

High variability in the attractiveness of municipally-planted ecorative plants to pollinators

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packages

```
library(ggplot2)
library(readxl)
library(forcats)
library(glmTMB)
library(dplyr)
library(DHARMa)
library(multcomp)
library(emmeans)
library(eoffice)
library(gridExtra)
library(car)
```

input data, subsetting

```
data <- read_excel("municipal_pollinator_data_merged_bumblebees.xlsx",
  sheet = "global_database_goodnames")

ants <- subset (data, insect_group == "Ants")
flies <- subset (data, insect_group == "Other flies")
honeybees <- subset (data, insect_group == "Honey bees")
wasps <- subset (data, insect_group == "Wasps")
wildbees <- subset (data, insect_group == "Wild bees")

bees_and_wildbees <- rbind(honeybees, wildbees)
bees_wildbees_flies_wasps <- rbind(honeybees, wildbees, flies, wasps)
```

plots

plot of all insect visitation rates for all cultivars

First some summary statistics: mean visitation rate for each cultivar

```
mean_insectsM2 <- data %>%
  group_by(cultivar) %>%
  summarise(mean_insects_m2 = mean(insects_m2_full_coverage, na.rm = TRUE))
```

```
mean_insectsM2
```

```
## # A tibble: 35 x 2
##   cultivar                                mean_insects_m2
##   <chr>                                <dbl>
## 1 "Achillea filipendulina"              0.160
## 2 "Alcaltheae spp."                    0.529
## 3 "Anemone japonica"                   0.914
## 4 "Aster ageratoides"                  1.61
## 5 "Begonia semperflorens \"Eureka Scarlet\"" 0.377
## 6 "Begonia semperflorens \"Eureka White\""  0.318
## 7 "Begonia semperflorens \"red\""          0.735
## 8 "Begonia semperflorens \"white\""        0.334
## 9 "Bistorta affinis"                   0.857
## 10 "Campanula persicifolia"             0.828
## # i 25 more rows
```

now some descriptive plots

```
# mean bar plot
all_insects_by_cultivar_plot <- ggplot(data, aes(x = reorder(cultivar, insects_m2_full_coverage), y = insects_m2_full_coverage)) +
  scale_y_continuous(expand = c(0, 0)) +
  coord_cartesian(ylim = c(0, 6)) +
  stat_summary(fun.y = "mean", geom = "bar", size = 3) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 0, hjust = 1, vjust = 0.3),
```

```

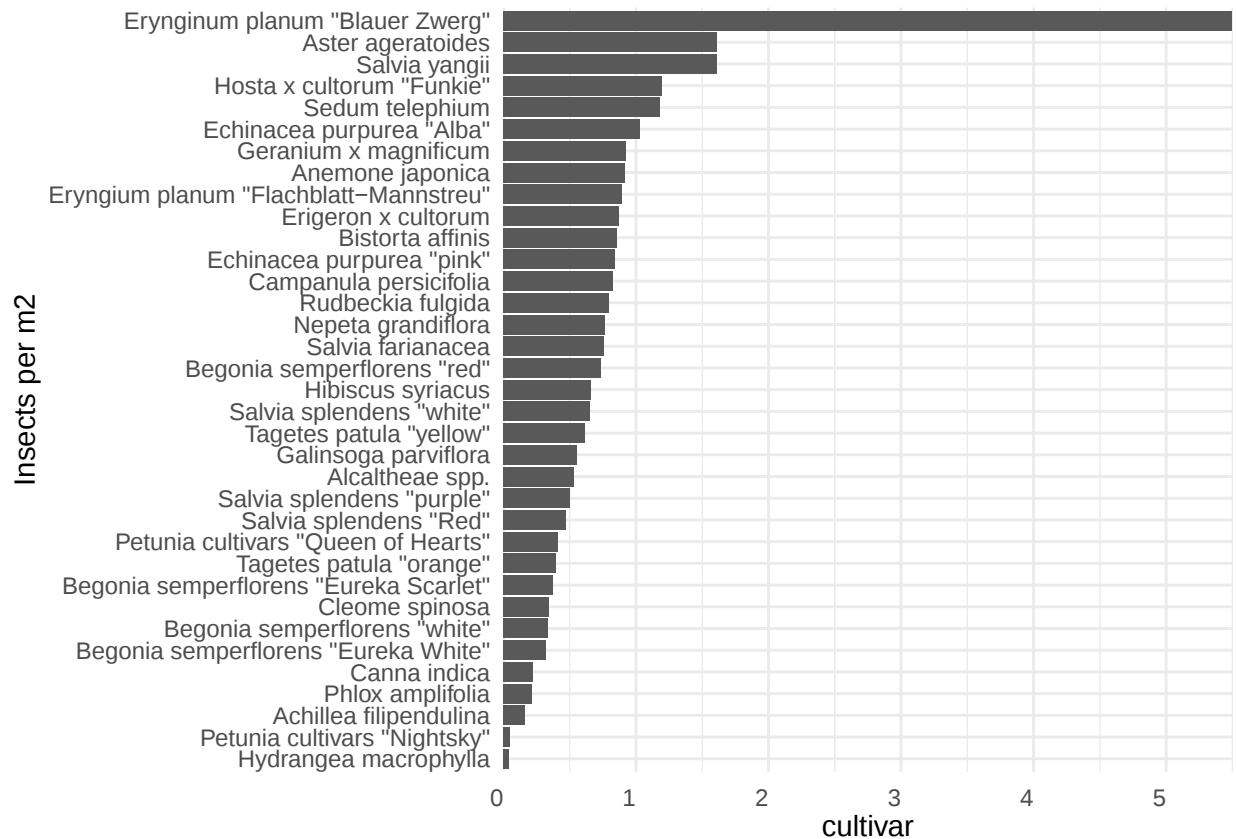
axis.text.y = element_text(angle = 0, hjust = 1, vjust = 0.5)) + # Set angle to 0 for the Y-axis
labs(x = "Insects per m2", y = "cultivar")

# Rotate the plot by 90 degrees
all_insects_by_cultivar_plot <- all_insects_by_cultivar_plot + coord_flip()

## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.

plot (all_insects_by_cultivar_plot)

```



```

#topptx (all_insects_by_cultivar_plot, "fig2_all_insects_by_cultivar_plot.pptx", width = 6, height = 8)

