FPA2020 Lecture 2: R basics

R, Rstudio, Rmarkdown

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Contents

1 How to use R via Rstudio

1.1 R

- Before starting the course, please visit the following website and download the applications which we will use in the course.
- First, please visit the following web site and download "R 3.6.xx" compatible with your OS. Below is for Windows as an example (sorry for this old screenshot):`https://cran.r-project.org/`

Download R-3.5.2 for Windows. The R-project for statistical c... https://cran.r-project.org/bin/windows/base/

R-3.5.2 for Windows (32/64 bit)

Download R 3.5.2 for Windows (79 megabytes, 32/64 bit)
Installation and other instructions
New features in this version

If you want to double-check that the package you have downloaded matches the package distributed by CRAN, you can compare the md5sum of the .exe to the fingerprint on the master server. You will need a version of md5sum for windows: both graphical and command line versions are available.

Frequently asked questions

- Does R run under my version of Windows?
- How do I update packages in my previous version of R?
- Should I run 32-bit or 64-bit R?

Please see the R FAQ for general information about R and the R Windows FAQ for Windows-specific information.

Other builds

- Patches to this release are incorporated in the r-patched snapshot build.
- A build of the development version (which will eventually become the next major release of R) is available in the r-devel snapshot build.
- Previous releases

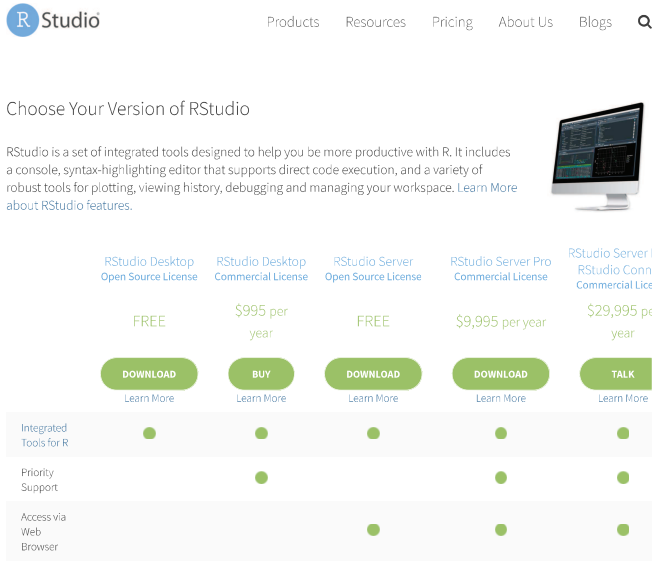
Note to webmasters: A stable link which will redirect to the current Windows binary release is <CRAN MIRROR>/bin/windows/base/release.htm.

%

1.2 Rstudio

- Then please visit the web site below and download the free version of "RStudio Desktop": https://www.rstudio.com/products/rstudio/download/

Download RStudio - RStudio https://www.rstudio.com/products/rstudio/download/



%

1.3 Rmarkdown

I will explain how you can create a memo/report of your analysis with R in a easy way with Rmarkdown. I'm writing this handout using it.

1.4 Required libraries

Please install the following packages in R by using a command before the seminar. The syntax to install packages is as follow (there are another ways though).

```
install.packages("package name")
```

```
install.packages("knitr")
install.packages("rmarkdown")
install.packages("kableExtra")

install.packages("ggplot2")
install.packages("gridExtra")

install.packages("mgcv")
install.packages("fields")
install.packages("ggmap")
install.packages("marmap")
install.packages("mapdata")

install.packages("tidyverse")
install.packages("shiny")
```

1.5 calling libraries

Then you can call those libraries.

```
library(knitr)
library(rmarkdown)
library(kableExtra)

library(ggplot2)
library(gridExtra)

library(mgcv)
library(fields)
library(ggmap)
library(marmap)
library(mapdata)

library(tidyverse)
library(shiny)
```

