

# data\_visualization\_hackathon

Sohrab Khan

2024-07-26

## Hackathon: Data Visualization in R

### Load and Install Repositories and Packages

```
library(tidyverse)
```

```
## — Attaching core tidyverse packages — tidyverse 2.0.0 —
## ✓ dplyr      1.1.4      ✓ readr      2.1.5
## ✓ forcats    1.0.0      ✓ stringr    1.5.1
## ✓ ggplot2    3.5.1      ✓ tibble     3.2.1
## ✓ lubridate  1.9.3      ✓ tidyr      1.3.1
## ✓ purrr      1.0.2
## — Conflicts — tidyverse_conflicts() —
## ✗ dplyr::filter() masks stats::filter()
## ✗ dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(ggplot2)
library(readxl)
library(dplyr)
```

### Create a data folder manually or use R code mentioned below

```
dir.create("hackathon_data_visualization")
```

```
## Warning in dir.create("hackathon_data_visualization"):  
## 'hackathon_data_visualization' already exists
```

# Download example data

```
url <- "https://raw.githubusercontent.com/AMMnet/AMMnet-Hackathon/main/01_data-vis/data/"  
  
download.file(paste0(url,"mockdata_cases.csv"),  
              destfile = "hackathon_data_visualization/mockdata_cases.csv")  
  
download.file("https://raw.githubusercontent.com/AMMnet/AMMnet-Hackathon/main/01_data-vis/data/mosq_mock.csv", destfile = "hackathon_data_visualization/mosq_mock.csv")
```

# Load example data

```
library(readr)  
malaria_data <- read_csv("hackathon_data_visualization/mockdata_cases.csv")
```

```
## Rows: 514 Columns: 10  
## — Column specification —————  
## Delimiter: ","  
## chr (2): location, ages  
## dbl (8): month, year, total, positive, xcoord, ycoord, prev, time_order_loc  
##  
## 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.
```

```
View(malaria_data)  
mosq_data <- read_csv("hackathon_data_visualization/mosq_mock.csv")
```

```
## Rows: 104 Columns: 19  
## — Column specification —————  
## Delimiter: ","  
## chr (4): Village, Method, Location, hour  
## dbl (15): session, Compound.ID, ag.Male, Ag.unfed, Ag.halfed, Ag.fed, Ag.gr...  
##  
## 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.
```

```
View(mosq_data)
```

# Characterize means Exploring our data

## How many rows and columns

```
dim(malaria_data)
```

```
## [1] 514 10
```

## General information

```
head(malaria_data)
```

```
## # A tibble: 6 × 10
##   location month  year ages  total positive xcoord ycoord prev time_order_loc
##   <chr>      <dbl> <dbl> <chr>  <dbl>    <dbl> <dbl> <dbl> <dbl>      <dbl>
## 1 mordor      1  2018 15_abo... 122      30 -20.5  30.2 0.246          1
## 2 mordor      2  2018 15_abo... 168      57 -20.1  30.3 0.339          2
## 3 mordor      3  2018 15_abo...  97      20 -20.1  30.4 0.206          3
## 4 mordor      4  2018 15_abo...  91      23 -20.0  30.5 0.253          4
## 5 mordor      5  2018 15_abo...  67      19 -20.7  30.7 0.284          5
## 6 mordor      6  2018 15_abo... 107      25 -19.2  30.5 0.234          6
```

```
summary(malaria_data)
```

```
##   location          month          year          ages
## Length:514      Min.   : 1.000   Min.   :2018   Length:514
## Class :character 1st Qu.: 4.000   1st Qu.:2018   Class :character
## Mode  :character Median : 7.000   Median :2019   Mode  :character
##                Mean   : 6.486   Mean   :2019
##                3rd Qu.: 9.000   3rd Qu.:2020
##                Max.   :12.000   Max.   :2020
##   total          positive          xcoord          ycoord
## Min.   : 20.0   Min.   : -1.00   Min.   : -21.84   Min.   :28.52
## 1st Qu.: 46.0   1st Qu.: 14.00   1st Qu.: -20.39   1st Qu.:29.64
## Median :103.0   Median : 33.00   Median : -20.06   Median :29.99
## Mean   :141.5   Mean   : 47.81   Mean   : -20.04   Mean   :30.00
## 3rd Qu.:206.0   3rd Qu.: 67.00   3rd Qu.: -19.71   3rd Qu.:30.32
## Max.   :611.0   Max.   :264.00   Max.   : -18.79   Max.   :31.81
##   prev          time_order_loc
## Min.   : -0.04545   Min.   : 1.00
## 1st Qu.: 0.24615   1st Qu.: 9.00
## Median : 0.33016   Median :18.00
## Mean   : 0.31518   Mean   :17.65
## 3rd Qu.: 0.39024   3rd Qu.:26.00
## Max.   : 0.53488   Max.   :35.00
```

## Exploring individual columns of the data

```
malaria_data$location # values for a single column
```

[illegible]

[illegible]

```
unique(malaria_data$location) # unique values for a single column
```

```
## [1] "mordor"      "narnia"      "neverwhere" "oz"          "wonderland"
```

```
table(malaria_data$location) # frequencies for a single column
```

```
##
##      mordor      narnia neverwhere      oz wonderland
##         105         104          96      104         105
```

```
table(malaria_data$location, malaria_data$ages) # frequencies for multiple column
```

```
##
##           15_above 5_to_14 under_5
##      mordor         35      35      35
##      narnia         35      35      34
##      neverwhere      32      32      32
##      oz             35      35      34
##      wonderland      35      35      35
```

## Check for if there are any missing values- NA

```
sum(is.na(malaria_data))
```

```
## [1] 0
```

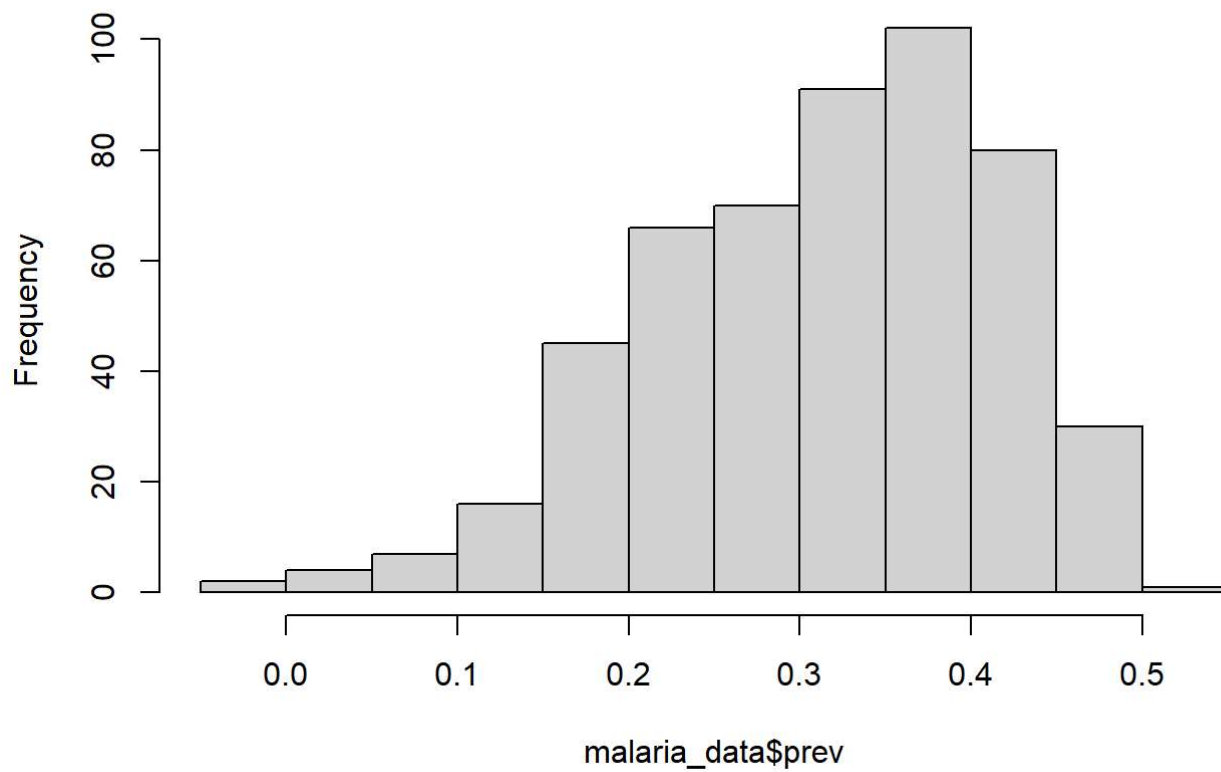
# Exploratory Visualizations Using Base R Functions

## Single variable or column comparison

**\*\*Histogram or Frequency Chart**

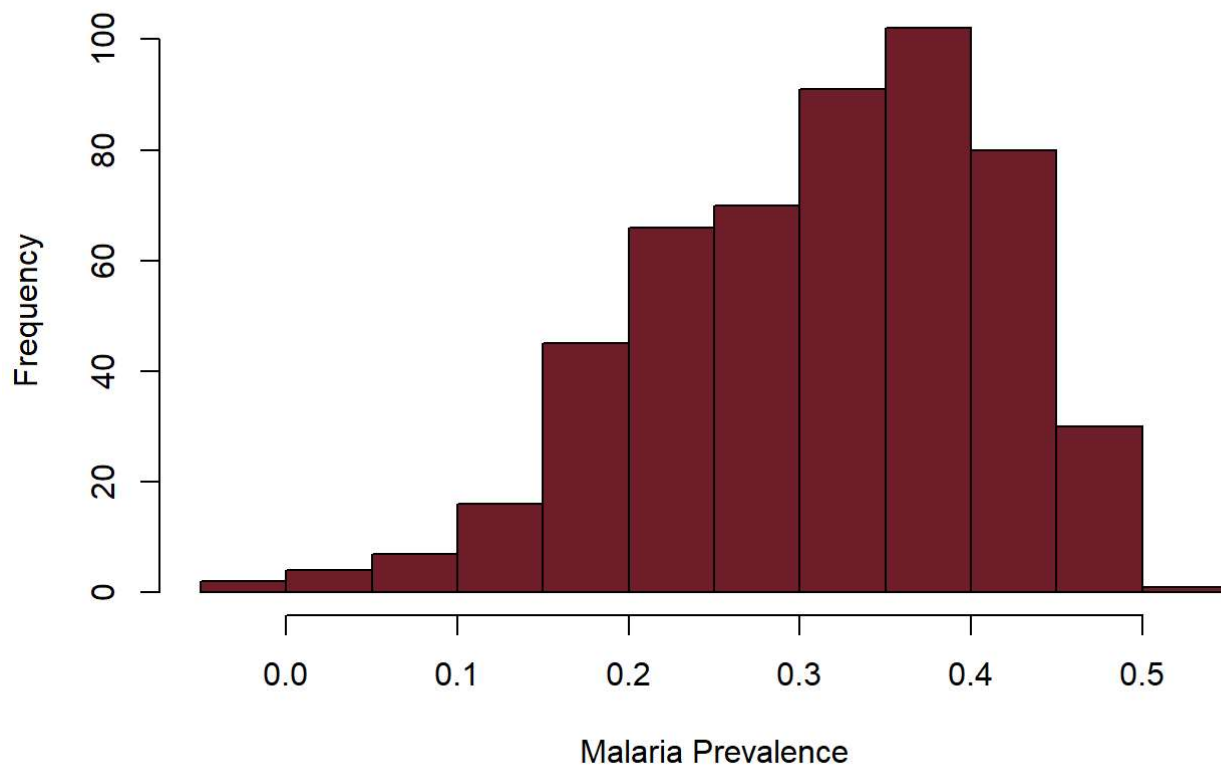
```
hist(malaria_data$prev)
```

**Histogram of malaria\_data\$prev**



```
hist(malaria_data$prev,  
     breaks = 10, # breaks mean how many individual bars do we need to group  
     main = "Distribution of Malaria Prevalence",  
     xlab = "Malaria Prevalence",  
     ylab = "Frequency",  
     col = "#701f28",  
     border = "black")
```

