Scale analysis and final models

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Contents

Before you begin

This script is number 5 of 6 in a series of scripts used to replicate the analyses presented in the paper: "Life on the edge: Industrial footprint and edge effects variably affect the distribution of a boreal small mammal"

This script was used to fit, evaluate, and visualize all models of landscape structure and its influence on the spatial distribution of red squirrels in our study area. This includes all model fitting, model selection, diagnostics, and effects plots.

When running these scripts, please ensure that you have downloaded the complete GitHub repository. This will ensure you have all the files, data, and proper folder structure you will need to run this code and associated analyses.

Also make sure you open RStudio through the R project (OSM_red_squirrel_distribution.Rproj). This will automatically set your working directory to the correct place (wherever you saved the repository) and ensure you don't have to change the file paths for some of the data. This analysis was initially run in R v4.3.0. If you have any questions or concerns, please contact one of the authors (in order):

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0. Setup

```
rm(list = ls())
#library(MASS)
library(glmmTMB)
#library(lme4)
library(tidyverse)
library(MuMIn)
library(rphylopic)
library(corrr)
library(performance)
#library(PerformanceAnalytics)
library(broom.mixed)
library(cowplot)
library(writexl)

`%nin%` <- Negate(`%in%`)
```

1. Prepare the data for modeling

We will also apply standardized z-scaling to the data. This is done *per buffer* since technically they are different datasets.

1.1. Import the data

```
covs <- read_csv("./data/processed/OSM_all_covariates_HFI_SBFI_final.csv")
```

```
## Rows: 9460 Columns: 55
## -- Column specification ---------------------------------------------------
## Delimiter: ","
## chr  (2): array, site
## dbl (53): array_year, lat, long, easting_12n, northing_12n, buffer_dist, cfi...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
response <- read_csv("./data/processed/OSM_monthly_detections_2021_2022_2023.csv") %>%

  # Only species we want is red squirrel
  filter(species == "red squirrel") %>%

  # Only want detections column
  select(-species, -presence) %>%

  rename(squirrel = detections)
```

```
## Rows: 63934 Columns: 7
## -- Column specification ------------------------------------------------------
## Delimiter: ","
## chr (3): array, site, species
## dbl (4): month, year, presence, detections
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
# Add the covariates to the response variable
data <- response %>%

  left_join(covs, by = c("array", "site"))
```

```
## Warning in left_join(., covs, by = c("array", "site")): Detected an unexpected many-to-many relation
## i Row 1 of `x` matches multiple rows in `y`.
## i Row 1 of `y` matches multiple rows in `x`.
## i If a many-to-many relationship is expected, set `relationship =
##   "many-to-many"` to silence this warning.
```

```r
# Make sure there are 20 rows per site/month/year
data %>%

  group_by(site, month, year) %>%

  summarize(n_obs = n()) %>%

  arrange(n_obs)
```

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

```
## # A tibble: 4,918 x 4
## # Groups:   site, month [4,754]
##    site    month  year n_obs
##    <chr>   <dbl> <dbl> <int>
##  1 LU13_11     1  2023    22
##  2 LU13_11     2  2023    22
##  3 LU13_11     3  2023    22
##  4 LU13_11     4  2023    22
##  5 LU13_11     5  2023    22
##  6 LU13_11     6  2023    22
##  7 LU13_11     7  2023    22
##  8 LU13_11     8  2023    22
##  9 LU13_11     9  2022    22
## 10 LU13_11     9  2023    22
## # i 4,908 more rows
```

```r
# 20 for everything. Looks good!!

# z-scaling for variables WITHIN each buffer
data_scaled <- data %>%
```

```
  group_by(buffer_dist) %>%

  mutate(across(cfi_site:last_col(), ~ as.numeric(scale(.)))) %>%

  ungroup(.)

# The mean will be 0 even though we grouped first, since the mean for each buffer is still 0.
summary(data_scaled)
```

```
##     array              site               month             year
##  Length:108196      Length:108196      Min.   : 1.000   Min.   :2021
##  Class :character   Class :character   1st Qu.: 4.000   1st Qu.:2022
##  Mode  :character   Mode  :character   Median : 7.000   Median :2023
##                                        Mean   : 6.634   Mean   :2023
##                                        3rd Qu.:10.000   3rd Qu.:2024
##                                        Max.   :12.000   Max.   :2024
##
##     squirrel        array_year        lat             long
##  Min.   : 0.0000   Min.   :2021   Min.   :54.56   Min.   :-115.0
##  1st Qu.: 0.0000   1st Qu.:2022   1st Qu.:55.55   1st Qu.:-113.0
##  Median : 0.0000   Median :2022   Median :56.56   Median :-111.8
##  Mean   : 0.9339   Mean   :2022   Mean   :56.30   Mean   :-112.2
##  3rd Qu.: 1.0000   3rd Qu.:2023   3rd Qu.:57.10   3rd Qu.:-111.2
##  Max.   :70.0000   Max.   :2023   Max.   :57.56   Max.   :-110.1
##
##   easting_12n      northing_12n      buffer_dist       cfi_site
##  Min.   :254793   Min.   :6046183   Min.   :  50   Min.   :-1.0421
##  1st Qu.:375199   1st Qu.:6155882   1st Qu.:1000   1st Qu.:-0.6582
##  Median :448084   Median :6268110   Median :2375   Median :-0.3196
##  Mean   :427832   Mean   :6241258   Mean   :2393   Mean   : 0.0000
##  3rd Qu.:487051   3rd Qu.:6330343   3rd Qu.:3750   3rd Qu.: 0.2842
##  Max.   :559033   Max.   :6379755   Max.   :5000   Max.   : 6.7755
##
## cfi_site_with_harvest cfi_site_with_vegedges  harvest_0_15
##  Min.   :-1.1835        Min.   :-1.1245        Min.   :-0.4446
##  1st Qu.:-0.6693        1st Qu.:-0.6442        1st Qu.:-0.3841
##  Median :-0.3013        Median :-0.3122        Median :-0.3240
##  Mean   : 0.0000        Mean   : 0.0000        Mean   : 0.0000
##  3rd Qu.: 0.3302        3rd Qu.: 0.2777        3rd Qu.:-0.2203
##  Max.   : 6.7241        Max.   : 6.7198        Max.   : 8.8550
##
## harvest_gt_15      harvest_total      osm_industrial      pipe_trans
##  Min.   :-0.6256   Min.   :-0.67528   Min.   :-0.50992   Min.   :-0.9652
##  1st Qu.:-0.4893   1st Qu.:-0.56852   1st Qu.:-0.41059   1st Qu.:-0.6878
##  Median :-0.3716   Median :-0.41880   Median :-0.30491   Median :-0.3105
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.00000   Mean   : 0.0000
##  3rd Qu.:-0.1280   3rd Qu.:-0.03056   3rd Qu.:-0.04273   3rd Qu.: 0.2548
##  Max.   : 6.9091   Max.   : 5.08535   Max.   :10.57756   Max.   : 7.4013
##
##     railways          roads            seismic         seismic_lines
##  Min.   :-0.111   Min.   :-1.3575   Min.   :-1.0230   Min.   :-1.5413
##  1st Qu.:-0.091   1st Qu.:-0.5403   1st Qu.:-0.6049   1st Qu.:-0.6608
##  Median :-0.052   Median :-0.1591   Median :-0.3247   Median :-0.2403
##  Mean   : 0.000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
```

```
##    3rd Qu.:-0.038   3rd Qu.: 0.4028   3rd Qu.: 0.2055   3rd Qu.: 0.4071
##    Max.   :26.485   Max.   :15.0263   Max.   : 5.7997   Max.   : 5.0866
##    NA's   :4918
##  seismic_lines_3D      trails          veg_edges        wells_active
##    Min.   :-0.4103   Min.   :-1.0576   Min.   :-0.8885   Min.   :-0.56774
##    1st Qu.:-0.3846   1st Qu.:-0.6221   1st Qu.:-0.4756   1st Qu.:-0.47773
##    Median :-0.3565   Median :-0.2290   Median :-0.1844   Median :-0.38959
##    Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.00000
##    3rd Qu.:-0.2986   3rd Qu.: 0.2535   3rd Qu.: 0.1645   3rd Qu.:-0.01219
##    Max.   : 6.2937   Max.   :15.8529   Max.   :13.8053   Max.   :19.32623
##
##   wells_inactive    wells_total       pct_betu_pap        fire_0_15
##    Min.   :-0.9289   Min.   :-0.7841   Min.   :-0.09     Min.   :-0.3601
##    1st Qu.:-0.6250   1st Qu.:-0.5801   1st Qu.:-0.07     1st Qu.:-0.3444
##    Median :-0.3368   Median :-0.3392   Median :-0.07     Median :-0.3258
##    Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.00     Mean   : 0.0000
##    3rd Qu.: 0.1762   3rd Qu.: 0.1184   3rd Qu.:-0.05     3rd Qu.:-0.3000
##    Max.   :13.2921   Max.   : 8.9950   Max.   :20.22     Max.   : 4.5335
##                                        NA's   :59016
##    fire_gt_15        pct_lari_lar      lc_broadleaf      lc_coniferous
##    Min.   :-0.3240   Min.   :-0.6475   Min.   :-1.0151   Min.   :-2.37235
##    1st Qu.:-0.2827   1st Qu.:-0.5490   1st Qu.:-0.7086   1st Qu.:-0.70739
##    Median :-0.2498   Median :-0.3749   Median :-0.4357   Median :-0.07207
##    Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.00000
##    3rd Qu.:-0.2232   3rd Qu.: 0.1673   3rd Qu.: 0.4674   3rd Qu.: 0.61317
##    Max.   : 7.4090   Max.   : 9.4549   Max.   : 4.4843   Max.   : 2.74250
##
##     lc_herbs        lc_mixedwood       lc_shrubs         lc_water
##    Min.   :-0.7852   Min.   :-1.3024   Min.   :-0.3114   Min.   :-0.5413
##    1st Qu.:-0.6572   1st Qu.:-0.6833   1st Qu.:-0.2894   1st Qu.:-0.3722
##    Median :-0.3921   Median :-0.3053   Median :-0.2693   Median :-0.2429
##    Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
##    3rd Qu.: 0.2136   3rd Qu.: 0.4097   3rd Qu.:-0.2334   3rd Qu.:-0.1295
##    Max.   : 6.7377   Max.   : 5.8728   Max.   : 8.9180   Max.   :13.1921
##
##    lc_wetland      lc_wetland_treed   pct_pice_gla       pct_pice_mar
##    Min.   :-1.0140   Min.   :-1.7479   Min.   :-0.4873   Min.   :-2.1399
##    1st Qu.:-0.6385   1st Qu.:-0.7748   1st Qu.:-0.4199   1st Qu.:-0.9071
##    Median :-0.4023   Median :-0.1654   Median :-0.3262   Median : 0.1614
##    Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
##    3rd Qu.: 0.2744   3rd Qu.: 0.6188   3rd Qu.:-0.1272   3rd Qu.: 0.8697
##    Max.   : 6.0380   Max.   : 3.4576   Max.   : 9.5250   Max.   : 1.7085
##
##   pct_pinu_ban      pct_popu_tre     nonanthro_cai_mn   nonanthro_ed
##    Min.   :-0.3977   Min.   :-1.6340   Min.   :-1.6760   Min.   :-1.1470
##    1st Qu.:-0.3679   1st Qu.:-0.8626   1st Qu.:-0.7096   1st Qu.:-0.5623
##    Median :-0.3372   Median :-0.1685   Median :-0.1475   Median :-0.2731
##    Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
##    3rd Qu.:-0.1929   3rd Qu.: 0.8477   3rd Qu.: 0.6428   3rd Qu.: 0.2039
##    Max.   : 5.0205   Max.   : 2.5358   Max.   : 3.5209   Max.   : 5.1082
##
##   nonanthro_tca    landscape_cai_mn   landscape_ed      landscape_tca
##    Min.   :-3.1665   Min.   : NA       Min.   : NA       Min.   : NA
##    1st Qu.:-0.7096   1st Qu.: NA       1st Qu.: NA       1st Qu.: NA
```

```
##  Median : 0.1140    Median : NA       Median : NA      Median : NA
##  Mean   : 0.0000    Mean   :NaN       Mean   :NaN      Mean   :NaN
##  3rd Qu.: 0.8431    3rd Qu.: NA       3rd Qu.: NA      3rd Qu.: NA
##  Max.   : 1.6937    Max.   : NA       Max.   : NA      Max.   : NA
##                     NA's   :108196    NA's   :108196   NA's   :108196
##  nonanthro_cohesion  landscape_cohesion landscape_contag   landscape_mesh
##  Min.   :-17.73901   Min.   :-3.90056   Min.   :-3.07601   Min.   :-1.8860
##  1st Qu.: -0.09964   1st Qu.:-0.69566   1st Qu.:-0.72484   1st Qu.:-0.6640
##  Median :  0.26597   Median :-0.03058   Median :-0.08274   Median :-0.2884
##  Mean   :  0.00000   Mean   : 0.00000   Mean   : 0.00000   Mean   : 0.0000
##  3rd Qu.:  0.50409   3rd Qu.: 0.73933   3rd Qu.: 0.64601   3rd Qu.: 0.3927
##  Max.   :  0.88374   Max.   : 2.95922   Max.   : 4.08776   Max.   : 7.5132
##
##   landscape_np      landscape_shei      landscape_siei
##  Min.   :-1.1343   Min.   :-4.12918   Min.   :-4.3075
##  1st Qu.:-0.5236   1st Qu.:-0.64137   1st Qu.:-0.5770
##  Median :-0.2777   Median : 0.07569   Median : 0.2271
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.0000
##  3rd Qu.: 0.1454   3rd Qu.: 0.70654   3rd Qu.: 0.7397
##  Max.   : 7.0051   Max.   : 3.20495   Max.   : 1.9831
##
```

```
rm(covs, response)
```

1.2. Scale the data and store values

I also want to make sure we store the values we used to scale the data so that we can back-transform it into ecologically meaningful values for figures. Either it's annoying to fit models (typing scale() all the time or annoying to make plots. Would have been faster to write 'scale' in all the models but oh well… maybe I'll fix this one day and learn from my mistakes. Laziness does not pay off in the long run.

```
data_scaled_summary <- data %>%

  select(buffer_dist, cfi_site:last_col()) %>%

  group_by(buffer_dist) %>%

  pivot_longer(cols = 2:last_col(), values_to = "value", names_to = "variable") %>%

  group_by(buffer_dist, variable) %>%

  # Store the mean and the sd for backtransforming later (don't judge me)
  summarize(
    mean = mean(value, na.rm = TRUE),
    sd   = sd(value, na.rm = TRUE),
    .groups = "drop"
  )
```

2. Scale analysis:

Another nice way to visualize our results for the scale analysis is to plot the model weight for the global sub-models at each scale.

