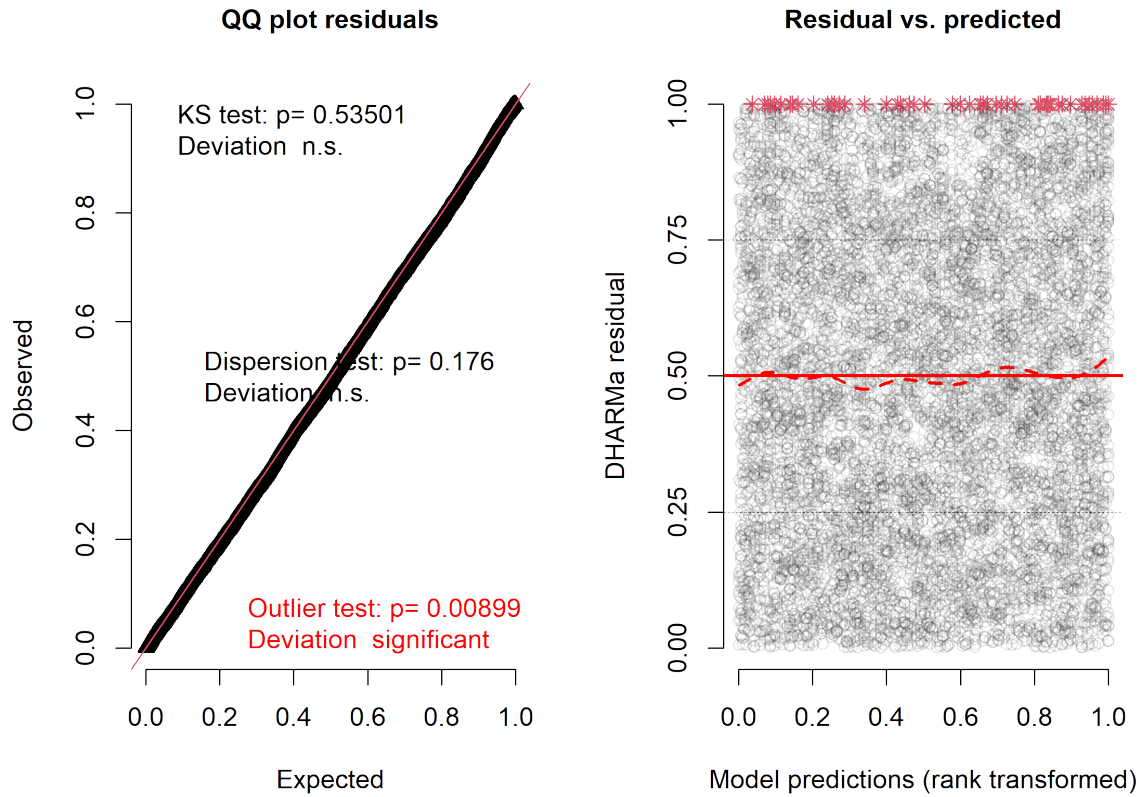
summary(nb.abund_frag_year)
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year * Diet * (FragSize.c + DeerPressure.c) +
## (1 | BlockID/SiteID) + (1 | CatID)
## Data: subset(cat.pois_ag, n_records >= min_N & !(CatID == "LYMADI" &
## Year == 2017))
##
##      AIC      BIC   logLik deviance df.resid
##  9210.5   9365.8  -4583.2   9166.5     8586
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.1406   0.3749
## BlockID         (Intercept) 0.1697   0.4120
## CatID           (Intercept) 1.9679   1.4028
## Number of obs: 8608, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 90
##
## Dispersion parameter for nbinom2 family (): 0.293
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.79673    0.32782  -45.14  < 2e-16 ***
## Year1          -0.84664    0.15061   -5.62  1.89e-08 ***
## Year2          -0.05212    0.12898   -0.40   0.6862
## DietGeneralist  0.20200    0.34668    0.58   0.5601
## FragSize.c      0.33626    0.14484    2.32   0.0203 *
```

```
## DeerPressure.c          0.06845    0.15334    0.45    0.6553
## Year1:DietGeneralist    0.52096    0.17233    3.02    0.0025 **
## Year2:DietGeneralist    0.10530    0.15259    0.69    0.4901
## Year1:FragSize.c        -0.04678    0.15403   -0.30    0.7613
## Year2:FragSize.c        -0.03883    0.13441   -0.29    0.7727
## Year1:DeerPressure.c    0.07052    0.15674    0.45    0.6528
## Year2:DeerPressure.c    0.05516    0.13867    0.40    0.6908
## DietGeneralist:FragSize.c -0.26335    0.11834   -2.23    0.0261 *
## DietGeneralist:DeerPressure.c -0.01368    0.11907   -0.11    0.9085
## Year1:DietGeneralist:FragSize.c 0.15647    0.17668    0.89    0.3758
## Year2:DietGeneralist:FragSize.c -0.08510    0.15894   -0.54    0.5923
## Year1:DietGeneralist:DeerPressure.c 0.23364    0.17683    1.32    0.1864
## Year2:DietGeneralist:DeerPressure.c -0.09251    0.16035   -0.58    0.5640
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

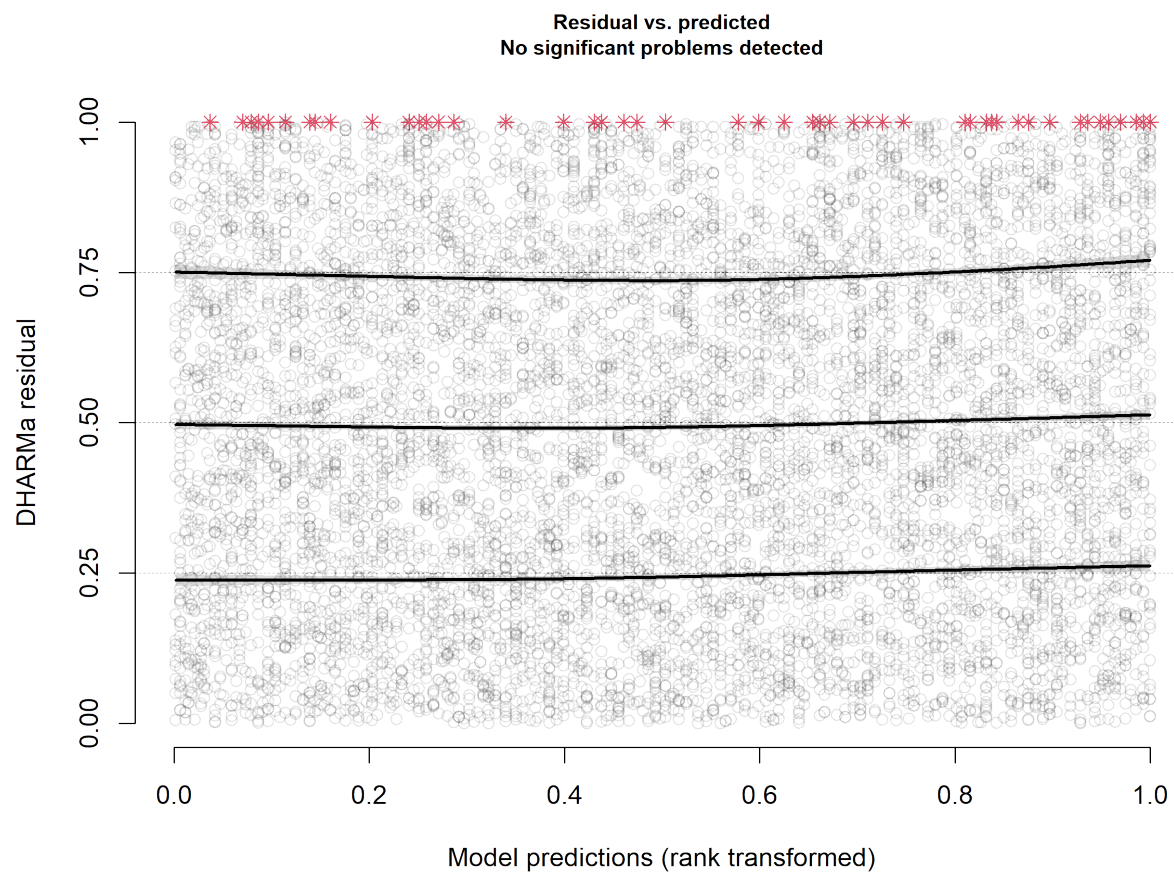
```
Anova(nb.abund_frag_year, 2) ## no variation in effects of fragmentation among years.
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Count
##
##           Chisq Df Pr(>Chisq)
## Year          98.5960  2 < 2.2e-16 ***
## Diet           0.5916  1  0.4417834
## FragSize.c      1.5913  1  0.2071434
## DeerPressure.c  0.3120  1  0.5764785
## Year:Diet       25.4606  2  2.96e-06 ***
## Year:FragSize.c  2.1205  2  0.3463777
## Year:DeerPressure.c 14.3311  2  0.0007728 ***
## Diet:FragSize.c  5.9507  1  0.0147113 *
## Diet:DeerPressure.c 0.1052  1  0.7457034
## Year:Diet:FragSize.c 0.7848  2  0.6754407
## Year:Diet:DeerPressure.c 1.7759  2  0.4115070
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sim_res <- simulateResiduals(nb.abund_frag_deer, integerResponse = TRUE)
plot(sim_res) ## some issues although the qqplot distributions look okay.
```

DHARMA residual



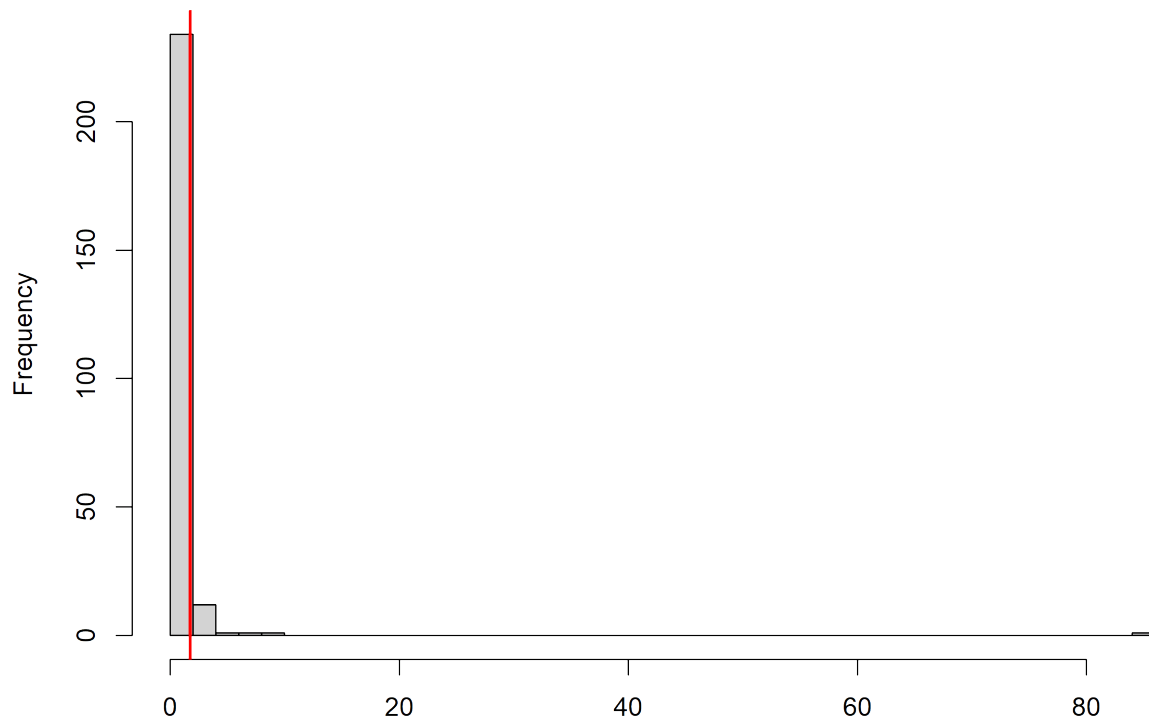
```
## residuals ~ predictions quantiles not working properly.
testQuantiles(sim_res) # seems okay
```



```
##  
## Test for location of quantiles via qgam  
##  
## data: simulationOutput  
## p-value = 0.2818  
## alternative hypothesis: both
```

```
testDispersion(sim_res) ## potentially problematic, but resolved by removing
```

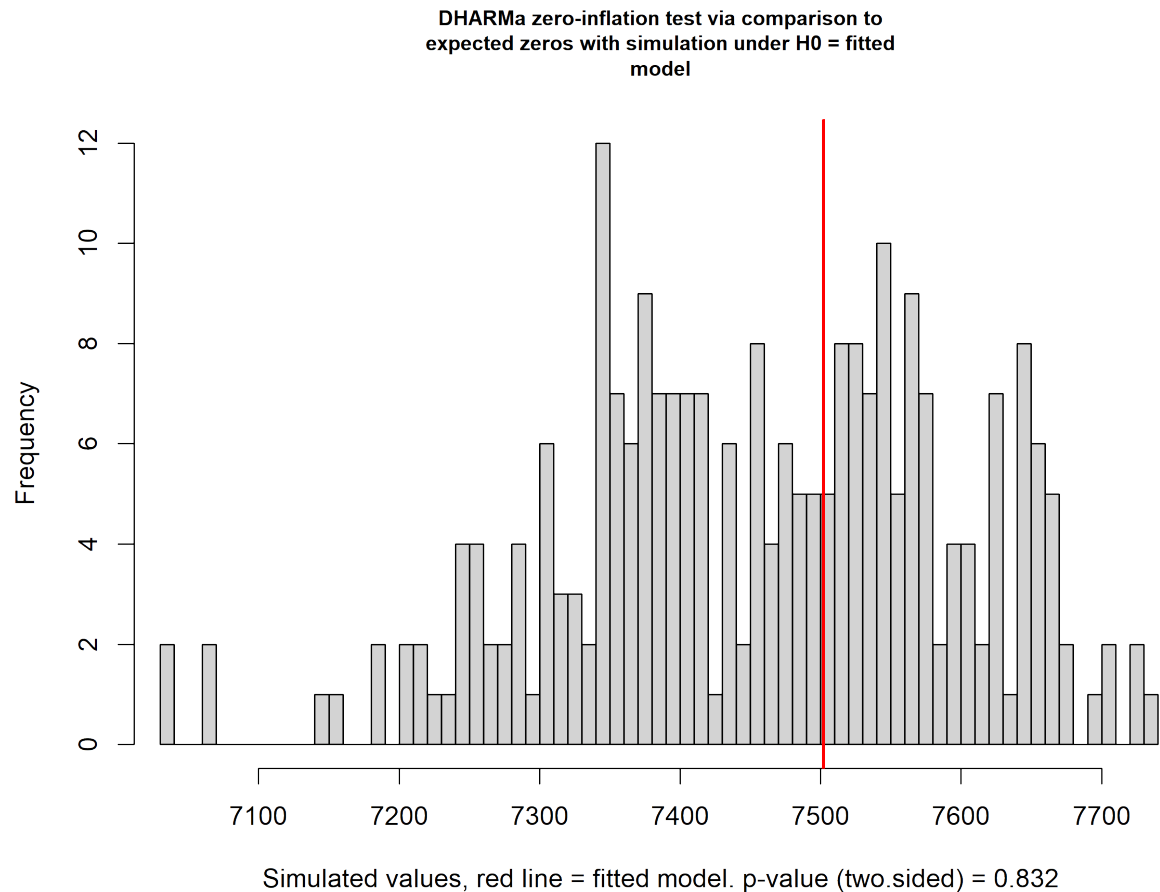
DHARMA nonparametric dispersion test via sd of
residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.176

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## dispersion = 1.7797, p-value = 0.176
## alternative hypothesis: two.sided

## Lymantria from 2017 and n < 3 species, without big changes in the results.
## Suggests the problem is being over-emphasized by the diagnostics
# sort(table(nb.abund_Frag$frame[outliers(sim_res), "CatID"])) ## nearly all lymantria
# testOutliers(nb.abund_Frag, type = "bootstrap") ## potentially problematic,
# but resolved by removing Lymantria. I think this is a false positive.
testZeroInflation(sim_res) # fine
```

