

Sticky Traps

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R Read Data

```
stickytrap.csv <- "/home/mwl04747/RTricks/12_Sticky_Traps/insect_sticky_trap_counts_15_traps.csv"

stickytrap.df <- read.csv(stickytrap.csv)

head(stickytrap.df)

##   Sticky.Trap.ID Distance..m.      Taxon Count
## 1          T0_1           0    Aedes aegypti   16
## 2          T0_1           0    Culex pipiens   29
## 3          T0_1           0 Anopheles gambiae   23
## 4          T0_1           0   Sciaridae spp.   23
## 5          T0_1           0 Cecidomyiidae spp.  23
## 6          T0_1           0 Chironomidae spp.  27

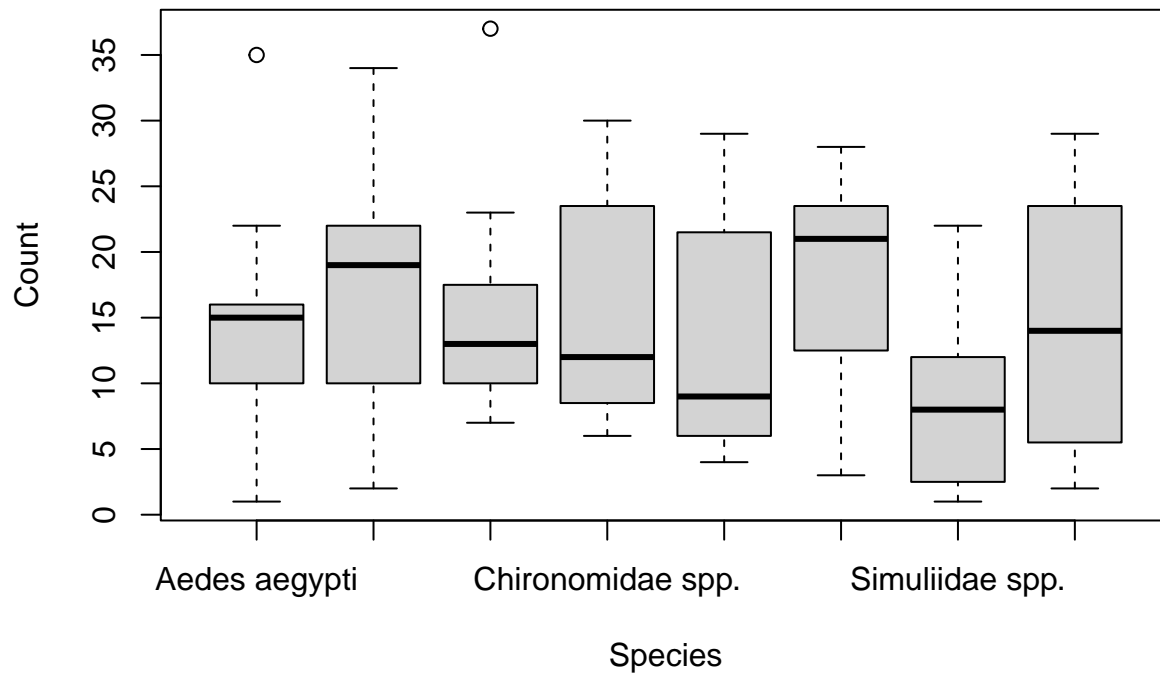
names(stickytrap.df)<- c("Trap", "Distance", "Species", "Count")

str(stickytrap.df)

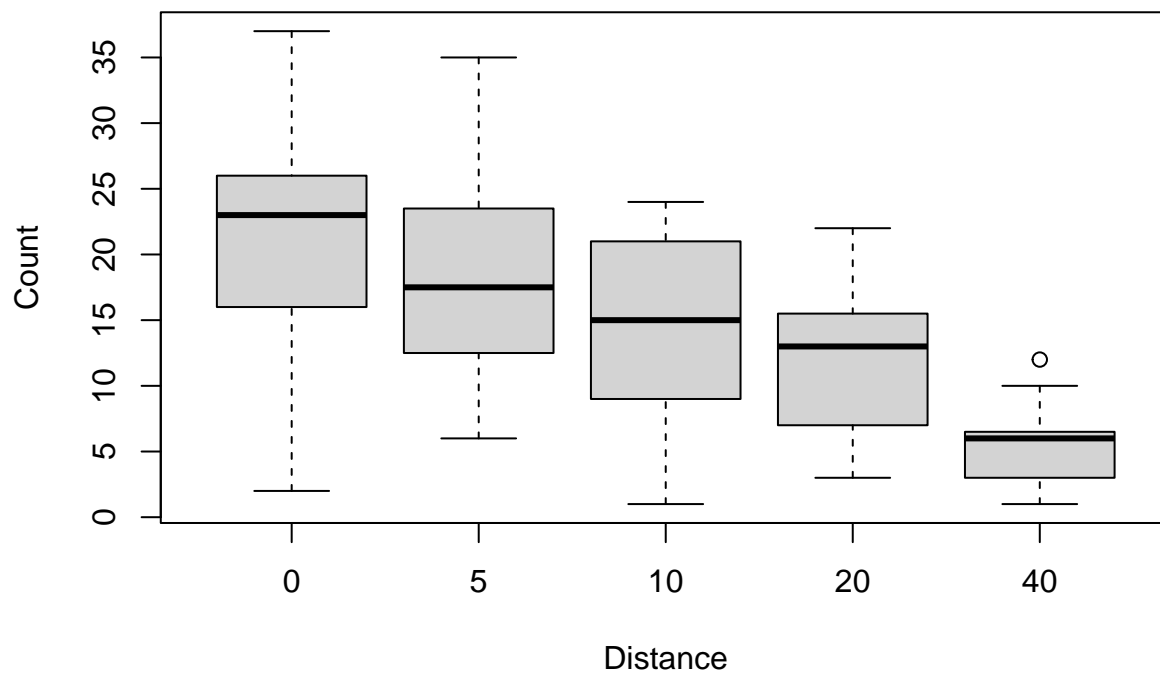
## 'data.frame':   120 obs. of  4 variables:
##  $ Trap      : chr  "T0_1" "T0_1" "T0_1" "T0_1" ...
##  $ Distance: int   0 0 0 0 0 0 0 0 0 0 ...
##  $ Species  : chr  "Aedes aegypti" "Culex pipiens" "Anopheles gambiae" "Sciaridae spp." ...
##  $ Count    : int  16 29 23 23 23 27 26 2 16 25 ...
```