2 A quick warming up (1)

2.1 Getting R sessions started with basic arithmetics and handling the list

```
a <- c(10,20,30,40,50); a
```

```
[1] 10 20 30 40 50
```

```
sum(a)
```

```
[1] 150
```

```
mean(a)
```

```
[1] 30
```

```
(-1)*a^2+100
```

```
[1]    0  -300  -800 -1500 -2400
```

```
a[c(1,3,5)]
```

```
[1] 10 30 50
```

```
a[-c(2,4)]
```

```
[1] 10 30 50
```

```
b <- seq(2,10,by=2); b
```

```
[1]  2  4  6  8 10
```

```
a+b
```

```
[1] 12 24 36 48 60
```

```
a*b
```

```
[1]  20  80 180 320 500
```

```
b/a
```

```
[1] 0.2 0.2 0.2 0.2 0.2
```

2.2 For loop

```
ss <- 0
 for(i in 1:10){
  ss <- ss + i
}
ss
```

```
[1] 55
```

```
# Just in case, this is done simply as follows:
sum(1:10)
```

```
[1] 55
```

3 A quick warming up (2)

We will conduct a very simple analysis for body proportion of Japanese fish species with statistical testing and visual presentation. We first read a data file named as "Horsemackerel.csv".

3.1 Reading data from csv file

```
# Read the data file
Data <- read.csv("Horsemackerel.csv", header=T)
head(Data)
```

```
  Species  TL  FL  SL HL BD   ED
1   Maaji 297 259 235 65 59 15.4
2   Maaji 285 263 255 65 61 15.2
3   Maaji 285 255 263 65 63 15.1
4   Maaji 319 275 269 71 63 16.6
5   Maaji 297 259 235 65 59 15.1
6   Maaji 194 172 160 45 42 13.6
```

```
# Extract the data column and create a new object "proportion"
Data$BD
```

```
 [1] 59 61 63 63 59 42 42 50 46 44 40 53 34 38 38 36 36 36 34 38 37 37 40 36 34
[26] 38 37 37 40 38 31 30 36 31 39 37 36 41 31 30 36 31 37 41 45 37 38 31 30 36
[51] 31 37 41 45 37 38 31 30 36 31 37 41 45 37 38 39 31 30 36 31 39 37 36 41 31
[76] 30 36 31 37 41 45 37 38 39 39 37 37 36 36 35
 [ reached getOption("max.print") -- omitted 85 entries ]
```

```
Data$SL
```

```
 [1] 235 255 263 269 235 160 174 182 171 168 152 203 137 149 150 145 146 145 136
[20] 148 137 145 155 145 136 148 137 145 155 145 118 122 138 133 142 129 134 152
[39] 137 143 157 150 148 150 175 166 161 137 143 157 150 148 150 175 166 161 137
[58] 143 157 150 148 150 175 166 161 141 118 122 138 133 142 129 134 152 137 143
[77] 157 150 148 150 175 166 161 205 213 215 221 189 193 197
 [ reached getOption("max.print") -- omitted 85 entries ]
```

```
Proportion <- Data$BD/Data$SL

# Add "Prop" into the current data set "Data"
Data <- cbind(Data, Prop=Proportion)
attach(Data)
```

3.2 Visual presentation

```
# Exracting data
SP <- as.numeric(Species)
SPname <- levels(Species)
SP
```

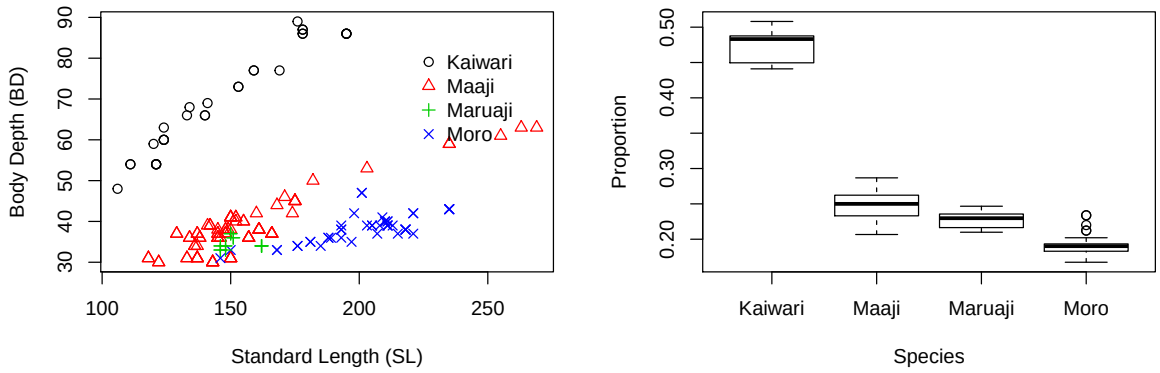
```
 [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[39] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[77] 2 2 2 2 2 2 2 4 4 4 4 4 4 4
 [ reached getOption("max.print") -- omitted 85 entries ]
```

```
SPname
```

```
[1] "Kaiwari" "Maaji"   "Maruaji" "Moro"
```

