

Final project

Daniel Gonzalez-Suarez

4/3/2020

Contents

Loading data and tidying it up.	1
Exploring the data	3
1. Outliers	3
2. Homogeneity of variance	6
3. Normality	8
4. Zeroes	12
5. Collinearity X	14
6. Relationships X and Y	22
7. Interactions	24
8. Independence of Y	25

Part II, Final Assignment

This is the second assingment for the Ecological Data Analysis in R course. In order to start, packages and functions will be loaded first.

Loading data and tidying it up.

Here, steps for tidying the dataset will be presented. Raw data was taken during completion of underwater transects, then input in Excel. Data will be imported as a .csv file.

```
df <- read.csv("./data/df_dgonzalezsuarez.csv")
head(df)
```

```
##      Dia  Provincia Latitud  Longitud  Localidad  SitioCodigo
## 1 19-Mar-16 Puntarenas 9.78203 -84.89076 ISLA_TORTUGA IT_SIN_TURISTAS
## 2 19-Mar-16 Puntarenas 9.78203 -84.89076 ISLA_TORTUGA IT_SIN_TURISTAS
## 3 19-Mar-16 Puntarenas 9.78203 -84.89076 ISLA_TORTUGA IT_SIN_TURISTAS
## 4 19-Mar-16 Puntarenas 9.78203 -84.89076 ISLA_TORTUGA IT_SIN_TURISTAS
## 5 19-Mar-16 Puntarenas 9.78203 -84.89076 ISLA_TORTUGA IT_SIN_TURISTAS
## 6 19-Mar-16 Puntarenas 9.78203 -84.89076 ISLA_TORTUGA IT_SIN_TURISTAS
##  Profundidad Transecto Area_.m2.  Phylum      Taxa
## 1           2           1         50 Chordata  Carangidae
## 2           2           1         50 Chordata  Haemulidae
## 3           2           1         50 Chordata  Pomacentridae
```

```
## 4      2      1      50 Chordata Pomacentridae
## 5      2      1      50 Chordata Pomacentridae
## 6      2      1      50 Chordata Pomacentridae
##           Especie NivelTrofico Talla_.cm. Abundancia Densidad_.org.m2.
## 1  Gnathanodon speciosus  Piscivoros      20      5      0.10
## 2   Haemulon maculicauda  Carnivoros      15      4      0.08
## 3 Microspathodon dorsalis  Herbivoros      25      2      0.04
## 4 Microspathodon dorsalis  Herbivoros      30      3      0.06
## 5   Abudefduf troschelii  Herbivoros      10      3      0.06
## 6   Abudefduf concolor    Herbivoros       5      5      0.10
```

```
tail(df)
```

```
##           Dia  Provincia Latitud  Longitud  Localidad SitioCodigo Profundidad
## 783 22-May-16 Guanacaste 10.9389 -85.73262 CUAJINIQUIL SR_HACHAL      2
## 784 22-May-16 Guanacaste 10.9389 -85.73262 CUAJINIQUIL SR_HACHAL      2
## 785 22-May-16 Guanacaste 10.9389 -85.73262 CUAJINIQUIL SR_HACHAL      2
## 786 22-May-16 Guanacaste 10.9389 -85.73262 CUAJINIQUIL SR_HACHAL      2
## 787 22-May-16 Guanacaste 10.9389 -85.73262 CUAJINIQUIL SR_HACHAL      2
## 788 22-May-16 Guanacaste 10.9389 -85.73262 CUAJINIQUIL SR_HACHAL      2
##           Transecto Area_.m2.  Phylum      Taxa      Especie NivelTrofico
## 783      1      50 Chordata Serranidae Serranus psittacinus  Carnivoros
## 784      1      50 Chordata Serranidae Serranus psittacinus  Carnivoros
## 785      1      50 Chordata Serranidae Serranus psittacinus  Carnivoros
## 786      1      50 Chordata Labridae  Thalassoma lucasanum  Carnivoros
## 787      1      50 Chordata Labridae  Thalassoma lucasanum  Carnivoros
## 788      1      50 Chordata Labridae  Thalassoma lucasanum  Carnivoros
##           Talla_.cm. Abundancia Densidad_.org.m2.
## 783      10      4      0.08
## 784      15      6      0.12
## 785      20      4      0.08
## 786      10      25     0.50
## 787      15      10     0.20
## 788      20      12     0.24
```

```
str(df)
```

```
## 'data.frame': 788 obs. of 16 variables:
## $ Dia : Factor w/ 4 levels "19-Mar-16","20-Mar-16",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Provincia : Factor w/ 2 levels "Guanacaste","Puntarenas": 2 2 2 2 2 2 2 2 2 2 ...
## $ Latitud : num 9.78 9.78 9.78 9.78 9.78 ...
## $ Longitud : num -84.9 -84.9 -84.9 -84.9 -84.9 ...
## $ Localidad : Factor w/ 3 levels "CUAJINIQUIL",...: 2 2 2 2 2 2 2 2 2 2 ...
## $ SitioCodigo : Factor w/ 7 levels "C_MATAPALITO",...: 5 5 5 5 5 5 5 5 5 5 ...
## $ Profundidad : num 2 2 2 2 2 2 2 2 2 2 ...
## $ Transecto : int 1 1 1 1 1 1 1 1 1 1 ...
## $ Area_.m2. : int 50 50 50 50 50 50 50 50 50 50 ...
## $ Phylum : Factor w/ 1 level "Chordata": 1 1 1 1 1 1 1 1 1 1 ...
## $ Taxa : Factor w/ 25 levels "Acanthuridae",...: 5 11 20 20 20 20 20 20 7 23 ...
## $ Especie : Factor w/ 58 levels "Abudefduf concolor",...: 25 29 40 40 2 1 55 55 18 22 ...
## $ NivelTrofico : Factor w/ 4 levels "Carnivoros","Herbivoros",...: 3 1 2 2 2 2 2 2 1 1 ...
## $ Talla_.cm. : int 20 15 25 30 10 5 10 15 15 15 ...
## $ Abundancia : int 5 4 2 3 3 5 6 8 1 1 ...
## $ Densidad_.org.m2.: num 0.1 0.08 0.04 0.06 0.06 0.1 0.12 0.16 0.02 0.02 ...
```

```
range(df$Talla_.cm.)
```

```
## [1] 5 100
```

```
range(df$Abundancia)
```

```
## [1] 1 212
```

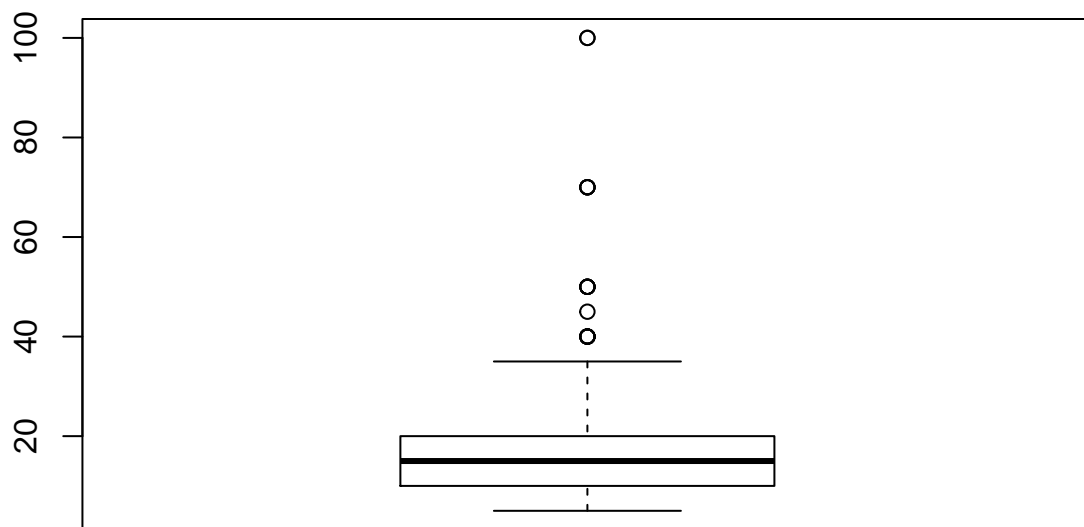
Everything looks good. Data was already in long format before importing it.