Boxplot

```
# using r base
boxplot(Count ~ Species, data = stickytrap.df)
```



```
boxplot(Count ~ Distance, data = stickytrap.df)
```



Linear Model

```
# using r base
lm1 <- lm(Count ~ Species + Distance, data = stickytrap.df)
summary(lm1)
```

```
##
```

```
## Call:
## lm(formula = Count ~ Species + Distance, data = stickytrap.df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.4042  -4.3771   0.3542   3.5271  17.1083
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    19.80417    1.75122   11.309 < 2e-16 ***
## SpeciesAnopheles gambiae    2.26667    2.31891    0.977  0.3305
## SpeciesCecidomyiidae spp.    1.13333    2.31891    0.489  0.6260
## SpeciesChironomidae spp.    1.60000    2.31891    0.690  0.4916
## SpeciesCulex pipiens    -0.40000    2.31891   -0.172  0.8634
## SpeciesSciaridae spp.     3.06667    2.31891    1.322  0.1887
## SpeciesSimuliidae spp.    -5.40000    2.31891   -2.329  0.0217 *
## SpeciesTipulidae spp.     0.33333    2.31891    0.144  0.8860
## Distance        -0.38250    0.04099  -9.331 1.24e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.351 on 111 degrees of freedom
## Multiple R-squared:  0.485, Adjusted R-squared:  0.4479
## F-statistic: 13.07 on 8 and 111 DF, p-value: 3.87e-13
```

```
anova(lm1)
```

```
## Analysis of Variance Table
##
## Response: Count
##      Df Sum Sq Mean Sq F value    Pr(>F)
## Species    7  704.6   100.7   2.4958  0.02029 *
## Distance    1 3511.3  3511.3  87.0651 1.243e-15 ***
## Residuals 111 4476.6    40.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Linear Model for each species

```
# using r base
```

```
lm2 <- lm(Count ~ Distance, data = subset(stickytrap.df, subset = Species == "Aedes aegypti"))
anova(lm2)
```

```
## Analysis of Variance Table
##
## Response: Count
##      Df Sum Sq Mean Sq F value    Pr(>F)
## Distance    1 480.00  480.00  11.451 0.004891 **
## Residuals 13 544.93   41.92
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

create a loop of species

```
species <- unique(stickytrap.df$Species)
```

```
#species
```

```
for (i in 1:length(species)) {  
  print(species[i])  
}
```

```
## [1] "Aedes aegypti"
```

```
## [1] "Culex pipiens"
```

```
## [1] "Anopheles gambiae"
```

```
## [1] "Sciaridae spp."
```

```
## [1] "Cecidomyiidae spp."
```