```

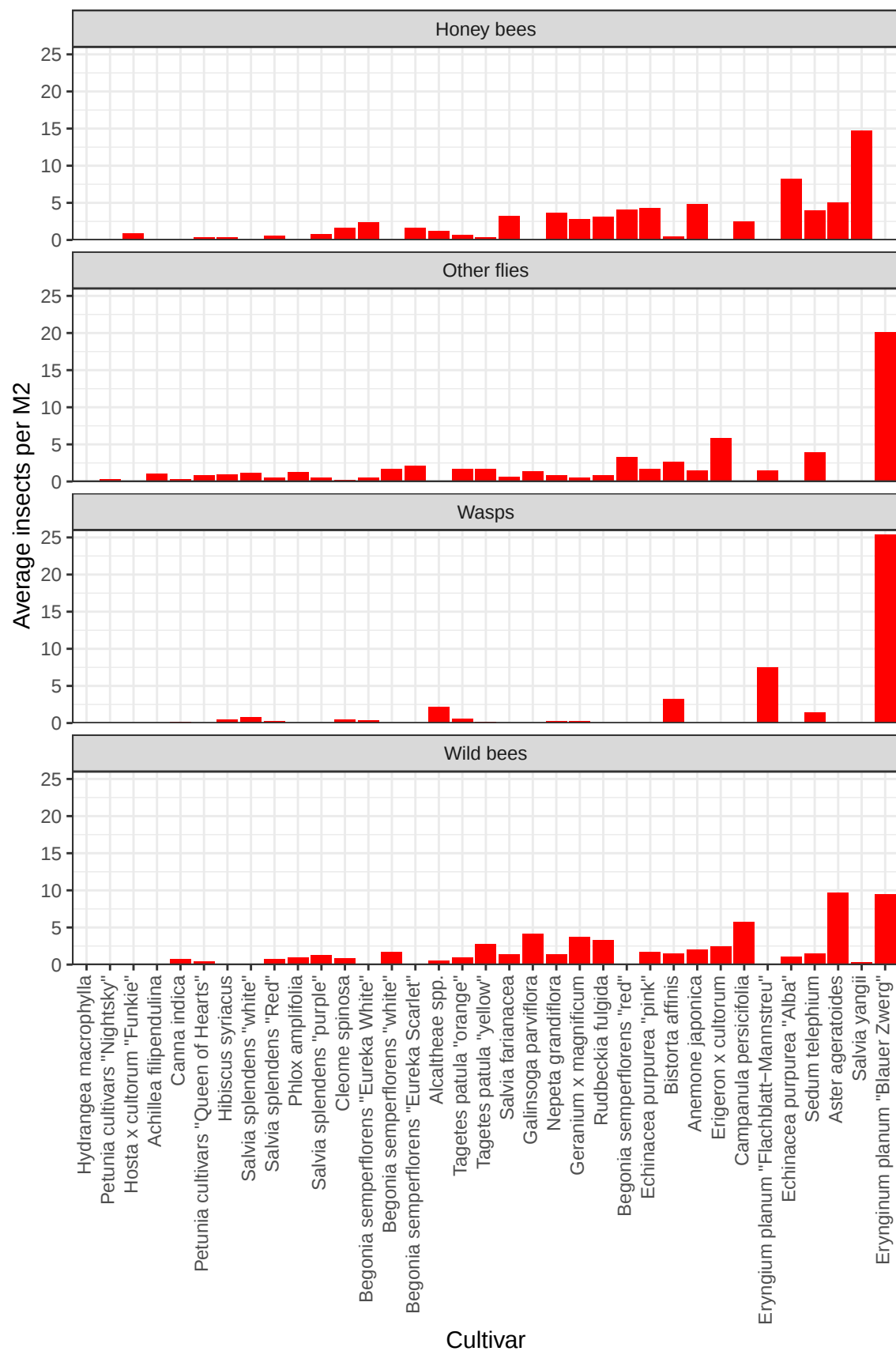
Now individual plots of cultivar attractiveness for the top 4 most common insect groups (honeybees wildbees flies ants wasps)

```

insectplot_facet_common <- ggplot (bees_wildbees_flies_wasps, aes(x = reorder(cultivar, insects_m2_full,
  facet_wrap(~ insect_group, nrow = 4, ncol = 1)+
  scale_y_continuous(expand = c(0, 0)) + # forces X axis to 0, but in this case is overridden by ribbon
  coord_cartesian(ylim = c(0, 26)) +
  stat_summary(fun.y = "mean", geom = "bar", size = 3, fill = "red") +
  ylab("Average insects per M2") +
  xlab("Cultivar") +
  theme_bw(15) +

```

```
theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.3))  
  
plot (insectplot_facet_common)
```



Total contributions of cultivars and insect groups, in terms of insects per m2

Contribution of each insect group to total

First some summary statistics

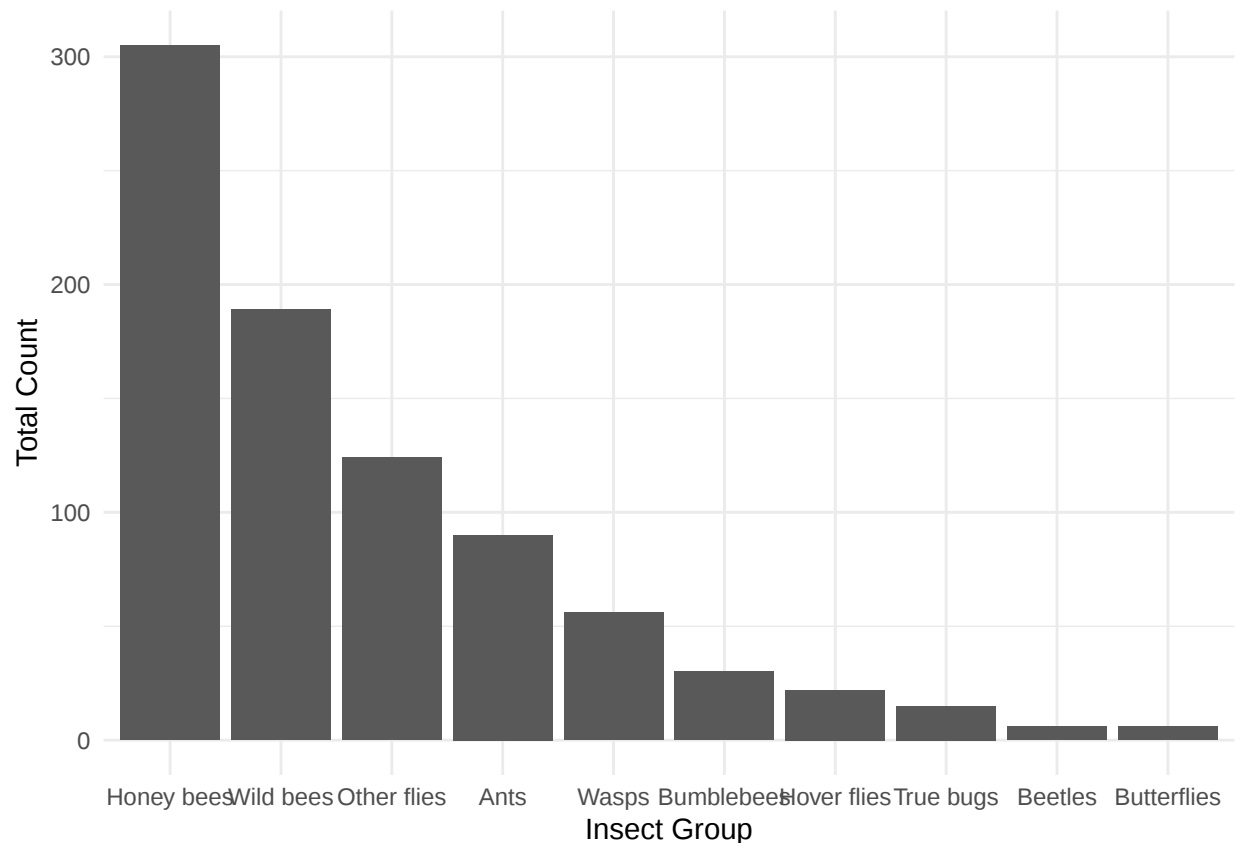
```
data_summary <- data %>%  
  group_by(insect_group) %>%  
  summarise(total_count = sum(count)) %>%  
  mutate(percentage = (total_count / sum(total_count)) * 100) %>%  
  arrange(desc(percentage))
```

data_summary

```
## # A tibble: 10 x 3  
##   insect_group total_count percentage  
##   <chr>         <dbl>      <dbl>  
## 1 Honey bees      305      36.2  
## 2 Wild bees       189      22.4  
## 3 Other flies     124      14.7  
## 4 Ants            90      10.7  
## 5 Wasps           56       6.64  
## 6 Bumblebees      30       3.56  
## 7 Hover flies     22       2.61  
## 8 True bugs       15       1.78  
## 9 Beetles         6        0.712  
## 10 Butterflies    6        0.712
```

first just one bar chart showing contribution of all insect groups

```
# Calculate the total count for each insect group  
total_counts <- data %>%  
  group_by(insect_group) %>%  
  summarise(total_count = sum(count)) %>%  
  arrange(desc(total_count)) # Order by total count in descending order  
  
# Create a bar chart  
insect_contribution_plot <- ggplot(total_counts, aes(x = reorder(insect_group, -total_count), y = total_count)) +  
  geom_bar(stat = "identity") +  
  labs(x = "Insect Group",  
       y = "Total Count") +  
  theme_minimal()  
  
plot (insect_contribution_plot)
```



```
#topptx (insect_contribution_plot, "insect_contribution_plot.pptx", width = 6, height = 6)
```

