Exploratory Analysis

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Introduction

Required Libraries

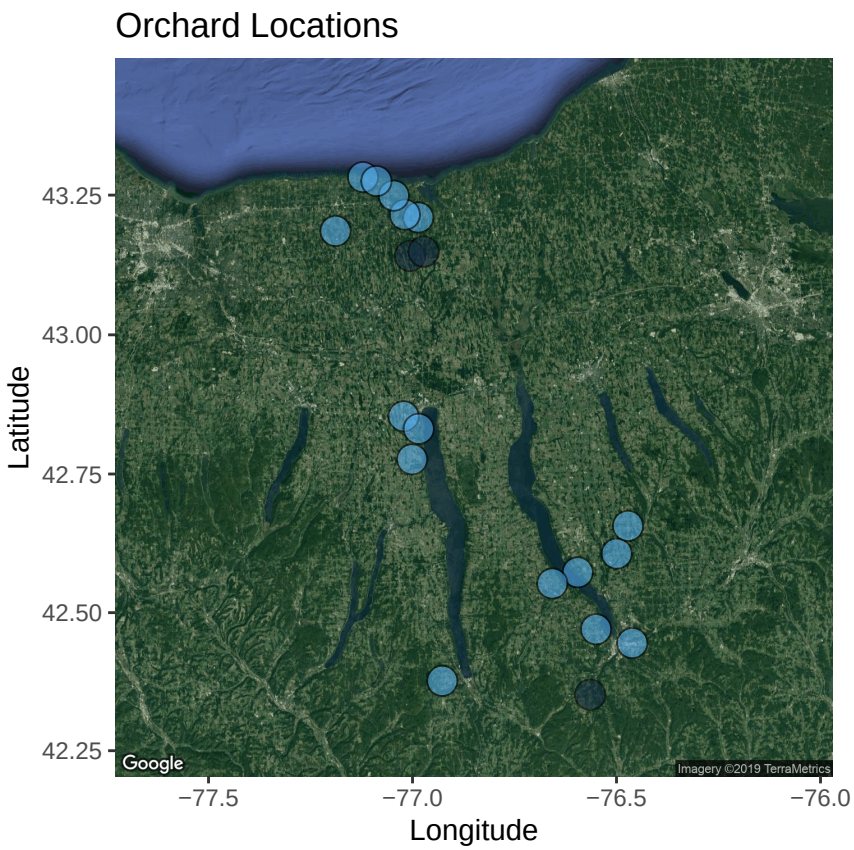
```
library(tidyverse)
library(ggmap)
library(leaps)
library(GGally)
```

Map Analysis

```
#Loading the data in from paper ~ downloaded from their resources as a .xlsx, created csv with useful p
data <- read.csv("data.csv") %>%
  #renaming as column name had a few unrecognised characters in front
  rename(orchard = contains("orchard"))

#Creating an indicator variable to show whether the Orchard appeared in both years or just 1 (0 -> No,
years <- data %>%
  select(orchard, year) %>%
  distinct() %>%
  count(orchard) %>%
  rename(both_years = n) %>%
  mutate(both_years = (both_years - 1)) %>%
  mutate(id = row_number())


data <- merge(data, years)

#Isolating the lat and long
lat_long <- data %>%
  select(lat,long,both_years) %>%
  distinct()

register_google(key = "AIzaSyB9Hpt0vTWrALpm0iUyJxW6C2IuHZylpC8")
map <- get_map(location = c(lon = mean(lat_long$lon), lat = mean(lat_long$lat)), zoom = 9,
                      maptype = "satellite", scale = 2)
```

```
## Source : https://maps.googleapis.com/maps/api/staticmap?center=42.85269,-76.850661&zoom=9&size=640x6
```

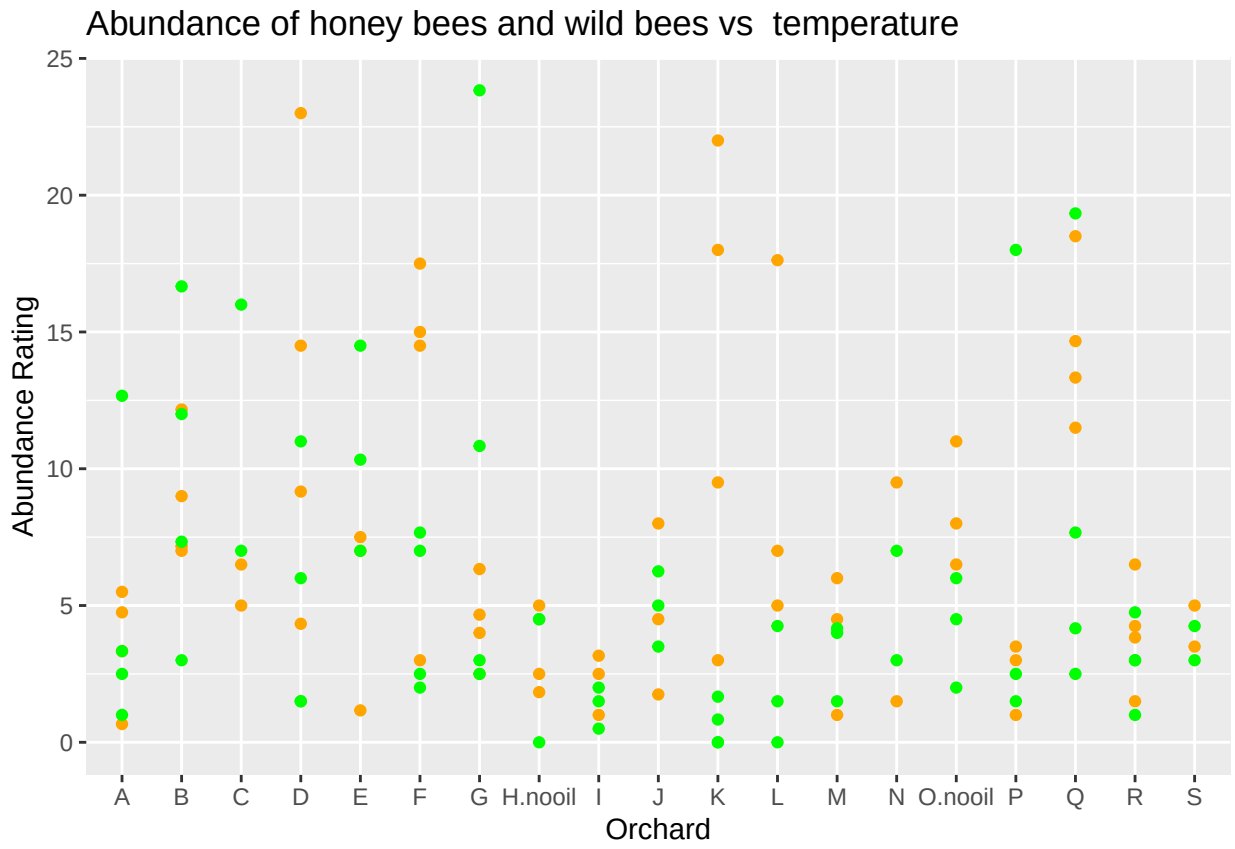
```
#~~~~~Plotting the locations of all the orchards:
plotted_map <- ggmap(map) +
  geom_point(data = lat_long, aes(x = long, y = lat, fill = both_years , alpha = 0.8), size = 5, shape =
  guides(fill = FALSE, alpha = FALSE, size = FALSE) +
  ggtitle("Orchard Locations") +
  xlab("Longitude") +
  ylab("Latitude")
plotted_map
```




```
##
```

Jumped Straight into this original look

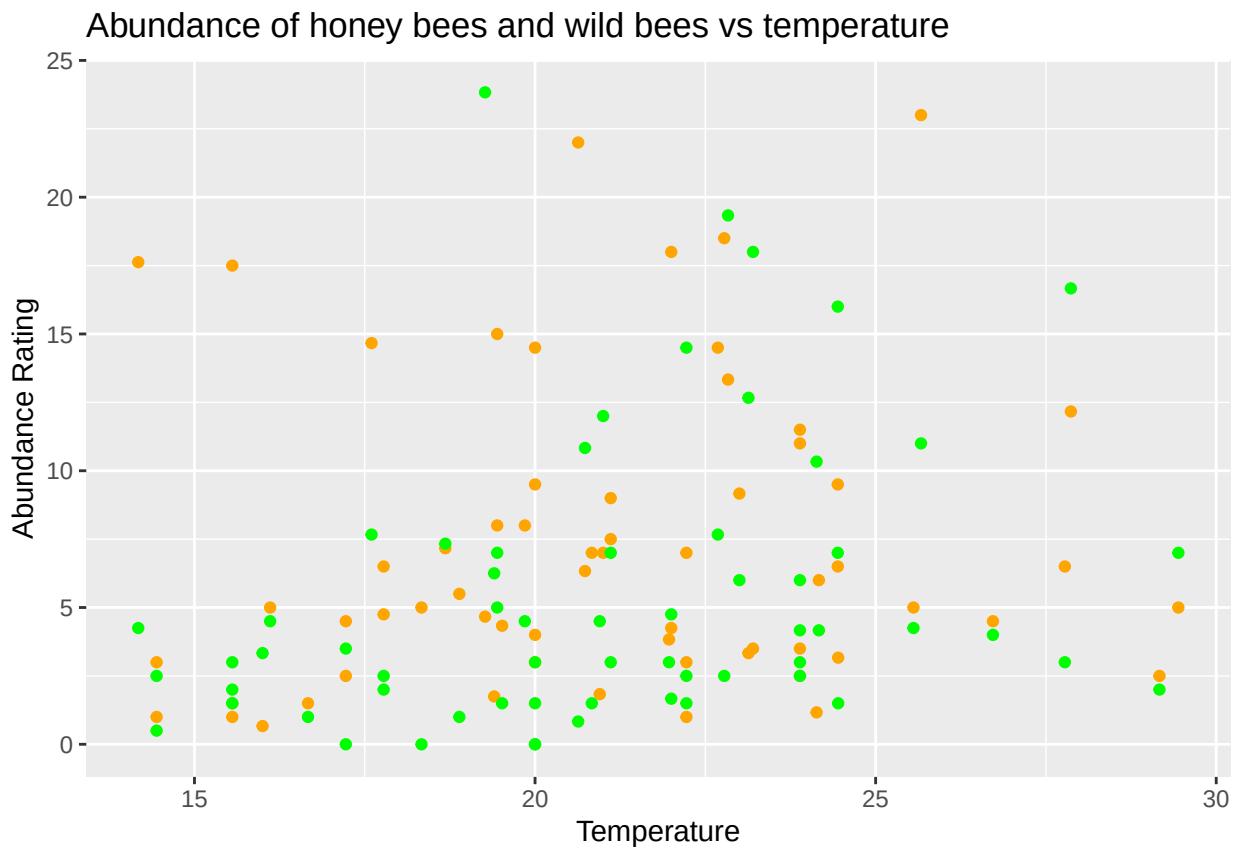
```
abundance_plot <- ggplot(data = data) +
  geom_point(aes(x = orchard, y = apisAb), colour = "orange") +
  geom_point(aes(x = orchard, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs  temperature") +
  xlab("Orchard") +
  ylab("Abundance Rating")
abundance_plot
```




```
abundance_summary <- data %>% summarise(
  honey_mean = round(mean(apisAb),2),
  wild_mean = round(mean(wildAbF), 2),
  honey_sd = round(sd(apisAb), 2),
  wild_sd = round(sd(wildAbF), 2)
)
abundance_summary
```