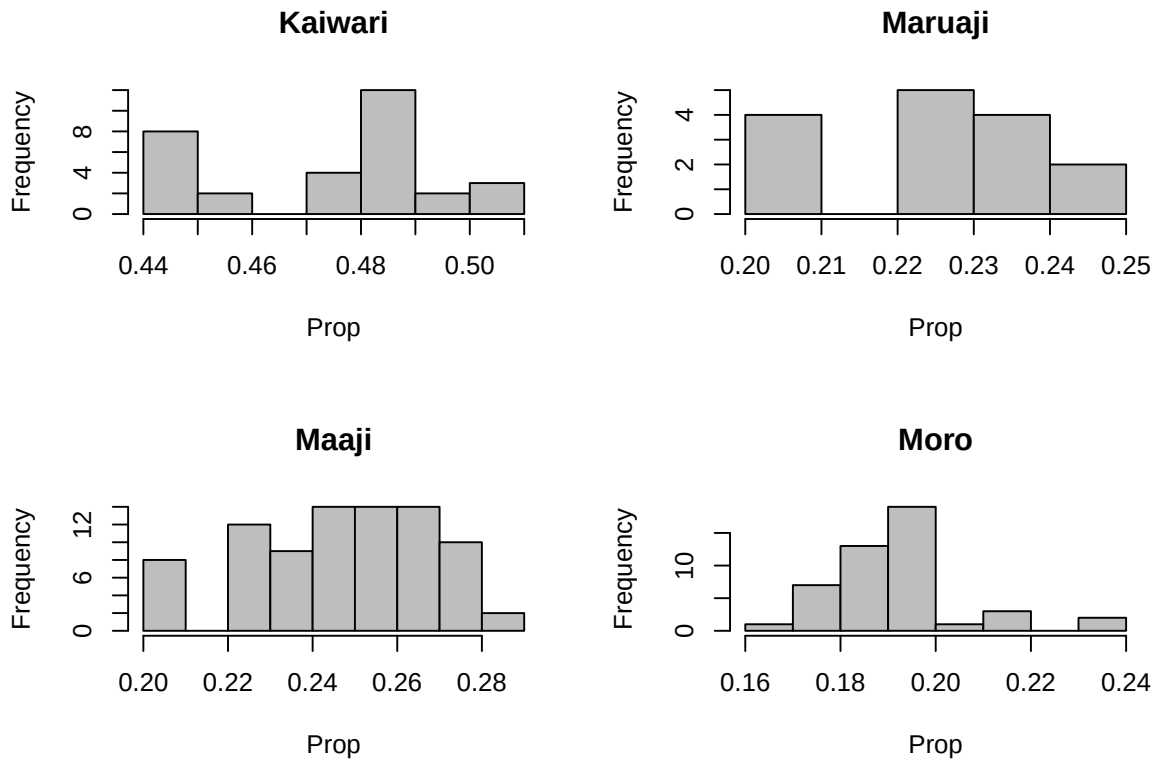
3.3 Scatter plot and boxplot

```
par(mfrow=c(1,2)) #Splitting screen
plot(BD~SL, pch=SP, col=SP, xlab="Standard Length (SL)", ylab="Body Depth (BD)")
legend(220, 85, legend=levels(Species), pch=1:4, col=1:4, bty="n")
boxplot(Prop~Species, ylab="Proportion")
```



