1940223_CIA3.R

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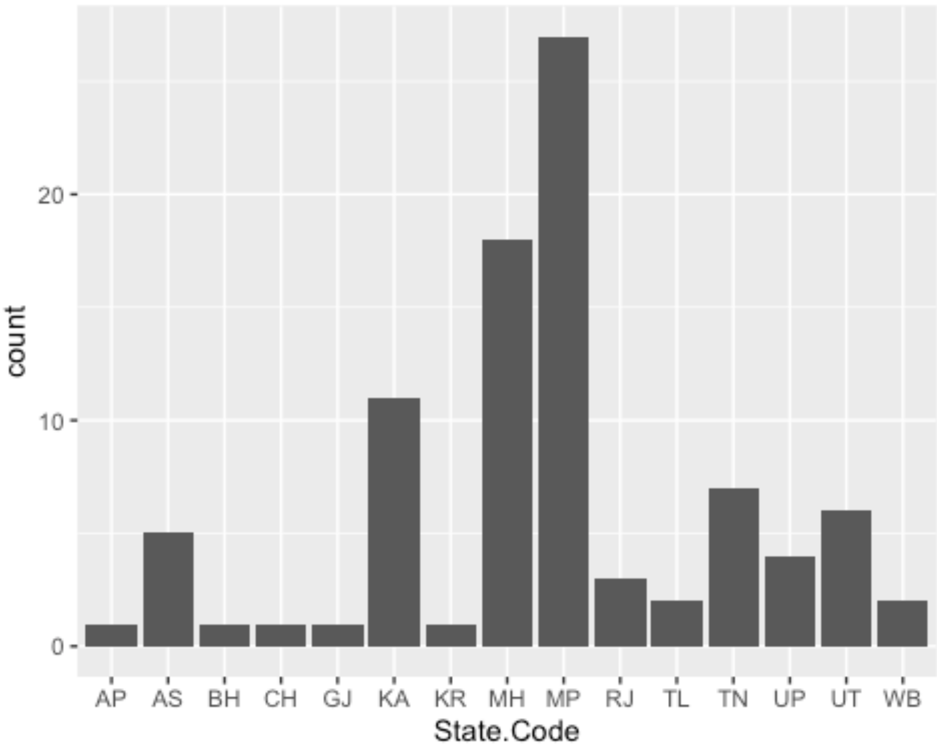
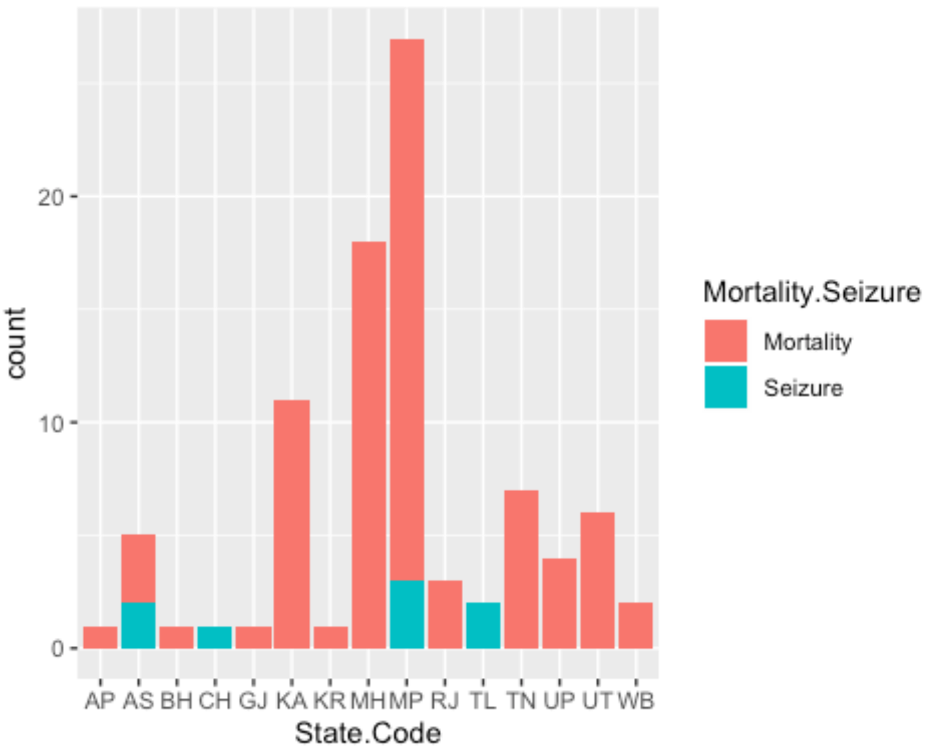
```
data = read.csv("NTCA - TIGERNET.csv")
#ABOUT THE DATASET
#Records: Mortalities and seizures of tigers.
#Country: India
#Year: 2018

#Libraries
library(ggplot2)
library(ggcorrplot)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##     filter, lag
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
attach(data)

head(select(data, 4:8), 6)
##   Mortality.Seizure State.Code          State  Sex  Age
## 1         Mortality         MH    Maharashtra <NA>   NA
## 2         Mortality         MH    Maharashtra <NA>  2.3
## 3         Mortality         MP  Mahya Pradesh <NA>  7.8
## 4         Mortality         MH    Maharashtra <NA>  4.0
## 5         Mortality         KR         Kerala Male 10.4
## 6         Mortality         MP Madhya Pradesh Male  2.0
#1.1
#Bar chart of observations according to state
bp1 = ggplot(data, aes(x = State.Code))
bp1 + geom_bar()
```