2.1. Natural sub-model:

```r
natural_scale <- purrr::map(unique(data$buffer_dist), ~{

  # Subset the data based on the current buffer distance
  data_subset <- data_scaled %>%

    filter(buffer_dist == .x)

  # Fit the initial model for the current buffer distance
  glmmTMB(squirrel ~

                     lc_coniferous +
                     lc_mixedwood +
                     lc_broadleaf +
                     lc_shrubs +
                     lc_herbs +
                     fire_0_15 +

                     (1|array/site),

                 data = data_subset,
                 family = nbinom2,
                 na.action = na.fail)
  }
) %>%

  set_names(unique(data$buffer_dist)) %>%

  # Model selection and AIC for each scale
  MuMIn::model.sel(natural_scale) %>%

  as.data.frame(.) %>%

  dplyr::mutate(buffer = as.numeric(rownames(.)),
                submodel = "NATURAL")
```

2.2. Anthro composition submodel:

```r
comp_scale <- purrr::map(unique(data$buffer_dist), ~{

  # Subset the data based on the current buffer distance
  data_subset <- data_scaled %>%

    filter(buffer_dist == .x)

  # Fit the initial model for the current buffer distance
  glmmTMB(squirrel ~

                     pipe_trans +
                     seismic +
                     wells_inactive +
                     #harvest_total +
                     wells_active +
                     osm_industrial +
```

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```
                           harvest_0_15 +
                           #roads +

                           (1|array/site),

                     data = data_subset,
                     family = nbinom2,
                     na.action = na.fail)

    }
) %>%

set_names(unique(data$buffer_dist)) %>%

# Model selection and AIC for each scale
MuMIn::model.sel(comp_scale) %>%

as.data.frame(.) %>%

dplyr::mutate(buffer = as.numeric(rownames(.)),
              submodel = "COMP")
```

2.3. Configuration sub-model:

```
config_scale <- purrr::map(unique(data$buffer_dist), ~{

  # Subset the data based on the current buffer distance
  data_subset <- data_scaled %>%

    filter(buffer_dist == .x)

  # Fit the initial model for the current buffer distance
  glmmTMB(squirrel ~

                     # configuration variables
                     landscape_shei +
                     nonanthro_ed +
                     landscape_mesh +

                     (1|array/site),

                   data = data_subset,
                   family = nbinom2,
                   na.action = na.fail)

    }
) %>%

set_names(unique(data$buffer_dist)) %>%

# Model selection and AIC for each scale
MuMIn::model.sel(config_scale) %>%

as.data.frame(.) %>%

dplyr::mutate(buffer = as.numeric(rownames(.)),
```

```
            submodel = "CONFIG")
```

2.4. Let's put it all together into a plot:

```r
# One big data frame
fig_scale <- bind_rows(natural_scale,
                       comp_scale,
                       config_scale) %>%

  # Plot the model weights as a line.
  ggplot(., aes(x = buffer, y = weight, color = submodel)) +

    geom_line(size = 1, alpha = 0.7) +

    # Old color scheme I didn't like (overwritten)
    scale_color_manual(values =c("#D24D57",
                                 "#1976D2",
                                 "#388E3C")) +

    scale_color_manual(values =c("goldenrod2","darkblue","forestgreen"),
                       labels =c("Disturbance \ncomposition", "Configuration", "Natural
                       ↪ \nlandcover")) +
    #scale_color_viridis_d() +

    theme_bw() +

    # Crop the axis since model weights are low
    scale_y_continuous(limits = c(0, 0.41), expand = expansion(add = c(0, 0))) +

    scale_x_continuous(expand = c(0,0), limits = c(0, 5100)) +

    #scale_x_log10(expand = c(0,0), limits = c(50, 5100)) +

    labs(x = "Buffer radius (m)",
         y = "AICc weight",
         color = "Covariate subset") +

    # Remove all grid lines
    theme(panel.grid = element_blank()) +

    # Squirrel icon for funsies. Wrong spp. but whatever.
    add_phylopic(
      uuid = get_uuid(name = "Sciurus vulgaris"),
      x = 3000,
      y = 0.34,
      height = 0.09
      ) +

    theme(
    legend.position = c(0.98, 0.99),         # Top-right corner
    legend.justification = c(1, 1)      # Anchor the legend's top-right
    )
```

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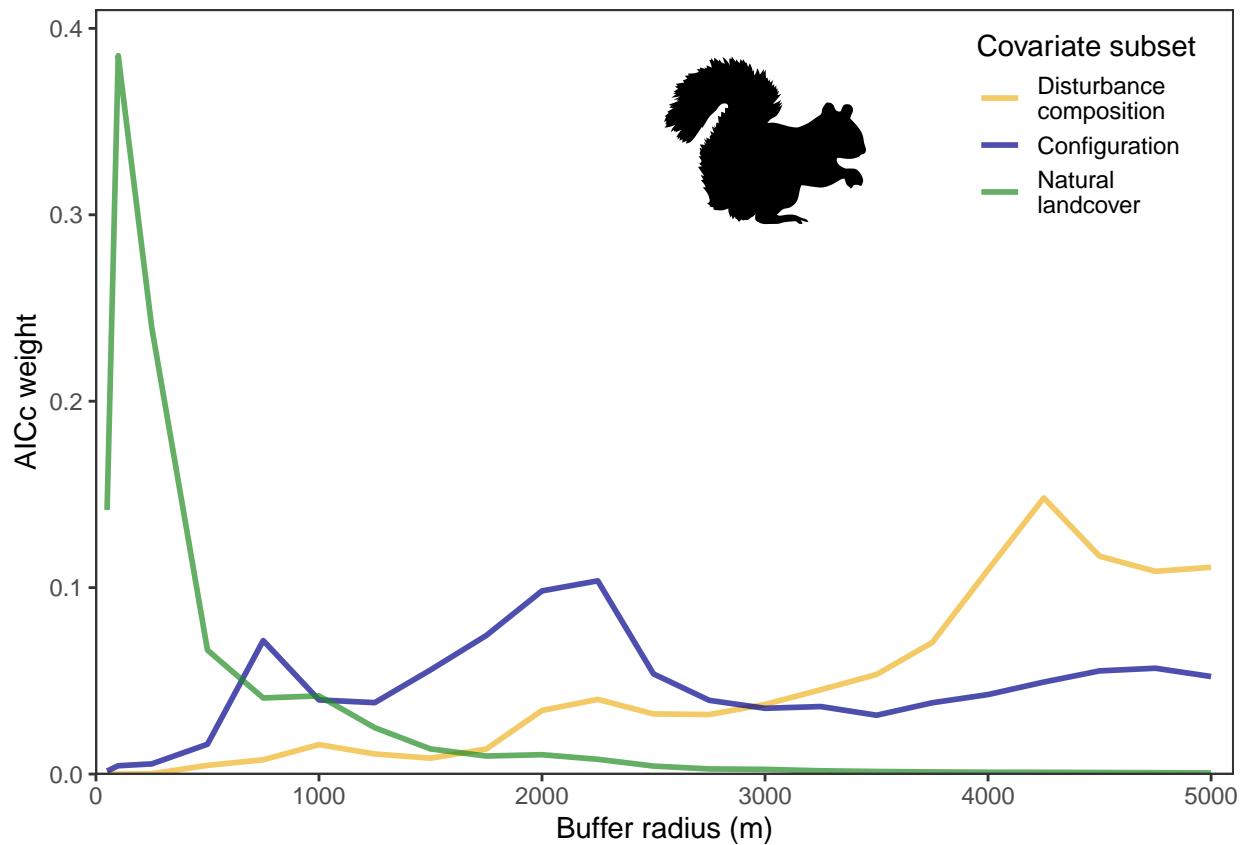
```
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

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

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

`fig_scale`


```
ggsave("./figures/redsquirrel_neg_binomial_submodel_scale_modelweight.png", width = 5, height =
↪  3.5, dpi = 500)

#ggsave("./figures/redsquirrel_neg_binomial_submodel_scale_modelweight_logscale.png", width = 7,
↪  height = 4, dpi = 500)
```

2.5. Identify top scales:

What are the numbers from the above scale analysis?

```
natural_scale$buffer[1]
```

```
## [1] 100
```

```
comp_scale$buffer[1]
```

```
## [1] 4250
```

```
config_scale$buffer[1]
```

```
## [1] 2250
```

Store them manually here before we move to the next step.

```
# Let's specify these values manually. This means we don't need to re-run this every time we open a
↪   new R session.
nat_buffer <- 100
comp_buffer <- 4250
config_buffer <- 2250
```

3. Construct the final dataset (best spatial scales)

We will pull out the predictors from the submodels **at the appropriate spatial scales** and merge this into one big dataset for final models. This selects a couple extra columns that we don't actually want to model but that's fine, this was efficient *#sueme*

```
data_final_scaled <- bind_cols(

  # response variables
  data_scaled %>%
    select(1:squirrel) %>%
    distinct(),

  # natural data scaled by natural buffer
  data_scaled %>%
    filter(buffer_dist == nat_buffer) %>%
    select(fire_0_15:lc_wetland_treed) %>%
    mutate(natural_buffer = nat_buffer), # won't use this column, just keeping track of the scale
    ↪   somehow

  # composition data scaled by composition buffer
  data_scaled %>%
    filter(buffer_dist == comp_buffer) %>%
    select(harvest_0_15:wells_total) %>%
    mutate(comp_buffer = comp_buffer), # won't use this column, just keeping track of the scale
    ↪   somehow

  # configuration data
  data_scaled %>%
    filter(buffer_dist == config_buffer) %>%
    select(contains("nonanthro") | contains("landscape") | contains("cfi")) %>%
```

```
    mutate(config_buffer = config_buffer) # won't use this column, just keeping track of the scale
    ↪  somehow
  ) %>%

  relocate(contains("buffer"), .after=("squirrel")) %>%

  select(-landscape_ed, -landscape_tca, -landscape_cai_mn)

summary(data_final_scaled)
```

```
##     array               site               month            year
## Length:4918        Length:4918        Min.   : 1.000   Min.   :2021
## Class :character   Class :character   1st Qu.: 4.000   1st Qu.:2022
## Mode  :character   Mode  :character   Median : 7.000   Median :2023
##                                       Mean   : 6.634   Mean   :2023
##                                       3rd Qu.:10.000   3rd Qu.:2024
##                                       Max.   :12.000   Max.   :2024
##     squirrel        natural_buffer  comp_buffer    config_buffer
## Min.   : 0.0000   Min.   :100     Min.   :4250   Min.   :2250
## 1st Qu.: 0.0000   1st Qu.:100     1st Qu.:4250   1st Qu.:2250
## Median : 0.0000   Median :100     Median :4250   Median :2250
## Mean   : 0.9339   Mean   :100     Mean   :4250   Mean   :2250
## 3rd Qu.: 1.0000   3rd Qu.:100     3rd Qu.:4250   3rd Qu.:2250
## Max.   :70.0000   Max.   :100     Max.   :4250   Max.   :2250
##    fire_0_15          fire_gt_15       pct_lari_lar      lc_broadleaf
## Min.   :-0.2844   Min.   :-0.190   Min.   :-0.3749   Min.   :-0.6332
## 1st Qu.:-0.2844   1st Qu.:-0.190   1st Qu.:-0.3749   1st Qu.:-0.6284
## Median :-0.2844   Median :-0.190   Median :-0.3749   Median :-0.5125
## Mean   : 0.0000   Mean   : 0.000   Mean   : 0.0000   Mean   : 0.0000
## 3rd Qu.:-0.2844   3rd Qu.:-0.190   3rd Qu.:-0.3232   3rd Qu.: 0.1606
## Max.   : 4.5335   Max.   : 7.409   Max.   : 8.3161   Max.   : 3.1892
##  lc_coniferous        lc_herbs          lc_mixedwood       lc_shrubs
## Min.   :-1.3520   Min.   :-0.52107   Min.   :-0.6342   Min.   :-0.2440
## 1st Qu.:-0.9249   1st Qu.:-0.52107   1st Qu.:-0.6203   1st Qu.:-0.2440
## Median :-0.1031   Median :-0.44105   Median :-0.4386   Median :-0.2440
## Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.0000
## 3rd Qu.: 0.8063   3rd Qu.: 0.03641   3rd Qu.: 0.1295   3rd Qu.:-0.2374
## Max.   : 2.2948   Max.   : 6.73769   Max.   : 5.1466   Max.   : 8.9180
##    lc_water          lc_wetland        lc_wetland_treed   harvest_0_15
## Min.   :-0.1678   Min.   :-0.56217   Min.   :-1.0134   Min.   :-0.4207
## 1st Qu.:-0.1678   1st Qu.:-0.54608   1st Qu.:-0.8433   1st Qu.:-0.4207
## Median :-0.1678   Median :-0.44292   Median :-0.3634   Median :-0.4207
## Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.0000
## 3rd Qu.:-0.1678   3rd Qu.: 0.02224   3rd Qu.: 0.6197   3rd Qu.:-0.1659
## Max.   :12.6617   Max.   : 5.23963   Max.   : 3.0220   Max.   : 4.9011
##  harvest_gt_15      harvest_total     osm_industrial      pipe_trans
## Min.   :-0.58153   Min.   :-0.6425   Min.   :-0.49935   Min.   :-0.9207
## 1st Qu.:-0.58153   1st Qu.:-0.6425   1st Qu.:-0.45973   1st Qu.:-0.8304
## Median :-0.47811   Median :-0.4576   Median :-0.36131   Median :-0.2868
## Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.0000
## 3rd Qu.: 0.04405   3rd Qu.: 0.1236   3rd Qu.: 0.01547   3rd Qu.: 0.4123
## Max.   : 5.46216   Max.   : 4.3829   Max.   : 8.60241   Max.   : 4.1597
##     railways           roads             seismic         seismic_lines
## Min.   :-0.102   Min.   :-1.0714   Min.   :-0.9918   Min.   :-1.5177
```

```
##  1st Qu.:-0.102   1st Qu.:-0.6144   1st Qu.:-0.5853   1st Qu.:-0.6680
##  Median :-0.102   Median :-0.2604   Median :-0.2973   Median :-0.1923
##  Mean   : 0.000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
##  3rd Qu.:-0.102   3rd Qu.: 0.3832   3rd Qu.: 0.2352   3rd Qu.: 0.4256
##  Max.   :13.822   Max.   : 5.0237   Max.   : 5.1278   Max.   : 3.5024
##  seismic_lines_3D     trails          veg_edges        wells_active
##  Min.   :-0.4013   Min.   :-1.0235   Min.   :-0.8285   Min.   :-0.53247
##  1st Qu.:-0.4013   1st Qu.:-0.7128   1st Qu.:-0.5413   1st Qu.:-0.52642
##  Median :-0.4013   Median :-0.2853   Median :-0.2484   Median :-0.41446
##  Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.00000
##  3rd Qu.:-0.2343   3rd Qu.: 0.3389   3rd Qu.: 0.2348   3rd Qu.: 0.05882
##  Max.   : 5.3692   Max.   : 4.4249   Max.   : 6.2924   Max.   : 6.35239
##  wells_inactive     wells_total      nonanthro_cai_mn   nonanthro_ed
##  Min.   :-0.8992   Min.   :-0.7462   Min.   :-1.6276   Min.   :-1.0673
##  1st Qu.:-0.6961   1st Qu.:-0.6125   1st Qu.:-0.6932   1st Qu.:-0.5441
##  Median :-0.4514   Median :-0.3564   Median :-0.1896   Median :-0.2889
##  Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000
##  3rd Qu.: 0.4679   3rd Qu.: 0.2336   3rd Qu.: 0.5964   3rd Qu.: 0.1271
##  Max.   : 3.9137   Max.   : 6.1091   Max.   : 2.6958   Max.   : 4.6367
##  nonanthro_tca     nonanthro_cohesion landscape_cohesion landscape_contag
##  Min.   :-2.8806   Min.   :-6.39094   Min.   :-2.60717   Min.   :-2.49910
##  1st Qu.:-0.6934   1st Qu.:-0.06247   1st Qu.:-0.74738   1st Qu.:-0.69574
##  Median : 0.1575   Median : 0.28132   Median :-0.06761   Median :-0.08636
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.00000   Mean   : 0.00000
##  3rd Qu.: 0.8542   3rd Qu.: 0.49120   3rd Qu.: 0.76526   3rd Qu.: 0.62715
##  Max.   : 1.6299   Max.   : 0.76886   Max.   : 2.39415   Max.   : 3.40955
##  landscape_mesh    landscape_np      landscape_shei     landscape_siei
##  Min.   :-1.0155   Min.   :-0.79501   Min.   :-3.52743   Min.   :-3.9765
##  1st Qu.:-0.6708   1st Qu.:-0.51403   1st Qu.:-0.60965   1st Qu.:-0.5383
##  Median :-0.2930   Median :-0.29480   Median : 0.08809   Median : 0.2545
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.00000   Mean   : 0.0000
##  3rd Qu.: 0.3122   3rd Qu.: 0.06182   3rd Qu.: 0.67378   3rd Qu.: 0.7550
##  Max.   : 7.4986   Max.   : 5.73543   Max.   : 2.64626   Max.   : 1.7992
##    cfi_site       cfi_site_with_harvest cfi_site_with_vegedges
##  Min.   :-0.9601   Min.   :-1.0134       Min.   :-1.0053
##  1st Qu.:-0.6491   1st Qu.:-0.6678       1st Qu.:-0.6476
##  Median :-0.3108   Median :-0.2978       Median :-0.3164
##  Mean   : 0.0000   Mean   : 0.0000       Mean   : 0.0000
##  3rd Qu.: 0.2936   3rd Qu.: 0.3319       3rd Qu.: 0.3033
##  Max.   : 5.9740   Max.   : 5.5758       Max.   : 5.3407
```

