

# PIPO

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Import Datasets:

```
Planting <- read.csv("/Users/sarahcarter/Downloads/PIPO COMPILED  
PLANTING DATA - PLANTING DATA.csv")  
Initial <- read.csv("/Users/sarahcarter/Downloads/PIPO INITIAL DATA -  
INITIAL DATA.csv")  
#str(Planting)
```

Initial H by provenance (all, planted and unplanted):

```
library(ggplot2)  
tapply(Initial$INITIAL.HEIGHT..cm., Initial$PROVENANCE, summary)
```

```
## [[1]]  
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's  
##      4.000   4.475   4.950   4.950   5.425   5.900    18  
##  
## $BD  
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's  
##      2.100   4.500   5.300   5.592   6.150  11.900    52  
##  
## $BH  
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.  
##      3.90    4.40    5.20    5.05   5.70    6.00  
##  
## $FC  
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's  
##      4.000   5.400   5.750   6.197   6.400  10.300    13  
##  
## $HM1  
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's  
##      3.600   5.450   5.850   5.888   6.500   7.200    20  
##  
## $HM6  
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's  
##      3.900   4.650   6.000   6.163   7.150  10.000     5
```

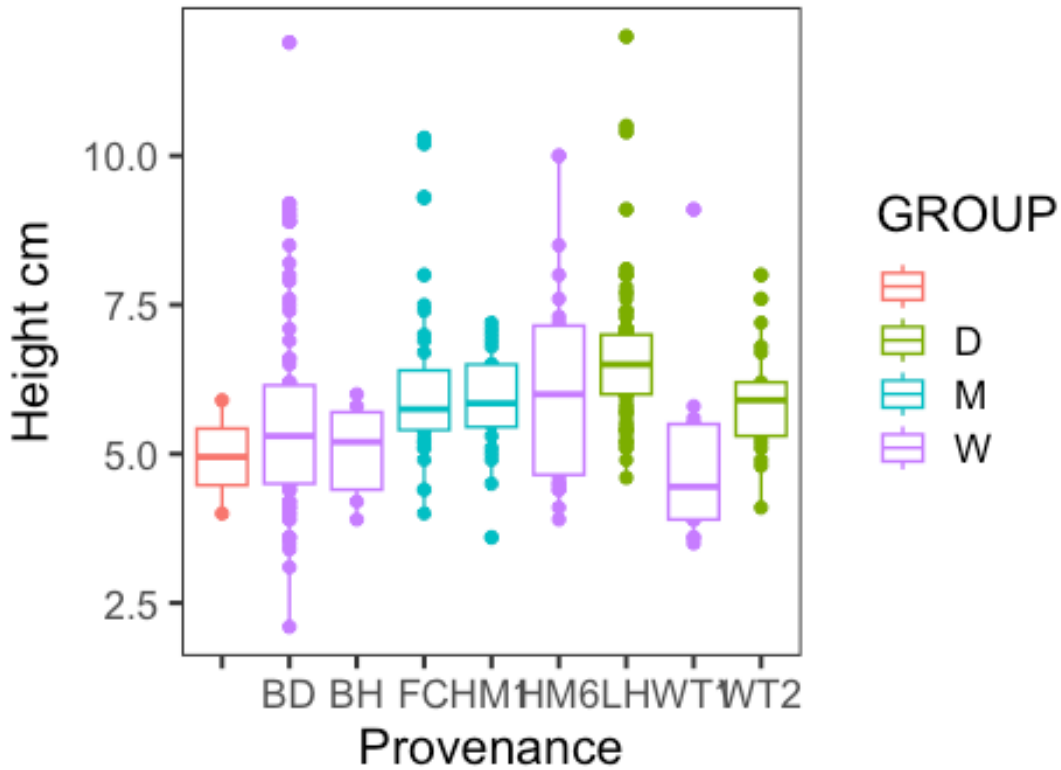
```
##
## $LH
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.600   6.000   6.500   6.611   7.000   12.000        53
##
## $WT1
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      3.50    3.90    4.45    4.80    5.50    9.10        12
##
## $WT2
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.100   5.300   5.900   5.943   6.200   8.000        23

ggplot(Initial, aes(x=PROVENANCE, y = INITIAL.HEIGHT..cm., col = GROUP))
+ geom_point() +
  geom_boxplot() +
    xlab("Provenance") +
    ylab(expression(paste("Height cm")) +
    theme_bw(base_size = 16) + theme(panel.grid.major =
element_blank(), panel.grid.minor = element_blank()) + ggtitle("
Initial Height by Provenance for all Seedlings")

## Warning: Removed 196 rows containing non-finite values
(`stat_boxplot()`).

## Warning: Removed 196 rows containing missing values
(`geom_point()`).
```

## Initial Height by Provenance for all



Initial H by provenance (PLANTED):

```
lapply(Planting$INITIAL.HEIGHT..cm., Planting$PROVENANCE, summary)
```

```
## [[1]]
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##         4         4         4         4         4         4         2
##
## $BD
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      2.100  4.700  5.400  5.667  6.100  11.900     20
##
## $BH
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##         4.2    4.6    5.0    5.0    5.4    5.8         3
##
```

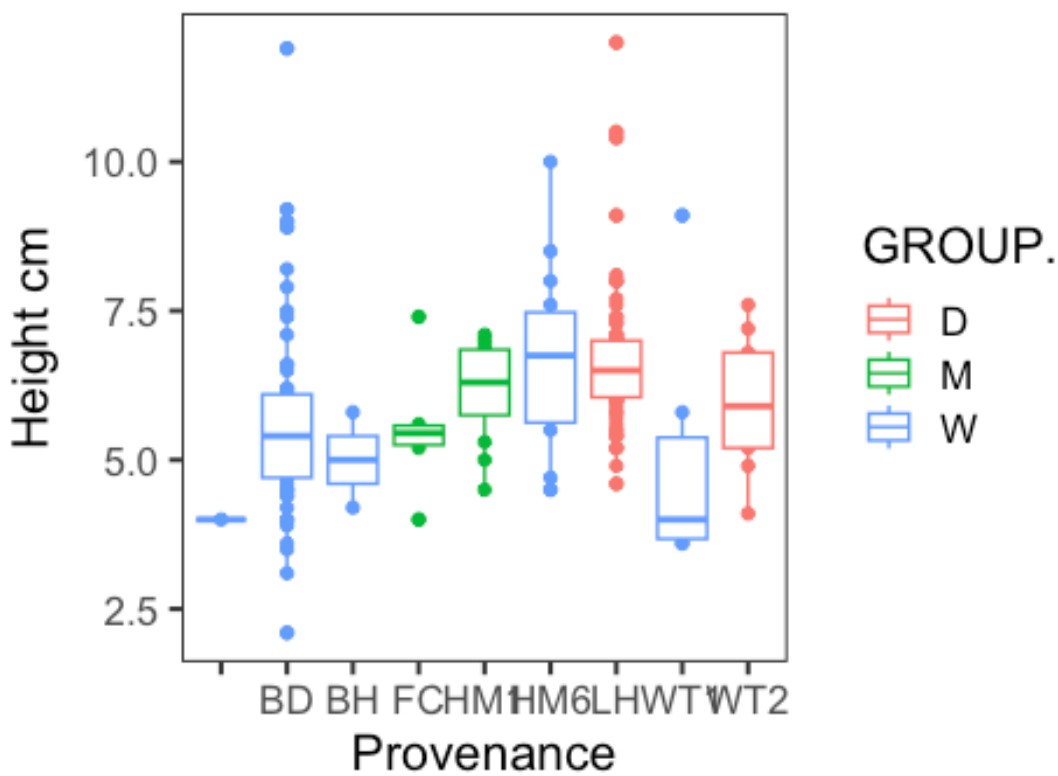
```
## $FC
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      4.000   5.250   5.450   5.517   5.575   7.400      29
##
## $HM1
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      4.500   5.750   6.300   6.173   6.850   7.100      14
##
## $HM6
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      4.500   5.625   6.750   6.650   7.475  10.000       7
##
## $LH
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      4.600   6.050   6.500   6.657   7.000  12.000      23
##
## $WT1
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      3.600   3.675   4.000   5.017   5.375   9.100       8
##
## $WT2
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      4.1      5.2      5.9      5.9      6.8      7.6      12
```

```
ggplot(Planting,aes(x=PROVENANCE,y = INITIAL.HEIGHT..cm., col =
GROUP.)) + geom_point() +
  geom_boxplot() +
    xlab("Provenance") +
    ylab(expression(paste("Height cm")))+
    theme_bw(base_size = 16) + theme(panel.grid.major =
element_blank(), panel.grid.minor = element_blank()) + ggtitle("
Initial Seedling Height by Provenance")
```

```
## Warning: Removed 118 rows containing non-finite values
(`stat_boxplot()`).
```

```
## Warning: Removed 118 rows containing missing values
(`geom_point()`).
```

