Meristem Size Anlysis

Libraries

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.1.3
```

```
library(car)
```

```
## Warning: package 'car' was built under R version 3.1.3
```

```
library(reshape2)
```

```
##ggplot custom theme

cbPalette <- c("#56B4E9","#999999", "#E69F00", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")

customTheme <- list(theme(axis.title.x = element_text(face="bold", size=30),
        axis.title.y = element_text(face="bold", size=30),
        axis.text.x  = element_text(size=16),
        axis.text.y  = element_text(size=16),
        legend.title = element_text(size=30),
        legend.text = element_text(size=20),
        strip.text.x = element_text(size = 20),
        strip.text.y = element_text(size = 20),
        strip.background = element_rect(fill="#b0c4de"),
        legend.position="none") )
```

```
merSize <- read.csv("../data/widthHeight_all.csv")
head(merSize)
```

```
##           label height width genotype rep
## 1 e2_001.01.tif  0.091 0.193       e2   1
## 2 e2_001.02.tif  0.138 0.203       e2   1
## 3 e2_001.03.tif  0.101 0.165       e2   1
## 4 e2_001.04.tif  0.164 0.218       e2   1
## 5 e2_001.05.tif  0.119 0.190       e2   1
## 6 e2_001.06.tif  0.140 0.199       e2   1
```

```
merSize <- merSize[, -1]

merSize$genotype <- gsub("e2", "e-2", merSize$genotype)
merSize$genotype <- gsub("wt", "WT", merSize$genotype)

head(merSize)
```

```
##   height width genotype rep
## 1  0.091 0.193      e-2   1
```

```
## 2  0.138 0.203      e-2  1
## 3  0.101 0.165      e-2  1
## 4  0.164 0.218      e-2  1
## 5  0.119 0.190      e-2  1
## 6  0.140 0.199      e-2  1
```

```
summary(merSize)
```

```
##     height          width          genotype            rep
##  Min.   :0.0250  Min.   :0.038  Length:80          Min.   :1.00
##  1st Qu.:0.0520  1st Qu.:0.159  Class :character   1st Qu.:1.00
##  Median :0.0735  Median :0.171  Mode  :character   Median :1.00
##  Mean   :0.0739  Mean   :0.168                     Mean   :1.36
##  3rd Qu.:0.0848  3rd Qu.:0.189                     3rd Qu.:2.00
##  Max.   :0.1640  Max.   :0.228                     Max.   :2.00
```

Visualization

Height

Height is significantly larger in *e-2*. There is also significant

```
ggplot(merSize, aes(genotype, height)) +
  geom_boxplot(alpha = .7) +
  geom_point(position = "jitter", alpha = .6, aes(color = genotype)) +
  theme_bw() +
  scale_x_discrete(limits=c("WT","e-2")) +
  scale_color_manual(values=cbPalette) +
  ylab("size (mm)") +
  customTheme
```
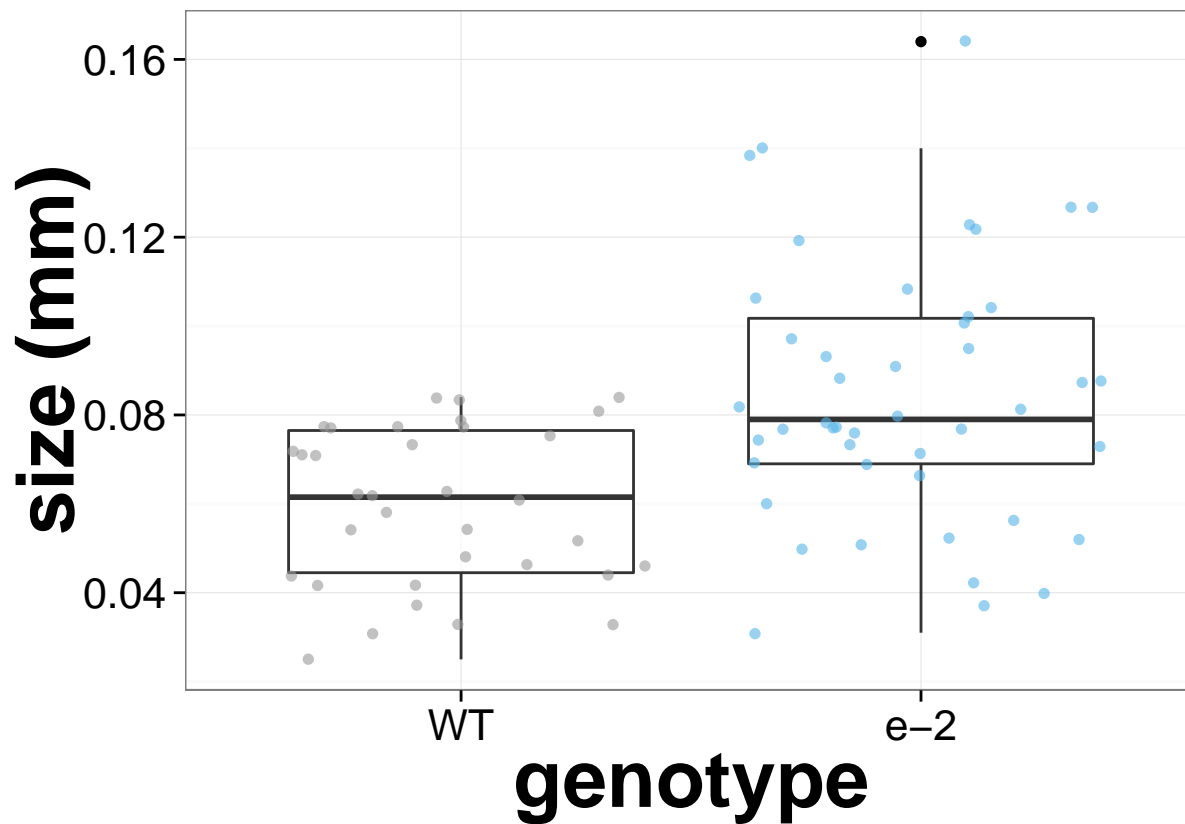
```r
t.test(merSize$height ~ merSize$genotype, var.eq=F, alt = "two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  merSize$height by merSize$genotype
## t = 4.773, df = 75.26, p-value = 8.729e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.01470 0.03577
## sample estimates:
## mean in group e-2  mean in group WT
##          0.08459           0.05935
```

Test for variance