Insect group visitation proportion by cultivar

This helps us see who the visitors are to each cultivar

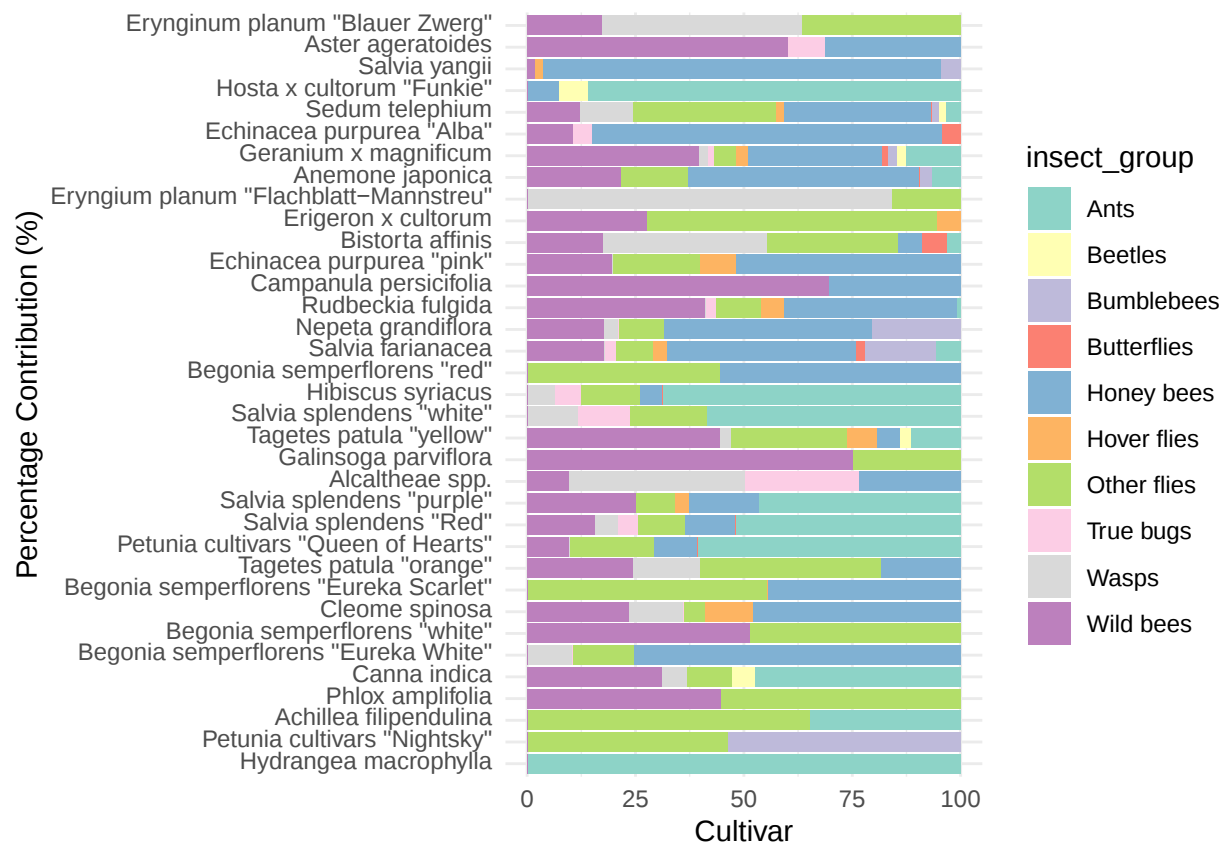
```
# Calculate the percentage contribution of 'insects_m2_full_coverage' for each 'insect_group' within ea
data_percent <- data %>%
  group_by(cultivar, insect_group) %>%
  summarise(total_insects_m2 = sum(insects_m2_full_coverage),
            original_values = mean(insects_m2_full_coverage)) %>%
  group_by(cultivar) %>%
  mutate(percentage = total_insects_m2 / sum(total_insects_m2) * 100)
```

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

```
# Create a stacked bar chart showing the percentage contribution
filledstackedplot_cultivar <- ggplot(data_percent, aes(x = reorder(cultivar, original_values), y = perc
  geom_bar(stat = "identity") +
  labs(y = "Cultivar", x = "Percentage Contribution (%)") + # Swap x and y axis labels
  scale_fill_brewer(palette = "Set3") +
  theme_minimal() +
  theme(axis.text.y = element_text(angle = 0, hjust = 1, vjust = 0.3)) +
```

```
coord_flip()

# Display the plot
plot(filledstackedplot_cultivar)
```



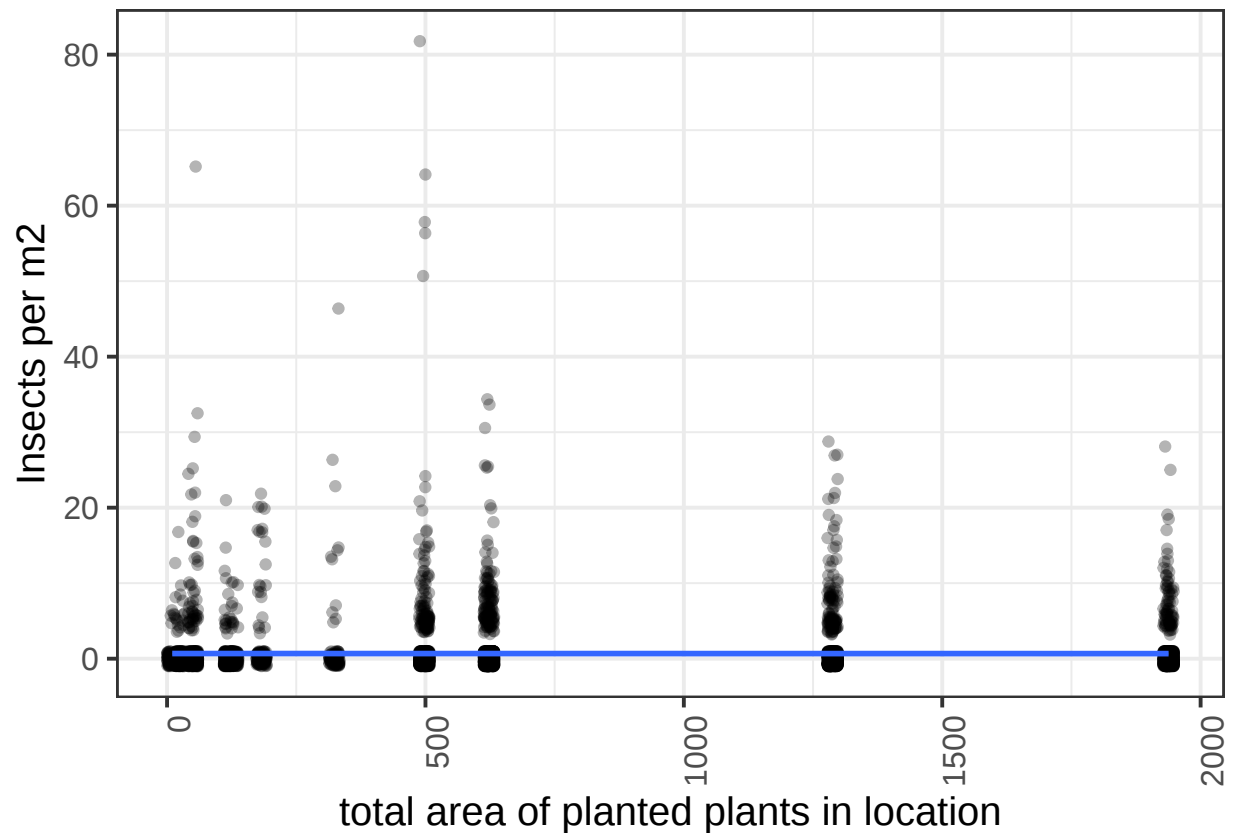
```
#topptx (filledstackedplot_cultivar, "fig3_filledstackedplot_cultivar.pptx", width = 6, height = 8)
```