# Initial Seedling Height by Provenance



Final H by provenance:

```
lapply(Planting$FINAL.HEIGHT..cm., Planting$PROVENANCE, summary)
```

```
## [[1]]
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      7.80   9.25   10.70   10.70  12.15   13.60     1
##
## $BD
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      4.200   6.600   8.100   8.618  10.975   13.600     27
##
## $BH
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      5.1    5.4    6.0    8.0   10.7   12.8     1
##
```

```

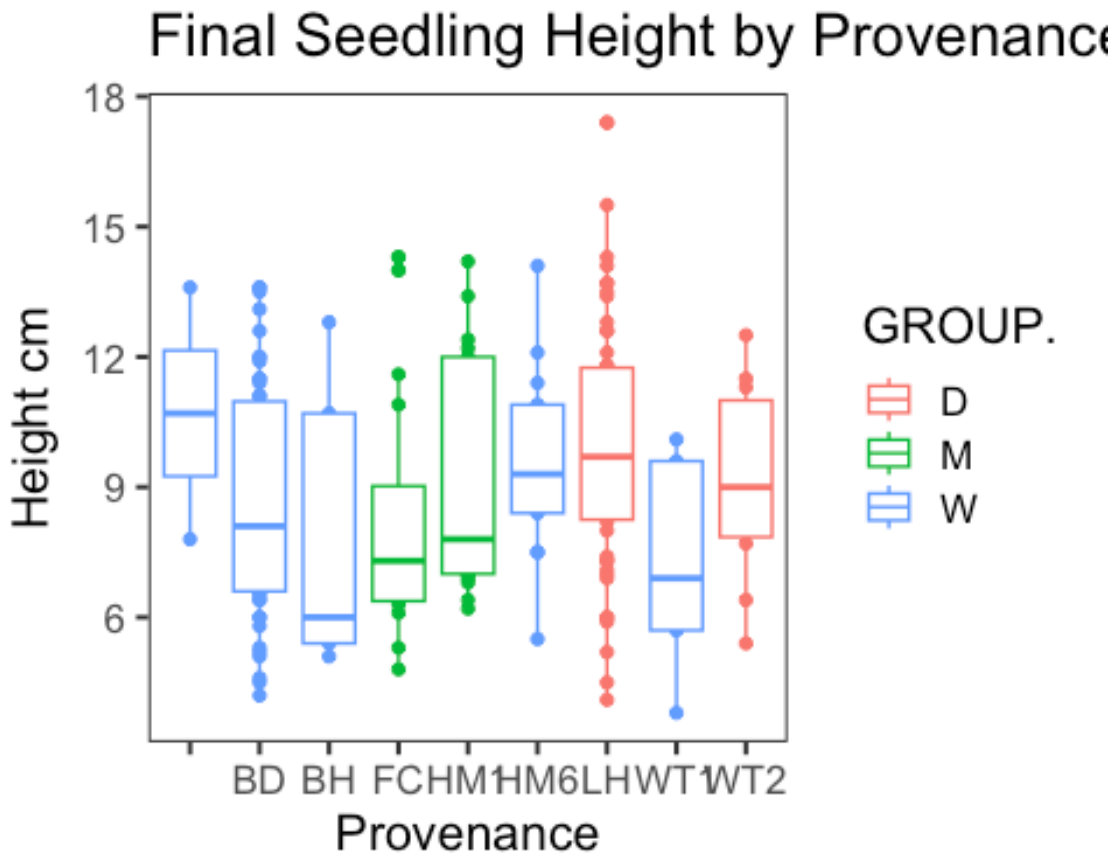
## $FC
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.800   6.375   7.300   8.325   9.025   14.300         19
##
## $HM1
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      6.200   7.000   7.800   9.094   12.000   14.200         8
##
## $HM6
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      5.500   8.400   9.300   9.469   10.900   14.100         8
##
## $LH
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.100   8.250   9.700   9.969   11.750   17.400        43
##
## $WT1
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      3.80    5.70    6.90    7.22    9.60   10.10         9
##
## $WT2
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      5.400   7.850   9.000   9.091   11.000   12.500        10

ggplot(Planting,aes(x=PROVENANCE,y = FINAL.HEIGHT..cm., col = GROUP.))
+ geom_point() +
  geom_boxplot() +
    xlab("Provenance") +
    ylab(expression(paste("Height cm")))+
    theme_bw(base_size = 16) + theme(panel.grid.major =
element_blank(), panel.grid.minor = element_blank()) + ggtitle("Final
Seedling Height by Provenance")

## Warning: Removed 126 rows containing non-finite values
(`stat_boxplot()`).

## Warning: Removed 126 rows containing missing values
(`geom_point()`).

```



Initial health of all groups:

```
#count(Initial, INITIAL.HEALTH, GROUP)
#count(Initial, INITIAL.HEALTH, PROVENANCE)
#Planting %>% count(INITIAL.HEALTH, GROUP.)
#Planting %>% count(INITIAL.HEALTH, PROVENANCE)
```

Final health:

```
#count(Planting, FINAL.HEALTH, GROUP.)
#count(Planting, FINAL.HEALTH, PROVENANCE)
#Planting %>% count(FINAL.HEALTH, GROUP.)
#Planting %>% count(FINAL.HEALTH, PROVENANCE)
```

Height Summary Data:

```
tapply(Planting$INITIAL.HEIGHT..cm., Planting$GROUP., summary)
```

```
## $D
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.100   6.000   6.500   6.576   7.000   12.000        35
##
## $M
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.000   5.300   6.200   5.941   6.800   7.400        44
##
## $W
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      2.100   4.500   5.400   5.743   6.500   11.900        39
```

```
tapply(Planting$FINAL.HEIGHT..cm., Planting$GROUP., summary)
```

```
## $D
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.100   8.025   9.650   9.823   11.600   17.400        53
##
## $M
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      4.800   6.900   7.600   8.721   11.000   14.300        28
##
## $W
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      3.800   6.600   8.300   8.687   10.800   14.100        45
```

Basal Diameter Summary Data:

```
tapply(Planting$INITIAL.DIAMETER..mm., Planting$GROUP., summary)
```

```
## $D
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      1.030   1.510   1.710   1.810   1.995   3.020        36
##
## $M
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      1.270   1.480   1.720   1.645   1.780   1.990        44
##
## $W
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.      NA's
##      0.990   1.510   1.660   1.728   1.940   2.730        39
```



```
tapply(Planting$FINAL.DIAMETER..mm., Planting$GROUP., summary)
```

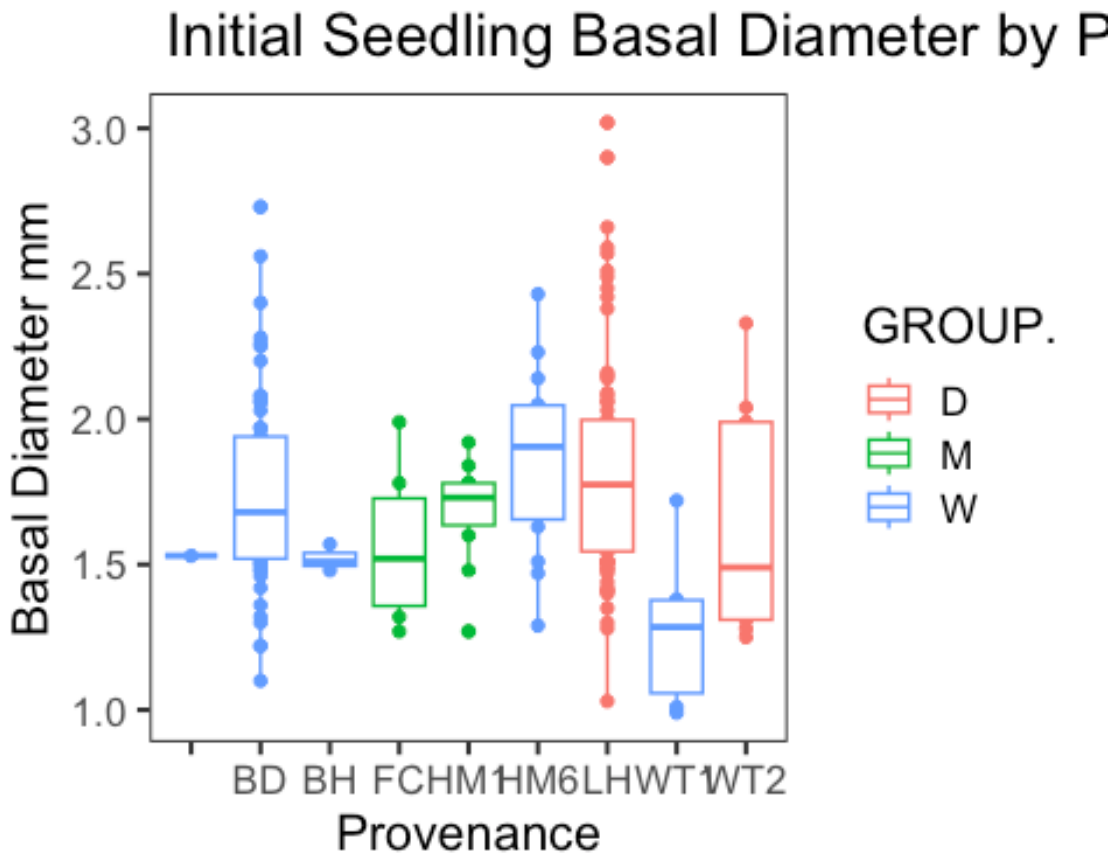
```
## $D
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      1.250   1.812   2.020   2.131   2.333   3.690    53
##
## $M
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      1.340   1.660   1.830   1.922   2.190   2.590    28
##
## $W
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##      1.31    1.80    2.08    2.14    2.40    3.39    45
```