```r
e2 <- subset(merSize, genotype == "e-2")
wt <- subset(merSize, genotype == "WT")

# Variance is over 5 times greater in e-2
var(e2$height)
```

```
## [1] 0.0008631
```

```
var(wt$height)
```

```
## [1] 0.0003125
```

```
sd(e2$height)
```

```
## [1] 0.02938
```

```
sd(wt$height)
```

```
## [1] 0.01768
```

```
#Here are two different tests for difference in variance. Both show that there is a difference in variri
var.test(e2$height, wt$height, alternative="two.sided")
```

```
##
##  F test to compare two variances
##
## data:  e2$height and wt$height
## F = 2.762, num df = 45, denom df = 33, p-value = 0.003047
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  1.426 5.180
## sample estimates:
## ratio of variances
##               2.762
```

```
leveneTest(merSize$height, merSize$genotype)
```

```
## Warning: merSize$genotype coerced to factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1    4.11  0.046 *
##       78
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Width

```
ggplot(merSize, aes(genotype, width)) +
  geom_boxplot(alpha = .7) +
  geom_point(position = "jitter", alpha = .6, aes(color = genotype)) +
  theme_bw() +
  scale_x_discrete(limits=c("WT","e-2")) +
  scale_color_manual(values=cbPalette) +
  ylab("size (mm)") +
  customTheme
```
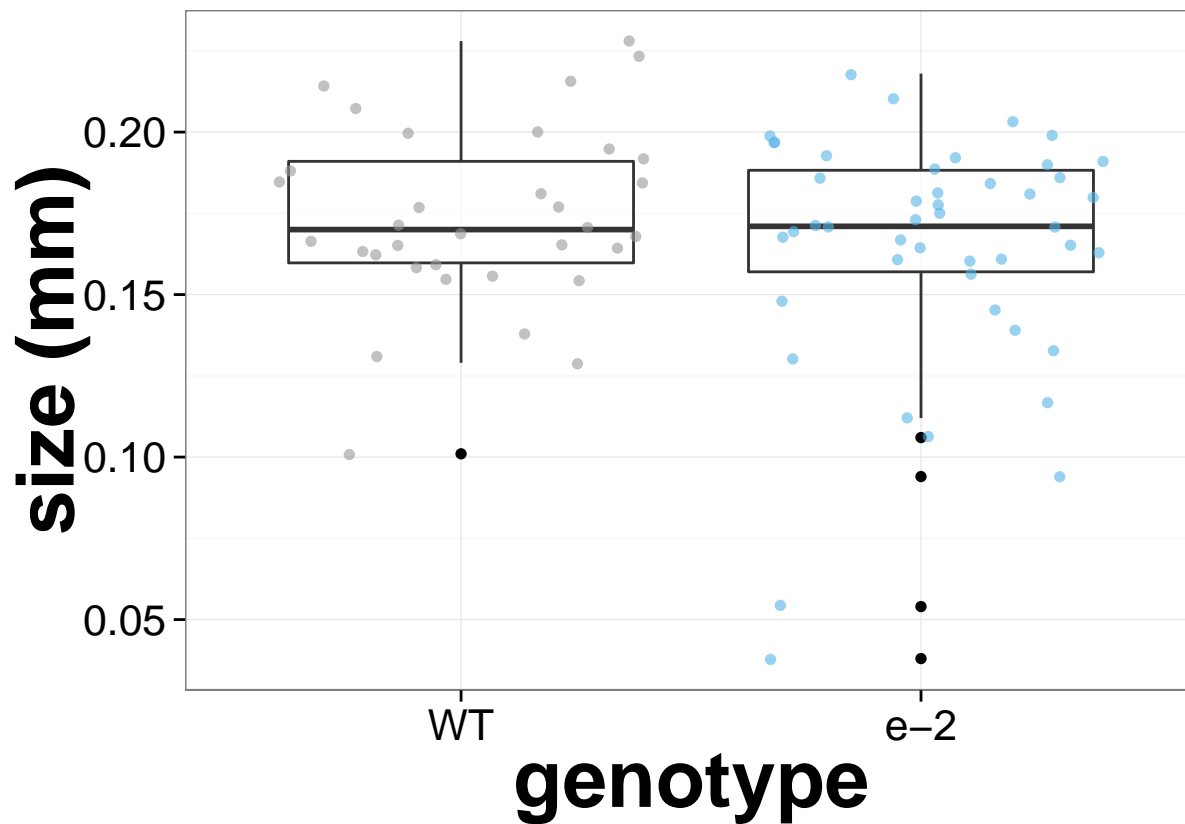
```r
t.test(merSize$width ~ merSize$genotype, var.eq=F, alt = "two.sided")
```

```
##
##  Welch Two Sample t-test
##
## data:  merSize$width by merSize$genotype
## t = -1.363, df = 78, p-value = 0.1767
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.02431  0.00455
## sample estimates:
## mean in group e-2  mean in group WT
##            0.1640            0.1739
```

Test for variance

```r
sopin1a <- subset(merSize, genotype == "e-2")
