

# Ellsworth Resurvey Data Analysis

---

## Goals and Approach

---

The primary goal of these preliminary analyses is to figure out how many plots should be resurveyed at Ellsworth in summer 2020. To do this, we used the pre-treatment survey data from 2006/2007 to quantify variance in density, height, and DBH of plots by block and stand type (for DF and WG stand types only; RA plots were not included due to low sample size). We then simulated data, assuming treatments effects proportional to stems removed (30%) for all response variables (density, height, and DBH), with the variance equivalent to the 2006/2007 data. Thus, this approach makes some assumptions that may not be accurate (variance remains constant in time, regardless of the treatment, and the treatment effects are proportional to the proportion of stems removed). However, the goal is to give us a sense of the approximate number of plots necessary to estimate a treatment effect, given observed variance at the plot and stand level.

## Summary of Conclusions

---

After looking at the simulated data, we concluded that we should collect data in ~25-30 plots per treatment within the WH stand types and ~15-20 plots per treatment within the DF stand types.

## Data Files

---

We used the following datafiles, which can be found in the Ellsworth GitHub repo (<https://github.com/AileneKane/ellsworth>) as well as in the “Ellsworth Science and Monitoring” shared folder on Box.

LIVETREES\_CLEAN\_04282008.csv

PLOT\_CLEAN\_11062008.csv

Ellsworth\_stands\_treatment\_data.csv

## Analysis of pre-treatment survey data

---

We load the above files and packages, and then put them together into a dataframe for analysis

There is some structure to the data, that may be important to account for in looking at treatment effects, and therefore should be kept in mind in resurveys: - Blocks (N,C,S), which are different geographical regions at Ellsworth -Standtype, which are different forest types at Ellsworth. -Note: There are 5 plots in which standtype is blank- what are these? we will ignore them for now! Here is a breakdown of the number of plots in each standtype by region and by:

```
table(plotd2$STAND.TYP,plotd2$BLOCK)
```

```
##
##           C  N  S
##           0  2  3
## DF-1       6 21  0
## DF-2       7  4 40
## RA-3       1  0  4
## WH/SS/RC-1 15  1  0
## WH/SS/RC-2 19  0 19
## WH/SS/RC-3 33  3 18
## WH/SS/RC-4  0 25  0
## WH/SS/RC-5  3  0  0
```

```
table(plotd2$STAND.TYP,plotd2$TRT)
```

```
##
##           CON ROAD THIN
##           2   0   3
## DF-1      16   0  11
## DF-2      23  12  16
## RA-3       1   3   1
## WH/SS/RC-1  1  10   5
```

```
## WH/SS/RC-2 22 7 9
## WH/SS/RC-3 7 21 26
## WH/SS/RC-4 12 0 13
## WH/SS/RC-5 0 3 0
```

Now lets look at effects of age on density, height, dbh, and crown, and quantify variation by region and stand-type using multilevel models.