Exploring the data

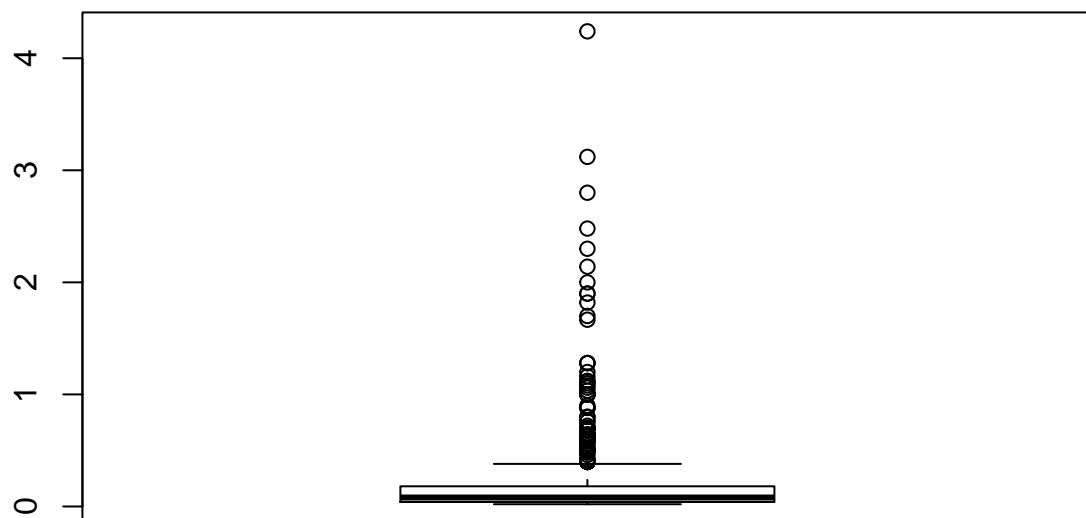
We are going to see visual representation of data.

1. Outliers

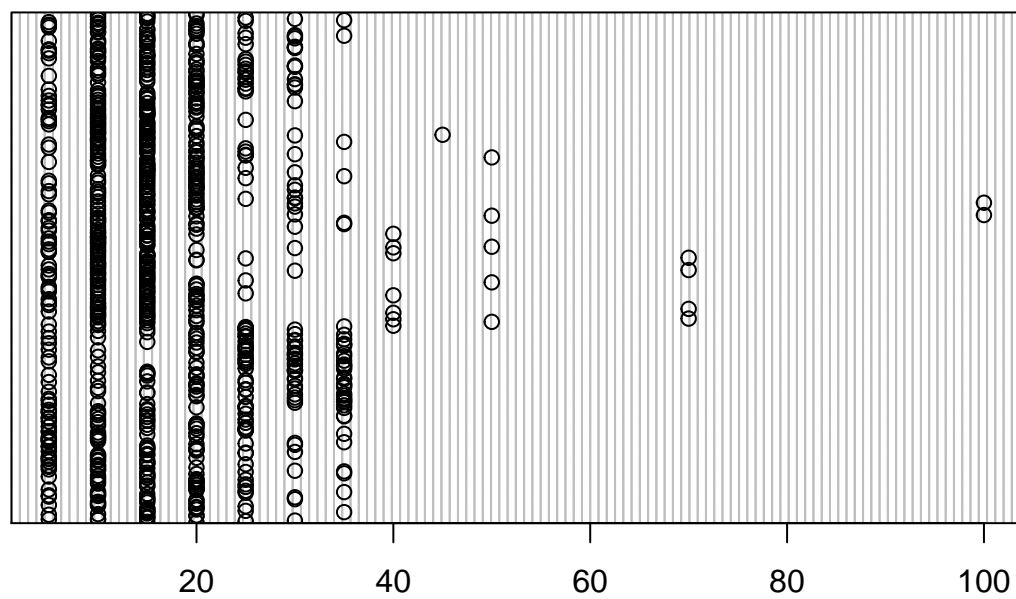
```
boxplot(df$Talla_.cm.)
```



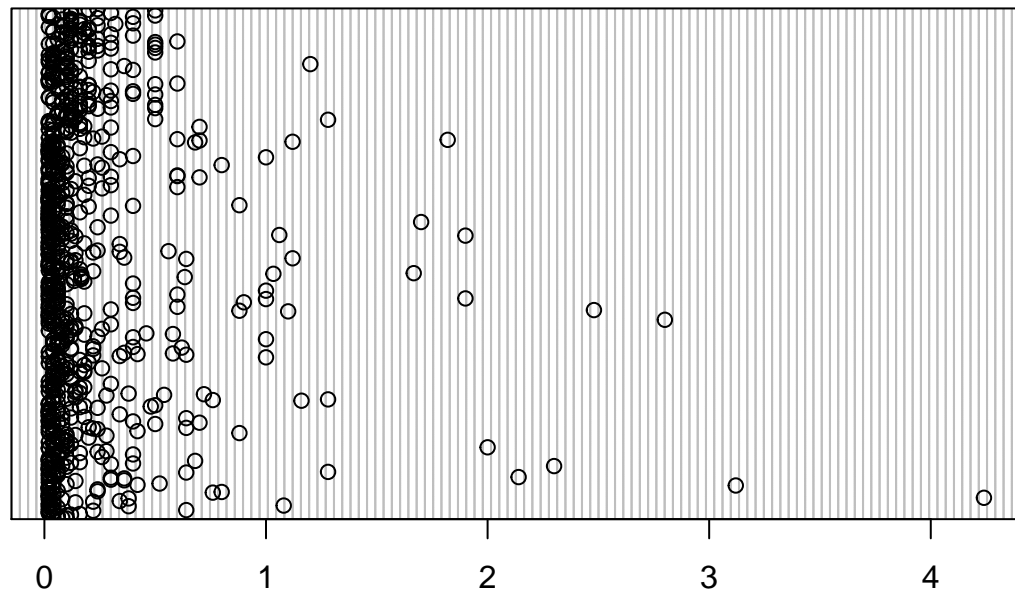
```
boxplot(df$Densidad_.org.m2.)
```



```
dotchart(df$Talla_.cm.)
```