total planted area size vs insect visitation rate

Various publications claim that there is no relationship between planted area size and insect visitation rates per unit area. I will quickly confirm visually.

```
ggplot (data, aes(x = total_area_cultivars, y = insects_m2_full_coverage)) +
geom_jitter(width = 10, height = 1, alpha = 0.3) +
geom_smooth(method = "lm") +
theme_bw(15) +
theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
labs( x = "total area of planted plants in location", y = "Insects per m2")
```

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



Confirmed. No apparent effect. Naturally, this is also heavily skewed by the zero inflation, but certainly nothing obvious here. A quick statistical analysis to be found in the stats part.

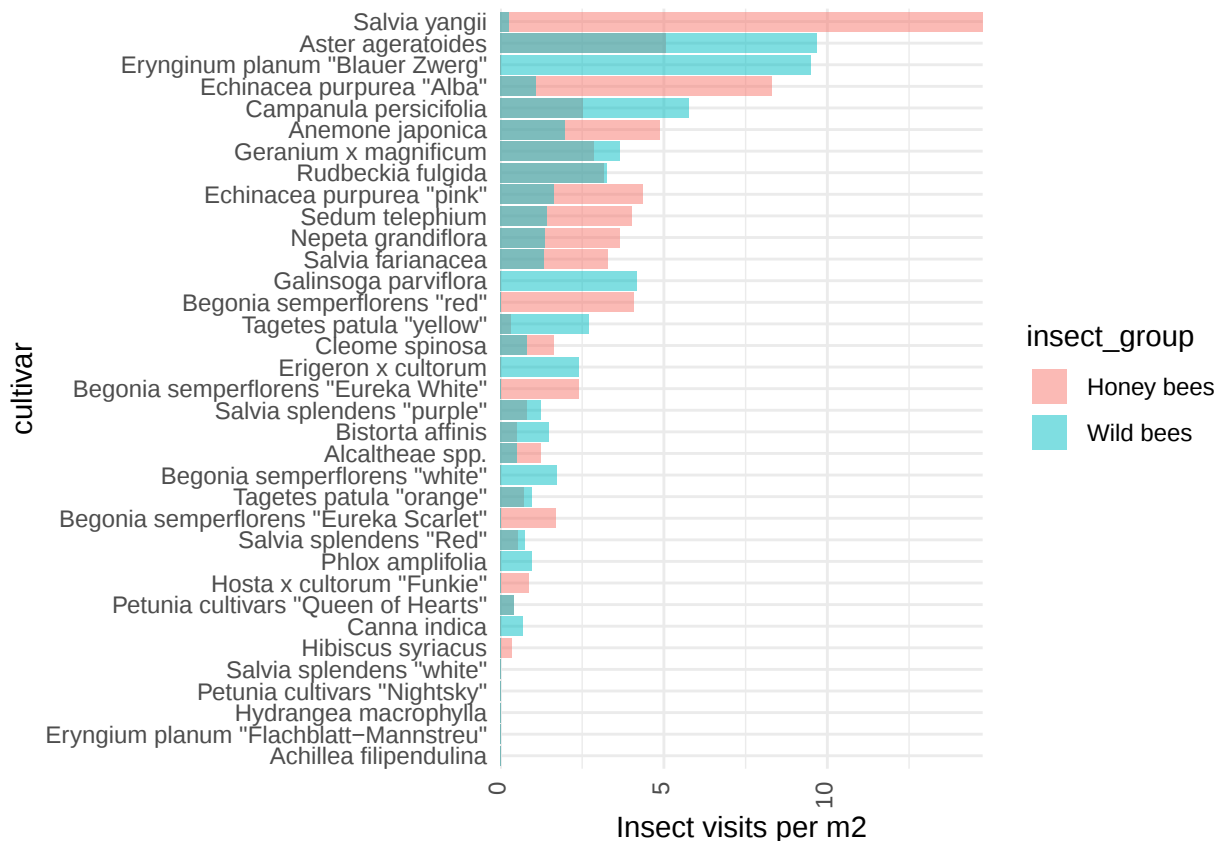
Wild bees and honeybees - plots

To reduce dimensionality and pursue clear questions, here we are focussing in on just wild bees and honeybees. Is there an overlap between wild bees and honeybees? What plants do wild bees like but honeybees don't?

```
fig3_honey_wildbees <- ggplot (bees_and_wildbees, aes(x = reorder(cultivar,insects_m2_full_coverage), y =
  scale_y_continuous(expand = c(0, 0)) + # forces X axis to 0, but in this case is overridden by ribbon
  coord_cartesian(ylim = c(0, 20)) +
  stat_summary(fun.y = "mean", geom = "bar", shape = 23, size = 3, alpha = 0.5) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.3)) + # hjust and vjust nudge the
  labs( x = "cultivar", y = "Insect visits per m2") +
  coord_flip()
```

```
## Coordinate system already present. Adding new coordinate system, which will
## replace the existing one.
```

```
plot (fig3_honey_wildbees)
```



```
#topptx (fig3_honey_wildbees, "fig3_wildvshoney.pptx", width = 6, height = 6)
```

some descriptive states here:

sum of count

```
# Calculate the sum of "count" for each combination of "cultivar" and "insect_group"
bees_and_wildbees %>%
  group_by(cultivar, insect_group) %>%
  summarise(total_count = sum(count))
```

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

```
## # A tibble: 70 x 3
## # Groups:   cultivar [35]
##   cultivar                insect_group total_count
##   <chr>                  <chr>          <dbl>
## 1 "Achillea filipendulina" Honey bees         0
## 2 "Achillea filipendulina" Wild bees         0
## 3 "Alcaltheae spp."       Honey bees         2
## 4 "Alcaltheae spp."       Wild bees          1
## 5 "Anemone japonica"      Honey bees        27
## 6 "Anemone japonica"      Wild bees        12
## 7 "Aster ageratoides"    Honey bees         7
```

```
## 8 "Aster ageratoides" Wild bees 13
## 9 "Begonia semperflorens \"Eureka Scarlet\"" Honey bees 4
## 10 "Begonia semperflorens \"Eureka Scarlet\"" Wild bees 0
## # i 60 more rows
```

```
bees_and_wildbees %>%
  group_by(insect_group) %>%
  summarise(total_count = sum(count))
```

```
## # A tibble: 2 x 2
##   insect_group total_count
##   <chr>         <dbl>
## 1 Honey bees      305
## 2 Wild bees       189
```

statistical analysis

Questions we want to ask: - do cultivars differ in attractiveness overall? - do cultivars differ in attractiveness for specific target groups? - does total patch area affect insect visitation rates - then do pairwise comparisons - which cultivars has more wild bees than honeybees?

do cultivars differ in attractiveness?