## Density

---

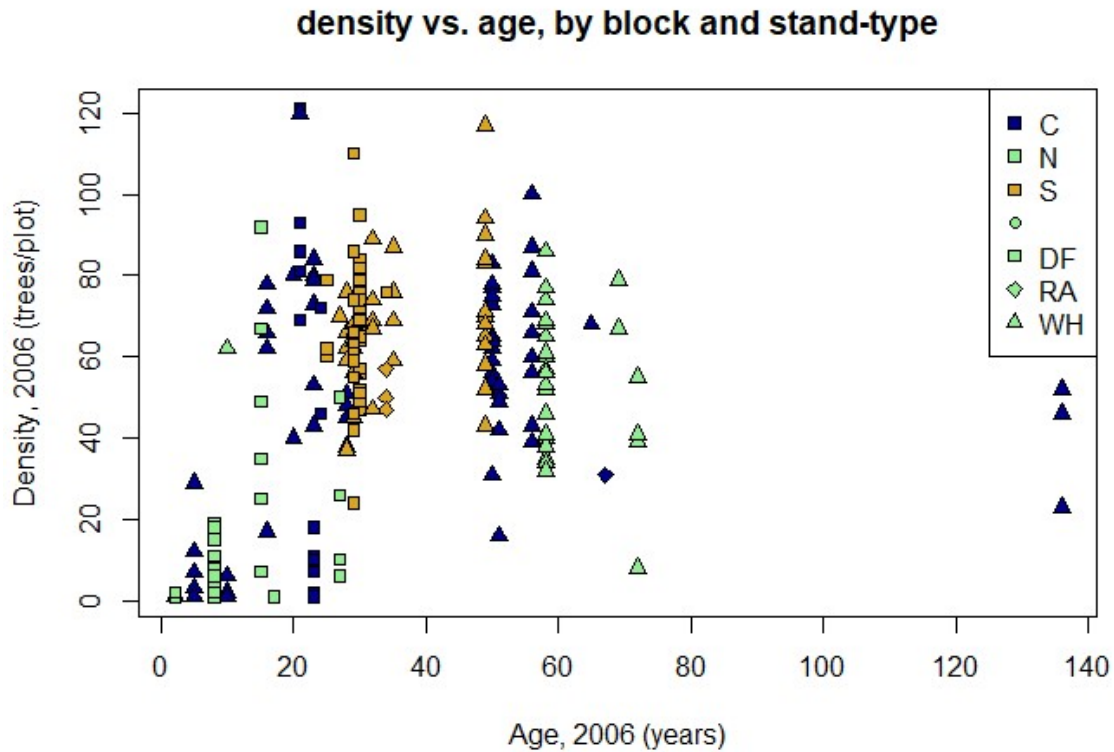
```
colors<-c("darkblue","lightgreen","goldenrod")
syms<-c(21,22,23,24)
blocks<-as.character(unique(plotd2$BLOCK))
treats<-unique(plotd2$TRT)
sttypes<-sort(unique(plotd2$stand.code))

plot(plotd2$AGE_BH_2006,plotd2$predens, pch=syms[as.numeric(as.factor(plotc

legend("topright", legend=c(blocks,sttypes),pch=c(22,22,22,syms),pt.bg=c(cc
```

<

>



```
densmod<-lmer(predens~AGE_BH_2006 + (1|BLOCK) + (1|STAND.TYPE), data=plotd2
den.standsd<-VarCorr(densmod,comp="Variance")[1]
den.blocksd<-VarCorr(densmod,comp="Variance")[2]
Bage.dens<-fixef(densmod)[2]
int.dens<-fixef(densmod)[1]
summary(densmod)#
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: predens ~ AGE_BH_2006 + (1 | BLOCK) + (1 | STAND.TYPE)
## Data: plotd2
##
## REML criterion at convergence: 1910.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5567 -0.5631 -0.1083  0.5731  3.9016
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## STAND.TYPE (Intercept) 500.57    22.373
```

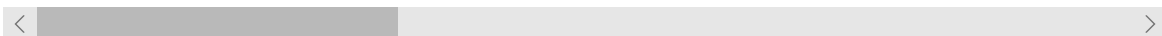
```
## BLOCK      (Intercept)  36.66    6.055
## Residual                365.33   19.114
## Number of obs: 216, groups:  STAND.TYPE, 8; BLOCK, 3
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  49.43120   11.43900   4.321
## AGE_BH_2006 -0.09828    0.16634  -0.591
##
## Correlation of Fixed Effects:
##              (Intr)
## AGE_BH_2006  -0.629
```

There is a weak negative effect of age on density, after accounting for variation in density and blocks. There is much higher variance in density by stand type than by block.

