

# Lab1

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## Tasks

### Task 1

Find the working directory

```
getwd()
```

```
## [1] "C:/Users/dezaf/Documents/Fall 2020/Stats/Labs/Lab1"
```

### Task 2

Read in the DDT data

```
ddt <- read.csv("DDT.csv")  
head(ddt)
```

```
##   RIVER MILE  SPECIES LENGTH WEIGHT DDT  
## 1   FCM     5 CCATFISH  42.5    732  10  
## 2   FCM     5 CCATFISH  44.0    795  16  
## 3   FCM     5 CCATFISH  41.5    547  23  
## 4   FCM     5 CCATFISH  39.0    465  21  
## 5   FCM     5 CCATFISH  50.5   1252  50  
## 6   FCM     5 CCATFISH  52.0   1255 150
```

### Task 3

- The qualitative variables are RIVER and SPECIES
- The quantitative variables are MILE< LENGTH< WEIGHT, and DDT
- 3
- Subset the ddt data set so that we see only those obs with Species, LMBASS and Weight bigger than 800gms

```
test <- with(ddt, ddt[SPECIES=="LMBASS" & WEIGHT>800,] )  
test
```

```
##   RIVER MILE SPECIES LENGTH WEIGHT DDT  
## 141   TRM  345  LMBASS     30    856 2.2  
## 144   TRM  345  LMBASS     36   1433 1.9
```

e. Subset the ddt data set so that we see only those obs where the river is SCM and DDT bigger than 4.0

```
test1 <- with(ddt, ddt[RIVER=="SCM" & DDT>4,])
test1
```

```
##      RIVER MILE  SPECIES LENGTH WEIGHT DDT
## 16    SCM      1 CCATFISH     45    984 9.1
## 17    SCM      1 CCATFISH     43    965 7.8
## 18    SCM      1 CCATFISH     45   1084 4.1
```

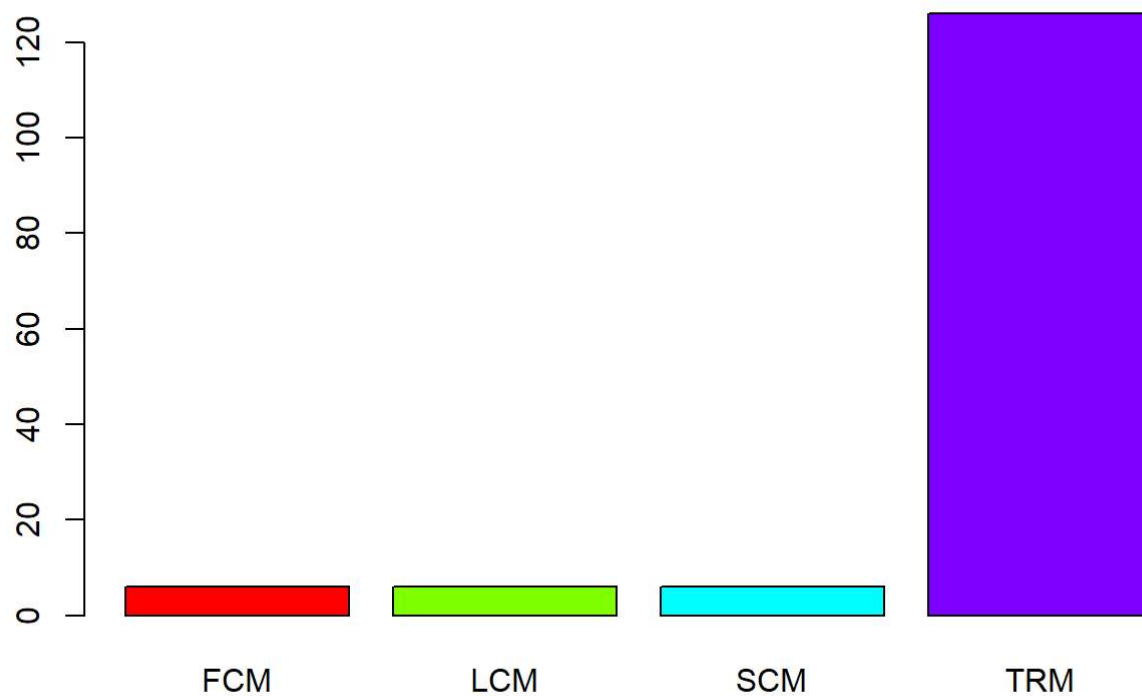
## Task 4

```
### Make a table of rivers
tb=with(ddt, RIVER)
tb
```

```
##      [1] "FCM" "FCM" "FCM" "FCM" "FCM" "FCM" "FCM" "LCM" "LCM" "LCM" "LCM" "LCM" "LCM"
##     [13] "SCM" "SCM" "SCM" "SCM" "SCM" "SCM" "SCM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [25] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [37] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [49] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [61] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [73] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [85] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##     [97] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##    [109] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##    [121] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
##    [133] "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM" "TRM"
```

```
### Make a color coded barplot of the rivers
tbb <- table(ddt$RIVER)
barplot(tbb, main = "Rivers", col = rainbow(4))
```

