lab9.R

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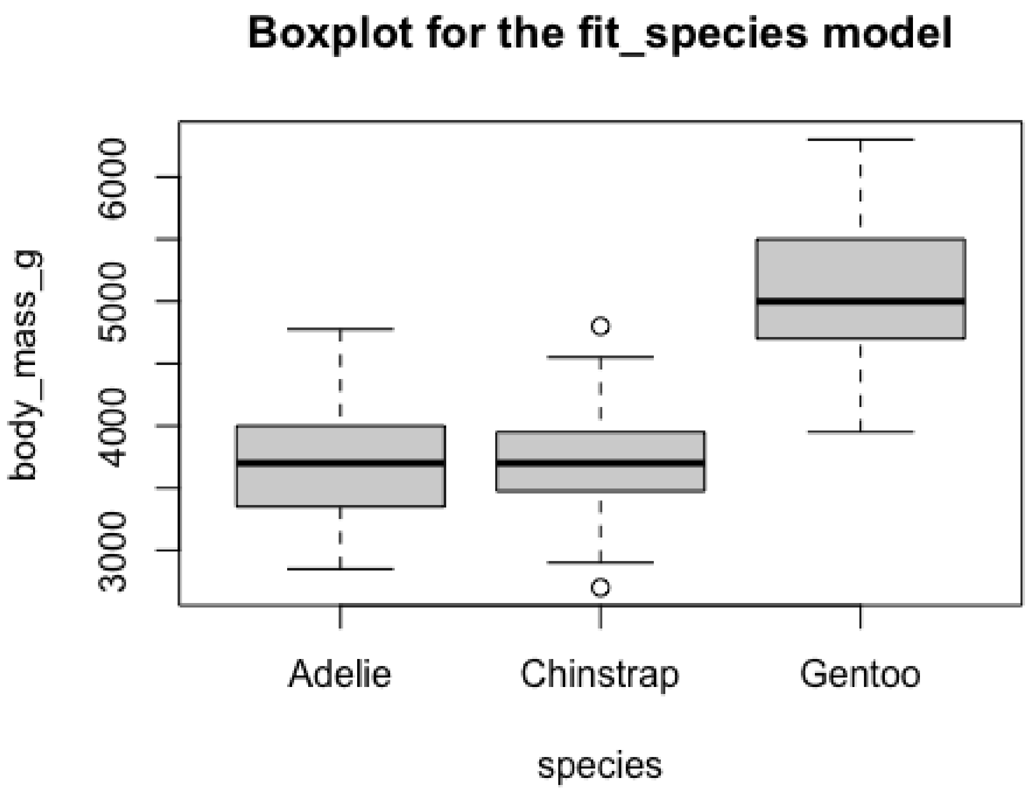
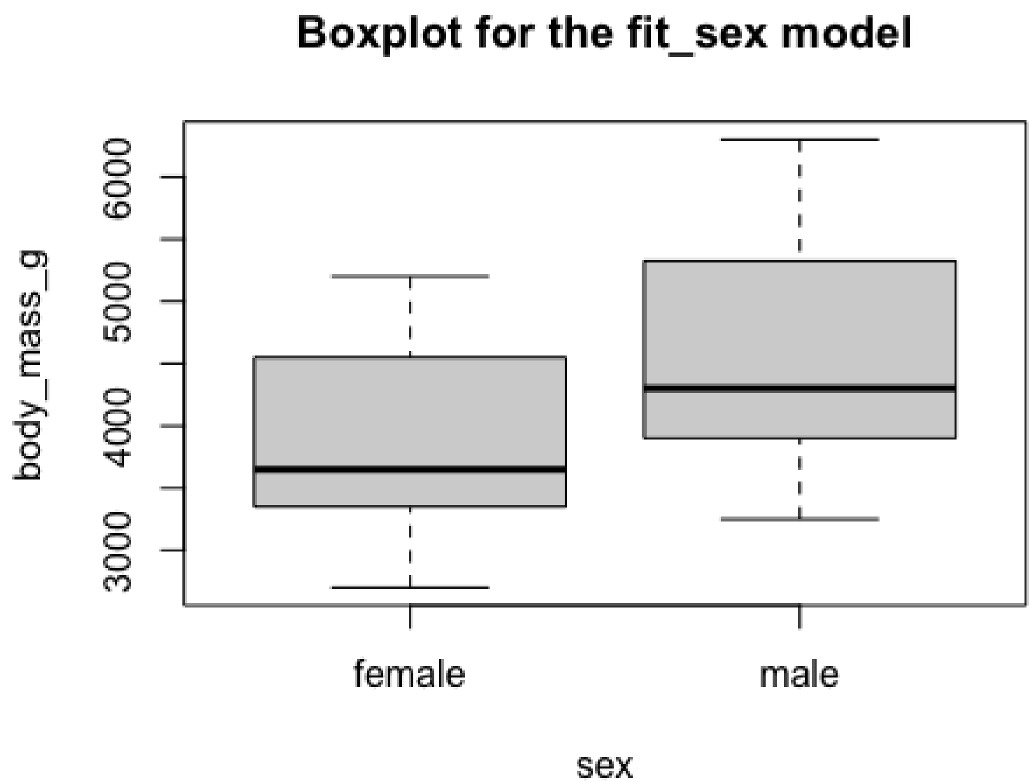
```
birds =
read.csv("/Users/stonehuang/Documents/environmental_data/data/bird.sta.csv")
hab =
read.csv("/Users/stonehuang/Documents/environmental_data/data/hab.sta.csv")

birdhab = merge(
  birds,
  hab, by=c("basin", "sub", "sta"))

# Create a contingency table for edge/interior and brown creeper
presence/absence
table(
  birdhab$s.edge,
  birdhab$BRCR > 0)

##
##     FALSE TRUE
##   E   144   29
##   I   559  314

br_creeper_table = table(
  birdhab$s.edge,
  birdhab$BRCR > 0)[, 2:1]

br_creeper_table

##
##     TRUE FALSE
##   E   29   144
##   I  314   559

#Q1. The presence/absence of Brown Creepers does not vary between the