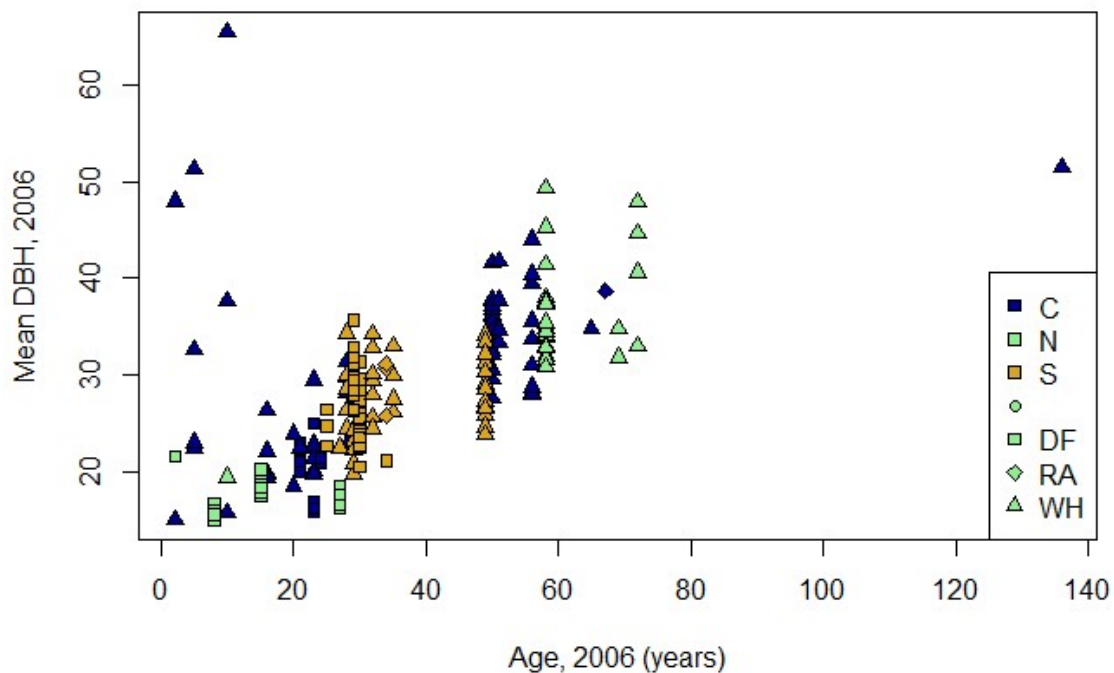
## DBH

---

```
plot(plotd2$AGE_BH_2006,plotd2$dbh.mn, pch=syms[as.numeric(as.factor(plotd2
legend("bottomright", legend=c(blocks,sttypes),pch=c(22,22,22,syms),pt.bg=c
```



DBH vs. age, by block and stand-type



```
dbhmod<-lmer(DBH~ AGE_BH_2006+(1|BLOCK) + (1|STAND.TYPE), data=treed2)
dbh.standsd<-VarCorr(dbhmod,comp="Variance")[1]
dbh.blocksd<-VarCorr(dbhmod,comp="Variance")[2]
summary(dbhmod)#positive effect of age on dbh, similar variance by TRT and E
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: DBH ~ AGE_BH_2006 + (1 | BLOCK) + (1 | STAND.TYPE)
## Data: treed2
##
## REML criterion at convergence: 84818.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5699 -0.6381 -0.1143  0.4534 15.3875
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## STAND.TYPE (Intercept)  54.12234   7.3568
## BLOCK       (Intercept)   0.03443   0.1855
## Residual                                101.59504 10.0794
```

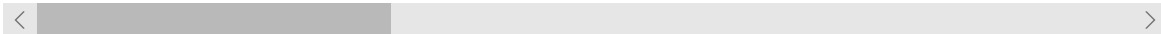
```
## Number of obs: 11365, groups:  STAND.TYPE, 8; BLOCK, 3
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept) 14.13399    2.73878   5.161
## AGE_BH_2006  0.32242    0.01829  17.627
##
## Correlation of Fixed Effects:
##              (Intr)
## AGE_BH_2006 -0.302
```

