## Angle Analysis

## **Plants**

- -Population 1 was done from photographs on older plants, where we could only retrieve the angle for L1 L4.
- -Population 2 was performed on plants around 20 days old and was calculated from histology.
- -Population 3 was measured from plants around 1 months old from only PIN1::GFP x e2/e2

## Analysis

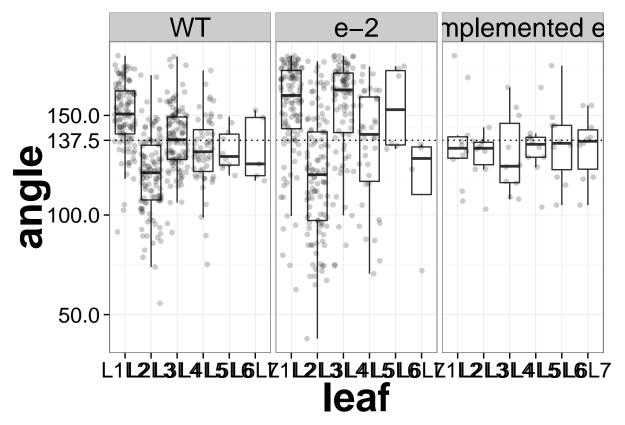
Libraries

```
library(reshape2)
library(ggplot2)
## Warning: package 'ggplot2' was built under R version 3.1.3
Do analysis on
angleData <- read.csv("../data/anglePopulation1&2&3.csv")
head(angleData)
     primordia leaf angle genotype plant population
## 1
               L2L3 37.89
                                e2
                                      E43
## 2
               L2L3 55.71
                               3130
                                      W13
                                                    1
## 3
               L1L2 62.54
                                      E30
                                                    1
                                e2
## 4
               L2L3 65.03
                                 e2
                                      E82
                                                    1
## 5
               L2L3 67.17
                                 e2
                                      E55
                                                    1
## 6
               L2L3 69.20
angleDataLeaf <- angleData[,c(2,3,4,5,6)]</pre>
angleDataSub <- subset(angleDataLeaf, leaf != "L7L8")</pre>
levels(angleDataSub$genotype) <- c("WT", "e-2", "complemented e-2")</pre>
```

Make a boxplot that illustrates angle divergence.

```
legend.title = element_text(size=30),
legend.text = element_text(size=20),
strip.text.x = element_text(size = 20),
legend.position="none")
```

```
## Warning: Removed 63 rows containing non-finite values (stat_boxplot).
## Warning: Removed 140 rows containing non-finite values (stat_boxplot).
## Warning: Removed 63 rows containing missing values (geom_point).
## Warning: Removed 140 rows containing missing values (geom_point).
```



Make a diagram illustrating how many plants of e2 and wt are distichous, spiral & other.

Spiral = Both L2L3 and L3L4 between 147.5 and 127.5. Decussate = Leaf L2L3 between 80 to 100 and L3L4 between 190 to 170. Other = Everything else.

At this point it may be beneficial to change to the wide format where each plant in a single observation by casting.

```
angleDataPlant <- angleData[,-c(6,1)]
castAngleData <- dcast(angleDataPlant, plant + genotype ~ leaf, value.var = "angle")</pre>
```

How many of each genotype

## summary(castAngleData\$genotype)

```
## 3130 e2 pin1.gfp.e2
## 114 123 11
```

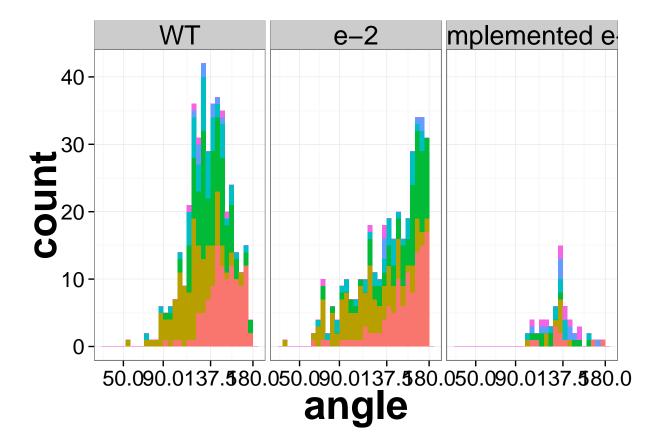
```
wtAngle <- subset(castAngleData, genotype == "3130")</pre>
#Spiral WT
wtSpiralL34 <- subset(wtAngle, L3L4 <= 150 & L3L4 >= 120)
dim(wtSpiralL34) #75
## [1] 75 9
wtDecL34 <- subset(wtAngle, L3L4 <= 195 & L3L4 >= 165)
dim(wtDecL34) #5
## [1] 5 9
##e2
e2Angle <- subset(castAngleData, genotype == "e2")</pre>
dim(e2Angle)
## [1] 123
#Spiral e2
e2SpiralL34 <- subset(e2Angle, L3L4 <= 150 & L3L4 >= 120)
dim(e2SpiralL34) #18
## [1] 18 9
e2DecL34 <- subset(e2Angle, L3L4 <= 195 & L3L4 >= 165)
dim(e2DecL34) #39
## [1] 39 9
39/88
## [1] 0.4432
44+39
## [1] 83
83/88
## [1] 0.9432
#How many plant were recorded for L3L4
summary(is.na(e2Angle$L3L4)) #87
            FALSE
                      TRUE
                              NA's
     Mode
## logical
                87
                     36
```

```
#0ther
88 - 39 -18 #=31
```