Let's look at the correlation among this final set of candidate variables at their respective spatial scales:

```r
data_final_corr <- data_final_scaled %>%

  select(9:ncol(.)) %>%

  corrr::correlate(., use = "pairwise.complete.obs",
                      method = "pearson",
                      diagonal = NA,
                      quiet = TRUE) %>%
  as_tibble() %>%

  mutate(across(everything(), ~ if_else(row_number() >= min(which(is.na(.))), NA, .))) %>%
```

```
  select(rev(names(.))) %>%

  relocate(term) %>%

  pivot_longer(cols = -term, names_to = "var2", values_to = "corr") %>%

  rename(var1 = term) %>%

  arrange(desc(abs(corr))) %>%

  drop_na(.)
```

```
## Warning: There was 1 warning in `mutate()`.
## i In argument: `across(...)`.
## Caused by warning in `min()`:
## ! no non-missing arguments to min; returning Inf
```

```
head(data_final_corr, 15)
```

```
## # A tibble: 15 x 3
##    var1                var2                    corr
##    <chr>               <chr>                  <dbl>
##  1 cfi_site            cfi_site_with_vegedges  0.981
##  2 landscape_contag    landscape_shei         -0.965
##  3 nonanthro_ed        landscape_np            0.957
##  4 landscape_shei      landscape_siei          0.950
##  5 wells_active        wells_total             0.944
##  6 seismic             nonanthro_ed            0.936
##  7 landscape_contag    landscape_siei         -0.931
##  8 nonanthro_cohesion  landscape_np           -0.930
##  9 seismic_lines_3D    nonanthro_ed            0.916
## 10 nonanthro_ed        nonanthro_cohesion     -0.913
## 11 seismic             seismic_lines_3D        0.911
## 12 seismic_lines_3D    landscape_np            0.907
## 13 seismic             nonanthro_cohesion     -0.900
## 14 harvest_gt_15       harvest_total           0.896
## 15 seismic             landscape_np            0.894
```

Let's make a table for the Supporting Information to show high correlations.

```
covs_formatted <- read_csv("./tables/OSM_all_covariates_formatted_names.csv")

xxx <- data_final_corr %>%
  filter(var1 != "cfi_site_with_harvest" & var2 != "cfi_site_with_harvest",
         var1 != "cfi_site_with_vegedges" & var2 != "cfi_site_with_vegedges",
         var1 != "nonanthro_cai_mn" & var2 != "nonanthro_cai_mn",
         var1 != "nonanthro_tca" & var2 != "nonanthro_tca") %>%
  left_join(covs_formatted, by = c("var1" = "Covariate")) %>%
  mutate(var1 = PrettyName) %>%
  select(-PrettyName) %>%
  left_join(covs_formatted, by = c("var2" = "Covariate")) %>%
  mutate(var2 = PrettyName) %>%
  select(-PrettyName) %>%
  drop_na() %>%
```

```
  filter(abs(corr)>0.50)

writexl::write_xlsx(xxx, "./tables/final_dataset_high_correlation.xlsx")
```

4. Fit models using the best-fit scales for each 'category' of variables.

nbinom2 allows the variance to increase with the square of the mean, which seemed to be the best fit to our data (vs nbinom1) in an initial exploration of AIC scores (huge drop in AICc)

```
m_null <- glmmTMB(squirrel ~ # Squirrel as response variable

                        #lc_coniferous +
                        #lc_mixedwood +
                        #lc_broadleaf +
                        #lc_shrubs +
                        #lc_herbs +
                        #fire_0_15 +

                        (1|array/site), # Nested random effects for every model

                     data = data_final_scaled, # Scaled data as the data
                     family = nbinom2,  # nbinom2 specification
                     na.action = na.fail) # fail the model if there are NAs. Probably a data
                     ↪  error.

# Not gonna annotate every model since it should be obvious by now.
m_fire <- glmmTMB(squirrel ~

                        #lc_coniferous +
                        #lc_mixedwood +
                        #lc_broadleaf +
                        #lc_shrubs +
                        #lc_herbs +
                        fire_0_15 +

                        (1|array/site),

                     data = data_final_scaled,
                     family = nbinom2,
                     na.action = na.fail)


m_forest <- glmmTMB(squirrel ~

                        lc_coniferous +
                        lc_mixedwood +
                        lc_broadleaf +
                        #lc_shrubs +
                        #lc_herbs +
                        #fire_0_15 +

                        (1|array/site),

                     data = data_final_scaled,
                     family = nbinom2,
                     na.action = na.fail)
```

```r
m_forest_fire <- glmmTMB(squirrel ~

                        lc_coniferous +
                        lc_mixedwood +
                        lc_broadleaf +
                        #lc_shrubs +
                        #lc_herbs +
                        fire_0_15 +

                        (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)


m_landcover <- glmmTMB(squirrel ~

                        lc_coniferous +
                        lc_mixedwood +
                        lc_broadleaf +
                        lc_shrubs +
                        lc_wetland +
                        lc_wetland_treed +
                        #fire_0_15 +

                        (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)

m_landcover_fire <- glmmTMB(squirrel ~

                        lc_coniferous +
                        lc_mixedwood +
                        lc_broadleaf +
                        lc_shrubs +
                        lc_wetland +
                        lc_wetland_treed +
                        fire_0_15 +

                        (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)

  m_seis_wells <- glmmTMB(squirrel ~
                        lc_coniferous +
                        lc_mixedwood +
                        lc_broadleaf +
                        fire_0_15 +

                        pipe_trans +
                        seismic +
                        wells_inactive +
                        #harvest_total +
```

```r
                          #wells_active +
                          #osm_industrial +
                          #harvest_0_15 +
                          #roads +

                          (1|array/site),

                  data = data_final_scaled,
                  family = nbinom2,
                  na.action = na.fail)

m_harvest <- glmmTMB(squirrel ~
                          lc_coniferous +
                          lc_mixedwood +
                          lc_broadleaf +
                          fire_0_15 +

                          #pipe_trans +
                          #seismic +
                          #wells_inactive +
                          #harvest_total +
                          #wells_active +
                          #osm_industrial +
                          harvest_0_15 +
                          #roads + +

                          (1|array/site),

                  data = data_final_scaled,
                  family = nbinom2,
                  na.action = na.fail)

m_harvest_seis <- glmmTMB(squirrel ~
                          lc_coniferous +
                          lc_mixedwood +
                          lc_broadleaf +
                          fire_0_15 +

                          pipe_trans +
                          seismic +
                          wells_inactive +
                          #harvest_total +
                          #wells_active +
                          #osm_industrial +
                          harvest_0_15 +
                          #roads +

                          (1|array/site),

                  data = data_final_scaled,
                  family = nbinom2,
                  na.action = na.fail)


m_active <- glmmTMB(squirrel ~
                          lc_coniferous +
                          lc_mixedwood +
                          lc_broadleaf +
                          fire_0_15 +
```

```r
                    #pipe_trans +
                    #seismic +
                    #wells_inactive +
                    #harvest_total +
                    wells_active +
                    osm_industrial +
                    #harvest_0_15 +
                    #roads +

                    (1|array/site),

                data = data_final_scaled,
                family = nbinom2,
                na.action = na.fail)

m_active_harvest <- glmmTMB(squirrel ~
                    lc_coniferous +
                    lc_mixedwood +
                    lc_broadleaf +
                    fire_0_15 +

                    #pipe_trans +
                    #seismic +
                    #wells_inactive +
                    #harvest_total +
                    wells_active +
                    osm_industrial +
                    harvest_0_15 +
                    #roads +

                    (1|array/site),

                data = data_final_scaled,
                family = nbinom2,
                na.action = na.fail)

m_active_seis <- glmmTMB(squirrel ~
                    lc_coniferous +
                    lc_mixedwood +
                    lc_broadleaf +
                    fire_0_15 +

                    pipe_trans +
                    seismic +
                    wells_inactive +
                    #harvest_total +
                    wells_active +
                    osm_industrial +
                    #harvest_0_15 +
                    #roads +

                    (1|array/site),
                data = data_final_scaled,
                family = nbinom2,
                na.action = na.fail)

m_active_seis_harvest <- glmmTMB(squirrel ~
                    lc_coniferous +
```

```
                        lc_mixedwood +
                        lc_broadleaf +
                        fire_0_15 +

                        pipe_trans +
                        seismic +
                        wells_inactive +
                        #harvest_total +
                        wells_active +
                        osm_industrial +
                        harvest_0_15 +
                        #roads +

                        (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)

  m_het <- glmmTMB(squirrel ~

                        # natural covariates
                        fire_0_15 +
                        lc_broadleaf +
                        lc_coniferous +
                        lc_mixedwood +

                        # configuration variables
                        landscape_shei +
                        #nonanthro_ed +
                        #landscape_mesh +

                        (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)

m_edge <- glmmTMB(squirrel ~

                        # natural covariates
                        fire_0_15 +
                        lc_broadleaf +
                        lc_coniferous +
                        lc_mixedwood +

                        # configuration variables
                        #landscape_shei +
                        nonanthro_ed +
                        #landscape_mesh +

                        (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)


  m_cohesion <- glmmTMB(squirrel ~
```

```r
                        # natural covariates
                        fire_0_15 +
                        lc_broadleaf +
                        lc_coniferous +
                        lc_mixedwood +

                        # configuration variables
                        nonanthro_cohesion +
                        #landscape_mesh +

                        (1|array/site),

                  data = data_final_scaled,
                  family = nbinom2,
                  na.action = na.fail)

m_cohesion_mesh <- glmmTMB(squirrel ~

                        # natural covariates
                        fire_0_15 +
                        lc_broadleaf +
                        lc_coniferous +
                        lc_mixedwood +

                        # configuration variables
                        nonanthro_cohesion +
                        landscape_mesh +

                        (1|array/site),

                  data = data_final_scaled,
                  family = nbinom2,
                  na.action = na.fail)

m_cohesion_shei <- glmmTMB(squirrel ~

                        # natural covariates
                        fire_0_15 +
                        lc_broadleaf +
                        lc_coniferous +
                        lc_mixedwood +

                        # configuration variables
                        nonanthro_cohesion +
                        #landscape_mesh +
                        landscape_shei +

                        (1|array/site),

                  data = data_final_scaled,
                  family = nbinom2,
                  na.action = na.fail)


m_conn <- glmmTMB(squirrel ~

                        # natural covariates
                        fire_0_15 +
```

```r
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +

                    # configuration variables
                    #landscape_shei +
                    #nonanthro_ed +
                    landscape_mesh +

                    (1|array/site),

                 data = data_final_scaled,
                 family = nbinom2,
                 na.action = na.fail)

m_edge_conn <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +

                    # configuration variables
                    #landscape_shei +
                    nonanthro_ed +
                    landscape_mesh +

                    (1|array/site),

                 data = data_final_scaled,
                 family = nbinom2,
                 na.action = na.fail)

m_het_conn <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +

                    # configuration variables
                    landscape_shei +
                    #nonanthro_ed +
                    landscape_mesh +

                    (1|array/site),

                 data = data_final_scaled,
                 family = nbinom2,
                 na.action = na.fail)

m_het_edge <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
```

```r
                    lc_mixedwood +

                    # configuration variables
                    landscape_shei +
                    nonanthro_ed +
                    #landscape_mesh +

                    (1|array/site),

                data = data_final_scaled,
                family = nbinom2,
                na.action = na.fail)

m_config <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +

                    # configuration variables
                    landscape_shei +
                    nonanthro_ed +
                    landscape_mesh +

                    (1|array/site),

                data = data_final_scaled,
                family = nbinom2,
                na.action = na.fail)

m_edge_cfi <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +

                    # configuration variables
                    #landscape_shei +
                    nonanthro_ed +
                    cfi_site +
                    #landscape_mesh +

                    (1|array/site),

                data = data_final_scaled,
                family = nbinom2,
                na.action = na.fail)

m_edgeXcfi <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +
```

```
                         # configuration variables
                         #landscape_shei +
                         nonanthro_ed +
                         cfi_site +
                         nonanthro_ed*cfi_site +
                         #landscape_mesh +

                         (1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)
```