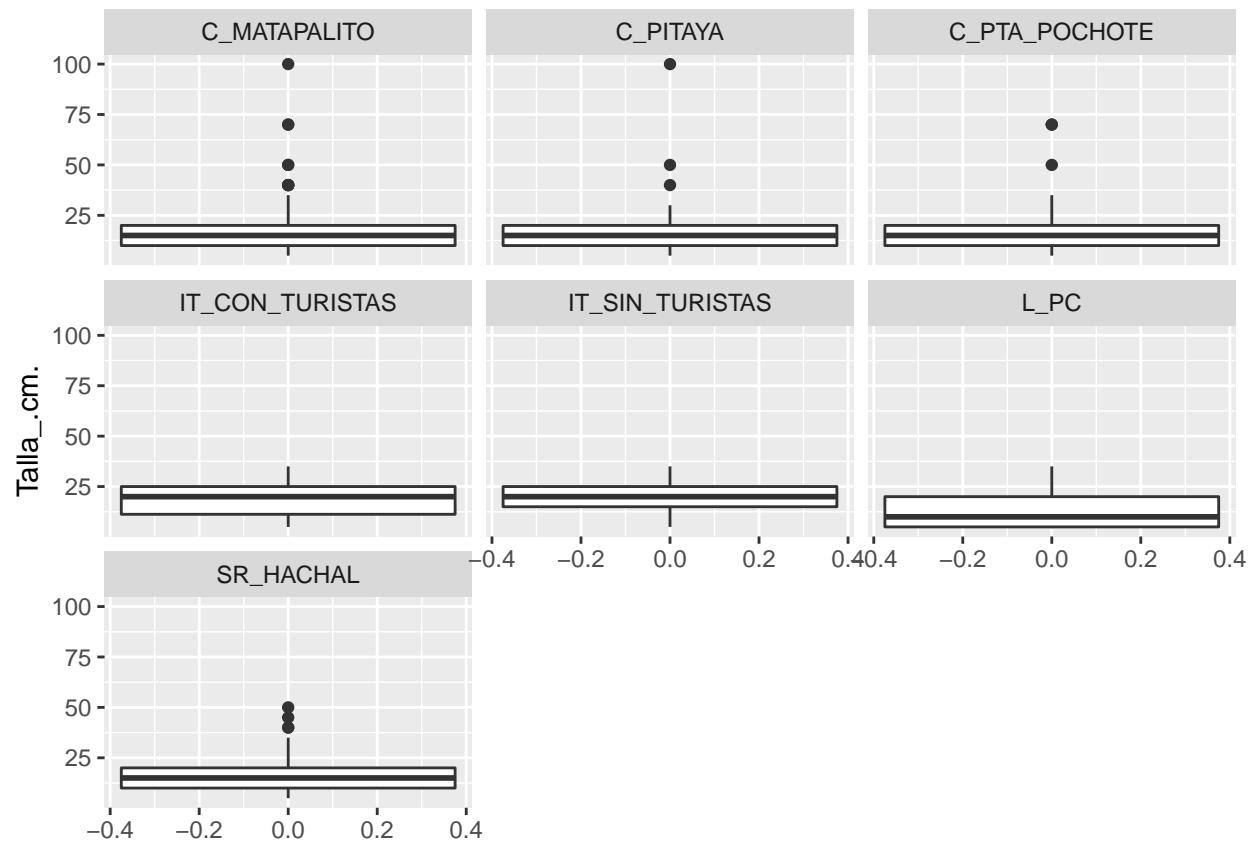
```
dotchart(df$Densidad_.org.m2.)
```



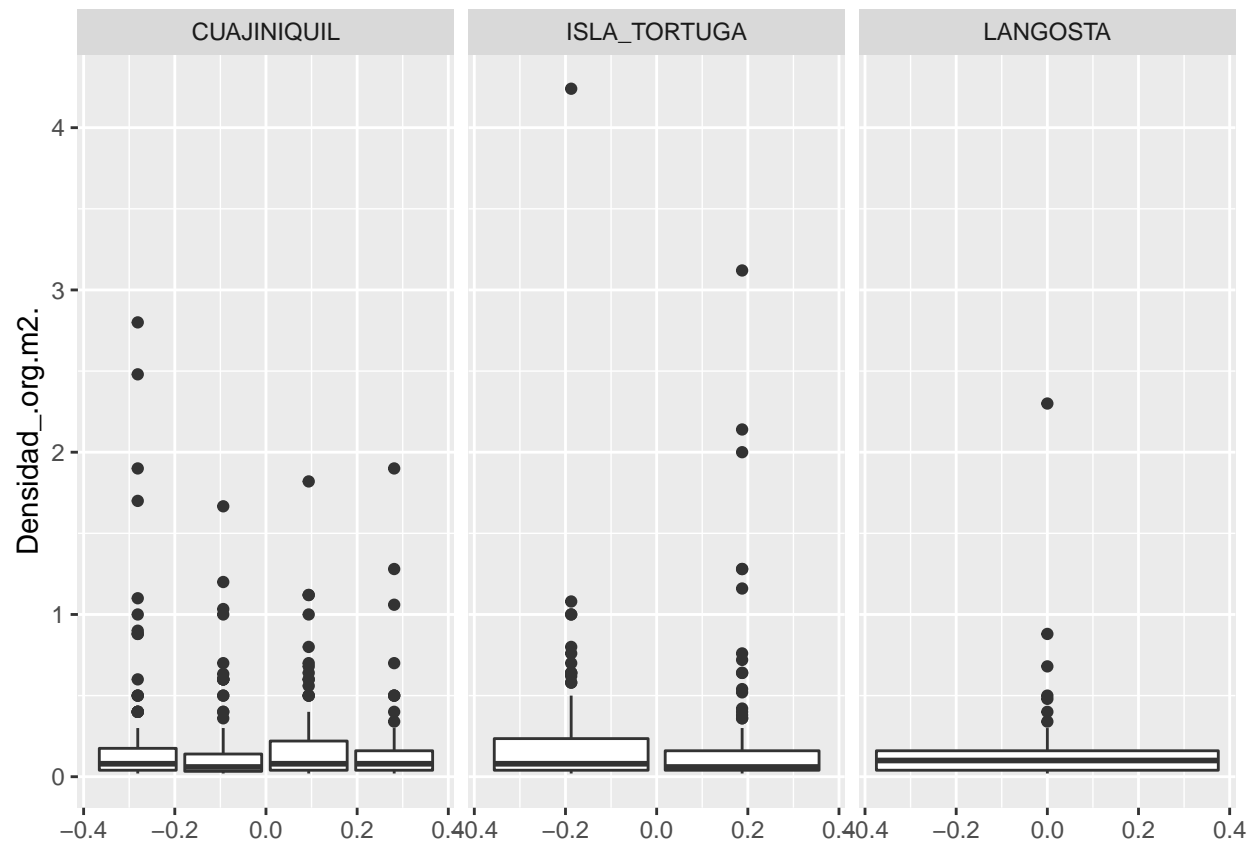
Many outliers, but there are no errors on data.

2. Homogeneity of variance

```
p <- ggplot(data=df, aes(X=Provincia, y=Talla_.cm.)) +  
  geom_boxplot() + facet_wrap(~SitioCodigo)  
p
```



```
p<- ggplot(data=df, aes(X=SitioCodigo, y=Densidad_.org.m2.)) +  
  geom_boxplot() + facet_wrap(~Localidad)  
p
```

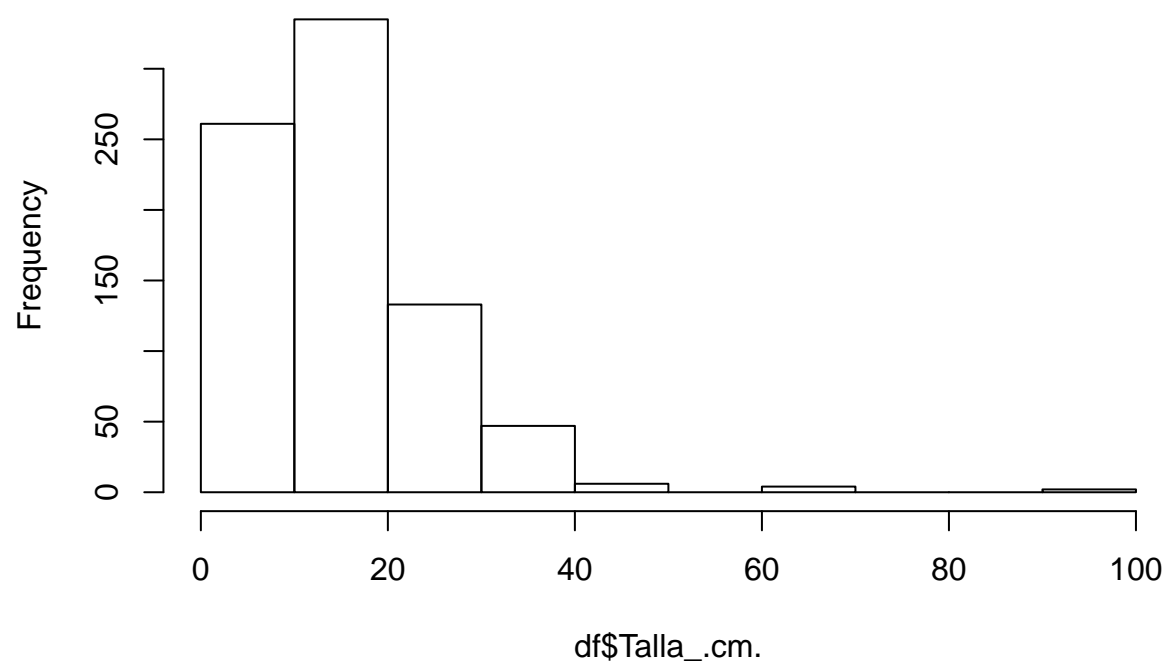


There is homogeneity of variance.

3. Normality

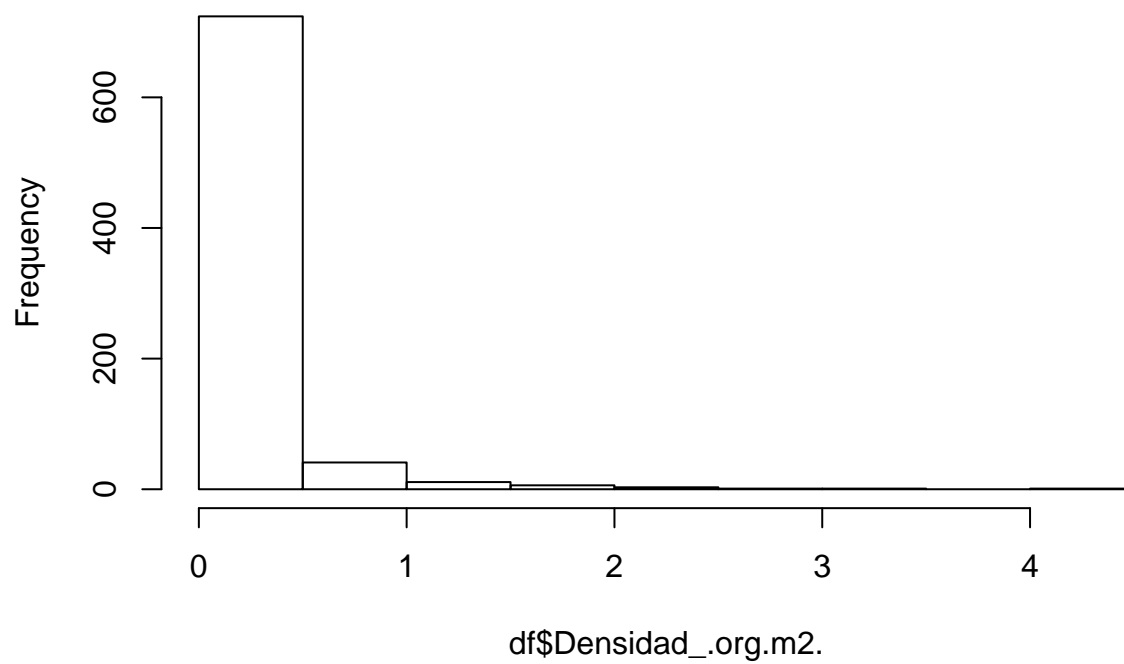
```
hist(df$Talla_.cm.)
```


Histogram of df\$Talla_.cm.