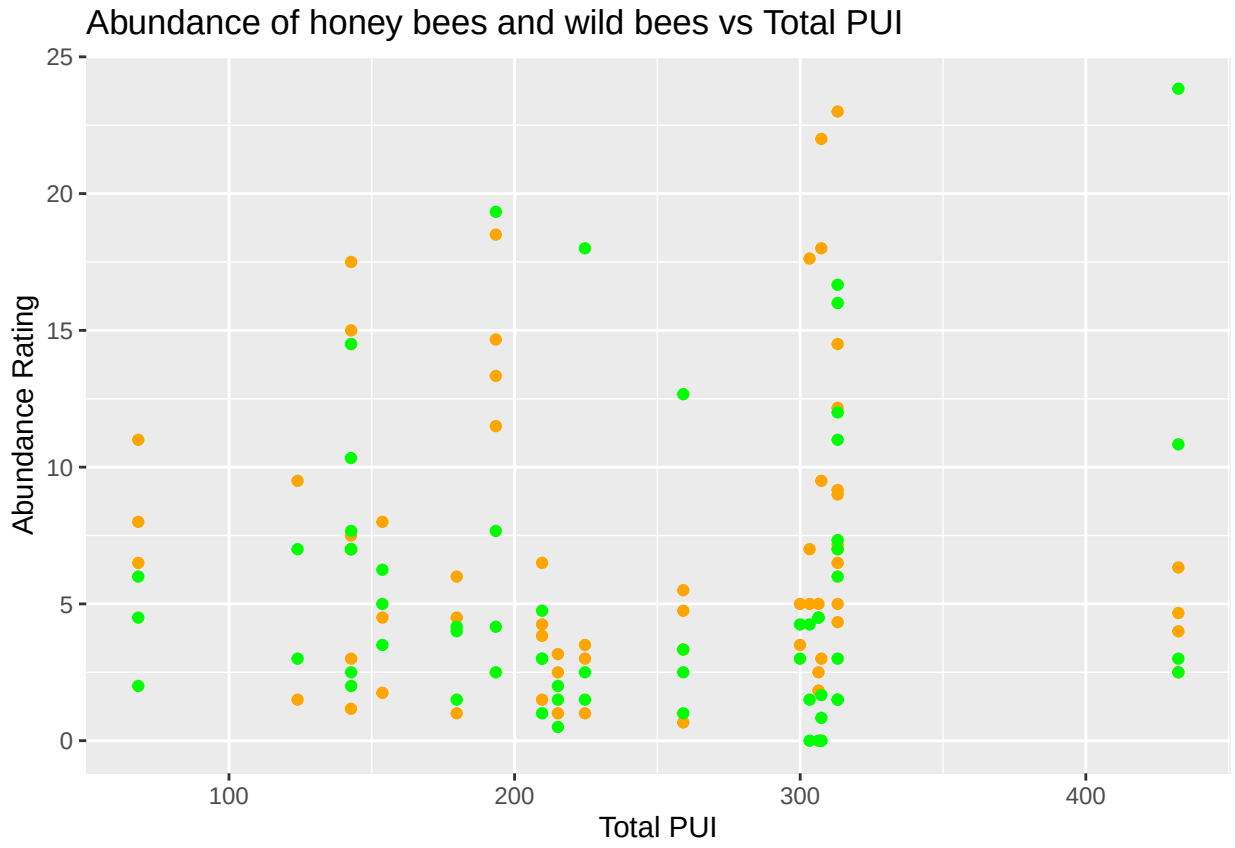
```
##   honey_mean wild_mean honey_sd wild_sd
## 1       7.19      5.41     5.51    5.21
```

```
#Looking at temperature vs bees
temperature_plot <- ggplot(data = data) +
  geom_point(aes(x = temp, y = apisAb), colour = "orange") +
  geom_point(aes(x = temp, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs temperature") +
  xlab("Temperature") +
  ylab("Abundance Rating")
temperature_plot
```

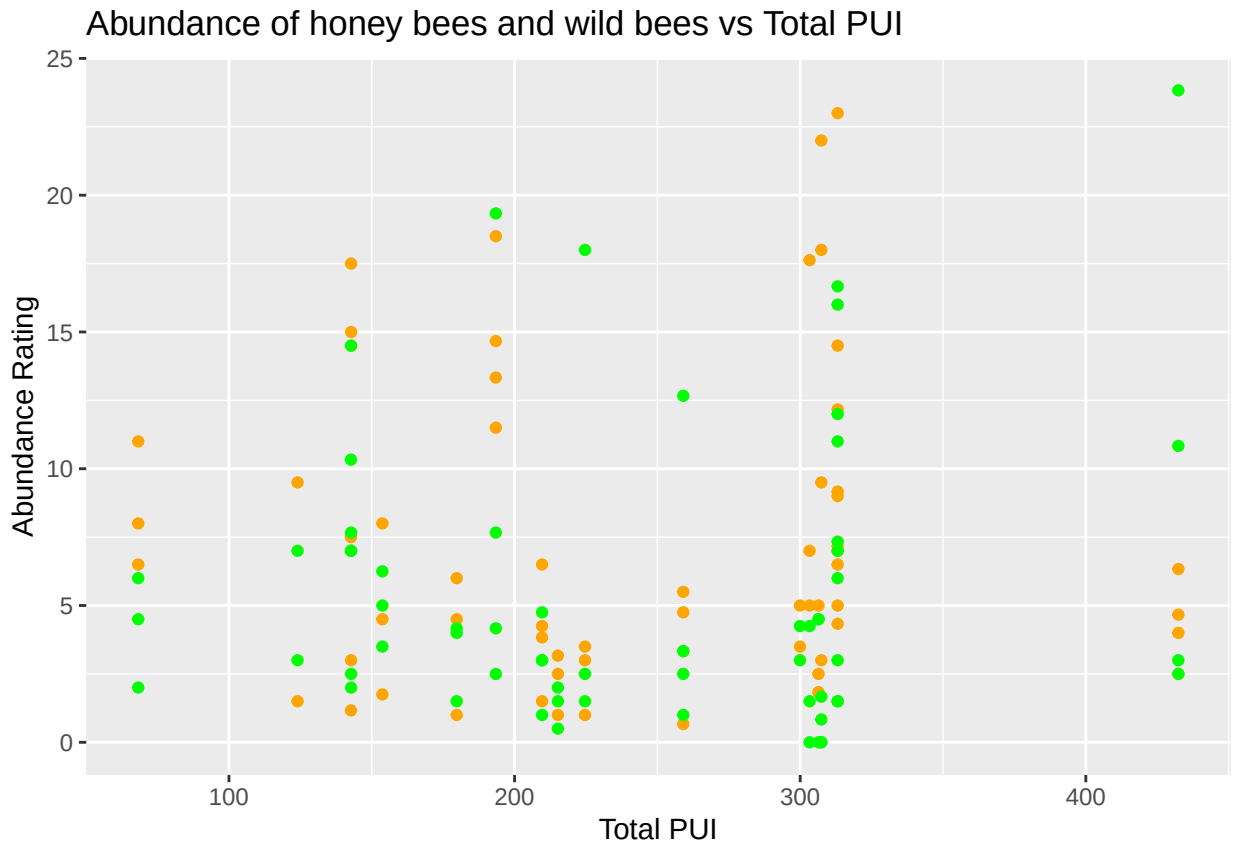



```r
#Looking at the data it seems a quadratic model would be the best fit, shown below
temperature_plot <- temperature_plot +
  stat_smooth(aes(x = temp, y = apisAb), method = "lm", formula = y ~ x + I(x^2), colour = "orange") +
  stat_smooth(aes(x = temp, y = wildAbF), method = "lm", formula = y ~ x + I(x^2), colour = "green") +
  theme_bw()



#Actually shows like nothing lol

log_data <- data %>%
  mutate(apisAb = log(apisAb), wildAbF = log(wildAbF))

temperature_plot_log <-  ggplot(data = log_data) +
  geom_point(aes(x = temp, y = apisAb), colour = "orange") +
  geom_point(aes(x = temp, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs temperature") +
  xlab("Temperature") +
  ylab("Abundance Rating")

#Doesn't show too much
pui_plot <-  ggplot(data = data) +
  geom_point(aes(x = eiqB11, y = apisAb), colour = "orange") +
  geom_point(aes(x = eiqB11, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs Total PUI") +
  xlab("Total PUI") +
```