## Rivers



```
### Make a table of the rivers crossed with the species of fish
```

```
rf <- table(ddt$RIVER, ddt$SPECIES)
```

```
rf
```

```
##
```

```
##      CCATFISH LMBASS SMBUFFALO
```

```
## FCM         6      0         0
```

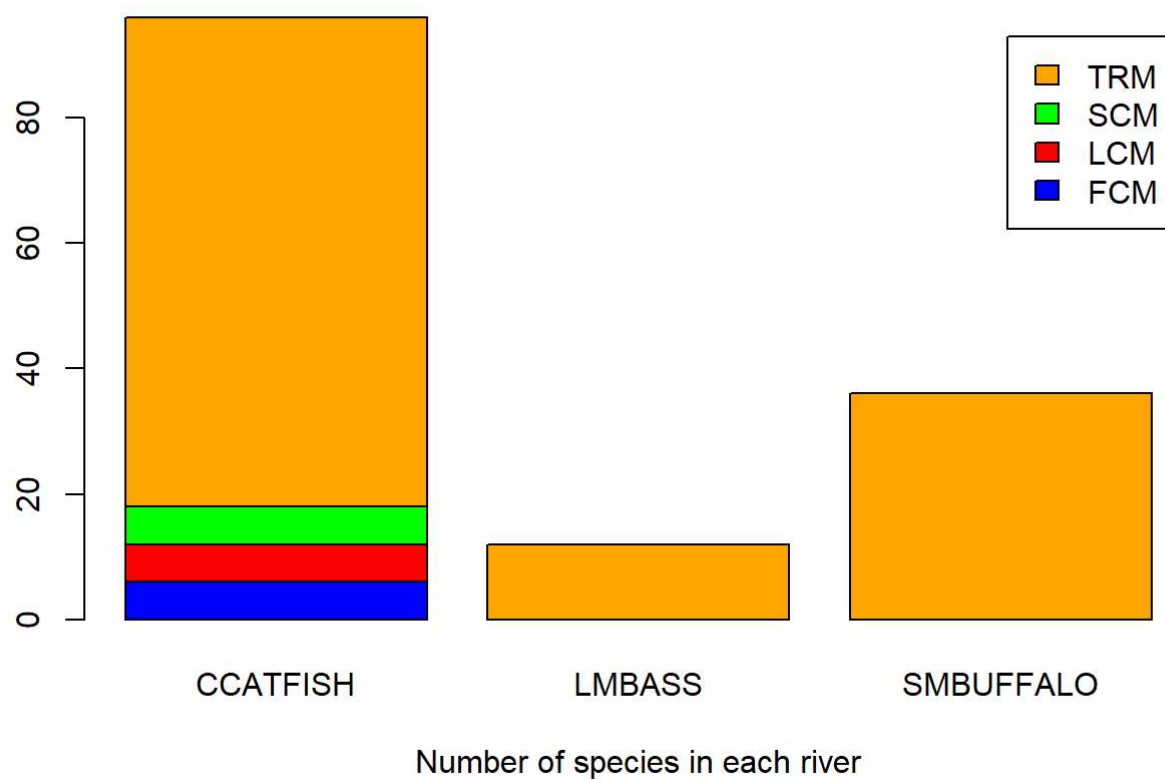
```
## LCM         6      0         0
```

```
## SCM         6      0         0
```

```
## TRM        78     12        36
```

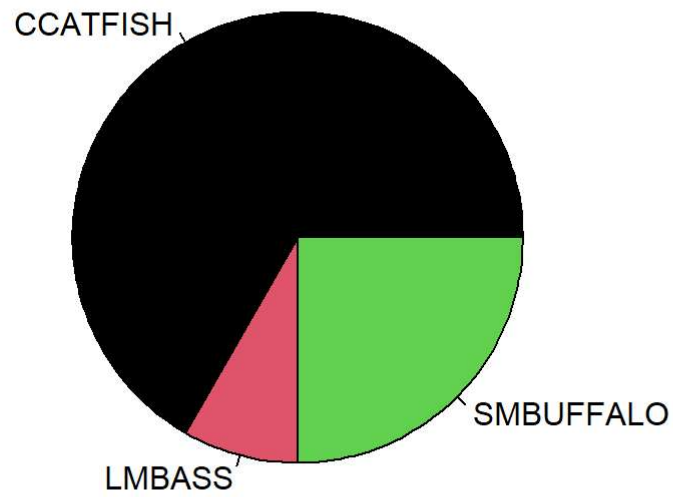
```
### Make a barplot of the rivers crossed with the species of fish
```

```
barplot(rf, xlab="Number of species in each river", col=c("blue","red","green","orange"),legend=
rownames(rf))
```