interior and edge of forest stands.
#Q2. Brown Creepers show a significant habitat preference because the p-value
is lower than 0.05.
chisq_BRCR = chisq.test(br_creeper_table)
chisq_BRCR

##
##  Pearson's Chi-squared test with Yates' continuity correction
##
```

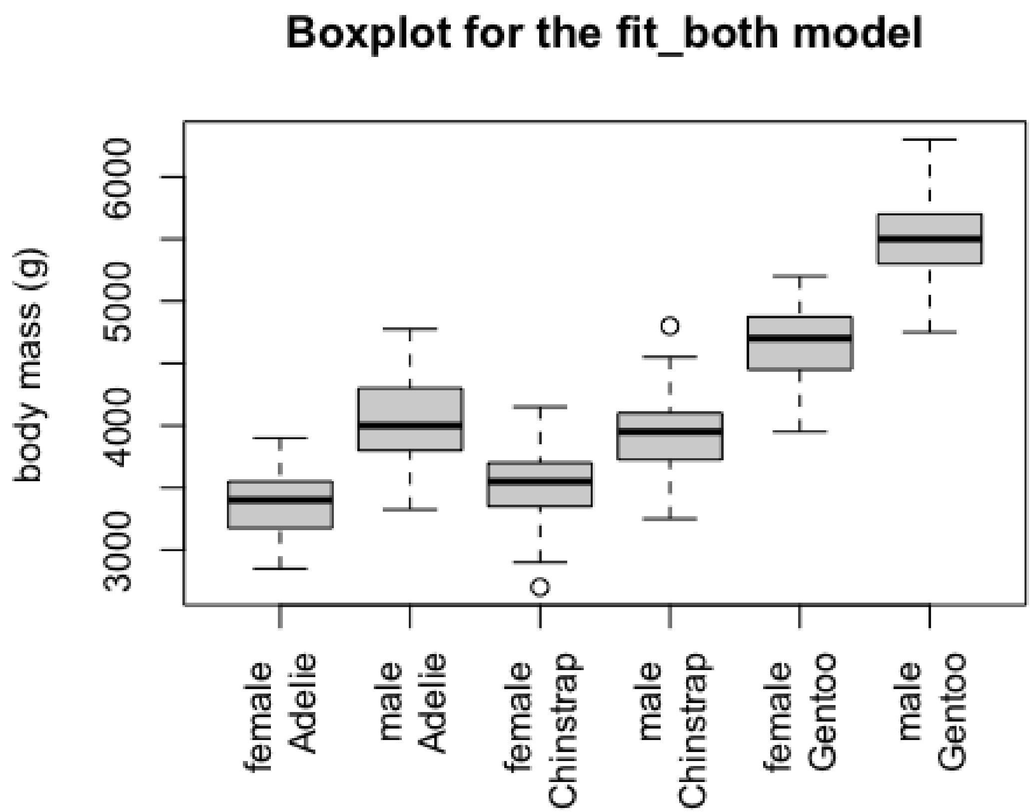
```
## data:  br_creeper_table
## X-squared = 23.3, df = 1, p-value = 1.386e-06

require(palmerpenguins)

## Loading required package: palmerpenguins

head(penguins)

## # A tibble: 6 × 8
##   species island bill_length_mm bill_depth_mm flipper_length_… body_mass_g
sex
##   <fct>   <fct>           <dbl>         <dbl>            <int>       <int>
<fct>
