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 Ellsowrth in summe, echo=TRUE, results="hide"r 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.

Summary

Data Files

We used the following datafiles, which can be 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. Here is a breakdown of the number of plots in each standtype by region:

```
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
```

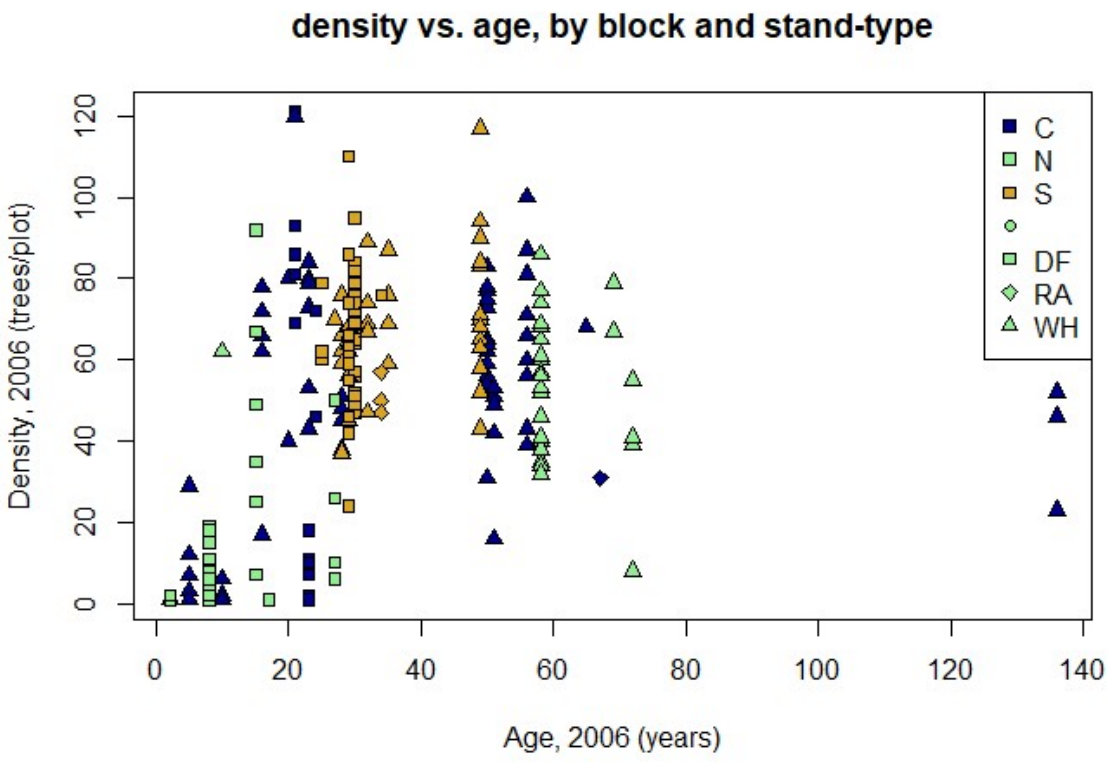
Now lets look at effects of age on density, height, dbh, and crown, and quantify variation by region and stand-type using multilevel models.

Density

```
colors<-c("darkblue","lightgreen","goldenrod")
symbs<-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=symbs[as.numeric(as.factor(plotc

legend("topright", legend=c(blocks,sttypes),pch=c(22,22,22,symbs),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.
```