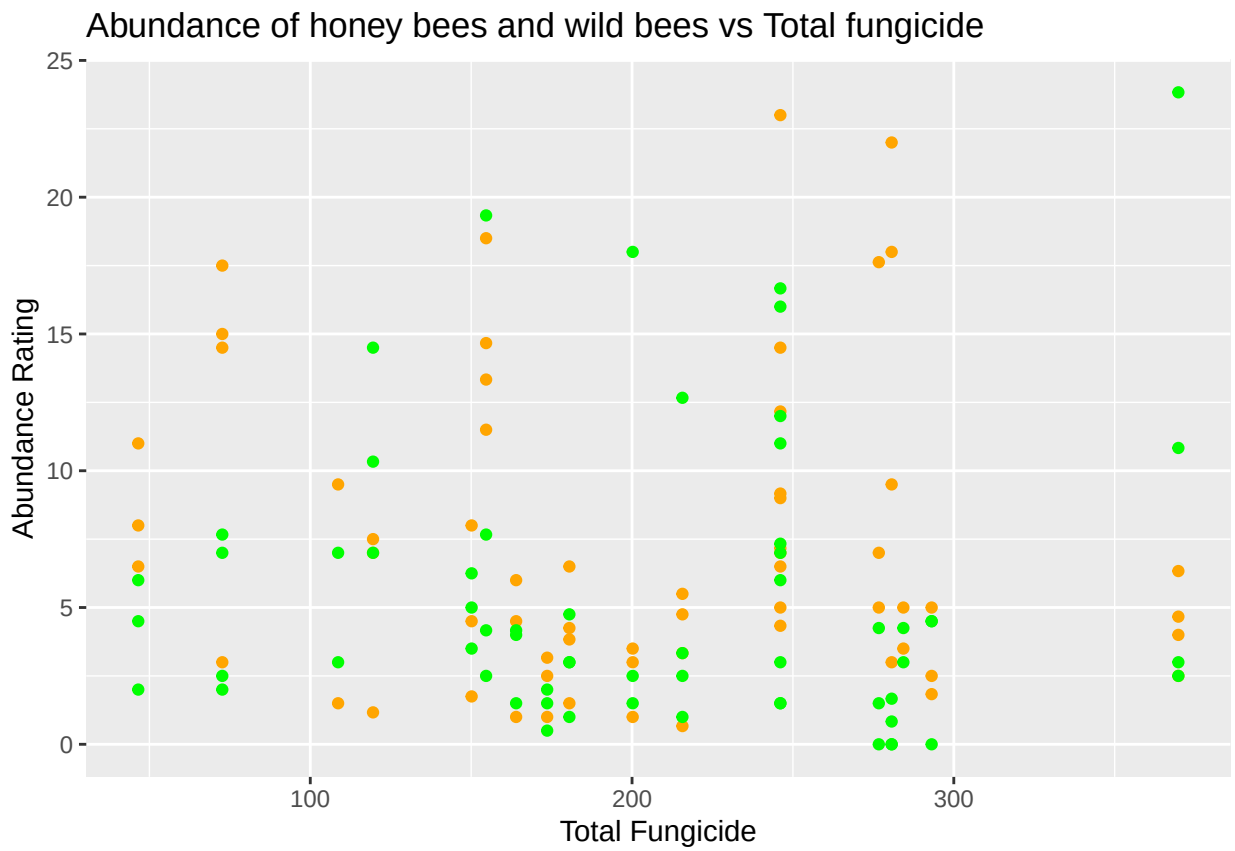
```
  ylab("Abundance Rating")
pui_plot
```



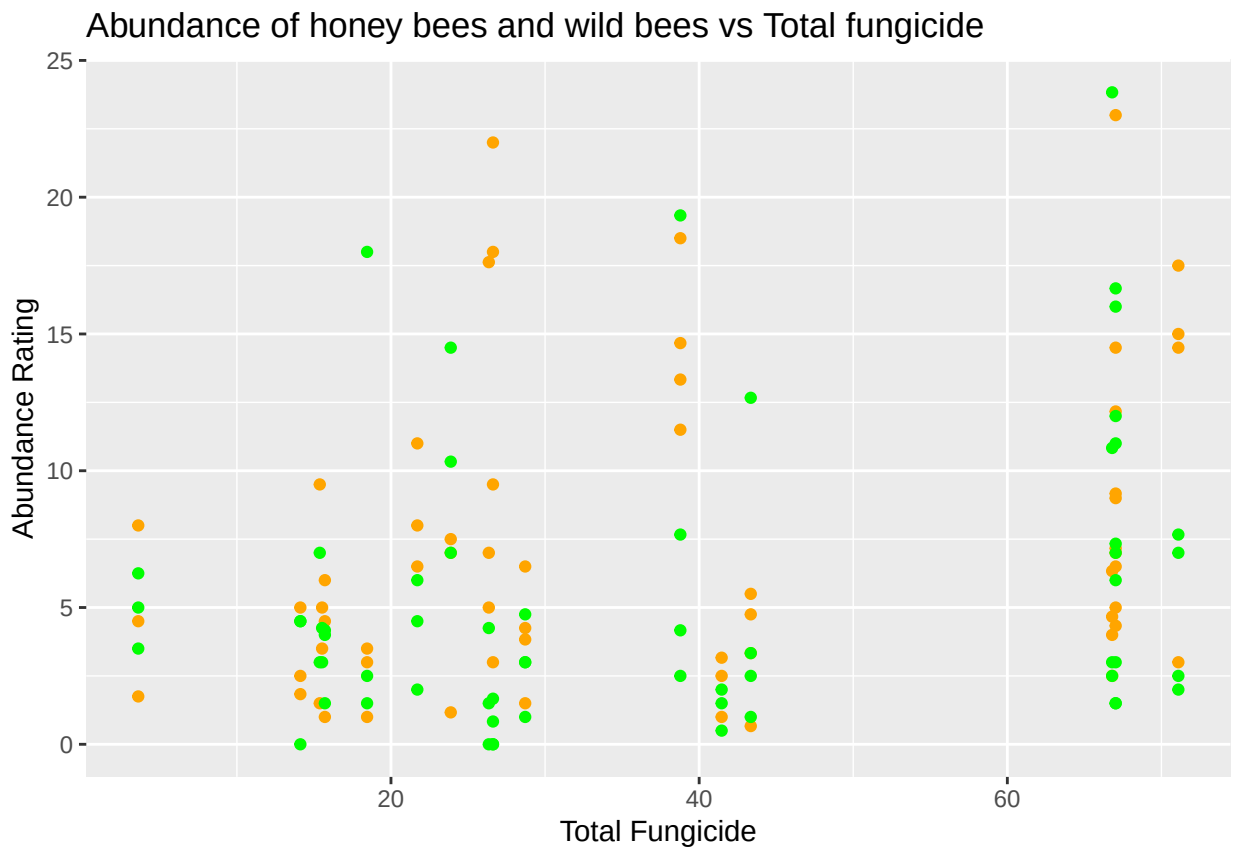

```
#Doesn't show too much
pui_plot <-  ggplot(data = data) +
  geom_point(aes(x = eiqB11, y = apisAb), colour = "orange") +
  geom_point(aes(x = eiqB11, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs Total PUI") +
  xlab("Total PUI") +
  ylab("Abundance Rating")
pui_plot
```




```
fungicide_plot <-  ggplot(data = data) +
  geom_point(aes(x = eiqB11.fun, y = apisAb), colour = "orange") +
  geom_point(aes(x = eiqB11.fun, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs Total fungicide") +
  xlab("Total Fungicide") +
  ylab("Abundance Rating")
fungicide_plot
```




```
Insectcide_plot <-  ggplot(data = data) +
  geom_point(aes(x = eiqB11.ins, y = apisAb), colour = "orange") +
  geom_point(aes(x = eiqB11.ins, y = wildAbF), colour = "green") +
  ggtitle("Abundance of honey bees and wild bees vs Total fungicide") +
  xlab("Total Fungicide") +
  ylab("Abundance Rating")
Insectcide_plot
```



Leaps

```
summary(regsubsets( apisAb ~ eiqB11 + eiqB11.np + eiqB11.fun    + eiqB11.ins +  eiqB11.ins.np +
                    eiqB11F.pre   + eiqB11F.blm   + eiqB11F.pos   + eiqB11I.pre   + eiqB11I.blm   +
                    eiqB11I.pos   + eiqB11I.pos.np    + eiqB11T.blm   + eiqB11T.pos   + size  + hive.a
, data = data, nvmax = 6))
```

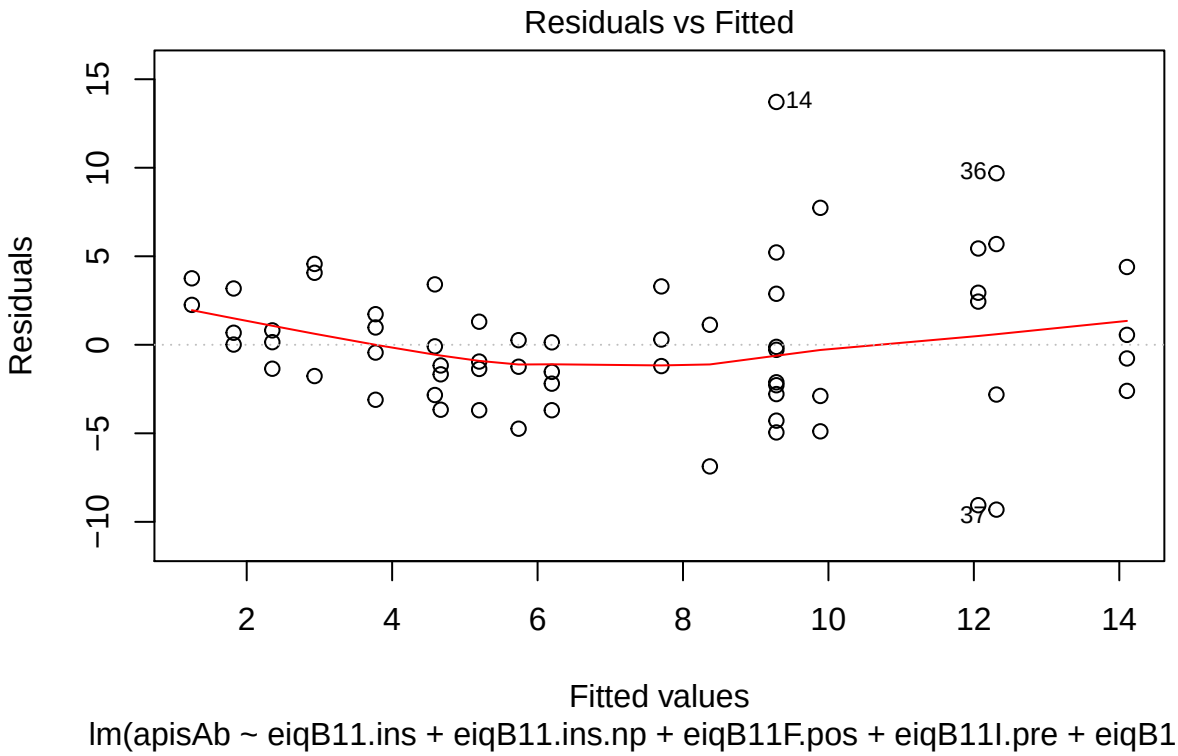
```
## Warning in leaps.setup(x, y, wt = wt, nbest = nbest, nvmax = nvmax,
## force.in = force.in, : 2 linear dependencies found
```