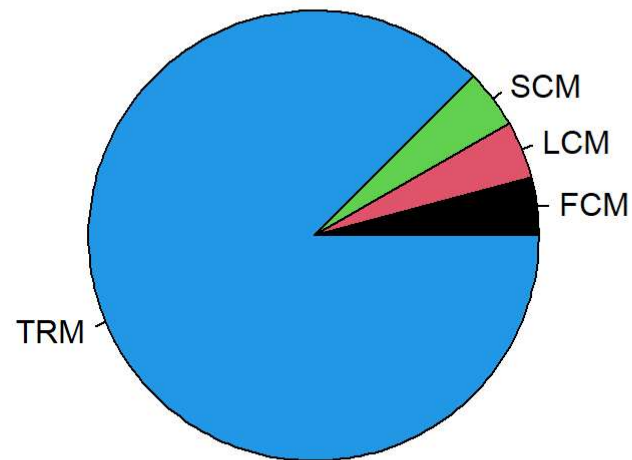


## Task 5

```
### Mle a pie chart of Fish Species  
fspec <- table(ddt$SPECIES)  
pie(fspect, col=1:3)
```

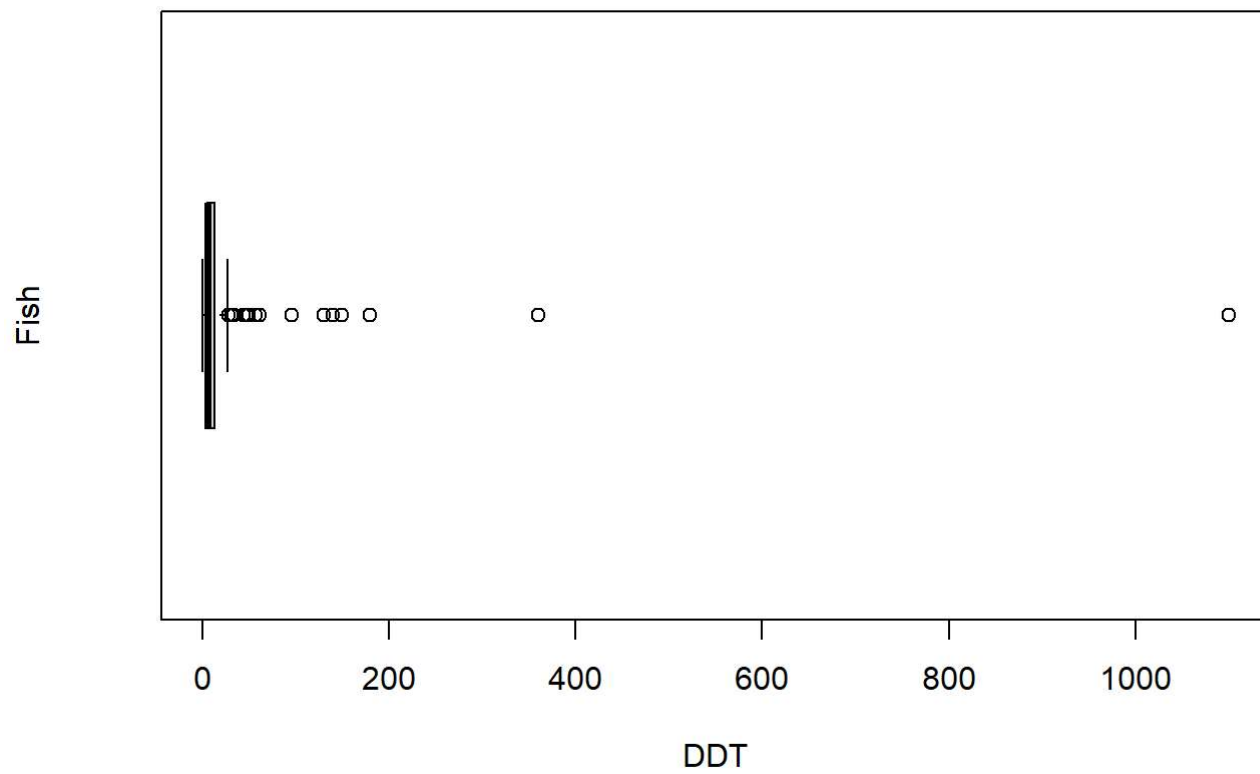


```
### Make a pie chart of RIVERS  
pie(tbb, col=1:4)
```