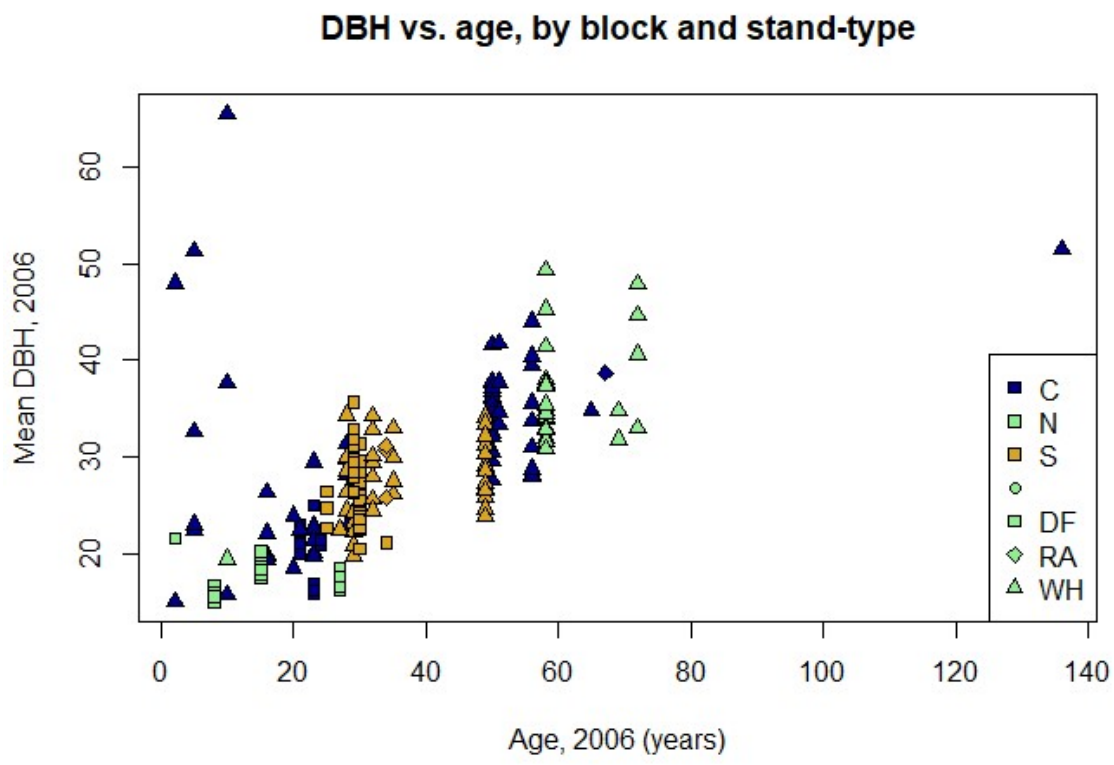
```
##  STAND.TYPE (Intercept) 500.57   22.373
##  BLOCK      (Intercept)  36.66    6.055
##  Residual                365.33   19.114
## Number of obs: 216, groups:  STAND.TYPE, 8; BLOCK, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 49.43120   11.43900   4.321
## AGE_BH_2006 -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=symbs[as.numeric(as.factor(plotd2

legend("bottomright", legend=c(blocks,sttypes),pch=c(22,22,22,symbs),pt.bg=c
```




```
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
```

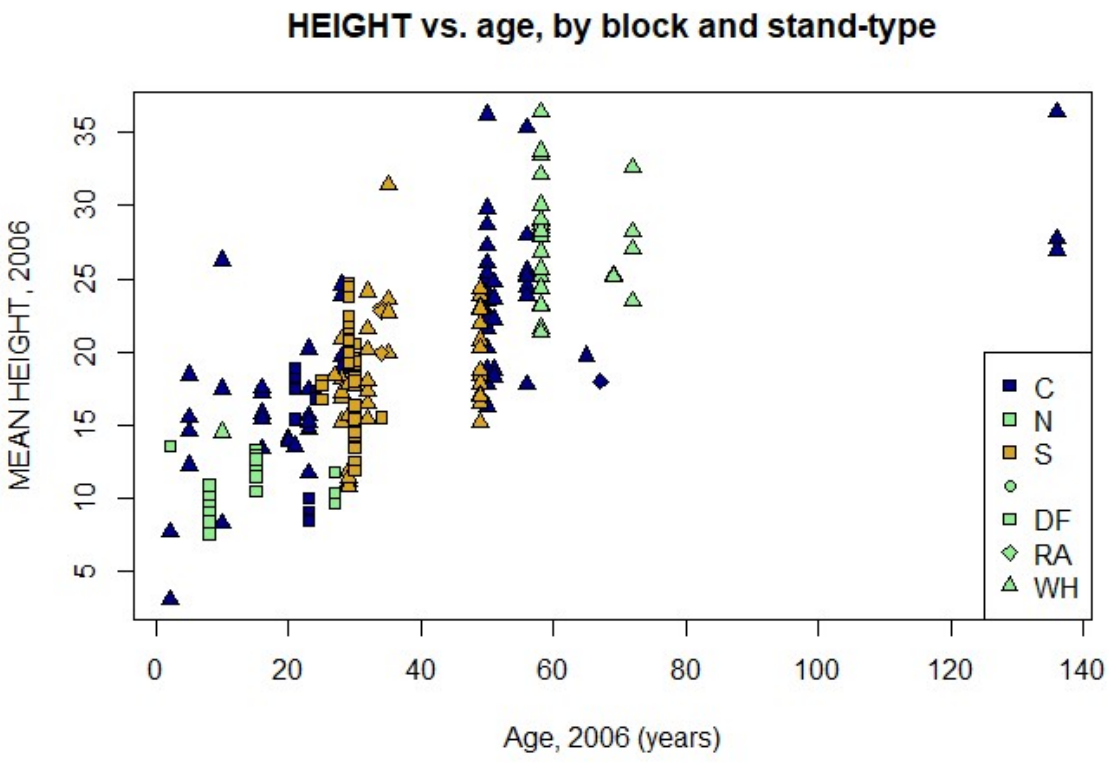
```
## Number of obs: 11365, groups:  STAND.TYPE, 8; BLOCK, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 14.13399    2.73878   5.161
## AGE_BH_2006  0.32242    0.01829  17.627
##
## Correlation of Fixed Effects:
##             (Intr)
## AGE_BH_2006 -0.302
```