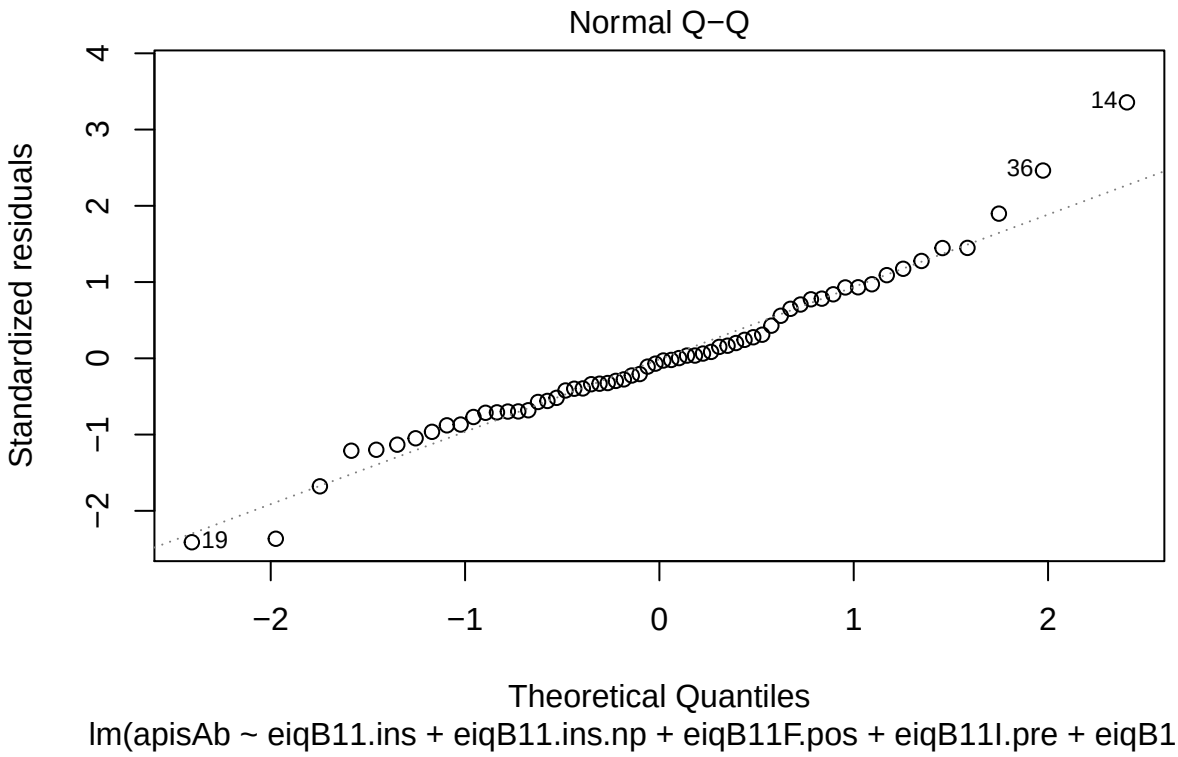
```
## Reordering variables and trying again:
```

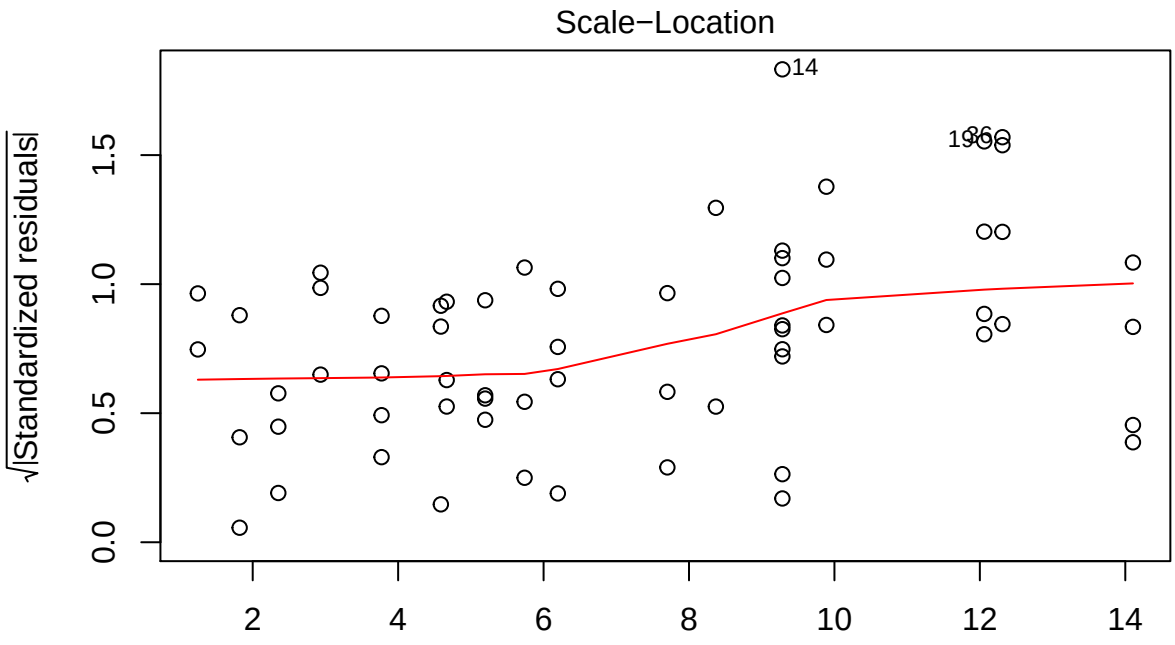
```
## Subset selection object
## Call: regsubsets.formula(apisAb ~ eiqB11 + eiqB11.np + eiqB11.fun +
##     eiqB11.ins + eiqB11.ins.np + eiqB11F.pre + eiqB11F.blm +
##     eiqB11F.pos + eiqB11I.pre + eiqB11I.blm + eiqB11I.pos + eiqB11I.pos.np +
##     eiqB11T.blm + eiqB11T.pos + size + hive.acr + X2000nat, data = data,
##     nvmax = 6)
## 17 Variables  (and intercept)
##                Forced in Forced out
## eiqB11             FALSE      FALSE
## eiqB11.np          FALSE      FALSE
## eiqB11.fun         FALSE      FALSE
## eiqB11.ins         FALSE      FALSE
## eiqB11F.pre        FALSE      FALSE
## eiqB11F.blm        FALSE      FALSE
```

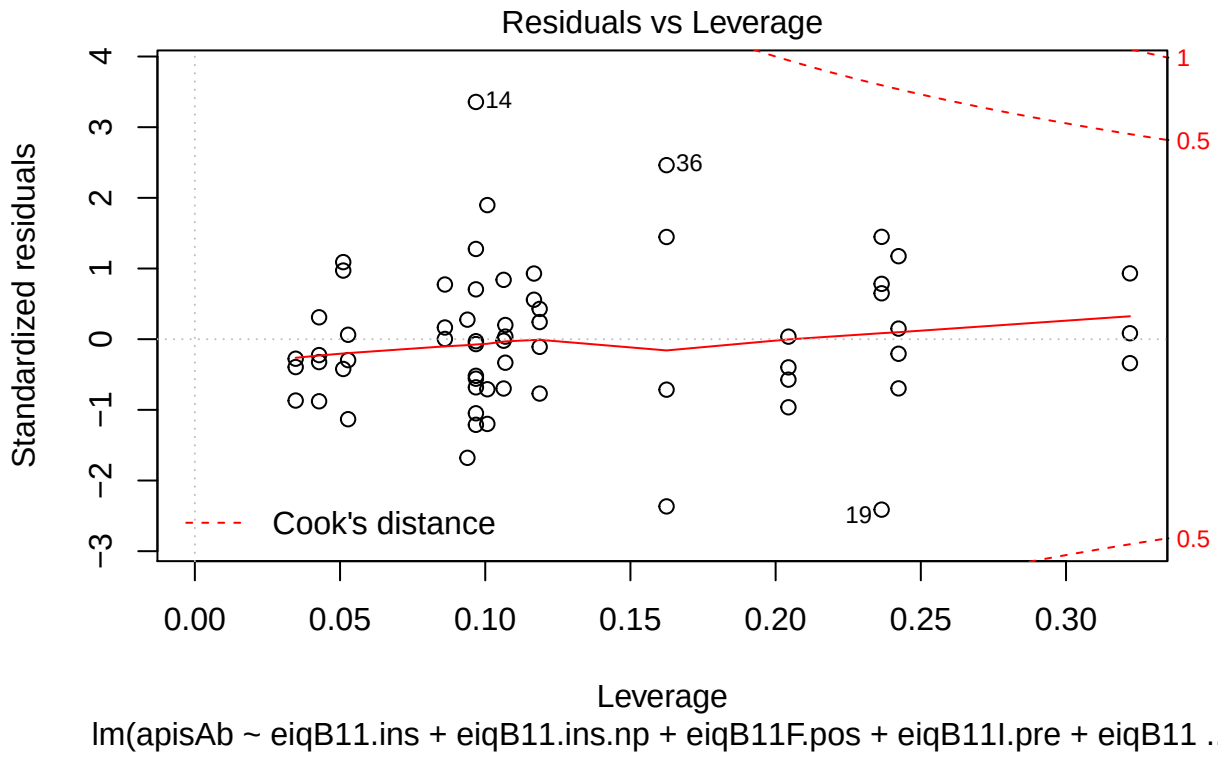
```
## eiqB11F.pos        FALSE      FALSE
## eiqB11I.pre        FALSE      FALSE
## eiqB11I.blm        FALSE      FALSE
## eiqB11I.pos        FALSE      FALSE
## eiqB11I.pos.np     FALSE      FALSE
## eiqB11T.blm        FALSE      FALSE
## size               FALSE      FALSE
## hive.acr           FALSE      FALSE
## X2000nat           FALSE      FALSE
## eiqB11.ins.np      FALSE      FALSE
## eiqB11T.pos        FALSE      FALSE
## 1 subsets of each size up to 7
## Selection Algorithm: exhaustive
##          eiqB11 eiqB11.np eiqB11.fun eiqB11.ins eiqB11.ins.np eiqB11F.pre
## 1  ( 1 ) " "    " "       " "        "*"        " "           " "
## 2  ( 1 ) " "    " "       " "        "*"        " "           " "
## 3  ( 1 ) " "    "*"       " "        " "        " "           "*"
## 4  ( 1 ) "*"    "*"       " "        " "        " "           "*"
## 5  ( 1 ) " "    " "       " "        " "        " "           "*"
## 6  ( 1 ) " "    " "       " "        "*"        "*"           " "
## 7  ( 1 ) " "    " "       " "        "*"        "*"           " "
##          eiqB11F.blm eiqB11F.pos eiqB11I.pre eiqB11I.blm eiqB11I.pos
## 1  ( 1 ) " "         " "         " "         " "         " "
## 2  ( 1 ) " "         "*"         " "         " "         " "
## 3  ( 1 ) " "         " "         " "         "*"         " "
## 4  ( 1 ) " "         " "         " "         "*"         " "
## 5  ( 1 ) " "         "*"         "*"         "*"         " "
## 6  ( 1 ) " "         "*"         "*"         "*"         "*"
## 7  ( 1 ) " "         "*"         "*"         "*"         "*"
##          eiqB11I.pos.np eiqB11T.blm eiqB11T.pos size hive.acr X2000nat
## 1  ( 1 ) " "            " "         " "         " "  " "      " "
## 2  ( 1 ) " "            " "         " "         " "  " "      " "
## 3  ( 1 ) " "            " "         " "         " "  " "      " "
## 4  ( 1 ) " "            " "         " "         " "  " "      " "
## 5  ( 1 ) "*"            " "         " "         " "  " "      " "
## 6  ( 1 ) " "            " "         " "         " "  " "      " "
## 7  ( 1 ) "*"            " "         " "         " "  " "      " "
```

```
#Let's look at a graph of the one with 7 variables:
#eiqB11.ins, eiqB11.ins.np eiqB11F.pos eiqB11I.pre eiqB11I.blm eiqB11I.pos eiqB11I.pos.np
lm_non_vary <- lm(apisAb ~ eiqB11.ins +  eiqB11.ins.np + eiqB11F.pos +
                    eiqB11I.pre +  eiqB11I.blm + eiqB11I.pos + eiqB11I.pos.np, data)
  plot(lm_non_vary)
```