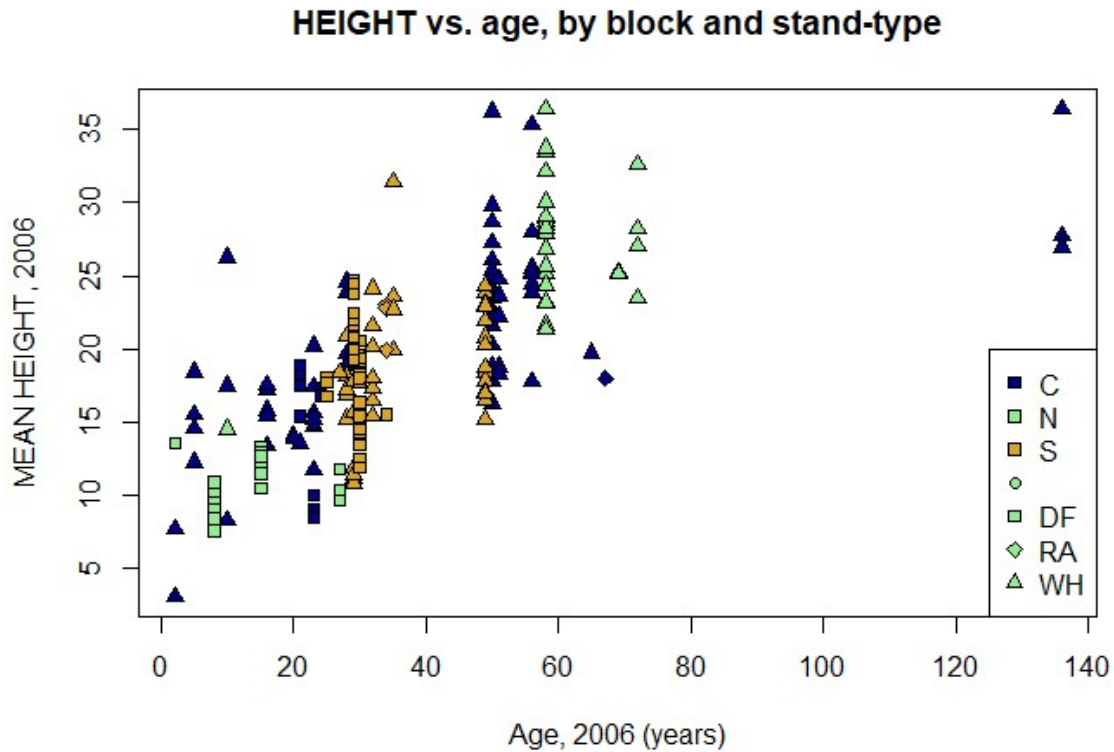
There is a positive effect of age on dbh, after accounting for variation in density and blocks. There is much higher variance in dbh by stand type than by block.

## Height

---

```
plot(plotd2$AGE_BH_2006,plotd2$ht.mn, pch=symbs[as.numeric(as.factor(plotd2$
legend("bottomright", legend=c(blocks,sttypes),pch=c(22,22,22,symbs),pt.bg=c
```





```
htmod<-lmer(HT~ AGE_BH_2006+(1|BLOCK) + (1|STAND.TYPE), data=treed2)
summary(htmod)#positive effect of age on ht, higher variance by TRT...
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: HT ~ AGE_BH_2006 + (1 | BLOCK) + (1 | STAND.TYPE)
## Data: treed2
##
## REML criterion at convergence: 14022.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3668 -0.6304 -0.0418  0.5464  4.9806
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## STAND.TYPE (Intercept) 21.74663  4.6633
## BLOCK        (Intercept)  0.08047  0.2837
## Residual                        35.52325  5.9601
## Number of obs: 2182, groups:  STAND.TYPE, 8; BLOCK, 3
##
## Fixed effects:
```



```
##           Estimate Std. Error t value
## (Intercept) 17.48581    1.92169   9.099
## AGE_BH_2006  0.05838    0.02098   2.782
##
## Correlation of Fixed Effects:
##           (Intr)
## AGE_BH_2006 -0.495
```