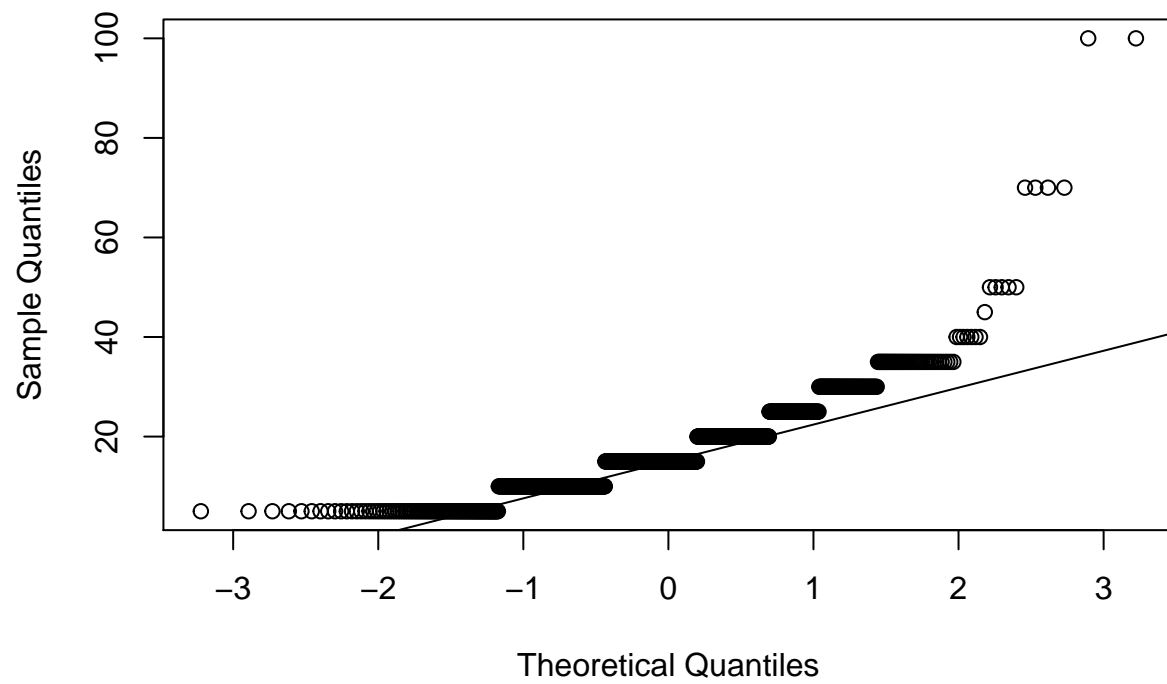
```
hist(df$Densidad_.org.m2.)
```

Histogram of df\$Densidad_.org.m2.

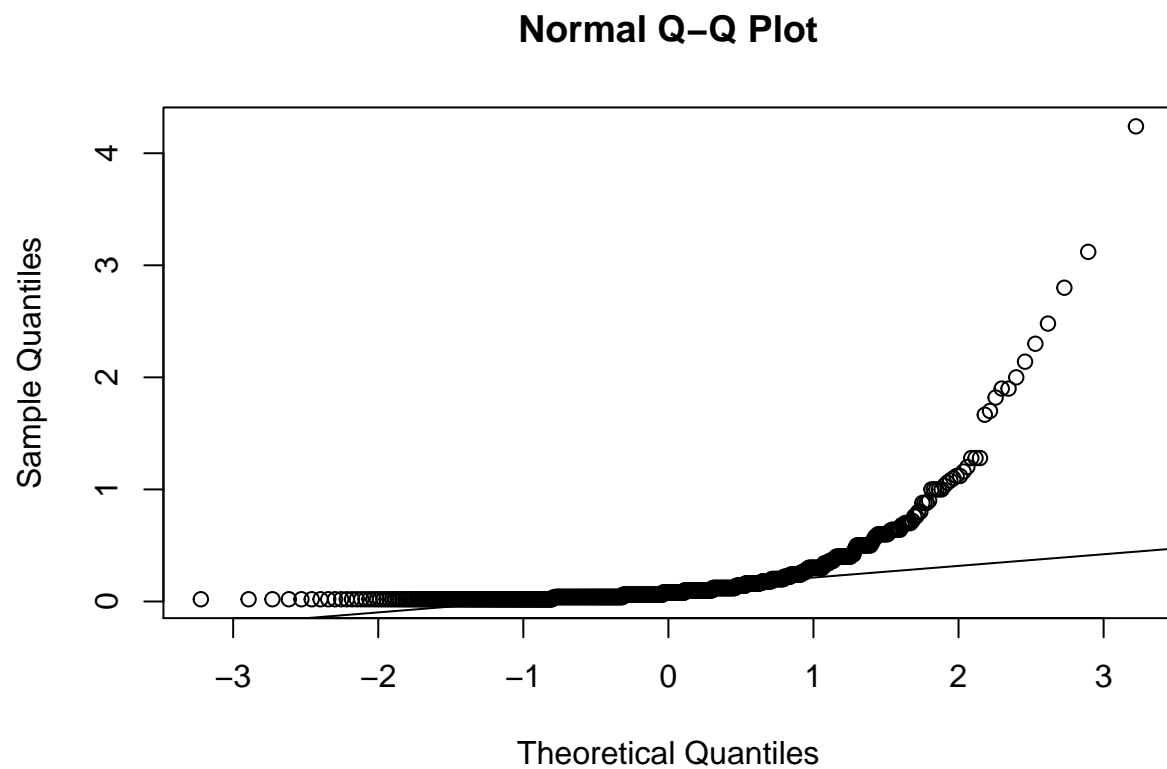


```
qqnorm(df$Talla_.cm.)  
qqline(df$Talla_.cm.)
```

Normal Q-Q Plot



```
qqnorm(df$Densidad_.org.m2.)  
qqline(df$Densidad_.org.m2.)
```



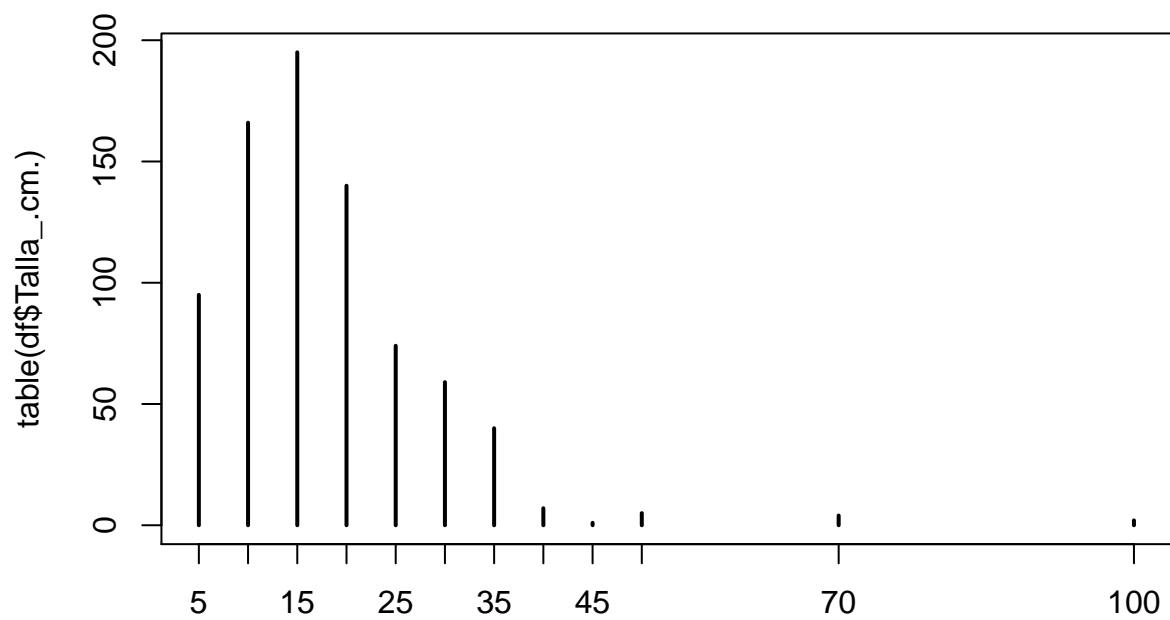
Data is not normal, as seen in histograms and confirmed by Q-Q plots.