```
##
## DHARMA zero-inflation test via comparison to expected zeros with
## simulation under H0 = fitted model
##
## data: simulationOutput
## ratioObsSim = 1.0062, p-value = 0.832
## alternative hypothesis: two.sided
```

A couple of tests are “significant” but the plots don’t look bad once we remove Lymantria 2017 and rare ($n < 3$) species.

Figures presenting model results

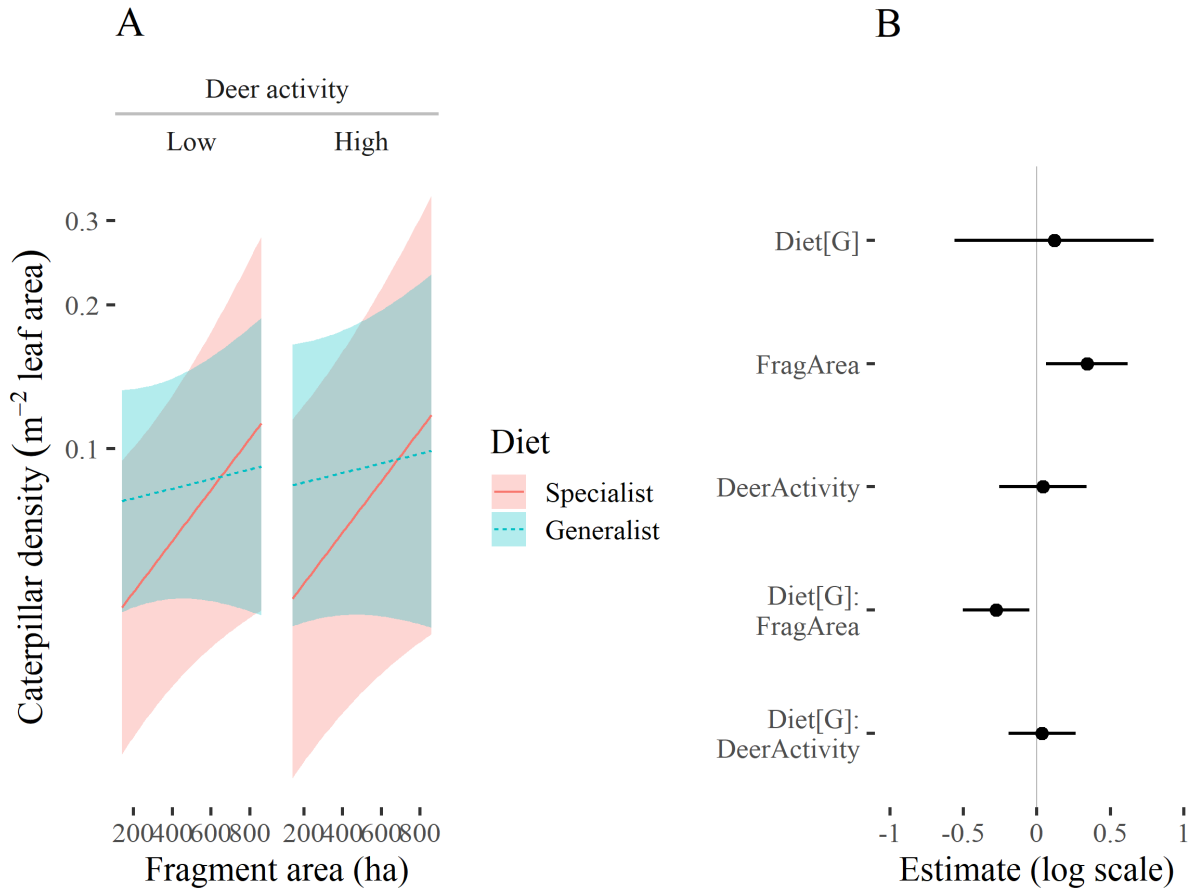
```
## plot from model
(deer_activity_plot <-
  (
    data.frame(
      ggpredict(nb.abund_frag_deer,
        terms = c("FragSize.c [-1.3:1.3 by=0.05]", "Diet",
          "DeerPressure.c [c(-1, 1)]" ))) %>%
      mutate(DeerPressure = factor(ifelse(facet == 1, "Low", "High"),
```



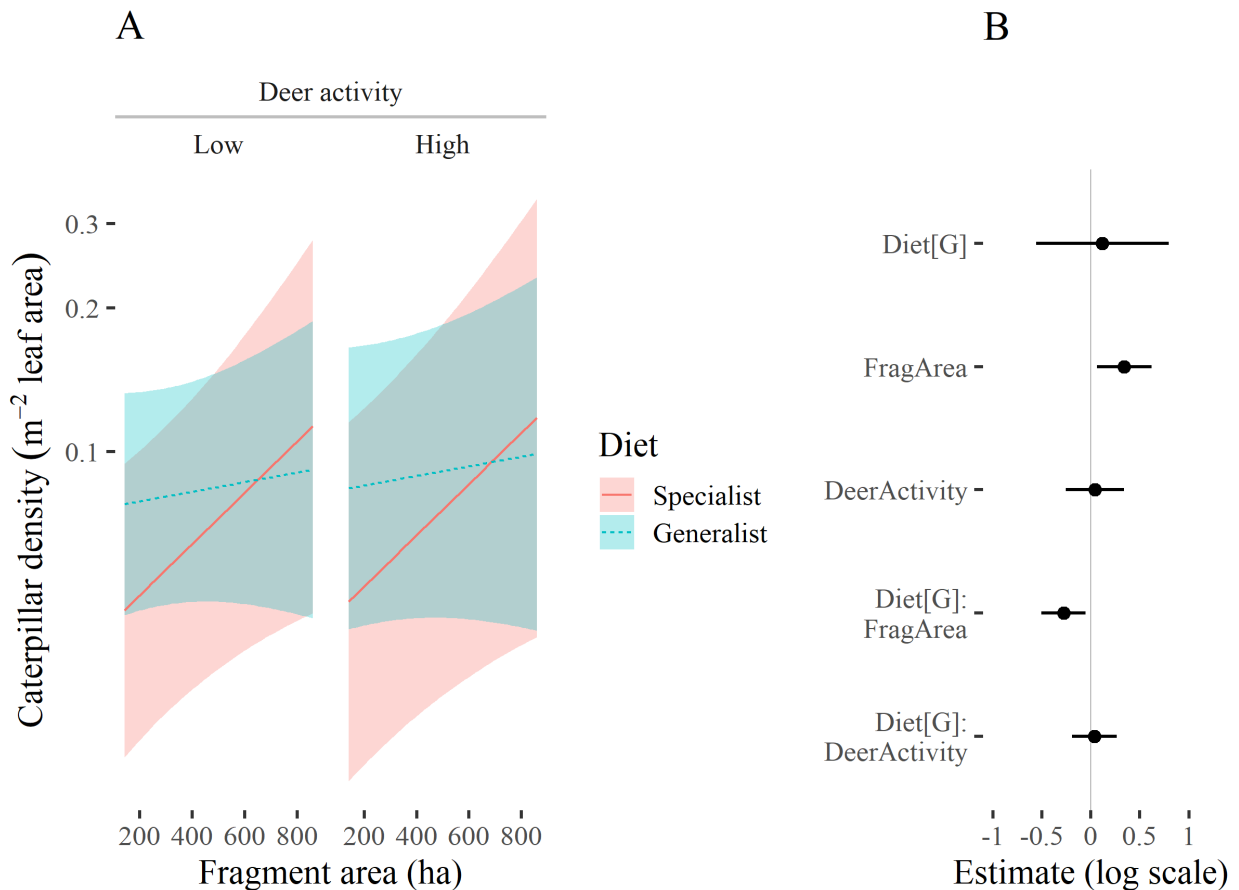
```

                                levels = c("Low", "High")),
  FragSize = x * sd(sites$FragSize) + 500,
  DeerLab = "Deer activity") %>%
ggplot(aes(x = FragSize, y = predicted, colour = group,
           linetype = group, fill = group,
           ymin = conf.low, ymax = conf.high)) +
ggh4x::facet_nested(~ DeerLab + DeerPressure, scales = "free_y",
                    nest_line = element_line()) +
geom_ribbon(colour = NA, alpha = 0.3) + geom_line() +
coord_trans(y = "log") +
labs(x = "Fragment area (ha)",
     y = expression(Caterpillar~density~(m^-2~leaf~area)),
     colour = "Diet", fill = "Diet", linetype = "Diet", title = "A") +
ggthemes::theme_tufte(base_size = 16) +
theme(ggh4x.facet.nestline = element_line(colour = "grey")) +
(plot_model(nb.abund_frag_deer, transform = NULL,
           rm.terms=c("Year1", "Year2"),
           axis.labels = rev(c("Diet[G]", "FragArea", "DeerActivity",
                              "Diet[G]:\nFragArea", "Diet[G]:\nDeerActivity")),
           vline.color = "grey70", colors = "black") + #ylim(0.5, 10) +
ggthemes::theme_tufte(base_size = 16) +
labs(title = NULL, y = "Estimate (log scale)") + ggtitle("B"))

```



```
(deer_activity_plot <- deer_activity_plot + plot_layout(widths = c(2/3, 1/3)))
```



```
ggsave(plot = deer_activity_plot,
        filename = "figures/Fig2_DeerMeanActivityPlot.pdf",
        width = 8, height = 5)
```

Variation among species in fragmentation effects

Exploring variation among caterpillar species in response to fragmentation.

```
## adding a random slope for frag size
nb.abund_frag_deer_rc <- glmmTMB::glmmTMB(
  Count ~ offset(LeafArea.Log) + Year +
    Diet * (FragSize.c + DeerPressure.c) +
    (1|BlockID/SiteID) + (FragSize.c|CatID), family = glmmTMB::nbinom2,
  contrasts = list(Year = "contr.sum"),
  control=glmmTMB::glmmTMBControl(parallel = parallel::detectCores(),
    collect = FALSE),
  data = subset(cat.pois_ag,
    n_records >= min_N & !(CatID == "LYMADI" & Year == 2017)))
```

```
summary(nb.abund_frag_deer_rc)
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + DeerPressure.c) +
## (1 | BlockID/SiteID) + (FragSize.c | CatID)
## Data: subset(cat.pois_ag, n_records >= min_N & !(CatID == "LYMADI" &
## Year == 2017))
##
##      AIC      BIC   logLik deviance df.resid
##  9205.4   9304.3  -4588.7   9177.4     8594
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev. Corr
## SiteID:BlockID (Intercept) 0.1429   0.3780
## BlockID        (Intercept) 0.1773   0.4210
## CatID          (Intercept) 2.2031   1.4843
##              FragSize.c  0.3607   0.6006   0.29
## Number of obs: 8608, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 90
##
## Dispersion parameter for nbinom2 family (): 0.302
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.97329    0.35088  -42.67  <2e-16 ***
## Year1           -0.50403    0.05518   -9.13  <2e-16 ***
## Year2            0.06824    0.05076    1.34   0.179
## DietGeneralist   0.27716    0.36998    0.75   0.454
## FragSize.c       0.15737    0.20421    0.77   0.441
## DeerPressure.c  -0.01573    0.15355   -0.10   0.918
## DietGeneralist:FragSize.c -0.16057    0.19788   -0.81   0.417
## DietGeneralist:DeerPressure.c 0.07554    0.11705    0.65   0.519
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(nb.abund_frag_deer, nb.abund_frag_deer_rc) ## improves the model substantially
## Data: subset(cat.pois_ag, n_records >= min_N & !(CatID == "LYMADI" & ...
## Models:
## nb.abund_frag_deer: Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + DeerPressure.c) + , z
## nb.abund_frag_deer: (1 | BlockID/SiteID) + (1 | CatID), zi=-0, disp=~1
## nb.abund_frag_deer_rc: Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + DeerPressure.c) +
## nb.abund_frag_deer_rc: (1 | BlockID/SiteID) + (FragSize.c | CatID), zi=-0, disp=~1
##
##      Df      AIC      BIC   logLik deviance  Chisq Chi Df
## nb.abund_frag_deer    12 9235.8 9320.5 -4605.9   9211.8
## nb.abund_frag_deer_rc  14 9205.4 9304.3 -4588.7   9177.4 34.383      2
##
##      Pr(>Chisq)
## nb.abund_frag_deer
## nb.abund_frag_deer_rc 3.419e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

## plot random slopes for each species
cat_reff <- tidy(nb.abund_frag_deer_rc, effects = "ran_vals") %>%
  filter(group == "CatID")
cat_reff <- left_join(cat_reff, abund, by = c("level" = "CatID")) %>%
  rename("n" = "n_records")
cat_reff$Diet <- as.factor(diet_c$Diet2[match(cat_reff$level, diet_c$CatID)])

cat_reff %<>% group_by(term, Diet) %>%
  mutate(qq = rank(estimate))

cat_reff %<>% left_join(.,
  group_by(catdata, CatID) %>%
    summarize(ScientificName = unique(ScientificName)),
  by = c("level" = "CatID"))

## find main host for each caterpillar
main_host <- cat %>% group_by(CatID, HostID) %>%
  summarize(n = sum(Count, na.rm = TRUE)) %>%
  slice(which.max(n)) %>% dplyr::select(-n)

## Sort hosts by importance for specialists
specialist_importance <- filter(cat, !is.na(Diet)) %>% group_by(HostID, Diet) %>%
  summarize(n = sum(Count, na.rm = TRUE)) %>%
  pivot_wider(names_from = Diet, values_from = n, values_fill = 0) %>%
  left_join(filter(species, Taxon == "Plantae") %>%
    select(PlantSciName = ScientificName, SpeciesID),
    by = c("HostID" = "SpeciesID")) %>%
  arrange(desc(Specialist)) %>%
  filter(HostID %in% main_host$HostID)

main_host <- mutate(
  main_host,
  PreferredHost = factor(HostID,
    levels = specialist_importance$HostID,
    labels = specialist_importance$PlantSciName))

cat_reff <- left_join(cat_reff, main_host, by = c("level" = "CatID"))
cat_reff %<>% mutate(ScientificName = gsub(" BOLD.*", "", ScientificName))
cat_reff$ScientificName[cat_reff$ScientificName == "Coryphista meadii"] <- "Rheumaptera meadii"
cat_reff %<>% mutate(label = paste0(ScientificName, " [", n, "]"))
cat_reff <- cat_reff %>% droplevels()

cat_reff$Diet <- relevel(cat_reff$Diet, "Specialist")

## intercept not very interesting
blup_plot <- filter(cat_reff, term == "FragSize.c") %>%
  mutate(estimate_c = ifelse(Diet == "Specialist",
    estimate +
      fixef(nb.abund_frag_deer_rc)$cond["FragSize.c"],
    estimate +
      fixef(nb.abund_frag_deer_rc)$cond["FragSize.c"] +
      fixef(nb.abund_frag_deer_rc)$cond["DietGeneralist:FragSize.c"]
  )) %>%

```

```

ggplot(aes(y = reorder_within(label, qq, term), x = estimate_c,
          xmin = estimate_c - std.error, xmax = estimate_c + std.error,
          color = PreferredHost, fill = PreferredHost, shape = PreferredHost)) +
geom_vline(xintercept = 0, col = "grey50", linetype = "dotted") +
geom_linerange(show.legend=FALSE) +
geom_point(size = 3) +
facet_wrap(~Diet, scales = "free_y") +
labs(x = "Area sensitivity (log scale)",
     y = "Lepidopteran species") +
scale_y_reordered() +
scale_x_continuous(breaks = seq(-1, 2, 1)) +
scale_color_viridis_d(name = "Preferred Host", direction=-1) +
scale_fill_viridis_d(name = "Preferred Host", direction=-1) +
scale_shape_manual(values=c(15:17, 25, 23, 0:6, 8:14),
                   name = "Preferred Host") +
ggthemes::theme_tufte(base_size = 12) +
theme(axis.text.y = element_text(face = "italic"),
      legend.text = element_text(face = "italic"))

ggsave(blup_plot, file = "figures/Fig3_speciesblups.pdf", height = 9)

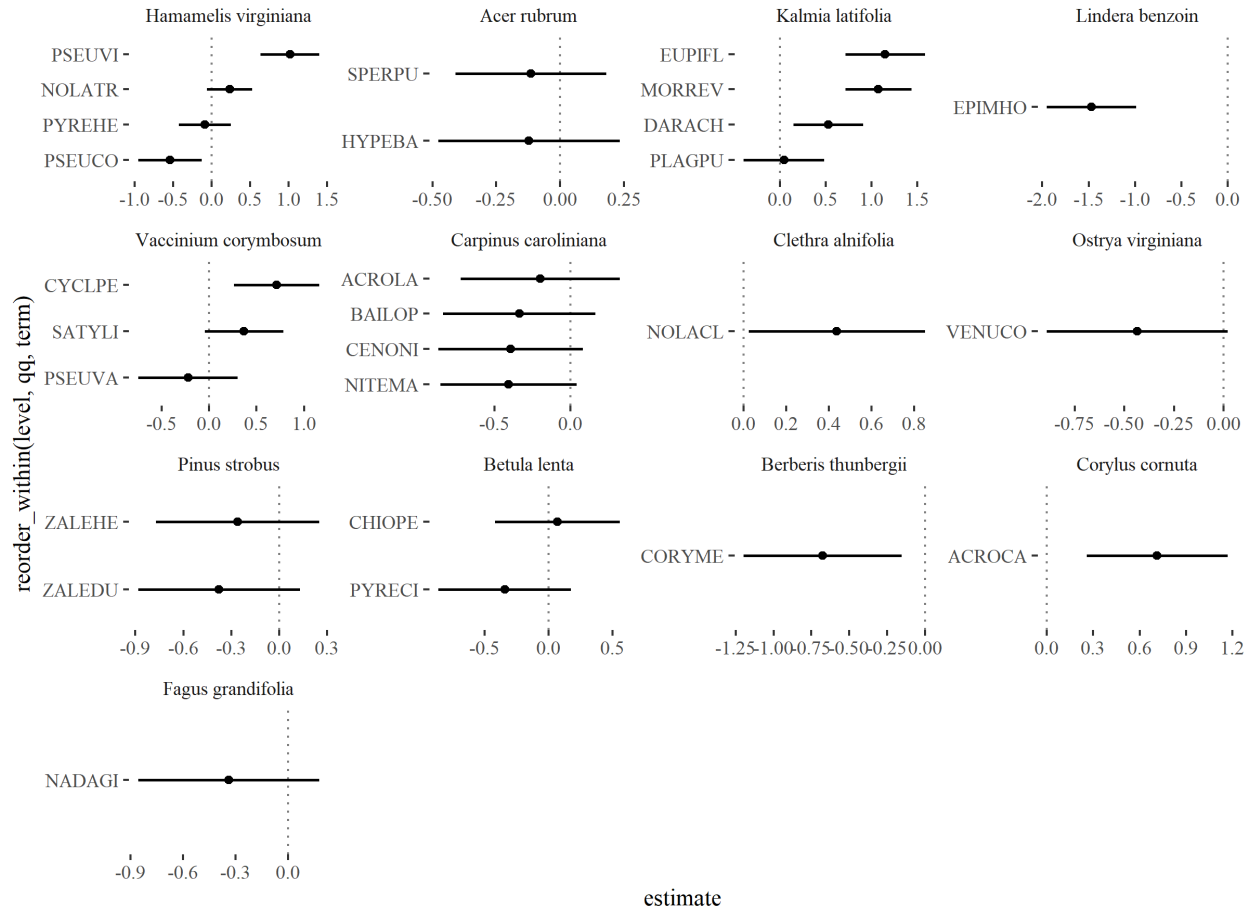
table(cat_reff$PreferredHost)
##
## Hamamelis virginiana      Acer rubrum      Kalmia latifolia
##                28                16                22
## Lindera benzoin Vaccinium corymbosum Carpinus caroliniana
##                6                10                52
## Clethra alnifolia Ostrya virginiana Lyonia ligustrina
##                2                4                2
## Pinus strobus Betula lenta Berberis thunbergii
##                4                12                2
## Corylus cornuta Quercus alba Fagus grandifolia
##                2                4                4
## Quercus velutina Acer saccharum Betula alleghaniensis
##                2                4                2
## Corylus americana
##                2

```