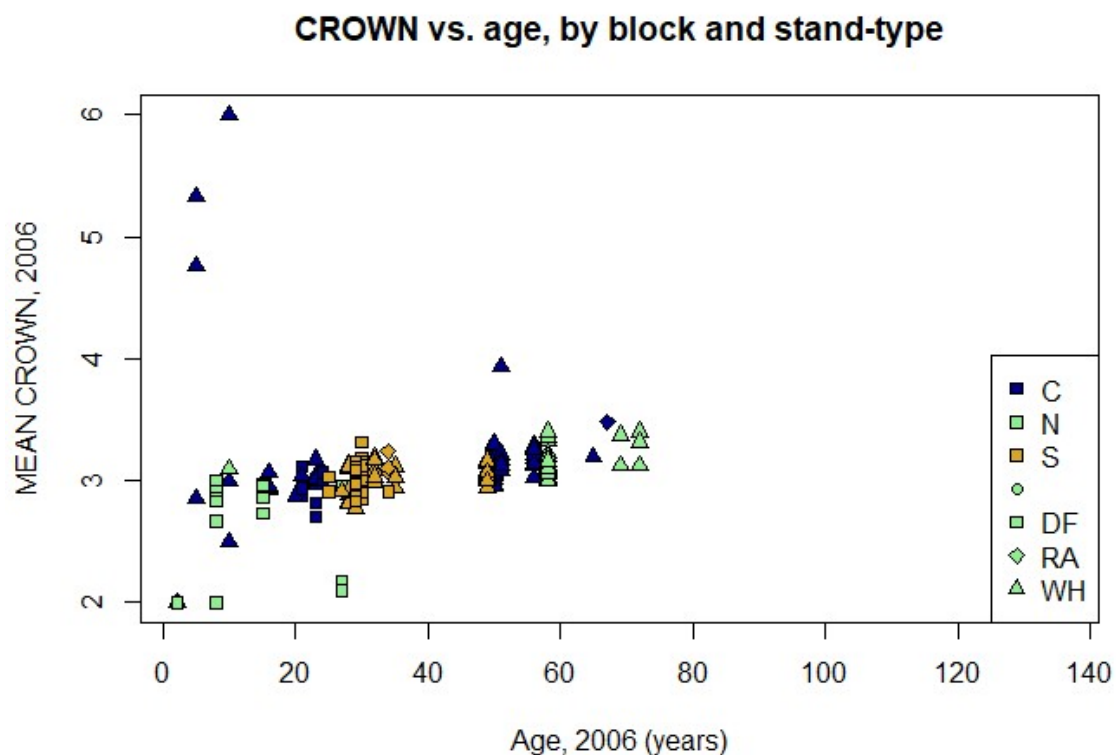
```
ht.standsd<-VarCorr(htmod,comp="Variance")[1]
ht.blocksd<-VarCorr(htmod,comp="Variance")[2]
```

There is a positive effect of age on height, after accounting for variation in density and blocks. There is much higher variance in height by stand type than by block.

## Crown

```
plot(plotd2$AGE_BH_2006,plotd2$crown.mn, pch=symbols[as.numeric(as.factor(plot
legend("bottomright", legend=c(blocks,sttypes),pch=c(22,22,22,symbols),pt.bg=c
```

< >



```
crownmod<-lmer(CROWN~ AGE_BH_2006+(1|BLOCK) + (1|STAND.TYPE), data=treed2)

summary(crownmod)#positive effect of age on crown, slightly higher variance
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: CROWN ~ AGE_BH_2006 + (1 | BLOCK) + (1 | STAND.TYPE)
## Data: treed2
##
## REML criterion at convergence: 16545.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -5.6792 -0.2866 -0.0561 -0.0175  5.7064
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## STAND.TYPE (Intercept) 0.16535   0.4066
## BLOCK      (Intercept) 0.01763   0.1328
## Residual                    0.24948   0.4995
## Number of obs: 11366, groups: STAND.TYPE, 8; BLOCK, 3
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  2.859453   0.168422  16.978
## AGE_BH_2006  0.006614   0.000916   7.221
##
## Correlation of Fixed Effects:
##              (Intr)
## AGE_BH_2006 -0.246
```

```
crown.standsd<-VarCorr(crownmod,comp="Variance")[1]
crown.blocksd<-VarCorr(crownmod,comp="Variance")[2]
```

There is a positive effect of age on crown, after accounting for variation in density and blocks. There is much higher variance in crown by stand type than by block.