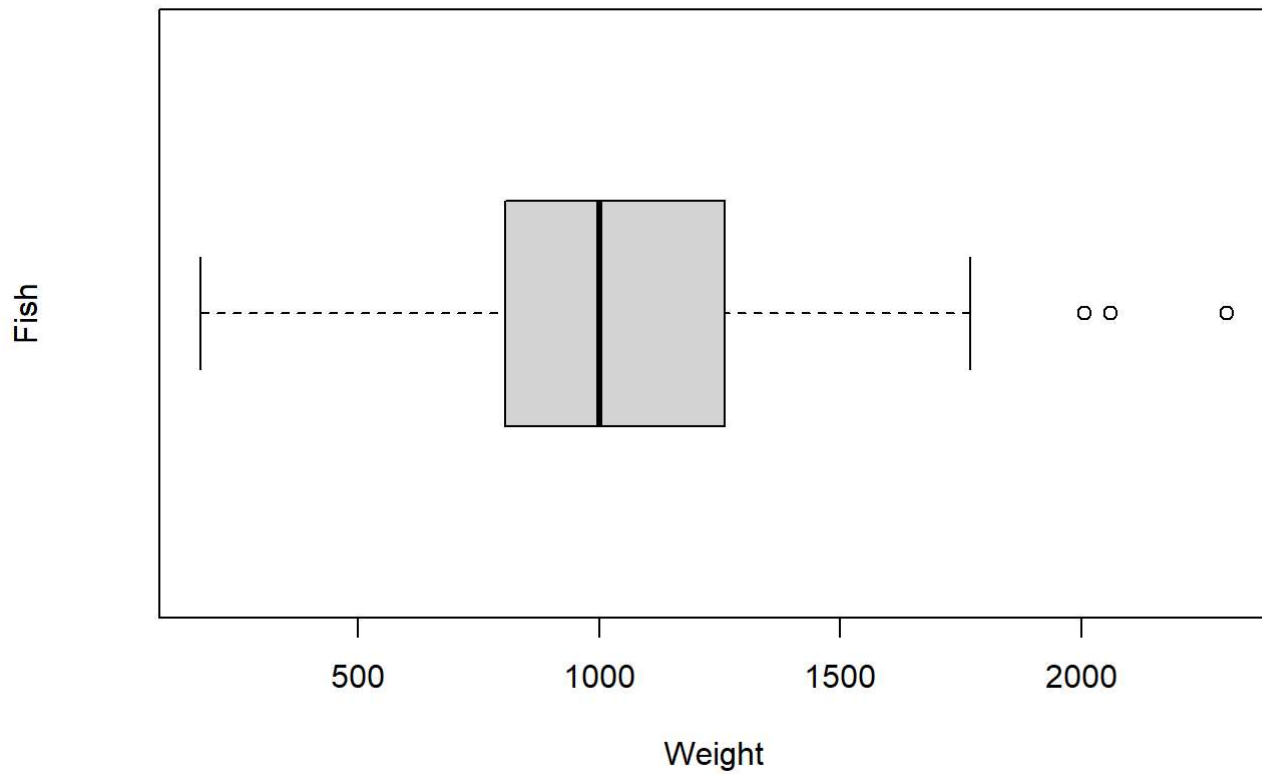


## Task 6

```
### Make a boxplot of the variable DDT  
boxplot(ddt$DDT, horizontal = TRUE, ylab="Fish",xlab="DDT")
```

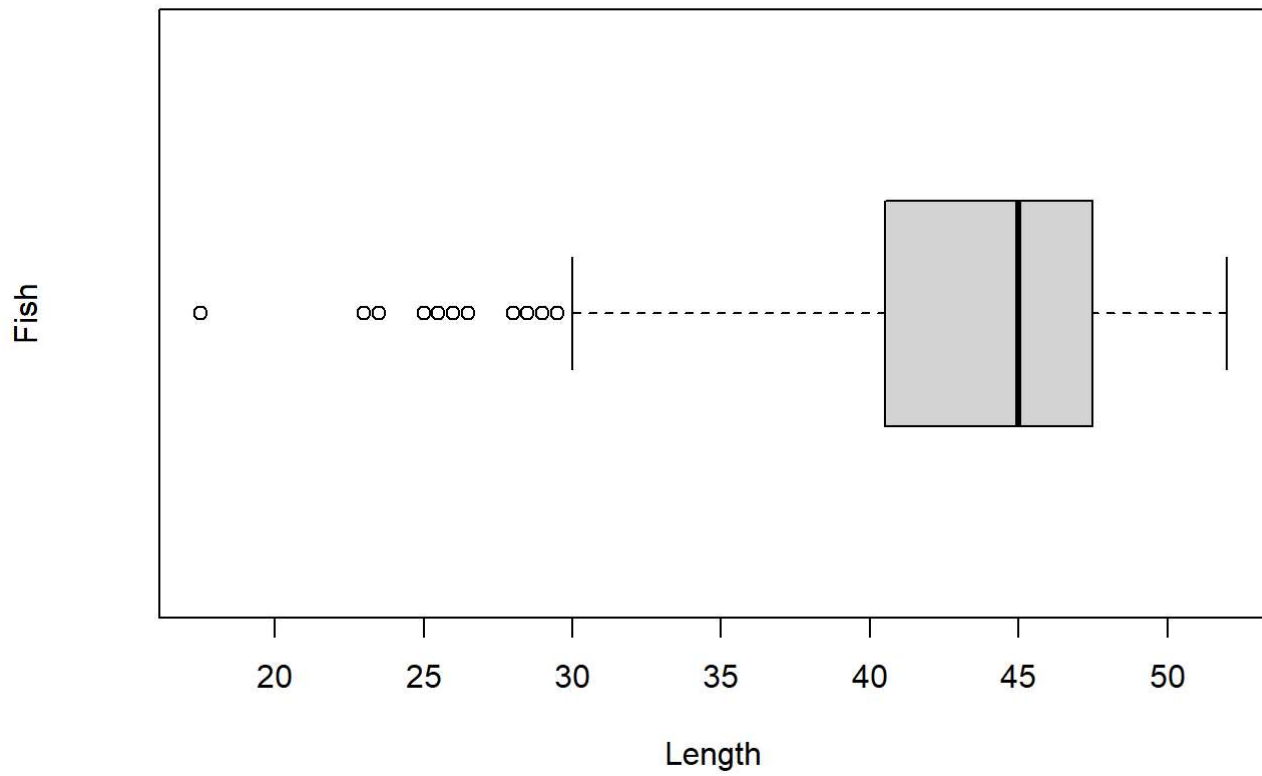


```
### Make a boxplot of the variable WEIGHT  
boxplot(ddt$WEIGHT, horizontal = TRUE, ylab="Fish",xlab="Weight")
```



```
### Make a boxplot of the variable LENGTH  
boxplot(ddt$LENGTH, horizontal = TRUE, ylab="Fish", xlab="Length")
```