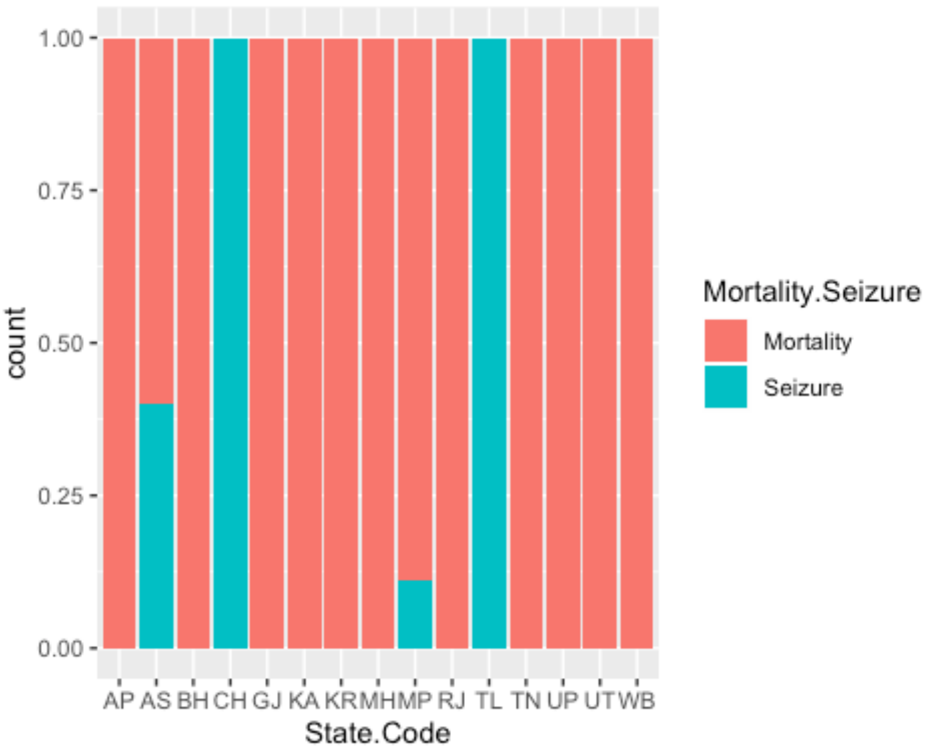



```
#INTERPRETATIONS
#a. Maximum observations are from Madhya Pradesh, followed by Maharshtra and Karnataka
#b. The range of frequencies is large
#   i.e. difference between least no. of observations and most no. of observations is large

#1.2
```

```
#1.2
#Segmented bar chart to see mortalities and seizure per state
bp2 = ggplot(data, aes(x = State.Code, fill = Mortality.Seizure))
#1. In absolute values
bp2 + geom_bar()
```