## 1 Adelie  Torge…           39.1          18.7              181        3750
male
## 2 Adelie  Torge…           39.5          17.4              186        3800
fema…
## 3 Adelie  Torge…           40.3          18                195        3250
fema…
## 4 Adelie  Torge…           NA            NA                 NA          NA
<NA>
## 5 Adelie  Torge…           36.7          19.3              193        3450
fema…
## 6 Adelie  Torge…           39.3          20.6              190        3650
male
## # … with 1 more variable: year <int>

#Q3
fit_species = lm(formula = body_mass_g ~ species, data = penguins)
#Q4
fit_sex = lm(formula = body_mass_g ~ sex, data = penguins)
#Q5
fit_both = lm(formula = body_mass_g ~ sex*species, data = penguins)

#Q6
boxplot(body_mass_g ~ species, data = penguins, main = "Boxplot for the
fit_species model")
```




```
#Q7
boxplot(body_mass_g ~ sex, data = penguins, main = "Boxplot for the fit_sex
model")
```



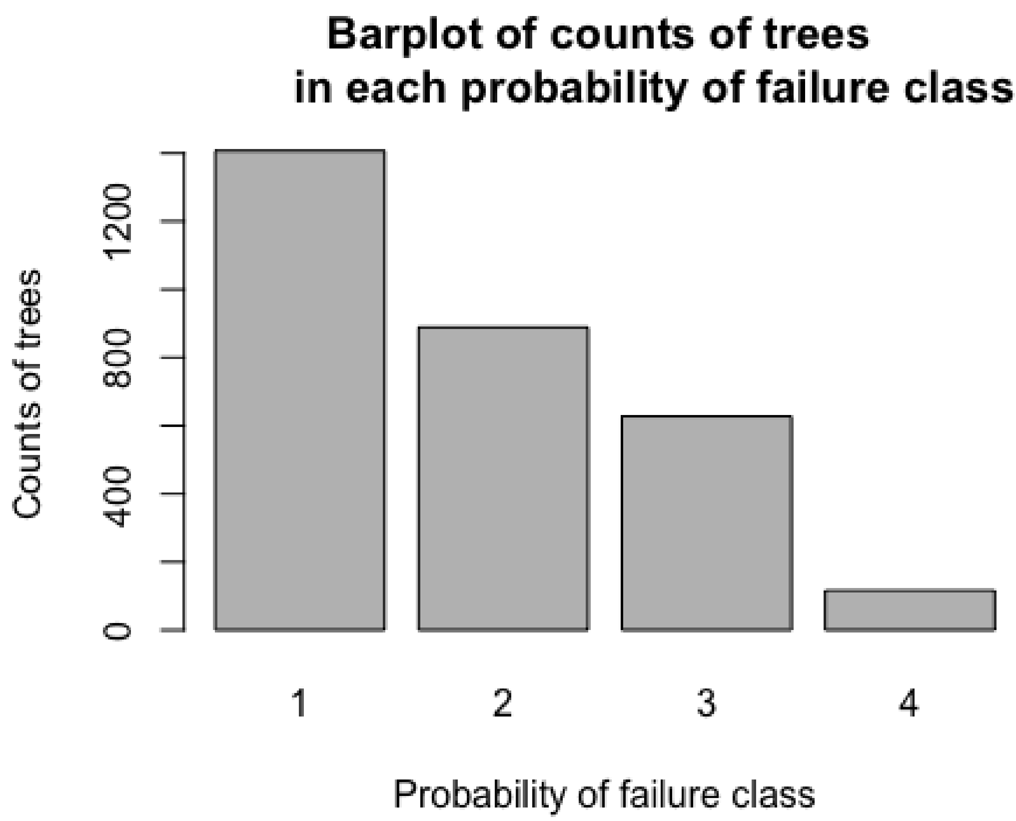

```
#Q8
boxplot(body_mass_g ~ sex*species, data = penguins, las = 3, names =
c("female \n Adelie", "male \n Adelie", "female \n Chinstrap", "male \n
Chinstrap", "female \n Gentoo", "male \n Gentoo"), ylab = "body mass (g)",
xlab = "", main = "Boxplot for the fit_both model")
```



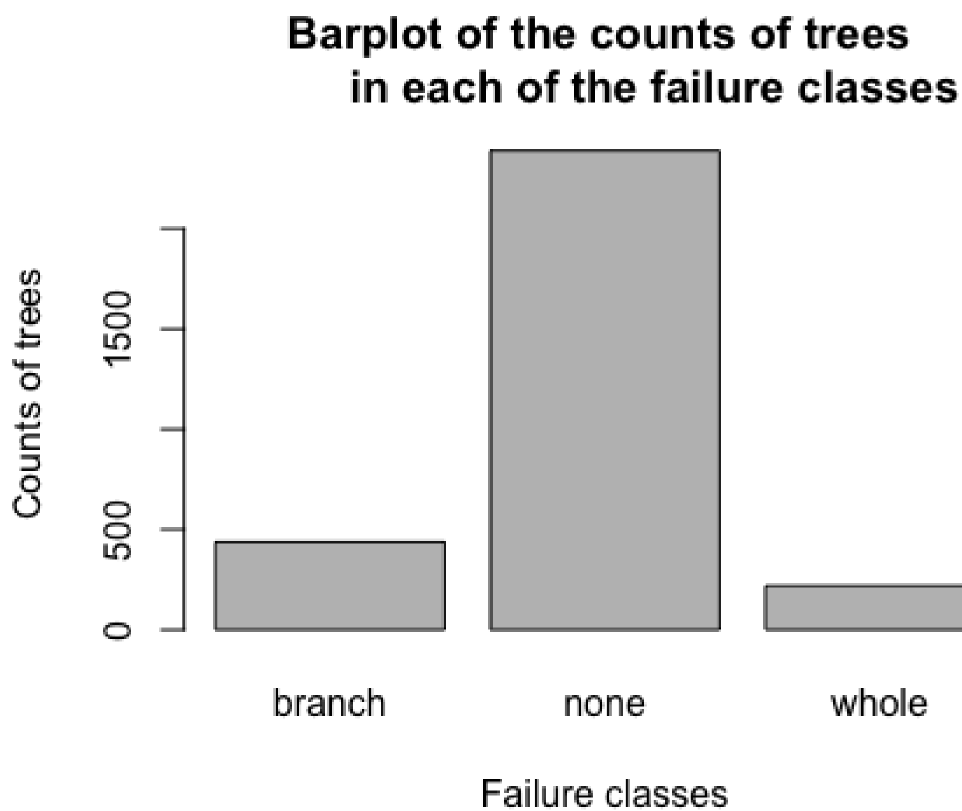

```
#Q9
#fit_species model may have problems fulfilling the homogeneity assumption
because the boxes have very different width.