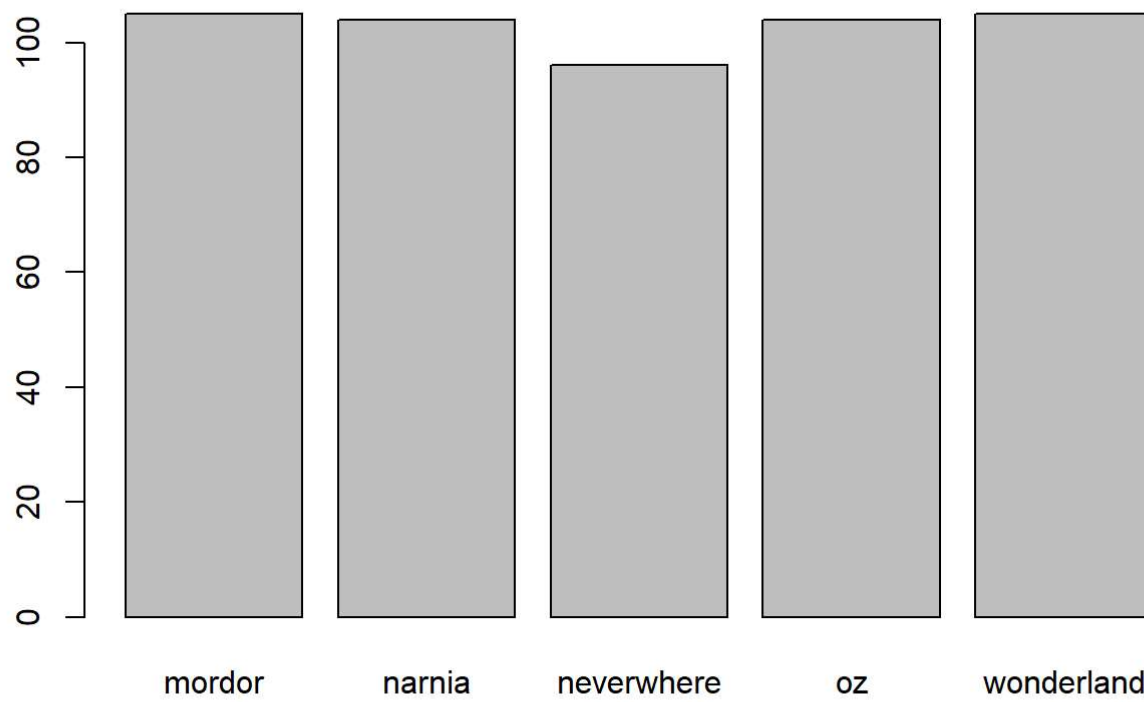
## Distribution of Malaria Prevalence



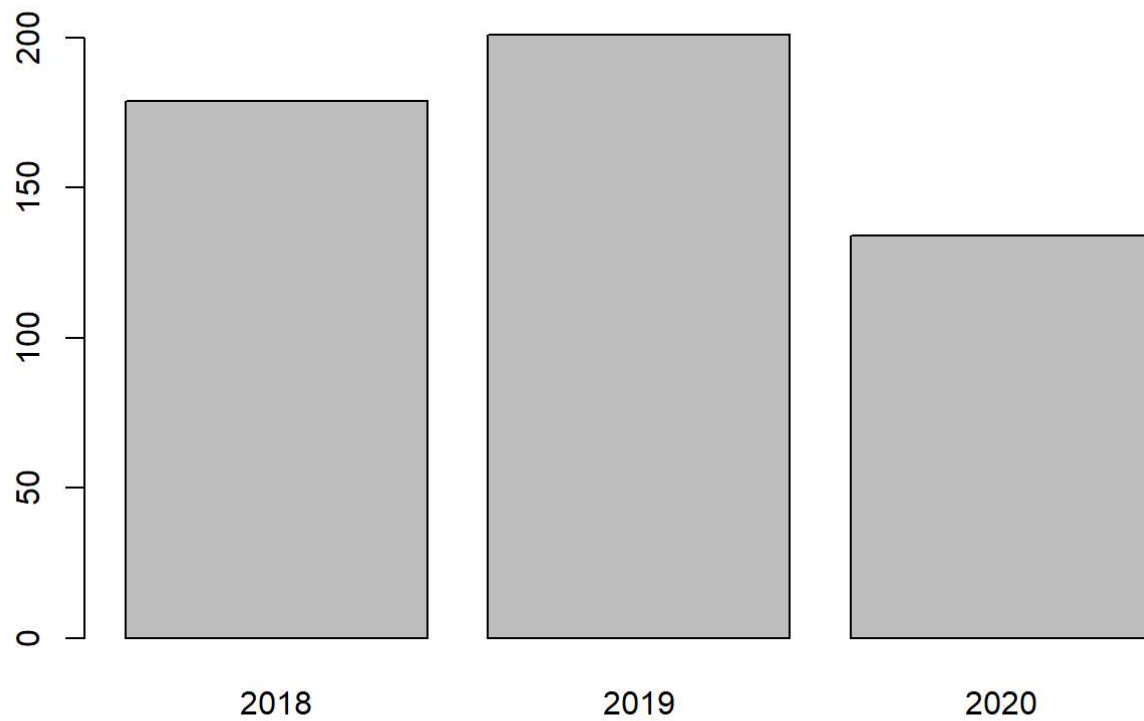
**Barplot-** tell us the number of counts within a categorical variable/ column

```
barplot(table(malaria_data$location))
```





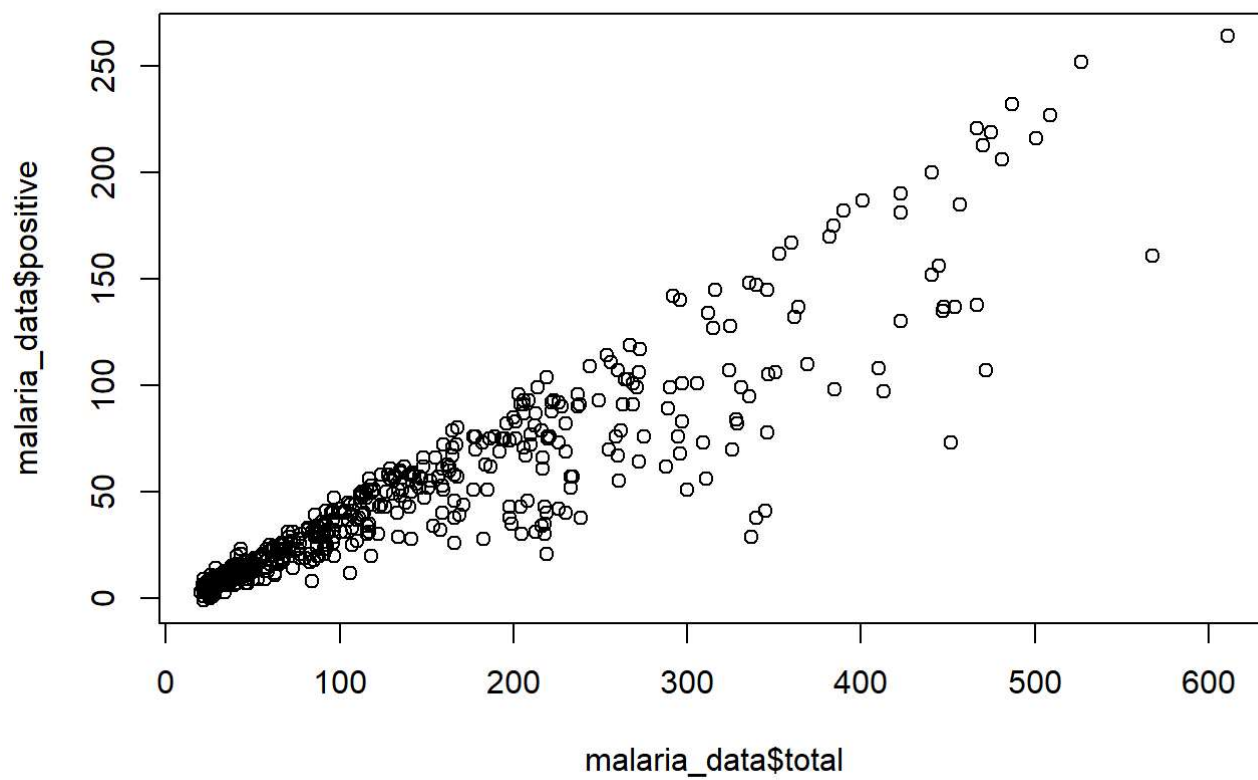
```
barplot(table(malaria_data$year))
```



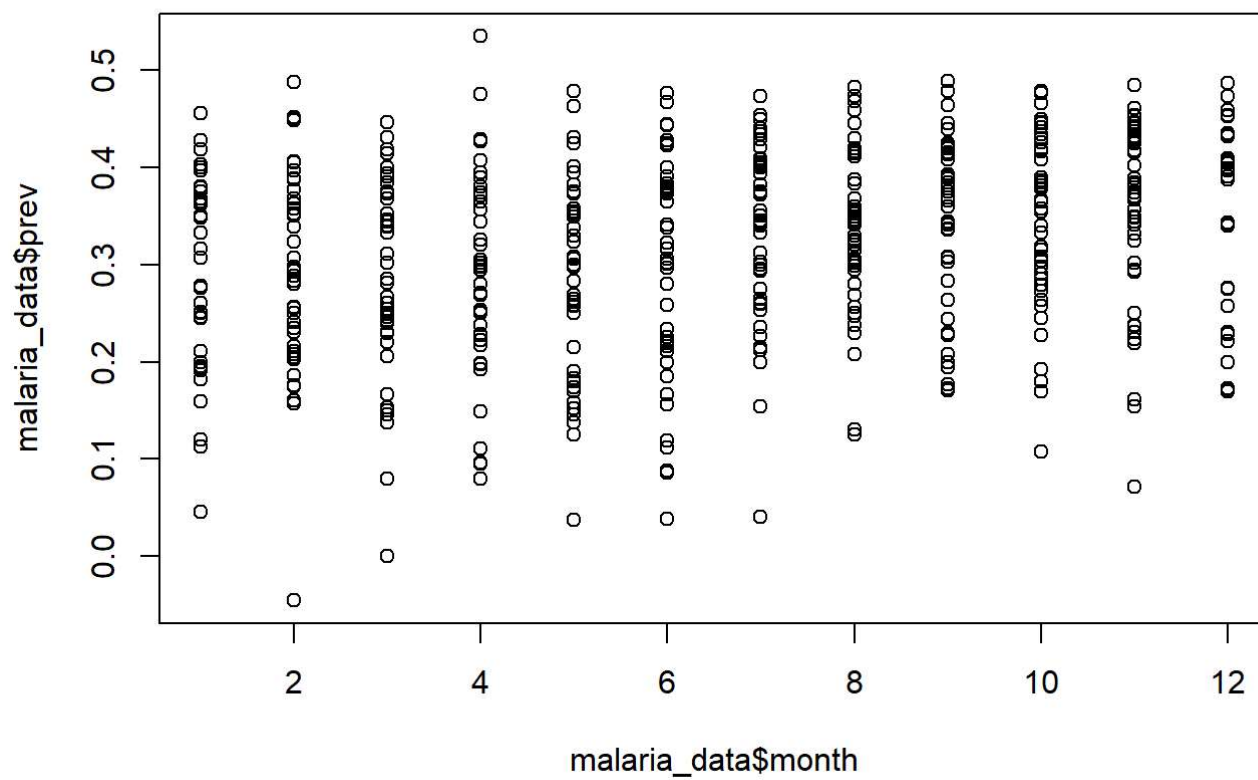
## Plotting Multiple column/ variable

### Scatterplot using R code - plot

```
plot(x = malaria_data$total, y = malaria_data$positive)
```

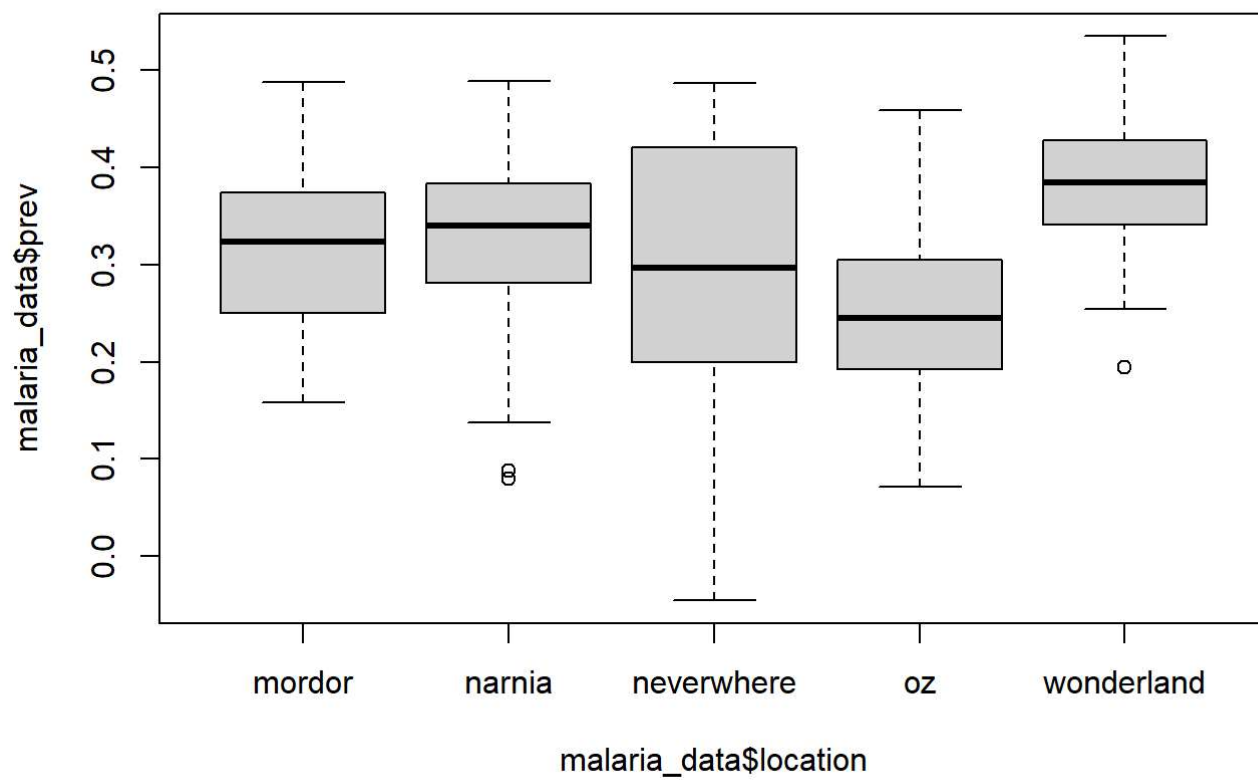


```
plot(x = malaria_data$month, y = malaria_data$prev)
```