Residuals vs Fitted
Residuals
Fitted values
lm(apisAb ~ eiqB11.ins + eiqB11.ins.np + eiqB11F.pos + eiqB11I.pre + eiqB11 ...
14
36
37
15
10
5
0
−5
−10
2
4
6
8
10
12
14


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(apisAb ~ eiqB11.ins + eiqB11.ins.np + eiqB11F.pos + eiqB11I.pre + eiqB11 ...
14
36
19
−2
−1
0
1
2
3
4


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
2
4
6
8
10
12
14
14
196
36
Fitted values
lm(apisAb ~ eiqB11.ins + eiqB11.ins.np + eiqB11F.pos + eiqB11I.pre + eiqB11 ...




```
summary(lm_non_vary)
```

```
##
## Call:
## lm(formula = apisAb ~ eiqB11.ins + eiqB11.ins.np + eiqB11F.pos +
##     eiqB11I.pre + eiqB11I.blm + eiqB11I.pos + eiqB11I.pos.np,
##     data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.3103 -2.5251 -0.2008  2.3934 13.7159
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       9.58254    2.00881   4.770 1.44e-05 ***
## eiqB11.ins     -613.24900  141.93474  -4.321 6.72e-05 ***
## eiqB11.ins.np    -0.62024    0.14172  -4.376 5.56e-05 ***
## eiqB11F.pos      -0.10990    0.03161  -3.477  0.00101 **
## eiqB11I.pre     613.89664  141.95438   4.325 6.63e-05 ***
## eiqB11I.blm     613.65610  141.93831   4.323 6.65e-05 ***
## eiqB11I.pos     613.47623  141.96140   4.321 6.70e-05 ***
## eiqB11I.pos.np    0.38638    0.16766   2.305  0.02506 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.299 on 54 degrees of freedom
```

```
## Multiple R-squared:  0.4612, Adjusted R-squared:  0.3914
## F-statistic: 6.604 on 7 and 54 DF,  p-value: 1.197e-05
```

```
  ###~~~~ With varying variables ~~~ neither of which appear as relevant at all...
summary(regsubsets( apisAb ~ temp+ bloom.index + eiqB11 + eiqB11.np + eiqB11.fun    + eiqB11.ins +  eiqB
                      eiqB11F.pre  + eiqB11F.blm   + eiqB11F.pos   + eiqB11I.pre   + eiqB11I.blm   +
                      eiqB11I.pos  + eiqB11I.pos.np    + eiqB11T.blm   + eiqB11T.pos   + size  + hive.a
                    , data = data, nvmax = 6))
```

```
## Warning in leaps.setup(x, y, wt = wt, nbest = nbest, nvmax = nvmax,
## force.in = force.in, : 2 linear dependencies found
```

```
## Reordering variables and trying again:
```

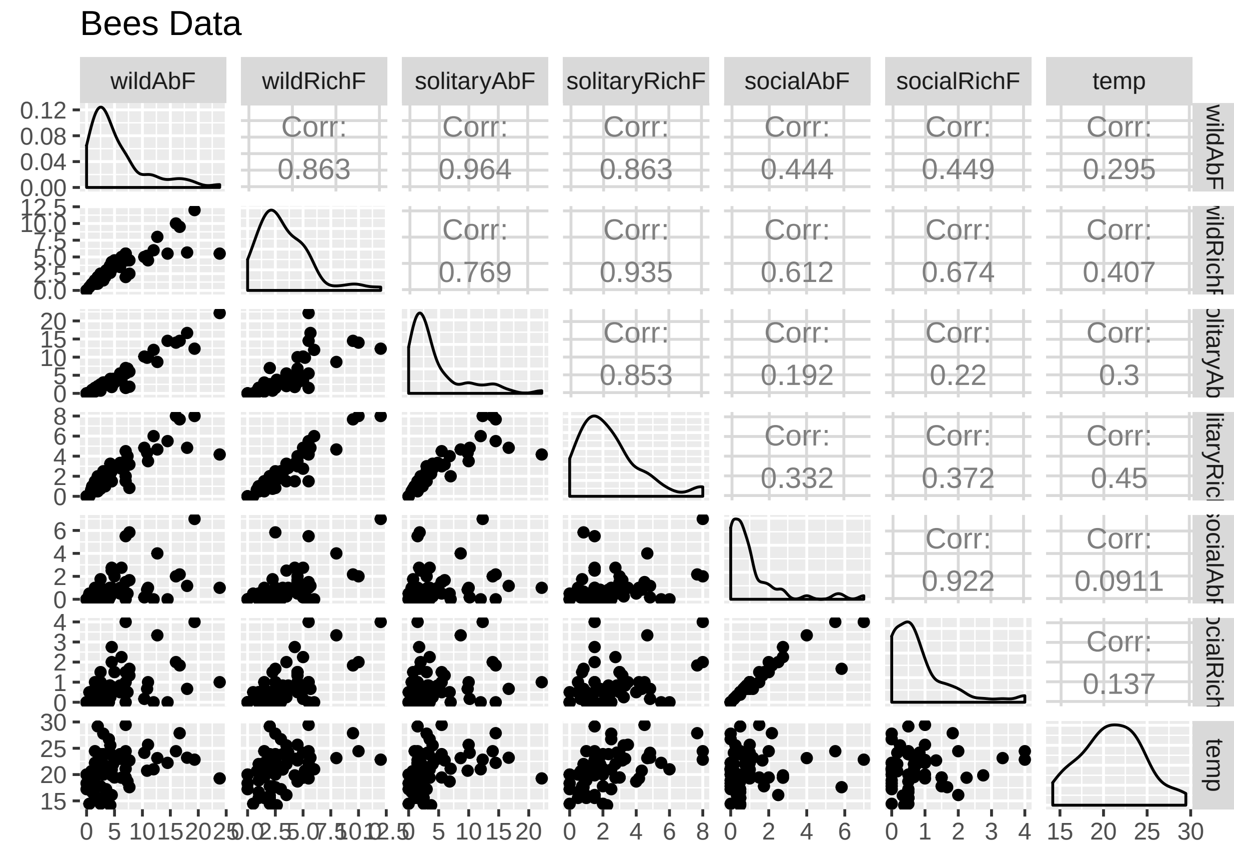
```
## Subset selection object
## Call: regsubsets.formula(apisAb ~ temp + bloom.index + eiqB11 + eiqB11.np +
##     eiqB11.fun + eiqB11.ins + eiqB11.ins.np + eiqB11F.pre + eiqB11F.blm +
##     eiqB11F.pos + eiqB11I.pre + eiqB11I.blm + eiqB11I.pos + eiqB11I.pos.np +
##     eiqB11T.blm + eiqB11T.pos + size + hive.acr + X2000nat, data = data,
##     nvmax = 6)
## 19 Variables  (and intercept)
##                Forced in Forced out
## temp               FALSE      FALSE
## bloom.index        FALSE      FALSE
## eiqB11             FALSE      FALSE
## eiqB11.np          FALSE      FALSE
## eiqB11.fun         FALSE      FALSE
## eiqB11.ins         FALSE      FALSE
## eiqB11F.pre        FALSE      FALSE
## eiqB11F.blm        FALSE      FALSE
## eiqB11F.pos        FALSE      FALSE
## eiqB11I.pre        FALSE      FALSE
## eiqB11I.blm        FALSE      FALSE
## eiqB11I.pos        FALSE      FALSE
## eiqB11I.pos.np     FALSE      FALSE
## eiqB11T.blm        FALSE      FALSE
## size               FALSE      FALSE
## hive.acr           FALSE      FALSE
## X2000nat           FALSE      FALSE
## eiqB11.ins.np      FALSE      FALSE
## eiqB11T.pos        FALSE      FALSE
## 1 subsets of each size up to 7
## Selection Algorithm: exhaustive
##          temp bloom.index eiqB11 eiqB11.np eiqB11.fun eiqB11.ins
## 1  ( 1 ) " "  " "          " "    " "       " "        "*"
## 2  ( 1 ) " "  " "          " "    " "       " "        "*"
## 3  ( 1 ) " "  " "          " "    "*"       " "        " "
## 4  ( 1 ) " "  " "          "*"    "*"       " "        " "
## 5  ( 1 ) " "  " "          " "    " "       " "        " "
## 6  ( 1 ) " "  " "          " "    " "       " "        "*"
## 7  ( 1 ) " "  " "          " "    " "       " "        "*"
##          eiqB11.ins.np eiqB11F.pre eiqB11F.blm eiqB11F.pos eiqB11I.pre
## 1  ( 1 ) " "           " "         " "         " "         " "
## 2  ( 1 ) " "           " "         " "         "*"         " "
## 3  ( 1 ) " "           "*"         " "         " "         " "
## 4  ( 1 ) " "           "*"         " "         " "         " "
```

```
## 5  ( 1 ) " "           "*"          " "          "*"          "*"
## 6  ( 1 ) "*"           " "          " "          "*"          "*"
## 7  ( 1 ) "*"           " "          " "          "*"          "*"
##          eiqB11I.blm eiqB11I.pos eiqB11I.pos.np eiqB11T.blm eiqB11T.pos
## 1  ( 1 ) " "         " "          " "             " "          " "
## 2  ( 1 ) " "         " "          " "             " "          " "
## 3  ( 1 ) "*"         " "          " "             " "          " "
## 4  ( 1 ) "*"         " "          " "             " "          " "
## 5  ( 1 ) "*"         " "          "*"             " "          " "
## 6  ( 1 ) "*"         "*"          " "             " "          " "
## 7  ( 1 ) "*"         "*"          "*"             " "          " "
##          size hive.acr X2000nat
## 1  ( 1 ) " "  " "      " "
## 2  ( 1 ) " "  " "      " "
## 3  ( 1 ) " "  " "      " "
## 4  ( 1 ) " "  " "      " "
## 5  ( 1 ) " "  " "      " "
## 6  ( 1 ) " "  " "      " "
## 7  ( 1 ) " "  " "      " "
```

```
 ##Both stepwise regressions so the same predictors as the best
hist_resid <- ggplot(data=data, aes(lm_non_vary$residuals)) +
  geom_histogram(binwidth = 1, color = "black", fill = "purple4") +
  theme(panel.background = element_rect(fill = "white"),
        axis.line.x=element_line(),
        axis.line.y=element_line()) +
  ggtitle("Histogram for Model Residuals")

#Probably need to look into best ways to plot/compare these
```