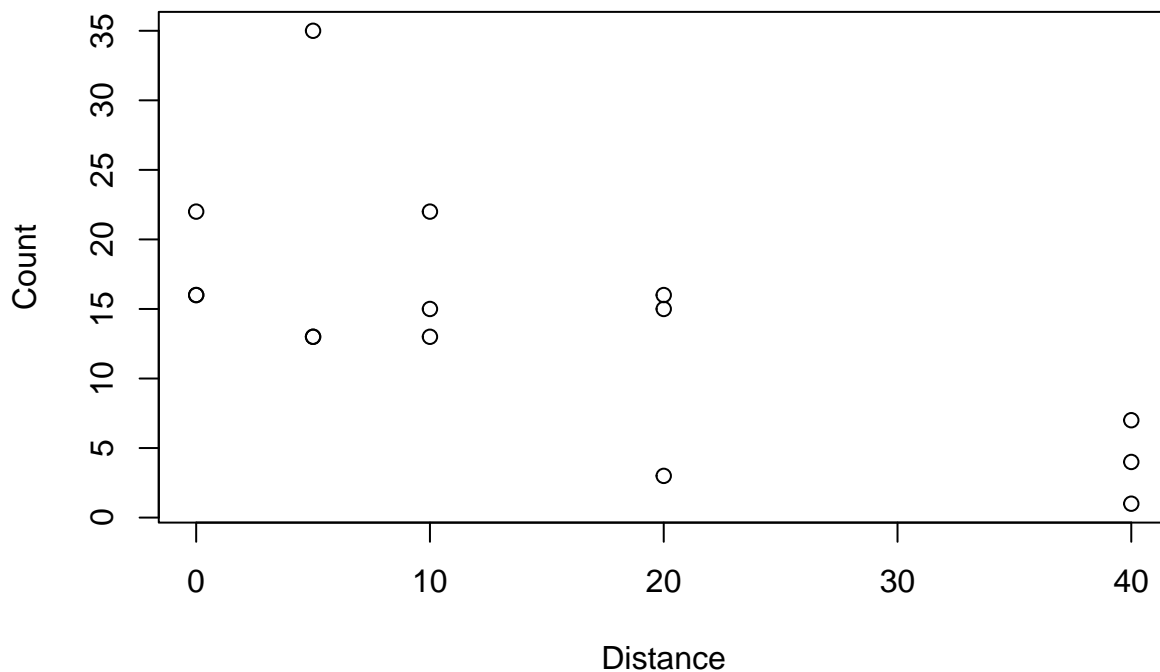
```
## [1] "Chironomidae spp."
```

```
## [1] "Tipulidae spp."
```