# How many plots do we need to capture treatment effects, amidst all the variation?

---

To figure out how many plots need to be resampled to capture the treatment effects, amidst all the variation among blocks and standtypes, we simulated a dataset of resampled data. To do this, we set expected effect sizes of treatment

## 1. RESPONSE VARIABLE = DENSITY

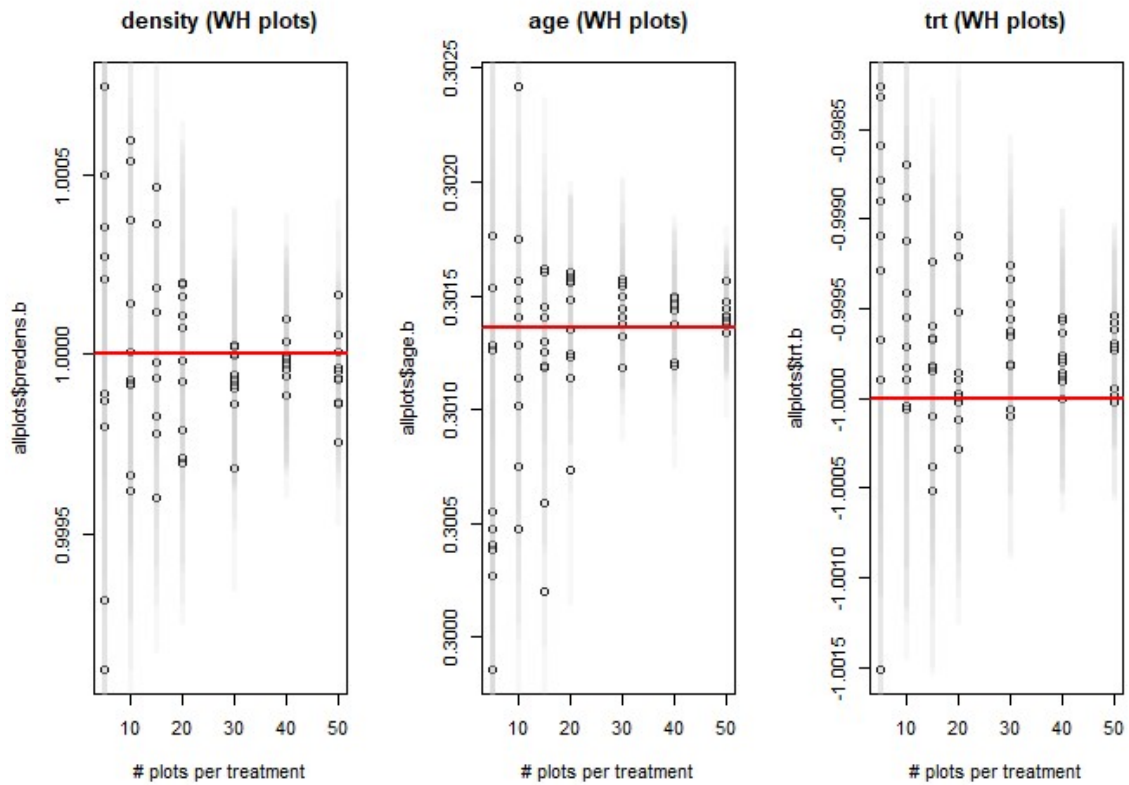
---

In all plots, the x axis is the number of plots per treatment.