GGTally

```
bees_data <- ggpairs(data = data, columns = 7:13, title = "Bees Data")
bees_data
```




```
predictor_data <- ggpairs(data = data, columns = 13:34, title = "Predictor Data")
predictor_data
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning: Removed 1 rows containing missing values (geom_point).

## Warning: Removed 1 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removing 1 row that contained a missing value

## Warning in (function (data, mapping, alignPercent = 0.6, method =
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```
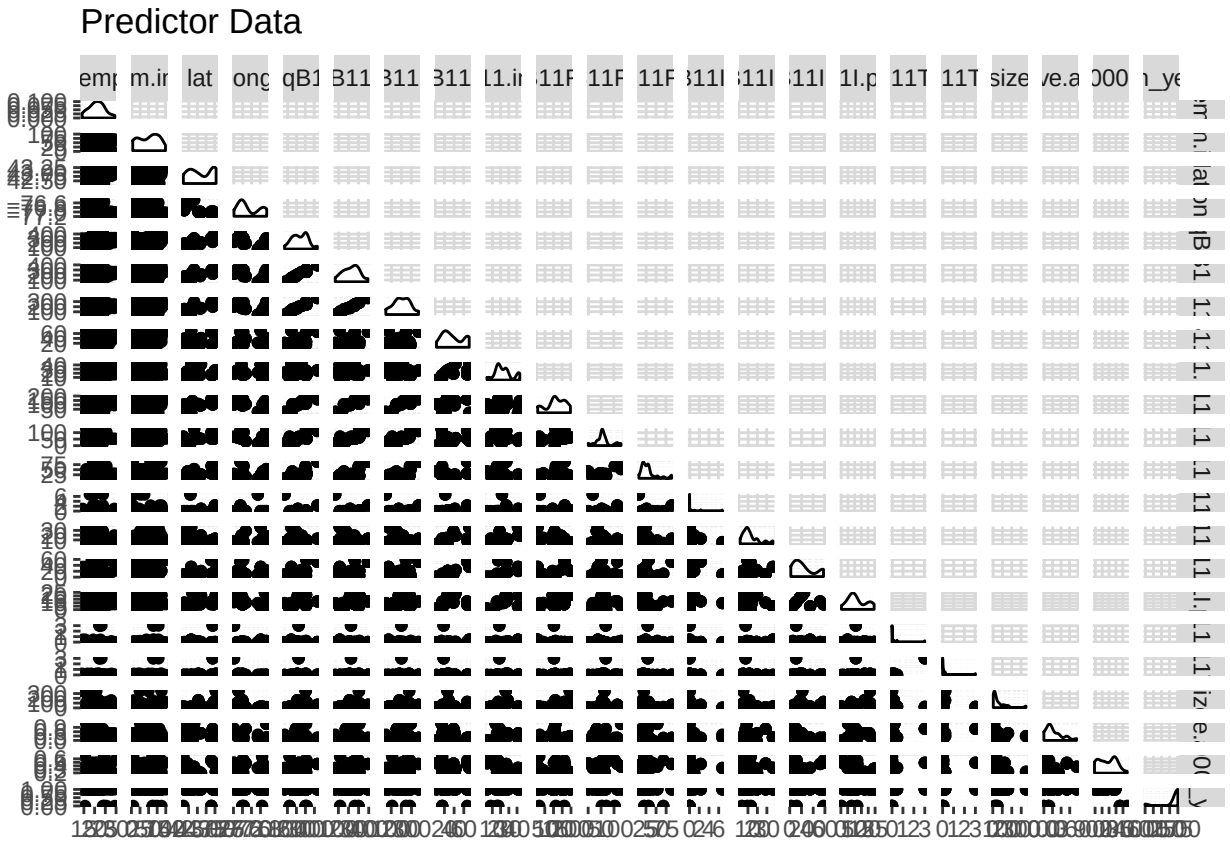
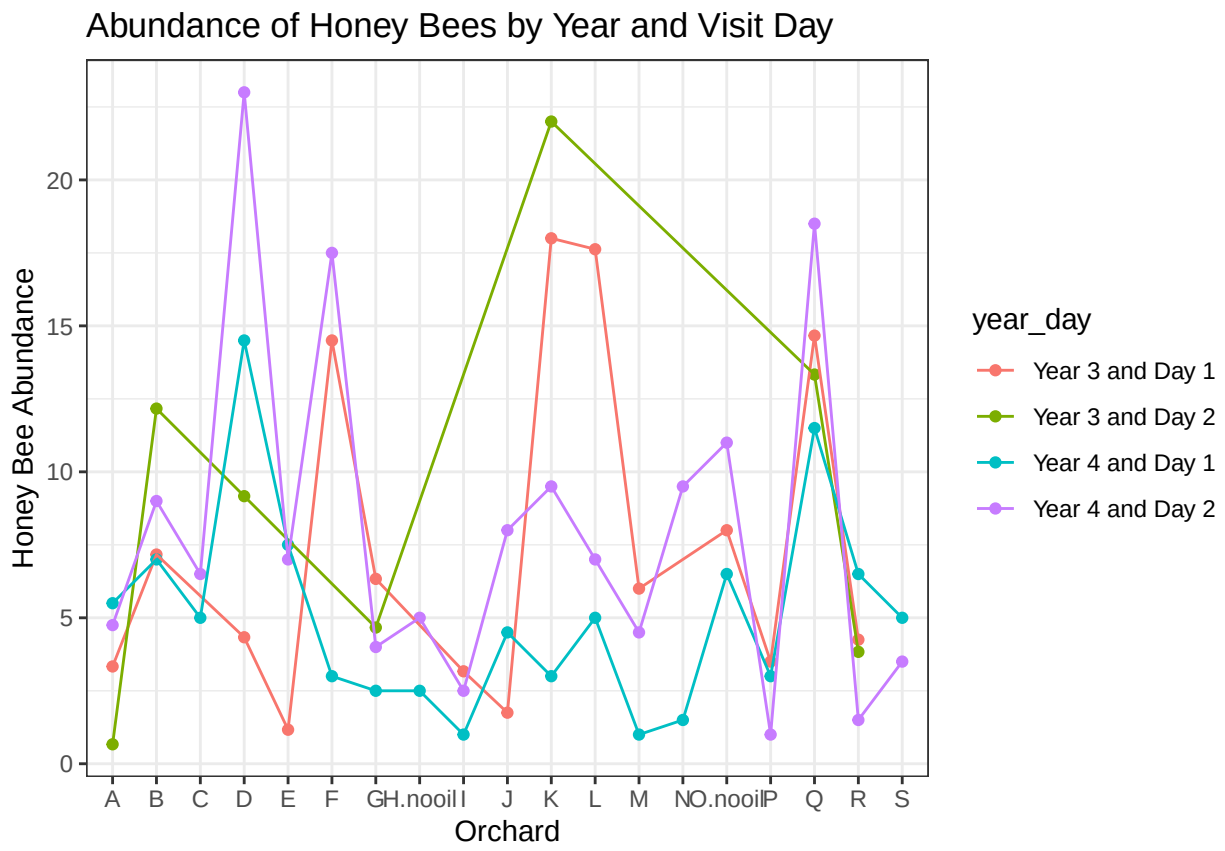



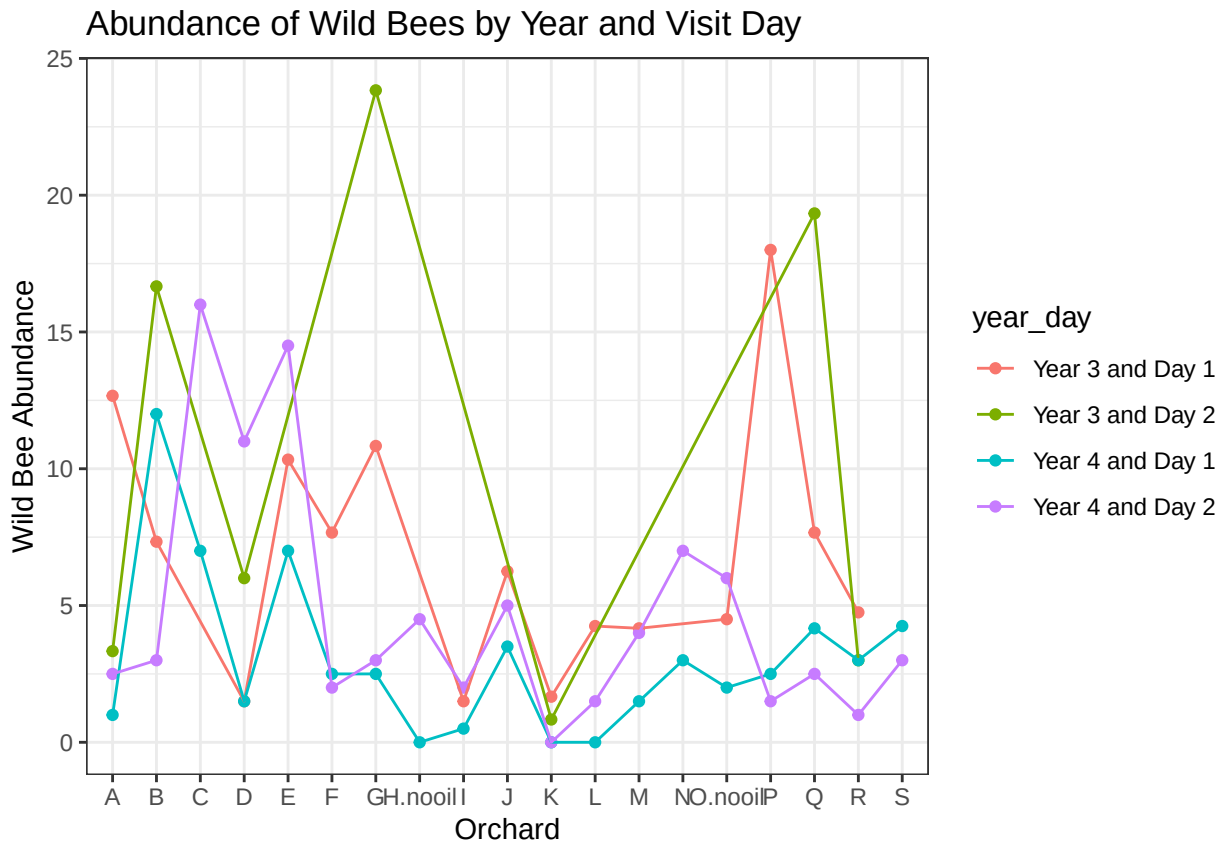
Looking at individual variables