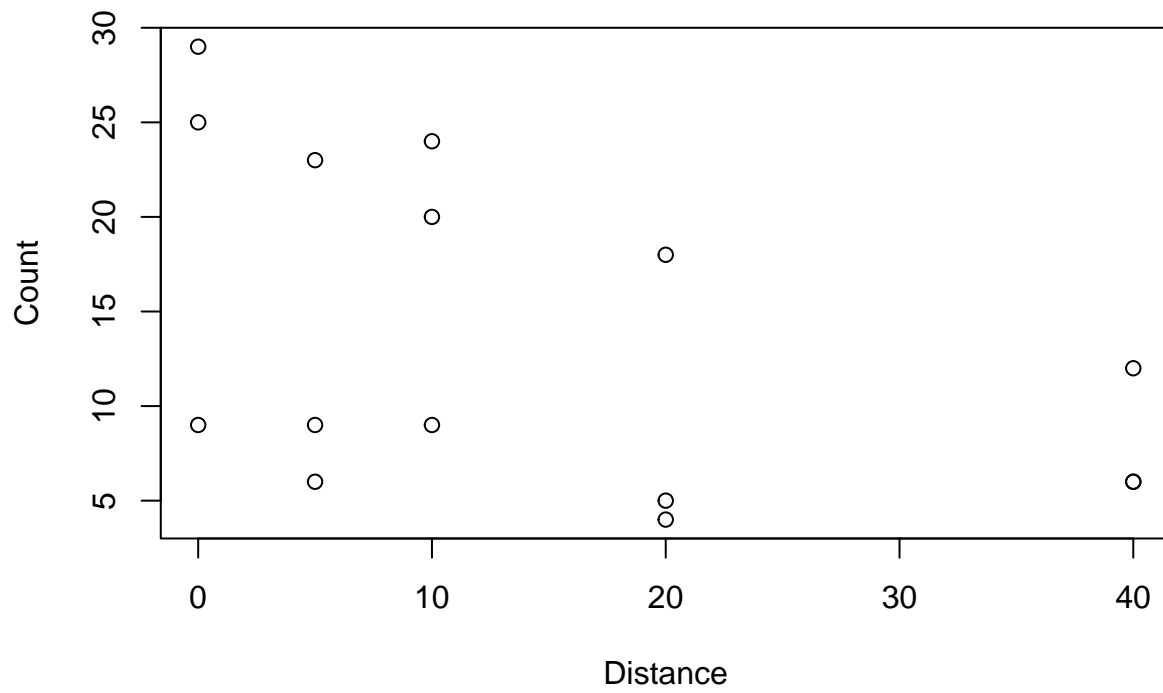
```
## [1] "Simuliidae spp."
```

plot with points

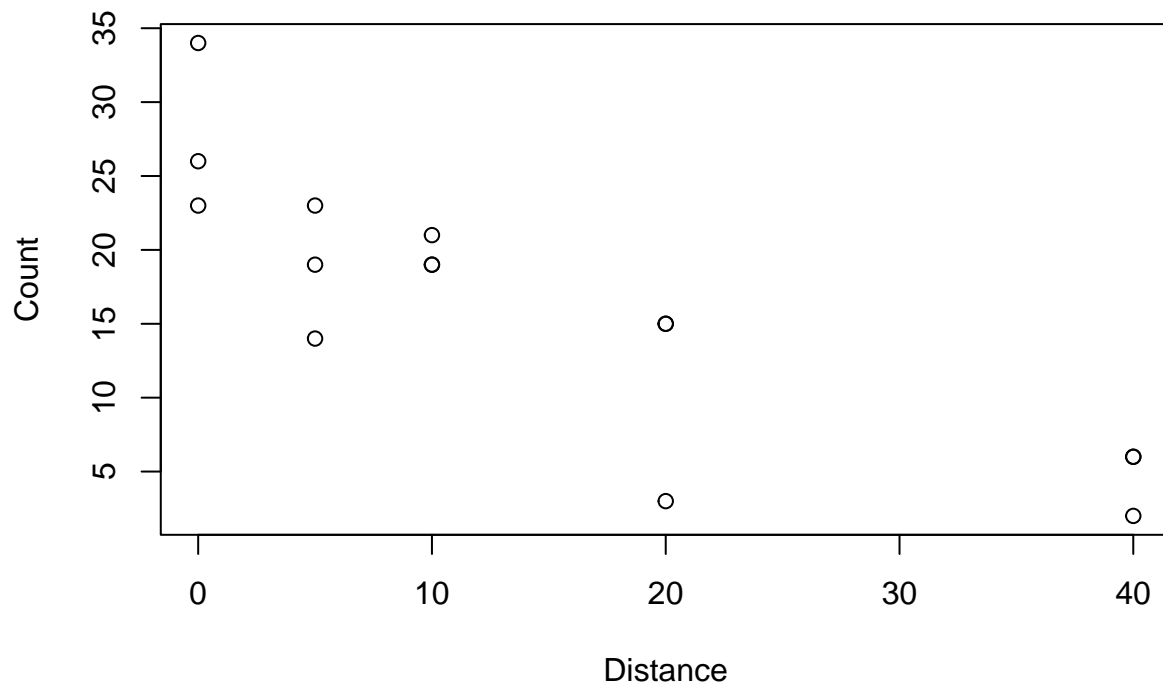
```
for (i in 1:length(species)) {  
  temp.df <- subset(stickytrap.df, subset = Species == species[i])  
  plot (Count ~ Distance, data = temp.df)  
  print(species[i])  
}
```