5. Perform model selection

Let's gather all the models into a list and perform model selection:

```
#rm(m_nat_comp_config2)

# Pull all models from the global environment
models <- mget(ls(pattern = "m_"))

# PErform model selection on them
models_rank <- MuMIn::model.sel(models) %>%

    as.data.frame(.) %>%

    select(-`disp((Int))`) %>%

    # Tidy up the disgusting glmmTMB names (thanks ChatGPT!!)
    rename_with(~ gsub("cond\\(|disp\\(|\\)|\\(", "", .)) %>%

    rename(intercept = `Int`) %>%

    mutate(model = rownames(.)) %>%

    # Model at the first row
    relocate(model)

models_rank
```

```
##                                     model intercept  fire_0_15 lc_broadleaf
## m_edgeXcfi                     m_edgeXcfi -1.427925 0.15769889   -0.5184199
## m_seis_wells                 m_seis_wells -1.572581 0.11240507   -0.4778583
## m_harvest_seis             m_harvest_seis -1.570776 0.09684067   -0.4733282
## m_edge_cfi                     m_edge_cfi -1.567200 0.16163124   -0.4928295
## m_edge_conn                   m_edge_conn -1.562466 0.19104506   -0.5133915
## m_active_seis               m_active_seis -1.572573 0.13022726   -0.4723316
## m_config                         m_config -1.559354 0.20258102   -0.5380583
## m_active_seis_harvest m_active_seis_harvest -1.570856 0.11423316   -0.4679858
## m_het_edge                     m_het_edge -1.561443 0.17179761   -0.5412209
## m_edge                             m_edge -1.566267 0.14768820   -0.5036329
## m_cohesion_mesh           m_cohesion_mesh -1.568183 0.21849236   -0.4991341
```

```
## m_cohesion                         m_cohesion -1.570700 0.17538729   -0.4934427
## m_cohesion_shei             m_cohesion_shei -1.566806 0.19961846   -0.5268128
## m_conn                             m_conn -1.567658 0.28029701   -0.4736139
## m_forest_fire               m_forest_fire -1.569886 0.23832582   -0.4704491
## m_het                               m_het -1.566800 0.26194637   -0.4950755
## m_harvest                       m_harvest -1.566950 0.20601272   -0.4674565
## m_het_conn                     m_het_conn -1.565877 0.29001804   -0.4889981
## m_active                         m_active -1.572968 0.27440936   -0.4499958
## m_active_harvest         m_active_harvest -1.569942 0.23895698   -0.4442878
## m_forest                         m_forest -1.580889         NA   -0.5103000
## m_landcover_fire         m_landcover_fire -1.570350 0.31937125   -0.7657364
## m_landcover                   m_landcover -1.579396         NA   -0.7986393
## m_fire                             m_fire -1.557730 0.28489807         NA
## m_null                             m_null -1.570733         NA         NA
##                   lc_coniferous lc_mixedwood osm_industrial wells_active
## m_edgeXcfi         -0.032283340   0.16358190             NA           NA
## m_seis_wells       -0.005779811   0.15468778             NA           NA
## m_harvest_seis     -0.003229019   0.15087108             NA           NA
## m_edge_cfi         -0.017969211   0.15372909             NA           NA
## m_edge_conn        -0.045979284   0.11772131             NA           NA
## m_active_seis      -0.003575806   0.15444343      0.1105531  -0.01413357
## m_config           -0.055956349   0.08846544             NA           NA
## m_active_seis_harvest -0.001126694  0.15039267      0.1126439  -0.01882282
## m_het_edge         -0.049405069   0.10145326             NA           NA
## m_edge             -0.033103091   0.15055022             NA           NA
## m_cohesion_mesh    -0.046715422   0.12522553             NA           NA
## m_cohesion         -0.036190489   0.15209934             NA           NA
## m_cohesion_shei    -0.051553523   0.10730891             NA           NA
## m_conn             -0.021979643   0.15116866             NA           NA
## m_forest_fire      -0.015128002   0.17173150             NA           NA
## m_het              -0.025436180   0.13820635             NA           NA
## m_harvest          -0.013254231   0.16388419             NA           NA
## m_het_conn         -0.027890557   0.13257960             NA           NA
## m_active            0.003295678   0.18029519      0.1233570   0.09076456
## m_active_harvest    0.007694183   0.17198065      0.1265564   0.10381425
## m_forest           -0.021489508   0.15286291             NA           NA
## m_landcover_fire   -0.319353140   0.02963789             NA           NA
## m_landcover        -0.316265282   0.01933788             NA           NA
## m_fire                       NA           NA             NA           NA
## m_null                       NA           NA             NA           NA
##                   harvest_0_15 pipe_trans    seismic wells_inactive
## m_edgeXcfi                  NA         NA         NA             NA
## m_seis_wells                NA  0.3052326 -0.4471425    0.005864648
## m_harvest_seis      0.07299016  0.3108955 -0.4382964    0.017820765
## m_edge_cfi                  NA         NA         NA             NA
## m_edge_conn                 NA         NA         NA             NA
## m_active_seis               NA  0.3015702 -0.4310483   -0.019989374
## m_config                    NA         NA         NA             NA
## m_active_seis_harvest 0.07650757  0.3099517 -0.4226267   -0.005497010
## m_het_edge                  NA         NA         NA             NA
## m_edge                      NA         NA         NA             NA
## m_cohesion_mesh             NA         NA         NA             NA
## m_cohesion                  NA         NA         NA             NA
## m_cohesion_shei             NA         NA         NA             NA
```

```
## m_conn                                  NA          NA             NA             NA
## m_forest_fire                           NA          NA             NA             NA
## m_het                                   NA          NA             NA             NA
## m_harvest                       0.10036954          NA             NA             NA
## m_het_conn                              NA          NA             NA             NA
## m_active                                NA          NA             NA             NA
## m_active_harvest                0.11765607          NA             NA             NA
## m_forest                                NA          NA             NA             NA
## m_landcover_fire                        NA          NA             NA             NA
## m_landcover                             NA          NA             NA             NA
## m_fire                                  NA          NA             NA             NA
## m_null                                  NA          NA             NA             NA
##                          nonanthro_cohesion landscape_mesh landscape_shei
## m_edgeXcfi                               NA             NA             NA
## m_seis_wells                             NA             NA             NA
## m_harvest_seis                           NA             NA             NA
## m_edge_cfi                               NA             NA             NA
## m_edge_conn                              NA     -0.2691175             NA
## m_active_seis                            NA             NA             NA
## m_config                                 NA     -0.2368008     0.11685528
## m_active_seis_harvest                    NA             NA             NA
## m_het_edge                               NA             NA     0.17376761
## m_edge                                   NA             NA             NA
## m_cohesion_mesh                   0.2292213     -0.2291634             NA
## m_cohesion                        0.2044128             NA             NA
## m_cohesion_shei                   0.2247754             NA     0.15869581
## m_conn                                   NA     -0.1948194             NA
## m_forest_fire                            NA             NA             NA
## m_het                                    NA             NA     0.12465232
## m_harvest                                NA             NA             NA
## m_het_conn                               NA     -0.1707704     0.07849967
## m_active                                 NA             NA             NA
## m_active_harvest                         NA             NA             NA
## m_forest                                 NA             NA             NA
## m_landcover_fire                         NA             NA             NA
## m_landcover                              NA             NA             NA
## m_fire                                   NA             NA             NA
## m_null                                   NA             NA             NA
##                          nonanthro_ed  cfi_site cfi_site:nonanthro_ed   lc_shrubs
## m_edgeXcfi                -0.08883836 0.2954803            -0.2561767          NA
## m_seis_wells                       NA        NA                    NA          NA
## m_harvest_seis                     NA        NA                    NA          NA
## m_edge_cfi                -0.37852471 0.2660567                    NA          NA
## m_edge_conn               -0.31100945        NA                    NA          NA
## m_active_seis                      NA        NA                    NA          NA
## m_config                  -0.32282048        NA                    NA          NA
## m_active_seis_harvest              NA        NA                    NA          NA
## m_het_edge                -0.28828172        NA                    NA          NA
## m_edge                    -0.26158022        NA                    NA          NA
## m_cohesion_mesh                    NA        NA                    NA          NA
## m_cohesion                         NA        NA                    NA          NA
## m_cohesion_shei                    NA        NA                    NA          NA
## m_conn                             NA        NA                    NA          NA
## m_forest_fire                      NA        NA                    NA          NA
```

```
## m_het                                  NA        NA                    NA          NA
## m_harvest                              NA        NA                    NA          NA
## m_het_conn                             NA        NA                    NA          NA
## m_active                               NA        NA                    NA          NA
## m_active_harvest                       NA        NA                    NA          NA
## m_forest                               NA        NA                    NA          NA
## m_landcover_fire                       NA        NA                    NA -0.22584267
## m_landcover                            NA        NA                    NA -0.01122732
## m_fire                                 NA        NA                    NA          NA
## m_null                                 NA        NA                    NA          NA
##                       lc_wetland lc_wetland_treed df   logLik      AICc
## m_edgeXcfi                    NA               NA 11 -4686.194 9394.442
## m_seis_wells                  NA               NA 11 -4687.487 9397.028
## m_harvest_seis                NA               NA 12 -4687.250 9398.564
## m_edge_cfi                    NA               NA 10 -4689.652 9399.348
## m_edge_conn                   NA               NA 10 -4689.873 9399.790
## m_active_seis                 NA               NA 13 -4686.866 9399.806
## m_config                      NA               NA 11 -4689.408 9400.869
## m_active_seis_harvest         NA               NA 14 -4686.606 9401.297
## m_het_edge                    NA               NA 10 -4691.011 9402.068
## m_edge                        NA               NA  9 -4692.103 9402.242
## m_cohesion_mesh               NA               NA 10 -4691.417 9402.879
## m_cohesion                    NA               NA  9 -4693.068 9404.173
## m_cohesion_shei               NA               NA 10 -4692.160 9404.365
## m_conn                        NA               NA  9 -4693.631 9405.299
## m_forest_fire                 NA               NA  8 -4694.841 9405.711
## m_het                         NA               NA  9 -4694.274 9406.585
## m_harvest                     NA               NA  9 -4694.382 9406.800
## m_het_conn                    NA               NA 10 -4693.424 9406.893
## m_active                      NA               NA 10 -4693.488 9407.021
## m_active_harvest              NA               NA 11 -4692.861 9407.775
## m_forest                      NA               NA  7 -4697.320 9408.663
## m_landcover_fire      -0.1640682       -0.2667872 11 -4693.915 9409.883
## m_landcover           -0.1353234       -0.3071780 10 -4695.846 9411.737
## m_fire                        NA               NA  5 -4704.376 9418.764
## m_null                        NA               NA  4 -4707.890 9423.789
##                           delta       weight
## m_edgeXcfi             0.000000 5.591327e-01
## m_seis_wells          2.586045 1.534484e-01
## m_harvest_seis        4.121863 7.119733e-02
## m_edge_cfi            4.906134 4.810182e-02
## m_edge_conn           5.348357 3.855972e-02
## m_active_seis         5.364269 3.825416e-02
## m_config              6.427454 2.248076e-02
## m_active_seis_harvest 6.855755 1.814707e-02
## m_het_edge            7.625992 1.234673e-02
## m_edge                7.800059 1.131758e-02
## m_cohesion_mesh       8.437427 8.229071e-03
## m_cohesion            9.731446 4.308820e-03
## m_cohesion_shei       9.923648 3.914011e-03
## m_conn               10.857026 2.454379e-03
## m_forest_fire        11.268831 1.997650e-03
## m_het                12.142867 1.290402e-03
## m_harvest            12.358630 1.158437e-03
```

```
## m_het_conn              12.450986 1.106159e-03
## m_active               12.578990 1.037581e-03
## m_active_harvest        13.333557 7.114916e-04
## m_forest               14.221449 4.564220e-04
## m_landcover_fire        15.441196 2.480286e-04
## m_landcover            17.295472 9.814110e-05
## m_fire                 24.322243 2.924200e-06
## m_null                 29.346857 2.370969e-07
```

```r
# Fetch the top model
top_model <- get(ls(pattern = rownames(models_rank[1]))[1])
```

```
## Warning in grep(pattern, all.names, value = TRUE): argument 'pattern' has
## length > 1 and only the first element will be used
```

```r
# Or explore any model manually using the same code...
top_model <- m_edgeXcfi
```

6. Model inspection and validation

6.0. A bit of set up for tables and figures

Let's read in the 'pretty' names of the covariates first. These will be what we use in figures and tables.

```r
covs_formatted <- read_csv("./tables/OSM_all_covariates_formatted_names.csv")
```

```
## Rows: 44 Columns: 2
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (2): Covariate, PrettyName
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

6.1. Check out a general summary:

```r
summary(top_model)
```

```
##  Family: nbinom2  ( log )
## Formula:
## squirrel ~ fire_0_15 + lc_broadleaf + lc_coniferous + lc_mixedwood +
##     nonanthro_ed + cfi_site + nonanthro_ed * cfi_site + (1 |     array/site)
## Data: data_final_scaled
##
##      AIC      BIC   logLik deviance df.resid
##   9394.4   9465.9  -4686.2   9372.4     4907
##
```