#Q10. The null hypothesis of the Bartlett test is that the variances are the
same among groups.
#Q11. 0.0501
bartlett.test(body_mass_g ~ species, data = penguins)

##
##  Bartlett test of homogeneity of variances
##
## data:  body_mass_g by species
## Bartlett's K-squared = 5.9895, df = 2, p-value = 0.05005

#Q12. 0.0319
bartlett.test(body_mass_g ~ sex, data = penguins)

##
##  Bartlett test of homogeneity of variances
##
## data:  body_mass_g by sex
## Bartlett's K-squared = 4.6017, df = 1, p-value = 0.03194
```

```
#Q13. 0.1741
dat_groups = aggregate(
  body_mass_g ~ sex*species,
  data = penguins,
  FUN = c)
str(dat_groups)

## 'data.frame':    6 obs. of  3 variables:
##  $ sex        : Factor w/ 2 levels "female","male": 1 2 1 2 1 2
##  $ species    : Factor w/ 3 levels "Adelie","Chinstrap",..: 1 1 2 2 3 3
##  $ body_mass_g:List of 6
##   ..$ : int  3800 3250 3450 3625 3200 3700 3450 3325 3400 3800 ...
##   ..$ : int  3750 3650 4675 3800 4400 4500 4200 3600 3950 3800 ...
##   ..$ : int  3500 3525 3950 3250 4150 3800 3700 3575 3700 3450 ...
##   ..$ : int  3900 3650 3725 3750 3700 3775 4050 4050 3300 4400 ...
##   ..$ : int  4500 4450 4550 4800 4400 4650 4650 4200 4150 4800 ...
##   ..$ : int  5700 5700 5400 5200 5150 5550 5850 5850 6300 5350 ...

bartlett.test(dat_groups$body_mass_g)

##
##  Bartlett test of homogeneity of variances
##
## data:  dat_groups$body_mass_g
## Bartlett's K-squared = 7.6908, df = 5, p-value = 0.1741

#Q14
#The fit_sex model has issues with heterogeneity. The p-value is lower than
0.05, so we reject the null hypothesis that the variances are the same among
groups.

#Q15
dat_fl =
read.csv("/Users/stonehuang/Documents/environmental_data/data/trees_FL.csv")
head(dat_fl)