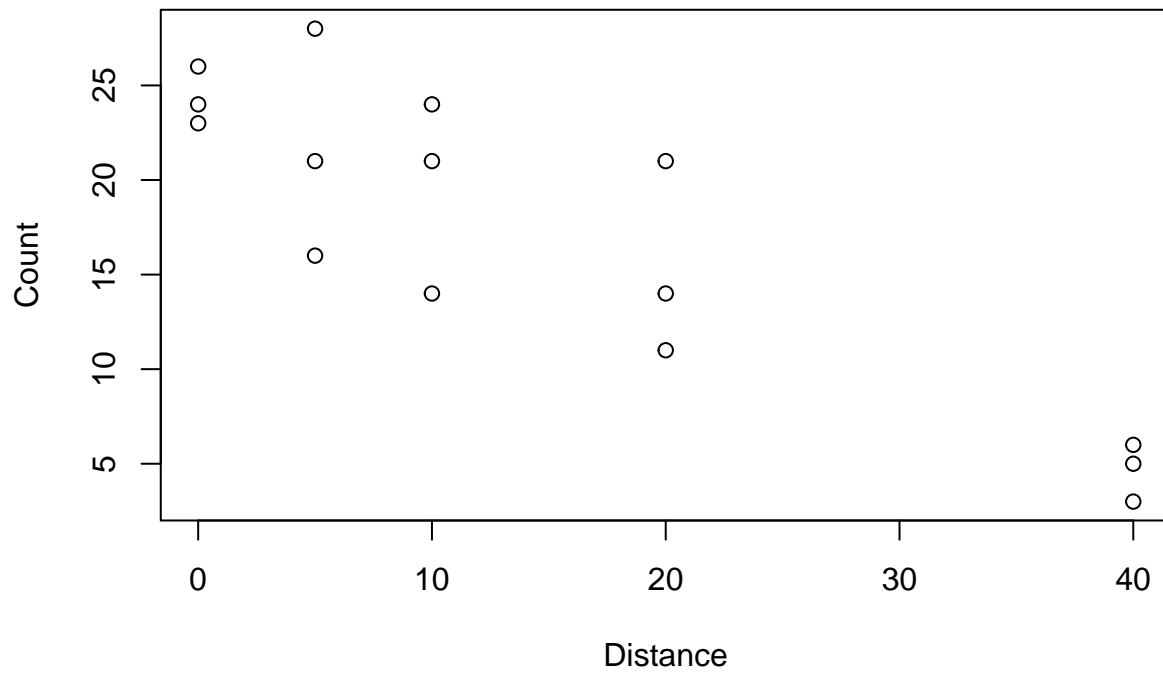
```
## [1] "Aedes aegypti"
```



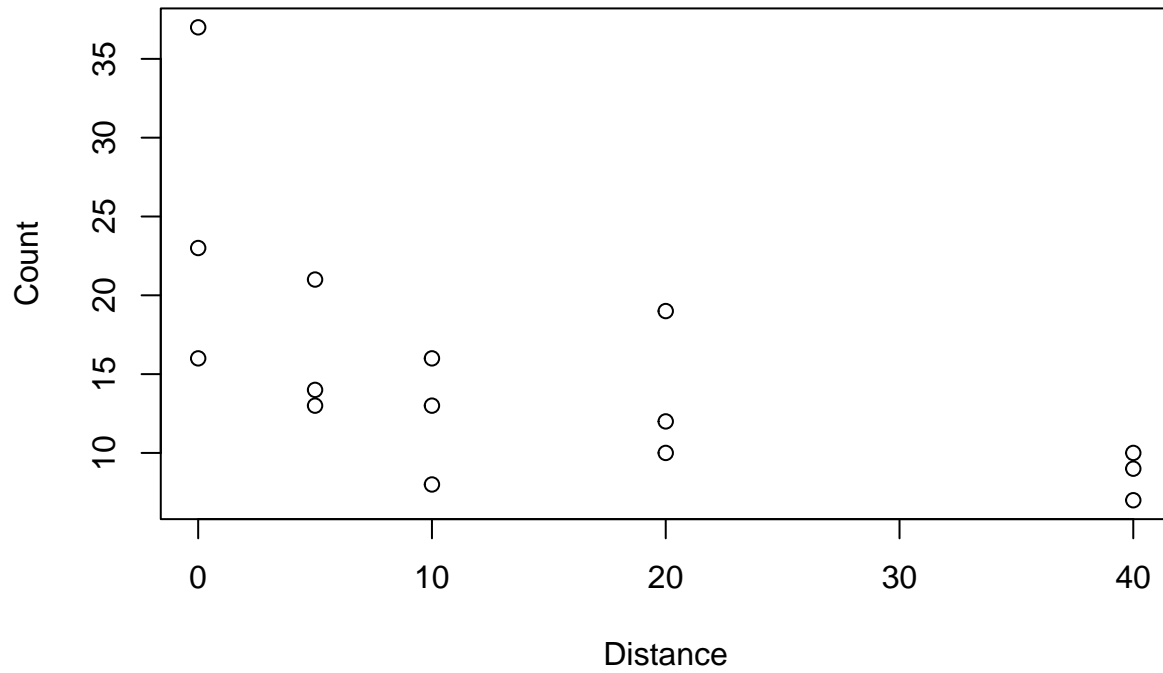
[1] "Culex pipiens"



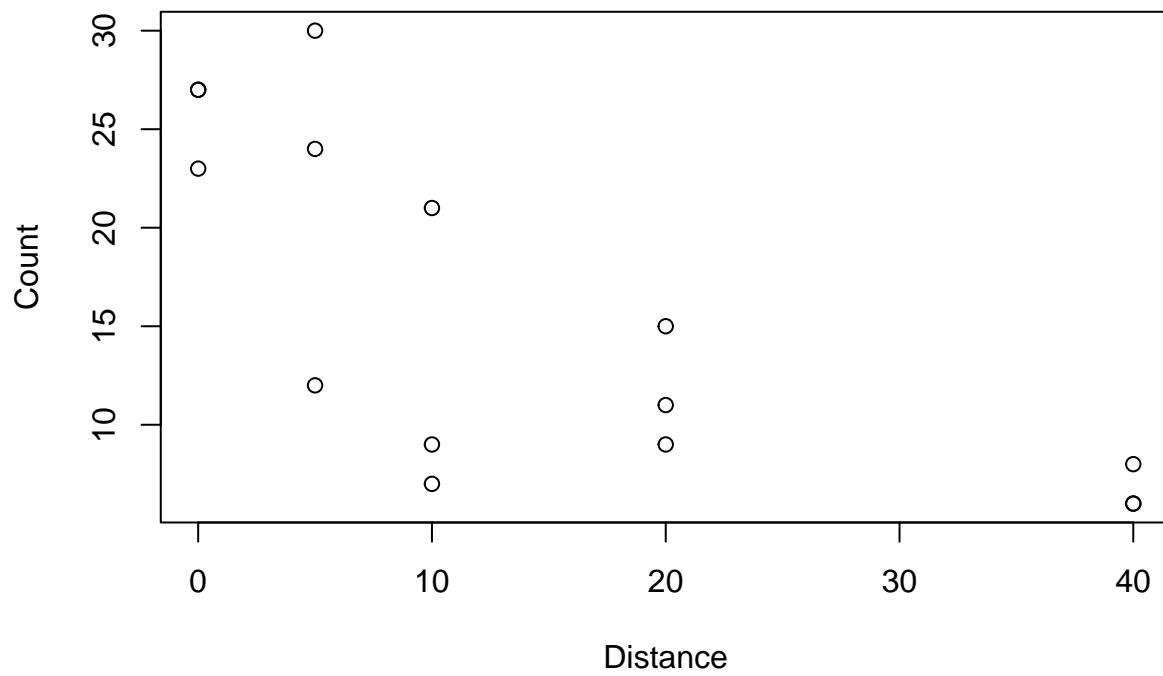
[1] "Anopheles gambiae"