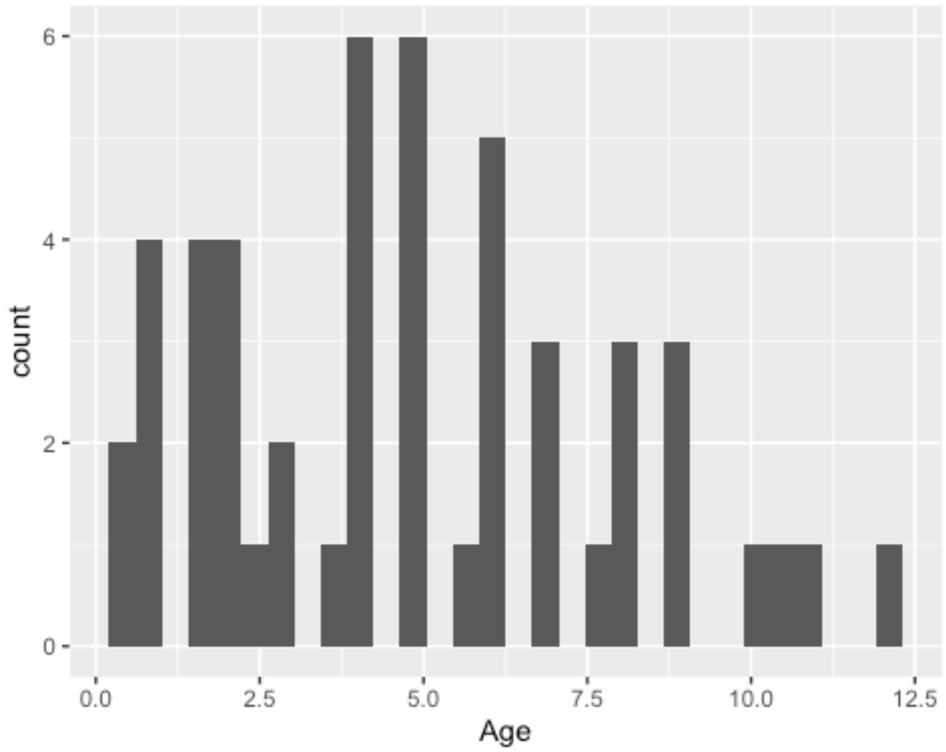



```
#INTERPRETATION
#a. Seizures recorded are very few compared to mortalities
#b. Seizures are recorded only in 4 states
#2. In proportion to the total observations from the state
bp2 + geom_bar(position = "fill")
```