```

filter(cat_reff, term == "FragSize.c" & Diet == "Specialist") %>%
ggplot(aes(y = reorder_within(level, qq, term), x = estimate,
          xmin = estimate - std.error, xmax = estimate + std.error)) +
geom_vline(xintercept = 0, col = "grey50", linetype = "dotted") +
geom_pointinterval() + scale_y_reordered() +
facet_wrap(~PreferredHost, scale = "free") +
ggthemes::theme_tufte()

```



```
## Is Epimecis having a disproportionate effect?
nb.abund_Frag_rc_red <-
  update(nb.abund_frag_deer_rc,
    data = subset(cat.pois_ag,
      n_records >= 3 &
        !(CatID %in% c("EPIMHO" , "CORYME")) &
        !(CatID == "LYMADI" & Year == 2017)))

summary(nb.abund_Frag_rc_red) ## the lack of a difference is largely
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + DeerPressure.c) +
## (1 | BlockID/SiteID) + (FragSize.c | CatID)
## Data: subset(cat.pois_ag, n_records >= 3 & !(CatID %in% c("EPIMHO",
## "CORYME")) & !(CatID == "LYMADI" & Year == 2017))
##
##      AIC      BIC   logLik deviance df.resid
##  8983.4   9082.0 -4477.7   8955.4     8402
##
## Random effects:
##
## Conditional model:
```

```
## Groups      Name      Variance Std.Dev. Corr
## SiteID:BlockID (Intercept) 0.1652  0.4064
## BlockID      (Intercept) 0.2174  0.4663
## CatID        (Intercept) 2.1290  1.4591
##              FragSize.c 0.2217  0.4709  0.22
## Number of obs: 8416, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 88
##
## Dispersion parameter for nbinom2 family (): 0.317
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.88816   0.35876  -41.50  <2e-16 ***
## Year1           -0.49474   0.05528   -8.95  <2e-16 ***
## Year2            0.05129   0.05095    1.01  0.3141
## DietGeneralist   0.20402   0.37049    0.55  0.5819
## FragSize.c       0.37506   0.19179    1.96  0.0505 .
## DeerPressure.c   -0.15476   0.16570   -0.93  0.3503
## DietGeneralist:FragSize.c -0.34454  0.17451  -1.97  0.0483 *
## DietGeneralist:DeerPressure.c 0.18646  0.12367    1.51  0.1316
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

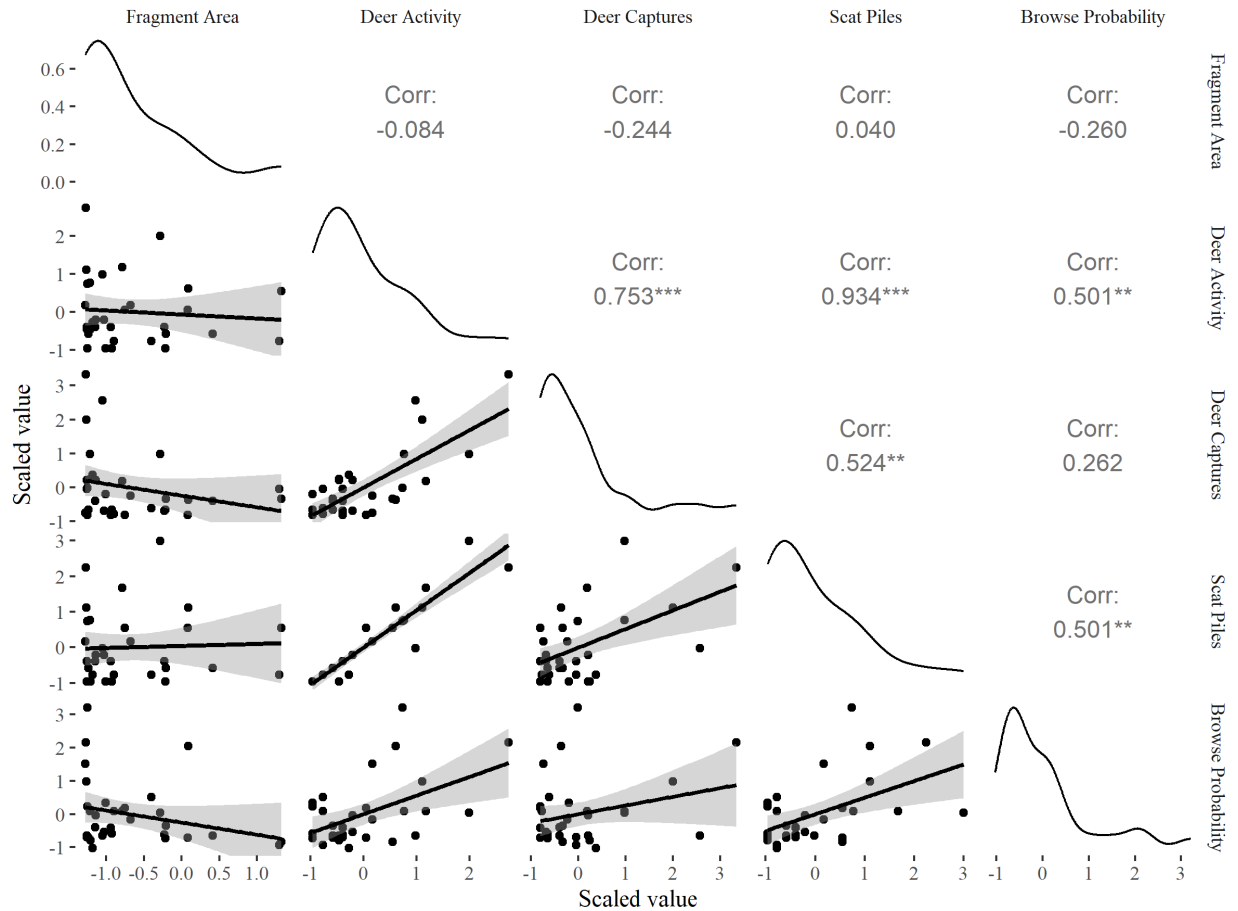
## driven by Epimices & Rheumaptera (specialists in small frags)
```

Seems like there is considerable variation among lep species. In particular, the specialists are a little right skewed. It is worth noticing that the species that respond most negatively to fragment area are Epimecis hortaria, which only ate Lindera benzoin in our data set and Coryphista meadii, a barberry specialist. Given Barberry is an invasive exotic, it represents a different mechanism. Epimices is restricted to Lindera in our dataset, but according to Wagner it eats Tulip tree (hence its common name Tulip-tree beauty). Perhaps this is an example of local specialization a la Fox & Morrow?

Alternative measures of deer effects

```
# measures of deer abundance
## plot of correlations among measures of deer pressure
sites2 <- rowwise(sites) %>%
  mutate(DeerPressure.c = mean(ScatPiles.c:DeerCaptures.c))
with(sites2, cor.test(FragSize.c, DeerPressure.c))
##
## Pearson's product-moment correlation
##
## data: FragSize.c and DeerPressure.c
## t = -0.46173, df = 30, p-value = 0.6476
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.4203823  0.2726793
## sample estimates:
##          cor
## -0.08400167
```

```
(deer_correlation_plot <- GGally::ggpairs(
  dplyr::select(sites2, FragSize.c, DeerPressure.c,
    DeerCaptures.c, ScatPiles.c, BrowseProb.c),
  lower = list(continuous = "smooth"),
  columnLabels= c("Fragment Area", "Deer Activity", "Deer Captures",
    "Scat Piles", "Browse Probability"),
  xlab = "Scaled value", ylab = "Scaled value") +
  ggthemes::theme_tufte())
```



```
ggsave(deer_correlation_plot, file = "figures/fig_s2_deercorrelations.pdf")

with(sites,
  {
    print(cor.test(FragSize.c, DeerCaptures.c))
    print(cor.test(FragSize.c, ScatPiles.c))
    print(cor.test(FragSize.c, BrowseProb.c))
  })

##
## Pearson's product-moment correlation
##
## data: FragSize.c and DeerCaptures.c
## t = -1.3805, df = 30, p-value = 0.1776
```



```

## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.5465224 0.1140054
## sample estimates:
##      cor
## -0.2444044
##
##
## Pearson's product-moment correlation
##
## data: FragSize.c and ScatPiles.c
## t = 0.22139, df = 30, p-value = 0.8263
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3127101 0.3836784
## sample estimates:
##      cor
## 0.04038772
##
##
## Pearson's product-moment correlation
##
## data: FragSize.c and BrowseProb.c
## t = -1.4736, df = 30, p-value = 0.151
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.55794788 0.09775071
## sample estimates:
##      cor
## -0.2597985

```

```

## deer camera captures
nb.abund_deercaptures <- glmmTMB::glmmTMB(
  Count ~ offset(LeafArea.Log) + Year +
    Diet * (FragSize.c + DeerCaptures.c) +
    (1|BlockID/SiteID) + (1|CatID), family = glmmTMB::nbinom2,
  contrasts = list(Year = "contr.sum"),
  control=glmmTMB::glmmTMBControl(parallel = 20, collect = FALSE),
  data = subset(cat.pois_ag,
    n_records >= min_N, !(CatID == "LYMADI" & Year == 2017)))
summary(nb.abund_deercaptures)
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + DeerCaptures.c) +
## (1 | BlockID/SiteID) + (1 | CatID)
## Data: subset(cat.pois_ag, n_records >= min_N, !(CatID == "LYMADI" &
## Year == 2017))
##
##      AIC      BIC   logLik deviance df.resid
##  9645.1   9729.9  -4810.5   9621.1     8628
##
## Random effects:
##

```

```
## Conditional model:
## Groups          Name          Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.1436  0.3789
## BlockID         (Intercept) 0.1894  0.4353
## CatID           (Intercept) 2.1584  1.4691
## Number of obs: 8640, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 90
##
## Dispersion parameter for nbinom2 family (): 0.281
##
## Conditional model:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -14.73251    0.34022  -43.30 < 2e-16 ***
## Year1                       -0.44176    0.05481   -8.06 7.67e-16 ***
## Year2                        0.03398    0.05137    0.66  0.5083
## DietGeneralist              0.17441    0.35986    0.48  0.6279
## FragSize.c                  0.32218    0.14513    2.22  0.0264 *
## DeerCaptures.c             -0.12470    0.12031   -1.04  0.3000
## DietGeneralist:FragSize.c   -0.23057    0.11559   -1.99  0.0461 *
## DietGeneralist:DeerCaptures.c 0.18208    0.09194    1.98  0.0477 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(nb.abund_deercaptures, 2)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Count
##               Chisq Df Pr(>Chisq)
## Year           81.4639  2 < 2e-16 ***
## Diet            0.7068  1  0.40052
## FragSize.c      1.7445  1  0.18657
## DeerCaptures.c  0.0219  1  0.88234
## Diet:FragSize.c  3.9790  1  0.04607 *
## Diet:DeerCaptures.c 3.9222  1  0.04765 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
nb.abund_scatter <- glmmTMB::glmmTMB(
  Count ~ offset(LeafArea.Log) + Year +
    Diet * (FragSize.c + ScatPiles.c) +
    (1|BlockID/SiteID) + (1|CatID), family = glmmTMB::nbinom2,
  contrasts = list(Year = "contr.sum"),
  control=glmmTMB::glmmTMBControl(parallel = 20, collect = FALSE),
  data = subset(cat.pois_ag,
    n_records >= min_N, !(CatID == "LYMADI" & Year == 2017)))
summary(nb.abund_scatter)
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + ScatPiles.c) +
## (1 | BlockID/SiteID) + (1 | CatID)
## Data: subset(cat.pois_ag, n_records >= min_N, !(CatID == "LYMADI" &
## Year == 2017))
##
##          AIC          BIC    logLik deviance df.resid
```

```
##    9645.7    9730.5   -4810.9    9621.7      8628
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.1339   0.3659
## BlockID         (Intercept) 0.1630   0.4037
## CatID           (Intercept) 2.1567   1.4686
## Number of obs: 8640, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 90
##
## Dispersion parameter for nbinom2 family (): 0.28
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.72792    0.33562  -43.88 < 2e-16 ***
## Year1          -0.44298    0.05483   -8.08 6.49e-16 ***
## Year2           0.03341    0.05139    0.65 0.5157
## DietGeneralist  0.13015    0.35923    0.36 0.7171
## FragSize.c      0.32451    0.14012    2.32 0.0206 *
## ScatPiles.c     0.10196    0.11552    0.88 0.3775
## DietGeneralist:FragSize.c -0.28288    0.11322   -2.50 0.0125 *
## DietGeneralist:ScatPiles.c 0.07213    0.08415    0.86 0.3914
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(nb.abund_scat, 2)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Count
##              Chisq Df Pr(>Chisq)
## Year          82.0212  2    < 2e-16 ***
## Diet           0.7225  1    0.39532
## FragSize.c     1.1277  1    0.28826
## ScatPiles.c    2.6453  1    0.10386
## Diet:FragSize.c 6.2429  1    0.01247 *
## Diet:ScatPiles.c 0.7346  1    0.39139
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
nb.abund_browse <- glmmTMB::glmmTMB(
  Count ~ offset(LeafArea.Log) + Year +
    Diet * (FragSize.c + BrowseProb.c) +
    (1|BlockID/SiteID) + (1|CatID), family = glmmTMB::nbinom2,
  contrasts = list(Year = "contr.sum"),
  control=glmmTMB::glmmTMBControl(parallel = 20, collect = FALSE),
  data = subset(cat.pois_ag,
    n_records >= min_N, !(CatID == "LYMADI" & Year == 2017)))
summary(nb.abund_browse)
## Family: nbinom2 ( log )
## Formula:
## Count ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c + BrowseProb.c) +
## (1 | BlockID/SiteID) + (1 | CatID)
```

```
## Data: subset(cat.pois_ag, n_records >= min_N, !(CatID == "LYMADI" &
##   Year == 2017))
##
##           AIC          BIC    logLik deviance df.resid
##    9646.0    9730.7  -4811.0   9622.0     8628
##
## Random effects:
##
## Conditional model:
##   Groups          Name          Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.1409   0.3753
## BlockID        (Intercept) 0.1914   0.4375
## CatID           (Intercept) 2.1603   1.4698
## Number of obs: 8640, groups: SiteID:BlockID, 32; BlockID, 13; CatID, 90
##
## Dispersion parameter for nbinom2 family (): 0.28
##
## Conditional model:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -14.67211    0.34017  -43.13 < 2e-16 ***
## Year1           -0.43940    0.05486   -8.01 1.15e-15 ***
## Year2            0.03273    0.05143    0.64 0.52453
## DietGeneralist   0.08486    0.36049    0.24 0.81390
## FragSize.c       0.38984    0.14428    2.70 0.00689 **
## BrowseProb.c     0.08873    0.12756    0.70 0.48669
## DietGeneralist:FragSize.c -0.33549    0.11755   -2.85 0.00432 **
## DietGeneralist:BrowseProb.c -0.16832    0.09671   -1.74 0.08179 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(nb.abund_browse, 2)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Count
##
##              Chisq Df Pr(>Chisq)
## Year           80.7288  2 < 2.2e-16 ***
## Diet            0.7104  1  0.399307
## FragSize.c      1.6001  1  0.205892
## BrowseProb.c    0.0868  1  0.768325
## Diet:FragSize.c  8.1462  1  0.004315 **
## Diet:BrowseProb.c 3.0289  1  0.081791 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
deerbrowse_plot <-
  plot_model(nb.abund_browse, transform = NULL,
    rm.terms=c("Year1", "Year2"),
    axis.labels = rev(c("Diet[G]", "FragArea", "DeerBrowse",
      "Diet[G]:\nFragArea", "Diet[G]:\nDeerBrowse")),
    vline.color = "grey70", colors = "black") + #ylim(0.5, 10) +
    ggthemes::theme_tufte() + labs(title = NULL, y = NULL)