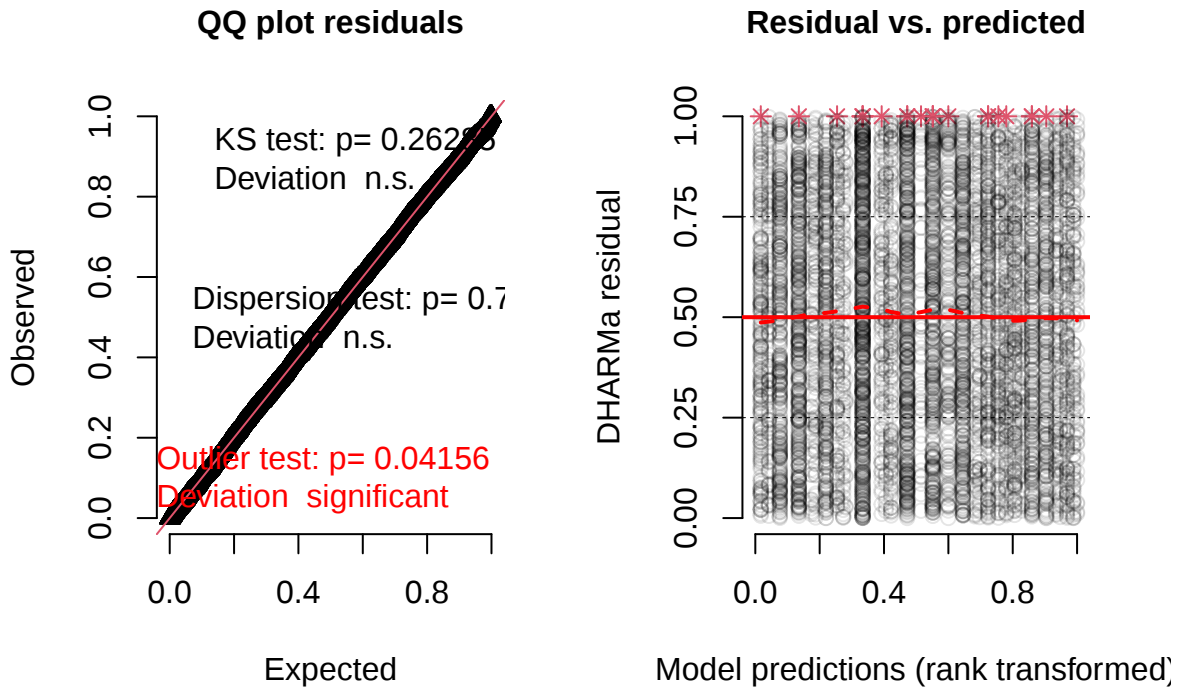
```
m1 <- glmmTMB(insects_m2_full_coverage ~ cultivar
              + (1 | location),
              ziformula=~1,
              family=nbinom1,
              data = data)
```

looking at results, testing model fit

```
# testing model fit
simulateResiduals(m1, n = 500, plot = T) #dharma
```

DHARMA: testOutliers with type = binomial may have inflated Type I error rates for integer-valued dis