3.4 Histogram of proportion by species

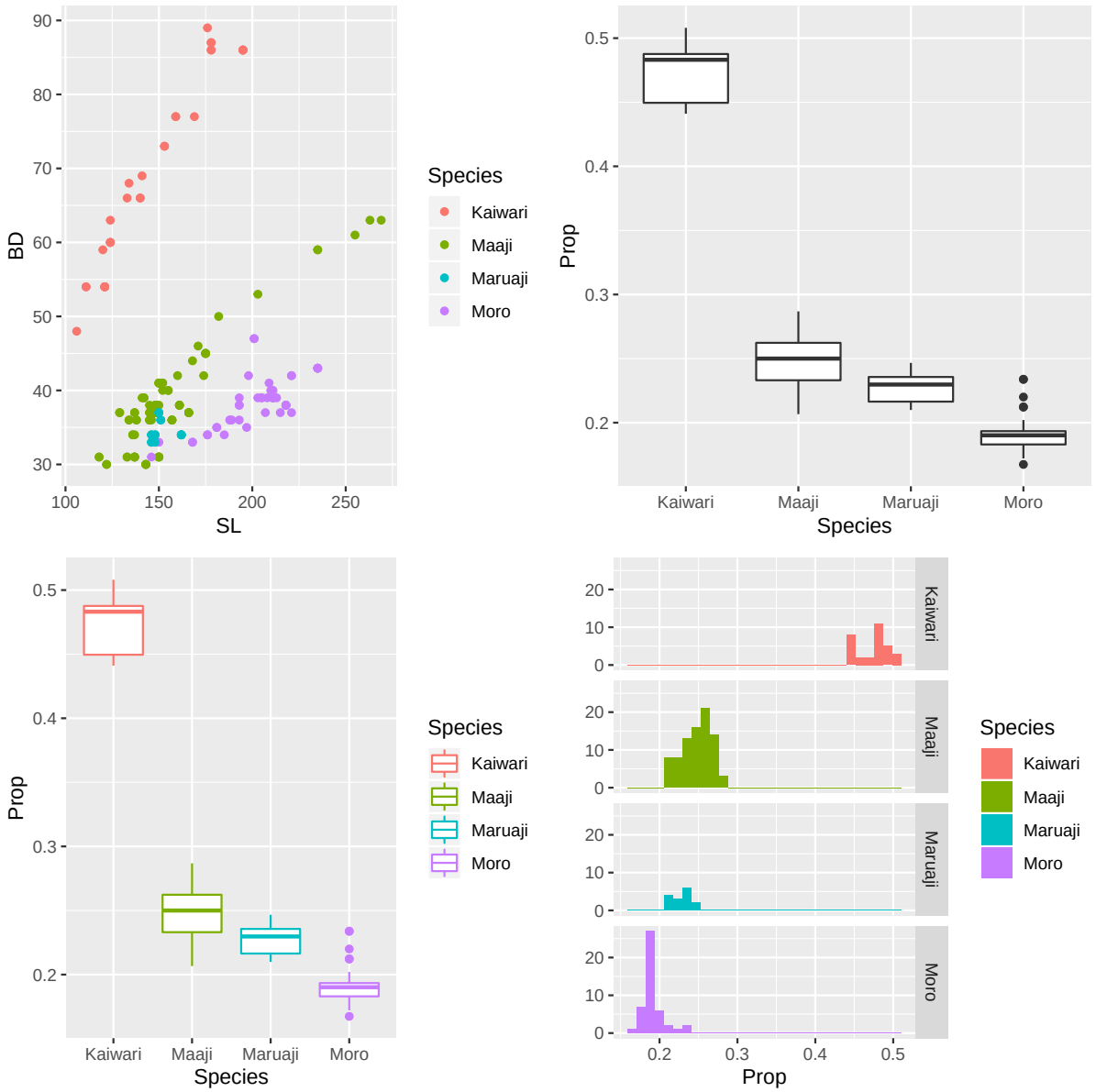
```
par(mfcol=c(2,2))
for(i in 1:length(SPname)) hist(Prop[SP==i], xlab="Prop", main=paste(SPname[i]), col="gray")
```