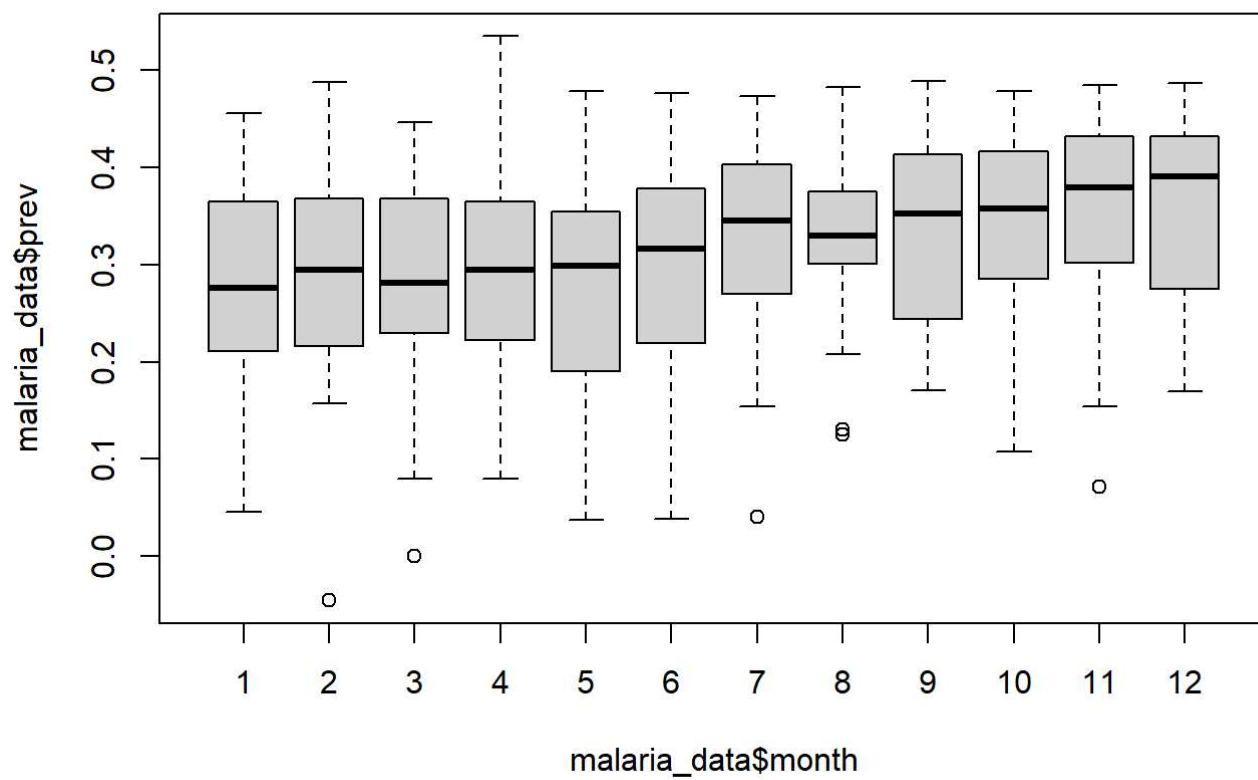


### Boxplot using R code - boxplot

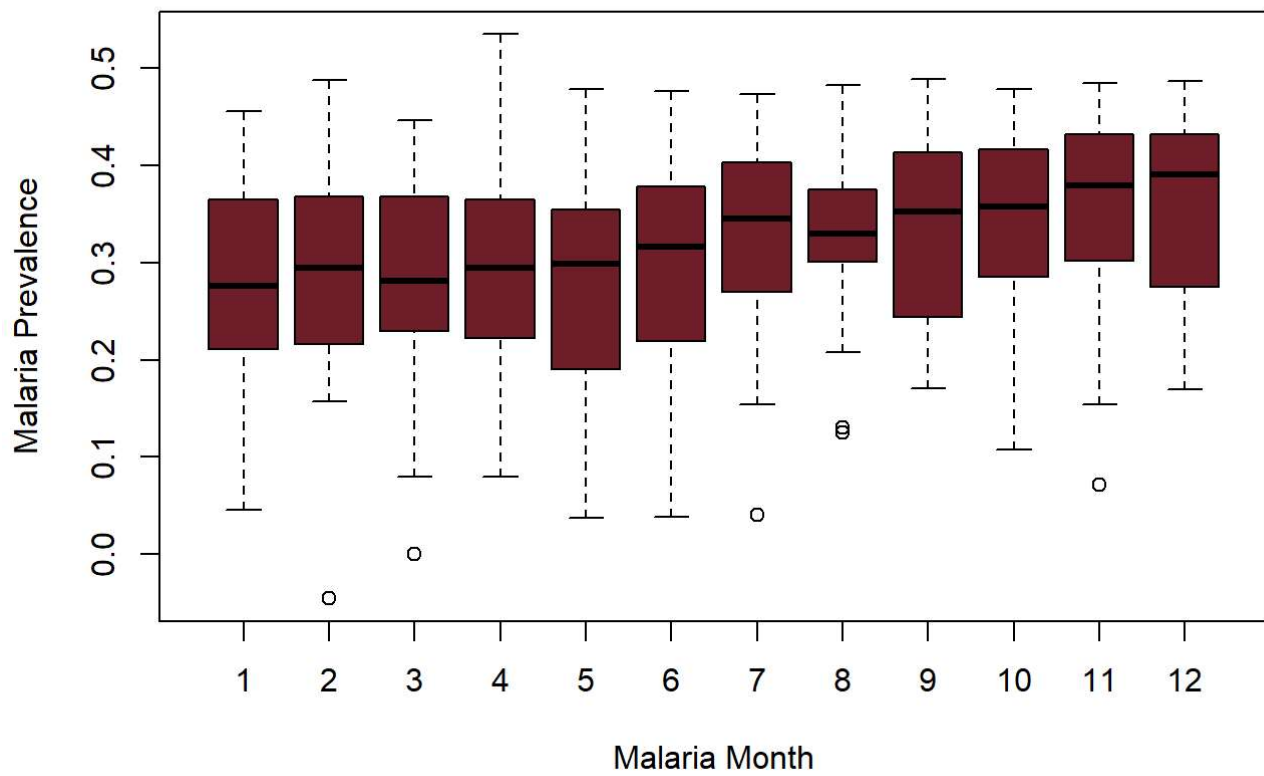
```
boxplot(malaria_data$prev ~ malaria_data$location)
```



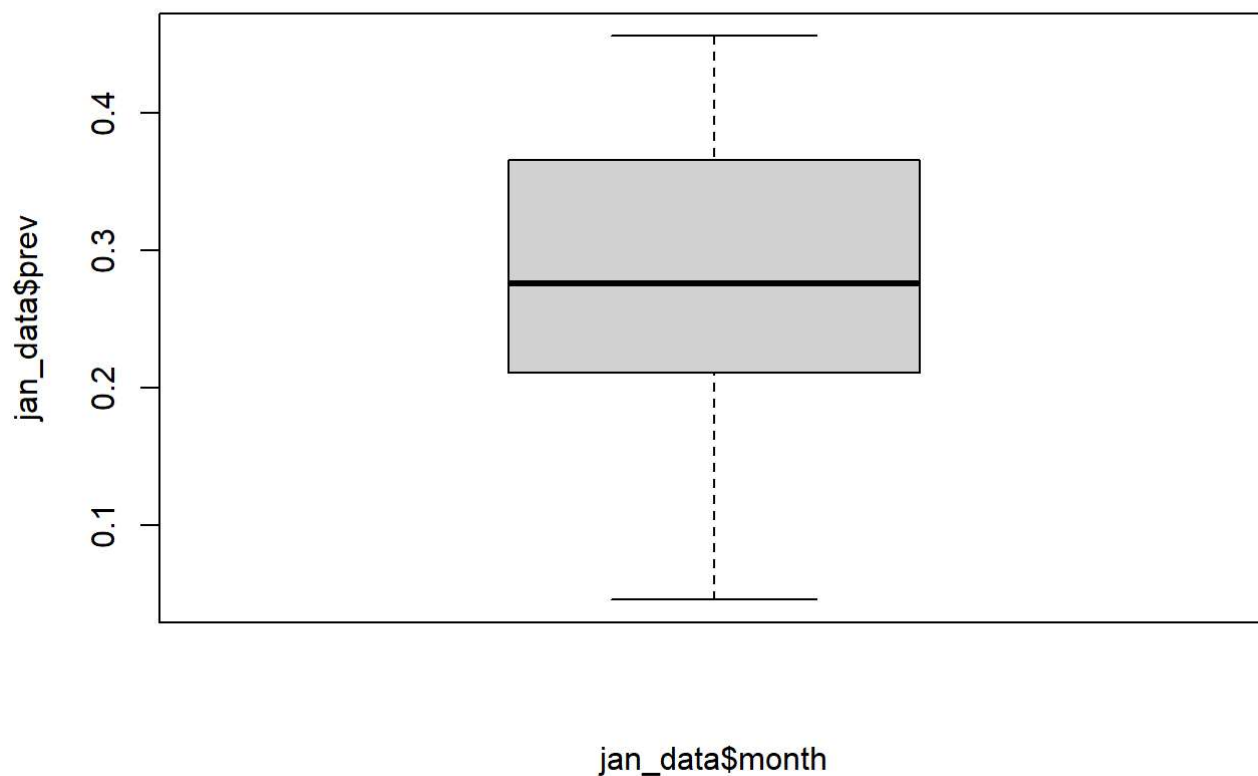
```
boxplot(malaria_data$prev ~ malaria_data$month)
```



```
boxplot(malaria_data$prev ~ malaria_data$month,  
        data = malaria_data,  
        xlab = "Malaria Month",  
        ylab = "Malaria Prevalence",  
        col = "#701f28",  
        border = "black")
```



```
jan_data <- filter(malaria_data, month==1)
boxplot(jan_data$prev ~ jan_data$month)
```



```
boxplot
```

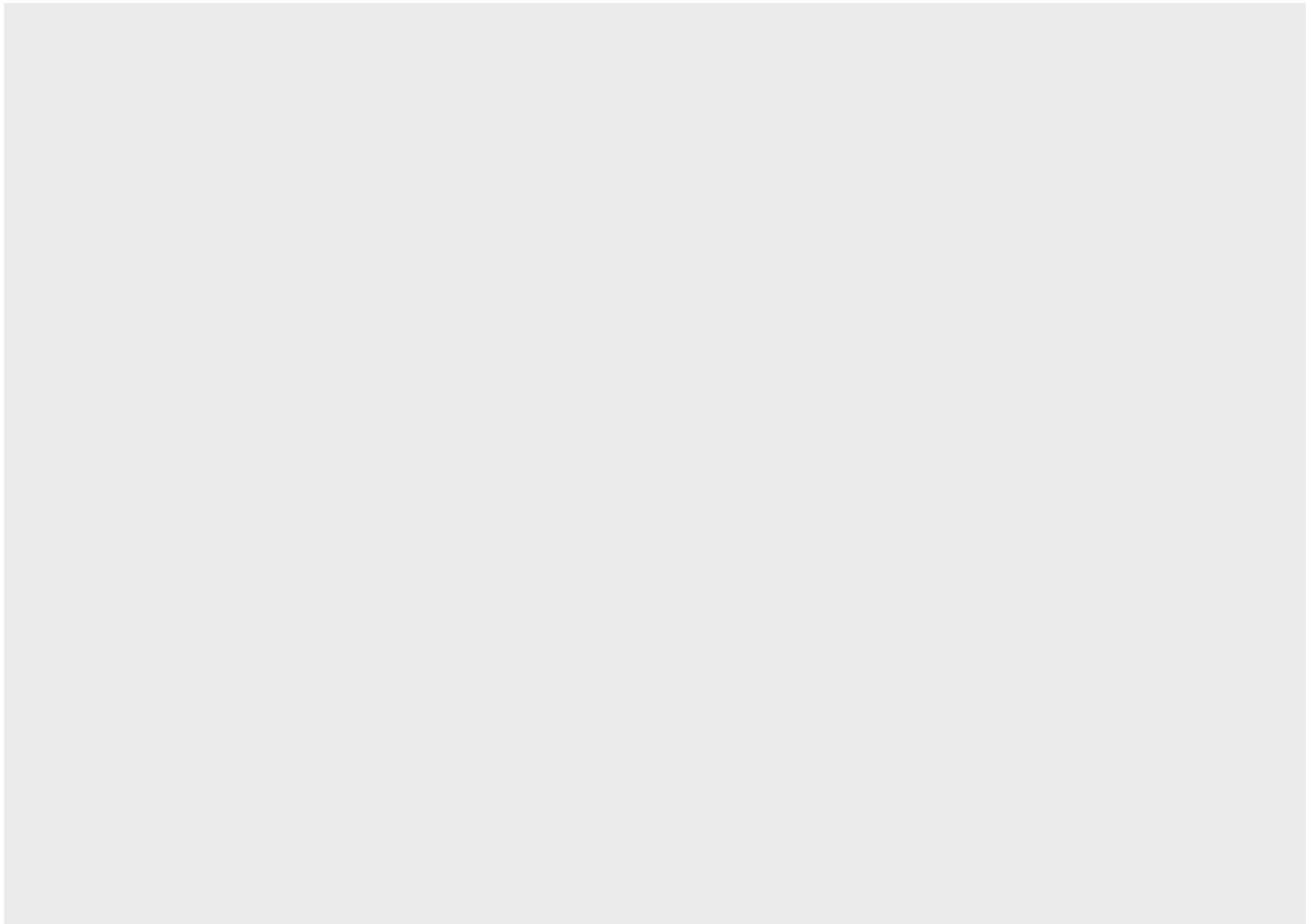
```
## function (x, ...)  
## UseMethod("boxplot")  
## <bytecode: 0x0000021c4ef14b58>  
## <environment: namespace:graphics>
```