Initial basal diameter by provenance:

```
ggplot(Planting, aes(x=PROVENANCE, y = INITIAL.DIAMETER..mm., col =
GROUP.)) + geom_point() +
  geom_boxplot() +
  xlab("Provenance") +
  ylab(expression(paste("Basal Diameter mm"))) +
  theme_bw(base_size = 16) + theme(panel.grid.major =
element_blank(), panel.grid.minor = element_blank()) + ggtitle("
Initial Seedling Basal Diameter by Provenance")

## Warning: Removed 119 rows containing non-finite values
(`stat_boxplot()`).

## Warning: Removed 119 rows containing missing values
(`geom_point()`).
```



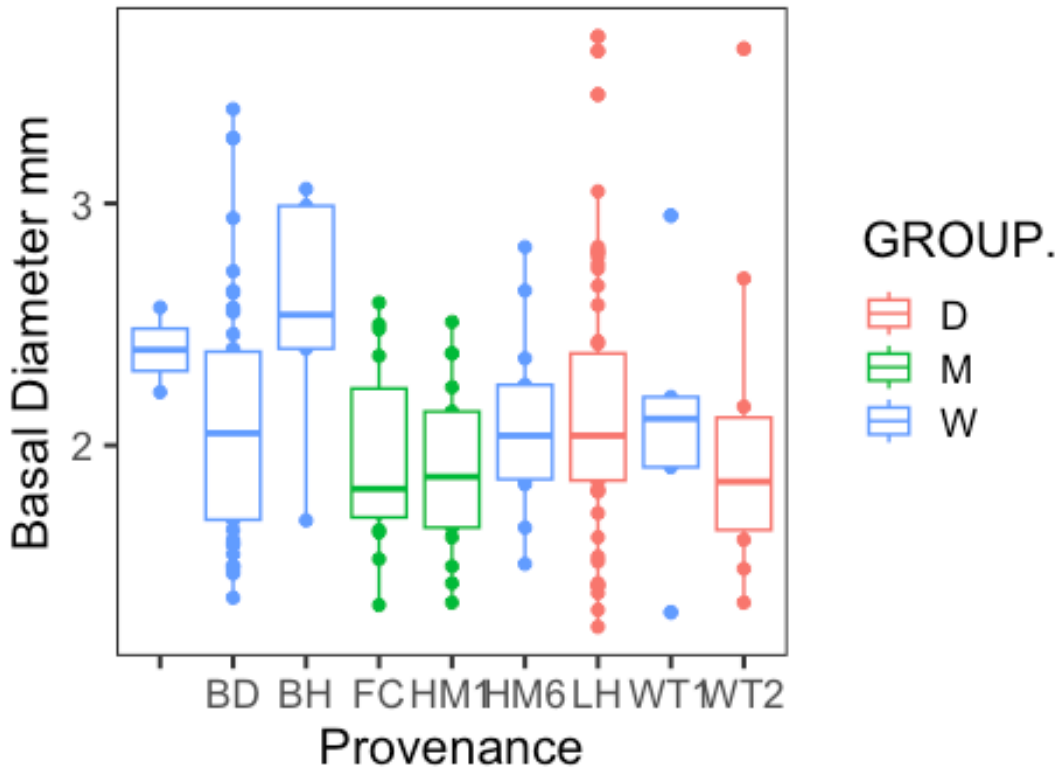
Final basal diameter by provenance:

```
ggplot(Planting, aes(x=PROVENANCE, y = FINAL.DIAMETER..mm., col =
GROUP.)) + geom_point() +
  geom_boxplot() +
  xlab("Provenance") +
  ylab(expression(paste("Basal Diameter mm"))) +
  theme_bw(base_size = 16) + theme(panel.grid.major =
element_blank(), panel.grid.minor = element_blank()) + ggtitle("Final
Seedling Basal Diameter by Provenance")
```

```
## Warning: Removed 126 rows containing non-finite values
(`stat_boxplot()`).
```

```
## Warning: Removed 126 rows containing missing values
(`geom_point()`).
```

## Final Seedling Basal Diameter by Pro



t-test for initial/final data (general):

```
library(car)

## Loading required package: carData

t.test(Planting$INITIAL.HEIGHT..cm., Planting$FINAL.HEIGHT..cm.,
paired = TRUE, mu = 0, conf.level = 0.95)

##
## Paired t-test
##
## data: Planting$INITIAL.HEIGHT..cm. and Planting$FINAL.HEIGHT..cm.
## t = -11.516, df = 122, p-value < 2.2e-16
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -3.332752 -2.355053
```

```

## sample estimates:
## mean difference
##      -2.843902

t.test(Planting$INITIAL.DIAMETER..mm., Planting$FINAL.DIAMETER..mm.,
paired = TRUE, mu = 0, conf.level = 0.95)

##
## Paired t-test
##
## data:  Planting$INITIAL.DIAMETER..mm. and
Planting$FINAL.DIAMETER..mm.
## t = -7.0849, df = 122, p-value = 9.725e-11
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.3839269 -0.2162357
## sample estimates:
## mean difference
##      -0.3000813

t.test(Planting$INITIAL.HEALTH, Planting$FINAL.HEALTH, paired = TRUE,
mu = 0, conf.level = 0.95)

##
## Paired t-test
##
## data:  Planting$INITIAL.HEALTH and Planting$FINAL.HEALTH
## t = -9.5343, df = 180, p-value < 2.2e-16
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -1.0449210 -0.6865707
## sample estimates:
## mean difference
##      -0.8657459

```

Filter data and new objects:

```

library(dplyr)

##
## Attaching package: 'dplyr'

```

```

## The following object is masked from 'package:car':
##
##      recode

## The following objects are masked from 'package:stats':
##
##      filter, lag

## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union

#by group only
dry <- Planting %>% filter(GROUP=="D")
wet <- Planting %>% filter(GROUP=="W")
mod <- Planting %>% filter(GROUP=="M")

#by site only
site1 <- Planting %>% filter(SITE=="1")
site2 <- Planting %>% filter(SITE=="2")

#by group and site
site1D <- Planting %>% filter(SITE=="1", GROUP=="D")
site2D <- Planting %>% filter(SITE=="2", GROUP=="D")
site1W <- Planting %>% filter(SITE=="1", GROUP=="W")
site2W <- Planting %>% filter(SITE=="2", GROUP=="W")
site1M <- Planting %>% filter(SITE=="1", GROUP=="M")
site2M <- Planting %>% filter(SITE=="2", GROUP=="M")

#by provenance
#W
BD <- Planting %>% filter(PROVENANCE=="BD")
BH <- Planting %>% filter(PROVENANCE=="BH")
WT1 <- Planting %>% filter(PROVENANCE=="WT1")
HM6 <- Planting %>% filter(PROVENANCE=="HM6")
#M
HM1 <- Planting %>% filter(PROVENANCE=="HM1")
FC <- Planting %>% filter(PROVENANCE=="FC")
#D
LH <- Planting %>% filter(PROVENANCE=="LH")
WT2 <- Planting %>% filter(PROVENANCE=="WT2")

