UI.morphology

```
setwd("/Users/jennahamlin/UIproject")
library(ggplot2)
library(arm)
```

This is for pollen tube growth analyses for HT transgenics

```
## Warning: package 'arm' was built under R version 3.2.5

## Loading required package: MASS

## Loading required package: Matrix

## Warning: package 'Matrix' was built under R version 3.2.5

## Loading required package: lme4

## Warning: package 'lme4' was built under R version 3.2.5

##
## arm (Version 1.9-3, built: 2016-11-21)

## Working directory is /Users/jennahamlin/UIproject
```

```
mydata<-read.csv("PT.measurements.HT.csv", header=T)
```

```
lm1<-lm(Percent ~ Type, data=mydata)

# Create a data frame 'estimates' to hold...
# the means, SDs, SEMs or interval bounds:
estimates <- expand.grid(Type=levels(mydata$Type))
# Add the mean heights to the dataframe
#estimates$Height  <- predict(lm1, newdata= estimates)
# alternatively, mean heights using tapply()
estimates$Height  <- tapply(mydata$Percent, mydata$Type, mean)

##### Means with 95% CIs
# add 95% CI upper and lower bounds to estimates dataframe
estimates$C95_lwr  <- predict(lm1, newdata= estimates, interval="confidence")[,2]
estimates$C95_upr  <- predict(lm1, newdata= estimates, interval="confidence")[,3]

estimates
```

```
##      Type    Height    C95_lwr    C95_upr
## 1 1079-A 0.7040828 0.6447546 0.7634111
## 2 1079-B 0.9760981 0.9464339 1.0057622
## 3 1080-A 0.9406750 0.8987235 0.9826264
## 4 1080-B 0.9253292 0.8910760 0.9595824
```

Plot of means with 95% CIs