## Step by Step Data Visualization using ggplot2

### Data

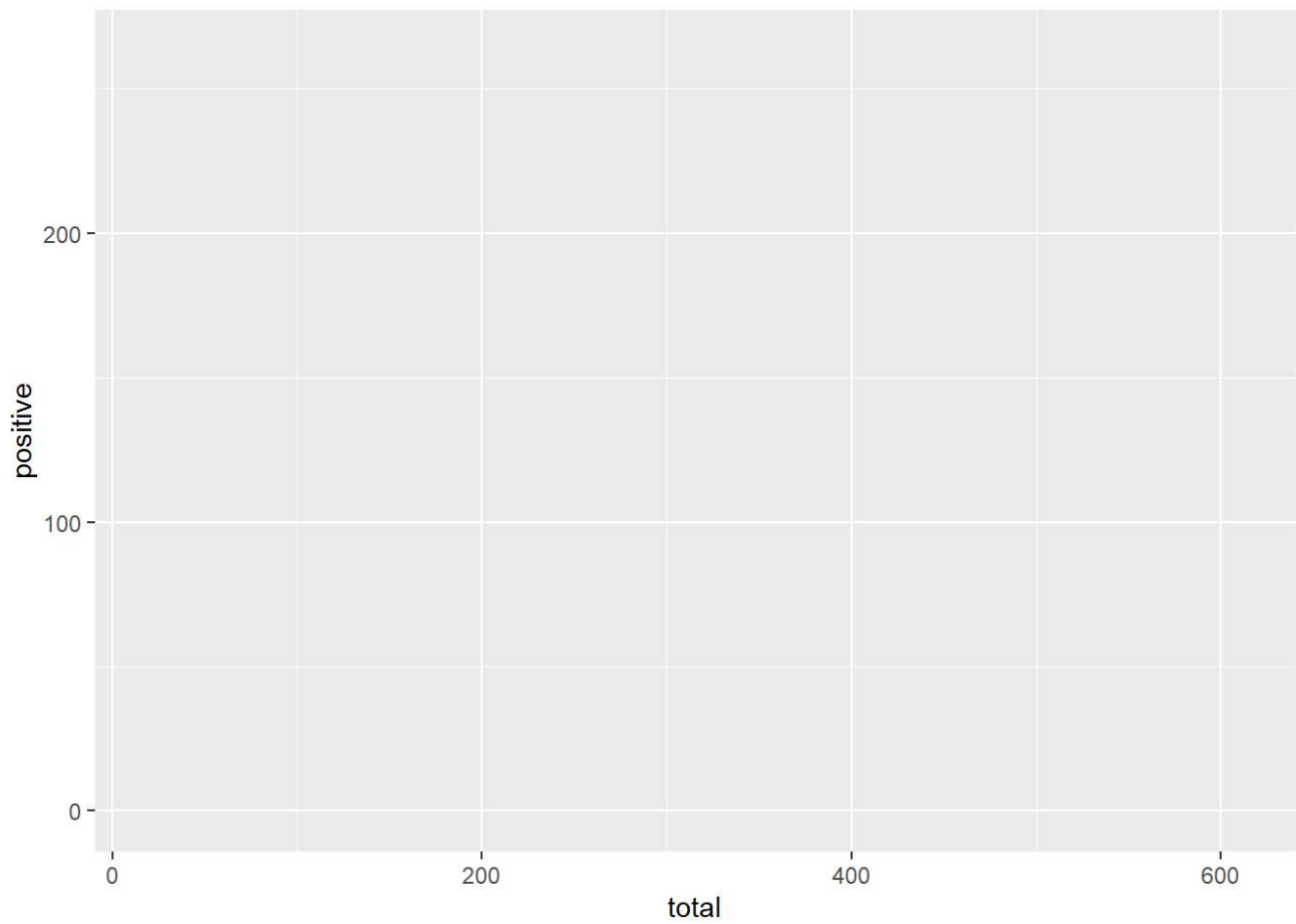
```
ggplot(data = malaria_data)
```





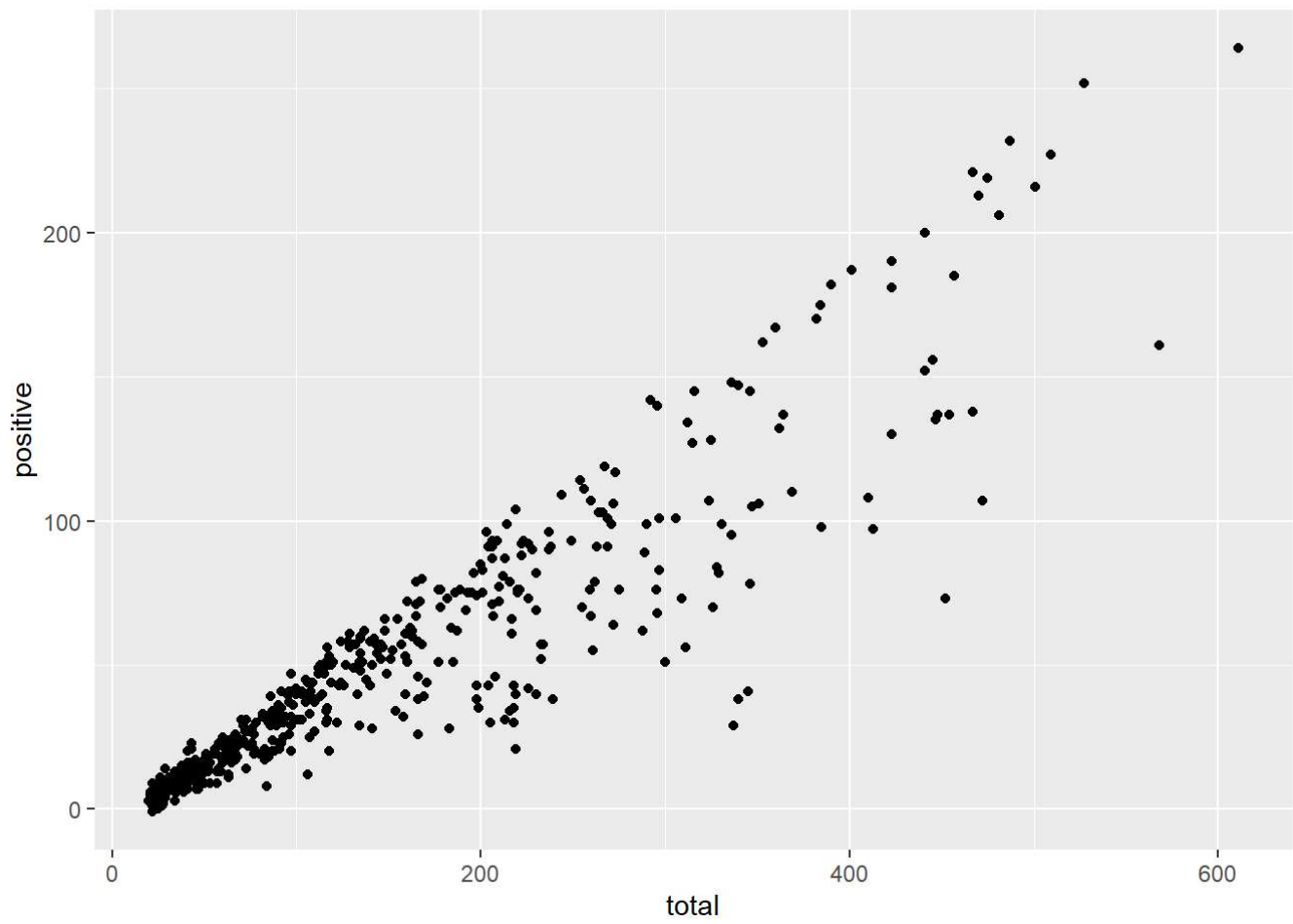
## Organize Data(aes())

```
ggplot(data = malaria_data, aes(x = total, y = positive))
```

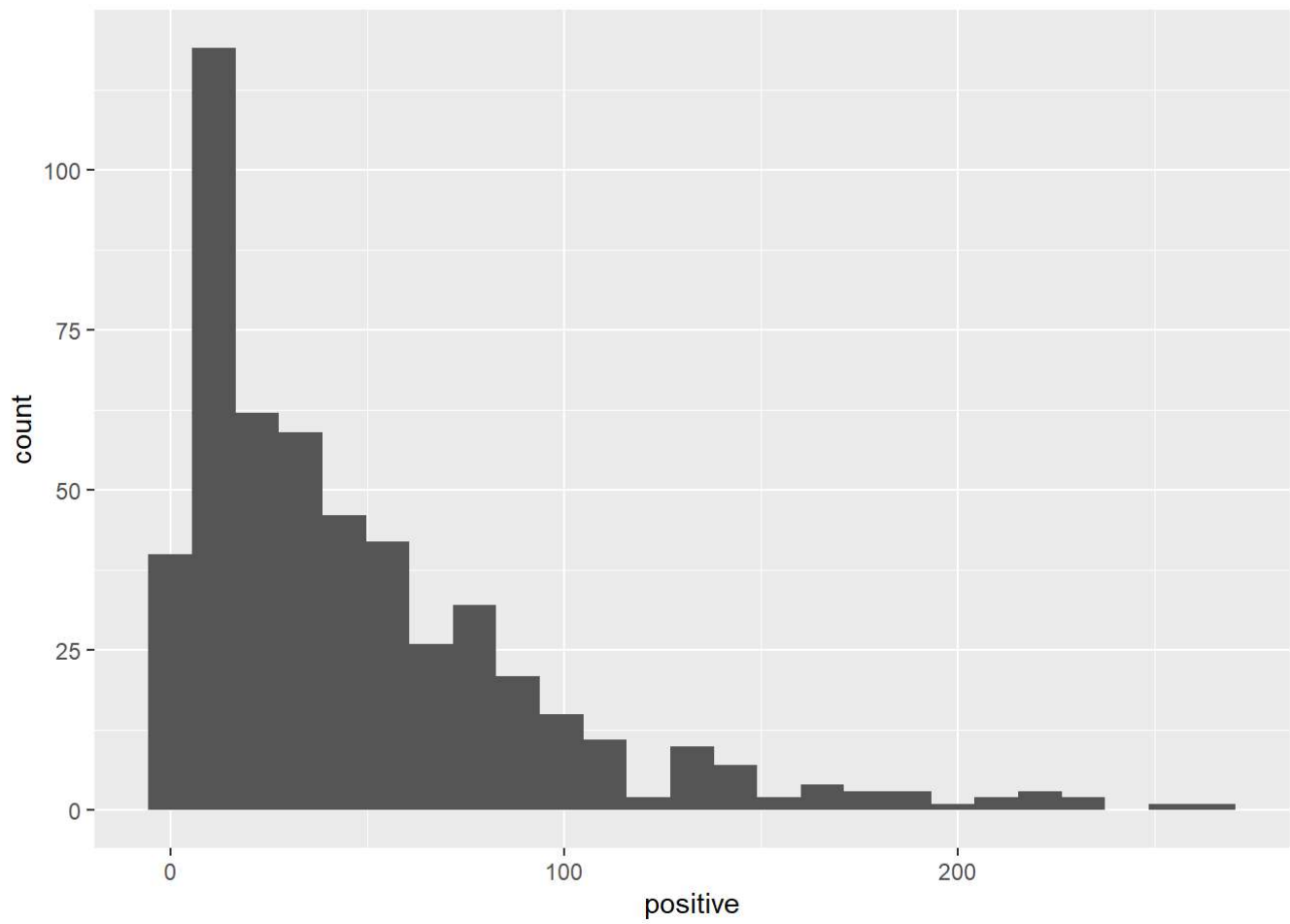


## Visualizing Data(geom\_)

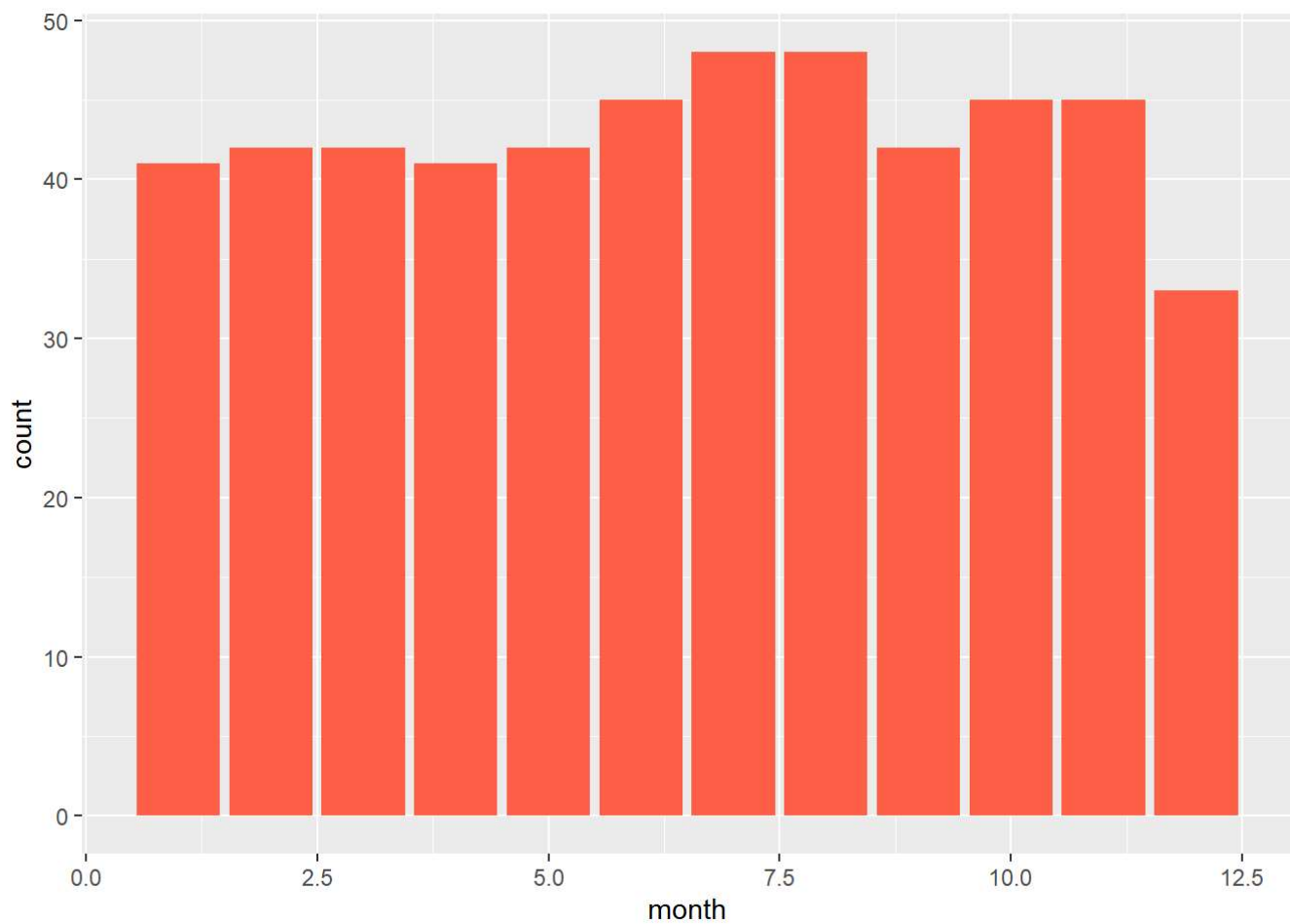
```
ggplot(data = malaria_data, aes(x = total, y = positive)) + geom_point()
```



```
ggplot(data = malaria_data, aes(x = positive)) + geom_histogram(bins = 25)
```