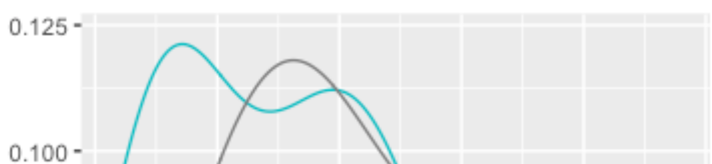


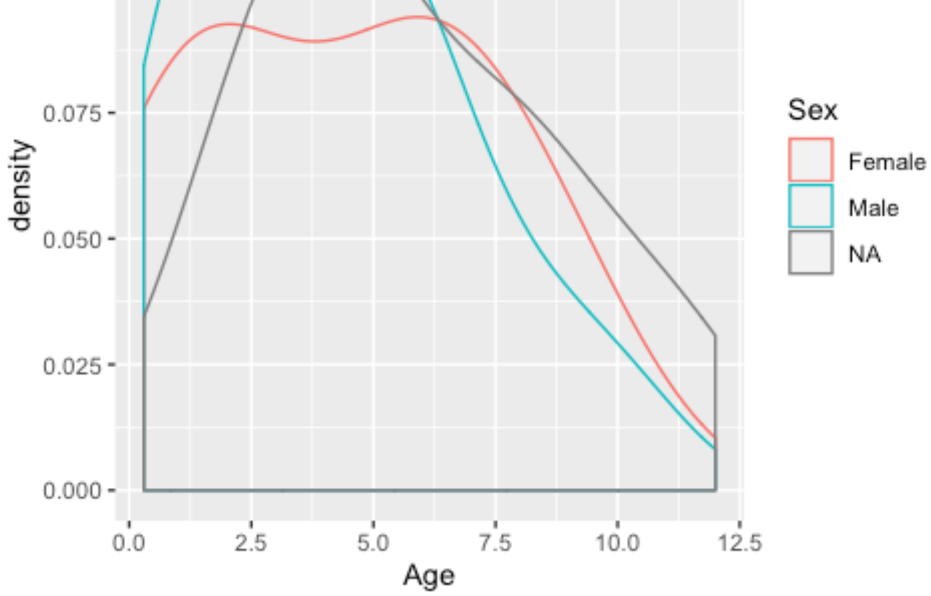

```
#INTERPRETATION
#a. Chandigarh and Telangana recorded seizures in 100% of the observations
#b. Most states recorded mortalities in 100% of the observations

#2.1
#Density plot and histogram according to tiger ages
dp1 = ggplot(data, aes(x = Age))
dp1 + geom_density(na.rm = TRUE)
```


```
dp1 + geom_histogram(na.rm = TRUE)
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

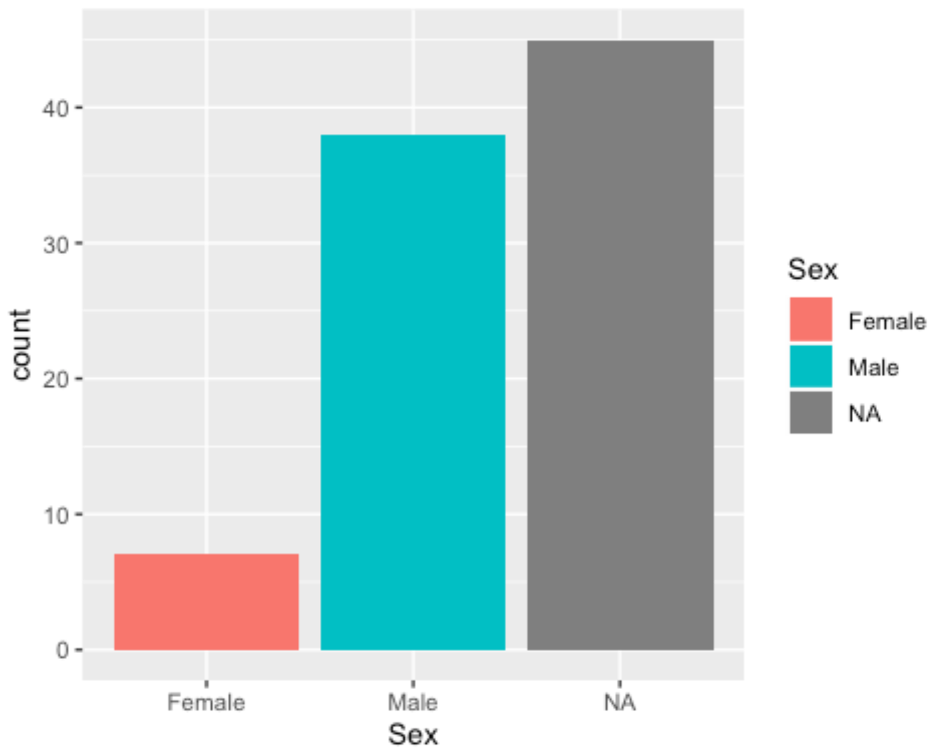



```
#INTERPRETATION
#a. Ages around 5 years is most highly recorded
#b. The observations get almost linearly fewer as the age rises beyond 4-5 years
#   i.e. after around 4-5 years, the number of observed tigers in inversely propotional to age
#c. Observations at the lower extreme of the ages are more numerous than at the higher extreme
#   i.e the density curve is positively skewed
#   This may indicate some combination of the following factors
#   -Infant mortality has risen
#   -Birth rate has fallen
#   (However, due to the significant number of unknown ages, the above conclusions are far from definitive)