```
## Random effects:
##
## Conditional model:
##  Groups      Name          Variance Std.Dev.
##  site:array  (Intercept) 2.502     1.5816
##  array       (Intercept) 0.410     0.6403
## Number of obs: 4918, groups:  site:array, 430; array, 10
##
## Dispersion parameter for nbinom2 family (): 0.811
##
## Conditional model:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -1.42793    0.23031  -6.200 5.65e-10 ***
## fire_0_15           0.15770    0.11215   1.406   0.1597
## lc_broadleaf       -0.51842    0.12835  -4.039 5.36e-05 ***
## lc_coniferous      -0.03228    0.11093  -0.291   0.7710
## lc_mixedwood        0.16358    0.09223   1.774   0.0761 .
## nonanthro_ed       -0.08884    0.16631  -0.534   0.5932
## cfi_site            0.29548    0.12080   2.446   0.0144 *
## nonanthro_ed:cfi_site -0.25618  0.10011  -2.559   0.0105 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6.2. Pseudo-R2

```
performance::r2(top_model)
```

```
## # R2 for Mixed Models
##
##   Conditional R2: 0.744
##      Marginal R2: 0.099
```

6.3. Check dispersion:

```
performance::check_overdispersion(top_model)
```
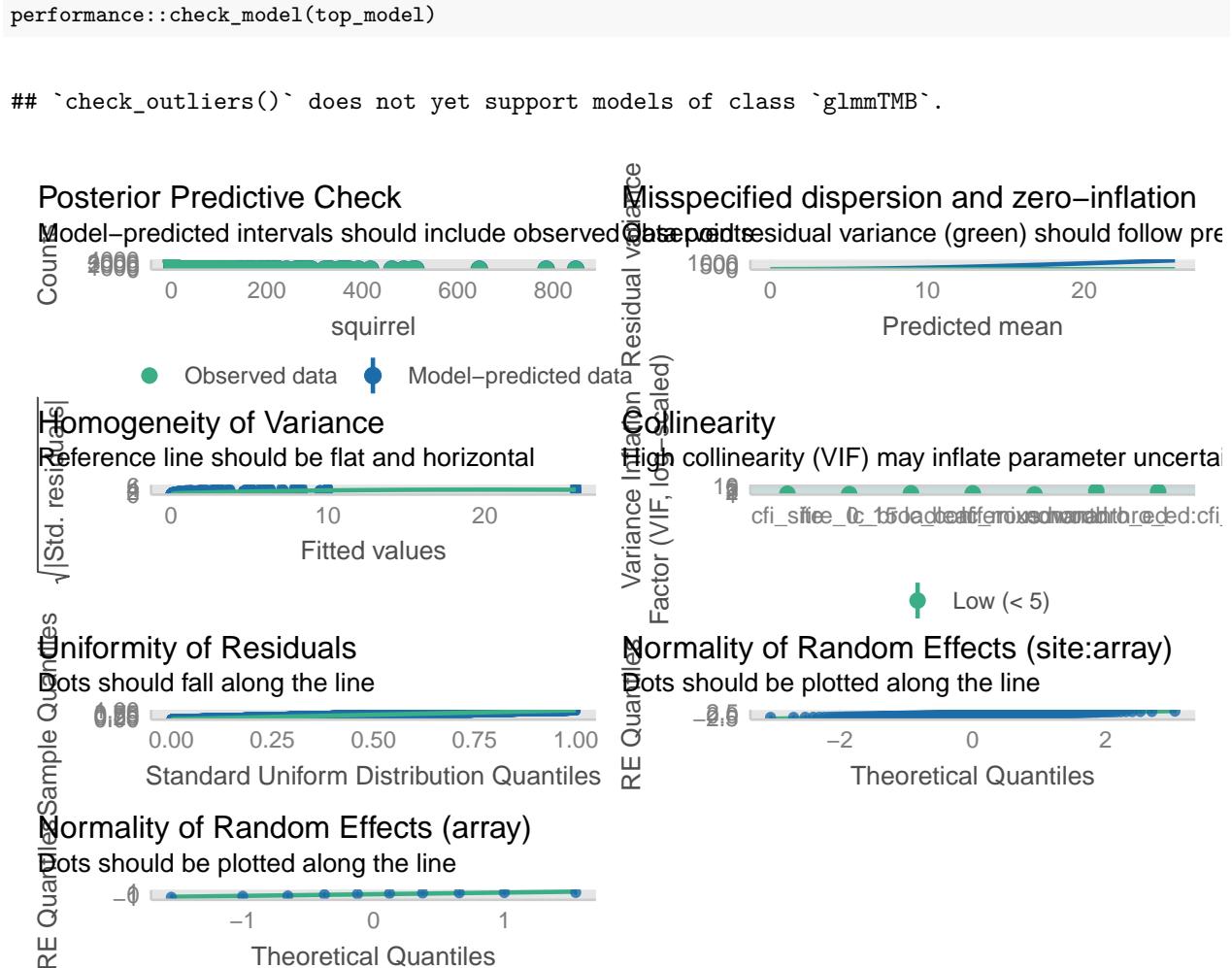
```
## # Overdispersion test
##
##  dispersion ratio = 0.179
##          p-value = 0.176
```

```
## No overdispersion detected.
```

Previous notes from fitting proportional binomial models: "The model is overdispersed. Variance is much higher than the mean which violates an assumption of the bernoilli distribution. A zero inflated bernoulli (ZIB) might be more appropriate. Re-binning the data into monthly occurrence frequency might also help eliminate a lot of the zeros that are (likely) the cause of this."

6.4. Check other diagnostics including VIFs.

```
performance::check_model(top_model)
```

```
## `check_outliers()` does not yet support models of class `glmmTMB`.
```



```
ggsave("./figures/top_model_neg_binomial_diagnostics.png", height = 12, width = 9)
```

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

```
## `geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```
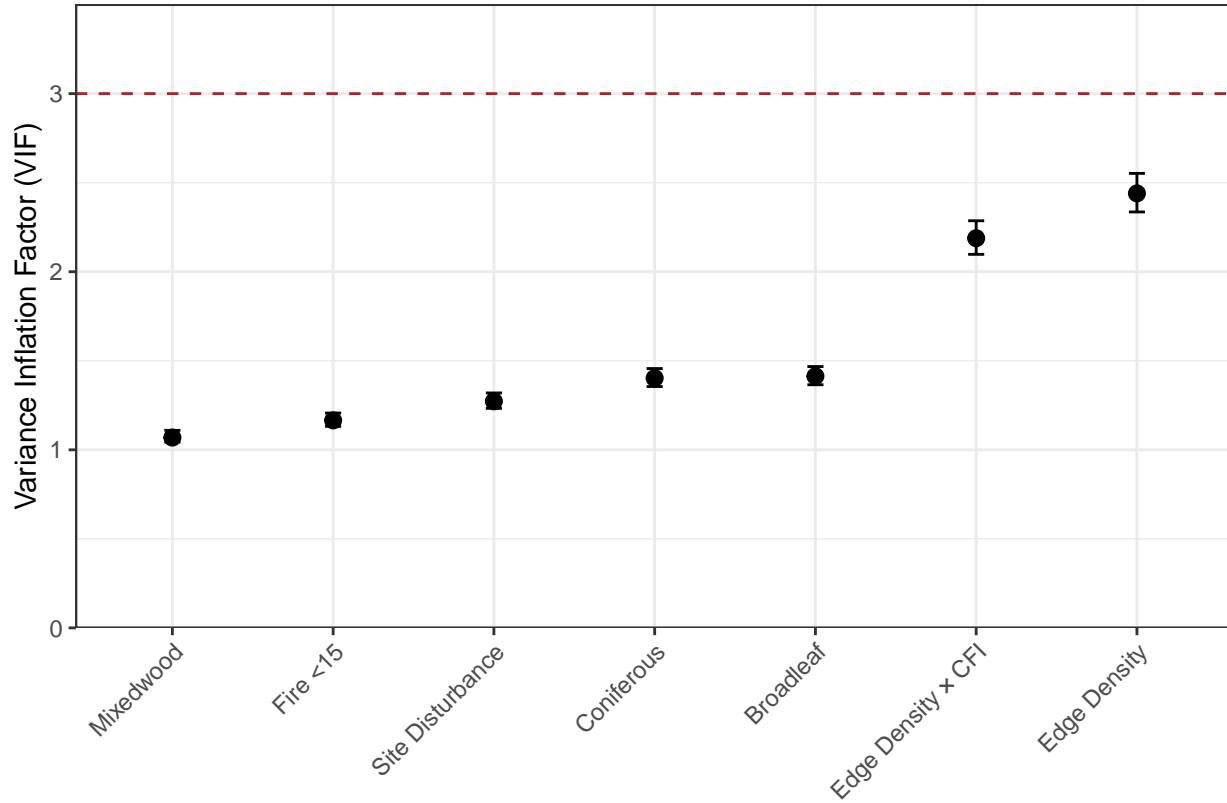
6.5. Variance inflation factors:

```
# vif from the car package
performance::check_collinearity(top_model) %>%

  as.data.frame(.) %>%

  # Add the pretty names
```

```r
  left_join(covs_formatted, by = c("Term" = "Covariate")) %>%

  # Manual fix for a couple of them
  mutate(PrettyName = case_when(
    Term == "nonanthro_ed:cfi_site" ~ "Edge Density × CFI",
    TRUE ~ PrettyName)) %>%

  # plot with ggplot
  ggplot(aes(x = reorder(PrettyName, VIF), # reorders from smallest VIF to largest (not sure I want
  ↪  like this)
             y = VIF)) +

    geom_hline(yintercept = 3, linetype='dashed', col = 'firebrick') +

    # Error bars behind the points
    geom_errorbar(aes(ymin = VIF_CI_low, ymax = VIF_CI_high), width = 0.1) +  # Error bars

    # plot as points
    geom_point(size = 2.5) +

    # add labels
    labs(x = '',
         y = 'Variance Inflation Factor (VIF)') +

    scale_y_continuous(limits = c(0, 3.2), expand = expansion(add = c(0, 0.3))) +

    # set theme
    theme_bw() +

    theme(axis.text.x = element_text(angle = 45, hjust = 1))  # Rotate x-axis labels by 45 degrees
```

```
ggsave("./figures/top_model_neg_binomial_VIF.png", dpi=500, width = 5, height = 3.5)
```

6.6. Likelihood ratio test for random effect structure:

```
m_edgeXcfi_noranef <- glmmTMB(squirrel ~

                    # natural covariates
                    fire_0_15 +
                    lc_broadleaf +
                    lc_coniferous +
                    lc_mixedwood +

                    # configuration variables
                    #landscape_shei +
                    nonanthro_ed +
                    cfi_site +
                    nonanthro_ed*cfi_site,
                    #landscape_mesh +

                    #(1|array/site),

                    data = data_final_scaled,
                    family = nbinom2,
                    na.action = na.fail)
```

```
summary(m_edgeXcfi_noranef)
```

```
##  Family: nbinom2  ( log )
## Formula:
## squirrel ~ fire_0_15 + lc_broadleaf + lc_coniferous + lc_mixedwood +
##     nonanthro_ed + cfi_site + nonanthro_ed * cfi_site
## Data: data_final_scaled
##
##      AIC      BIC   logLik deviance df.resid
##  10710.8   10769.4  -5346.4  10692.8     4909
##
##
## Dispersion parameter for nbinom2 family (): 0.186
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.12680    0.04487  -2.826  0.00471 **
## fire_0_15             0.21237    0.03793   5.600 2.15e-08 ***
## lc_broadleaf         -0.54628    0.05178 -10.550  < 2e-16 ***
## lc_coniferous        -0.22706    0.04452  -5.101 3.39e-07 ***
## lc_mixedwood         -0.06637    0.04303  -1.542  0.12296
## nonanthro_ed         -0.16580    0.06878  -2.411  0.01593 *
## cfi_site              0.35124    0.05050   6.955 3.52e-12 ***
## nonanthro_ed:cfi_site -0.22707    0.04611  -4.924 8.47e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m_edgeXcfi_noranef, m_edgeXcfi)
```

```
## Data: data_final_scaled
## Models:
## m_edgeXcfi_noranef: squirrel ~ fire_0_15 + lc_broadleaf + lc_coniferous + lc_mixedwood + , zi=~0, di
## m_edgeXcfi_noranef:     nonanthro_ed + cfi_site + nonanthro_ed * cfi_site, zi=~0, disp=~1
## m_edgeXcfi: squirrel ~ fire_0_15 + lc_broadleaf + lc_coniferous + lc_mixedwood + , zi=~0, disp=~1
## m_edgeXcfi:     nonanthro_ed + cfi_site + nonanthro_ed * cfi_site + (1 | , zi=~0, disp=~1
## m_edgeXcfi:     array/site), zi=~0, disp=~1
##                    Df     AIC     BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## m_edgeXcfi_noranef  9 10710.8 10769.4 -5346.4  10692.8
## m_edgeXcfi         11  9394.4  9465.9 -4686.2   9372.4 1320.5      2  < 2.2e-16
##
## m_edgeXcfi_noranef
## m_edgeXcfi            ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7. Interpret results

7.1. Model summary

```
summary(top_model)
```

```
##  Family: nbinom2  ( log )
## Formula:
## squirrel ~ fire_0_15 + lc_broadleaf + lc_coniferous + lc_mixedwood +
##     nonanthro_ed + cfi_site + nonanthro_ed * cfi_site + (1 |     array/site)
## Data: data_final_scaled
##
##      AIC      BIC   logLik deviance df.resid
##   9394.4   9465.9  -4686.2   9372.4     4907
##
## Random effects:
##
## Conditional model:
##  Groups      Name        Variance Std.Dev.
##  site:array (Intercept) 2.502    1.5816
##  array      (Intercept) 0.410    0.6403
## Number of obs: 4918, groups:  site:array, 430; array, 10
##
## Dispersion parameter for nbinom2 family (): 0.811
##
## Conditional model:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -1.42793    0.23031  -6.200 5.65e-10 ***
## fire_0_15             0.15770    0.11215   1.406   0.1597
## lc_broadleaf         -0.51842    0.12835  -4.039 5.36e-05 ***
## lc_coniferous        -0.03228    0.11093  -0.291   0.7710
## lc_mixedwood          0.16358    0.09223   1.774   0.0761 .
## nonanthro_ed         -0.08884    0.16631  -0.534   0.5932
## cfi_site              0.29548    0.12080   2.446   0.0144 *
## nonanthro_ed:cfi_site -0.25618   0.10011  -2.559   0.0105 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.2. Odds ratio plots for the conditional model:

```
# Custom order for the x-axis covariates
custom_order <- c(
  "Broadleaf",
  "Mixedwood",
  "Coniferous",
  "Fire <15",
  "Site Disturbance",
  "Edge Density",
  "Edge Density × \nSite Disturbance"
  )
```
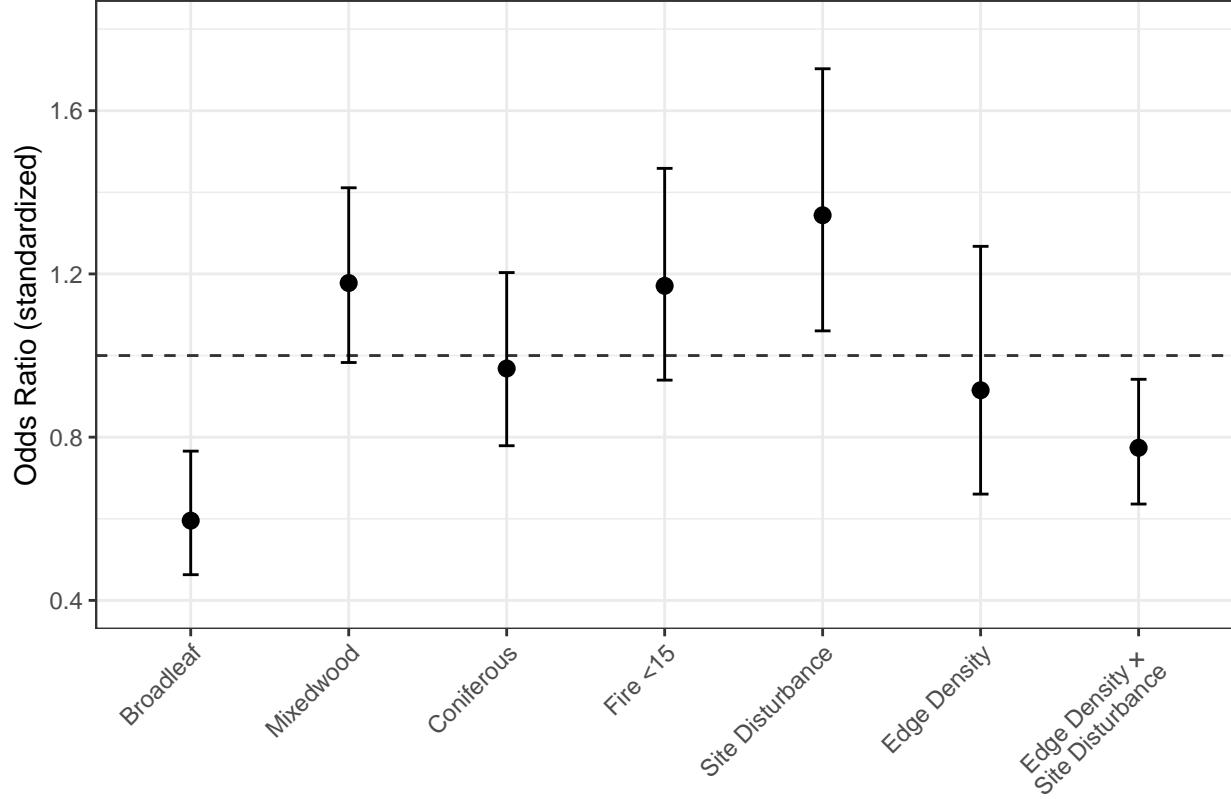
```r
odds_fig_top <-

confint(top_model) %>%

  as_tibble(rownames = "term") %>%

  # Rename the columns manually
  set_names(c('term', 'lower', 'upper', 'estimate')) %>%

  # Go from log odds back to odds
  mutate(across(c('lower', 'upper', 'estimate'), exp)) %>%

  # Remove things we dont wanna plot
  filter(term %nin% c('(Intercept)', 'Std.Dev.(Intercept)|array',
  ↪  'Std.Dev.(Intercept)|site:array')) %>%

  # PRetty names
  left_join(covs_formatted, by = c("term" = "Covariate")) %>%

  # Fix a couple manually
  mutate(PrettyName = case_when(
    term == "nonanthro_ed:cfi_site" ~ "Edge Density × \nSite Disturbance",
    TRUE ~ PrettyName)) %>%

  # Apply the custom order for covariates
  mutate(PrettyName = factor(PrettyName, levels = custom_order)) %>%

  # Plot it!!
  ggplot(., aes(x = PrettyName)) +

    geom_hline(yintercept = 1, linetype='dashed', col = 'grey20') +

    # Error bars behind the points
    geom_errorbar(aes(x = PrettyName, ymin = lower, ymax = upper), width = 0.1) +  # Error bars

    # plot as points
    geom_point(aes(y = estimate), size = 2.5) +

        scale_y_continuous(limits = c(0.4, 1.8)) +

    # add labels
    labs(x = '',
        y = 'Odds Ratio (standardized)') +

      annotate("text",
          x = 0.5,          # Left edge of panel
          y = 1.8,           # Top edge of panel
          label = " ",
          hjust = 0,                 # Left-aligned
          vjust = 1,                 # Top-aligned
          size = 5) +                    # Adjust size as needed

    # set theme
    theme_bw() +

    theme(plot.title = element_text(face = "bold")) +

    theme(axis.text.x = element_text(angle = 45, hjust = 1)) #+   # Rotate x-axis labels by 45
    ↪  degrees
```

```
    #add_phylopic(
    #    uuid = get_uuid(name = "Sciurus vulgaris"),
    #    x = 6.6,
    #    y = 1.6,
    #    height = 0.22
    #  )

odds_fig_top
```



```
ggsave(odds_fig_top, file = "./figures/top_model_neg_binomial_odds_ratios.png", width = 5, height =
↪  3.5)
```

7.3. Odds ratio plots for the second-place model

```
# Custom order for the x-axis covariates
custom_order <- c(
  "Broadleaf",
  "Mixedwood",
  "Coniferous",
  "Fire <15",
  "Inactive Well Sites",
  "Seismic Lines",
  "Pipelines & \nTransmission Lines"
```

```
  )

odds_fig_second <-

# Exact same code as before, not annotating because I'm lazy.
confint(m_seis_wells) %>%

  as_tibble(rownames = "term") %>%

  set_names(c('term', 'lower', 'upper', 'estimate')) %>%

  mutate(across(c('lower', 'upper', 'estimate'), exp)) %>%

  filter(term %nin% c('(Intercept)', 'Std.Dev.(Intercept)|array',
  ↳  'Std.Dev.(Intercept)|site:array')) %>%

  left_join(covs_formatted, by = c("term" = "Covariate")) %>%

  mutate(PrettyName = case_when(
    term == "nonanthro_ed:cfi_site" ~ "Edge Density × CFI",
    term == "pipe_trans" ~ "Pipelines & \nTransmission Lines",
    TRUE ~ PrettyName)) %>%

  mutate(PrettyName = factor(PrettyName, levels = custom_order)) %>%

  ggplot(., aes(x = PrettyName)) +

    geom_hline(yintercept = 1, linetype='dashed', col = 'grey20') +

    geom_errorbar(aes(x = PrettyName, ymin = lower, ymax = upper), width = 0.1) +  # Error bars

    # add labels
    labs(x = '',
         y = '') +

    # plot as bars
    geom_point(aes(y = estimate), size = 2.5) +

    scale_y_continuous(limits = c(0.4, 1.8)) +

      # set theme
    theme_bw() +

    theme(axis.text.x = element_text(angle = 45, hjust = 1)) +   # Rotate x-axis labels by 45
    ↳   degrees

    annotate("text",
          x = 0.5,          # Left edge of panel
          y = 1.8,           # Top edge of panel
          label = " ΔAICc=2.59",
          hjust = 0,                  # Left-aligned
          vjust = 1,                  # Top-aligned
          size = 5)                     # Adjust size as needed



    #add_phylopic(
    #  uuid = get_uuid(name = "Sciurus vulgaris"),
    #  x = 6.6,
```
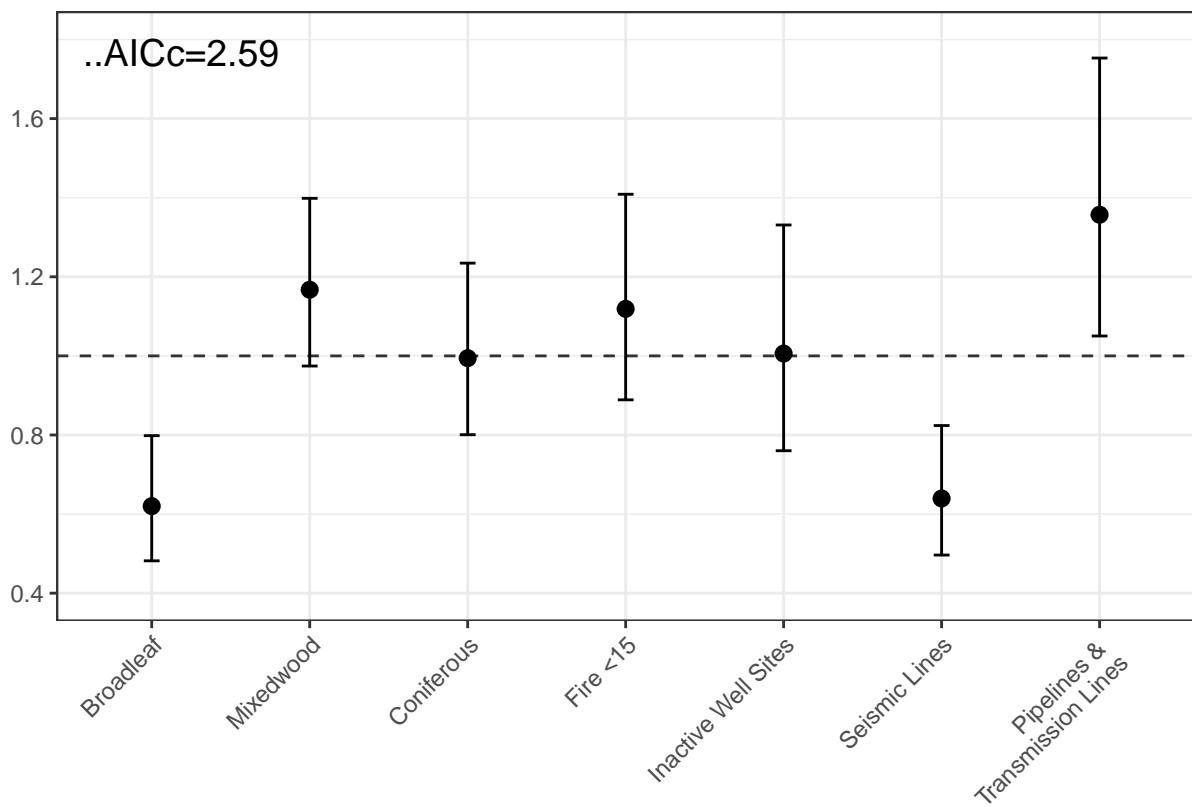
```
    #   y = 1.6,
    #   height = 0.22
    #   )

odds_fig_second
```

```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on ' ΔAICc=2.59' in 'mbcsToSbcs': dot substituted for <ce>
```

```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on ' ΔAICc=2.59' in 'mbcsToSbcs': dot substituted for <94>
```



```
ggsave(odds_fig_second, file= "./figures/second_place_model_neg_binomial_odds_ratios.png", width =
↪  5, height = 3.5)
```

7.4. Export the combined top and second-ranking model figures in one!

```
ggpubr::ggarrange(odds_fig_top, odds_fig_second,
                  ncol = 2,
                  nrow = 1,
                  align = "hv",
                  labels = c("A", "B")  # Add plot labels
                  )
```
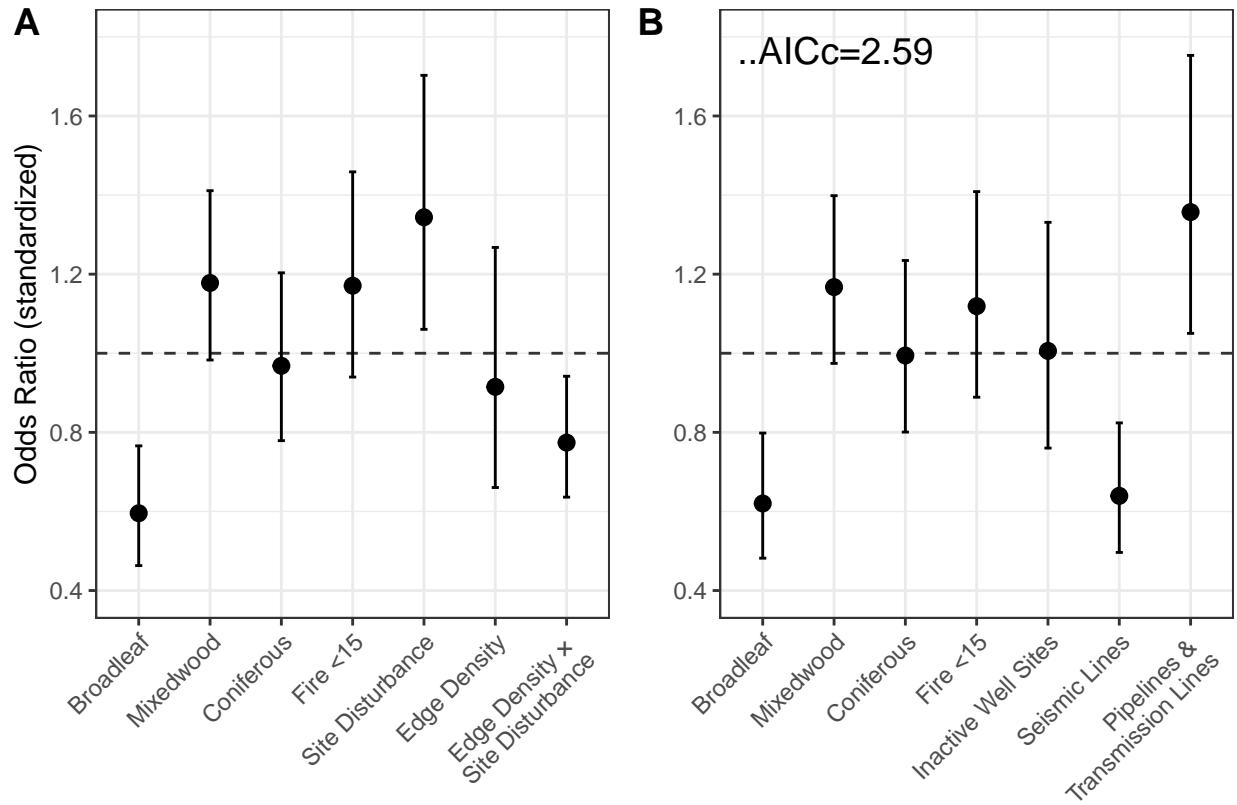
```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on ' ΔAICc=2.59' in 'mbcsToSbcs': dot substituted for <ce>

## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :
## conversion failure on ' ΔAICc=2.59' in 'mbcsToSbcs': dot substituted for <94>
```



```
ggsave("./figures/odds_ratio_top_model_second_model.png", width = 7, height = 4.2, dpi = 700)
```

8. Plot conditional effects

We will use our scaling summary here to backtransform the data into ecologically meaningful values. This is a bit hacky but it works.

8.1. Decid:

```
# Get just the row that contains the mean and SD for backtransforming....
# Hacky I KNOW don't judge me we had 2 weeks to do this
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == nat_buffer,
         variable == "lc_broadleaf")
```

```
# Use ggeffects to predict at all values of lc_broadleaf in the dataset
f_decid <- ggeffects::ggpredict(top_model, terms = c("lc_broadleaf [all]")) %>%

  as.data.frame() %>%

  # Apply the backtransform to the values for the x axis, predictions unchanged :)
  mutate(x = x * backtransform$sd + backtransform$mean) %>%

  ggplot(., aes(x = x, y = predicted)) +

    geom_line(size = 0.5) +  # Set lines to black

    # Confidence ribbon in front of the line
    geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.4, fill = 'forestgreen') +

    # Show unscaled data points for just the buffer distances that we want.
    geom_rug(data = data%>%filter(buffer_dist==nat_buffer), aes(x = lc_broadleaf), color =
    ↪  "grey20", inherit.aes = FALSE) +

    labs(x = "Broadleaf",
         y = NULL) +

    scale_x_continuous(expand = c(0, 0)) +  # Remove left blank space

    theme_bw() +

    theme(panel.grid = element_blank()) #+
```

```
## You are calculating adjusted predictions on the population-level (i.e.
##    `type = "fixed"`) for a *generalized* linear mixed model.
##    This may produce biased estimates due to Jensen's inequality. Consider
##    setting `bias_correction = TRUE` to correct for this bias.
##    See also the documentation of the `bias_correction` argument.
```

```
    # Squirrel icon for fun
    #add_phylopic(
    #  uuid = get_uuid(name = "Sciurus vulgaris"),
    #  x = 0.89,
    #  y = 0.46,
    #  height = 0.11
    #  )

ggsave(f_decid, file = "./figures/top_model_neg_binomial_broadleaf.png", dpi=400, width = 6, height
↪  = 4)
```

8.2. Conifer:

```
# Get just the row that contains the mean and SD for backtransforming...
# Yep, still hacky - but fast and it works
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == nat_buffer,
         variable == "lc_coniferous")

# Use ggeffects to predict at all values of lc_coniferous in the dataset
```

```r
f_conifer <- ggeffects::ggpredict(top_model, terms = c("lc_coniferous [all]")) %>%

  as.data.frame() %>%

  # Backtransform the x-axis values to their original scale (predictions stay in response scale)
  mutate(x = x * backtransform$sd + backtransform$mean) %>%

  # Plot predictions with ggplot2
  ggplot(., aes(x = x, y = predicted)) +

    geom_line(size = 0.5) +  # Black line for model prediction

    # Add a confidence ribbon (plotted underneath the line)
    geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.4, fill = 'forestgreen') +

    # Add raw data rug for just the buffer distance of interest (in unscaled space)
    geom_rug(data = data %>% filter(buffer_dist == nat_buffer),
             aes(x = lc_coniferous),
             color = "grey20", inherit.aes = FALSE) +

    # Axis labels
    labs(x = "Coniferous",
         y = NULL) +

    # Remove empty space on left side of x axis
    scale_x_continuous(expand = c(0, 0)) +

    # Minimal clean theme
    theme_bw() +

    theme(panel.grid = element_blank())# +

    # Squirrel icon for fun (lower left corner this time)
    #add_phylopic(
    #  uuid = get_uuid(name = "Sciurus vulgaris"),
    #  x = 0.08,
    #  y = 0.4,
    #  height = 0.06
    #)

# Save the figure
ggsave(f_conifer, file = "./figures/top_model_neg_binomial_conifer.png", dpi = 400, width = 6,
↪  height = 4)
```

8.3. Mixedwood:

```r
# Get just the row that contains the mean and SD for backtransforming...
# Still using our quick-and-dirty approach by filtering to the variable and buffer of interest
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == nat_buffer,
         variable == "lc_mixedwood")

# Use ggeffects to predict model outcomes across all observed lc_mixedwood values (scaled units)
f_mixedwood <- ggeffects::ggpredict(top_model, terms = c("lc_mixedwood [all]")) %>%

  as.data.frame() %>%
```

```r
  # Backtransform x values to original scale (predicted values are already in response scale)
  mutate(x = x * backtransform$sd + backtransform$mean) %>%

  # Start the plot
  ggplot(., aes(x = x, y = predicted)) +

    geom_line(size = 0.5) +  # Model prediction line (thin, black)

    # Confidence interval ribbon under the line
    geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.4, fill = 'forestgreen') +

    # Rug plot to show actual unscaled values from the selected buffer
    geom_rug(data = data %>% filter(buffer_dist == nat_buffer),
             aes(x = lc_mixedwood),
             color = "grey20", inherit.aes = FALSE) +

    # Axis labels
    labs(x = "Mixedwood",
         y = NULL) +

    # Tighten up left side of the x-axis
    scale_x_continuous(expand = c(0, 0)) +

    # Clean and minimal styling
    theme_bw() +
    theme(panel.grid = element_blank()) #+

    # Icon again! Now in the upper-left corner for variety
    #add_phylopic(
    #  uuid = get_uuid(name = "Sciurus vulgaris"),
    #  x = 0.06,
    #  y = 1.4,
    #  height = 0.28
    #)

# Save to file
ggsave(f_mixedwood, file = "./figures/top_model_neg_binomial_mixedwood.png", dpi = 400, width = 6,
↪  height = 4)
```

8.4. Recent fire

```r
# Get just the row that contains the mean and SD for backtransforming...
# Same trick, different variable (recent fire in this case)
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == nat_buffer,
         variable == "fire_0_15")

# Use ggeffects to predict at all observed values of fire_0_15 (in scaled units)
f_fire <- ggeffects::ggpredict(top_model, terms = c("fire_0_15 [all]")) %>%

  as.data.frame() %>%

  # Backtransform x-axis to original scale, leave predictions as-is
  mutate(x = x * backtransform$sd + backtransform$mean) %>%
```

```
  # Plot it
  ggplot(., aes(x = x, y = predicted)) +

    geom_line(size = 0.5) +  # Prediction line (black, thin)

    # Confidence interval ribbon in orange
    geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.4, fill = 'forestgreen') +

    # Add raw data rug for this buffer distance only (unscaled)
    geom_rug(data = data %>% filter(buffer_dist == nat_buffer),
             aes(x = fire_0_15),
             color = "grey20", inherit.aes = FALSE) +

    # Axis labels
    labs(x = "Fire (0-15 years)",
         y = NULL) +

    # No extra white space on x-axis
    scale_x_continuous(expand = c(0, 0)) +

    # Clean theme with grid off
    theme_bw() +
    theme(panel.grid = element_blank())

    # Optional: squirrel icon, currently disabled
    # add_phylopic(
    #   uuid = get_uuid(name = "Sciurus vulgaris"),
    #   x = 0.08,
    #   y = 1.32,
    #   height = 0.26
    # )

# Save the plot
ggsave(f_fire, file = "./figures/top_model_neg_binomial_fire.png", dpi = 400, width = 6, height =
↪  4)
```

8.5. Cumulative site disturbance:

```
# Get just the row that contains the mean and SD for backtransforming...
# This time for cumulative site disturbance (cfi_site), using the config buffer (might need to
↪   change to comp buffer later)
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == config_buffer,
         variable == "cfi_site")

# Use ggeffects to predict across all observed values of cfi_site (scaled)
f_cfi <- ggeffects::ggpredict(top_model, terms = c("cfi_site [all]")) %>%

  as.data.frame() %>%

  # Backtransform x-axis values to original scale
  mutate(x = x * backtransform$sd + backtransform$mean) %>%

  # Begin plot
  ggplot(., aes(x = x, y = predicted)) +
```

```r
  geom_line(size = 0.5) +  # Black prediction line

  # Confidence ribbon (red tone for disturbance)
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.4, fill = 'goldenrod3') +

  # Add raw data rug for this buffer distance only
  geom_rug(data = data %>% filter(buffer_dist == config_buffer),
           aes(x = cfi_site),
           color = "grey20", inherit.aes = FALSE) +

  # Axis labels
  labs(x = "Site disturbance",
       y = NULL) +

  # Remove padding on left of x-axis
  scale_x_continuous(expand = c(0, 0), limits = c(0, 0.302)) +

  scale_y_continuous(limits = c(0, 1.8)) +

  # Minimalist, clean plot theme
  theme_bw() +
  theme(panel.grid = element_blank())

  # Optional squirrel icon (commented out for now)
  # add_phylopic(
  #   uuid = get_uuid(name = "Sciurus vulgaris"),
  #   x = 0.04,
  #   y = 5.6,
  #   height = 1.2
  # )

# Save the plot
ggsave(f_cfi, file = "./figures/top_model_neg_binomial_cfi.png", dpi = 400, width = 6, height = 4)
```

```
## Warning: Removed 7 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

8.6. Edge density:

```r
# Get just the row that contains the mean and SD for backtransforming...
# This time for cumulative site disturbance (cfi_site), using the config buffer (might need to
↪   change to comp buffer later)
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == config_buffer,
         variable == "nonanthro_ed")

# Use ggeffects to predict across all observed values of cfi_site (scaled)
f_edge <- ggeffects::ggpredict(top_model, terms = c("nonanthro_ed [all]")) %>%

  as.data.frame() %>%

  # Backtransform x-axis values to original scale
  mutate(x = x * backtransform$sd + backtransform$mean) %>%

  # Begin plot
```

```r
  ggplot(., aes(x = x, y = predicted)) +

    geom_line(size = 0.5) +    # Black prediction line

    # Confidence ribbon (red tone for disturbance)
    geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = 0.48, fill = 'darkblue') +

    # Add raw data rug for this buffer distance only
    geom_rug(data = data %>% filter(buffer_dist == config_buffer),
             aes(x = nonanthro_ed),
             color = "grey20", inherit.aes = FALSE) +

    # Axis labels
    labs(x = "Edge density",
         y = NULL) +

    # Remove padding on left of x-axis
    scale_x_continuous(expand = c(0, 0), limits = c(2, 202.85)) +

    scale_y_continuous(limits = c(0, 0.48)) +

    # Minimalist, clean plot theme
    theme_bw() +
    theme(panel.grid = element_blank())

    # Optional squirrel icon (commented out for now)
    # add_phylopic(
    #    uuid = get_uuid(name = "Sciurus vulgaris"),
    #    x = 0.04,
    #    y = 5.6,
    #    height = 1.2
    # )

# Save the plot
ggsave(f_edge, file = "./figures/top_model_neg_binomial_edge.png", dpi = 400, width = 6, height =
  ↪ 4)
```

```
## Warning: Removed 37 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

8.6. Edge x CFI interaction

```r
# Get just the row that contains the mean and SD for backtransforming...
# This time for non-anthropogenic edge density (nonanthro_ed), using config buffer
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == config_buffer,
         variable == "nonanthro_ed")

# Predict squirrel occurrence across full range of nonanthro_ed
# for two quantiles (20th and 89th) of cumulative site disturbance (cfi_site)
f_edge_cfi <- ggeffects::ggpredict(

  top_model,
  terms = c(
    "nonanthro_ed [all]",
```

45

```r
  paste0("cfi_site [",
         quantile(data_final_scaled$cfi_site, 0.89), ", ",
         quantile(data_final_scaled$cfi_site, 0.20), "]")
  )
) %>%

as.data.frame() %>%

# Backtransform x values from scaled to original units (m/ha)
mutate(x = x * backtransform$sd + backtransform$mean) %>%

# Plot predictions and confidence ribbons, colored by cfi quantile group
ggplot(., aes(x = x, y = predicted, color = group)) +

  geom_line(size = 0.5) +  # Thin black line for predictions

  # Confidence interval ribbons, filled by group
  geom_ribbon(
    aes(ymin = conf.low, ymax = conf.high, fill = group),
    alpha = 0.4, color = NA
  ) +

  # Manually assign colors to line and fill for visual distinction
  scale_color_manual(
    values = c('grey20', 'grey20'),  # Lines stay neutral
    labels = c(  # Hacky way to get the labels to the unscaled values
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$cfi_site, 0.20), 3)),
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$cfi_site, 0.89), 3))
    )
  ) +
  scale_fill_manual(
    values = c('darkblue', 'darkred'),  # Fill colors for clarity
    labels = c(
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$cfi_site, 0.20), 3)),
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$cfi_site, 0.89), 3))
    )
  ) +

# OR JUST LABEL THEM AS QUANTILES

    # Manually assign colors to line and fill for visual distinction
  scale_color_manual(
    values = c('grey20', 'grey20'),  # Lines stay neutral
    labels = c("10% quantile", "90% quantile")
  ) +
  scale_fill_manual(
    values = c('dodgerblue2', 'darkred'),  # Fill colors for clarity
    labels = c("10% quantile", "90% quantile")
  ) +

  # Rug plot shows actual values of edge density in the unscaled data
  geom_rug(
    data = data %>% filter(buffer_dist == config_buffer),
    aes(x = nonanthro_ed),
    alpha = 0.5,
    color = "grey20",
    inherit.aes = FALSE
  ) +
```

```
    # Axes and legend
    labs(
      x = "Anthropogenic edge density (m per Ha)",
      y = "Expected count",
      color = "Site \ndisturbance",
      fill = "Site \ndisturbance"
    ) +

    # Trim x and y axis range to what's observed and relevant
    scale_x_continuous(limits = c(2, 202.85), expand = c(0, 0)) +
    scale_y_continuous(limits = c(0, 1.1), expand = c(0, 0)) +

    # Clean, minimal theme
    theme_bw() +
    theme(panel.grid = element_blank()) +
    theme(
      legend.position = "right",
      legend.margin = margin(0, 0, 0, 0),
      legend.box.margin = margin(0, 0, 0, -5),   # Pull legend closer to plot
      plot.margin = margin(5, 5, 5, 5)             # Optional: adjust plot margins
    ) +

    # Optional: add a squirrel icon again for flair :)
     add_phylopic(
       uuid = get_uuid(name = "Sciurus vulgaris"),
       x = 180,
       y = 0.95,
       height = 0.23
     )
```

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

```
# Save it!
ggsave(f_edge_cfi, file = "./figures/top_model_edge_cfi_interaction.png", dpi = 400, width = 7,
↪   height = 4)
```