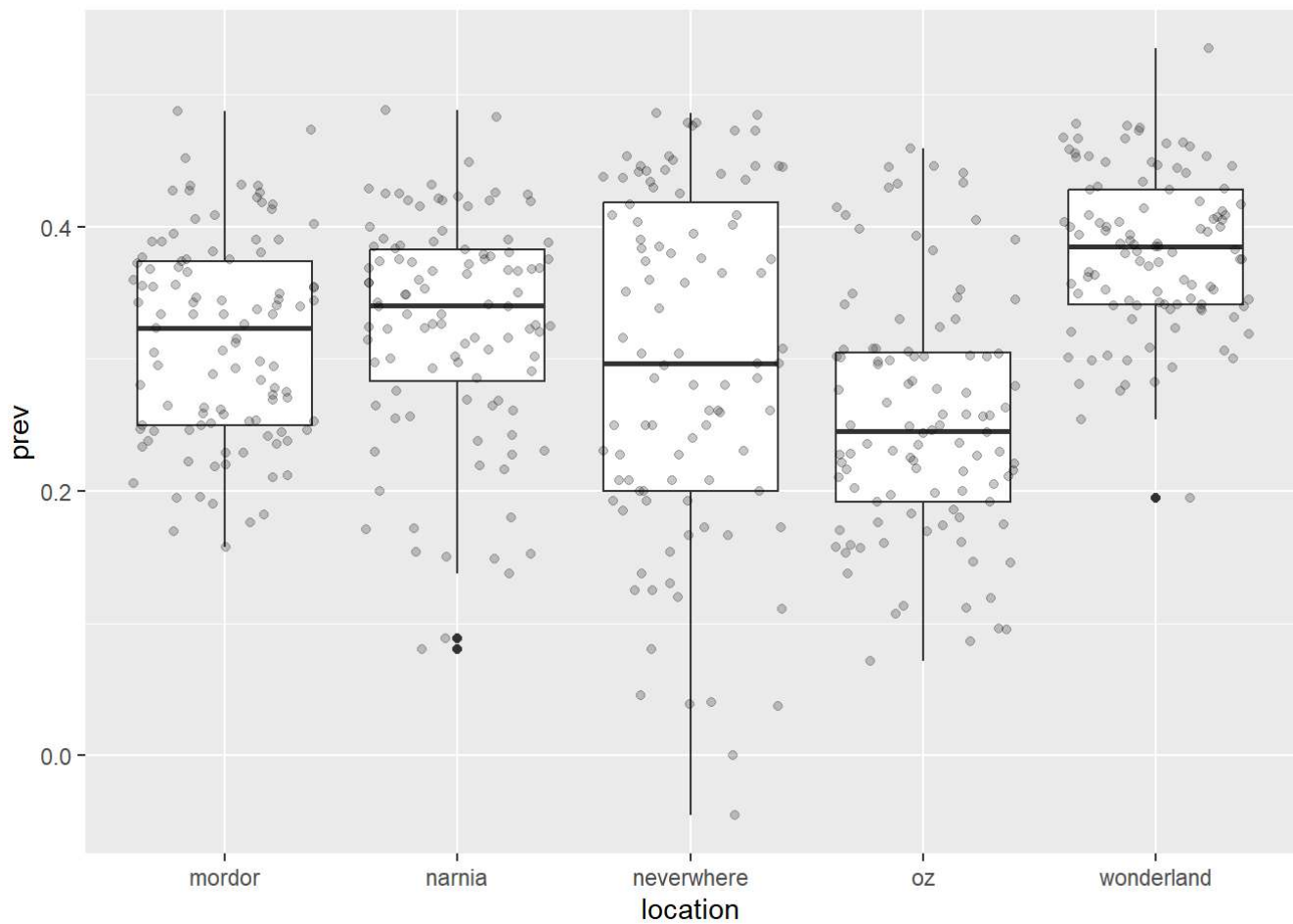


```
ggplot(data = malaria_data, aes(x = month)) + geom_bar(fill = "tomato")
```

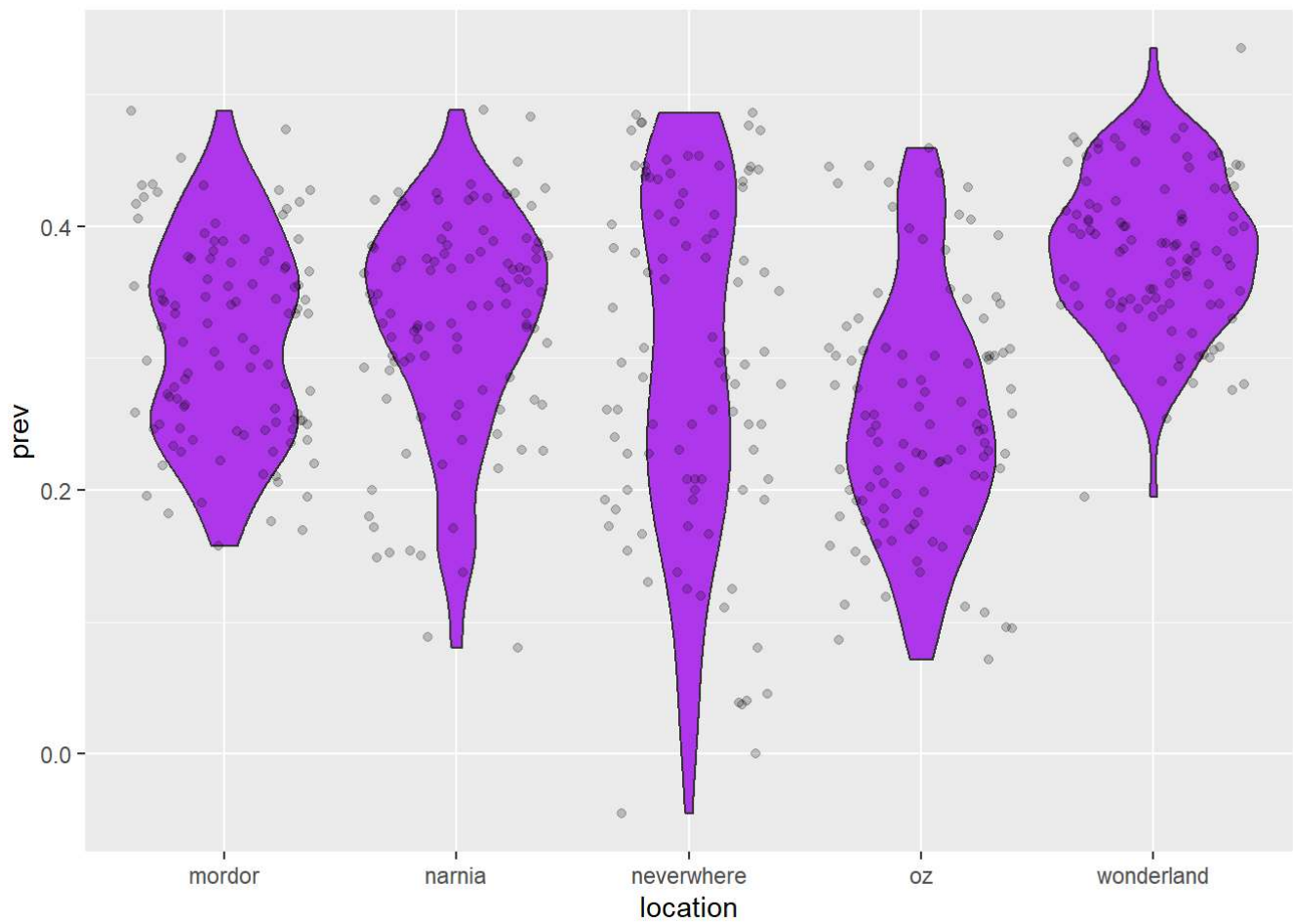


## Add multiple geoms\_

```
ggplot(data = malaria_data, aes(x = location, y = prev)) + geom_boxplot()+  
  geom_jitter(alpha = 0.2) #Boxplot shows value for the range but they don't show distr  
ibution
```

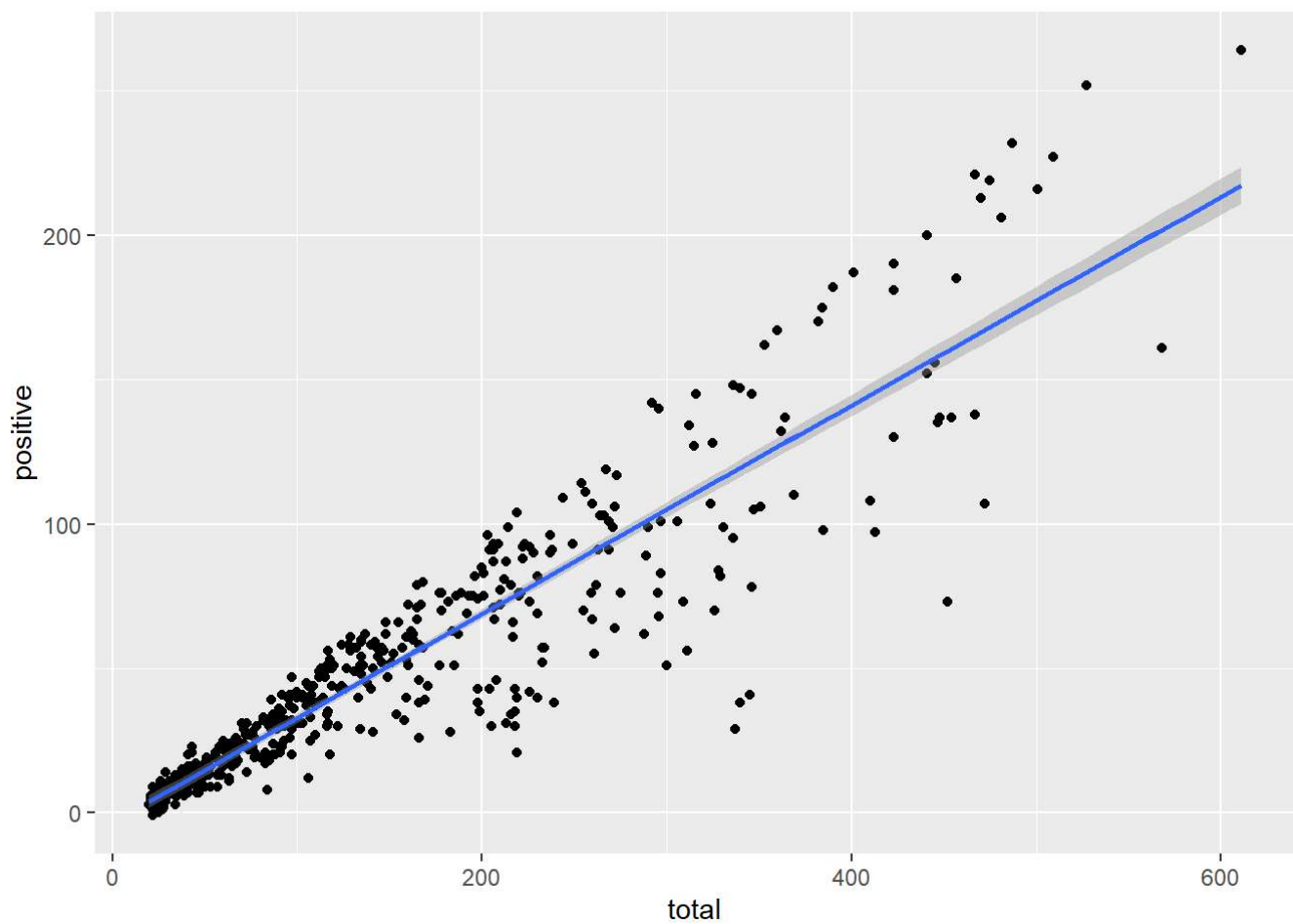


```
ggplot(data = malaria_data, aes(x = location, y = prev)) + geom_violin(fill= "darkorchid2")+  
  geom_jitter(alpha = 0.2) #Similar to the boxplot but the shape is different shows distribution
```



```
ggplot(data = malaria_data, aes(x = total, y = positive)) + geom_point() + geom_smooth  
(method = "lm")
```

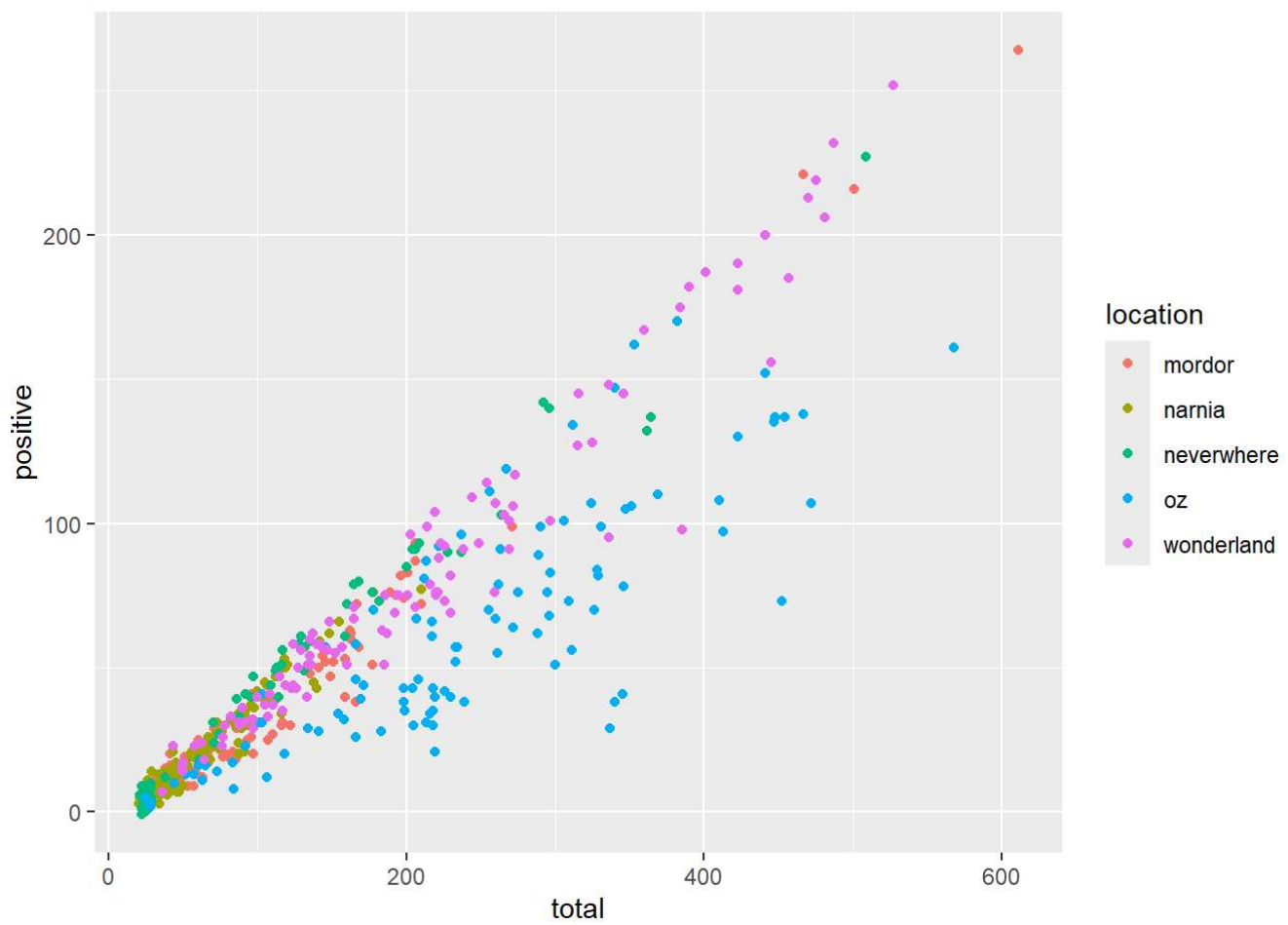
```
## `geom_smooth()` using formula = 'y ~ x'
```