deercap_plot <-
```

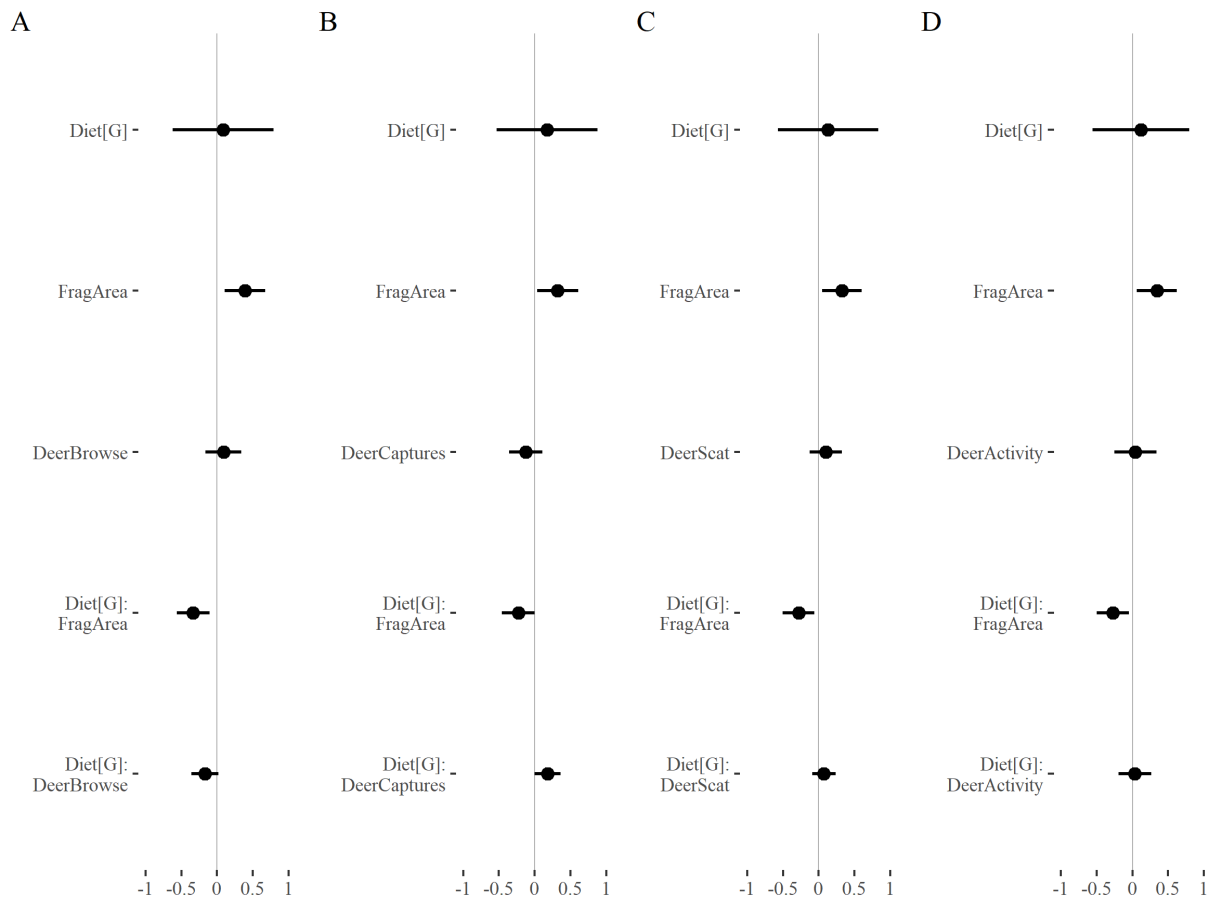
```

plot_model(nb.abund_deercaptures, transform = NULL,
           rm.terms=c("Year1", "Year2"),
           axis.labels = rev(c("Diet[G]", "FragArea", "DeerCaptures",
                               "Diet[G]:\nFragArea", "Diet[G]:\nDeerCaptures")),
           vline.color = "grey70", colors = "black") + # ylim(0.5, 10) +
ggthemes::theme_tufte() + labs(title = NULL, y = NULL)

deerscat_plot <-
  plot_model(nb.abund_scatter, transform = NULL,
            rm.terms=c("Year1", "Year2"),
            axis.labels = rev(c("Diet[G]", "FragArea", "DeerScat",
                                "Diet[G]:\nFragArea", "Diet[G]:\nDeerScat")),
            vline.color = "grey70", colors = "black") + #ylim(0.5, 10) +
ggthemes::theme_tufte() + labs(title = NULL, y = NULL)

## Using the average of all types (after standardization)
((deerbrowse_plot | deercap_plot | deerscat_plot )|
  (plot_model(nb.abund_frag_deer, transform = NULL,
             rm.terms=c("Year1", "Year2"),
             axis.labels = rev(c("Diet[G]", "FragArea", "DeerActivity",
                                 "Diet[G]:\nFragArea", "Diet[G]:\nDeerActivity")),
             vline.color = "grey70", colors = "black") +
    ggthemes::theme_tufte() + labs(title = NULL, y = NULL))) +
  plot_annotation(tag_levels = "A")

```



Patterns are similar in all cases

```
deer_comp_plot <- (deerbrowse_plot | deercap_plot | deerscat_plot ) +
  ggthemes::theme_tufte() + labs(title = NULL, y = NULL) +
  plot_annotation(tag_levels = "A")

ggsave(deer_comp_plot, file = "figures/fig_s3_deercompplot.pdf",
  width = 6, height = 2.5)
```

The effects of deer activity are a little complicated

- Mean deer activity measure has no effect on either diet.
- Specialists don't respond to any metric.
- Generalists are affected in opposite directions by deer captures (positively!?) and deer browse (negatively, albeit marginally non-significantly). However the effects are small, and they are not/barely significant. Probably not a real effect.

Species richness and model

```

richness.all <- cat %>% filter(Year != 2015 & n_records > min_N) %>%
  mutate(Year = droplevels(Year)) %>%
  # left_join(abund, by = "CatID") %>%
  filter(!is.na(Diet) ) %>% mutate(CatID = droplevels(CatID)) %>%
  group_by(BlockID, SiteID, Year, Diet, CatID) %>%
  summarize(Count = sum(Count, na.rm = TRUE)) %>%
  ungroup() %>%
  complete(Year, nesting(BlockID, SiteID), Diet,
    fill = list(Count = 0)) %>%
  group_by(BlockID, SiteID, Year, Diet) %>%
  summarize(species = n_distinct(CatID),
    shannon = diversity(Count, index = "shannon"),
    invsimpsons = diversity(Count, index = "simpson")) %>%
  left_join(LeafArea, by = c("Year", "BlockID", "SiteID")) %>%
  left_join(
    dplyr::select(sites, SiteID, FragSize:ScatPredict, FragSize.c:ScatPredict.c),
    by = c("SiteID")) %>%
  mutate(Diet = releval(Diet, "Specialist"),
    DeerPressure.c = mean(c(DeerCaptures.c, ScatPiles.c, BrowseProb.c)))

mod_rich_all <- glmmTMB(species ~ #offset(LeafArea.Log) +
  Year +
  Diet * (FragSize.c + DeerPressure.c) +
  (1|BlockID/SiteID),
  family = nbinom2,
  contrasts = list(Year = "contr.sum"),
  data = richness.all)

summary(mod_rich_all)
## Family: nbinom2 ( log )
## Formula: species ~ Year + Diet * (FragSize.c + DeerPressure.c) + (1 |
## BlockID/SiteID)
## Data: richness.all
##
##      AIC      BIC   logLik deviance df.resid
##    886.0    921.9   -432.0    864.0     181
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.05597  0.2366
## BlockID      (Intercept) 0.06868  0.2621
## Number of obs: 192, groups: SiteID:BlockID, 32; BlockID, 13
##
## Dispersion parameter for nbinom2 family (): 44.6
##
## Conditional model:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.85706    0.13353   6.419 1.38e-10 ***
## Year1           -0.19368    0.04825  -4.014 5.97e-05 ***
## Year2            0.07162    0.04554   1.573  0.116
## DietGeneralist    1.44086    0.10499  13.724 < 2e-16 ***

```

```
## FragSize.c          0.18132    0.11748    1.543    0.123
## DeerPressure.c      -0.06634    0.12365   -0.536    0.592
## DietGeneralist:FragSize.c -0.05504    0.10964   -0.502    0.616
## DietGeneralist:DeerPressure.c -0.04249    0.11121   -0.382    0.702
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod_rich_all)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: species
##              Chisq Df Pr(>Chisq)
## Year          16.5955  2  0.0002491 ***
## Diet         342.6029  1 < 2.2e-16 ***
## FragSize.c      2.9612  1  0.0852847 .
## DeerPressure.c   1.3058  1  0.2531528
## Diet:FragSize.c   0.2520  1  0.6157016
## Diet:DeerPressure.c 0.1460  1  0.7023906
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod_shan <- glmmTMB(shannon ~ offset(LeafArea.Log) + Year +
                    Diet * (FragSize.c + BrowseProb.c) +
                    (1|BlockID/SiteID),
                    family = gaussian,
                    contrasts = list(Year = "contr.sum"),
                    data = richness.all)

summary(mod_shan)
## Family: gaussian (identity)
## Formula: shannon ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c +
## BrowseProb.c) + (1 | BlockID/SiteID)
## Data: richness.all
##
##      AIC      BIC   logLik deviance df.resid
##    341.5    377.3   -159.7    319.5     181
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## SiteID:BlockID (Intercept) 8.575e-02 2.928e-01
## BlockID      (Intercept) 4.492e-10 2.119e-05
## Residual                2.574e-01 5.074e-01
## Number of obs: 192, groups: SiteID:BlockID, 32; BlockID, 13
##
## Dispersion estimate for gaussian family (sigma^2): 0.257
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -12.03598    0.10494 -114.69 < 2e-16 ***
## Year1         -0.52051    0.05178  -10.05 < 2e-16 ***
```



```
## Year2                0.19994    0.05178    3.86 0.000113 ***
## DietGeneralist       0.83694    0.10496    7.97 1.54e-15 ***
## FragSize.c           0.06096    0.10848    0.56 0.574169
## BrowseProb.c         0.10661    0.07704    1.38 0.166377
## DietGeneralist:FragSize.c -0.04456    0.10850   -0.41 0.681305
## DietGeneralist:BrowseProb.c -0.04414    0.07705   -0.57 0.566743
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod_shan)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: shannon
##               Chisq Df Pr(>Chisq)
## Year           102.8457  2    <2e-16 ***
## Diet           140.4279  1    <2e-16 ***
## FragSize.c       0.1695  1    0.6805
## BrowseProb.c     1.6061  1    0.2050
## Diet:FragSize.c   0.1687  1    0.6813
## Diet:BrowseProb.c 0.3282  1    0.5667
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod_simp <- glmmTMB(invsimpsons ~ offset(LeafArea.Log) + Year +
  Diet * (FragSize.c + DeerPressure.c) +
  (1|BlockID/SiteID),
  family = gaussian,
  contrasts = list(Year = "contr.sum"),
  data = richness.all)
```

```
summary(mod_simp)
## Family: gaussian (identity)
## Formula:
## invsimpsons ~ offset(LeafArea.Log) + Year + Diet * (FragSize.c +
##   DeerPressure.c) + (1 | BlockID/SiteID)
## Data: richness.all
##
##      AIC      BIC   logLik deviance df.resid
##    247.4    283.3   -112.7    225.4     181
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.
## SiteID:BlockID (Intercept) 1.424e-01 3.773e-01
## BlockID      (Intercept) 3.451e-10 1.858e-05
## Residual                1.361e-01 3.689e-01
## Number of obs: 192, groups: SiteID:BlockID, 32; BlockID, 13
##
## Dispersion estimate for gaussian family (sigma^2): 0.136
##
## Conditional model:
##                                     Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)          -1.213e+01  1.089e-01 -111.32 < 2e-16 ***
## Year1                -2.608e-01  3.765e-02  -6.93 4.27e-12 ***
## Year2                7.177e-02  3.765e-02   1.91 0.0566 .
## DietGeneralist       9.408e-02  7.572e-02   1.24 0.2141
## FragSize.c          -8.374e-02  1.118e-01  -0.75 0.4537
## DeerPressure.c       1.192e-01  1.009e-01   1.18 0.2371
## DietGeneralist:FragSize.c 4.664e-03  7.769e-02   0.06 0.9521
## DietGeneralist:DeerPressure.c -9.646e-04  7.011e-02  -0.01 0.9890
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod_simp)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: invsimpsons
##              Chisq Df Pr(>Chisq)
## Year          51.2327  2  7.498e-12 ***
## Diet           2.9111  1   0.08797 .
## FragSize.c     0.6034  1   0.43730
## DeerPressure.c  1.5771  1   0.20918
## Diet:FragSize.c  0.0036  1   0.95213
## Diet:DeerPressure.c 0.0002  1   0.98902
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

No clear relationship between fragment size and species richness of either specialists or generalists. A slight trend that diversity of generalists decreased in heavily browsed sites.

Host abundance model

Model of host abundance vs. fragment size.

Model of potential hostplants in the adjacent vegetation plots (inner ring).

```
n_distinct(host_abund$CatID) ## number of species
## [1] 190
```

```
## Filter out species with unknown diets and make specialists the reference
host_abund %<>% filter(!is.na(Diet)) %>%
  mutate(Diet = factor(Diet, levels = c("Specialist", "Generalist")))

host_BA %<>% filter(!is.na(Diet)) %>%
  mutate(Diet = factor(Diet, levels = c("Specialist", "Generalist")))

host_BA <- mutate(
  host_BA,
  DeerPressure.c = mean(c(DeerCaptures.c, ScatPiles.c, BrowseProb.c)),
  plotarea = nplots * 0.01)

## Add number of records of each species
```

```

host_abund %<>% left_join(abund, by = "CatID")
host_BA %<>% left_join(abund, by = "CatID")
summary(host_BA)
##      SiteID          CatID          N          nplots
## Length:5248      Length:5248      Min.   : 0.0      Min.   :3
## Class :character  Class :character  1st Qu.: 0.0      1st Qu.:3
## Mode  :character  Mode  :character  Median : 0.0      Median :3
##                                     Mean  : 3695.5      Mean   :3
##                                     3rd Qu.: 763.1      3rd Qu.:3
##                                     Max.   :86653.5      Max.   :3
##
##      STID          BlockID          Block
## Min.   : 1.00      Length:5248      BishopSwamp: 492
## 1st Qu.: 8.75      Class :character  Bolton      : 492
## Median :16.50      Mode  :character  Meshomasic : 492
## Mean   :16.50                                     Middletown : 492
## 3rd Qu.:24.25                                     NyeHolman  : 492
## Max.   :32.00                                     Scotland   : 492
##                                     (Other)    :2296
##
##      Site          FragSize          ForestProp1km          FragRatio1km
## BabcockRd          : 164      Min.   : 2.973      Min.   :0.3140      Min.   : 0.758
## BeaverBrook_large : 164      1st Qu.: 24.736      1st Qu.:0.6348      1st Qu.: 1.466
## BeaverBrook_small : 164      Median : 121.427      Median :0.7040      Median : 1.926
## BishopSwamp_medium: 164      Mean   : 230.546      Mean   :0.6630      Mean   : 2.611
## BishopSwamp_small : 164      3rd Qu.: 393.990      3rd Qu.:0.7488      3rd Qu.: 2.382
## ChoateKollerEC     : 164      Max.   :1013.980      Max.   :0.8220      Max.   :17.741
## (Other)            :4264
## ForestProp1kmRadius FragRatio1kmRadius CoreConnected          SizeClass
## Min.   :0.3420      Min.   :0.090      Min.   : 0.0000      large :1804
## 1st Qu.:0.7275      1st Qu.:0.455      1st Qu.: 0.2557      medium:1148
## Median :0.7870      Median :0.757      Median : 1.7655      small :2296
## Mean   :0.7787      Mean   :1.128      Mean   : 12.6614
## 3rd Qu.:0.8902      3rd Qu.:1.322      3rd Qu.: 6.2248
## Max.   :0.9590      Max.   :7.177      Max.   :175.5920
##
## Hunted          ScatPiles          BrowseProb          DeerCaptures
## no :1804      Min.   :0.000      Min.   :0.01584      Min.   : 0.00
## yes:3444      1st Qu.:0.020      1st Qu.:0.04620      1st Qu.: 4.75
##                                     Median :0.060      Median :0.07055      Median : 15.00
##                                     Mean   :0.102      Mean   :0.10175      Mean   : 25.41
##                                     3rd Qu.:0.160      3rd Qu.:0.11831      3rd Qu.: 32.00
##                                     Max.   :0.420      Max.   :0.36986      Max.   :130.00
##
## BrowseProb_old          ScatPredict          Latitude          Longitude
## Min.   :0.02500      Min.   :0.01900      Min.   :41.43      Min.   : -72.88
## 1st Qu.:0.06925      1st Qu.:0.03650      1st Qu.:41.59      1st Qu.: -72.50
## Median :0.11150      Median :0.06350      Median :41.71      Median : -72.42
## Mean   :0.14316      Mean   :0.09566      Mean   :41.70      Mean   : -72.40
## 3rd Qu.:0.18025      3rd Qu.:0.14275      3rd Qu.:41.81      3rd Qu.: -72.24
## Max.   :0.44700      Max.   :0.32800      Max.   :41.91      Max.   : -72.08
##
##
##                                     SiteNotes
##                                     :4100