```
## Warning: Removed 74 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

8.7. CFI x Edge interaction

Do edges change the effect of site disturbance? This is a sort of backwards interpretation but I'm curious nonetheless.

```
# Backtransform helper: grab mean and SD for cumulative site disturbance (cfi_site)
backtransform <- data_scaled_summary %>%
  filter(buffer_dist == config_buffer,
         variable == "cfi_site")

# Predict squirrel occurrence across full range of cfi_site,
# at two values of edge density (nonanthro_ed)
```

```
f_cfi_edge <- ggeffects::ggpredict(

  top_model,
  terms = c(
    "cfi_site [all]",
    paste0("nonanthro_ed [",
           quantile(data_final_scaled$cfi_site, 0.89), ", ",
           quantile(data_final_scaled$cfi_site, 0.20), "]")
  )
) %>%

as.data.frame() %>%

# Backtransform x (cfi_site) from scaled units to proportion
mutate(x = x * backtransform$sd + backtransform$mean) %>%

ggplot(., aes(x = x, y = predicted, color = group)) +

  # Prediction lines
  geom_line(size = 0.5) +

  # Confidence bands by group (edge density levels)
  geom_ribbon(
    aes(ymin = conf.low, ymax = conf.high, fill = group),
    alpha = 0.4, color = NA
  ) +

  # Set color and fill manually for clarity
  scale_color_manual(
    values = c('grey20', 'grey20'),
    labels = c( # Hacky way to get the labels to the unscaled values
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$nonanthro_ed, 0.20),
        ↪ 1)),
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$nonanthro_ed, 0.80),
        ↪ 1))
    )
  ) +
  scale_fill_manual(
    values = c('darkblue', 'goldenrod3'),
    labels = c(
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$nonanthro_ed, 0.20),
        ↪ 1)),
      paste0(round(quantile((data %>% filter(buffer_dist == config_buffer))$nonanthro_ed, 0.80),
        ↪ 1))
    )
  ) +

  # Rug for cfi values (unscaled) used in data
  geom_rug(
    data = data %>% filter(buffer_dist == config_buffer),
    aes(x = cfi_site),
    color = "grey20",
    inherit.aes = FALSE
  ) +

  # Axis labels and legend tweaks
  labs(
    x = "Cumulative site disturbance",
    y = "Expected count",
```

```
        color = "edge \ndensity \n(m/Ha)",
        fill = "edge \ndensity \n(m/Ha)"
    ) +

    # Match x-axis range to data
    scale_x_continuous(limits = c(0, 0.229), expand = c(0, 0)) +
    scale_y_continuous(limits = c(0, 2.0)) +

    # Clean look
    theme_bw() +
    theme(panel.grid = element_blank())

    # Optional mascot
    # add_phylopic(
    #    uuid = get_uuid(name = "Sciurus vulgaris"),
    #    x = 0.04,
    #    y = 1.7,
    #    height = 0.2
    # )

# Save the figure
ggsave(f_cfi_edge, file = "./figures/top_model_cfi_edge_interaction.png", dpi = 400, width = 7,
↪   height = 4)
```

```
## Warning: Removed 32 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

8.8. Combined plot:

```
f_full_right <- cowplot::plot_grid(f_edge, f_cfi, ncol = 1, align = "v", axis = "lr")
```

```
## Warning: Removed 37 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

```
## Warning: Removed 7 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

```
f_full_top <- plot_grid(f_edge_cfi, f_full_right, ncol = 2, rel_widths = c(3, 1))
```
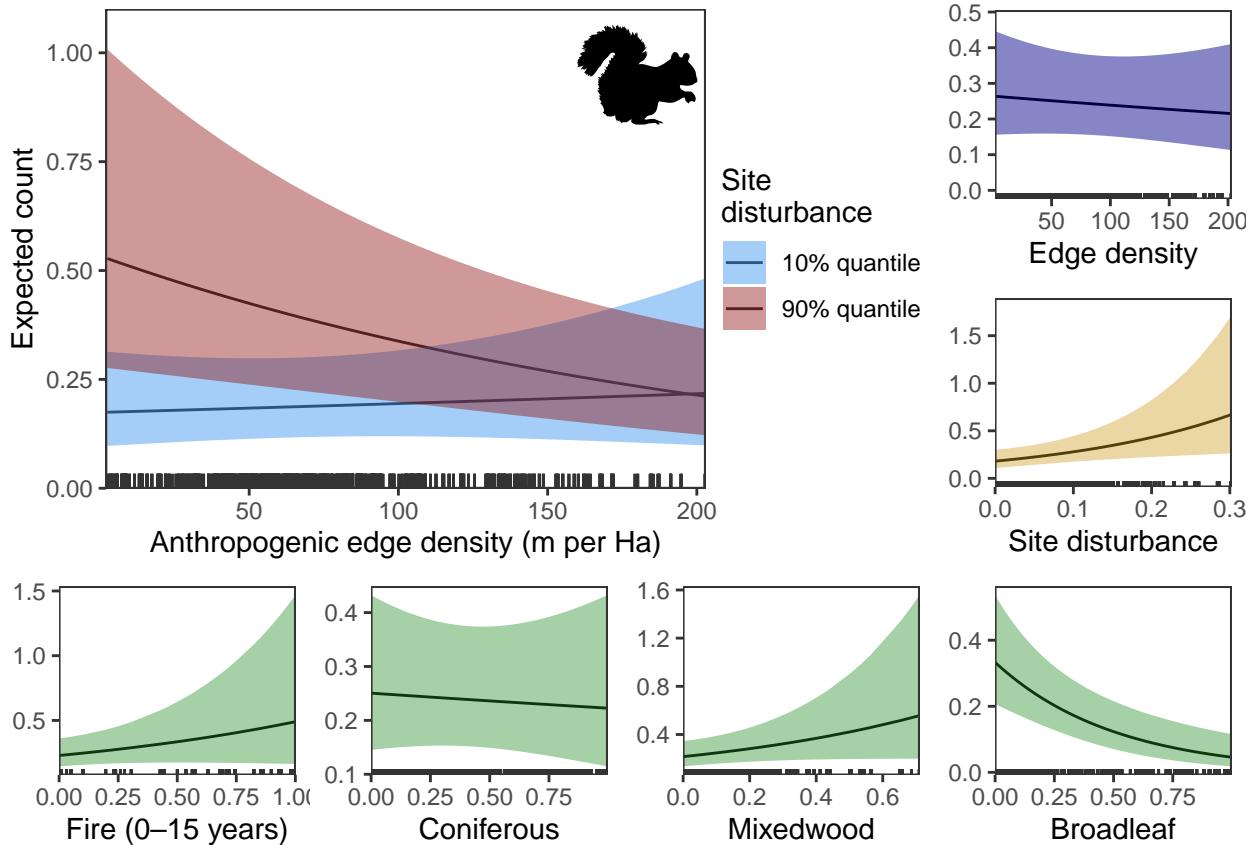
```
## Warning: Removed 74 rows containing missing values or values outside the scale range
## (`geom_line()`).
```

```
f_full_bottom <- plot_grid(f_fire, f_conifer, f_mixedwood, f_decid, nrow = 1, align = "v", axis =
↪   "lr")

f_full <- plot_grid(f_full_top, f_full_bottom, ncol = 1, rel_heights = c(2, 1), align = "v", axis =
↪   "l")

plot(f_full)
```

```
ggsave(f_full, file = "./figures/top_model_all_effects.png", width = 9, height = 6, dpi = 500)
```

9. Make a pretty AIC table for the report

```r
models_rank_table <- models_rank %>%

  # Select the model name and all columns up to (but not including) the 'df' column
  select(model, 1:(which(names(.) == "df") - 1)) %>%

  # Reshape from wide to long format: each row is now a model-predictor pair
  pivot_longer(cols = -model, names_to = "predictor", values_to = "value") %>%

  # Remove predictors that were not included in a model (i.e., NA values)
  drop_na(value) %>%

  # Join with a table of formatted covariate names for nicer labels in the output
  left_join(covs_formatted, by = c("predictor" = "Covariate")) %>%

  # Manually overwrite PrettyName for specific interaction terms
  mutate(PrettyName = case_when(
    predictor == "cfi_site:nonanthro_ed" ~ "Edge Density × CFI",
    TRUE ~ PrettyName)) %>%

  # Group by model to prepare for collapsing predictors into formula strings
```

```r
  group_by(model) %>%

  # Combine all covariates into a single formula string per model
  summarize(formula = paste(PrettyName, collapse = " + ")) %>%

  # Clean up the formula strings for display
  mutate(
    formula = str_replace(formula, "NA \\+", ""),      # Remove 'NA +' if present at the beginning
    formula = str_replace(formula, "NA", "1"),          # Replace 'NA' (empty models) with
    ↪   intercept-only model '1'
    formula = str_replace(formula, ":", " * "),        # Replace ':' with '*' to show interactions
    ↪   more clearly
    formula = str_replace(
      formula,
      "Fire <15 \\+ Broadleaf \\+ Coniferous \\+ Mixedwood +",
      "CORE "                                          # Group common landcover types under "CORE"
    )
  ) %>%

  # Reattach AIC info by joining back with the full model ranking table
  left_join(models_rank %>% select(model, df:ncol(.)),
            by = "model") %>%

  # Order models by ΔAICc (delta)
  arrange(delta) %>%

  # Select and rename final columns for table output
  select(
    "Hypothesis" = "model",
    "Covariates" = "formula",
    df,
    AICc,
    "ΔAICc" = "delta",
    "AICw" = "weight"
  )

# Export the formatted model selection table to Excel
writexl::write_xlsx(models_rank_table, "./tables/OSM_model_selection_summary.xlsx")
```

10. Make a pretty model summary table

10.1. for the top model

```r
# Extract fixed effects from the top model, including confidence intervals
fixed_effects <- broom.mixed::tidy(top_model, effects = "fixed", conf.int = TRUE) %>%

  # Round estimates, standard errors, test statistics, p-values, and confidence intervals to 3
  ↪   decimal places
  mutate(across(c(estimate, std.error, statistic, p.value, conf.low, conf.high), ~ round(.x, 3)))
  ↪   %>%

  # Remove the 'component' column, as it is not needed
  select(-component) %>%
```

```r
  # Rename columns for more understandable names
  rename_with(~ c("Type", "Term", "Estimate", "SE", "z", "p", "CI Low", "CI High")) %>%

  # Join with formatted covariate names for prettier labels
  left_join(covs_formatted, by = c("Term" = "Covariate")) %>%

  # Replace term names with pretty labels
  mutate(Covariate = case_when(
    Term == "nonanthro_ed:cfi_site" ~ "Edge Density × CFI",   # Human-readable label for
↪  interaction
    is.na(PrettyName) ~ "Intercept",                          # Replace NA PrettyName with
      ↪  "Intercept"
    TRUE ~ PrettyName)) %>%

  # Drop the 'Term' and 'PrettyName' columns after formatting
  select(-Term, -PrettyName)

# Extract random effects from the top model, including confidence intervals
random_effects <- broom.mixed::tidy(top_model, effects = "ran_pars", conf.int = TRUE) %>%

  # Modify the group names for better readability
  mutate(group = case_when(
    group == "site:array" ~ "Site [nested]",  # Rename 'site:array' to 'Site [nested]'
    group == "array" ~ "Array",               # Rename 'array' to 'Array'
    TRUE ~ group),                            # Keep other group names unchanged

  # Add a new column 'effect' to indicate random effects
  effect = "Random") %>%

  # Select relevant columns and rename them for clarity
  select("Type" = "effect", "Covariate" = group, "SD (intercept)" = "estimate")

# Combine both fixed and random effects into one summary table
# Add a 'Table' column to distinguish between fixed and random effects
top_model_summary <- bind_rows(
  tibble(Table = "Fixed Effects", fixed_effects),
  tibble(Table = "Random Effects", random_effects)
)

# Export the summary table to an Excel file
writexl::write_xlsx(top_model_summary, "./tables/OSM_top_model_summary.xlsx")
```

10.2. For the second place model

```r
# Exact same code as before so not gonna re-type the annotations... you get the deal.
fixed_effects <- broom.mixed::tidy(m_seis_wells, effects = "fixed", conf.int = TRUE) %>%

  mutate(across(c(estimate, std.error, statistic, p.value, conf.low, conf.high), ~ round(.x, 3)))
  ↪  %>%

  select(-component) %>%

  rename_with(~ c("Type", "Term", "Estimate", "SE", "z", "p", "CI Low", "CI High")) %>%

  left_join(covs_formatted, by = c("Term" = "Covariate")) %>%
```

```
  mutate(Covariate = case_when(
    Term == "nonanthro_ed:cfi_site" ~ "Edge Density × CFI",
    is.na(PrettyName) ~ "Intercept",
    TRUE ~ PrettyName)) %>%

  select(-Term, -PrettyName)

fixed_effects
```

```
## # A tibble: 8 x 8
##    Type  Estimate    SE      z      p `CI Low` `CI High` Covariate
##    <chr>    <dbl> <dbl>  <dbl>  <dbl>    <dbl>     <dbl> <chr>
## 1 fixed    -1.57  0.247 -6.37  0        -2.06     -1.09 Intercept
## 2 fixed    -0.006 0.11  -0.052 0.958    -0.222     0.211 Coniferous
## 3 fixed     0.155 0.092  1.68  0.093    -0.026     0.335 Mixedwood
## 4 fixed    -0.478 0.129 -3.71  0        -0.73     -0.225 Broadleaf
## 5 fixed     0.112 0.117  0.957 0.339    -0.118     0.343 Fire <15
## 6 fixed     0.305 0.131  2.34  0.02      0.049     0.561 Pipelines & Transmission~
## 7 fixed    -0.447 0.129 -3.46  0.001    -0.701    -0.194 Seismic Lines
## 8 fixed     0.006 0.143  0.041 0.967    -0.274     0.286 Inactive Well Sites
```

```
random_effects <- broom.mixed::tidy(top_model, effects = "ran_pars", conf.int = TRUE) %>%

    mutate(group = case_when(
      group == "site:array" ~ "Site [nested]",
      group == "array" ~ "Array",
      TRUE ~ group),

    effect = "Random") %>%

  select("Type" = "effect", "Covariate" = group, "SD (intercept)" = "estimate")

# Add a title for each table and stack them
top_model_summary <- bind_rows(
  tibble(Table = "Fixed Effects", fixed_effects),
  tibble(Table = "Random Effects", random_effects)
)

writexl::write_xlsx(top_model_summary, "./tables/OSM_second_place_model_summary.xlsx")
```