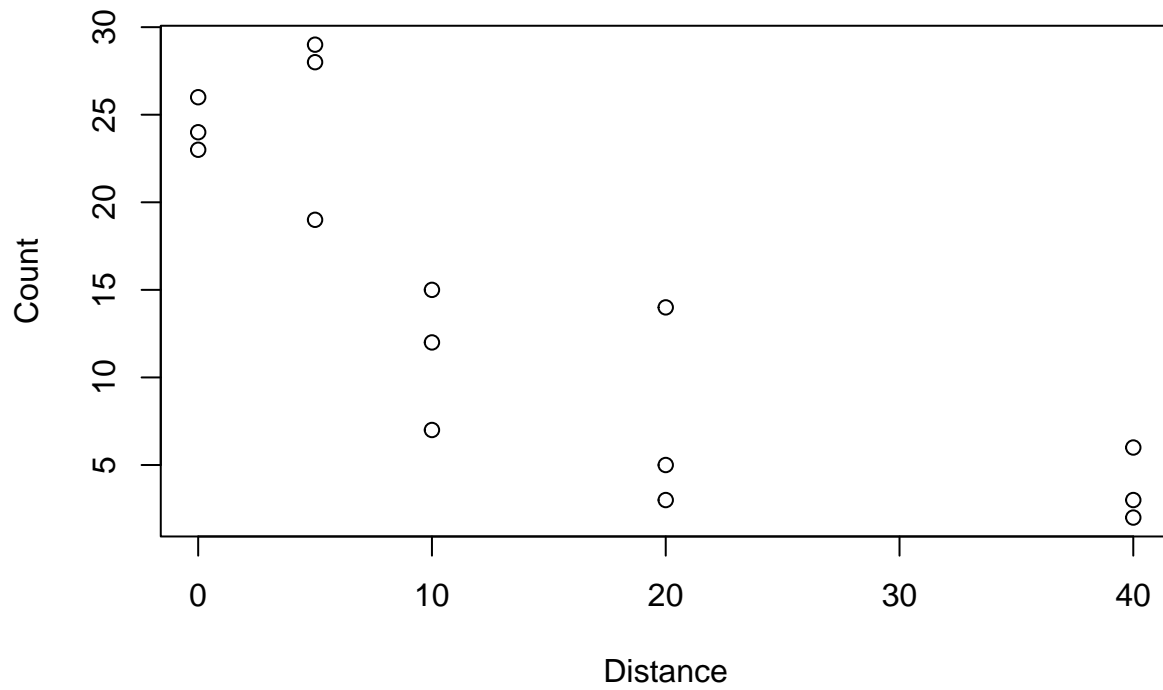
[1] "Sciariidae spp."



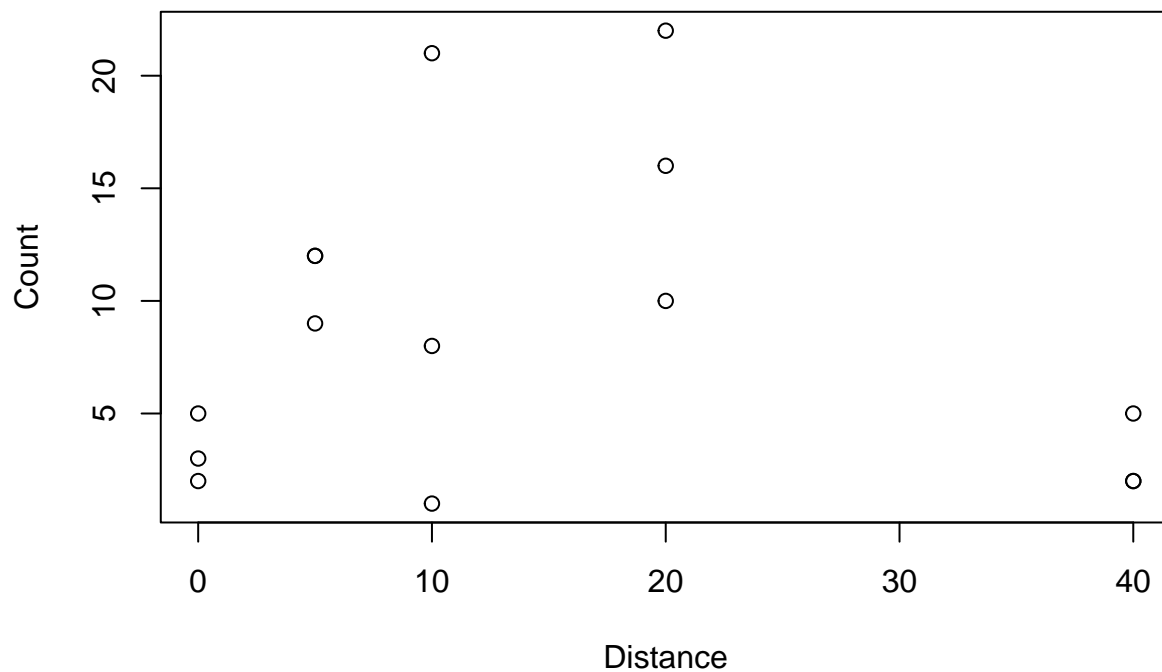
[1] "Cecidomyiidae spp."



[1] "Chironomidae spp."



[1] "Tipulidae spp."