4. Zeroes

```
range(df$Talla_.cm.)
```

```
## [1] 5 100
```

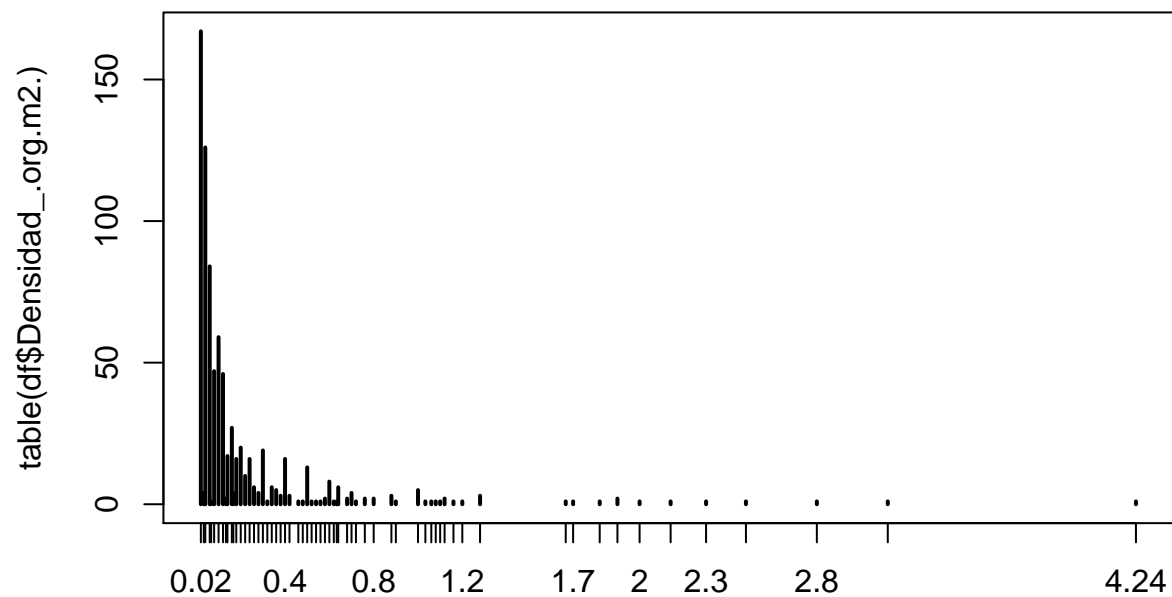
```
plot(table(df$Talla_.cm.))
```



```
range(df$Densidad_.org.m2.)
```

```
## [1] 0.02 4.24
```

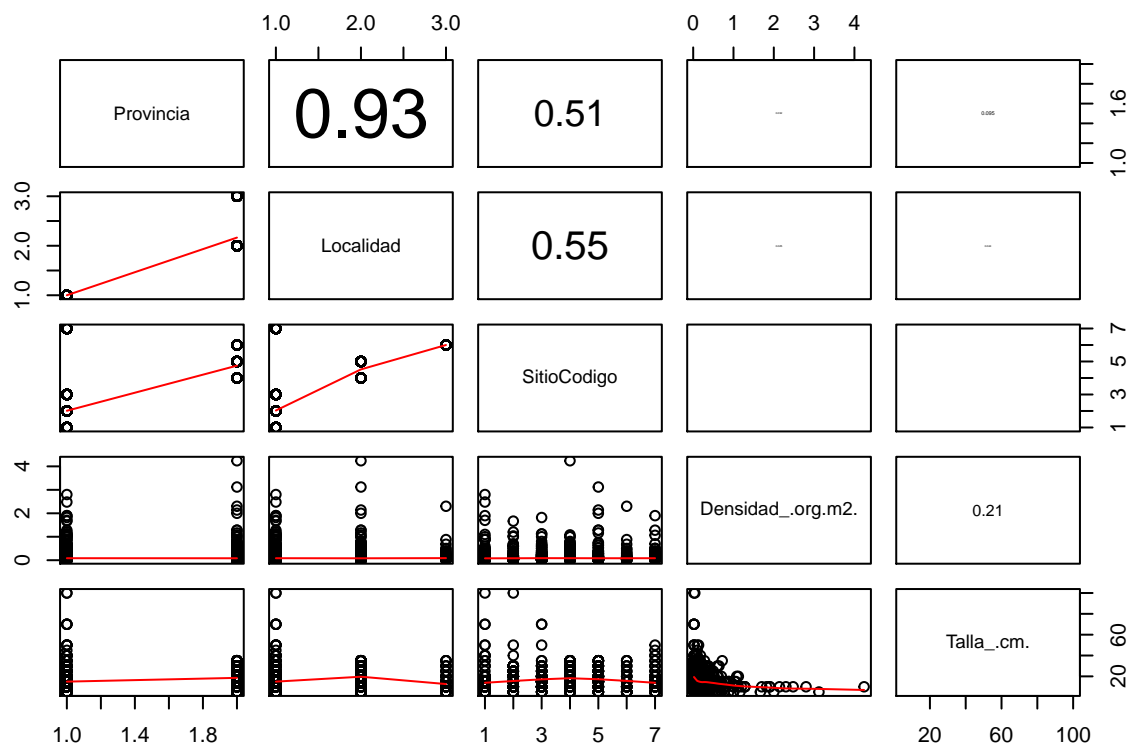
```
plot(table(df$Densidad_.org.m2.))
```



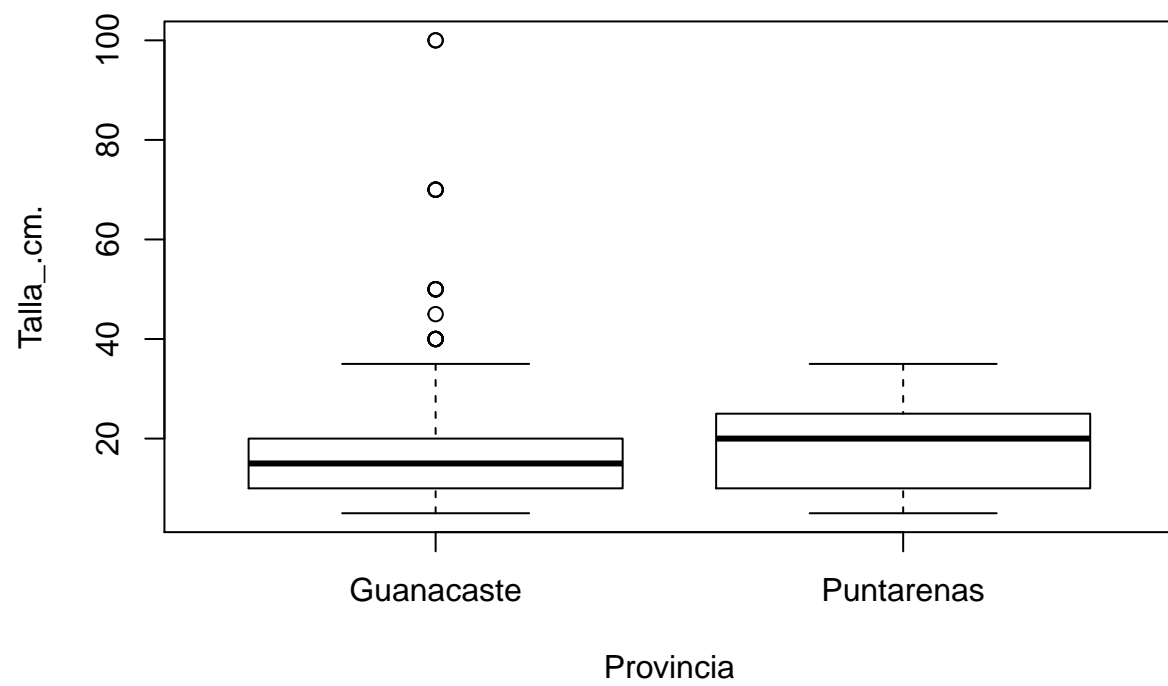
There are no zeroes in either continuous variable.