3.5 More colourful visual presentation by "ggplot"

A library "ggplot2" provides us with beautiful figures, but it requires a bit training of syntax, so I shall use a quicker version of command on ggplot.

```
plot1 <- qplot(SL, BD, col=Species)
plot2 <- qplot(Species, Prop, geom="boxplot")
plot3 <- qplot(Species, Prop, geom="boxplot", col=Species)
plot4 <- qplot(Prop, facets=Species~., fill=Species, data=Data)
grid.arrange(plot1, plot2, plot3, plot4, nrow=2, ncol=2)
```



3.6 Summary statistics

```
y <- split(Prop, Species)
y$Kaiwari
```

```
 [1] 0.4893617 0.5074627 0.5056818 0.5080645 0.4916667 0.4556213 0.4528302
 [8] 0.4962406 0.4714286 0.4771242 0.4838710 0.4887640 0.4842767 0.4838710
[15] 0.4842767 0.4887640 0.4714286 0.4771242 0.4838710 0.4864865 0.4831461
[22] 0.4410256 0.4462810 0.4410256 0.4462810 0.4410256 0.4462810 0.4831461
[29] 0.4864865 0.4410256 0.4462810
```

```
length(y$Kaiwari)
```

```
[1] 31
```

```
sapply(y, length)
```

```
Kaiwari   Maaji Maruaji    Moro
     31      83      15      46
```

```
lapply(y, length)
```

```
$Kaiwari
[1] 31

$Maaji
[1] 83

$Maruaji
[1] 15

$Moro
[1] 46
```

```
Ns <- sapply(y, length)
Mean <- sapply(y, mean)
SD <- sapply(y, sd)
data.frame(Nsample=Ns, Mean, SD)
```

```
        Nsample      Mean         SD
Kaiwari      31 0.4738781 0.02159171
Maaji        83 0.2477849 0.02045780
Maruaji      15 0.2273268 0.01283770
Moro         46 0.1908011 0.01381693
```

3.7 Example of one sample test (Null hypothesis, H0:mu=0.2)

```
lapply(y, t.test, mu=0.2)
```

```
$Kaiwari

    One Sample t-test

data:  X[[i]]
t = 70.624, df = 30, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0.2
95 percent confidence interval:
 0.4659582 0.4817980
sample estimates:
mean of x
0.4738781


$Maaji

    One Sample t-test

data:  X[[i]]
t = 21.28, df = 82, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0.2
95 percent confidence interval:
```

```
 0.2433179 0.2522520
sample estimates:
mean of x
0.2477849


$Maruaji

    One Sample t-test

data:  X[[i]]
t = 8.2442, df = 14, p-value = 9.634e-07
alternative hypothesis: true mean is not equal to 0.2
95 percent confidence interval:
 0.2202175 0.2344360
sample estimates:
mean of x
0.2273268


$Moro

    One Sample t-test

data:  X[[i]]
t = -4.5155, df = 45, p-value = 4.527e-05
alternative hypothesis: true mean is not equal to 0.2
95 percent confidence interval:
 0.1866980 0.1949042
sample estimates:
mean of x
0.1908011
```

```
res.t.test <- lapply(y, t.test, mu=0.2)
```

3.8 Two sample test (if the mean is equal between two speciesor not)

```
# variance same?
var.test(y[[2]],y[[3]])
```

```

    F test to compare two variances

data:  y[[2]] and y[[3]]
F = 2.5395, num df = 82, denom df = 14, p-value = 0.05378
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.9838916 5.1560229
sample estimates:
ratio of variances
          2.539471
```

```
# t-test
t.test(y[[2]],y[[3]], var.equal=T)
```

```
    Two Sample t-test

data:  y[[2]] and y[[3]]
t = 3.7332, df = 96, p-value = 0.0003205
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.009580294 0.031336083
sample estimates:
mean of x mean of y
0.2477849 0.2273268
```

```
t.test(y[[2]],y[[3]])
```

```
    Welch Two Sample t-test

data:  y[[2]] and y[[3]]
t = 5.1098, df = 28.765, p-value = 1.91e-05
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.01226681 0.02864956
sample estimates:
mean of x mean of y
0.2477849 0.2273268
```