```

```
#by provenance and site
```

```
BD1 <- Planting %>% filter(SITE=="1", PROVENANCE=="BD")
BD2 <- Planting %>% filter(SITE=="2", PROVENANCE=="BD")
BH1 <- Planting %>% filter(SITE=="1", PROVENANCE=="BH")
BH2 <- Planting %>% filter(SITE=="2", PROVENANCE=="BH")
WT11 <- Planting %>% filter(SITE=="1", PROVENANCE=="WT1")
WT12 <- Planting %>% filter(SITE=="2", PROVENANCE=="WT1")
HM61 <- Planting %>% filter(SITE=="1", PROVENANCE=="HM6")
HM62 <- Planting %>% filter(SITE=="2", PROVENANCE=="HM6")
```

```
#M
```

```
HM11 <- Planting %>% filter(SITE=="1", PROVENANCE=="HM1")
HM12 <- Planting %>% filter(SITE=="2", PROVENANCE=="HM1")
FC1 <- Planting %>% filter(SITE=="1", PROVENANCE=="FC")
FC2 <- Planting %>% filter(SITE=="2", PROVENANCE=="FC")
```

```
#D
```

```
LH1 <- Planting %>% filter(SITE=="1", PROVENANCE=="LH1")
LH2 <- Planting %>% filter(SITE=="2", PROVENANCE=="LH1")
WT21 <- Planting %>% filter(SITE=="1", PROVENANCE=="WT2")
WT22 <- Planting %>% filter(SITE=="2", PROVENANCE=="WT2")
```

```
#Differences:
```

```
heightdiff <- (Planting$FINAL.HEIGHT..cm. -
Planting$INITIAL.HEIGHT..cm.)
diameterdiff <- (Planting$FINAL.DIAMETER..mm. -
Planting$INITIAL.DIAMETER..mm.)
healthdiff <- (Planting$FINAL.HEALTH - Planting$INITIAL.HEALTH)
```

t-tests:

Initial/final H by site:

```
t.test(site1$INITIAL.HEIGHT..cm., site1$FINAL.HEIGHT..cm., paired =
TRUE, mu = 0, conf.level = 0.95)
```

```
##
```

```
## Paired t-test
```

```
##
```

```
## data: site1$INITIAL.HEIGHT..cm. and site1$FINAL.HEIGHT..cm.
```

```
## t = -7.334, df = 62, p-value = 5.67e-10
```

```
## alternative hypothesis: true mean difference is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -2.486544 -1.421393
## sample estimates:
## mean difference
## -1.953968

t.test(site2$FINAL.HEIGHT..cm., site2$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: site2$FINAL.HEIGHT..cm. and site2$INITIAL.HEIGHT..cm.
## t = 9.7142, df = 59, p-value = 7.534e-14
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 3.000044 4.556623
## sample estimates:
## mean difference
## 3.778333
```

Initial/final H by site and group:

```
#site1
#wet
t.test(site1W$FINAL.HEIGHT..cm., site1W$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: site1W$FINAL.HEIGHT..cm. and site1W$INITIAL.HEIGHT..cm.
## t = 3.9545, df = 28, p-value = 0.0004747
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.7180143 2.2612960
## sample estimates:
## mean difference
## 1.489655

#dry
t.test(site1D$FINAL.HEIGHT..cm., site1D$INITIAL.HEIGHT..cm., paired =
TRUE)
```

```
##
## Paired t-test
##
## data: site1D$FINAL.HEIGHT..cm. and site1D$INITIAL.HEIGHT..cm.
## t = 6.1142, df = 27, p-value = 1.567e-06
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 1.570863 3.157709
## sample estimates:
## mean difference
## 2.364286

#mod
t.test(site1M$FINAL.HEIGHT..cm., site1M$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: site1M$FINAL.HEIGHT..cm. and site1M$INITIAL.HEIGHT..cm.
## t = 2.0459, df = 5, p-value = 0.09615
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.5856146 5.1522813
## sample estimates:
## mean difference
## 2.283333

#site2
#wet
t.test(site2W$FINAL.HEIGHT..cm., site2W$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: site2W$FINAL.HEIGHT..cm. and site2W$INITIAL.HEIGHT..cm.
## t = 6.6304, df = 29, p-value = 2.871e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 2.703912 5.116088
## sample estimates:
```



```

## mean difference
##          3.91

#dry
t.test(site2D$FINAL.HEIGHT..cm., site2D$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: site2D$FINAL.HEIGHT..cm. and site2D$INITIAL.HEIGHT..cm.
## t = 7.5756, df = 21, p-value = 1.951e-07
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  3.188841 5.602068
## sample estimates:
## mean difference
##          4.395455

#mod
t.test(site2M$FINAL.HEIGHT..cm., site2M$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: site2M$FINAL.HEIGHT..cm. and site2M$INITIAL.HEIGHT..cm.
## t = 2.1629, df = 7, p-value = 0.06732
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.1480886 3.3230886
## sample estimates:
## mean difference
##          1.5875

```

Initial/final height by provenance:

```

#wet
t.test(BD$FINAL.HEIGHT..cm., BD$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##

```

```

## data:  BD$FINAL.HEIGHT..cm. and BD$INITIAL.HEIGHT..cm.
## t = 5.5866, df = 39, p-value = 1.942e-06
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  1.743167 3.721833
## sample estimates:
## mean difference
##          2.7325

t.test(BH$FINAL.HEIGHT..cm., BH$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data:  BH$FINAL.HEIGHT..cm. and BH$INITIAL.HEIGHT..cm.
## t = 1.4237, df = 2, p-value = 0.2905
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -1.011042 2.011042
## sample estimates:
## mean difference
##          0.5

t.test(WT1$FINAL.HEIGHT..cm., WT1$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data:  WT1$FINAL.HEIGHT..cm. and WT1$INITIAL.HEIGHT..cm.
## t = 1.1846, df = 2, p-value = 0.3579
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -5.878559 10.345225
## sample estimates:
## mean difference
##          2.233333

t.test(HM6$FINAL.HEIGHT..cm., HM6$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##

```

```

## data: HM6$FINAL.HEIGHT..cm. and HM6$INITIAL.HEIGHT..cm.
## t = 4.7151, df = 11, p-value = 0.0006345
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 1.484082 4.082585
## sample estimates:
## mean difference
## 2.783333

#mod
t.test(HM1$FINAL.HEIGHT..cm., HM1$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: HM1$FINAL.HEIGHT..cm. and HM1$INITIAL.HEIGHT..cm.
## t = 3.0527, df = 8, p-value = 0.01576
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.6223473 4.4665415
## sample estimates:
## mean difference
## 2.544444

t.test(FC$FINAL.HEIGHT..cm., FC$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: FC$FINAL.HEIGHT..cm. and FC$INITIAL.HEIGHT..cm.
## t = 1.0906, df = 4, p-value = 0.3368
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -1.082123 2.482123
## sample estimates:
## mean difference
## 0.7

#dry
t.test(LH$FINAL.HEIGHT..cm., LH$INITIAL.HEIGHT..cm., paired = TRUE)

```

```
##
## Paired t-test
##
## data: LH$FINAL.HEIGHT..cm. and LH$INITIAL.HEIGHT..cm.
## t = 8.4233, df = 44, p-value = 1.003e-10
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 2.498606 4.070283
## sample estimates:
## mean difference
## 3.284444

t.test(WT2$FINAL.HEIGHT..cm., WT2$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: WT2$FINAL.HEIGHT..cm. and WT2$INITIAL.HEIGHT..cm.
## t = 3.1791, df = 4, p-value = 0.03356
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.3825233 5.6574767
## sample estimates:
## mean difference
## 3.02
```

Initial/final H by site and provenance:

```
#wet
t.test(BD1$FINAL.HEIGHT..cm., BD1$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: BD1$FINAL.HEIGHT..cm. and BD1$INITIAL.HEIGHT..cm.
## t = 2.8732, df = 20, p-value = 0.0094
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.3770509 2.3753300
## sample estimates:
## mean difference
## 1.37619
```

```

t.test(BD2$FINAL.HEIGHT..cm., BD2$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: BD2$FINAL.HEIGHT..cm. and BD2$INITIAL.HEIGHT..cm.
## t = 5.5965, df = 18, p-value = 2.602e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 2.643055 5.820102
## sample estimates:
## mean difference
## 4.231579

#t.test(BH1$FINAL.HEIGHT..cm., BH1$INITIAL.HEIGHT..cm., paired = TRUE)
t.test(BH2$FINAL.HEIGHT..cm., BH2$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: BH2$FINAL.HEIGHT..cm. and BH2$INITIAL.HEIGHT..cm.
## t = 1.1818, df = 1, p-value = 0.4471
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -6.338413 7.638413
## sample estimates:
## mean difference
## 0.65

#t.test(WT11$FINAL.HEIGHT..cm., WT11$INITIAL.HEIGHT..cm., paired =
TRUE)
t.test(WT12$FINAL.HEIGHT..cm., WT12$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: WT12$FINAL.HEIGHT..cm. and WT12$INITIAL.HEIGHT..cm.
## t = 1.069, df = 1, p-value = 0.4788
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -33.74799 39.94799

```

```

## sample estimates:
## mean difference
##          3.1

t.test(HM61$FINAL.HEIGHT..cm., HM61$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: HM61$FINAL.HEIGHT..cm. and HM61$INITIAL.HEIGHT..cm.
## t = 3.5352, df = 5, p-value = 0.01665
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.6184624 3.9148710
## sample estimates:
## mean difference
##          2.266667

t.test(HM62$FINAL.HEIGHT..cm., HM62$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: HM62$FINAL.HEIGHT..cm. and HM62$INITIAL.HEIGHT..cm.
## t = 3.275, df = 5, p-value = 0.02208
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.7097853 5.8902147
## sample estimates:
## mean difference
##          3.3

#mod
t.test(HM11$FINAL.HEIGHT..cm., HM11$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: HM11$FINAL.HEIGHT..cm. and HM11$INITIAL.HEIGHT..cm.