5. Collinearity X

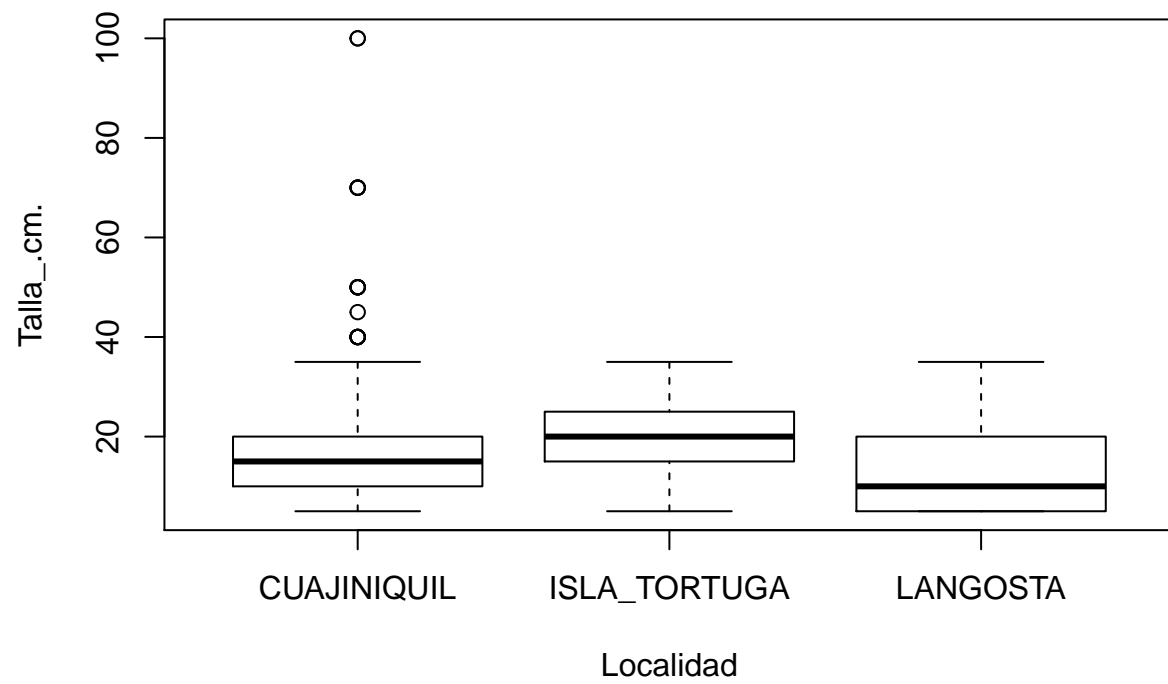
```
pairs(~ Provincia + Localidad + SitioCodigo + Densidad_.org.m2. + Talla_.cm.,
      lower.panel=panel.smooth, upper.panel=panel.cor,
      data=df)
```



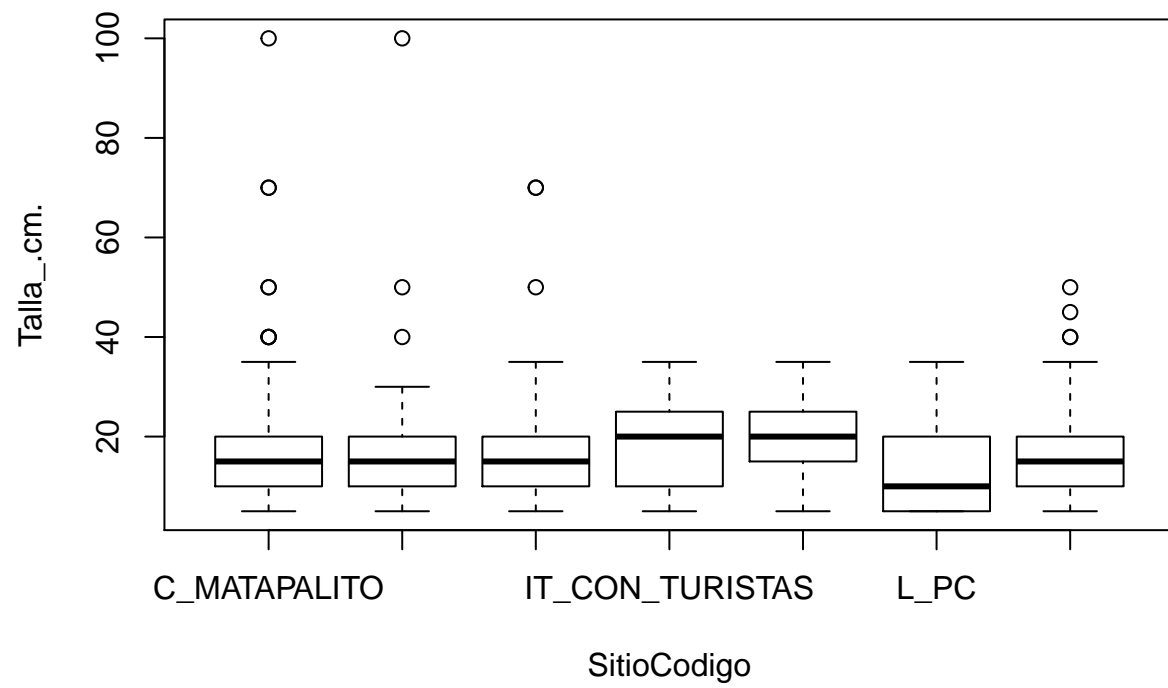
```
plot(Talla_.cm. ~ Provincia, data=df)
```



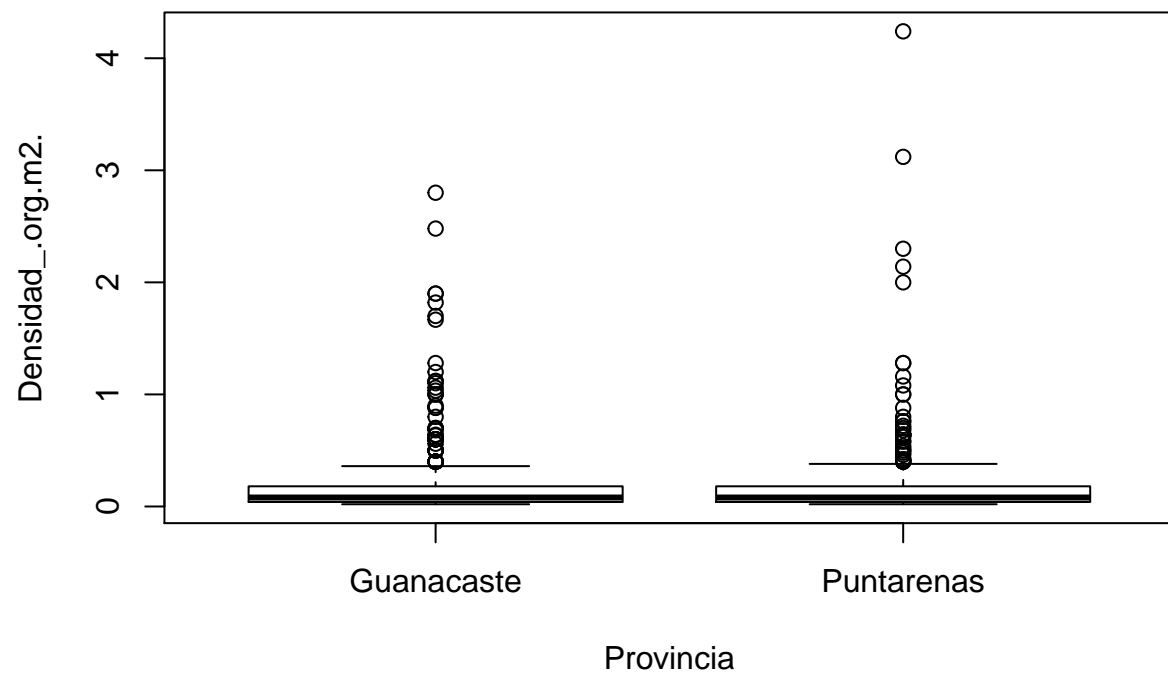
```
plot(Talla_.cm. ~ Localidad, data=df)
```