```

```
## Deer archery and spring turkey hunting only. : 164
## Deer archery, small game, waterfowl, and turkey hunting only. : 328
## Original center at 41.432518, -72.537878 : 164
## Original center at 41.62039, -72.139329, initial apex SUB at 41.62372, -72.138024: 164
## Original center at 41.637134, -72.091974, but shifted due to dirt road : 164
## Original center at 41.718437, -72.446922. Moved after 2017 deer surveys : 164
## FragSize.c ForestProp1km.c FragRatio1km.c FragSize.Logc
## Min. :-1.2783 Min. :-0.8844 Min. :-0.07087 Min. :-2.1493
## 1st Qu.:-1.2223 1st Qu.: 0.6407 1st Qu.: 0.13647 1st Qu.:-1.2665
## Median :-0.9736 Median : 0.9700 Median : 0.27117 Median :-0.5959
## Mean :-0.6930 Mean : 0.7749 Mean : 0.47169 Mean :-0.7194
## 3rd Qu.:-0.2726 3rd Qu.: 1.1827 3rd Qu.: 0.40478 3rd Qu.:-0.1000
## Max. : 1.3219 Max. : 1.5310 Max. : 4.90247 Max. : 0.2965
##
## ScatPiles.c BrowseProb.c DeerCaptures.c BrowseProb_old.c
## Min. :-0.9603 Min. :-1.0294 Min. :-0.8092 Min. :-1.1465
## 1st Qu.:-0.7720 1st Qu.:-0.6657 1st Qu.:-0.6579 1st Qu.:-0.7172
## Median :-0.3954 Median :-0.3739 Median :-0.3314 Median :-0.3072
## Mean : 0.0000 Mean : 0.0000 Mean : 0.0000 Mean : 0.0000
## 3rd Qu.: 0.5462 3rd Qu.: 0.1985 3rd Qu.: 0.2100 3rd Qu.: 0.3599
## Max. : 2.9943 Max. : 3.2128 Max. : 3.3314 Max. : 2.9484
##
## ScatPredict.c Diet DeerPressure.c plotarea
## Min. :-0.9536 Specialist:1984 Min. :-0.7816 Min. :0.03
## 1st Qu.:-0.7359 Generalist:3264 1st Qu.:-0.5077 1st Qu.:0.03
## Median :-0.4000 Median :-0.3507 Median :0.03
## Mean : 0.0000 Mean : 0.0000 Mean :0.03
## 3rd Qu.: 0.5858 3rd Qu.: 0.3856 3rd Qu.:0.03
## Max. : 2.8903 Max. : 2.5769 Max. :0.03
##
## n_records
## Min. : 1
## 1st Qu.: 1
## Median : 3
## Mean : 72
## 3rd Qu.: 15
## Max. :7950
##
```

```
# ## Fit the model of abundance - using basal area in paper, but results similar
# mod_hosts <- glmmTMB(N ~ Diet * FragSize.c +
#                       offset(log(nplots)) +
#                       # (1/CatID) +
#                       (1/BlockID/SiteID),
#                       ziformula = ~ 1 + Diet * FragSize.c,
#                       family = nbinom2,
#                       data = subset(host_abund,
#                                     n_records >= min_N),
#                       control=glmmTMB::glmmTMBControl(parallel = 20))

#summary(mod_hosts) ## No effects on the mean (but there are differences
# in zero inflation)
```

```

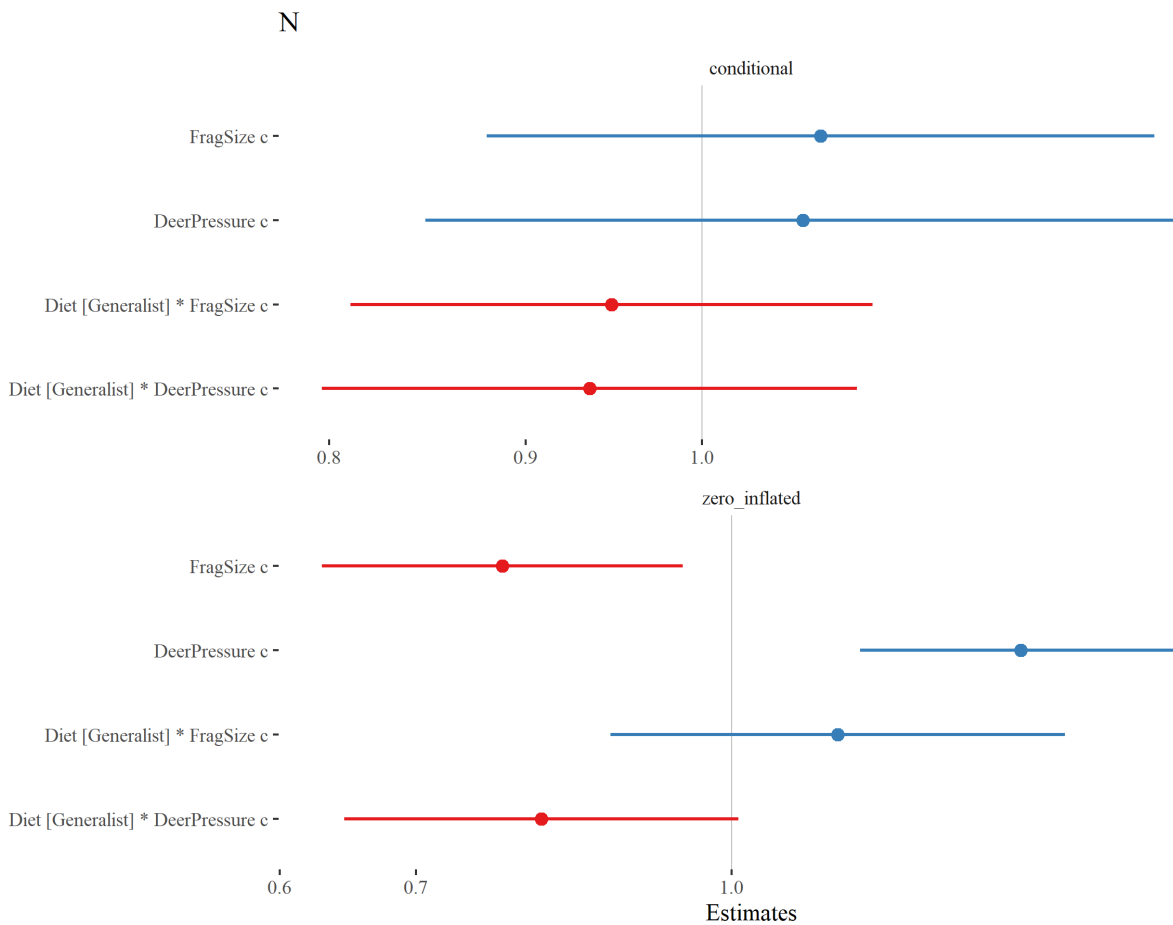
## Model based on basal area instead of abundance
mod_hosts <- glmmTMB(N ~ Diet * (FragSize.c + DeerPressure.c) +
  offset(log(nplots)) +
  (1|CatID) + ## removed because diagnostics better without
  (1|BlockID/SiteID),
  ziformula = ~ 1 + Diet * (FragSize.c + DeerPressure.c),
  #dispformula = ~ Diet,
  family = ziGamma(link = "log"),
  data = subset(host_BA,
    n_records >= min_N ),
  control=glmmTMB::glmmTMBControl(
    parallel = parallel::detectCores()))
summary(mod_hosts) ## No effects on the mean
## Family: Gamma ( log )
## Formula:
## N ~ Diet * (FragSize.c + DeerPressure.c) + offset(log(nplots)) +
## (1 | CatID) + (1 | BlockID/SiteID)
## Zero inflation: ~1 + Diet * (FragSize.c + DeerPressure.c)
## Data: subset(host_BA, n_records >= min_N)
##
##      AIC      BIC  logLik deviance df.resid
## 38279.2 38374.7 -19123.6 38247.2      2864
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## CatID      (Intercept) 4.20192  2.0499
## SiteID:BlockID (Intercept) 0.06848  0.2617
## BlockID      (Intercept) 0.67525  0.8217
## Number of obs: 2880, groups: CatID, 90; SiteID:BlockID, 32; BlockID, 13
##
## Dispersion estimate for Gamma family (sigma^2): 1
##
## Conditional model:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      3.70306    0.47949   7.723 1.14e-14 ***
## DietGeneralist      3.16192    0.50378   6.276 3.47e-10 ***
## FragSize.c         0.07116    0.10200   0.698  0.485
## DeerPressure.c      0.06065    0.11544   0.525  0.599
## DietGeneralist:FragSize.c -0.05410    0.07974  -0.678  0.498
## DietGeneralist:DeerPressure.c -0.06722    0.08178  -0.822  0.411
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Zero-inflation model:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -0.35925    0.10169  -3.533 0.000411 ***
## DietGeneralist   -0.88103    0.12813  -6.876 6.15e-12 ***
## FragSize.c       -0.25926    0.10416  -2.489 0.012811 *
## DeerPressure.c    0.32700    0.09259   3.532 0.000413 ***
## DietGeneralist:FragSize.c  0.12012    0.13113   0.916 0.359638
## DietGeneralist:DeerPressure.c -0.21531    0.11370  -1.894 0.058279 .

```

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

```
## but there are differences in the zero-inflation component -
## fewer zeros in large fragments for both diet breadths
```

```
plot_model(mod_hosts, vline.color = "grey", rm.terms = "Diet [Generalist]") +
  ggthemes::theme_tufte()
```

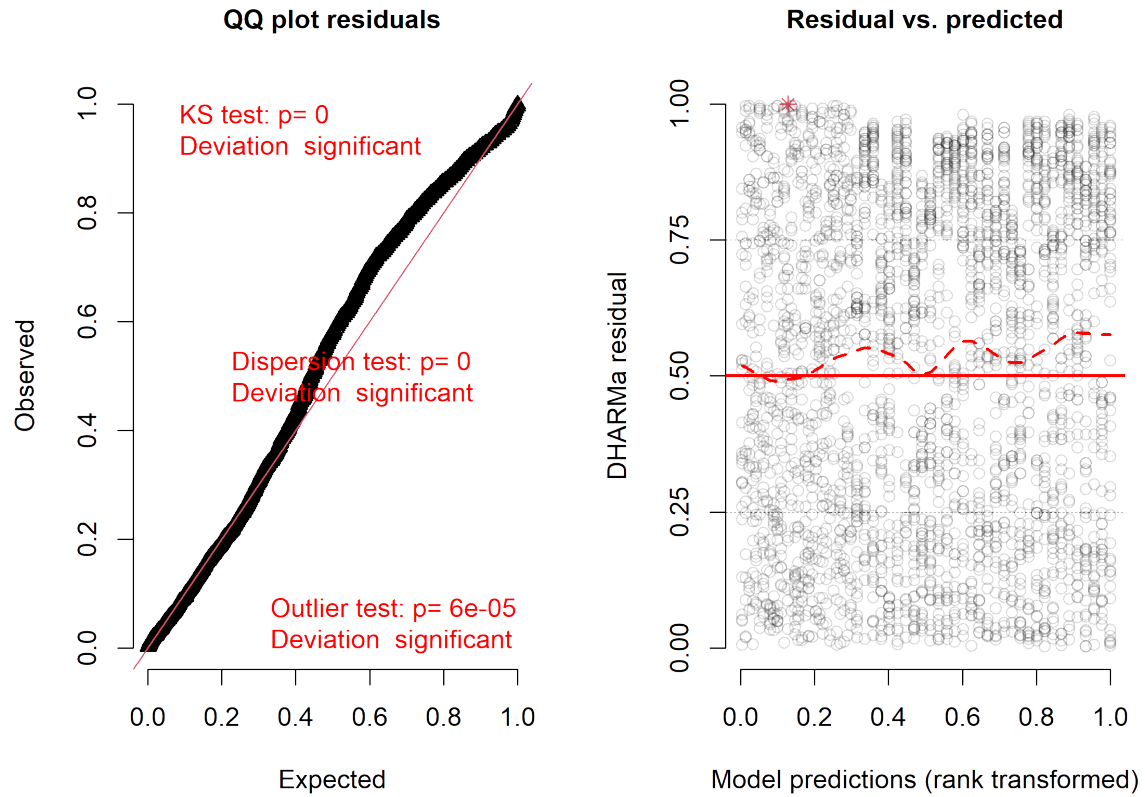


```
## worth noting that the slope is smaller for generalists, even though
## there is not significant interaction between slope and diet.
```

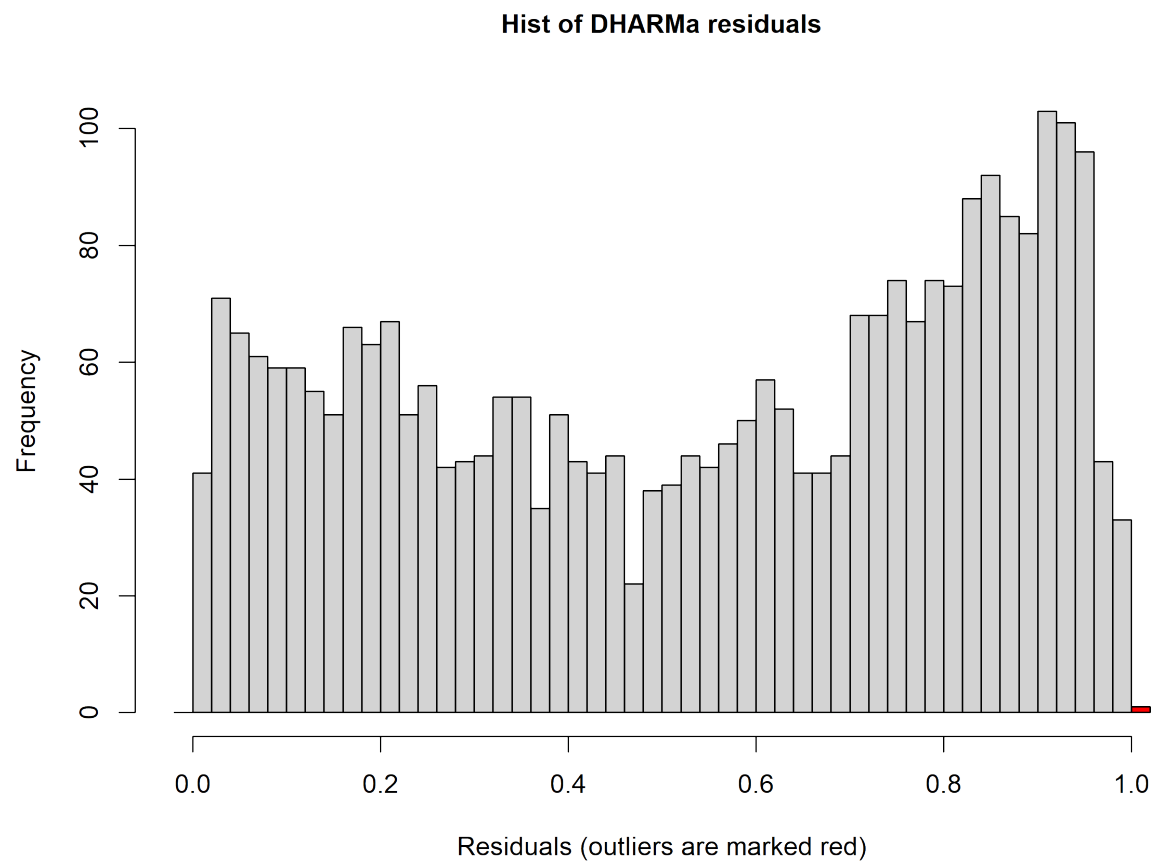
Diagnostics for host-abundance model

```
sim_res_host <- simulateResiduals(mod_hosts)
plot(sim_res_host) ## ok. Some deviations, that go away with removing
```

DHARMA residual

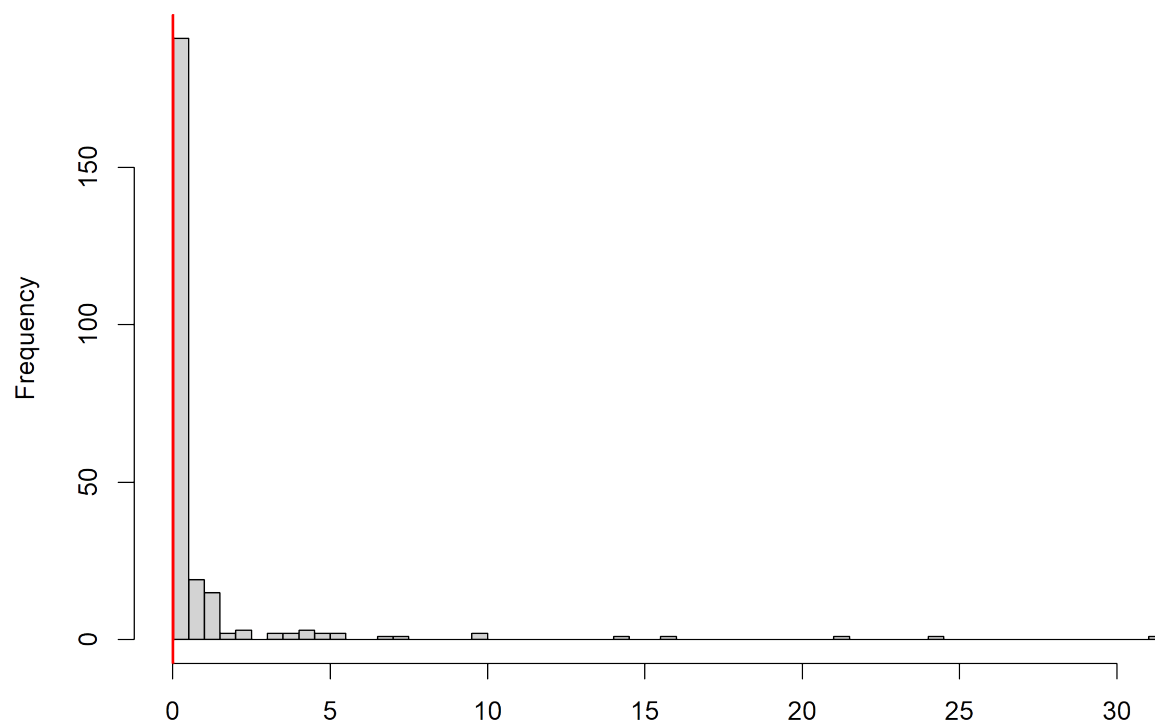


```
## random effect of caterpillar ID  
hist(sim_res_host) ##
```



```
testDispersion(sim_res_host) ## highly UNDER dispersed with CatID random effect
```