DHARMA residual



```
## Object of Class DHARMA with simulated residuals based on 500 simulations with refit = FALSE . See ?DHARMA
##
## Scaled residual values: 0.7908908 0.966 0.988 0.4696725 0.3231412 0.5229729 0.06865622 0.1879041 0.8
```

```
# top level summary
Anova (m1)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: insects_m2_full_coverage
##           Chisq Df Pr(>Chisq)
## cultivar 416.29 34 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#adjust for multiple comparisons
adjX <- glht(m1) # multcomp
summary(adjX, test = adjusted("BH"))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: glmmTMB(formula = insects_m2_full_coverage ~ cultivar + (1 |
```

```

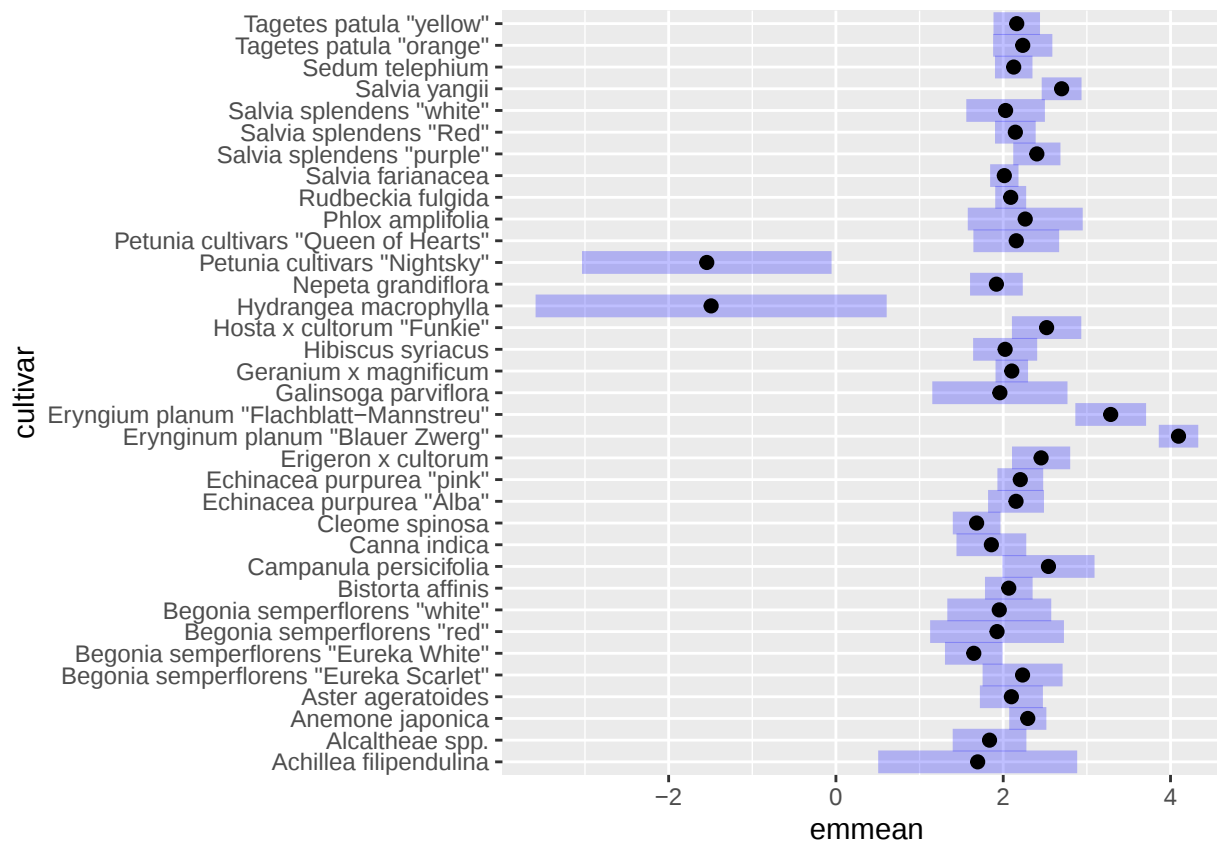
##      location), data = data, family = nbinom1, ziformula = ~1,
##      dispformula = ~1)
##
## Linear Hypotheses:
##
##                                     Estimate Std. Error z value
## (Intercept) == 0                    1.69469    0.60692   2.792
## cultivarAlcaltheae spp. == 0         0.14181    0.64412   0.220
## cultivarAnemone japonica == 0        0.59901    0.61460   0.975
## cultivarAster ageratoides == 0       0.40294    0.62316   0.647
## cultivarBegonia semperflorens "Eureka Scarlet" == 0 0.53668    0.65169   0.824
## cultivarBegonia semperflorens "Eureka White" == 0 -0.04651    0.62876  -0.074
## cultivarBegonia semperflorens "red" == 0          0.23150    0.72878   0.318
## cultivarBegonia semperflorens "white" == 0         0.25822    0.68265   0.378
## cultivarBistorta affinis == 0        0.37178    0.62214   0.598
## cultivarCampanula persicifolia == 0    0.84611    0.66669   1.269
## cultivarCanna indica == 0            0.16360    0.64022   0.256
## cultivarCleome spinosa == 0          -0.01248    0.62178  -0.020
## cultivarEchinacea purpurea "Alba" == 0    0.45830    0.62413   0.734
## cultivarEchinacea purpurea "pink" == 0    0.50941    0.61761   0.825
## cultivarErigeron x cultorum == 0        0.75820    0.63069   1.202
## cultivarEryngium planum "Blauer Zwerg" == 0    2.40088    0.61694   3.892
## cultivarEryngium planum "Flachblatt-Mannstreu" == 0 1.59038    0.64522   2.465
## cultivarGalinsoga parviflora == 0        0.26557    0.73107   0.363
## cultivarGeranium x magnificum == 0       0.40775    0.60995   0.669
## cultivarHibiscus syriacus == 0          0.32815    0.63489   0.517
## cultivarHosta x cultorum "Funkie" == 0      0.82405    0.64045   1.287
## cultivarHydrangea macrophylla == 0       -3.18657    1.22587  -2.599
## cultivarNepeta grandiflora == 0         0.22392    0.62556   0.358
## cultivarPetunia cultivars "Night sky" == 0   -3.23855    0.97183  -3.332
## cultivarPetunia cultivars "Queen of Hearts" == 0 0.46119    0.66103   0.698
## cultivarPhlox amplifolia == 0          0.56841    0.69933   0.813
## cultivarRudbeckia fulgida == 0          0.39484    0.60951   0.648
## cultivarSalvia farianacea == 0          0.31851    0.61009   0.522
## cultivarSalvia splendens "purple" == 0      0.70736    0.62108   1.139
## cultivarSalvia splendens "Red" == 0        0.45030    0.61740   0.729
## cultivarSalvia splendens "white" == 0       0.33364    0.65074   0.513
## cultivarSalvia yangii == 0             1.00350    0.61436   1.633
## cultivarSedum telephium == 0           0.43070    0.61380   0.702
## cultivarTagetes patula "orange" == 0       0.53862    0.63136   0.853
## cultivarTagetes patula "yellow" == 0      0.46713    0.62104   0.752
##
##                                     Pr(>|z|)
## (Intercept) == 0                    0.06106 .
## cultivarAlcaltheae spp. == 0         0.87580
## cultivarAnemone japonica == 0        0.78809
## cultivarAster ageratoides == 0       0.78809
## cultivarBegonia semperflorens "Eureka Scarlet" == 0 0.78809
## cultivarBegonia semperflorens "Eureka White" == 0 0.96872
## cultivarBegonia semperflorens "red" == 0          0.84762
## cultivarBegonia semperflorens "white" == 0         0.84044
## cultivarBistorta affinis == 0        0.78835
## cultivarCampanula persicifolia == 0    0.78809
## cultivarCanna indica == 0            0.87314
## cultivarCleome spinosa == 0          0.98398
## cultivarEchinacea purpurea "Alba" == 0    0.78809

```

```
## cultivarEchinacea purpurea "pink" == 0 0.78809
## cultivarErigeron x cultorum == 0 0.78809
## cultivarEryngium planum "Blauer Zwerg" == 0 0.00349 **
## cultivarEryngium planum "Flachblatt-Mannstreu" == 0 0.09595 .
## cultivarGalinsoga parviflora == 0 0.84044
## cultivarGeranium x magnificum == 0 0.78809
## cultivarHibiscus syriacus == 0 0.78835
## cultivarHosta x cultorum "Funkie" == 0 0.78809
## cultivarHydrangea macrophylla == 0 0.08171 .
## cultivarNepeta grandiflora == 0 0.84044
## cultivarPetunia cultivars "Nightsky" == 0 0.01507 *
## cultivarPetunia cultivars "Queen of Hearts" == 0 0.78809
## cultivarPhlox amplifolia == 0 0.78809
## cultivarRudbeckia fulgida == 0 0.78809
## cultivarSalvia farianacea == 0 0.78835
## cultivarSalvia splendens "purple" == 0 0.78809
## cultivarSalvia splendens "Red" == 0 0.78809
## cultivarSalvia splendens "white" == 0 0.78835
## cultivarSalvia yangii == 0 0.59723
## cultivarSedum telephium == 0 0.78809
## cultivarTagetes patula "orange" == 0 0.78809
## cultivarTagetes patula "yellow" == 0 0.78809
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- BH method)
```

```
#emmeans
```

```
meanie <- emmeans(m1, pairwise ~ cultivar)
# print (meanie) # no point plotting all pairwise comparisons for all pairs - we'd have a heck of a lot
plot (meanie)
```



honey vs wild bees - pairwise comps

Going to use the raw count, because we're going to compare only within cultivar. Means we can use poisson distribution too

Going to only look at top 6 most attractive cultivars:

```
unique(data$cultivar)
```