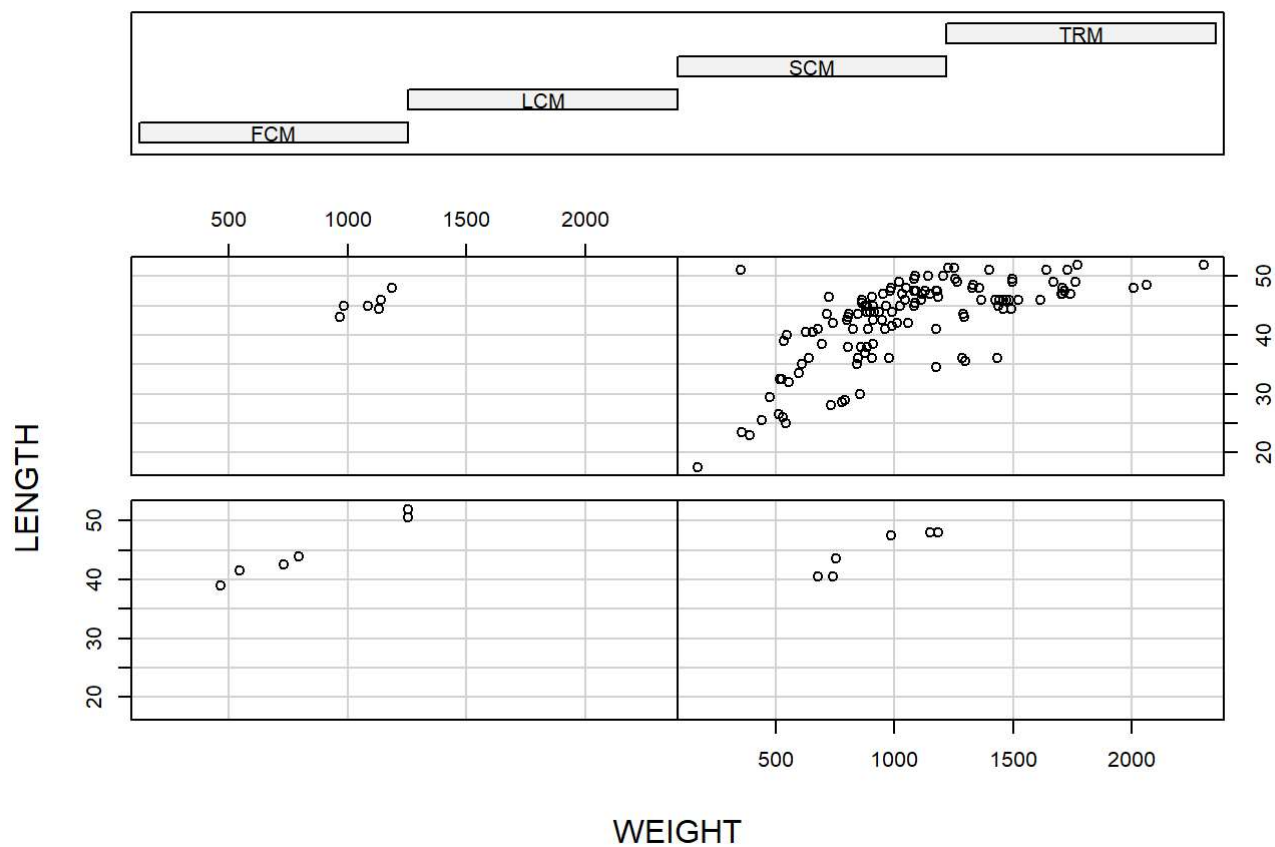




## Task 7

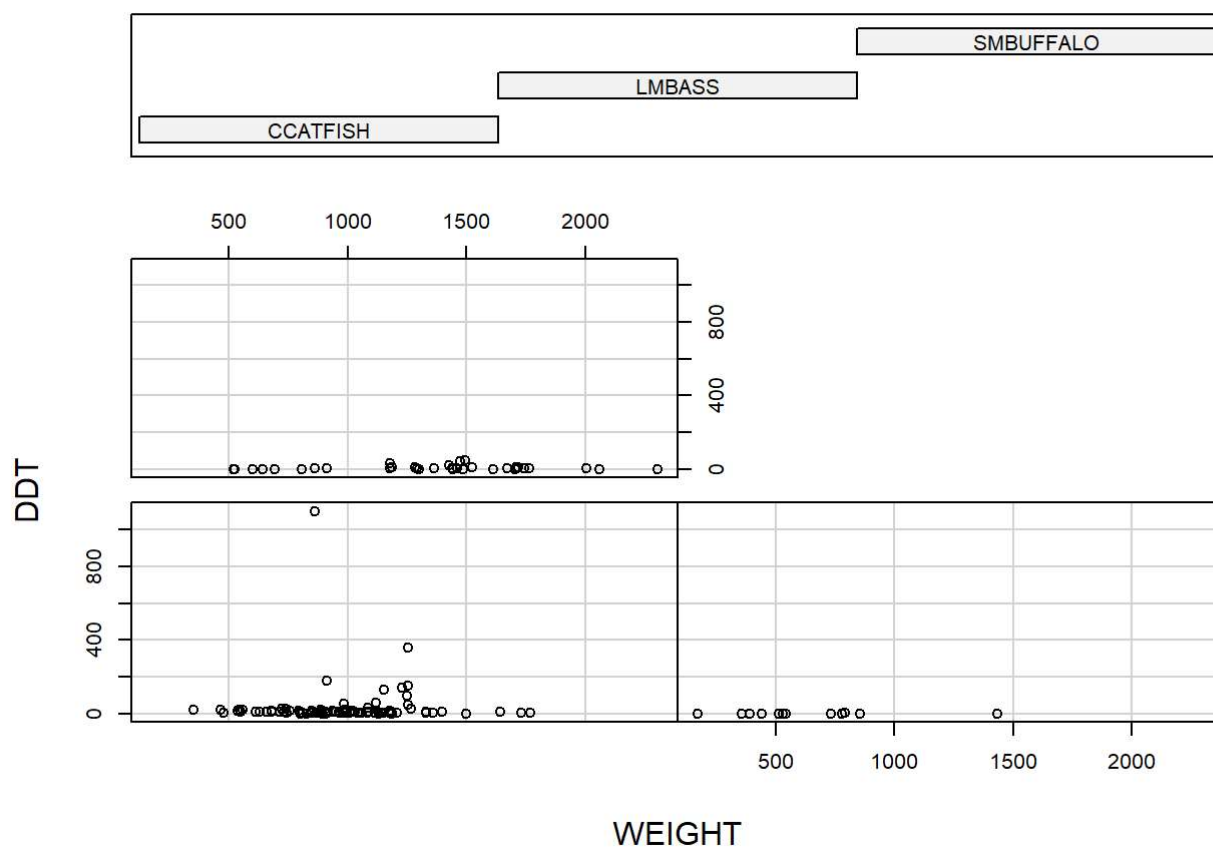
```
### Make a coplot of length vs weight given river  
coplot(LENGTH~WEIGHT|RIVER, data=ddt)
```