##   DBH_in HeighttoTop_ft     Species CanopyWidth_ft  MostSignificantDefect
## 1    8.0           12.5 Chinese elm             13                   Dead
## 2    8.0           16.0 Chinese elm             20                  Decay
## 3    5.5           15.5 Crapemyrtle             15 Poor Tree Architecture
## 4    6.2           14.0 Crapemyrtle             24 Poor Tree Architecture
## 5   16.0           17.0 Crapemyrtle             27 Poor Tree Architecture
## 6   15.2           20.0 Crapemyrtle             19 Poor Tree Architecture
##   Failure_Standardized ProbabilityofFailure
## 1                whole                    4
## 2                whole                    3
## 3                whole                    1
## 4                whole                    1
## 5                 none                    2
## 6                 none                    2
```

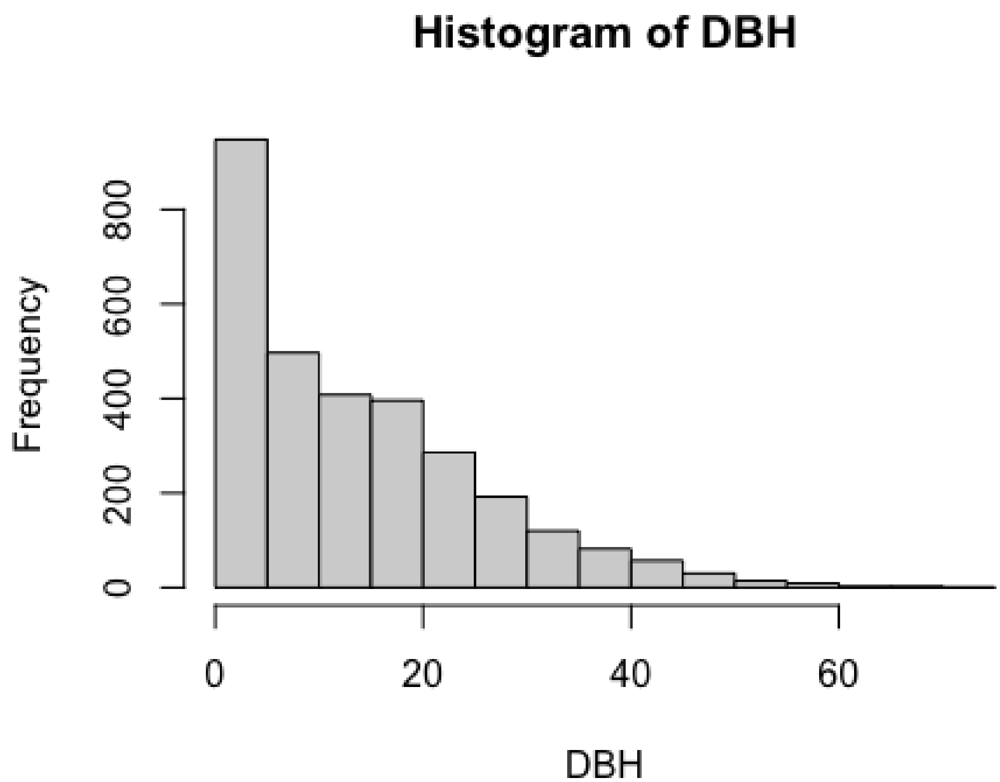
```
barplot(table(dat_fl$ProbabilityofFailure), ylab = "Counts of trees", xlab =
"Probability of failure class", main = "Barplot of counts of trees
        in each probability of failure class")
```



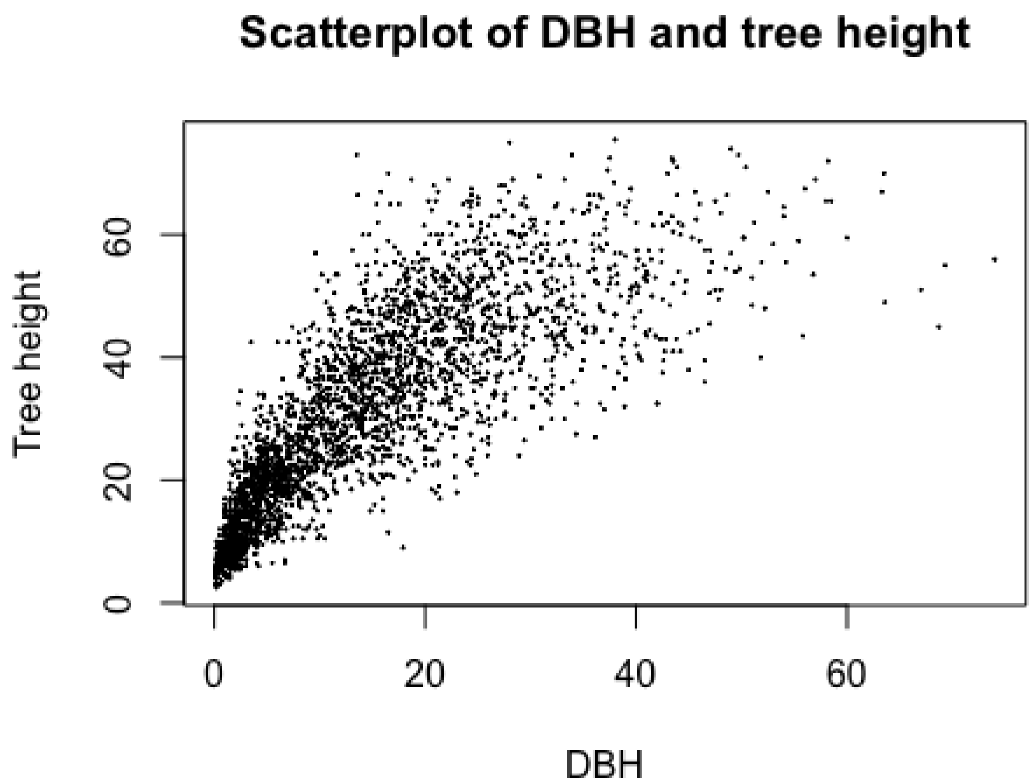

```
barplot(table(dat_fl$Failure_Standardized), ylab = "Counts of trees", xlab =
"Failure classes", main = "Barplot of the counts of trees
        in each of the failure classes")
```




```
hist(dat_fl$DBH_in, xlab = "DBH", main = "Histogram of DBH")
```




```
plot(dat_fl$HeighttoTop_ft ~ dat_fl$DBH_in, ylab = "Tree height", xlab =
"DBH", main = "Scatterplot of DBH and tree height", cex = 0.1)
```




```
#Q16. The null hypothesis for the Kolmogorov-Smirnov test is that there is no
difference in DBH between whole-tree failures and intact trees.
#Q17. 0.02125. The distribution of DBH is not the same for the two groups.
The p-value is lower than 0.05 so we reject the null hypothesis.
whole = subset(dat_fl, Failure_Standardized == "whole")
none = subset(dat_fl, Failure_Standardized == "none")