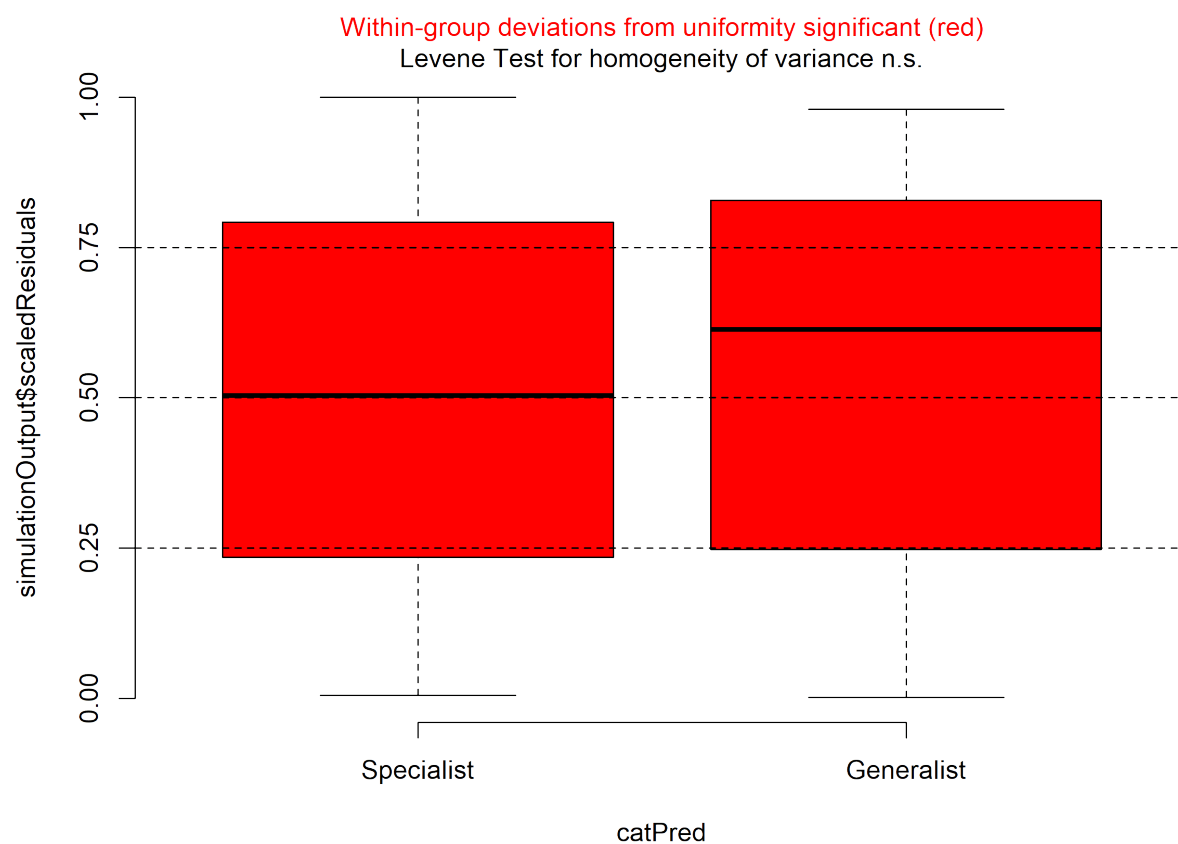

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## dispersion = 0.0025831, p-value < 2.2e-16
## alternative hypothesis: two.sided
```

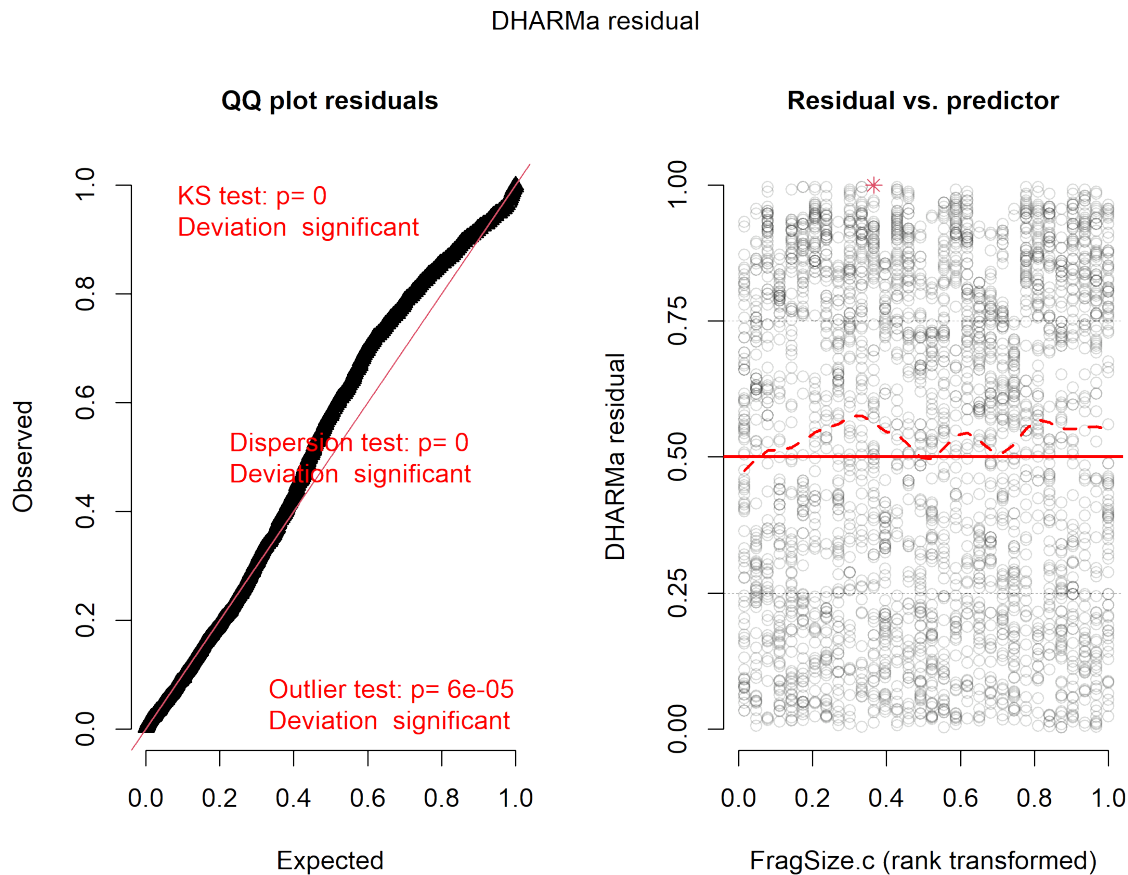
```
testCategorical(sim_res_host, mod_hosts$frame$Diet) ## more variance for generalists
```



```
## $uniformity
## $uniformity$details
## catPred: Specialist
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: dd[x, ]
## D = 0.049796, p-value = 0.02755
## alternative hypothesis: two-sided
##
## -----
## catPred: Generalist
##
## Asymptotic one-sample Kolmogorov-Smirnov test
##
## data: dd[x, ]
## D = 0.12851, p-value < 2.2e-16
## alternative hypothesis: two-sided
##
##
## $uniformity$p.value
## [1] 2.755071e-02 2.416931e-29
##
## $uniformity$p.value.cor
```

```
## [1] 2.755071e-02 4.833862e-29
##
##
## $homogeneity
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group  1  0.2394 0.6247
##      2878
```

```
plot(sim_res_host, form = mod_hosts$frame$FragSize.c) ## looks ok
```



Diagnostics are okay once we remove the random effect for caterpillar ID. Removing it gets rid of the underdispersion and

Not perfect, but visually acceptable and no issues with dispersion etc.

Note we need the zero-inflation term (really zero hurdle) because there are zeros outside the support for a gamma distribution.

After we do that looks like

1. there are no effects of fragmentation for either diet group on host abundance
2. Probability that a host is *absent* decreases with fragment size for specialist *and* generalists. There is no effect of diet x fragsize.

This is slightly complex to interpret, but most reasonable explanation is that larger forest fragments are more likely to contain hosts for caterpillars, but conditional on them containing them there is no effect on their abundance.

Deer effects on host abundance

Would be useful to also look at the effects of deer on host abundance.

```
mod_hosts_dc <- glmmTMB(N ~ Diet * (FragSize.c + DeerCaptures.c) +
  offset(log(nplots)) +
  (1|BlockID/SiteID),
  ziformula = ~ 1 + Diet * (FragSize.c + DeerCaptures.c),
  family = ziGamma(link = "log"),
  data = subset(host_BA,
    n_records > min_N),
  control=glmmTMB::glmmTMBControl(parallel = 20))

mod_hosts_sp <- glmmTMB(N ~ Diet * (FragSize.c + ScatPiles.c) +
  offset(log(nplots)) +
  (1|BlockID/SiteID),
  ziformula = ~ 1 + Diet * (FragSize.c + ScatPiles),
  family = ziGamma(link = "log"),
  data = subset(host_BA,
    n_records > min_N),
  control=glmmTMB::glmmTMBControl(parallel = 20))

mod_hosts_bp <- glmmTMB(N ~ Diet * (FragSize.c + BrowseProb.c) +
  offset(log(nplots)) +
  (1|BlockID/SiteID),
  ziformula = ~ 1 + Diet * (FragSize.c + BrowseProb.c),
  family = ziGamma(link = "log"),
  data = subset(host_BA,
    n_records > min_N),
  control=glmmTMB::glmmTMBControl(parallel = 20))

summary(mod_hosts_dc)
## Family: Gamma ( log )
## Formula:
## N ~ Diet * (FragSize.c + DeerCaptures.c) + offset(log(nplots)) +
## (1 | BlockID/SiteID)
## Zero inflation: ~1 + Diet * (FragSize.c + DeerCaptures.c)
## Data: subset(host_BA, n_records > min_N)
##
##      AIC      BIC   logLik deviance df.resid
## 37487.4 37575.1 -18728.7 37457.4      2545
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## SiteID:BlockID (Intercept) 0.004683 0.06844
## BlockID      (Intercept) 0.703814 0.83894
## Number of obs: 2560, groups: SiteID:BlockID, 32; BlockID, 13
##
```

```
## Dispersion estimate for Gamma family (sigma^2): 2.33
##
## Conditional model:
##
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.50494    0.25478  21.606 <2e-16 ***
## DietGeneralist    2.58667    0.11594  22.311 <2e-16 ***
## FragSize.c       -0.05808    0.10967  -0.530  0.5964
## DeerCaptures.c    0.20336    0.09390   2.166  0.0303 *
## DietGeneralist:FragSize.c  0.13724    0.12153   1.129  0.2588
## DietGeneralist:DeerCaptures.c -0.16768    0.09587  -1.749  0.0803 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Zero-inflation model:
##
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -0.60545    0.11862  -5.104 3.33e-07 ***
## DietGeneralist   -0.74976    0.14547  -5.154 2.55e-07 ***
## FragSize.c       -0.38821    0.12190  -3.185  0.00145 **
## DeerCaptures.c    0.11039    0.07981   1.383  0.16662
## DietGeneralist:FragSize.c  0.26119    0.14947   1.747  0.08057 .
## DietGeneralist:DeerCaptures.c -0.05606    0.09787  -0.573  0.56680
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod_hosts_dc, 2) ## no effect of deer captures
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: N
##
##           Chisq Df Pr(>Chisq)
## Diet      849.3101  1 < 2e-16 ***
## FragSize.c    0.5867  1  0.44369
## DeerCaptures.c  1.6405  1  0.20025
## Diet:FragSize.c  1.2753  1  0.25878
## Diet:DeerCaptures.c  3.0593  1  0.08028 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#
summary(mod_hosts_sp)
## Family: Gamma ( log )
## Formula:
## N ~ Diet * (FragSize.c + ScatPiles.c) + offset(log(nplots)) +
## (1 | BlockID/SiteID)
## Zero inflation: ~1 + Diet * (FragSize.c + ScatPiles)
## Data: subset(host_BA, n_records > min_N)
##
##           AIC      BIC   logLik deviance df.resid
## 37473.1 37560.8 -18721.5 37443.1      2545
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
```

```
## SiteID:BlockID (Intercept) 0.007103 0.08428
## BlockID (Intercept) 0.736450 0.85817
## Number of obs: 2560, groups: SiteID:BlockID, 32; BlockID, 13
##
## Dispersion estimate for Gamma family (sigma^2): 2.33
##
## Conditional model:
##
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 5.46006 0.25934 21.054 <2e-16 ***
## DietGeneralist 2.61215 0.11288 23.141 <2e-16 ***
## FragSize.c -0.12773 0.10635 -1.201 0.2298
## ScatPiles.c 0.24566 0.09933 2.473 0.0134 *
## DietGeneralist:FragSize.c 0.18400 0.11541 1.594 0.1109
## DietGeneralist:ScatPiles.c -0.24013 0.09794 -2.452 0.0142 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Zero-inflation model:
##
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.9353 0.1460 -6.404 1.52e-10 ***
## DietGeneralist -0.5029 0.1781 -2.824 0.004740 **
## FragSize.c -0.4580 0.1213 -3.775 0.000160 ***
## ScatPiles 2.7050 0.7434 3.639 0.000274 ***
## DietGeneralist:FragSize.c 0.3058 0.1478 2.069 0.038535 *
## DietGeneralist:ScatPiles -2.0686 0.9103 -2.272 0.023064 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod_hosts_sp, 2) ## negative effect of scat piles on both specialists
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: N
##
## Chisq Df Pr(>Chisq)
## Diet 851.1058 1 < 2e-16 ***
## FragSize.c 0.0347 1 0.85224
## ScatPiles.c 0.7320 1 0.39222
## Diet:FragSize.c 2.5417 1 0.11087
## Diet:ScatPiles.c 6.0110 1 0.01422 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# # that disappears for generalists. Frag size effect stays
#
summary(mod_hosts_bp) ##deer browse increases zeros for specialists, not generalists.
## Family: Gamma ( log )
## Formula:
## N ~ Diet * (FragSize.c + BrowseProb.c) + offset(log(nplots)) +
## (1 | BlockID/SiteID)
## Zero inflation: ~1 + Diet * (FragSize.c + BrowseProb.c)
## Data: subset(host_BA, n_records > min_N)
##
## AIC BIC logLik deviance df.resid
## 37475.5 37563.2 -18722.8 37445.5 2545
```

```
##
## Random effects:
##
## Conditional model:
##      Groups      Name      Variance Std.Dev.
## SiteID:BlockID (Intercept) 5.916e-08 0.0002432
## BlockID      (Intercept) 7.355e-01 0.8575949
## Number of obs: 2560, groups: SiteID:BlockID, 32; BlockID, 13
##
## Dispersion estimate for Gamma family (sigma^2): 2.33
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.50432    0.25918  21.238 < 2e-16 ***
## DietGeneralist    2.57817    0.11707  22.022 < 2e-16 ***
## FragSize.c       -0.05653    0.10661  -0.530 0.59594
## BrowseProb.c      0.25596    0.09805   2.610 0.00904 **
## DietGeneralist:FragSize.c 0.12770    0.12109   1.055 0.29164
## DietGeneralist:BrowseProb.c -0.16168    0.09715  -1.664 0.09606 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Zero-inflation model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)     -0.57513    0.11953  -4.812 1.50e-06 ***
## DietGeneralist  -0.77407    0.14627  -5.292 1.21e-07 ***
## FragSize.c      -0.34160    0.12304  -2.776 0.0055 **
## BrowseProb.c     0.25571    0.08146   3.139 0.0017 **
## DietGeneralist:FragSize.c 0.22462    0.15061   1.491 0.1359
## DietGeneralist:BrowseProb.c -0.17406    0.09922  -1.754 0.0794 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(mod_hosts_bp)
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: N
##              Chisq Df Pr(>Chisq)
## Diet          849.3692 1 < 2e-16 ***
## FragSize.c      0.5300 1 0.46661
## BrowseProb.c    4.6149 1 0.03170 *
## Diet:FragSize.c 1.1120 1 0.29164
## Diet:BrowseProb.c 2.7697 1 0.09606 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# ## Looking at all 3 together.
summary(mod_hosts_dc)$coef
## $cond
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.50493985 0.25478419 21.6062852 1.567652e-103
## DietGeneralist    2.58667083 0.11593902 22.3106151 2.914606e-110
## FragSize.c       -0.05807758 0.10966636 -0.5295843 5.964002e-01
```