```
day_data <- data %>%
  filter(day %in% c("1","2")) %>%
  mutate(year_day = ifelse(str_detect(day, "1") & str_detect(year, "3"), '11',
                           ifelse(str_detect(day, "2") & str_detect(year, "3"), '12',
```

```
                            ifelse(str_detect(day, "1") & str_detect(year, "4"), '21',
                             ifelse(str_detect(day, "2") & str_detect(year, "4"), '22', "55"))))) %>%
  mutate(year_day = factor(year_day, labels = c("Year 3 and Day 1","Year 3 and Day 2", "Year 4 and Day
  na.omit()


#checking data as there should be a result for each
tibble(counts = c(count(day_data %>%
        filter(year_day == "Year 3 and Day 1")),
count(day_data %>%
        filter(year_day == "Year 3 and Day 2")),
count(day_data %>%
        filter(year_day == "Year 4 and Day 1")),
count(day_data %>%
        filter(year_day == "Year 4 and Day 2")))) %>%
  view()

honey_by_year_day <- day_data %>%
  ggplot(aes(x = orchard, y = apisAb, colour = year_day)) +
  geom_point() +
  geom_line(aes(group = year_day)) +
  theme_bw() +
  ggtitle("Abundance of Honey Bees by Year and Visit Day") +
  ylab("Honey Bee Abundance") +
  xlab("Orchard")
honey_by_year_day
```




```
wild_by_year_day <- day_data %>%
  ggplot(aes(x = orchard, y = wildAbF, colour = year_day)) +
  geom_point() +
  geom_line(aes(group = year_day)) +
  theme_bw() +
  ggtitle("Abundance of Wild Bees by Year and Visit Day") +
  ylab("Wild Bee Abundance") +
  xlab("Orchard")
wild_by_year_day
```

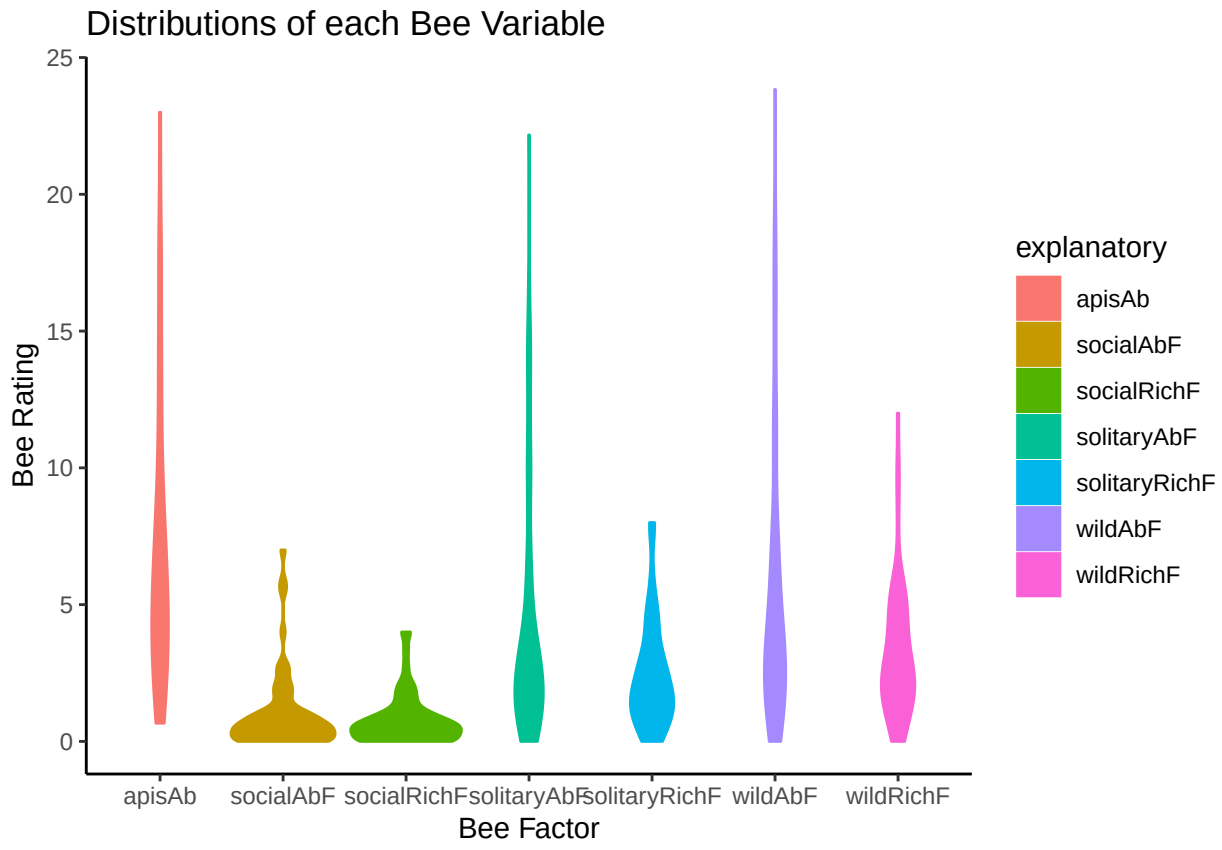



```
wild_temp_by_year_day <- day_data %>%
  ggplot(aes(x = temp, y = wildAbF, colour =  year_day)) +
  geom_point() +
  geom_line(aes(group = year_day )) +
  theme_classic()

honey_temp_by_year_day <- day_data %>%
  ggplot(aes(x = temp, y = apisAb, colour =  year_day)) +
  geom_point() +
  geom_line(aes(group = year_day )) +
  theme_classic()

#think of somehow quantifying bees as the "yield" variable
decision_data <- tibble(
  before = c("Apply Fungicide","Apply Insecticide", "Apply Both", "Apply Nothing"),
  during = c("a","b","c","d"),
  bee_yield = c(300,200,300,400)
)
```

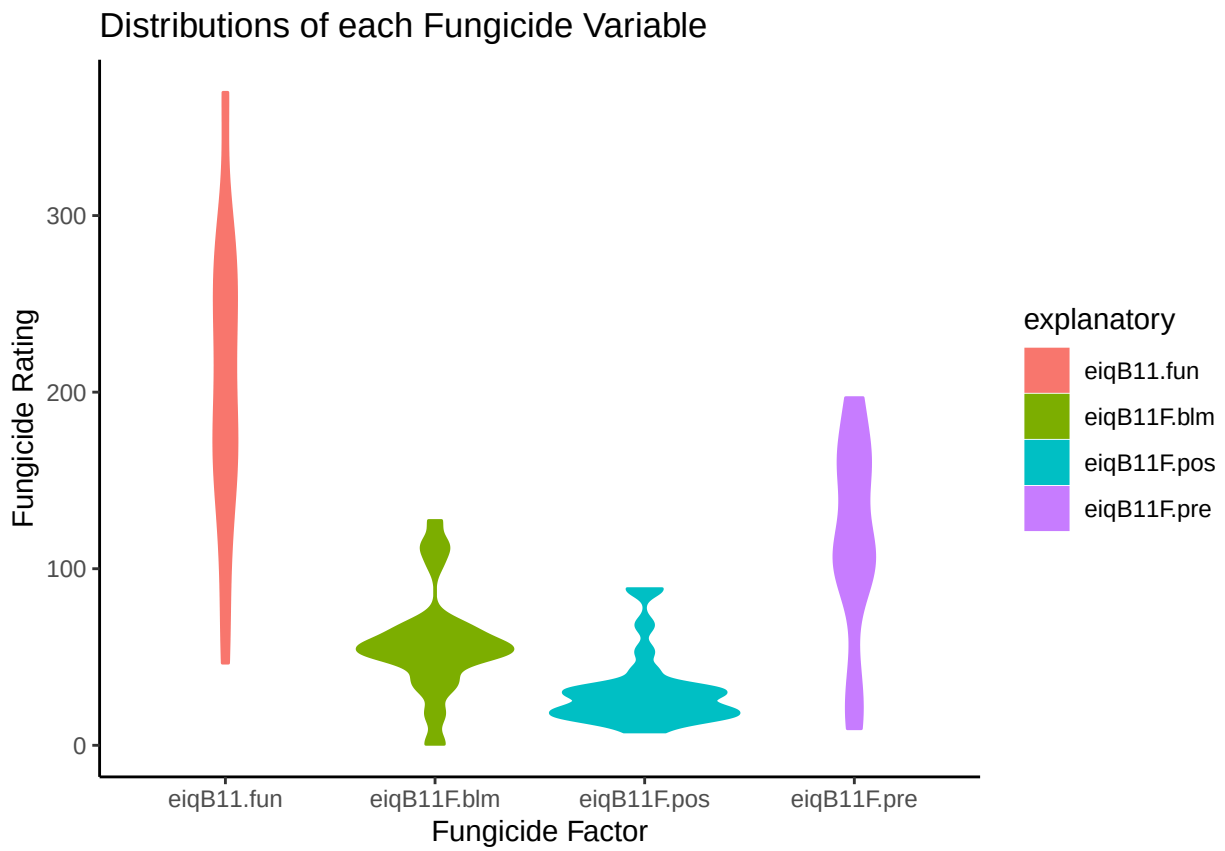
Code post 25/10