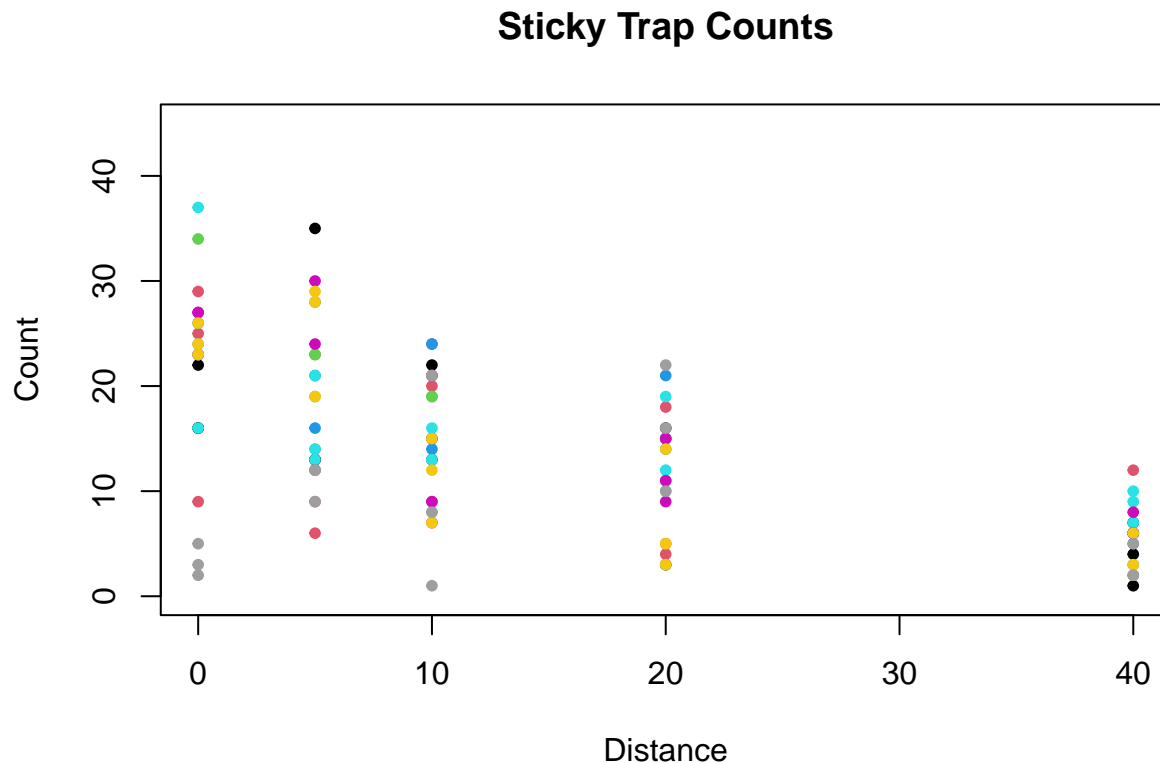
```
## [1] "Simuliidae spp."
```

Single Plot with Multiple Line

plot counts by distance but don't put points on the plot but scale xlim and ylim

```
plot(Count ~ Distance, data = stickytrap.df,
     xlim = c(0, 40),
     ylim = c(0, 45),
     type = "n",
     main = "Sticky Trap Counts",
     xlab = "Distance",
     ylab = "Count",
     cex.main = 1.2)

for (i in 1:length(species)) {
  points(Count ~ Distance, data = subset(stickytrap.df, subset=Species == species[i]),
        col = i,
        pch = 20)
}
```

plot counts by distance but don't put points on the plot but scale xlim and ylim

Avoid psuedo replication

```
# calculate mean and sd for each species
stickytrap.mean <- aggregate(Count ~ Species + Distance, data = stickytrap.df, FUN = mean)

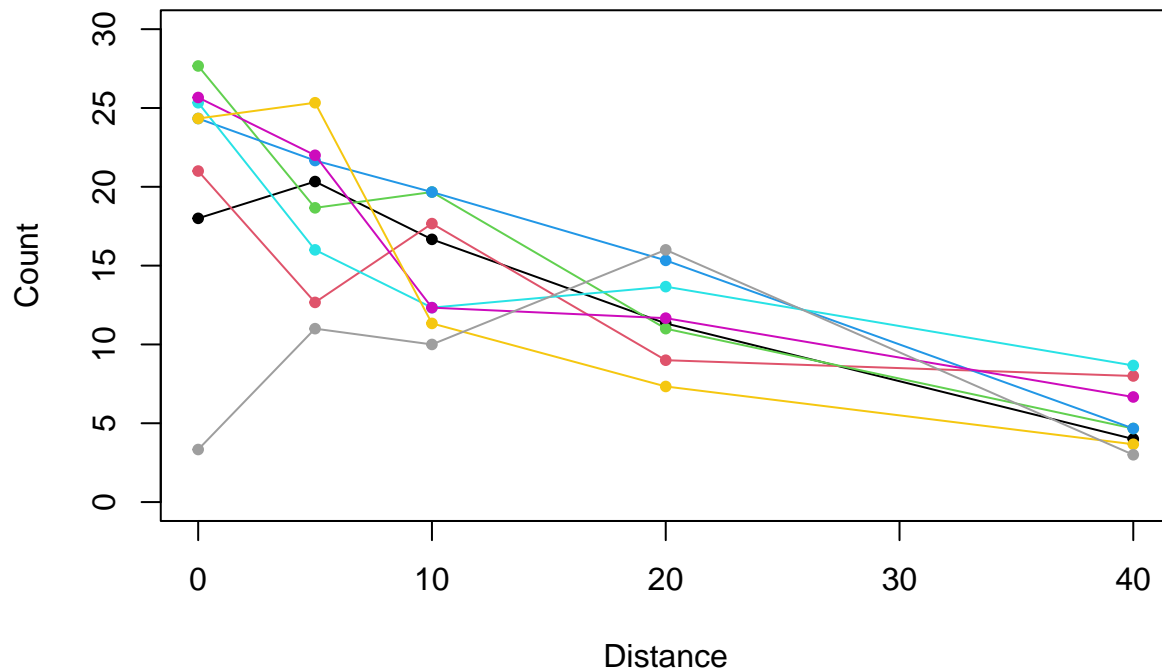
stickytrap.sd <- aggregate(Count ~ Species + Distance, data = stickytrap.df, FUN = sd)

plot(Count ~ Distance, data = stickytrap.mean,
     xlim = c(0, 40),
     ylim = c(0, 30),
     type = "n",
     main = "Sticky Trap Counts",
     xlab = "Distance",
     ylab = "Count",
     cex.main = 1.2)

for (i in 1:length(species)) {
  points(Count ~ Distance, data = subset(stickytrap.mean, subset=Species == species[i]),
        col = i,
        pch = 20)
  lines(Count ~ Distance, data = subset(stickytrap.mean, subset=Species == species[i]),
        col = i)
```

```
}
```