```
## DeerCaptures.c          0.20335996 0.09389816 2.1657501 3.033029e-02
## DietGeneralist:FragSize.c 0.13724271 0.12153051 1.1292860 2.587772e-01
## DietGeneralist:DeerCaptures.c -0.16767681 0.09586560 -1.7490821 8.027682e-02
##
## $zi
##              Estimate Std. Error   z value    Pr(>|z|)
## (Intercept)    -0.60544944 0.11862220 -5.1040145 3.325228e-07
## DietGeneralist  -0.74976143 0.14547245 -5.1539752 2.550217e-07
## FragSize.c     -0.38821174 0.12189563 -3.1847879 1.448602e-03
## DeerCaptures.c  0.11038868 0.07980997 1.3831440 1.666207e-01
## DietGeneralist:FragSize.c 0.26118635 0.14947126 1.7474018 8.056766e-02
## DietGeneralist:DeerCaptures.c -0.05605623 0.09786842 -0.5727714 5.667995e-01
##
## $disp
## NULL
```

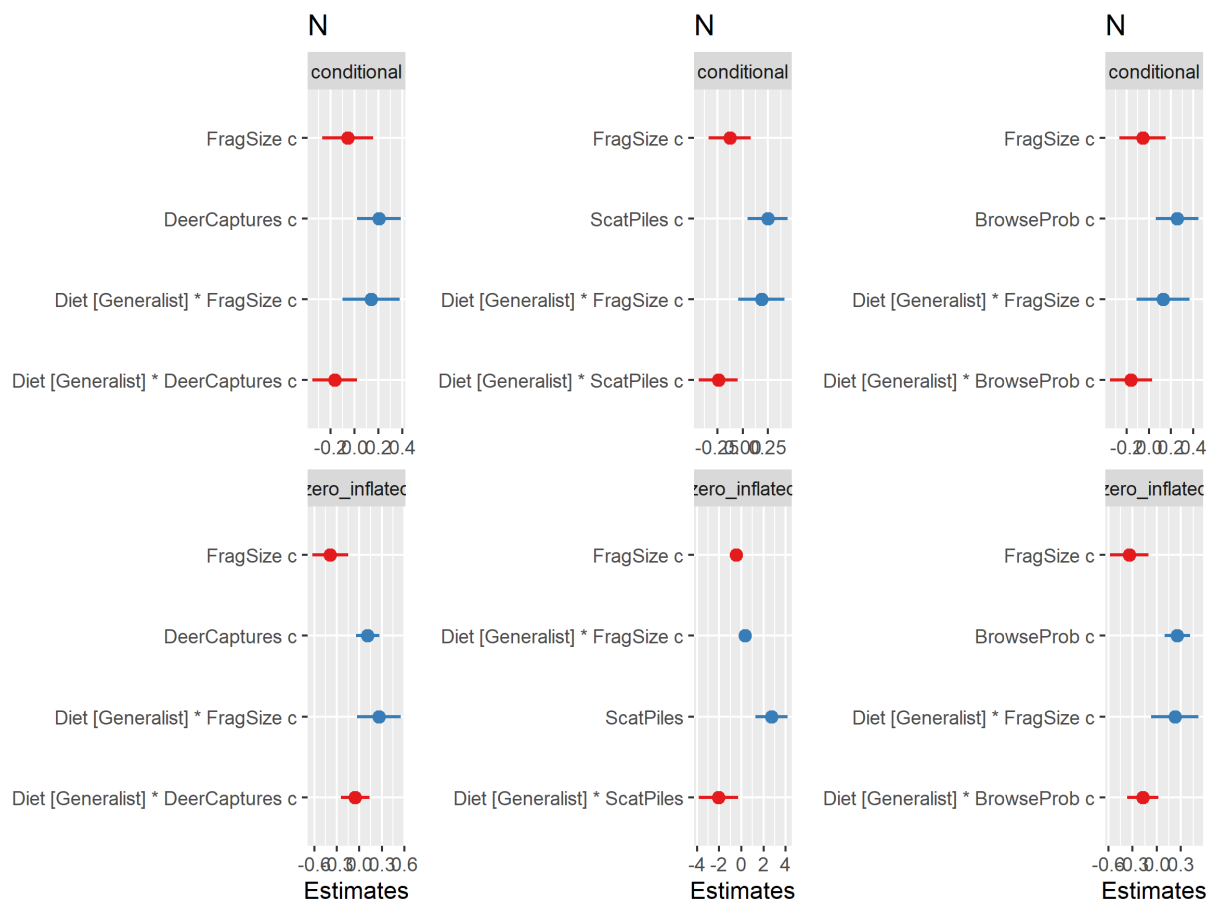
```
summary(mod_hosts_sp)$coef
## $cond
##              Estimate Std. Error   z value    Pr(>|z|)
## (Intercept)    5.4600638 0.25934025 21.053669 2.116433e-98
## DietGeneralist  2.6121515 0.11287936 23.141090 1.787393e-118
## FragSize.c     -0.1277261 0.10635334 -1.200960 2.297667e-01
## ScatPiles.c     0.2456635 0.09932975 2.473212 1.339048e-02
## DietGeneralist:FragSize.c 0.1840002 0.11541316 1.594274 1.108747e-01
## DietGeneralist:ScatPiles.c -0.2401330 0.09794453 -2.451724 1.421735e-02
##
## $zi
##              Estimate Std. Error   z value    Pr(>|z|)
## (Intercept)   -0.9352523 0.1460478 -6.403739 1.516172e-10
## DietGeneralist -0.5028813 0.1780638 -2.824163 4.740426e-03
## FragSize.c     -0.4579790 0.1213109 -3.775249 1.598477e-04
## ScatPiles      2.7050168 0.7433668 3.638872 2.738344e-04
## DietGeneralist:FragSize.c 0.3057836 0.1477843 2.069121 3.853477e-02
## DietGeneralist:ScatPiles -2.0685537 0.9103028 -2.272380 2.306358e-02
##
## $disp
## NULL
```

```
summary(mod_hosts_bp)$coef
## $cond
##              Estimate Std. Error   z value    Pr(>|z|)
## (Intercept)    5.50432369 0.25917935 21.2375089 4.301020e-100
## DietGeneralist  2.57816770 0.11706972 22.0224989 1.753246e-107
## FragSize.c     -0.05653207 0.10661402 -0.5302498 5.959387e-01
## BrowseProb.c    0.25596276 0.09805447 2.6104140 9.043271e-03
## DietGeneralist:FragSize.c 0.12769576 0.12109333 1.0545235 2.916433e-01
## DietGeneralist:BrowseProb.c -0.16167671 0.09714696 -1.6642487 9.606274e-02
##
## $zi
##              Estimate Std. Error   z value    Pr(>|z|)
## (Intercept)   -0.5751327 0.11953258 -4.811514 1.497910e-06
## DietGeneralist -0.7740730 0.14627399 -5.291938 1.210267e-07
## FragSize.c     -0.3415956 0.12303603 -2.776387 5.496677e-03
```



```
## BrowseProb.c          0.2557053 0.08146119 3.138983 1.695351e-03
## DietGeneralist:FragSize.c 0.2246172 0.15060994 1.491384 1.358608e-01
## DietGeneralist:BrowseProb.c -0.1740649 0.09921888 -1.754353 7.937010e-02
##
## $disp
## NULL
```

```
#
#
# ## now visually
plot_model(mod_hosts_dc, transform = NULL, rm.terms = "Diet [Generalist]") |
  plot_model(mod_hosts_sp, transform = NULL, rm.terms = "Diet [Generalist]") |
  plot_model(mod_hosts_bp, transform = NULL, rm.terms = "Diet [Generalist]")
```



```
#
# ## Both diet groups are positively associated with fragment size.
# ## Specialists decrease with deer activity; not generalists
#
```

Plot of host abundance vs. fragment area and deer activity

Plots showing relationships between fragment area and combined host densities

```
#####
## Plot for paper
#####
hostprob_plot <- ggpredict(mod_hosts,
  c("FragSize.c", "Diet", "DeerPressure.c [-1, 1]"),
  condition = c(nplots = 1),
  type = "zi_prob") %>% data.frame() %>%
  mutate(
    across(c(predicted, conf.low, conf.high), ~ 1 - .x),
    FragSize = x * sd(sites$FragSize) + 500,
    DeerAbund = factor(ifelse(facet == 1, "High", "Low"),
      levels = c("Low", "High")),
    DeerLab = "Deer Activity") %>%
  ggplot(aes(x = FragSize, y = predicted,
    colour = group, fill = group, linetype = group,
    ymin = conf.low, ymax = conf.high)) +
  geom_ribbon(alpha = 0.3, colour = NA) + geom_line() +
  ggh4x::facet_nested( ~ DeerLab + DeerAbund,
    nest_line = element_line()) +
  labs(x = NULL,
    y = expression(paste("Pr (Host occurrence)")),
    colour = "Diet", fill = "Diet", linetype = "Diet", title = "A") +
  scale_x_continuous(breaks = seq(200, 800, 200)) +
  ggthemes::theme_tufte() +
  theme(ggh4x.facet.nestline = element_line(colour = "grey"))

hostdens_plot <- ggpredict(mod_hosts,
  c("FragSize.c", "Diet", "DeerPressure.c [-1, 1]"),
  type = "fe") %>% data.frame() %>%
  mutate(
    FragSize = x * sd(sites$FragSize) + 500,
    DeerAbund = factor(ifelse(facet == 1, "High", "Low"),
      levels = c("Low", "High")),
    DeerLab = "Deer Activity",
    Diet = ifelse(group == 1, "Specialist", "Generalist")) %>%
  ggplot(aes(x = FragSize, y = predicted,
    colour = group, fill = group, linetype = group,
    ymin = conf.low, ymax = conf.high)) +
  geom_ribbon(alpha = 0.3, colour = NA) + geom_line() +
  facet_grid(Diet ~ DeerAbund) +
  labs(x = "Fragment area (ha)",
    y = expression(paste("Total host basal area (", ha^-1, ")")),
    colour = "Diet", fill = "Diet", linetype = "Diet", title = "C") +
  coord_trans(y = "log10") +
  scale_x_continuous(breaks = seq(200, 800, 200)) +
  scale_y_continuous(breaks = c(c(50, 100, 150, 200),
    c(2000, 4000, 6000, 8000))) +
  ggthemes::theme_tufte() +
  theme(strip.text = element_blank())

## Tree plots
hostabund_treepoint <- plot_model(mod_hosts, transform = NULL,
```

```

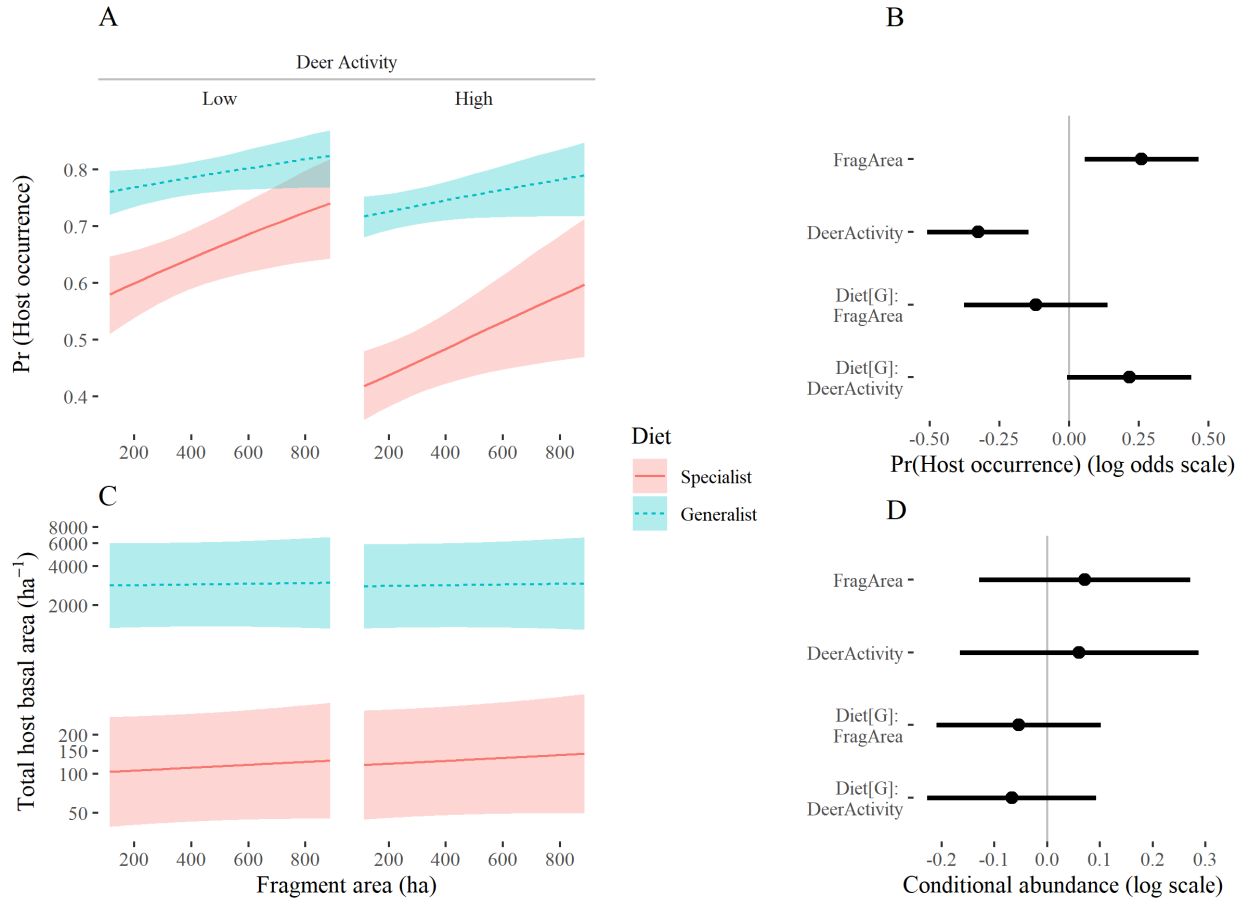
rm.terms = "Diet [Generalist]")
xlab <- c("FragArea", "DeerActivity",
         "Diet[G]: \n FragArea", "Diet[G]: \n DeerActivity")

hostabund_treeplot <-
  (filter(hostabund_treeplot$data, wrap.facet == "zero_inflated") %>%
    ggplot(aes(x = term, y = -estimate,
              ymin = -conf.low, ymax = -conf.high#,
              #colour = ifelse(estimate > 0, "N", "P")
            )) +
    geom_hline(yintercept = 0, colour = "grey") +
    geom_pointinterval(size = 4) +
    labs(x = NULL, y = "Pr(Host occurrence) (log odds scale)", title = "B") +
    scale_colour_discrete(guide = NULL) +
    scale_x_discrete(labels = rev(xlab)) +
    coord_flip() + ggthemes::theme_tufte() +
    theme(plot.title = element_text(hjust = -0.1))) /

  (filter(hostabund_treeplot$data, wrap.facet == "conditional") %>%
    ggplot(aes(x = term, y = estimate,
              ymin = conf.low, ymax = conf.high #,
              #colour = ifelse(estimate > 0, "N", "P")
            )) +
    geom_hline(yintercept = 0, colour = "grey") +
    geom_pointinterval(size = 4) +
    labs(x = NULL,
         y = "Conditional abundance (log scale)",
         title = "D") +
    scale_colour_discrete(guide = NULL) +
    scale_x_discrete(labels = rev(xlab)) +
    coord_flip() + ggthemes::theme_tufte() +
    theme(plot.title = element_text(hjust = -0.1)))

(hostabundplot <-
  ((hostprob_plot / hostdens_plot +
   plot_layout(guides = "collect")) | hostabund_treeplot) +
  plot_layout(widths = c(2, 1.2))
)

```



```
ggsave(hostabundplot, file = "figures/Figure_5_host_abund_plot.pdf",
        width = 7, height = 5)
tidy(mod_hosts)
## # A tibble: 15 x 8
##   effect component group      term estimate std.error statistic  p.value
##   <chr>    <chr>   <chr>    <chr>    <dbl>      <dbl>      <dbl>    <dbl>
## 1 fixed    cond    <NA>    (Int~    3.70      0.479      7.72  1.14e-14
## 2 fixed    cond    <NA>    Diet~    3.16      0.504      6.28  3.47e-10
## 3 fixed    cond    <NA>    Frag~    0.0712    0.102      0.698  4.85e- 1
## 4 fixed    cond    <NA>    Deer~    0.0607    0.115      0.525  5.99e- 1
## 5 fixed    cond    <NA>    Diet~   -0.0541    0.0797    -0.678  4.98e- 1
## 6 fixed    cond    <NA>    Diet~   -0.0672    0.0818    -0.822  4.11e- 1
## 7 fixed    zi     <NA>    (Int~   -0.359    0.102     -3.53  4.11e- 4
## 8 fixed    zi     <NA>    Diet~   -0.881    0.128     -6.88  6.15e-12
## 9 fixed    zi     <NA>    Frag~   -0.259    0.104     -2.49  1.28e- 2
##10 fixed    zi     <NA>    Deer~    0.327    0.0926     3.53  4.13e- 4
##11 fixed    zi     <NA>    Diet~    0.120    0.131     0.916  3.60e- 1
##12 fixed    zi     <NA>    Diet~   -0.215    0.114     -1.89  5.83e- 2
##13 ran_pars cond    CatID    sd__~    2.05     NA        NA     NA
##14 ran_pars cond    SiteID:Block~ sd__~    0.262     NA        NA     NA
##15 ran_pars cond    BlockID    sd__~    0.822     NA        NA     NA
```

Vegetation ordination

Visualising the relationship between fragment area and vegetation composition. We extract the data for the inner vegetation plots and use NMDS to find the main axes of variation (we use 3 because stress was >0.2 when we use only 2).