```
data_2012 <- day_data %>%
  filter(year == 4)

#Looking at violin plots of the data
```

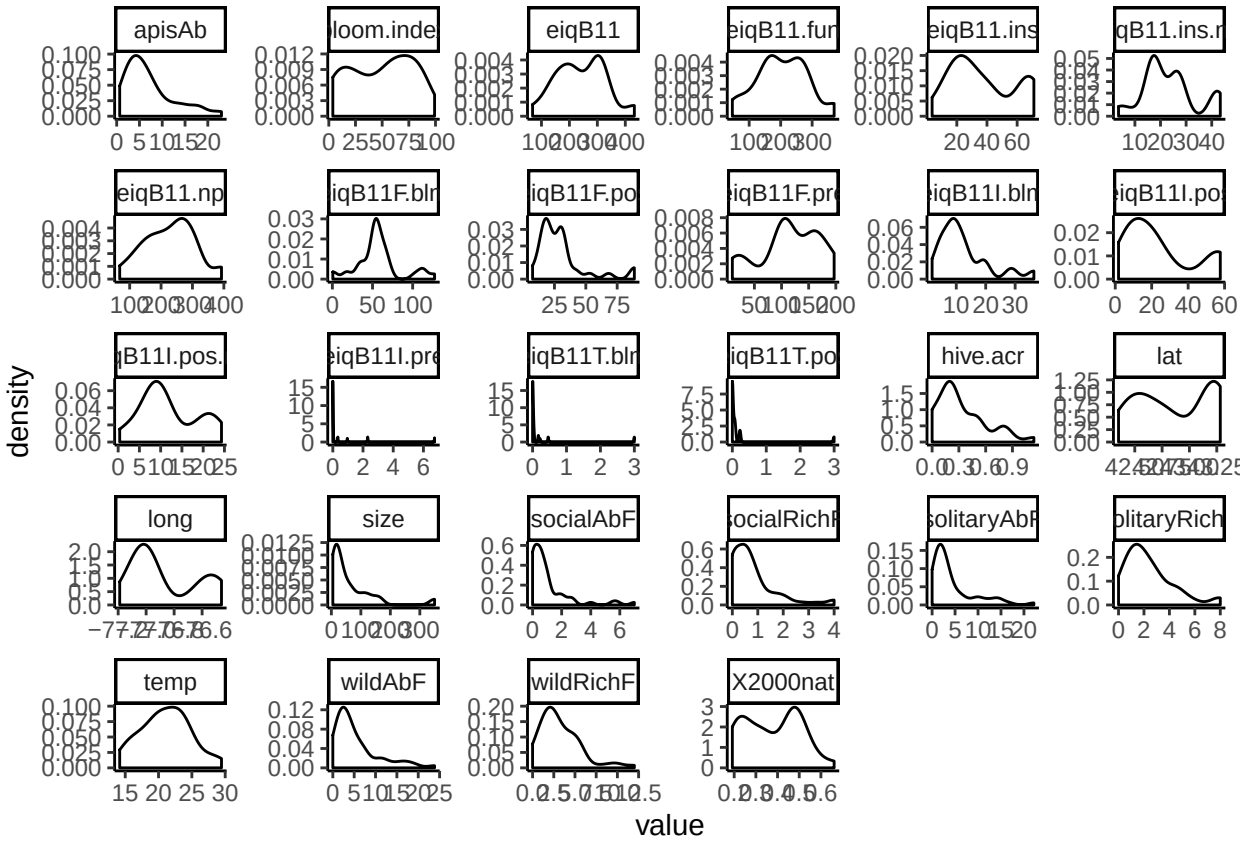
```
violin_data <- day_data %>%
  select(c("region":"X2000nat")) %>%
  gather(key = "explanatory", value = "value",-region, -day) %>%
  na.omit()

violin_plot <- function(x, xlab, ylab, title){
 x %>% ggplot() +
    geom_violin(aes(x = factor(explanatory), y = value, fill = explanatory, colour = explanatory)) +
    ylab(ylab) +
    xlab(xlab) +
    ggtitle(title) +
    theme(legend.position = "none") +
    theme_classic()
}

violin_plot_bees <- violin_data %>%
  subset(explanatory %in% colnames(day_data[4:12])) %>%
  violin_plot("Bee Factor", "Bee Rating", "Distributions of each Bee Variable")
violin_plot_bees
```



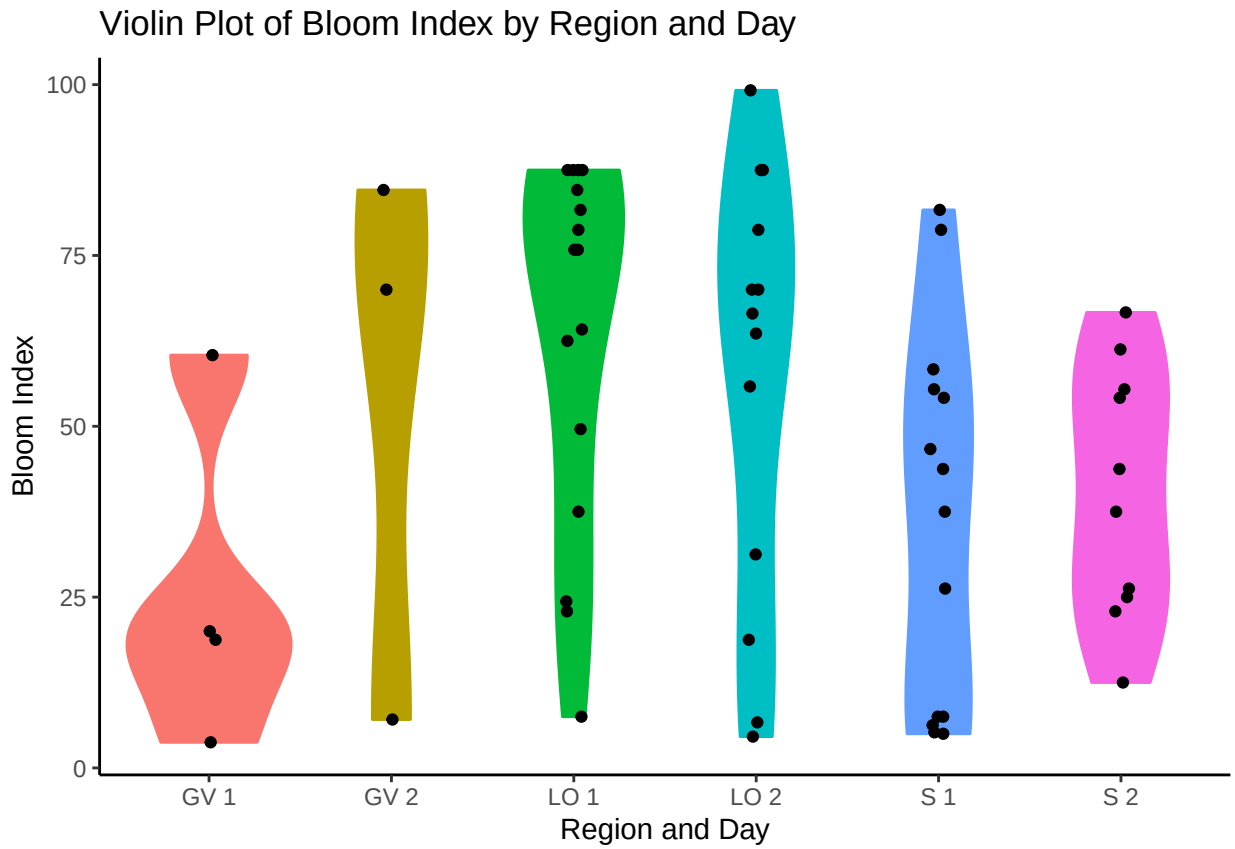

```
violin_plot_fungicides <- violin_data %>%
  subset(explanatory %in% colnames(day_data[c(19,22,23,24)])) %>%
  violin_plot("Fungicide Factor","Fungicide Rating","Distributions of each Fungicide Variable")
violin_plot_fungicides
```




```
violin_plot_insecticide <- violin_data %>%
  subset(explanatory %in% colnames(day_data[c(20,21,25:28)])) %>%
  violin_plot("Insecticide Factor", "Insecticide Rating", "Distributions of each Insecticide Variable")

#Distributions of all variables
distributions <- violin_data %>%
  ggplot() +
  geom_density(aes(value)) +
  facet_wrap(~explanatory, scales = "free") +
  theme_classic()
distributions
```




```
#Bloom values - particularly not ideal as it looks like the day 1 / day 2 actually is just random
#lol not even in relation to bloom levels
bloom_plot <- day_data %>%
  group_by(region, day) %>%
  mutate(group = paste(region, day)) %>%
  ggplot(aes(x= group, y = bloom.index)) +
  geom_violin(aes(fill = group, colour = group)) +
  geom_jitter(height = 0, width = 0.05) +
  theme_classic() +
  theme(legend.position = "none") +
  labs(x = "Region and Day", y = "Bloom Index", title = "Violin Plot of Bloom Index by Region and Day")
bloom_plot
```


Violin Plot of Bloom Index by Region and Day
Bloom Index
100
75
50
25
0
GV 1
GV 2
LO 1
LO 2
S 1
S 2
Region and Day