Sticky Trap Counts

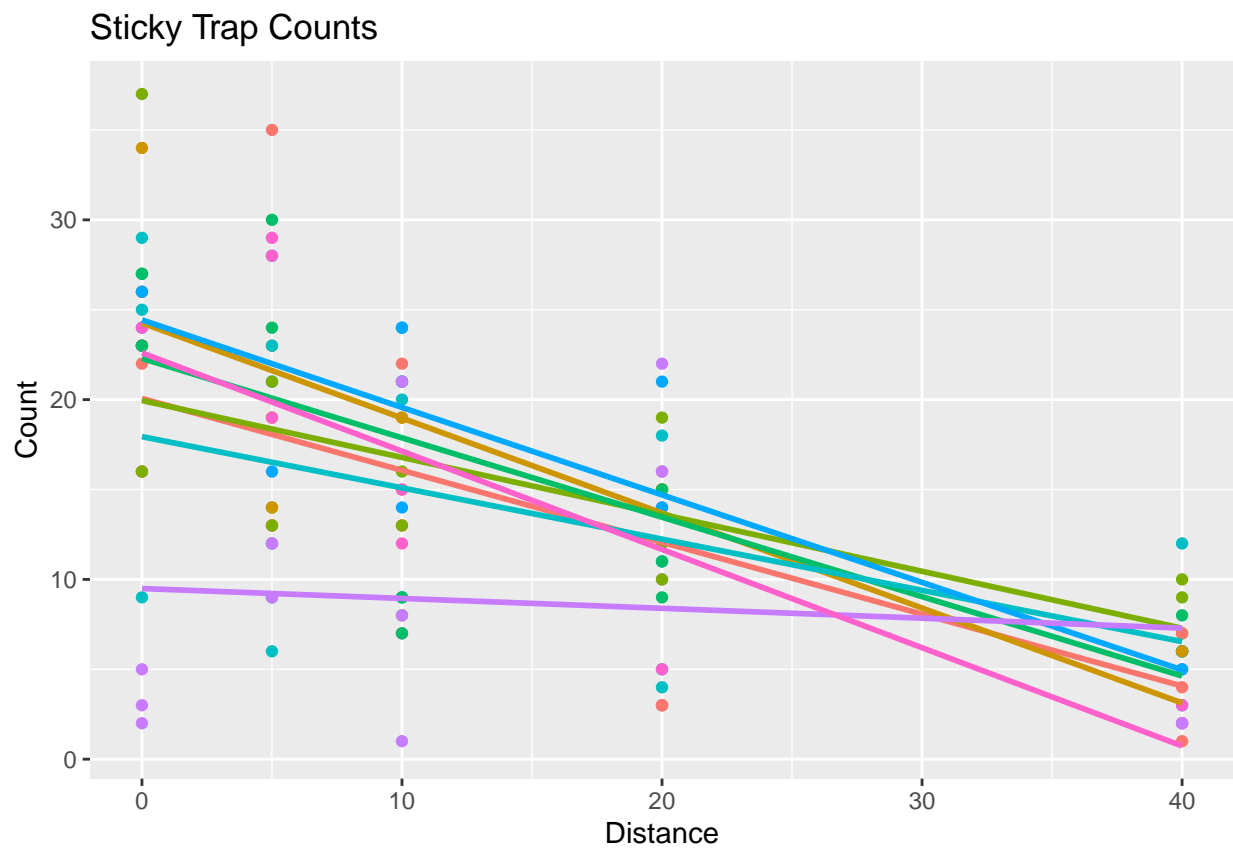


Using ggplot2

```
# plot counts by distance for each species with ggplot2, with a linear model for each species
library(ggplot2)

# plot counts by distance for each species with ggplot2, with a linear model for each species
# add legend
ggplot(stickytrap.df, aes(x = Distance, y = Count, color = factor(Species))) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
# facet_wrap(~ Species) +
  labs(title = "Sticky Trap Counts",
       x = "Distance",
       y = "Count") +
  theme(legend.position = "topright",
        legend.text = element_text(size = 8))

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



add legend