3.9 Analysis of variance (test if all the mean are equal or not)

Under an assumption of "common variance" across species,

```
res.lm <- lm(Prop~Species)
summary(res.lm)
```

```
Call:
lm(formula = Prop ~ Species)

Residuals:
      Min        1Q    Median        3Q       Max
-0.041118 -0.012597  0.002215  0.011178  0.043030

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     0.473878   0.003342  141.80   <2e-16 ***
SpeciesMaaji   -0.226093   0.003917  -57.73   <2e-16 ***
SpeciesMaruaji -0.246551   0.005852  -42.13   <2e-16 ***
SpeciesMoro    -0.283077   0.004324  -65.47   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.01861 on 171 degrees of freedom
Multiple R-squared:  0.9653,    Adjusted R-squared:  0.9647
F-statistic:  1584 on 3 and 171 DF,  p-value: < 2.2e-16
```

```
res.lm <- lm(Prop~Species-1)
summary(res.lm)
```

```

Call:
lm(formula = Prop ~ Species - 1)

Residuals:
      Min        1Q    Median        3Q       Max
-0.041118 -0.012597  0.002215  0.011178  0.043030

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
SpeciesKaiwari 0.473878   0.003342  141.80   <2e-16 ***
SpeciesMaaji   0.247785   0.002042  121.32   <2e-16 ***
SpeciesMaruaji 0.227327   0.004804   47.32   <2e-16 ***
SpeciesMoro    0.190801   0.002743   69.55   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.01861 on 171 degrees of freedom
Multiple R-squared:  0.9959,    Adjusted R-squared:  0.9958
F-statistic: 1.048e+04 on 4 and 171 DF,  p-value: < 2.2e-16
```

```
res.anova1 <- anova(res.lm)
res.anova1
```

```
Analysis of Variance Table

Response: Prop
           Df  Sum Sq Mean Sq F value    Pr(>F)
Species     4 14.5072  3.6268   10476 < 2.2e-16 ***
Residuals 171  0.0592  0.0003
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In case of "heterogeneity in variance",

```
res.bartlett <- bartlett.test(Prop~Species)
res.bartlett
```

```

    Bartlett test of homogeneity of variances

data:  Prop by Species
Bartlett's K-squared = 12.515, df = 3, p-value = 0.005813
```

```
res.anova2 <- oneway.test(Prop~Species, var.equal = FALSE)
res.anova2
```

```
    One-way analysis of means (not assuming equal variances)

data:  Prop and Species
F = 1373.1, num df = 3.00, denom df = 54.97, p-value < 2.2e-16
```

3.10 Pairwise t-test

```
pairwise.t.test(Prop,Species)
```

```
    Pairwise comparisons using t tests with pooled SD

data:  Prop and Species

        Kaiwari Maaji   Maruaji
Maaji   < 2e-16 -       -
Maruaji < 2e-16 0.00013 -
Moro    < 2e-16 < 2e-16 9.8e-10

P value adjustment method: holm
```

```
pairwise.t.test(Prop,Species, pool.sd = FALSE)
```

```
    Pairwise comparisons using t tests with non-pooled SD

data:  Prop and Species

        Kaiwari Maaji   Maruaji
Maaji   < 2e-16 -       -
Maruaji < 2e-16 1.9e-05 -
Moro    < 2e-16 < 2e-16 1.9e-09

P value adjustment method: holm
```

```
pairwise.t.test(Prop,Species, pool.sd = FALSE, p.adj = "bonf")
```

```
    Pairwise comparisons using t tests with non-pooled SD

data:  Prop and Species

        Kaiwari Maaji   Maruaji
Maaji   < 2e-16 -       -
Maruaji < 2e-16 0.00011 -
Moro    < 2e-16 < 2e-16 5.7e-09

P value adjustment method: bonferroni
```