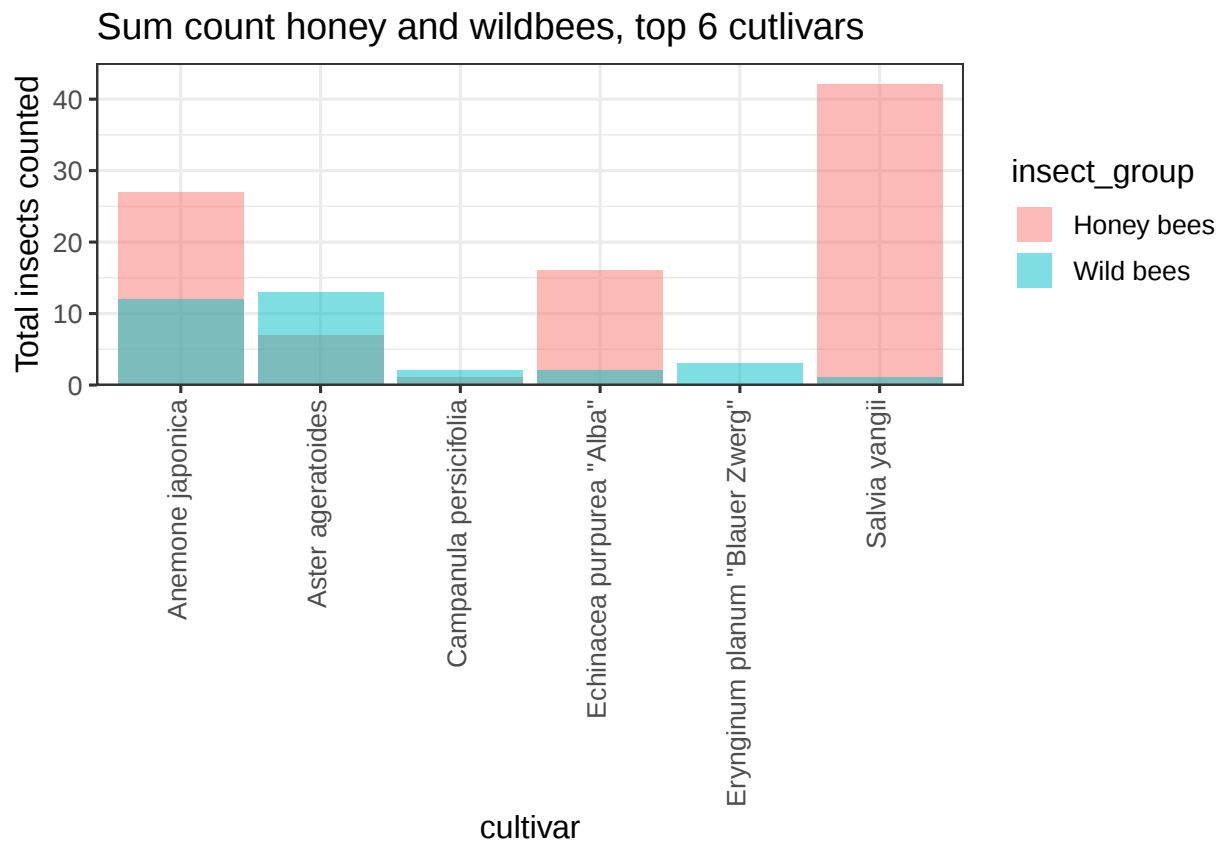
```
# List of cultivars to filter
selected_cultivars <- c("Salvia yangii", "Aster ageratoides", "Eryngium planum \"Blauer Zwerg\"", "Ech")

# Creating a subset dataset containing only the specified cultivars
top6cultivars <- bees_and_wildbees[bees_and_wildbees$cultivar %in% selected_cultivars, ]
```

make a figure, check all is in order

```
ggplot(top6cultivars, aes(x = cultivar, y = count, fill = insect_group)) +
  scale_y_continuous(expand = c(0, 0)) + # forces X axis to 0, but in this case is overridden by ribbon
  coord_cartesian(ylim = c(0, 45)) +
  stat_summary(fun.y = "sum", geom = "bar", shape = 23, size = 3, alpha = 0.5) +
  theme_bw(12) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.3)) + # hjust and vjust nudge the :
  labs(x = "cultivar", y = "Total insects counted", title = "Sum count honey and wildbees, top 6 cutlives")
```

```
## Warning in stat_summary(fun.y = "sum", geom = "bar", shape = 23, size = 3, :
## Ignoring unknown parameters: 'shape'
```



ok now lets see if we get do sensible modelling and pairwise comparisons with this

##NOTE IM USING THE RAW COUNT HERE, NOT THE M2 VARIABLE.

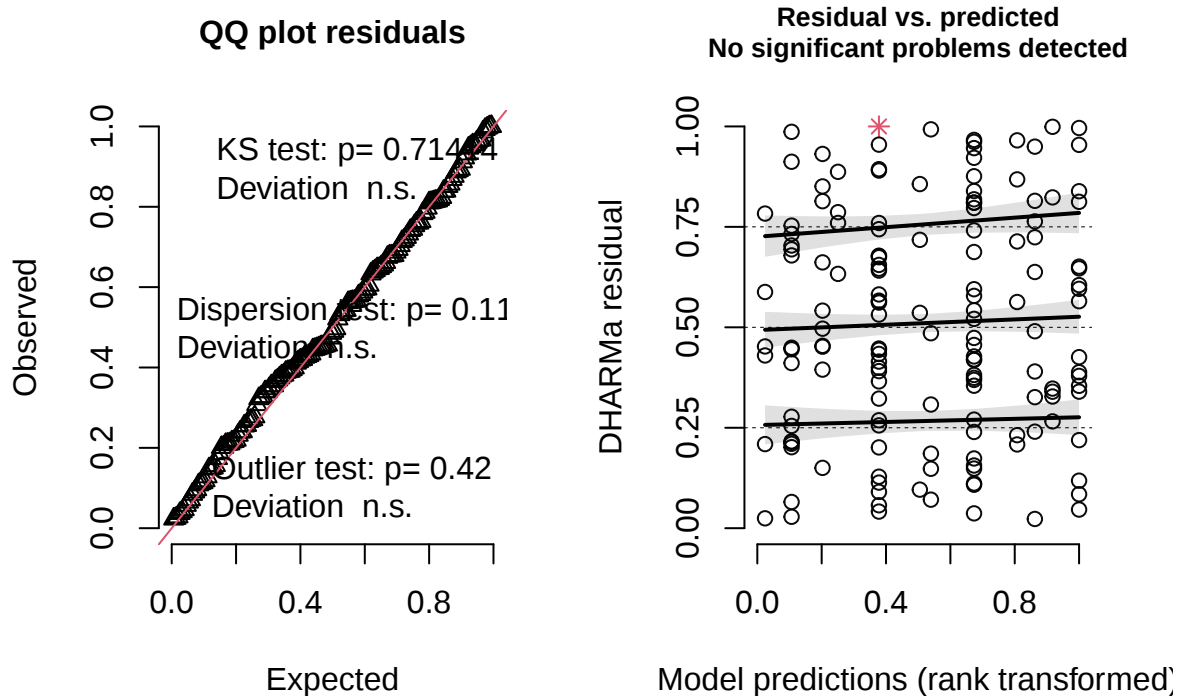
```
#model
m2beestop6 <- glmmTMB(count ~ as.factor(cultivar) * insect_group
  + (1 | location),
  ziformula=~1,
  family=poisson,
  data = top6cultivars)
```

```
Anova (m2beestop6)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: count
##
##              Chisq Df Pr(>Chisq)
## as.factor(cultivar)  9.0092  5  0.108698
## insect_group        6.8307  1  0.008960 **
## as.factor(cultivar):insect_group 19.5148  5  0.001541 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Dharma
simulateResiduals(m2beestop6, n = 500, plot = T) #dharma
```