```

```

## t = 1.532, df = 2, p-value = 0.2652
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -5.847654 12.314321
## sample estimates:
## mean difference
## 3.233333

t.test(HM12$FINAL.HEIGHT..cm., HM12$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: HM12$FINAL.HEIGHT..cm. and HM12$INITIAL.HEIGHT..cm.
## t = 2.6195, df = 5, p-value = 0.04712
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.04111933 4.35888067
## sample estimates:
## mean difference
## 2.2

t.test(FC1$FINAL.HEIGHT..cm., FC1$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##
## data: FC1$FINAL.HEIGHT..cm. and FC1$INITIAL.HEIGHT..cm.
## t = 1.4286, df = 2, p-value = 0.2893
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -2.682476 5.349143
## sample estimates:
## mean difference
## 1.333333

t.test(FC2$FINAL.HEIGHT..cm., FC2$INITIAL.HEIGHT..cm., paired = TRUE)

##
## Paired t-test
##

```

```

## data: FC2$FINAL.HEIGHT..cm. and FC2$INITIAL.HEIGHT..cm.
## t = -5, df = 1, p-value = 0.1257
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.8853102 0.3853102
## sample estimates:
## mean difference
## -0.25

#dry
#t.test(LH1$FINAL.HEIGHT..cm., LH1$INITIAL.HEIGHT..cm., paired = TRUE)
#t.test(LH2$FINAL.HEIGHT..cm., LH2$INITIAL.HEIGHT..cm., paired = TRUE)
t.test(WT21$FINAL.HEIGHT..cm., WT21$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: WT21$FINAL.HEIGHT..cm. and WT21$INITIAL.HEIGHT..cm.
## t = 1.5166, df = 2, p-value = 0.2686
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -4.470305 9.336972
## sample estimates:
## mean difference
## 2.433333

t.test(WT22$FINAL.HEIGHT..cm., WT22$INITIAL.HEIGHT..cm., paired =
TRUE)

##
## Paired t-test
##
## data: WT22$FINAL.HEIGHT..cm. and WT22$INITIAL.HEIGHT..cm.
## t = 39, df = 1, p-value = 0.01632
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 2.62938 5.17062
## sample estimates:
## mean difference
## 3.9

```



Initial/final health by site and provenance:

```
#wet
t.test(BD1$FINAL.HEALTH, BD1$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data: BD1$FINAL.HEALTH and BD1$INITIAL.HEALTH
## t = 4.6777, df = 32, p-value = 5.058e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.5594141 1.4224040
## sample estimates:
## mean difference
## 0.9909091

t.test(BD2$FINAL.HEALTH, BD2$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data: BD2$FINAL.HEALTH and BD2$INITIAL.HEALTH
## t = 2.6811, df = 24, p-value = 0.01306
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## 0.1519287 1.1680713
## sample estimates:
## mean difference
## 0.66

#t.test(BH1$FINAL.HEALTH, BH1$INITIAL.HEALTH, paired = TRUE)
t.test(BH2$FINAL.HEALTH, BH2$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data: BH2$FINAL.HEALTH and BH2$INITIAL.HEALTH
## t = NaN, df = 1, p-value = NA
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## NaN NaN
```

```

## sample estimates:
## mean difference
##          0

#t.test(WT11$FINAL.HEALTH, WT11$INITIAL..HEALTH, paired = TRUE)
t.test(WT12$FINAL.HEALTH, WT12$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data:  WT12$FINAL.HEALTH and WT12$INITIAL.HEALTH
## t = 2.6, df = 3, p-value = 0.08038
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.3640289  3.6140289
## sample estimates:
## mean difference
##          1.625

t.test(HM61$FINAL.HEALTH, HM61$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data:  HM61$FINAL.HEALTH and HM61$INITIAL.HEALTH
## t = 1.5275, df = 7, p-value = 0.1705
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.4110075  1.9110075
## sample estimates:
## mean difference
##          0.75

t.test(HM62$FINAL.HEALTH, HM62$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data:  HM62$FINAL.HEALTH and HM62$INITIAL.HEALTH
## t = NaN, df = 5, p-value = NA
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:

```

```

## NaN NaN
## sample estimates:
## mean difference
##          0

#mod
t.test(HM11$FINAL.HEALTH, HM11$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data:  HM11$FINAL.HEALTH and HM11$INITIAL.HEALTH
## t = NaN, df = 2, p-value = NA
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## NaN NaN
## sample estimates:
## mean difference
##          0

t.test(HM12$FINAL.HEALTH, HM12$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data:  HM12$FINAL.HEALTH and HM12$INITIAL.HEALTH
## t = 1.536, df = 6, p-value = 0.1755
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.3812568  1.6669711
## sample estimates:
## mean difference
##      0.6428571

t.test(FC1$FINAL.HEALTH, FC1$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data:  FC1$FINAL.HEALTH and FC1$INITIAL.HEALTH
## t = 1.7321, df = 2, p-value = 0.2254
## alternative hypothesis: true mean difference is not equal to 0

```

```

## 95 percent confidence interval:
## -1.484138 3.484138
## sample estimates:
## mean difference
## 1

t.test(FC2$FINAL.HEALTH, FC2$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data: FC2$FINAL.HEALTH and FC2$INITIAL.HEALTH
## t = 1, df = 2, p-value = 0.4226
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -2.752211 4.418877
## sample estimates:
## mean difference
## 0.8333333

#dry
#t.test(LH1$FINAL.HEALTH, LH1$INITIAL.HEALTH, paired = TRUE)
#t.test(LH2$FINAL.HEALTH, LH2$INITIAL.HEALTH, paired = TRUE)
t.test(WT21$FINAL.HEALTH, WT21$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##
## data: WT21$FINAL.HEALTH and WT21$INITIAL.HEALTH
## t = 2.1787, df = 5, p-value = 0.08124
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.2248212 2.7248212
## sample estimates:
## mean difference
## 1.25

t.test(WT22$FINAL.HEALTH, WT22$INITIAL.HEALTH, paired = TRUE)

##
## Paired t-test
##

```

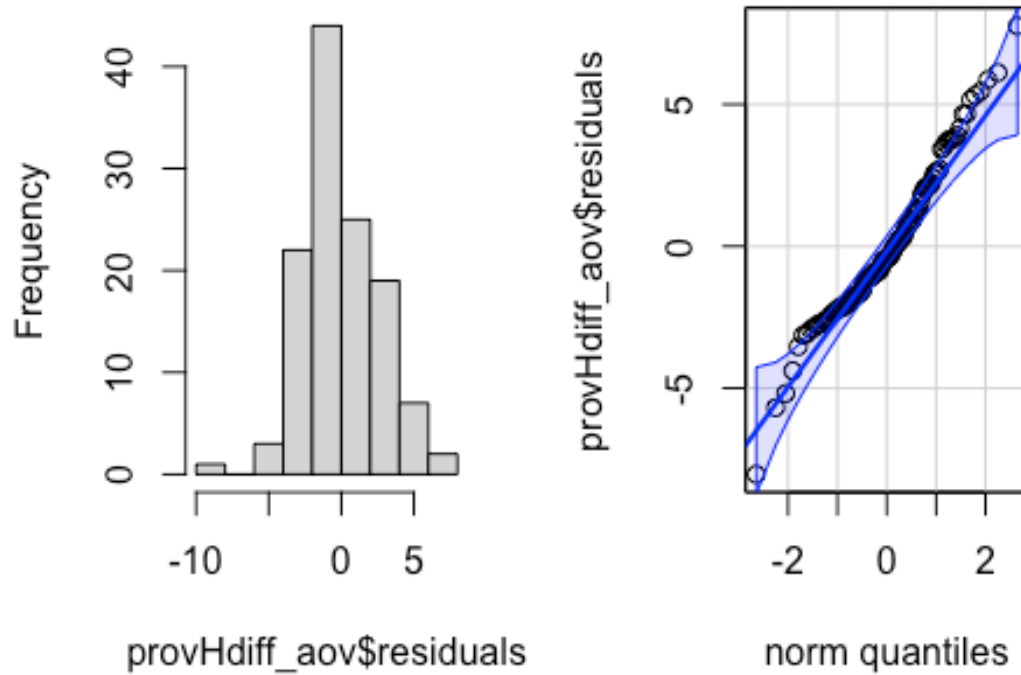
```
## data: WT22$FINAL.HEALTH and WT22$INITIAL.HEALTH
## t = 0.76249, df = 2, p-value = 0.5254
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -3.869063 5.535730
## sample estimates:
## mean difference
## 0.8333333
```