#2.2
#Density plot of age considering the two sexes
dp2 = ggplot(data, aes(x = Age, colour = Sex))
dp2 + geom_density(na.rm = TRUE)
```

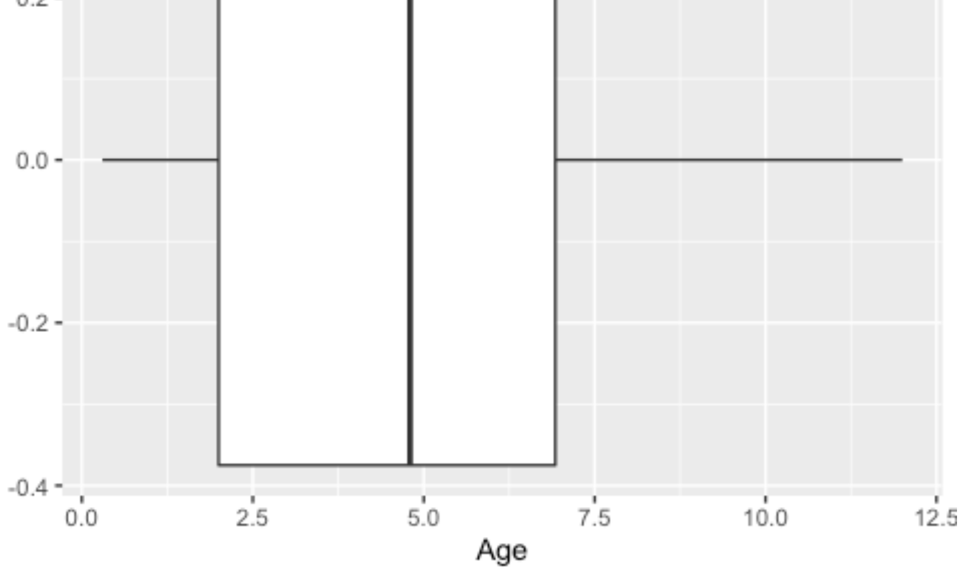




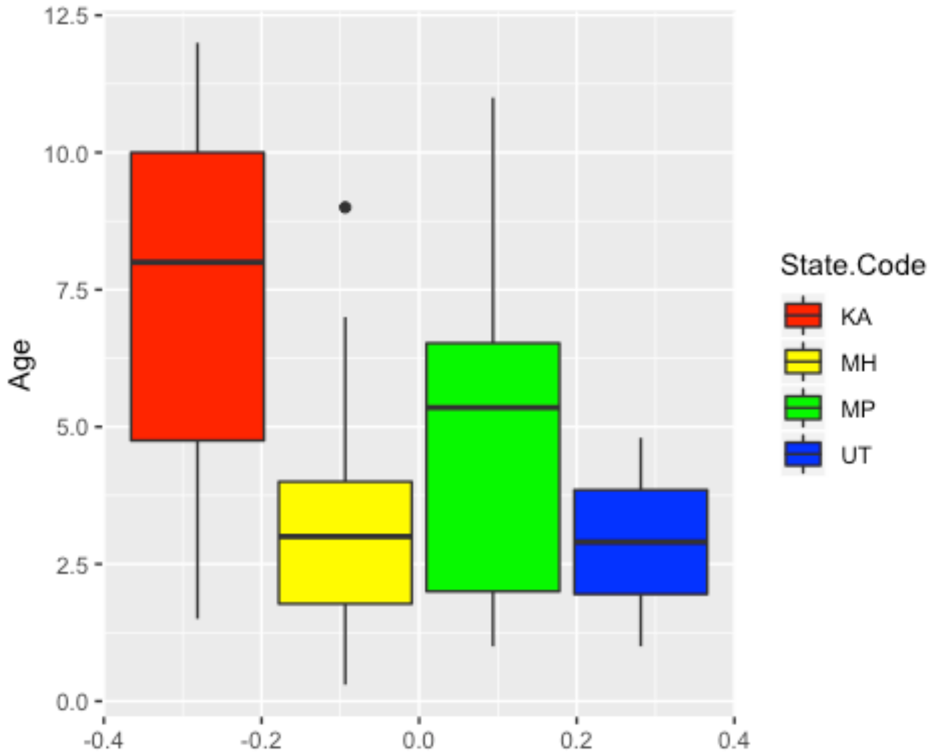

```
#Supporting graph
bp3 = ggplot(data, aes(x = Sex, fill = Sex))
bp3 + geom_bar()
```




```
#INTERPRETATION
#The supporting graph shows that the different density plots do not represent absolute values, only
proportions
#a. There are many more males with lower ages than with higher ages
#   i.e. between 0 and 7
#b. The maximum number of males are with ages around 1.5
#c. The female records follow a similar pattern to male records
#d. The ages are more flatly spread than they are for males
#   Hence, a larger proportion of the female population has higher ages
#   i.e. between 7 and 12.5
#e. The maximum number of females are with ages around 7