WH stand types

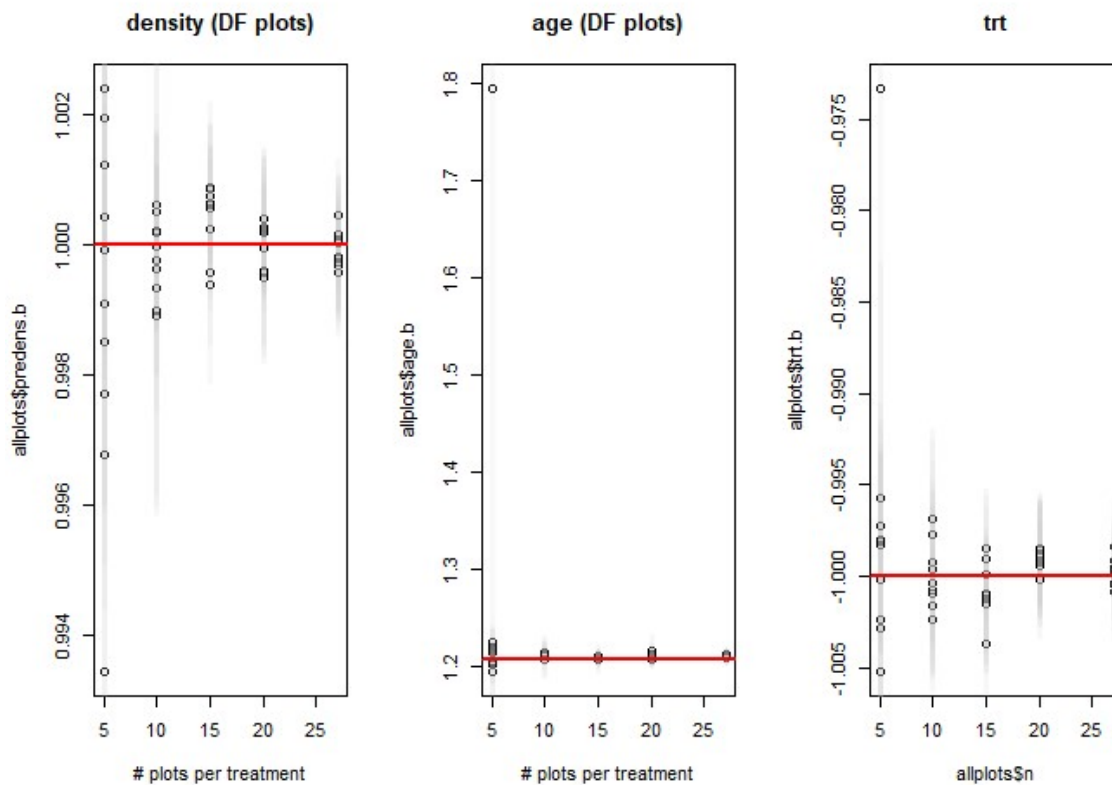
```
#4. set expected effect sizes for simulating data
#fit model for
par(mfrow=c(1,3))
plot(allplots$n,allplots$predens.b,main="density (WH plots)",ylim= range(all
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$predens.b.lc[i],allplots$n[i],allplots$predens.b.uc[i])
}
abline(h=predens.b, lwd=2, col="red")
plot(allplots$n,allplots$age.b,main="age (WH plots)",ylim=range(allplots$age
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$age.b.lc[i],allplots$n[i],allplots$age.b.uc[i])
}
abline(h=age.b, lwd=2, col="red")
plot(allplots$n,allplots$trt.b,main="trt (WH plots)",ylim=range(allplots$trt
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$trt.b.lc[i],allplots$n[i],allplots$trt.b.uc[i])
}
abline(h=trt.b, lwd=2, col="red")
```