ANOVA/KW Tests:

Height diff:

```
#by provenance
#Tests for normalcy
provHdiff_aov <- aov(heightdiff ~ PROVENANCE, data = Planting)
par(mfrow = c(1, 2))
hist(provHdiff_aov$residuals)
library(car)
qqPlot(provHdiff_aov$residuals, id = FALSE)
```

## Histogram of provHdiff\_aov\$residuals



```
shapiro.test(provHdiff_aov$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  provHdiff_aov$residuals
## W = 0.97143, p-value = 0.0103
```

```
#not normal
```

```
kruskal.test(heightdiff ~ PROVENANCE, data = Planting)
```

```
##
##  Kruskal-Wallis rank sum test
##
```

```

## data: heightdiff by PROVENANCE
## Kruskal-Wallis chi-squared = 13.735, df = 8, p-value = 0.08894

library(FSA)

## Registered S3 methods overwritten by 'FSA':
##   method      from
##   confint.boot car
##   hist.boot    car

## ## FSA v0.9.4. See citation('FSA') if used in publication.
## ## Run fishR() for related website and fishR('IFAR') for related
## book.

##
## Attaching package: 'FSA'

## The following object is masked from 'package:car':
##
##   bootCase

dunnTest(heightdiff ~ PROVENANCE, data = Planting, method = "holm")

## Warning: PROVENANCE was coerced to a factor.

## Warning: Some rows deleted from 'x' and 'g' because missing data.

## Dunn (1964) Kruskal-Wallis multiple comparison

##   p-values adjusted with the Holm method.

##   Comparison      Z    P.unadj    P.adj
## 1      - BD  1.7269680 0.08417340 1.0000000
## 2      - BH  2.3889956 0.01689451 0.5744132
## 3      BD - BH  1.6874984 0.09150756 1.0000000
## 4      - FC  2.3918845 0.01676212 0.5866741
## 5      BD - FC  1.8378236 0.06608840 1.0000000
## 6      BH - FC -0.1895069 0.84969554 1.0000000
## 7      - HM1  1.7121478 0.08686943 1.0000000
## 8      BD - HM1  0.1527119 0.87862546 0.8786255
## 9      BH - HM1 -1.4307183 0.15251097 1.0000000
## 10     FC - HM1 -1.4619126 0.14376515 1.0000000
## 11     - HM6  1.5857194 0.11280297 1.0000000
## 12     BD - HM6 -0.2976019 0.76600704 1.0000000

```

```
## 13    BH - HM6 -1.7166694 0.08603960 1.0000000
## 14    FC - HM6 -1.8217661 0.06849048 1.0000000
## 15    HM1 - HM6 -0.3499040 0.72641077 1.0000000
## 16      - LH   1.4456029 0.14828861 1.0000000
## 17    BD - LH -1.3200004 0.18683489 1.0000000
## 18    BH - LH -2.1751310 0.02962030 0.9774699
## 19    FC - LH -2.4577644 0.01398048 0.5032974
## 20    HM1 - LH -0.9398518 0.34729357 1.0000000
## 21    HM6 - LH -0.5813980 0.56097226 1.0000000
## 22      - WT1  1.7816238 0.07481060 1.0000000
## 23    BD - WT1  0.5158957 0.60592725 1.0000000
## 24    BH - WT1 -0.8589534 0.39036624 1.0000000
## 25    FC - WT1 -0.7708322 0.44080643 1.0000000
## 26    HM1 - WT1  0.3787195 0.70489614 1.0000000
## 27    HM6 - WT1  0.6301698 0.52858351 1.0000000
## 28    LH - WT1  0.9989607 0.31781374 1.0000000
## 29      - WT2  1.4110582 0.15822746 1.0000000
## 30    BD - WT2 -0.4272977 0.66916252 1.0000000
## 31    BH - WT2 -1.6607463 0.09676440 1.0000000
## 32    FC - WT2 -1.6988410 0.08934915 1.0000000
## 33    HM1 - WT2 -0.4643920 0.64236694 1.0000000
## 34    HM6 - WT2 -0.1967578 0.84401710 1.0000000
## 35    LH - WT2  0.1785301 0.85830668 1.0000000
## 36    WT1 - WT2 -0.7004073 0.48367299 1.0000000
```

Initial H between groups and provenance:

```
#Tests for normalcy
```

```
InH_aov <- aov(INITIAL.HEIGHT..cm. ~ GROUP., data = Planting)
```

```
par(mfrow = c(1, 2))
```

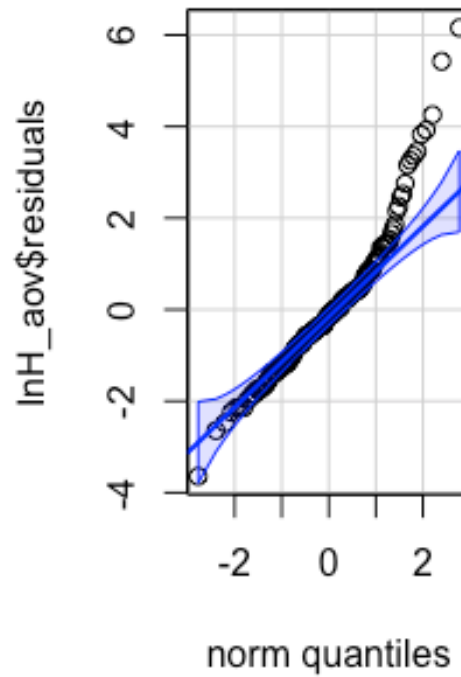
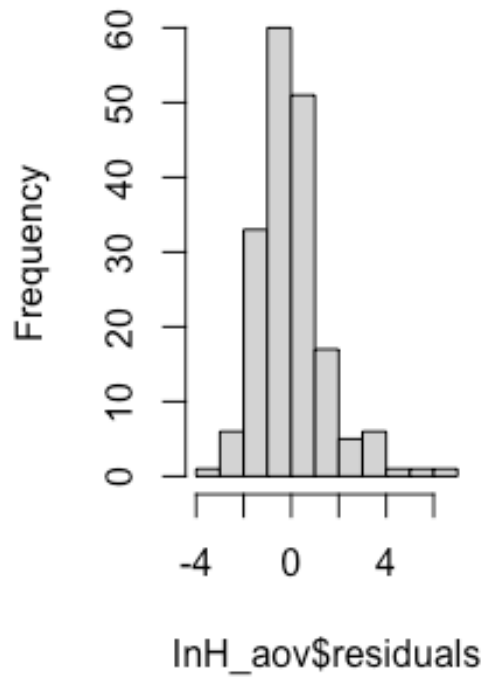
```
hist(InH_aov$residuals)
```

```
library(car)
```

```
qqPlot(InH_aov$residuals, id = FALSE)
```