#3.1
#Boxplot for ages
bxp1 = ggplot(data, aes(y = Age))
bxp1 + geom_boxplot() + coord_flip()
## Warning: Removed 40 rows containing non-finite values (stat_boxplot).
```

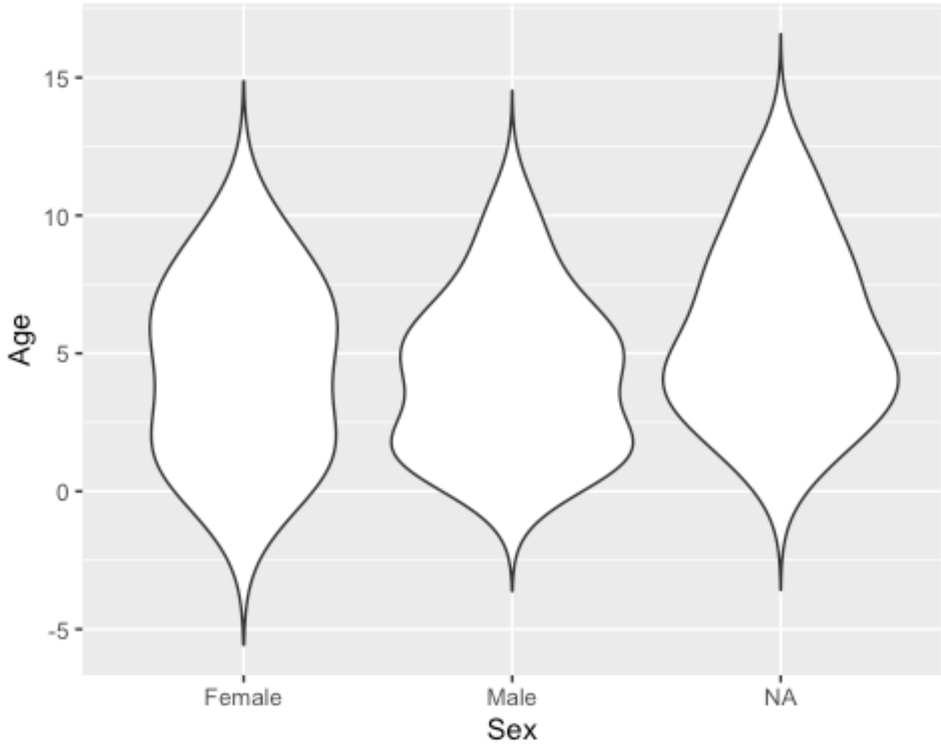



```
#INTERPRETATION
#We can see that
#a. The mean is between 4 to 5
#b. There are no outliers
#   i.e. every value is within an interquartile range from the previous quartile
#c. The 1st quartile is between 2 and 2.5
#d. The 3rd quartile is between 7 and 7.5
#e. The minimum is about 0.25
#f. The maximum is about 12

#3.2
#Boxplot for ages with regard to 4 states
tmp = data
s1 = filter(data, State.Code == "MH")
s2 = filter(data, State.Code == "KA")
s3 = filter(data, State.Code == "MP")
s4 = filter(data, State.Code == "UT")
tmp = union(union(union(s1, s2), s3), s4)
bxp2 = ggplot(tmp, aes(y = Age, fill = State.Code))
bxp2 + geom_boxplot() + scale_fill_manual(values = c("red", "yellow", "green", "blue"))
## Warning: Removed 25 rows containing non-finite values (stat_boxplot).
```

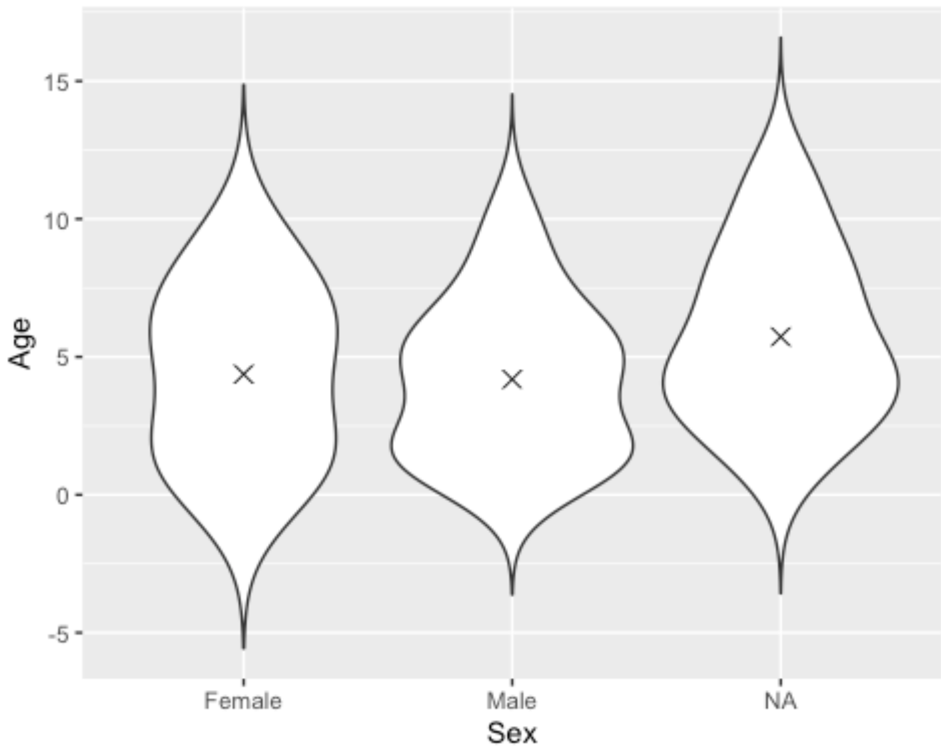