ks.test(whole$DBH_in, none$DBH_in)

## Warning in ks.test(whole$DBH_in, none$DBH_in): p-value will be approximate
in
## the presence of ties

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  whole$DBH_in and none$DBH_in
## D = 0.10643, p-value = 0.02125
## alternative hypothesis: two-sided

#Q18. Tree height increases with increasing DBH. The relationship is curved
and monotonic.
#Q19. Spearman
cor.test(
  dat_fl$DBH_in,
```

```
  dat_fl$HeighttoTop_ft,
  method='spearman',
  exact=FALSE)
```

```
##
##  Spearman's rank correlation rho
##
## data:  dat_fl$DBH_in and dat_fl$HeighttoTop_ft
## S = 541454081, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.8850462
```

#Q20. p-value < 2.2e-16.I conclude that the two variables are significantly correlated.

#Q21. X-squared = 202.65, p-value < 2.2e-16

```
dat_fl$fail = factor(dat_fl$Failure_Standardized != "none")
levels(dat_fl$fail) = c("No Fail", "Fail")
fl_table_2 = table(
  dat_fl$ProbabilityofFailure,
  dat_fl$fail)
fl_table_2
```

```
##
##     No Fail Fail
##   1    1239  168
##   2     670  219
##   3     421  206
##   4      53   63
```

```
chisq_trees = chisq.test(fl_table_2)
chisq_trees
```

```
##
##  Pearson's Chi-squared test
##
## data:  fl_table_2
## X-squared = 202.65, df = 3, p-value < 2.2e-16
```

#Q22. -136

```
round(
  chisq_trees$observed - chisq_trees$expected,
  digits = 0)
```

```
##
##     No Fail Fail
##   1     136 -136
##   2     -27   27
```

```
## 3 -71 71
## 4 -38 38

#Q23. There were fewer tree failures than expected by chance in failure
probability category #1.
#Q24. There more tree failures than expected by chance in failure probability
category #4.
#Q25. I conclude that the probability of failure rating system is effective!
There were more tree failures than expected in higher failure probability
categories.
```