Given : RIVER



```
### Make a coplot of DDT Vs Weight given species
coplot(DDT~WEIGHT|SPECIES, data = ddt)
```

Given : SPECIES

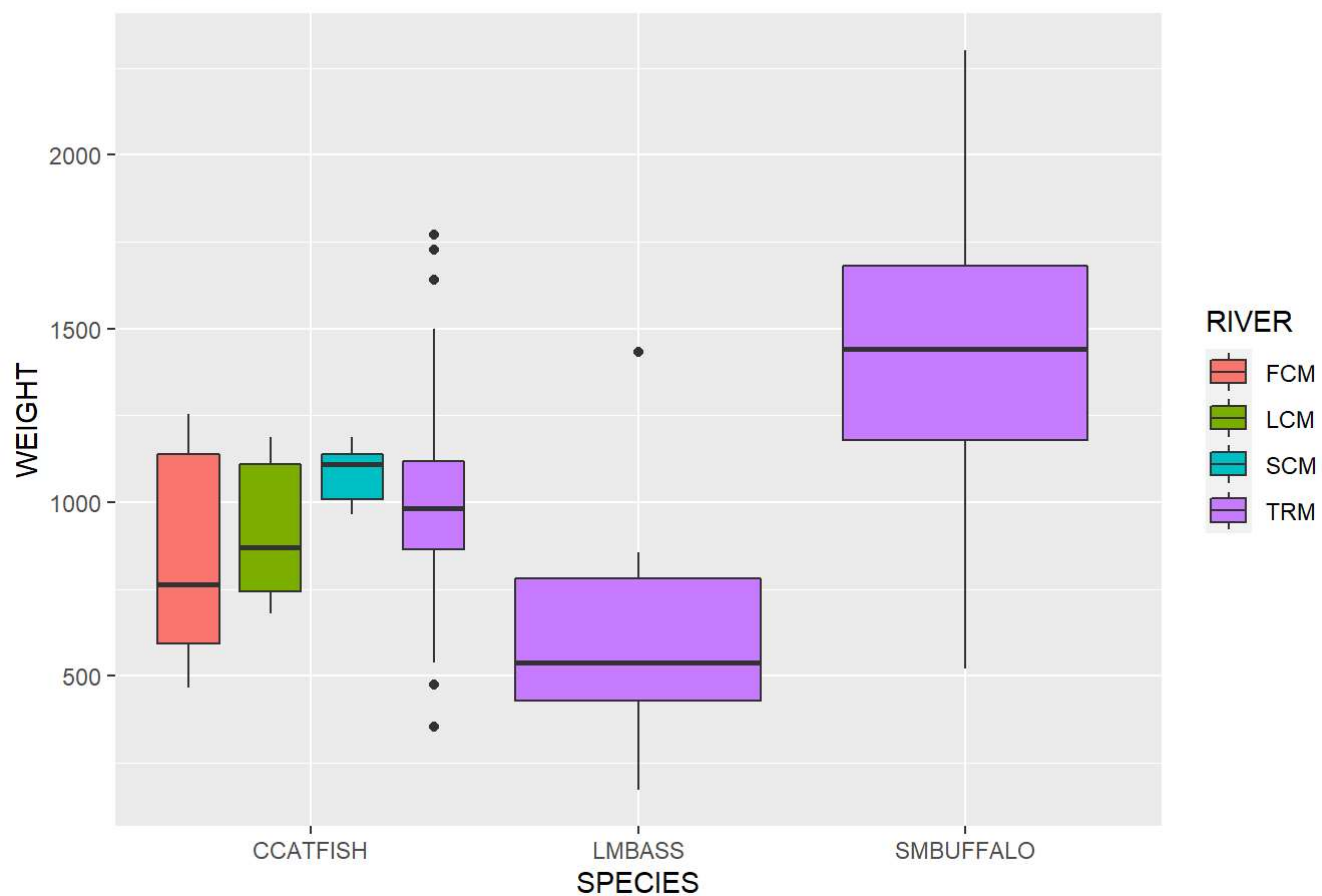


## Task 8

```
library(ggplot2)

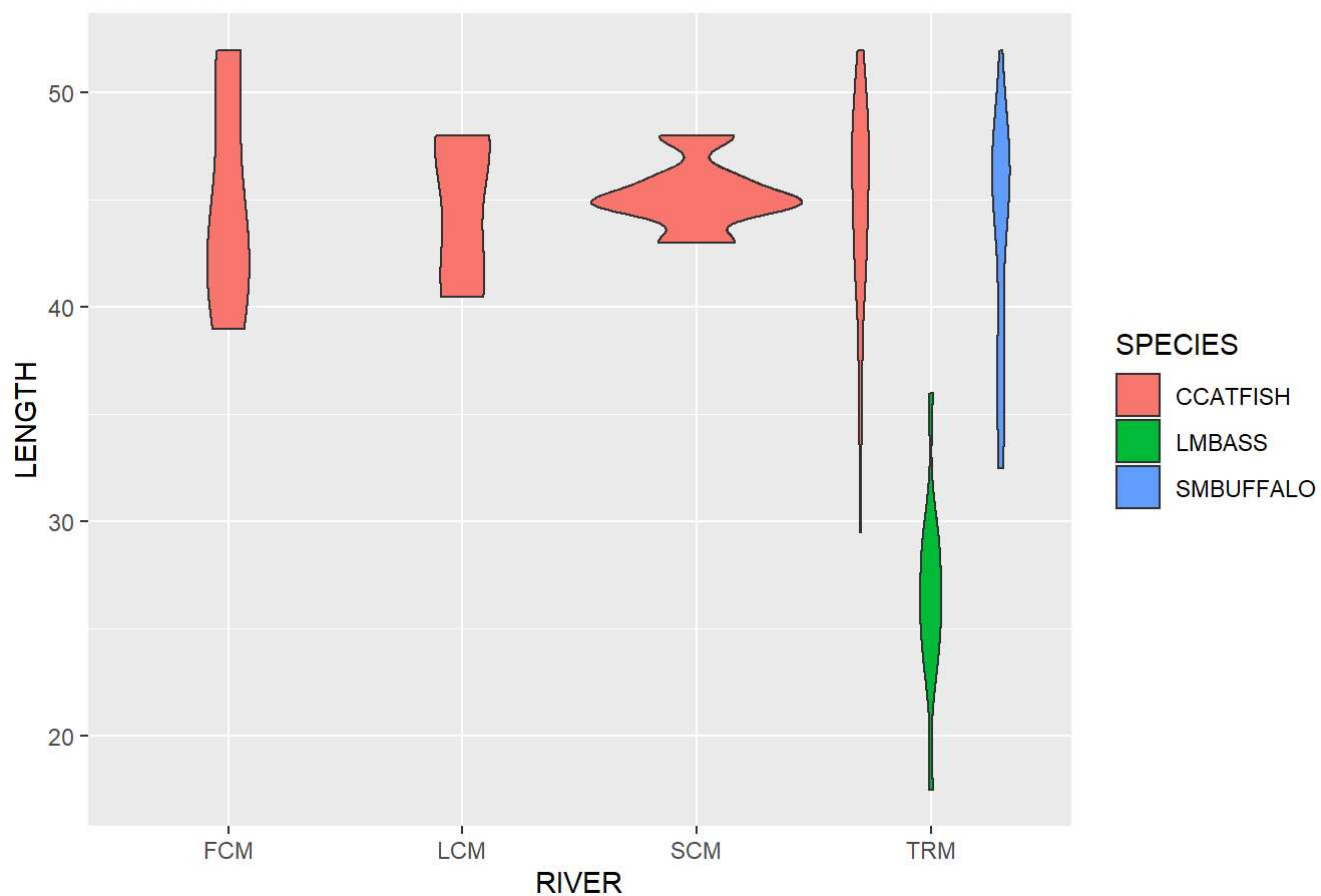
p <- ggplot(ddt, aes(x=SPECIES, y=WEIGHT, fill = RIVER))+geom_boxplot(position = position_dodge(
1))
p + ggtitle("Fabrizio Deza")
```

## Fabrizio Deza



```
vio <- ggplot(ddt, aes(x=RIVER, y=LENGTH, fill=SPECIES))+geom_violin()  
vio + ggtitle("Fabrizio Deza")
```

## Fabrizio Deza



```
sca <- ggplot(ddt, aes(x=WEIGHT, y=LENGTH, fill = SPECIES, color=SPECIES)) + geom_point()  
sca + ggtitle("Fabrizio Deza")
```

Fabrizio Deza