## [1] 31

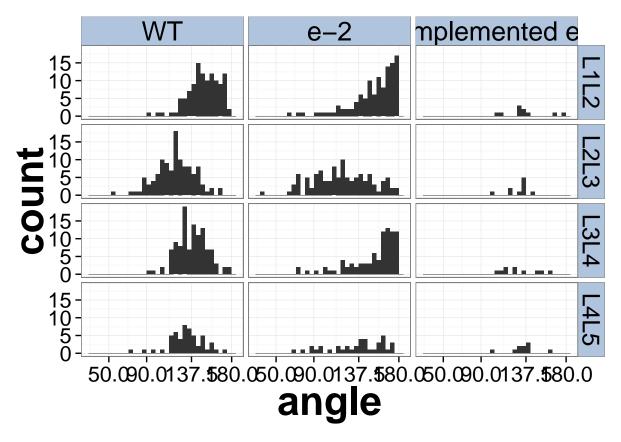
A few other ways to look at this data

```
## stat_bin: binwidth defaulted to range/30. Use 'binwidth = x' to adjust this.
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```



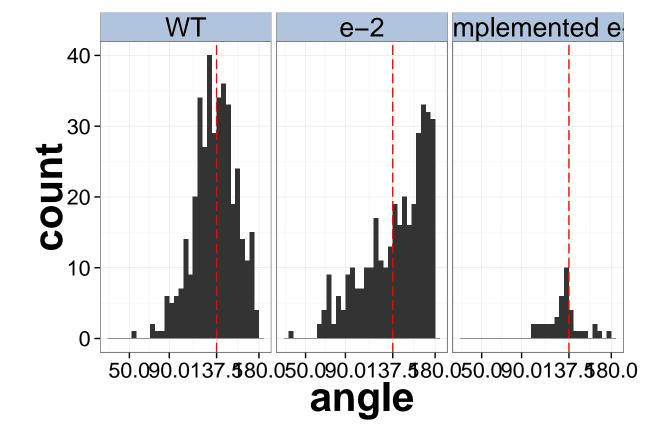
```
angleDataSubL12 <- subset(angleDataSub, leaf == "L1L2")</pre>
angleDataSubL23 <- subset(angleDataSub, leaf == "L2L3")</pre>
angleDataSubL34 <- subset(angleDataSub, leaf == "L3L4")</pre>
angleDataSubL45 <- subset(angleDataSub, leaf == "L4L5")</pre>
angleDataSubSub <- rbind(angleDataSubL12, angleDataSubL23, angleDataSubL34, angleDataSubL45)
ggplot(angleDataSubSub, aes(angle)) +
  geom_bar() +
  facet_grid(leaf~genotype) +
  scale_color_brewer(palette="Dark2") +
  theme bw() +
  scale x continuous(breaks=c(50, 90, 137.5, 180, 200)) +
  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 = 18),
        strip.background = element_rect(fill="#b0c4de"),
        legend.position="none"
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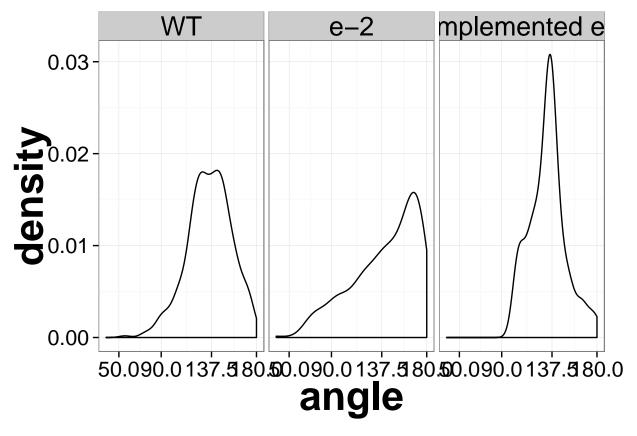


```
ggplot(angleDataSubSub, aes(angle)) +
  geom_bar() +
  facet_grid(.~genotype) +
  theme_bw() +
  scale_x_continuous(breaks=c(50, 90, 137.5, 180, 200)) +
  geom_vline(xintercept=137.5, color = "red", linetype= "longdash") +
  theme(axis.title.x = element_text(face="bold", size=30),
        axis.title.y = 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 = 18),
        strip.background = element_rect(fill="#b0c4de"),
        legend.position="none"
```

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```
## Warning: Removed 63 rows containing non-finite values (stat_density).
## Warning: Removed 140 rows containing non-finite values (stat_density).
```



```
## Warning: Removed 1 rows containing non-finite values (stat_density).
## Warning: Removed 62 rows containing non-finite values (stat_density).
## Warning: Removed 10 rows containing non-finite values (stat_density).
## Warning: Removed 14 rows containing non-finite values (stat_density).
## Warning: Removed 36 rows containing non-finite values (stat_density).
## Warning: Removed 80 rows containing non-finite values (stat_density).
```