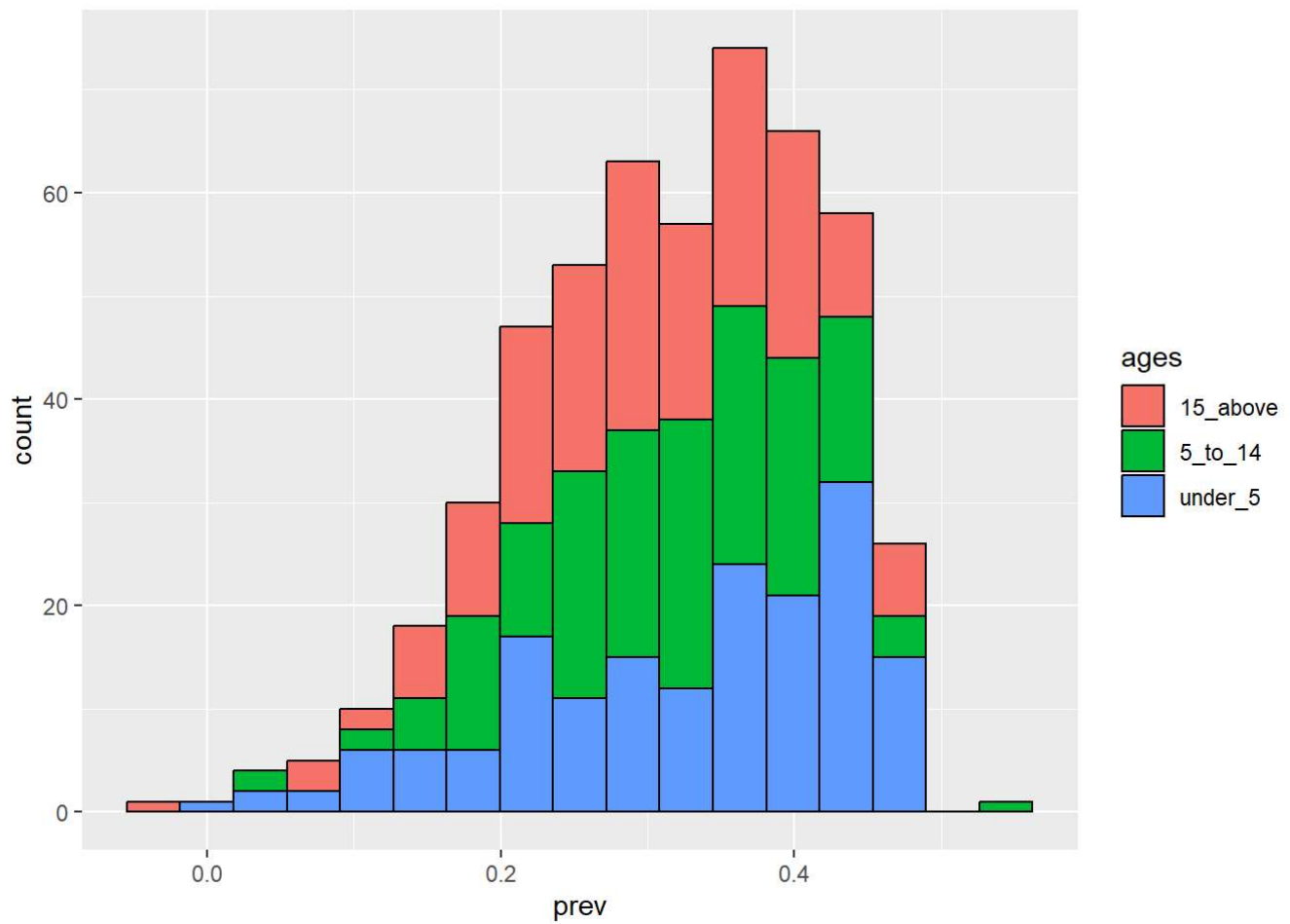
## Extending the aesthetic

```
ggplot(data = malaria_data, aes(x = total, y = positive, colour = location)) + geom_point()
```

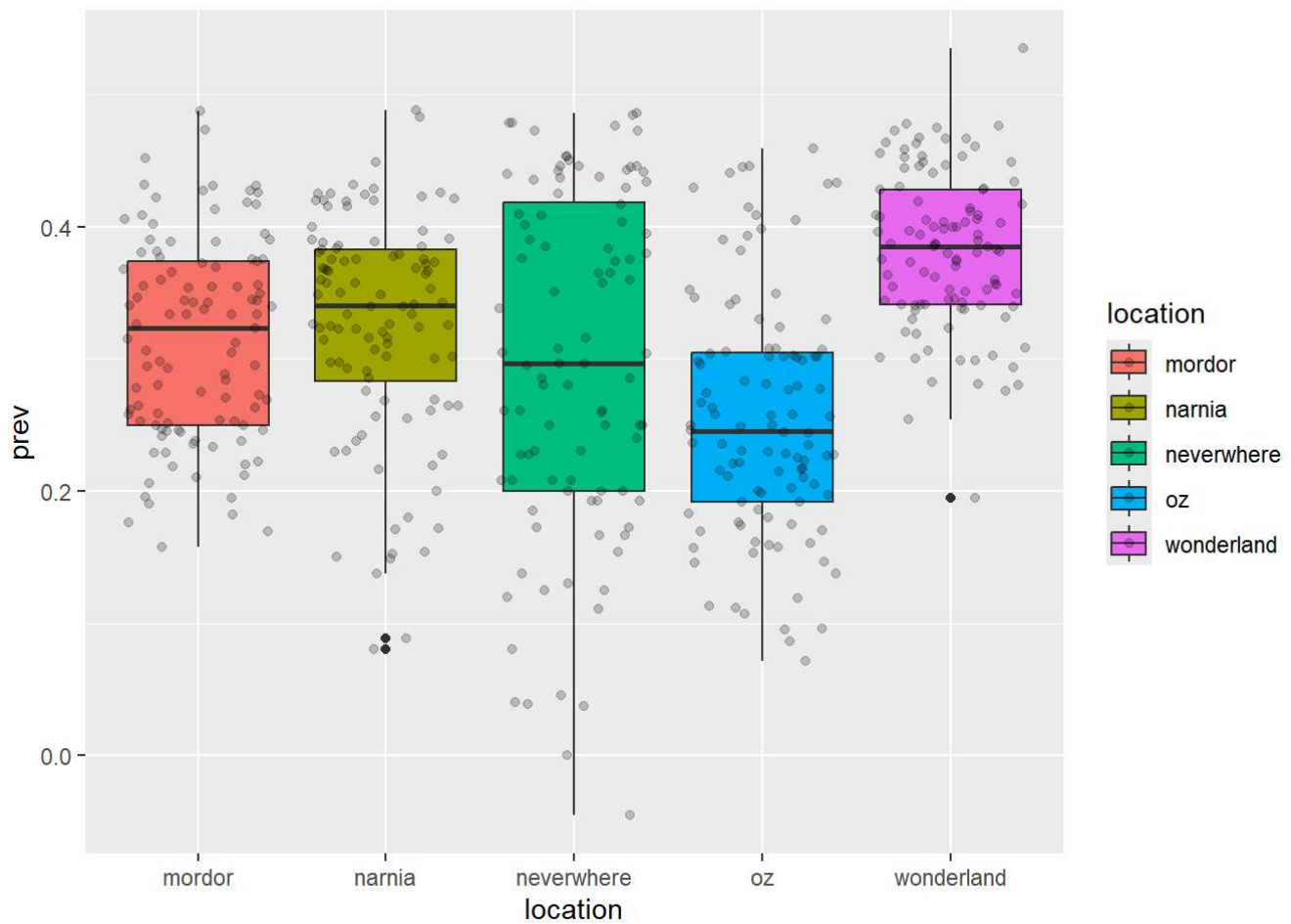




```
ggplot(data = malaria_data, aes(x = prev, fill = ages)) + geom_histogram(colour = "black", bins = 17)
```

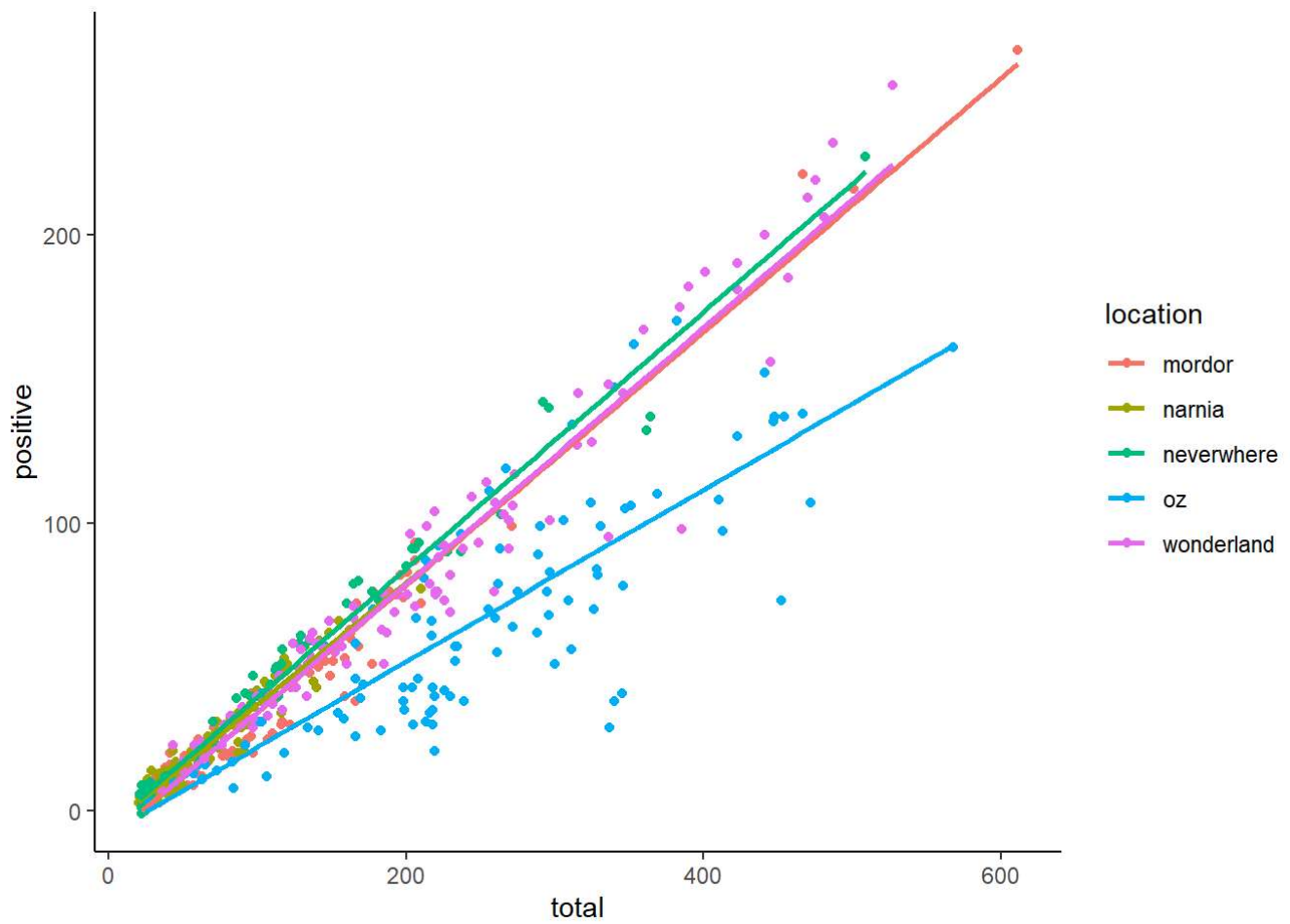


```
ggplot(data = malaria_data, aes(x = location, y = prev, fill = location)) + geom_boxplo
t()+
  geom_jitter(alpha = 0.2)
```