## histogram of InH\_aov\$residuals



```
shapiro.test(InH_aov$residuals)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  InH_aov$residuals  
## W = 0.92505, p-value = 4.629e-08
```

```
#not normal
```

```
kruskal.test(INITIAL.HEIGHT..cm. ~ GROUP., data = Planting)
```

```
##  
##  Kruskal-Wallis rank sum test  
##
```

```

## data:  INITIAL.HEIGHT..cm. by GROUP.
## Kruskal-Wallis chi-squared = 21.18, df = 2, p-value = 2.517e-05

library(FSA)
dunnTest(INITIAL.HEIGHT..cm. ~ GROUP., data = Planting, method =
"holm")

## Warning: GROUP. was coerced to a factor.

## Warning: Some rows deleted from 'x' and 'g' because missing data.

## Dunn (1964) Kruskal-Wallis multiple comparison

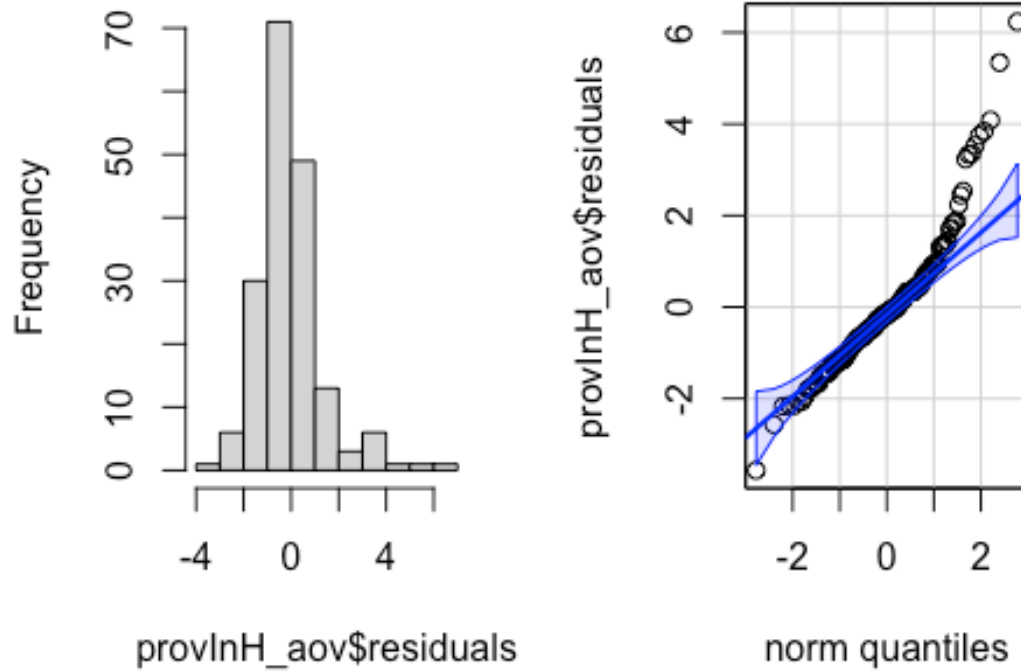
##  p-values adjusted with the Holm method.

##      Comparison          Z      P.unadj      P.adj
## 1      D - M 1.627822 1.035626e-01 2.071251e-01
## 2      D - W 4.590920 4.412962e-06 1.323889e-05
## 3      M - W 1.057096 2.904676e-01 2.904676e-01

#by provenance
#Tests for normalcy
provInH_aov <- aov(INITIAL.HEIGHT..cm. ~ PROVENANCE, data = Planting)
par(mfrow = c(1, 2))
hist(provInH_aov$residuals)
library(car)
qqPlot(provInH_aov$residuals, id = FALSE)

```

## ogram of provInH\_aov\$re



```
shapiro.test(provInH_aov$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  provInH_aov$residuals
## W = 0.90919, p-value = 3.732e-09
```

```
#not normal
```

```
kruskal.test(INITIAL.HEIGHT..cm. ~ PROVENANCE, data = Planting)
```

```
##
##  Kruskal-Wallis rank sum test
##
```

```

## data: INITIAL.HEIGHT..cm. by PROVENANCE
## Kruskal-Wallis chi-squared = 37.068, df = 8, p-value = 1.118e-05

library(FSA)
dunnTest(INITIAL.HEIGHT..cm. ~ PROVENANCE, data = Planting, method =
"holm")

## Warning: PROVENANCE was coerced to a factor.

## Warning: Some rows deleted from 'x' and 'g' because missing data.

## Dunn (1964) Kruskal-Wallis multiple comparison
## p-values adjusted with the Holm method.

##      Comparison      Z      P.unadj      P.adj
## 1      - BD -1.1013407 2.707484e-01 1.0000000000
## 2      - BH -0.4989514 6.178136e-01 1.0000000000
## 3      BD - BH  0.9028802 3.665895e-01 1.0000000000
## 4      - FC -0.9671566 3.334658e-01 1.0000000000
## 5      BD - FC  0.1545000 8.772155e-01 1.0000000000
## 6      BH - FC -0.6625718 5.076048e-01 1.0000000000
## 7      - HM1 -1.6209444 1.050296e-01 1.0000000000
## 8      BD - HM1 -1.7674550 7.715206e-02 1.0000000000
## 9      BH - HM1 -1.7147474 8.639155e-02 1.0000000000
## 10     FC - HM1 -1.2775334 2.014140e-01 1.0000000000
## 11     - HM6 -1.8375783 6.612456e-02 1.0000000000
## 12     BD - HM6 -2.6522335 7.996121e-03 0.2718681297
## 13     BH - HM6 -2.0841183 3.714941e-02 1.0000000000
## 14     FC - HM6 -1.7572000 7.888373e-02 1.0000000000
## 15     HM1 - HM6 -0.5188560 6.038612e-01 1.0000000000
## 16     - LH -1.9461958 5.163122e-02 1.0000000000
## 17     BD - LH -4.8268405 1.387161e-06 0.0000499378
## 18     BH - LH -2.3488883 1.882955e-02 0.6025457035
## 19     FC - LH -2.1554476 3.112682e-02 0.9649315519
## 20     HM1 - LH -0.8242003 4.098257e-01 1.0000000000
## 21     HM6 - LH -0.1959655 8.446372e-01 1.0000000000
## 22     - WT1 -0.6286518 5.295771e-01 1.0000000000
## 23     BD - WT1  1.0063851 3.142304e-01 1.0000000000
## 24     BH - WT1 -0.1454972 8.843183e-01 0.8843183339
## 25     FC - WT1  0.6332845 5.265479e-01 1.0000000000
## 26     HM1 - WT1  1.9979534 4.572172e-02 1.0000000000

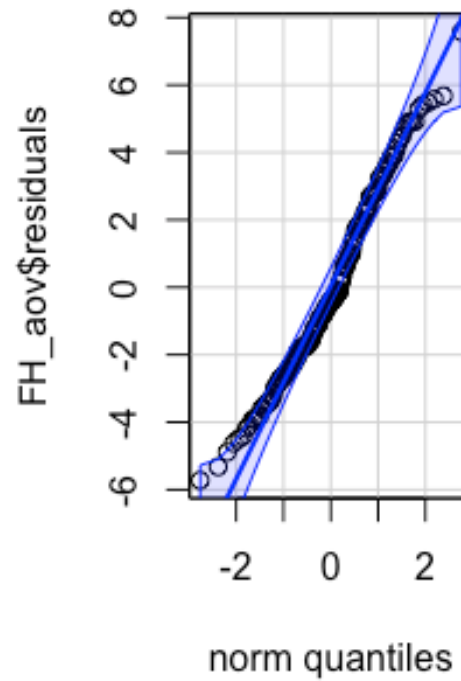
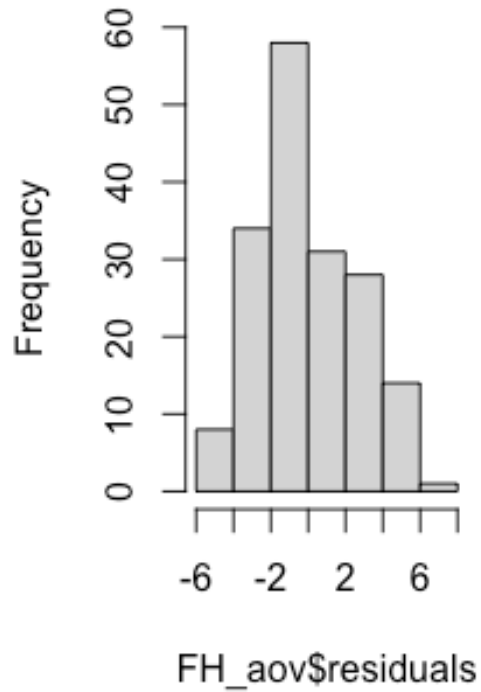
```

```
## 27  HM6 - WT1  2.5065123 1.219288e-02 0.4023650969
## 28   LH - WT1  3.0172387 2.550889e-03 0.0892811118
## 29      - WT2 -1.3093748 1.904074e-01 1.0000000000
## 30   BD - WT2 -0.7506383 4.528704e-01 1.0000000000
## 31   BH - WT2 -1.2060942 2.277812e-01 1.0000000000
## 32   FC - WT2 -0.6366685 5.243408e-01 1.0000000000
## 33  HM1 - WT2  0.6959783 4.864424e-01 1.0000000000
## 34  HM6 - WT2  1.2214772 2.219054e-01 1.0000000000
## 35   LH - WT2  1.6410987 1.007769e-01 1.0000000000
## 36  WT1 - WT2 -1.3303969 1.833875e-01 1.0000000000
```

Final H between groups and provenance:

```
#Tests for normalcy
FH_aov <- aov(FINAL.HEIGHT..cm. ~ GROUP., data = Planting)
par(mfrow = c(1, 2))
hist(FH_aov$residuals)
library(car)
qqPlot(FH_aov$residuals, id = FALSE)
```