```
[1] 0.3862998 0.2749778 0.2098242
```

Call:

```
metaMDS(comm = ., distance = "bray", k = 3, trymax = 50, trace = 0,          maxit = 1000, parallel = paral
```

global Multidimensional Scaling using monoMDS

Data: wisconsin(sqrt(.))

Distance: bray

Dimensions: 3

Stress: 0.2098255

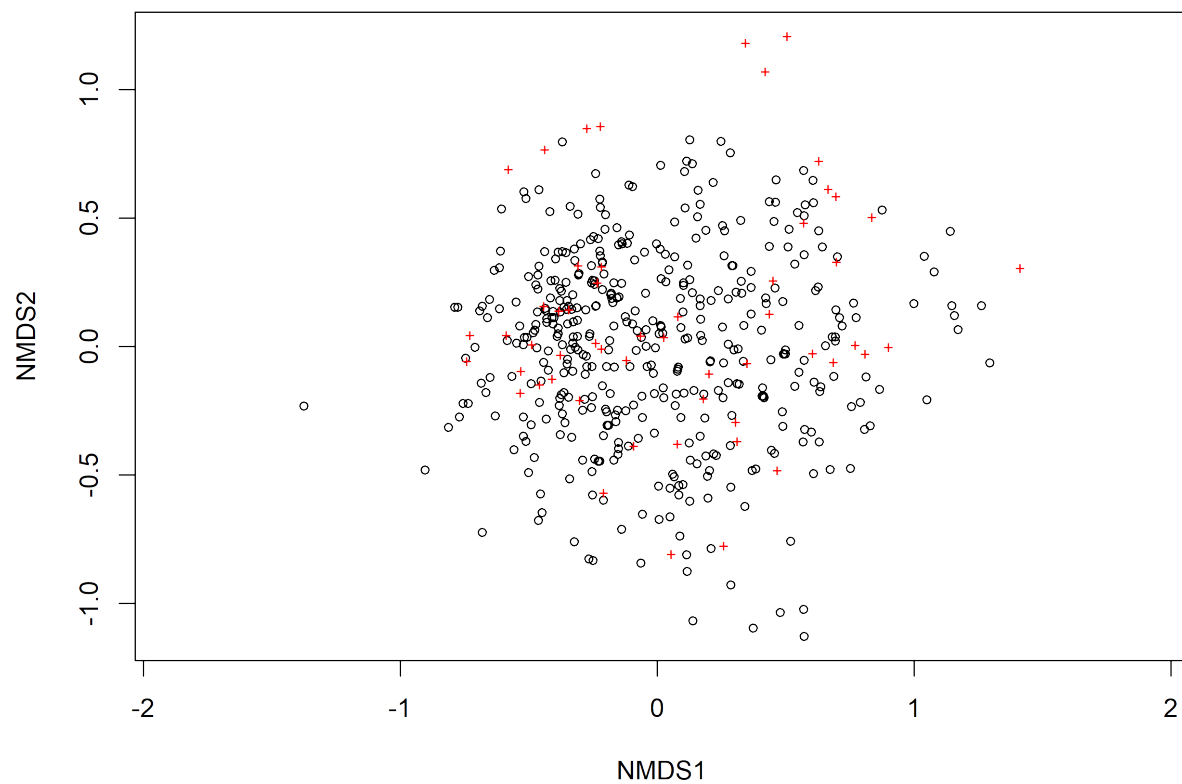
Stress type 1, weak ties

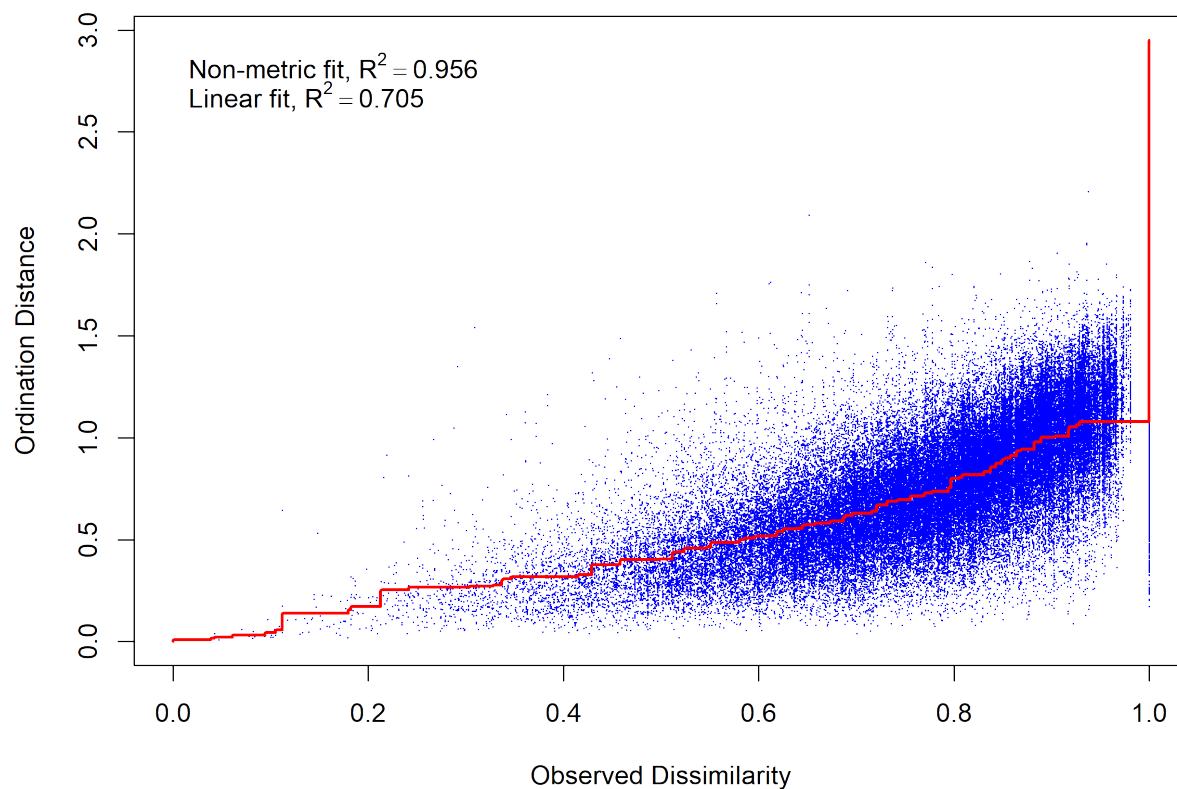
Best solution was not repeated after 64 tries

The best solution was from try 17 (random start)

Scaling: centring, PC rotation, halfchange scaling

Species: expanded scores based on 'wisconsin(sqrt(.))'





***VECTORS

	NMDS1	NMDS2	NMDS3	r2	Pr(>r)
log(FragSize)	-0.73646	-0.67589	0.02820	0.1532	0.001 ***
DeerPressure.c	0.63223	0.54484	-0.55085	0.0493	0.022 *

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

Blocks: strata

Permutation: free

Number of permutations: 999

Family: gaussian

Link function: identity

Formula:

log(FragSize) ~ s(NMDS1, NMDS2, NMDS3)

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.5988	0.1355	33.93	<2e-16 ***

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

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(NMDS1,NMDS2,NMDS3)	29.01	29.01	4.247	<2e-16 ***

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

R-sq.(adj) = 0.23

lmer.REML = 1539.1 Scale est. = 1.7107 n = 436

Family: gaussian

Link function: identity

Formula:

DeerPressure.c ~ s(NMDS1, NMDS2, NMDS3)

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.0504	0.2176	0.232	0.817

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(NMDS1,NMDS2,NMDS3)	29.84	29.84	2.147	0.000579 ***

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

R-sq.(adj) = 0.0477

lmer.REML = 852.47 Scale est. = 0.31665 n = 436

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 999

adonis2(formula = vegmat2 ~ log(FragSize) + splines::ns(DeerPressure.c, df = 3), data = vegmat, strata =

	Df	SumOfSqs	R2	F	Pr(>F)
log(FragSize)	1	3.633	0.02348	10.6881	0.001 ***
splines::ns(DeerPressure.c, df = 3)	3	4.589	0.02966	4.5002	0.001 ***
Residual	431	146.490	0.94686		
Total	435	154.712	1.00000		

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

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 999

adonis2(formula = vegmat2 ~ log(FragSize) + DeerCaptures.c, data = vegmat, strata = vegmat\$BlockID)

	Df	SumOfSqs	R2	F	Pr(>F)
log(FragSize)	1	3.633	0.02348	10.6027	0.001 ***
DeerCaptures.c	1	2.724	0.01761	7.9509	0.003 **
Residual	433	148.355	0.95891		
Total	435	154.712	1.00000		

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

Ordination plot

Develop a plot of the ordination

```
##
env_df <- fortify(ord_frag) %>%
  mutate(Label = c("Fragment Area", "Deer Pressure"))

ord_site <- bind_cols(filter(fortify(ord), score == "sites"),
  dplyr::select(vegmat, BlockID:DeerPressure.c))

ord_mod_fragsize <- gamm4(log(FragSize) ~ s(NMDS1, NMDS2, k = 50, bs="ts"),
  random = ~(1|BlockID),
  data = ord_site)

ord_mod_deer <- gamm4(BrowseProb ~ s(NMDS1, NMDS2, k = 50, bs="ts"),
  random = ~(1|BlockID),
  data = ord_site)

preddat <- expand_grid(NMDS1 = seq(-1, 1.5, 0.05), NMDS2 = seq(-1, 1.3, 0.05))
preddat$fragsize_pred <- exp(predict(ord_mod_fragsize$gam, newdata = preddat))
preddat$browse_pred <- predict(ord_mod_deer$gam, newdata = preddat)

#preddat %<>% mutate(NMDS1 = NMDS1, NMDS2 = NMDS2)

ordspec_df <- filter(fortify(ord), score == "species")
ordspec_df$FragCentroid <- exp(predict(ord_mod_fragsize$gam, newdata = ordspec_df))
ordspec_df$DeerCentroid <- predict(ord_mod_deer$gam, newdata = ordspec_df)

ordspec_df %<>% left_join(group_by(vegdata_ord, Tree, TreeFamily, HostID) %>%
  summarize(N = sum(is.na(Dead) | Dead == "no")),
  by = c("label" = "HostID"))

propspec <- cat %>%
  filter(n_records >= min_N) %>%
  group_by(HostID, Diet) %>%
  summarise(Count = sum(Count, na.rm = TRUE)) %>%
  filter(!is.na(Diet)) %>%
  pivot_wider(names_from = Diet, values_from = Count, values_fill = 0) %>%
  mutate(PropSpecialist = Specialist/(Generalist + Specialist),
    Total = Specialist + Generalist)

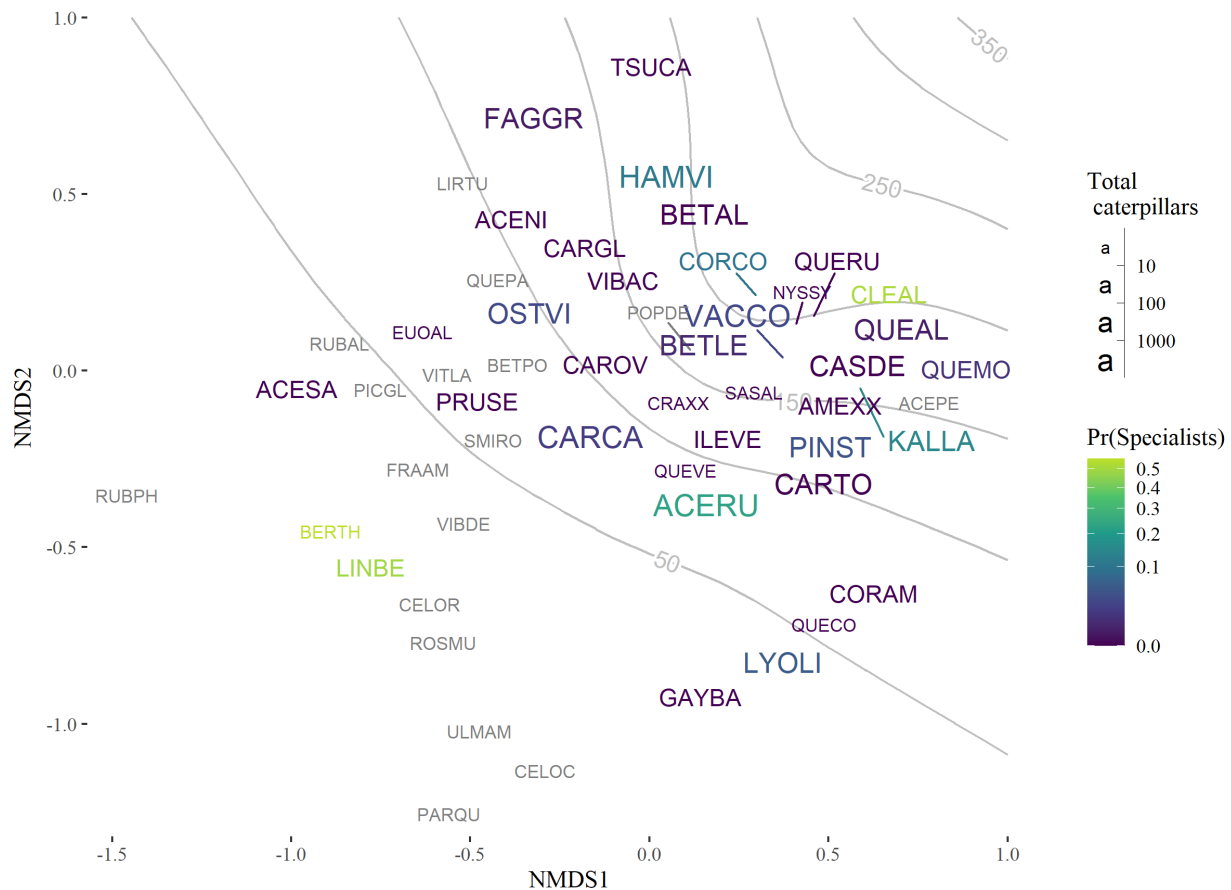
ordspec_df %<>%
  left_join(propspec, by = c("label" = "HostID")) %>%
  mutate(Total.c = replace_na(Total, 1)) #
# set plants with no values as 1 to allow plotting (but in smallest text).

## the axes have ended up aligning so largest fragments are nearer the origin.
## which is less intuitive. Flipping both x and y axes for clarity.
##
```



```
ord_plot <- ggplot(mapping = aes(x = -NMDS1, y = -NMDS2)) +
  geom_contour(data = preddat, aes(z = fragsize_pred), color = "grey") +
  metR::geom_text_contour(data = preddat, aes(z = fragsize_pred), color = "grey",
    stroke = 0.15) +
  geom_text_repel(data = ordspec_df, max.overlaps = 20,
    aes(label = label, colour = PropSpecialist, size = Total.c)) +
  # geom_segment(data = env_df, aes(x = 0, y = 0, xend = NMDS1, yend = NMDS2),
  #   arrow = arrow(length = unit(0.01, "npc")))) +
  #geom_label_repel(data = env_df, aes(label = Label)) +
  scale_size_binned(trans = "log10", range = c(1.5, 5)) +
  scale_colour_viridis_c(end = 0.9, trans = "sqrt") + ggthemes::theme_tufte() +
  labs(x = "NMDS1", y = "NMDS2", colour = "Pr(Specialists)", size = "Total\n caterpillars")
```

ord_plot



```
ggsave(ord_plot, filename = "figures/fig4_fragmentation_ordination.pdf")

## Pull out deer sensitivity and fragment sensitivity of each tree species
ordspec_df %>% arrange(FragCentroid) %>%
  dplyr::select(-starts_with("NMDS"), -score, -Total) %>%
  mutate(FragCentroid = round(FragCentroid),
    Generalist = replace_na(Generalist, 0),
```

```

Specialist = replace_na(Specialist, 0)) %>%
relocate(c(FragCentroid, DeerCentroid), .before = Generalist) %>%
write.csv(., file = "tables/HostSpeciesSummaries.csv")

```

Session Info

```

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 datasets  utils      methods    base
##
## other attached packages:
## [1] tidytext_0.4.2      ggeffects_1.6.0      car_3.1-2
## [4] carData_3.0-5       knitr_1.47           broom.mixed_0.2.9.5
## [7] DHARMA_0.4.6        performance_0.11.0   sjPlot_2.8.16
## [10] gamm4_0.2-6         mgcv_1.9-1           nlme_3.1-164
## [13] lme4_1.1-35.3       Matrix_1.7-0         glmmTMB_1.1.9
## [16] ggvegan_0.1.999     vegan_2.6-6.1        lattice_0.22-6
## [19] permute_0.9-7       ggrepel_0.9.5        ggh4x_0.2.8
## [22] GGally_2.2.1        ggdist_3.3.2         patchwork_1.2.0
## [25] magrittr_2.0.3      lubridate_1.9.3      forcats_1.0.0
## [28] stringr_1.5.1       dplyr_1.1.4          purrr_1.0.2
## [31] readr_2.1.5         tidyr_1.3.1          tibble_3.2.1
## [34] ggplot2_3.5.1       tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] rlang_1.1.3         furrr_0.3.1          compiler_4.4.0
## [4] systemfonts_1.1.0   vctr_0.6.5           crayon_1.5.2
## [7] pkgconfig_2.0.3     fastmap_1.2.0        backports_1.5.0
## [10] labeling_0.4.3      utf8_1.2.4           rmarkdown_2.27
## [13] tzdb_0.4.0          nloptr_2.0.3         ragg_1.3.2
## [16] bit_4.0.5           xfun_0.44            cachem_1.1.0
## [19] highr_0.11          SnowballC_0.7.1      sjmisc_2.8.10
## [22] broom_1.0.6         parallel_4.4.0       cluster_2.1.6
## [25] R6_2.5.1            stringi_1.8.4        RColorBrewer_1.1-3

```

```

## [28] parallelly_1.37.1    boot_1.3-30          numDeriv_2016.8-1.1
## [31] Rcpp_1.0.12          splines_4.4.0        timechange_0.3.0
## [34] tidyselect_1.2.1     rstudioapi_0.16.0    abind_1.4-5
## [37] yaml_2.3.8           TMB_1.9.11          codetools_0.2-20
## [40] sjlabelled_1.2.0     listenv_0.9.1        plyr_1.8.9
## [43] withr_3.0.0          evaluate_0.23        future_1.33.2
## [46] isoband_0.2.7        ggstats_0.6.0        pillar_1.9.0
## [49] janeaustenr_1.0.0    checkmate_2.3.1      renv_1.0.7
## [52] insight_0.19.11      distributional_0.4.0 generics_0.1.3
## [55] vroom_1.6.5          rprojroot_2.0.4      metR_0.15.0
## [58] hms_1.1.3            munsell_0.5.1        scales_1.3.0
## [61] minqa_1.2.7          globals_0.16.3       glue_1.7.0
## [64] tools_4.4.0          data.table_1.15.4    tokenizers_0.3.0
## [67] grid_4.4.0           datawizard_0.10.0    colorspace_2.1-0
## [70] cli_3.6.2            textshaping_0.4.0    fansi_1.0.6
## [73] ggthemes_5.1.0       viridisLite_0.4.2    sjstats_0.19.0
## [76] gtable_0.3.5         digest_0.6.35        farver_2.1.2
## [79] memoise_2.0.1        htmltools_0.5.8.1    lifecycle_1.0.4
## [82] bit64_4.0.5          MASS_7.3-60.2

```