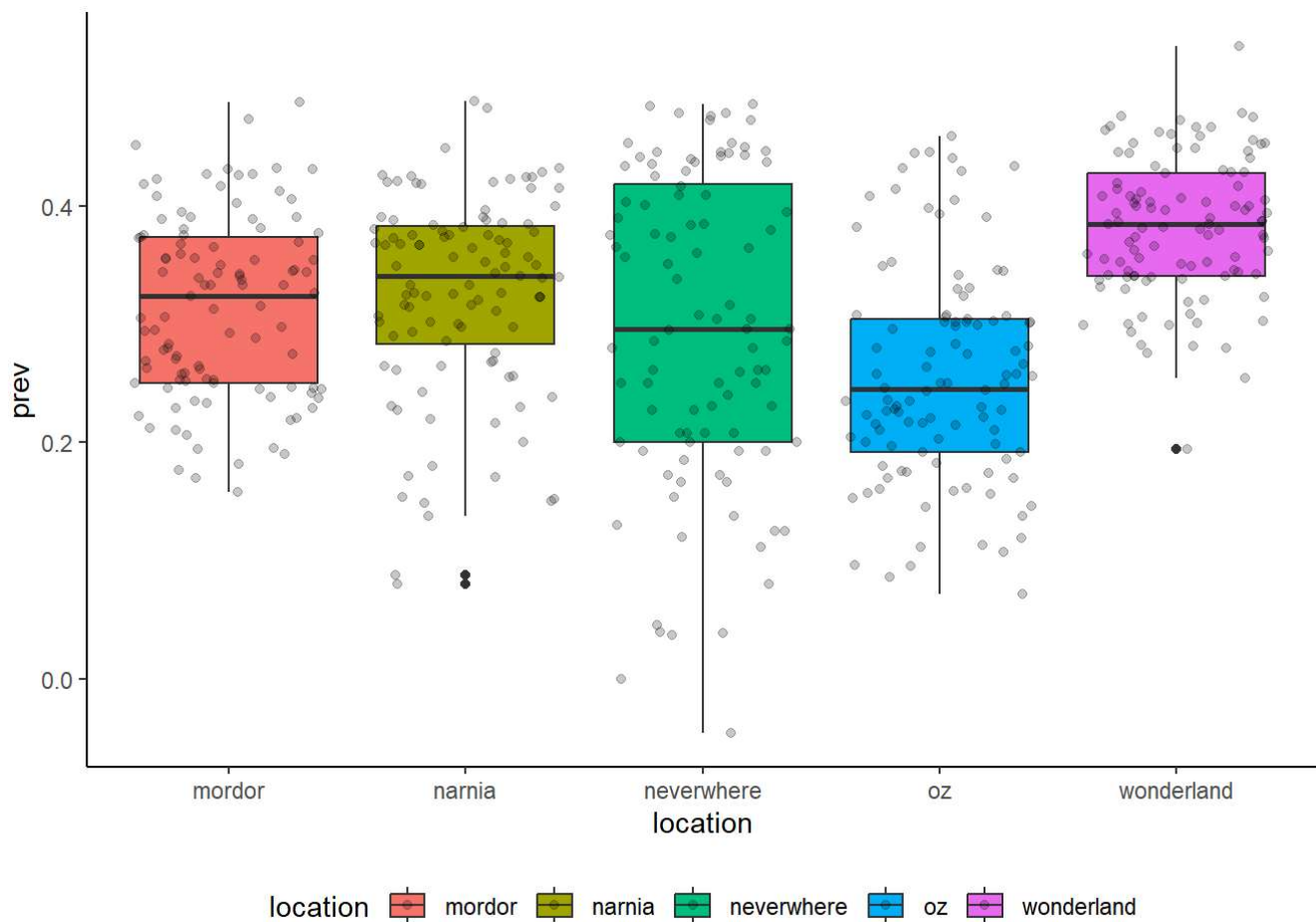


```
ggplot(data = malaria_data, aes(x = total, y = positive, colour = location)) + geom_point() +  
geom_smooth(method = "lm", se = FALSE) + theme_classic()
```

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

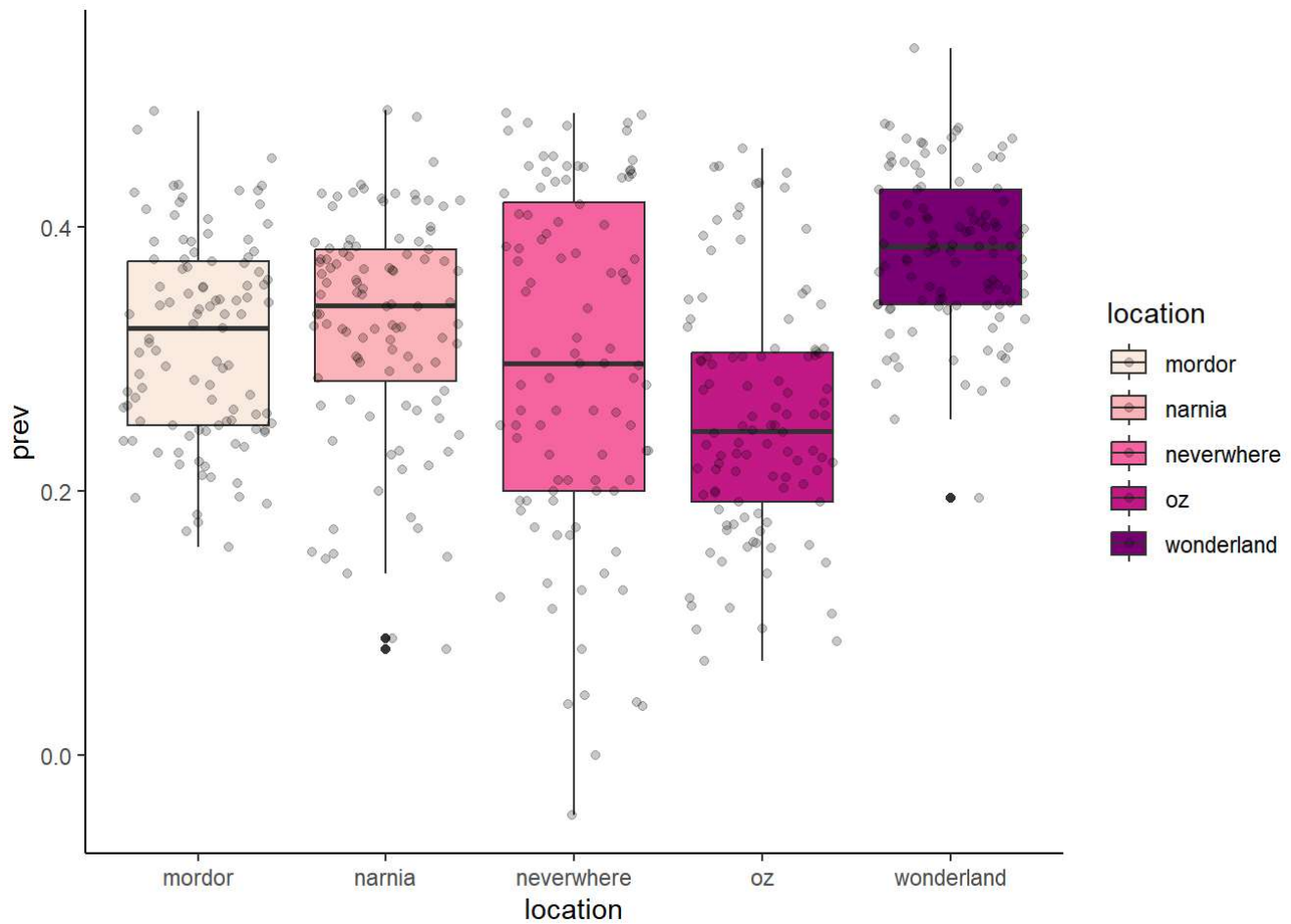


```
ggplot(data = malaria_data, aes(x = location, y = prev, fill = location)) + geom_boxplot() +
  geom_jitter(alpha = 0.2) + theme_classic() + theme(legend.position = "bottom")
```



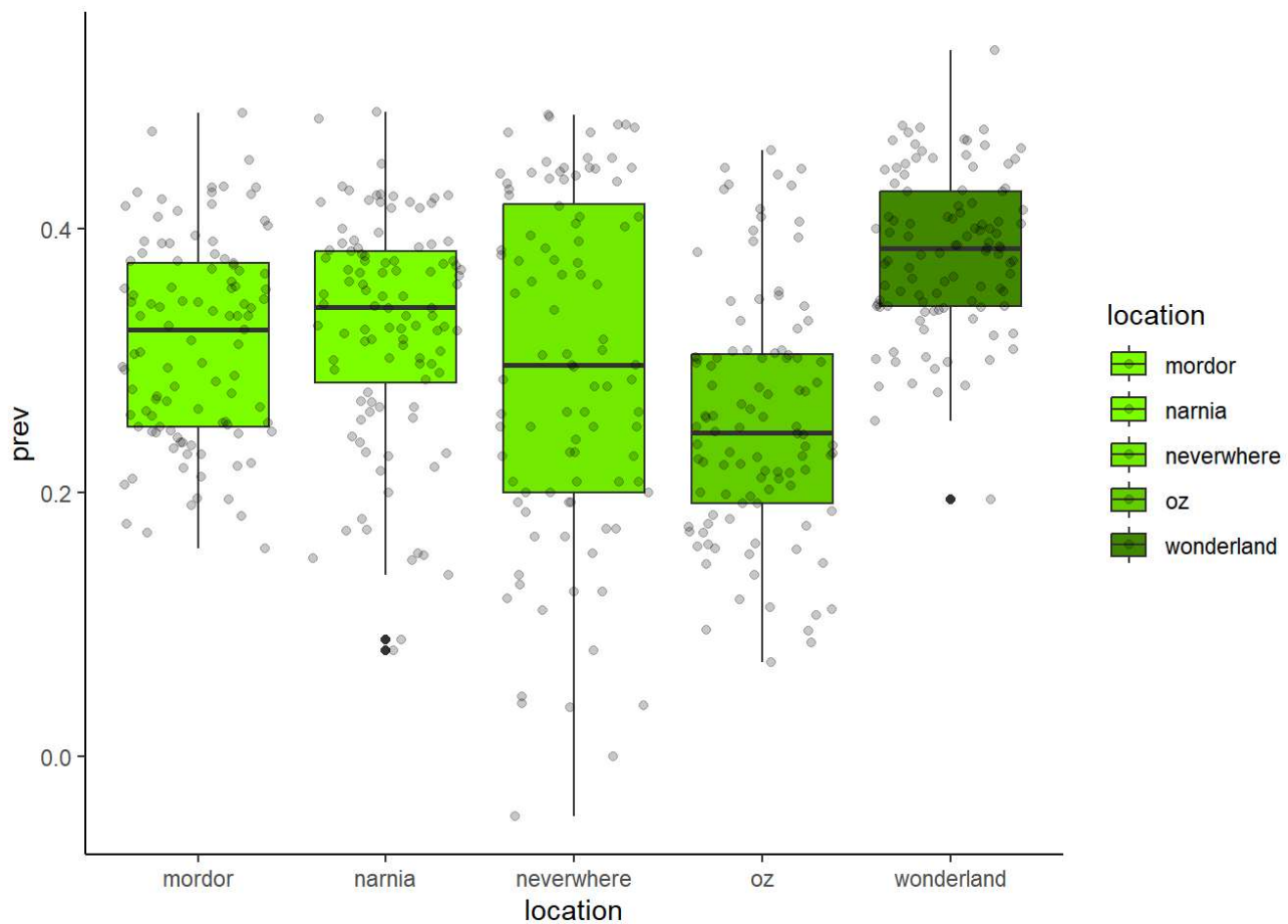
## Add colour Palette automatic using scale\_fill\_brewer

```
ggplot(data = malaria_data, aes(x = location, y = prev, fill = location)) + geom_boxplot() +  
  geom_jitter(alpha = 0.2) + theme_classic() + scale_fill_brewer(palette = "RdPu")
```



## Add colour manually

```
ggplot(data = malaria_data, aes(x = location, y = prev, fill = location)) + geom_boxplot() +
  geom_jitter(alpha = 0.2) + theme_classic() + scale_fill_manual(values = c("chartreuse", "chartreuse1", "chartreuse2", "chartreuse3", "chartreuse4"))
```

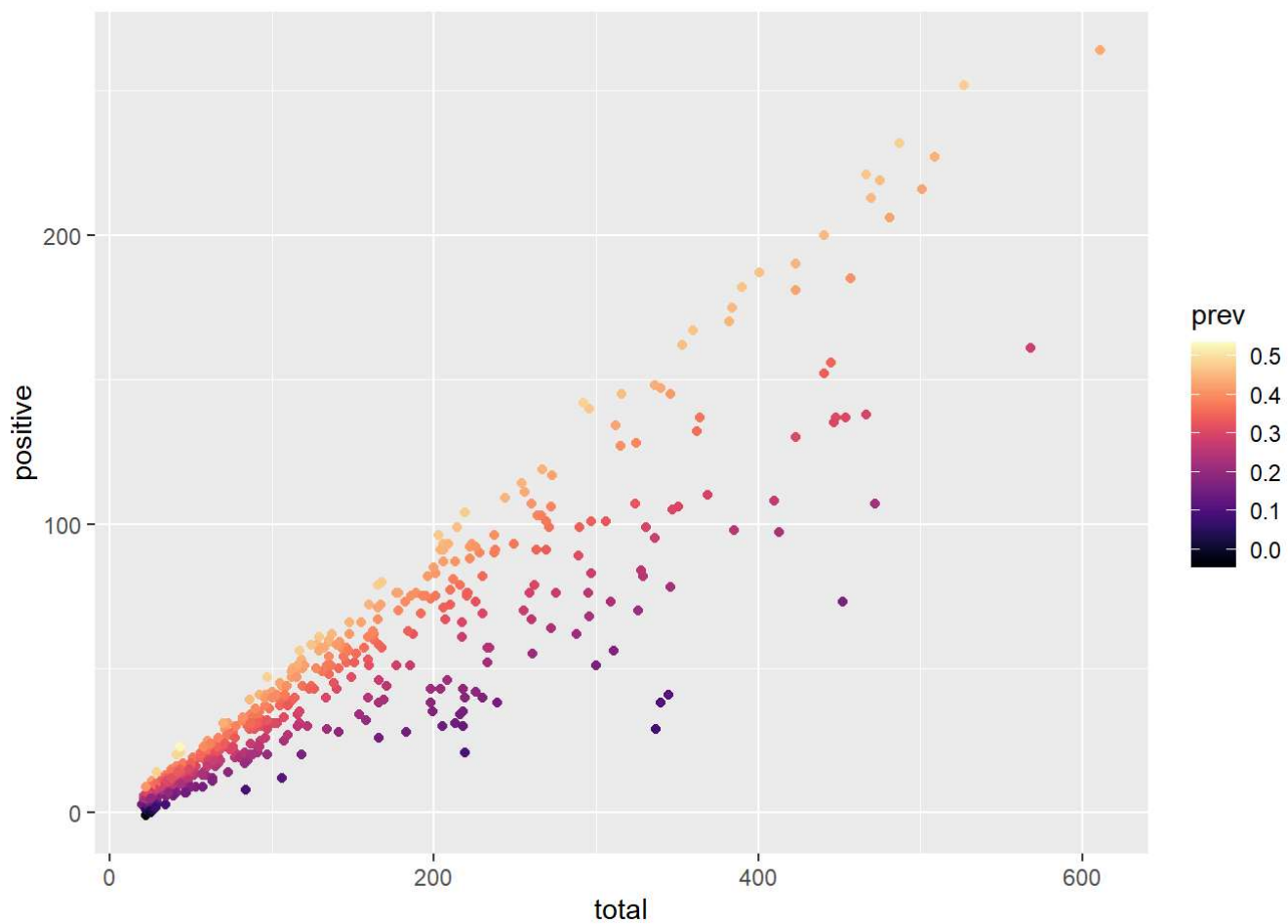


## Use viridis package to create custom color palettes

```
library(viridis)
```

```
## Loading required package: viridisLite
```