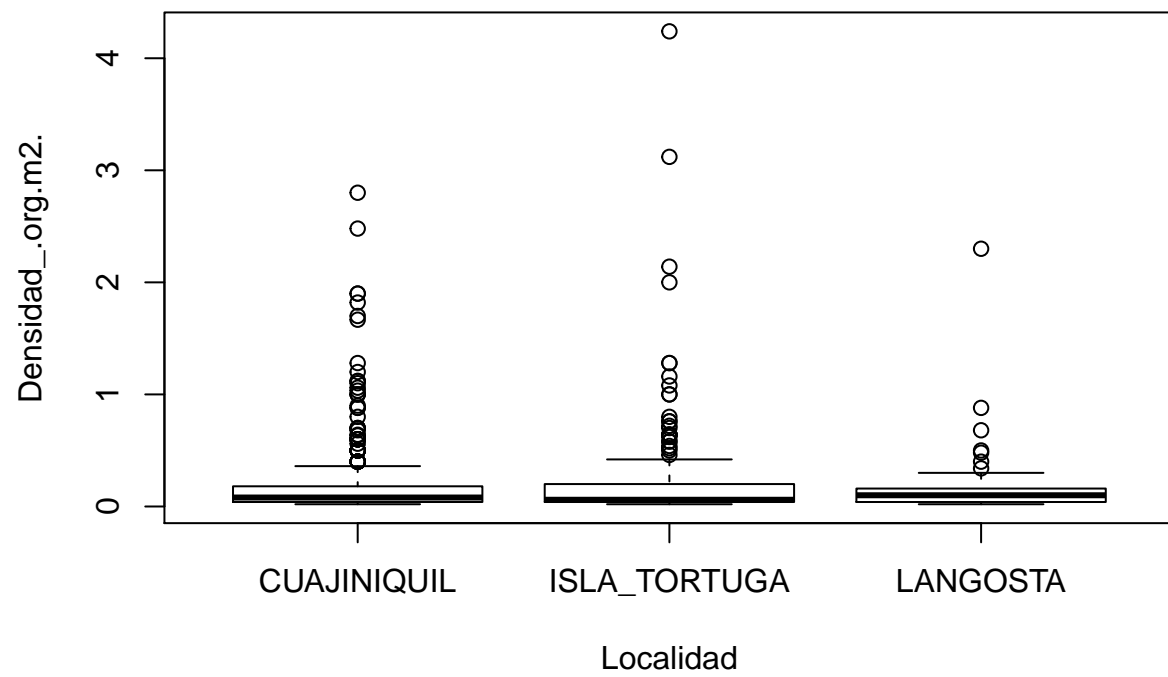
```
plot(Talla_.cm. ~ SitioCodigo, data=df)
```



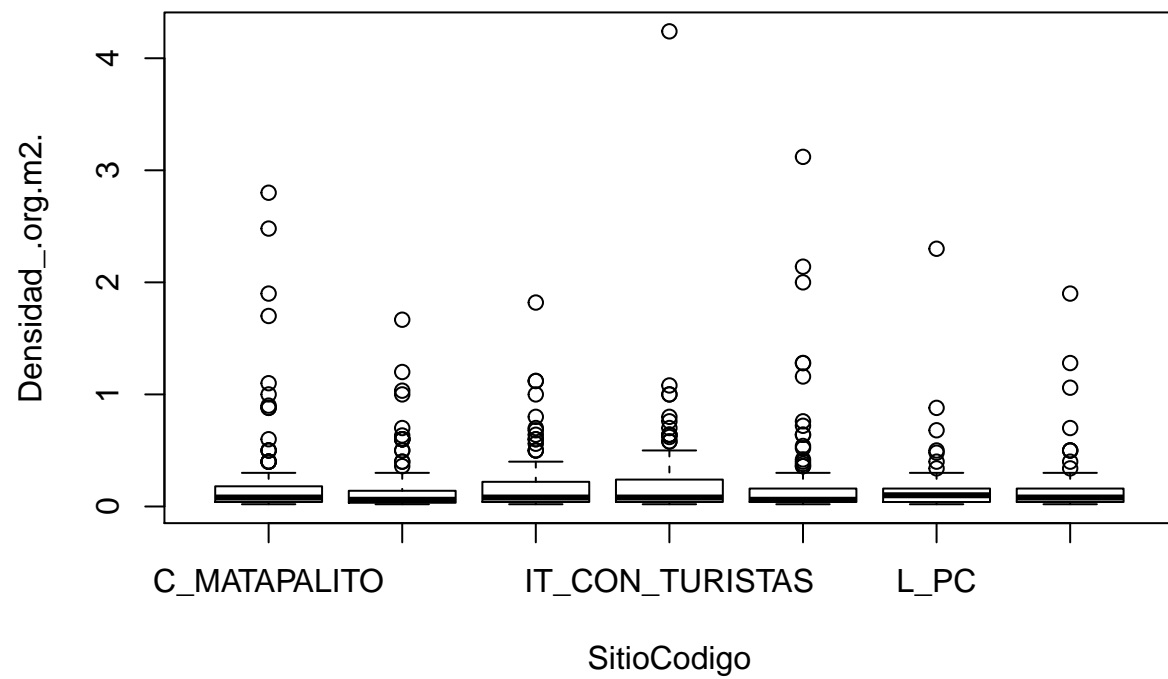
```
plot(Densidad_.org.m2. ~ Provincia, data=df)
```



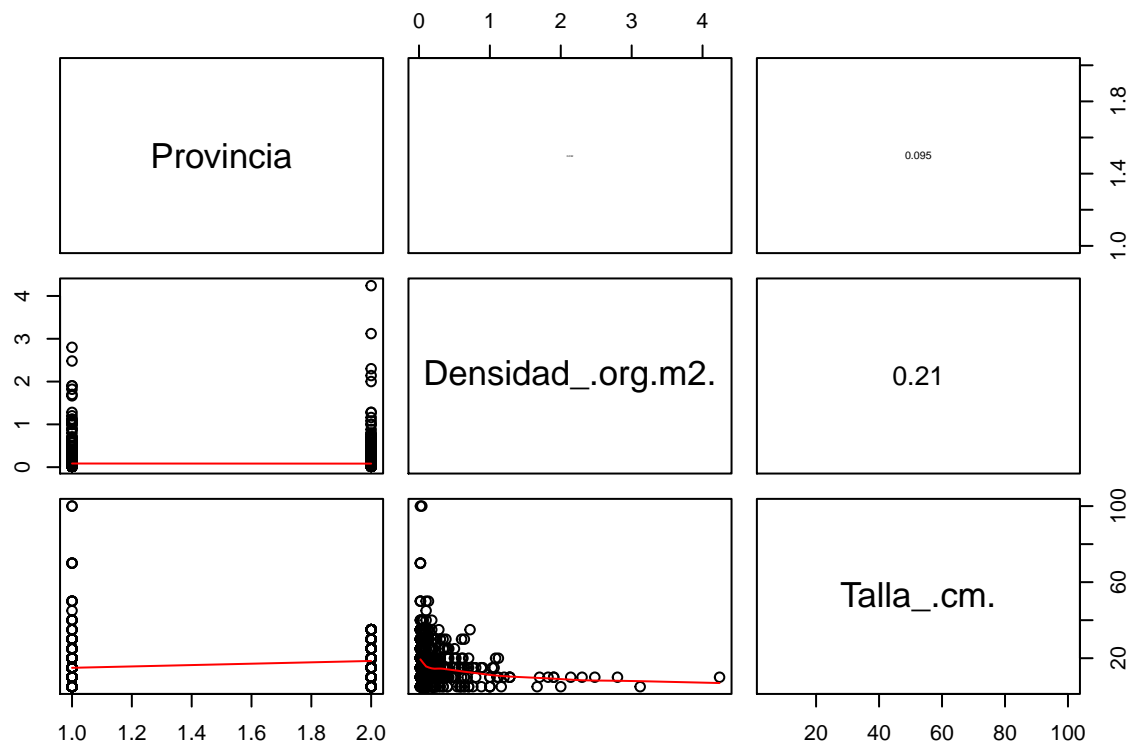
```
plot(Densidad_.org.m2. ~ Localidad, data=df)
```



```
plot(Densidad_.org.m2. ~ SitioCodigo, data=df)
```