DHARMA residual



```
## Object of Class DHARMA with simulated residuals based on 500 simulations with refit = FALSE . See ?DHARMA
##
## Scaled residual values: 0.7831745 0.9960342 0.3899917 0.8681415 0.3261663 0.8148226 0.3691393 0.4257...
```

```
adjX <- glht(m2beestop6) # multcomp
summary(adjX, test = adjusted("BH"))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: glmmTMB(formula = count ~ as.factor(cultivar) * insect_group +
## (1 | location), data = top6cultivars, family = poisson, ziformula = ~1,
## dispformula = ~1)
##
## Linear Hypotheses:
##
## (Intercept) == 0 Estimate -9.271e-02
## as.factor(cultivar)Aster ageratoides == 0 8.551e-03
## as.factor(cultivar)Campanula persicifolia == 0 -1.264e+00
## as.factor(cultivar)Echinacea purpurea "Alba" == 0 5.316e-01
## as.factor(cultivar)Eryngium planum "Blauer Zwerg" == 0 -1.957e+01
```

```

## as.factor(cultivar)Salvia yangii == 0          9.413e-01
## insect_groupWild bees == 0                    -7.861e-01
## as.factor(cultivar)Aster ageratoides:insect_groupWild bees == 0    1.389e+00
## as.factor(cultivar)Campanula persicifolia:insect_groupWild bees == 0 1.451e+00
## as.factor(cultivar)Echinacea purpurea "Alba":insect_groupWild bees == 0 -1.266e+00
## as.factor(cultivar)Erynginum planum "Blauer Zwerg":insect_groupWild bees == 0 1.992e+01
## as.factor(cultivar)Salvia yangii:insect_groupWild bees == 0         -2.897e+00
## Std. Error
## (Intercept) == 0          2.922e-01
## as.factor(cultivar)Aster ageratoides == 0    5.530e-01
## as.factor(cultivar)Campanula persicifolia == 0 1.038e+00
## as.factor(cultivar)Echinacea purpurea "Alba" == 0 3.520e-01
## as.factor(cultivar)Erynginum planum "Blauer Zwerg" == 0 8.003e+03
## as.factor(cultivar)Salvia yangii == 0        3.252e-01
## insect_groupWild bees == 0          3.624e-01
## as.factor(cultivar)Aster ageratoides:insect_groupWild bees == 0    6.188e-01
## as.factor(cultivar)Campanula persicifolia:insect_groupWild bees == 0 1.300e+00
## as.factor(cultivar)Echinacea purpurea "Alba":insect_groupWild bees == 0 8.461e-01
## as.factor(cultivar)Erynginum planum "Blauer Zwerg":insect_groupWild bees == 0 8.003e+03
## as.factor(cultivar)Salvia yangii:insect_groupWild bees == 0         1.080e+00
## z value
## (Intercept) == 0          -0.317
## as.factor(cultivar)Aster ageratoides == 0    0.015
## as.factor(cultivar)Campanula persicifolia == 0 -1.217
## as.factor(cultivar)Echinacea purpurea "Alba" == 0 1.510
## as.factor(cultivar)Erynginum planum "Blauer Zwerg" == 0 -0.002
## as.factor(cultivar)Salvia yangii == 0        2.894
## insect_groupWild bees == 0          -2.169
## as.factor(cultivar)Aster ageratoides:insect_groupWild bees == 0    2.244
## as.factor(cultivar)Campanula persicifolia:insect_groupWild bees == 0 1.116
## as.factor(cultivar)Echinacea purpurea "Alba":insect_groupWild bees == 0 -1.496
## as.factor(cultivar)Erynginum planum "Blauer Zwerg":insect_groupWild bees == 0 0.002
## as.factor(cultivar)Salvia yangii:insect_groupWild bees == 0         -2.682
## Pr(>|z|)
## (Intercept) == 0          0.9980
## as.factor(cultivar)Aster ageratoides == 0    0.9980
## as.factor(cultivar)Campanula persicifolia == 0 0.3831
## as.factor(cultivar)Echinacea purpurea "Alba" == 0 0.2694
## as.factor(cultivar)Erynginum planum "Blauer Zwerg" == 0 0.9980
## as.factor(cultivar)Salvia yangii == 0        0.0439
## insect_groupWild bees == 0          0.0902
## as.factor(cultivar)Aster ageratoides:insect_groupWild bees == 0    0.0902
## as.factor(cultivar)Campanula persicifolia:insect_groupWild bees == 0 0.3964
## as.factor(cultivar)Echinacea purpurea "Alba":insect_groupWild bees == 0 0.2694
## as.factor(cultivar)Erynginum planum "Blauer Zwerg":insect_groupWild bees == 0 0.9980
## as.factor(cultivar)Salvia yangii:insect_groupWild bees == 0         0.0439
##
## (Intercept) == 0
## as.factor(cultivar)Aster ageratoides == 0
## as.factor(cultivar)Campanula persicifolia == 0
## as.factor(cultivar)Echinacea purpurea "Alba" == 0
## as.factor(cultivar)Erynginum planum "Blauer Zwerg" == 0
## as.factor(cultivar)Salvia yangii == 0          *
## insect_groupWild bees == 0                      .

```

```
## as.factor(cultivar)Aster ageratoides:insect_groupWild bees == 0
## as.factor(cultivar)Campanula persicifolia:insect_groupWild bees == 0
## as.factor(cultivar)Echinacea purpurea "Alba":insect_groupWild bees == 0
## as.factor(cultivar)Eryngium planum "Blauer Zwerg":insect_groupWild bees == 0
## as.factor(cultivar)Salvia yangii:insect_groupWild bees == 0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- BH method)
```

```
#pairwise
meanie <- emmeans(m2beestop6, pairwise ~ insect_group|cultivar)
summary(meanie)
```

```
## $emmeans
## cultivar = Anemone japonica:
##   insect_group  emmean      SE df asymp.LCL asymp.UCL
## Honey bees    -0.0927    0.292 Inf  -6.65e-01    0.480
## Wild bees     -0.8788    0.371 Inf  -1.61e+00   -0.152
##
## cultivar = Aster ageratoides:
##   insect_group  emmean      SE df asymp.LCL asymp.UCL
## Honey bees    -0.0842    0.551 Inf  -1.16e+00    0.995
## Wild bees      0.5184    0.462 Inf  -3.87e-01    1.424
##
## cultivar = Campanula persicifolia:
##   insect_group  emmean      SE df asymp.LCL asymp.UCL
## Honey bees    -1.3566    1.045 Inf  -3.40e+00    0.692
## Wild bees     -0.6912    0.760 Inf  -2.18e+00    0.799
##
## cultivar = Echinacea purpurea "Alba":
##   insect_group  emmean      SE df asymp.LCL asymp.UCL
## Honey bees      0.4389    0.342 Inf  -2.32e-01    1.109
## Wild bees     -1.6128    0.758 Inf  -3.10e+00   -0.128
##
## cultivar = Eryngium planum "Blauer Zwerg":
##   insect_group  emmean      SE df asymp.LCL asymp.UCL
## Honey bees   -19.6665  8003.425 Inf  -1.57e+04 15666.758
## Wild bees    -0.5284    0.699 Inf  -1.90e+00    0.841
##
## cultivar = Salvia yangii:
##   insect_group  emmean      SE df asymp.LCL asymp.UCL
## Honey bees      0.8486    0.269 Inf   3.22e-01    1.375
## Wild bees     -2.8349    1.031 Inf  -4.86e+00   -0.813
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $contrasts
## cultivar = Anemone japonica:
##   contrast      estimate      SE df z.ratio p.value
## Honey bees - Wild bees    0.786    0.362 Inf   2.169  0.0301
##
## cultivar = Aster ageratoides:
##   contrast      estimate      SE df z.ratio p.value
```

```

## Honey bees - Wild bees  -0.603    0.499 Inf  -1.207  0.2276
##
## cultivar = Campanula persicifolia:
## contrast      estimate      SE  df z.ratio p.value
## Honey bees - Wild bees  -0.665    1.248 Inf  -0.533  0.5940
##
## cultivar = Echinacea purpurea "Alba":
## contrast      estimate      SE  df z.ratio p.value
## Honey bees - Wild bees   2.052    0.766 Inf   2.679  0.0074
##
## cultivar = Eryngium planum "Blauer Zwerg":
## contrast      estimate      SE  df z.ratio p.value
## Honey bees - Wild bees -19.138 8003.425 Inf  -0.002  0.9981
##
## cultivar = Salvia yangii:
## contrast      estimate      SE  df z.ratio p.value
## Honey bees - Wild bees   3.684    1.020 Inf   3.612  0.0003
##
## Results are given on the log (not the response) scale.

```