## histogram of FH\_aov\$residuals



```
shapiro.test(FH_aov$residuals)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  FH_aov$residuals  
## W = 0.97946, p-value = 0.01124
```

```
#not normal
```

```
kruskal.test(FINAL.HEIGHT..cm. ~ GROUP., data = Planting)
```

```
##  
##  Kruskal-Wallis rank sum test  
##
```

```

## data: FINAL.HEIGHT..cm. by GROUP.
## Kruskal-Wallis chi-squared = 7.4192, df = 2, p-value = 0.02449

library(FSA)
dunnTest(FINAL.HEIGHT..cm. ~ GROUP., data = Planting, method = "holm")

## Warning: GROUP. was coerced to a factor.

## Warning: Some rows deleted from 'x' and 'g' because missing data.

## Dunn (1964) Kruskal-Wallis multiple comparison

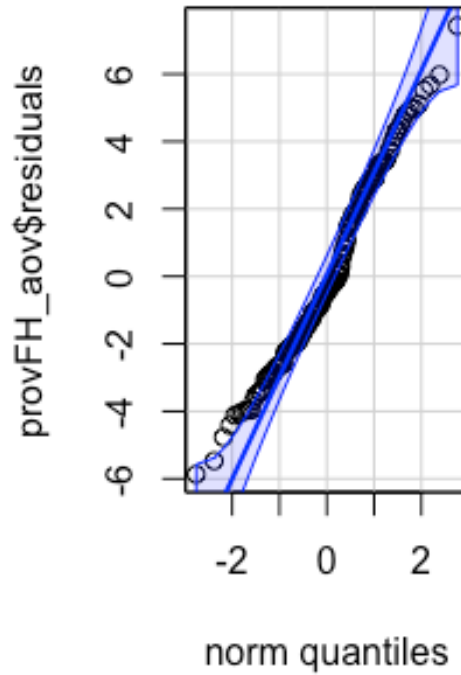
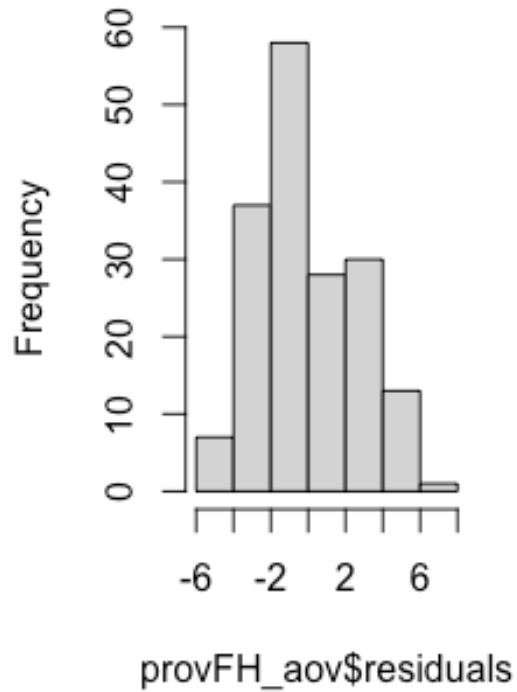
## p-values adjusted with the Holm method.

## Comparison      Z      P.unadj      P.adj
## 1      D - M  2.0854281 0.03703046 0.07406093
## 2      D - W  2.4673967 0.01360995 0.04082985
## 3      M - W -0.1349062 0.89268600 0.89268600

#by provenance
#Tests for normalcy
provFH_aov <- aov(FINAL.HEIGHT..cm. ~ PROVENANCE, data = Planting)
par(mfrow = c(1, 2))
hist(provFH_aov$residuals)
library(car)
qqPlot(provFH_aov$residuals, id = FALSE)

```

histogram of provFH\_aov\$resi



```
shapiro.test(provFH_aov$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  provFH_aov$residuals
## W = 0.97595, p-value = 0.004109
```

*#not normal*

```
kruskal.test(FINAL.HEIGHT..cm. ~ PROVENANCE, data = Planting)
```

```
##
##  Kruskal-Wallis rank sum test
##
```



```

## data: FINAL.HEIGHT..cm. by PROVENANCE
## Kruskal-Wallis chi-squared = 12.895, df = 8, p-value = 0.1155

library(FSA)
dunnTest(FINAL.HEIGHT..cm. ~ PROVENANCE, data = Planting, method =
"holm")

## Warning: PROVENANCE was coerced to a factor.

## Warning: Some rows deleted from 'x' and 'g' because missing data.

## Dunn (1964) Kruskal-Wallis multiple comparison
## p-values adjusted with the Holm method.

##      Comparison           Z      P.unadj      P.adj
## 1      - BD    0.9843006 0.32496774 1.0000000
## 2      - BH    1.1817720 0.23729618 1.0000000
## 3      BD - BH    0.5947280 0.55202533 1.0000000
## 4      - FC    1.1399646 0.25430107 1.0000000
## 5      BD - FC    0.5054664 0.61323130 1.0000000
## 6      BH - FC   -0.2610884 0.79402437 1.0000000
## 7      - HM1    0.7592825 0.44768360 1.0000000
## 8      BD - HM1  -0.5064604 0.61253349 1.0000000
## 9      BH - HM1  -0.8278055 0.40778067 1.0000000
## 10     FC - HM1  -0.8250445 0.40934634 1.0000000
## 11     - HM6    0.4684972 0.63942908 1.0000000
## 12     BD - HM6  -1.1368840 0.25558677 1.0000000
## 13     BH - HM6  -1.2026803 0.22910007 1.0000000
## 14     FC - HM6  -1.3367228 0.18131314 1.0000000
## 15     HM1 - HM6 -0.5747198 0.56548079 1.0000000
## 16     - LH    0.2966227 0.76675460 1.0000000
## 17     BD - LH   -2.5397216 0.01109407 0.3993867
## 18     BH - LH   -1.6596426 0.09698637 1.0000000
## 19     FC - LH   -2.2582655 0.02392911 0.8375189
## 20     HM1 - LH  -1.2759514 0.20197269 1.0000000
## 21     HM6 - LH  -0.4615111 0.64443197 1.0000000
## 22     - WT1    1.3977183 0.16219768 1.0000000
## 23     BD - WT1    0.9799254 0.32712293 1.0000000
## 24     BH - WT1    0.2856701 0.77513082 1.0000000
## 25     FC - WT1    0.6137272 0.53939563 1.0000000
## 26     HM1 - WT1    1.1829400 0.23683293 1.0000000

```

```
## 27  HM6 - WT1  1.5460130 0.12210143 1.0000000
## 28   LH - WT1  2.0464417 0.04071293 1.0000000
## 29      - WT2  0.6586174 0.51014147 1.0000000
## 30   BD - WT2 -0.6110738 0.54115072 1.0000000
## 31   BH - WT2 -0.8945013 0.37105371 1.0000000
## 32   FC - WT2 -0.8902545 0.37332926 1.0000000
## 33  HM1 - WT2 -0.1584549 0.87409839 0.8740984
## 34  HM6 - WT2  0.3672051 0.71346607 1.0000000
## 35   LH - WT2  0.8863745 0.37541575 1.0000000
## 36  WT1 - WT2 -1.2294792 0.21889218 1.0000000
```

Correlation:

```
cor.test(Planting$INITIAL.HEIGHT..cm., Planting$INITIAL.DIAMETER..mm.,
method=c("spearman"))
```

```
## Warning in cor.test.default(Planting$INITIAL.HEIGHT..cm.,
## Planting$INITIAL.DIAMETER..mm., : Cannot compute exact p-value with
ties
```

```
##
## Spearman's rank correlation rho
##
## data: Planting$INITIAL.HEIGHT..cm. and
Planting$INITIAL.DIAMETER..mm.
## S = 588349, p-value = 4.192e-08
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.3946836
```

```
cor.test(Planting$FINAL.HEIGHT..cm., Planting$FINAL.DIAMETER..mm.,
method=c("spearman"))
```

```
## Warning in cor.test.default(Planting$FINAL.HEIGHT..cm.,
## Planting$FINAL.DIAMETER..mm., : Cannot compute exact p-value with
ties
```

```
##
## Spearman's rank correlation rho
##
## data: Planting$FINAL.HEIGHT..cm. and Planting$FINAL.DIAMETER..mm.
## S = 423936, p-value = 2.754e-13
```

```
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.5171439
```

#is there anything MANOVA is applicable for?

A new cool and fun plot to mess with:

```
library(ggplot2)
ggplot(Planting) +
  aes(x = GROUP., y = INITIAL.HEIGHT..cm., color = GROUP.) +
  geom_jitter() +
  theme(legend.position = "right")

## Warning: Removed 118 rows containing missing values
(`geom_point()`).
```