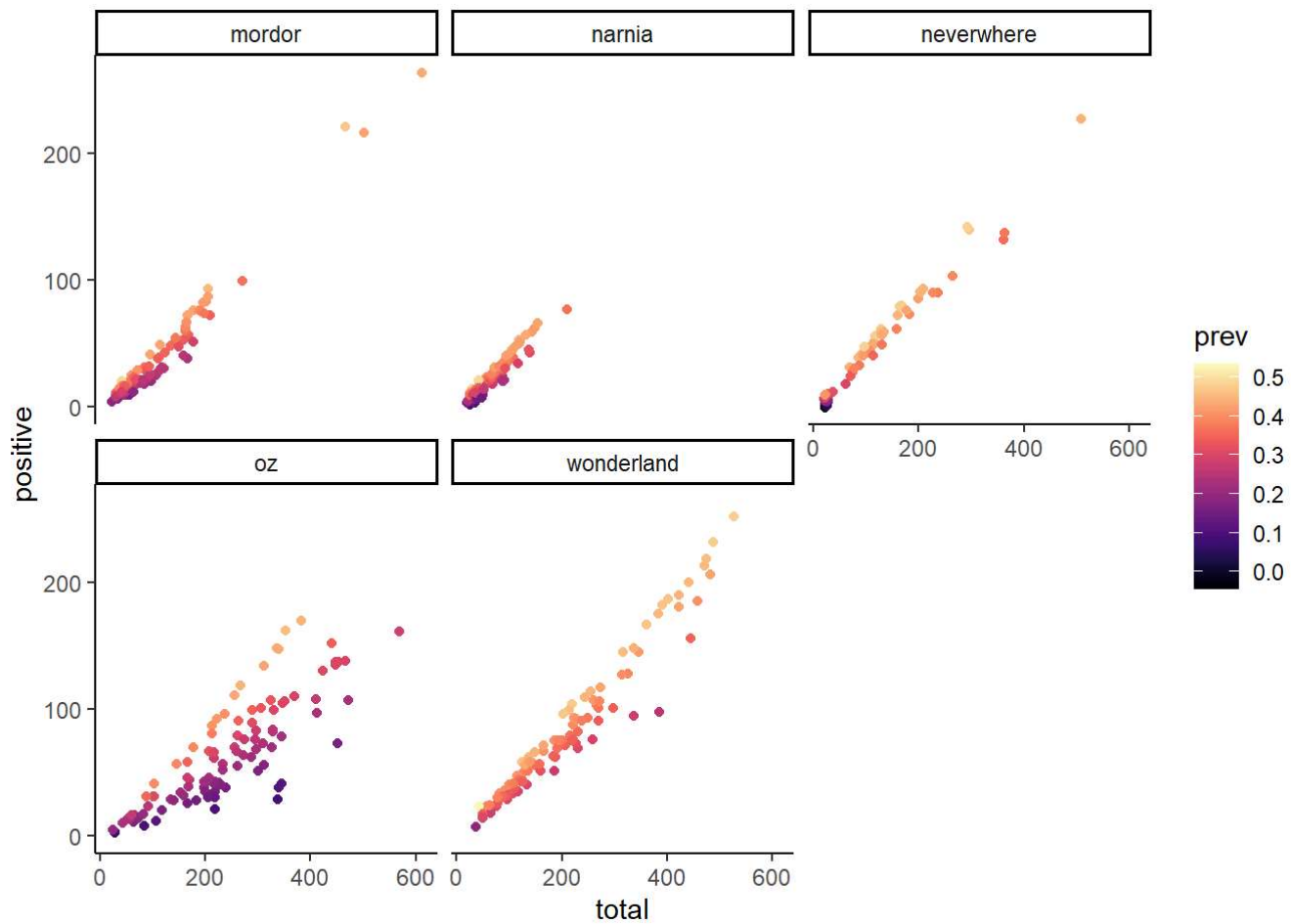
```
ggplot(data = malaria_data, aes(x = total, y = positive, colour = prev)) + geom_point()
+
  scale_color_viridis(option = "magma")
```



## Small multiple plots using facet

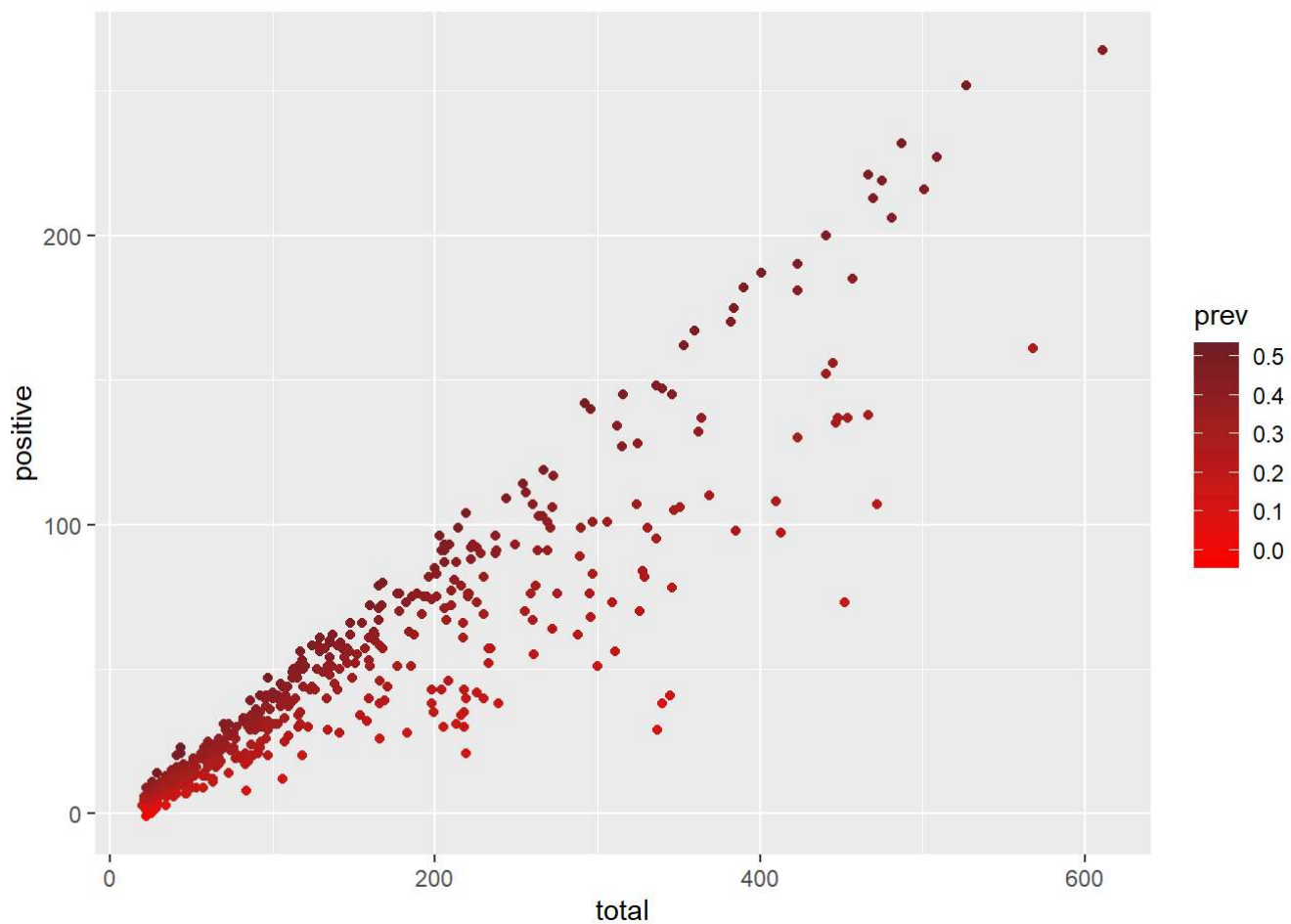
```
ggplot(data = malaria_data, aes(x = total, y = positive, colour = prev)) + geom_point()  
+  
  scale_color_viridis(option = "magma") +  
  facet_wrap(~location)+theme_classic()
```





## Visualize continous data on a spectrum using scale color gradient

```
ggplot(data = malaria_data, aes(x = total, y = positive, colour = prev)) + geom_point()
+
  scale_color_gradient(low = "red", high = "#701f28")
```

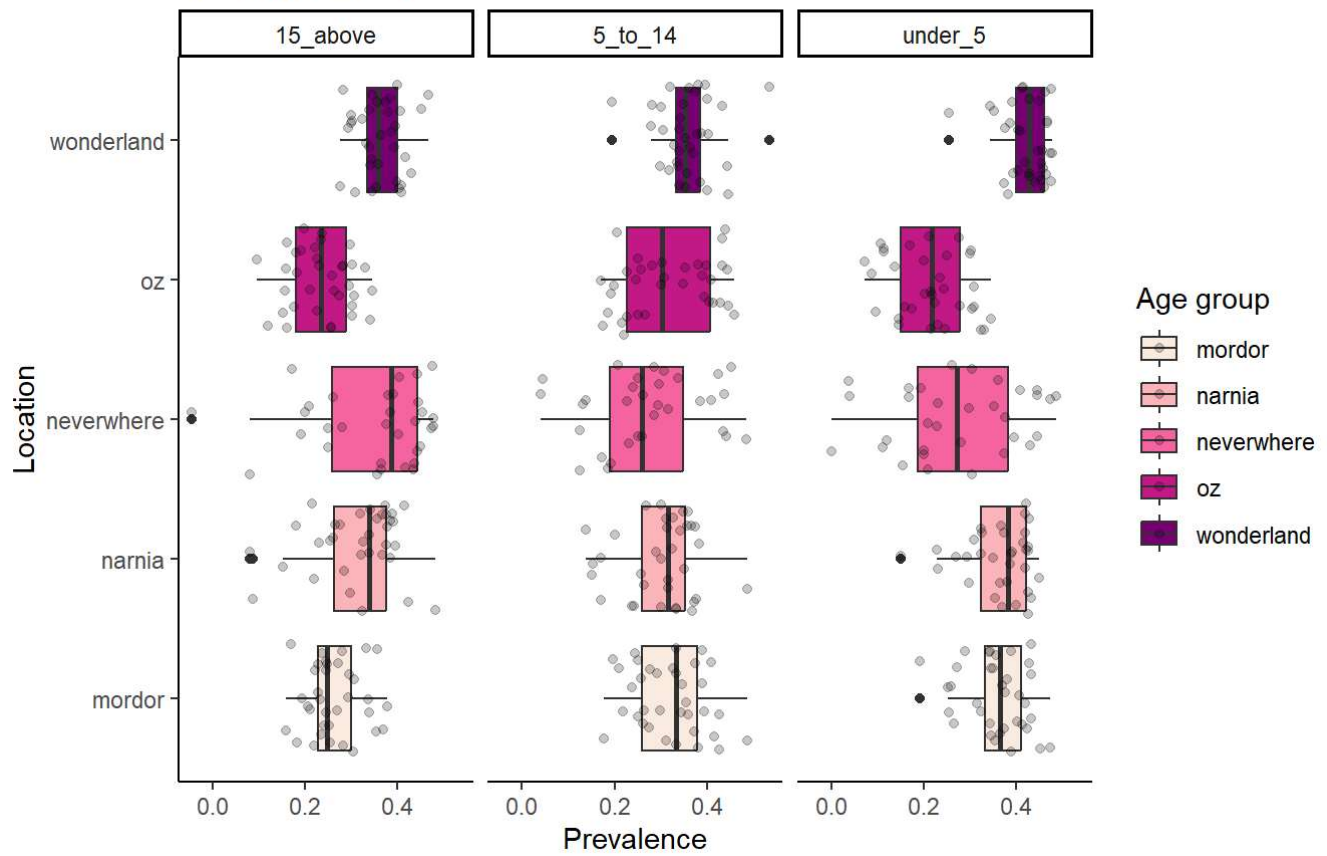


## Adding title, subtitle and flipping x and y axis

```
ggplot(data = malaria_data, aes(x = location, y = prev, fill = location)) + geom_boxplo
t()+
  geom_jitter(alpha = 0.2) +
  facet_wrap(~ages) +
  coord_flip() + # flips the x and y axis
  theme_classic() + scale_fill_brewer(palette = "RdPu")+
  labs(title = "Malaria Prevalence by Location and Age",
        subtitle = "Data from 2018 - 2020",
        x = "Location",
        y = "Prevalence",
        fill = "Age group")
```

# Malaria Prevalence by Location and Age

Data from 2018 - 2020



```
ggsave("malaria_age_prevalenceboxplot.png", width = 10, height = 6, units = "in", dpi = 300)
```