```
#INTERPRETATION
#Among these four states
#a. Tigers observed Karnataka have the highest median, minimum and maximum ages
#b. Karnataka and Madhya Pradesh would have negatively skewed distributions
#   This means that
#   1) Tigers below median age are more scattered accross the age spectrum
#   2) Tigers above median age are more concentrated in a smaller range of ages
```

```
#4.1
#Violin plot for age per sex
vp1 = ggplot(data, aes(x = Sex, y = Age))
vp1 + geom_violin(trim = FALSE)
## Warning: Removed 40 rows containing non-finite values (stat_ydensity).
```




```
vp1 + geom_violin(trim = FALSE) + stat_summary(fun.y = mean, geom = "point", na.rm =
TRUE, shape = "cross", size  = 3)
## Warning: Removed 40 rows containing non-finite values (stat_ydensity).
```

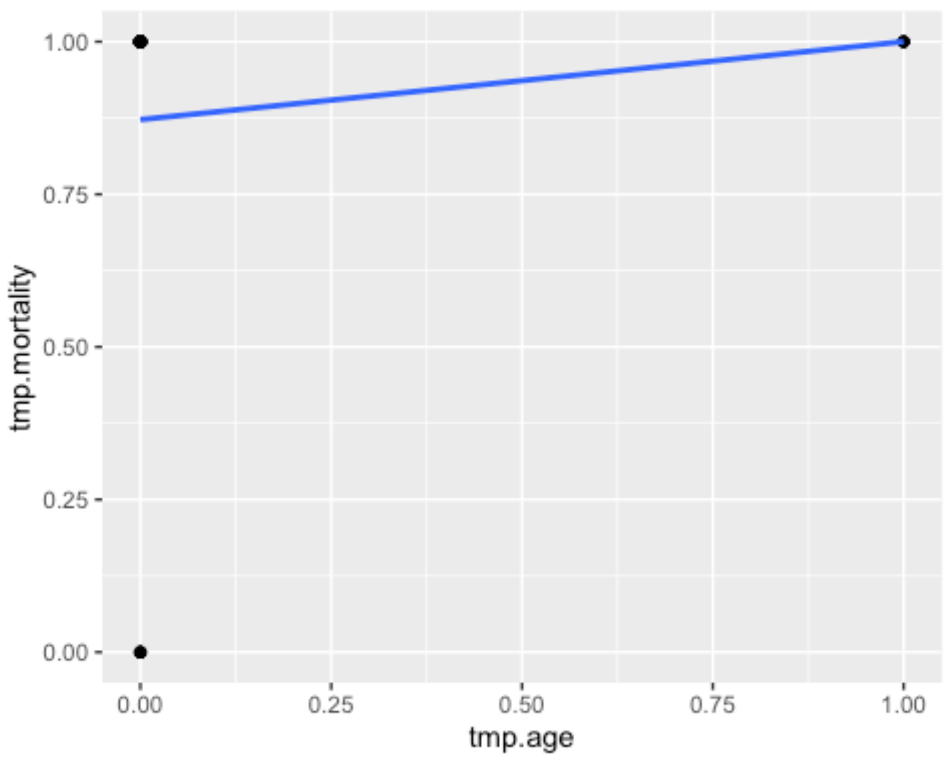



```
#INTERPRETATION
#The interpretations are similar to the density plot.
#a. As seen with the density plot, females are distributed similar to males accross ages
#   (They are also more evenly spread accross ages)
#b. The means of males, females and unrecorded genders are very similar
#c. The population is more concentrated around the young to mid-range ages

#4.2
#Violin and box plot for age with regard to mortalities and sex
vp2 = ggplot(data, aes(x = Mortality.Seizure, y = Age))
vp2 + geom_violin(trim = TRUE) + geom_boxplot( width = 0.1, aes(y = Age, fill = Sex)) +
scale_fill_brewer(palette = "Dark2")
```

```
scale_fill_brewer(palette = "Dark2")
## Warning: Removed 40 rows containing non-finite values (stat_ydensity).