wt <- subset(merSize, genotype == "WT")

# Variance is over 2 times greater in e-2
var(sopin1a$width)
```

```
## [1] 0.001388
```

```r
var(wt$width)
```

```
## [1] 0.0007608
```

```r
sd(sopin1a$width)
```

```
## [1] 0.03726
```

```r
sd(wt$width)
```

```
## [1] 0.02758
```

```r
#Here are two different tests for difference in variance.
var.test(sopin1a$width, wt$width, alternative="two.sided")
```

```
##
##  F test to compare two variances
##
## data:  sopin1a$width and wt$width
## F = 1.825, num df = 45, denom df = 33, p-value = 0.074
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.942 3.422
## sample estimates:
## ratio of variances
##               1.825
```

```r
leveneTest(merSize$width, merSize$genotype)
```

```
## Warning: merSize$genotype coerced to factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1    0.65   0.42
##       78
```

Both in one Plot

```r
head(merSize)
```

```
##   height width genotype rep
## 1  0.091 0.193      e-2   1
## 2  0.138 0.203      e-2   1
## 3  0.101 0.165      e-2   1
## 4  0.164 0.218      e-2   1
## 5  0.119 0.190      e-2   1
## 6  0.140 0.199      e-2   1
```

```
mdata <- melt(merSize, id=c("genotype","rep"))
head(mdata)
```

```
##    genotype rep variable value
## 1      e-2   1   height 0.091
## 2      e-2   1   height 0.138
## 3      e-2   1   height 0.101
## 4      e-2   1   height 0.164
## 5      e-2   1   height 0.119
## 6      e-2   1   height 0.140
```

```
ggplot(mdata, aes(genotype, value)) +
  geom_boxplot(alpha = .7, outlier.size = 0) +
  geom_point(position = "jitter", alpha = .6, aes(color = genotype)) +
  theme_bw() +
  scale_x_discrete(limits=c("WT","e-2")) +
  scale_color_manual(values=cbPalette) +
  customTheme +
  ylab("size (mm)") +
  facet_grid(.~variable)
```