DF stand type

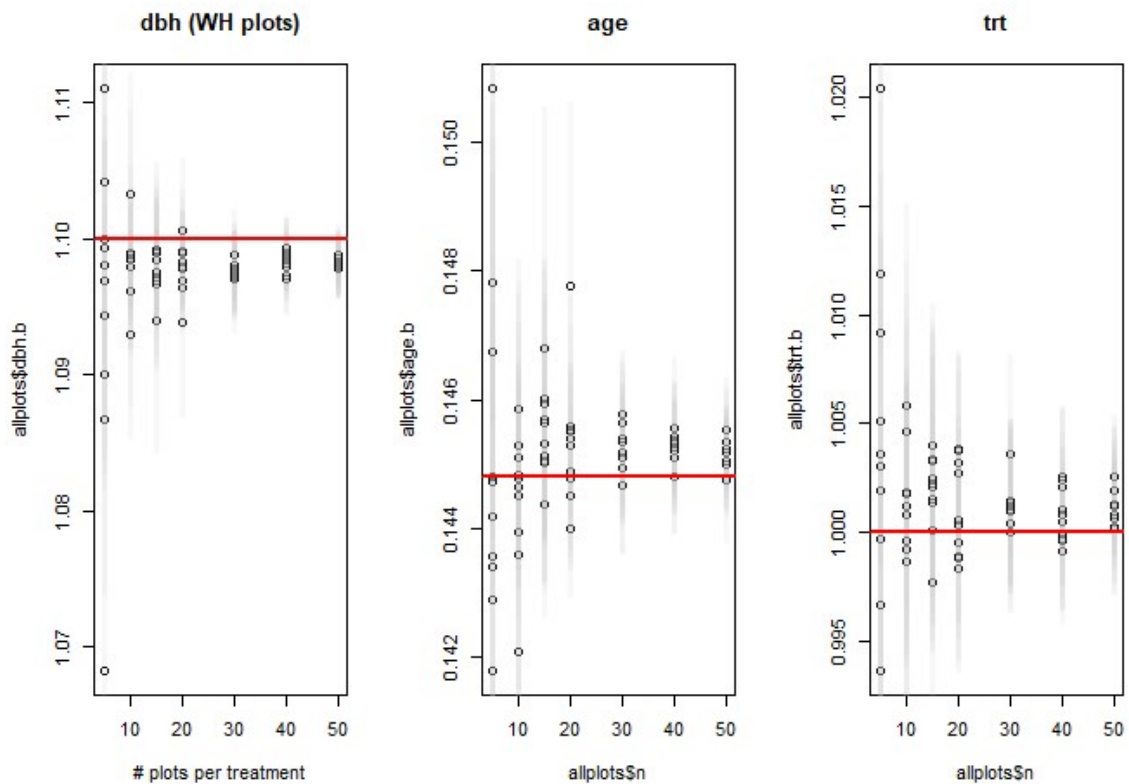
```
par(mfrow=c(1,3))
plot(allplots$n,allplots$predens.b,main="density (DF plots)",ylim= range(all
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$predens.b.lc[i],allplots$n[i],allplots$predens.b.uc[i])
}
abline(h=dens.b, lwd=2, col="red")
plot(allplots$n,allplots$age.b,main="age (DF plots)",ylim=range(allplots$age.b
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$age.b.lc[i],allplots$n[i],allplots$age.b.uc[i])
}
abline(h=age.b, lwd=2, col="red")
plot(allplots$n,allplots$trt.b,main="trt",ylim=range(allplots$trt.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$trt.b.lc[i],allplots$n[i],allplots$trt.b.uc[i])
}
abline(h=trt.b, lwd=2, col="red")
```



## 2. RESPONSE VARIABLE = DBH

WH standtypes

```
par(mfrow=c(1,3))
plot(allplots$n,allplots$dbh.b,main="dbh (WH plots)",ylim= range(allplots$dbh.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$dbh.b.lc[i],allplots$n[i],allplots$dbh.b.hc[i])
}
abline(h=dbh.b, lwd=2, col="red")
plot(allplots$n,allplots$age.b,main="age",ylim=range(allplots$age.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$age.b.lc[i],allplots$n[i],allplots$age.b.hc[i])
}
abline(h=age.b, lwd=2, col="red")
plot(allplots$n,allplots$trt.b,main="trt",ylim=range(allplots$trt.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$trt.b.lc[i],allplots$n[i],allplots$trt.b.hc[i])
}
abline(h=trt.b, lwd=2, col="red")
```



# Now for DF standtypes

```
par(mfrow=c(1,3))
plot(allplots$n,allplots$dbh.b,main="dbh (DF plots)",ylim= range(allplots$dbh.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$dbh.b.lc[i],allplots$n[i],allplots$dbh.b.uc[i])
}
abline(h=dbh.b, lwd=2, col="red")
plot(allplots$n,allplots$age.b,main="age",ylim=range(allplots$age.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$age.b.lc[i],allplots$n[i],allplots$age.b.uc[i])
}
abline(h=age.b, lwd=2, col="red")
plot(allplots$n,allplots$trt.b,main="trt",ylim=range(allplots$trt.b))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$trt.b.lc[i],allplots$n[i],allplots$trt.b.uc[i])
}
abline(h=trt.b, lwd=2, col="red")
```