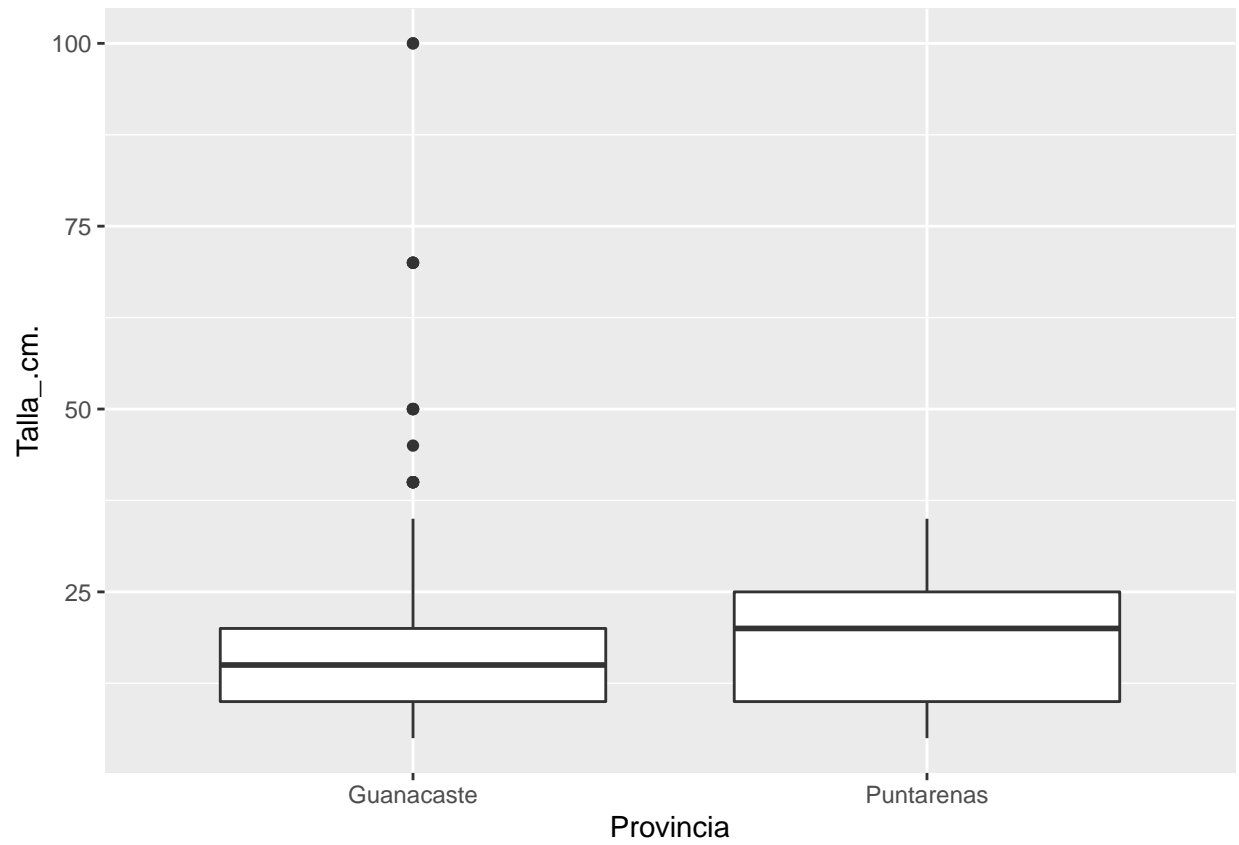
```
pairs(~ Provincia + Densidad_.org.m2. + Talla_.cm.,
      lower.panel=panel.smooth, upper.panel=panel.cor,
      data=df)
```



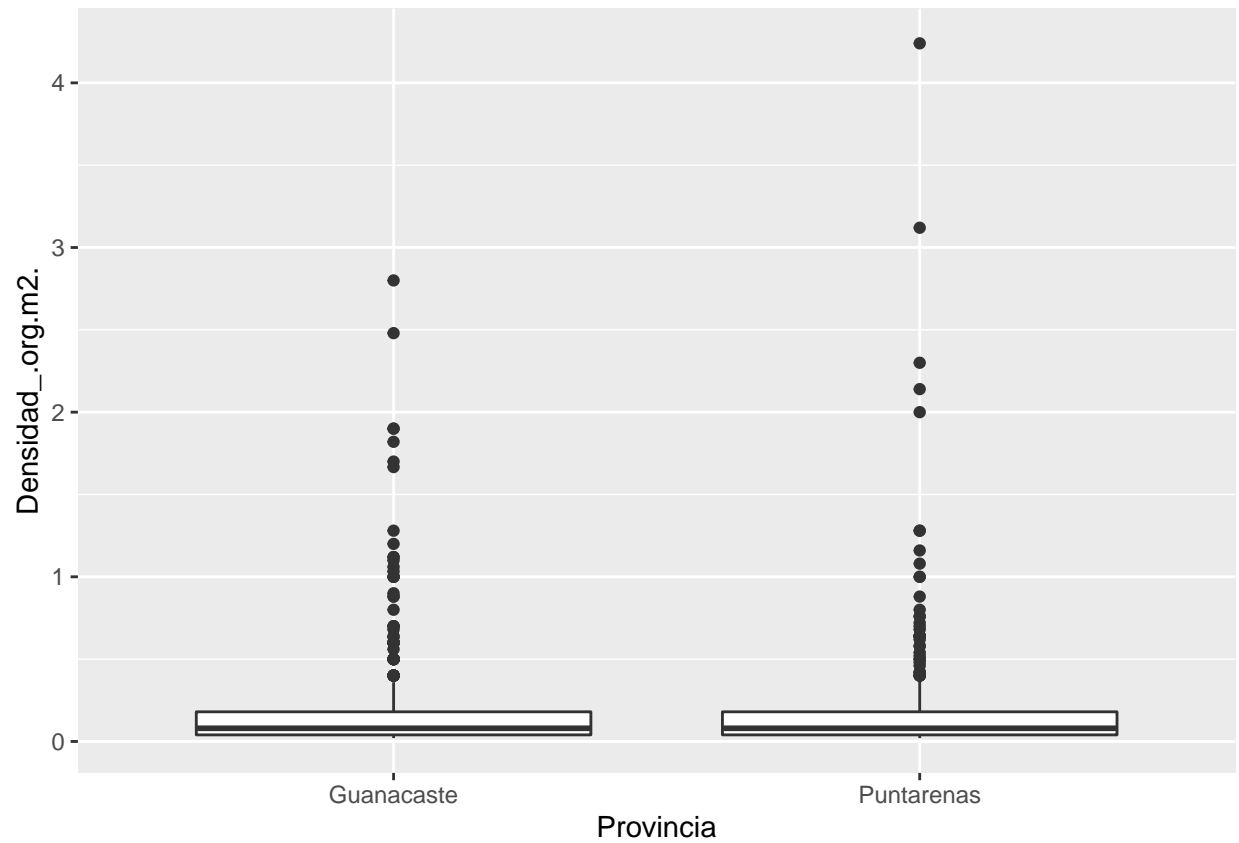
Our X variable will now be only Province

6. Relationships X and Y

```
p <- ggplot(df, aes(x=Provincia, y=Talla_.cm.)) +  
  geom_boxplot()  
p
```



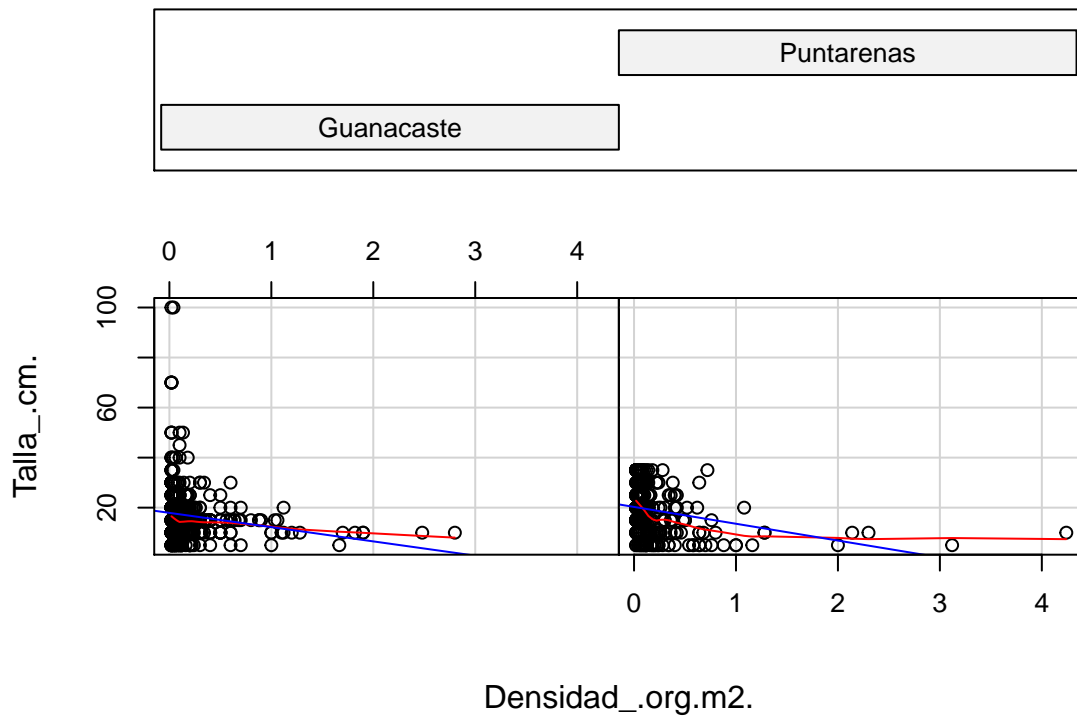
```
p <- ggplot(df, aes(x=Provincia, y=Densidad_.org.m2.)) +  
  geom_boxplot()  
p
```



7. Interactions

```
coplot(Talla_.cm. ~ Densidad_.org.m2. | Provincia ,
       data=df,
       panel=function(x,y,...) {
         panel.smooth(x,y,span=0.8,iter=5,...)
         abline(lm(y ~ x), col="blue") } )
```


Given : Provincia



There seems to be no interaction in Provinces.

8. Independence of Y

Both length and density could be dependent on Province because of fishing pressure effects.