## Warning: Removed 40 rows containing non-finite values (stat_boxplot).
```


```
#INTERPRETATION
#a. Recorded mortalities are higher at lower to mid-range ages
#b. Recorded seizures are only around mid-range ages
#c. No female seizures recorded
#d. From the box plot, the recorded ages of mortalities of females is lower on average than males

#5.1
#Classifying tigers as mature and cubs
data = mutate(data, Age.Group = factor(Age > 2, labels = c("Cub", "Mature")))

#6.1
#Finding age-wise data for each sex and mortality / seizure class
#Mean and standard deviation of ages
group_by(data, Sex, Mortality.Seizure) %>% summarise(mean(Age, na.rm = TRUE), sd(Age,
na.rm = TRUE))
## Warning: Factor `Sex` contains implicit NA, consider using
## `forcats::fct_explicit_na`
## Warning: Factor `Sex` contains implicit NA, consider using
## `forcats::fct_explicit_na`
## # A tibble: 5 x 4
## # Groups:   Sex [3]
##   Sex    Mortality.Seizure `mean(Age, na.rm = TRUE)` `sd(Age, na.rm = TRUE)`
##   <fct>  <fct>                                 <dbl>                   <dbl>
## 1 Female Mortality                              4.37                    3.20
## 2 Male   Mortality                              3.86                    2.71
## 3 Male   Seizure                                7.5                     2.12
## 4 <NA>   Mortality                              5.72                    3.33
## 5 <NA>   Seizure                                5.75                    2.35
#Minimum and maximum of ages
group_by(data, Sex, Mortality.Seizure) %>% summarise(min(Age, na.rm = TRUE), max(Age,
na.rm = TRUE))
## Warning: Factor `Sex` contains implicit NA, consider using
## `forcats::fct_explicit_na`

## Warning: Factor `Sex` contains implicit NA, consider using
## `forcats::fct_explicit_na`
## # A tibble: 5 x 4
## # Groups:   Sex [3]
##   Sex    Mortality.Seizure `min(Age, na.rm = TRUE)` `max(Age, na.rm = TRUE)`
##   <fct>  <fct>                                <dbl>                    <dbl>
## 1 Female Mortality                              0.3                      9
## 2 Male   Mortality                              0.5                     10.4
## 3 Male   Seizure                                6                        9
## 4 <NA>   Mortality                              1                       12
## 5 <NA>   Seizure                                3.5                      9
```

```r
## 5 <NA> Seizure 5.5 9
#7.1
#Correlation may not be meaningful or accurate as there are many unknown values, hence we may
not have sufficient to indicate relations.
#Also, I am calculating correlation for binary variables, and the available correlation methods may
not be appropriate.

#Correlation between age and mortality
j = 1
tmp.age = c(0)
tmp.mortality = c(0)
for(i in 1:90)
{
 if(!is.na(Age[i]) && !is.na(Mortality.Seizure))
 {
  tmp.age[j] = Age[i] > 10
  tmp.mortality[j] = Mortality.Seizure[i] == "Mortality"
  j = j + 1
 }
}
cor(tmp.age, tmp.mortality)
## [1] 0.09329556
#INTERPRETATION
#We see a very weak correlation between age being above 10 and mortality
#However, this could be because of the many missing values

#7.2
#Confirming that the vectors are of the same size
length(tmp.age)
## [1] 50
length(tmp.mortality)
## [1] 50
#Making a dataframe from the vectors
df = data.frame(tmp.age, tmp.mortality)
#Finding the regression
lm(tmp.mortality~tmp.age, data = df)
##
## Call:
## lm(formula = tmp.mortality ~ tmp.age, data = df)
##
## Coefficients:
## (Intercept)      tmp.age
##      0.8723       0.1277
#According to the result, mortality = 0.8723 + 0.1277*age
ggplot(df, aes(x = tmp.age, y = tmp.mortality)) + geom_point() + geom_smooth(method = "lm",
se = FALSE)
```




```r
#INTERPRETATION
#The above result is not meaningful, and is done mainly to show off my skills
#It is not meaningul, as it is not between two continuous variables
```

#It is not meaningful, as it is not between two continuous variables