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:
```

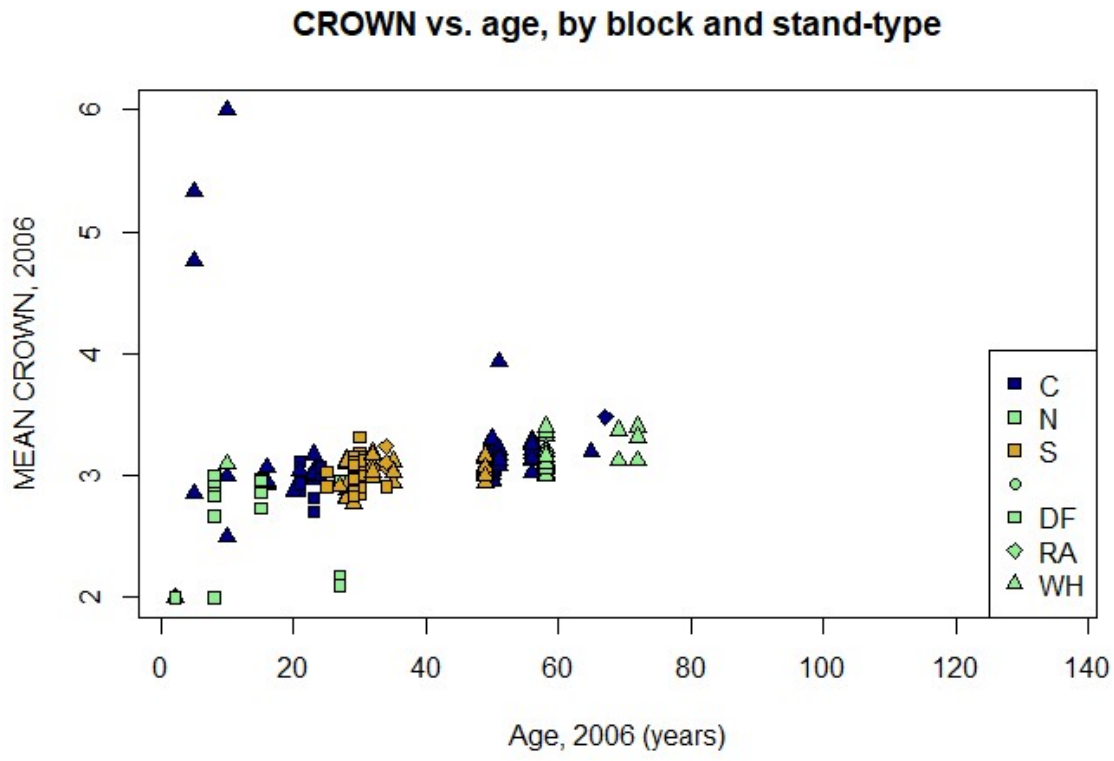
```
##             Estimate Std. Error t value
## (Intercept) 17.48581    1.92169   9.099
## AGE_BH_2006  0.05838    0.02098   2.782
##
## Correlation of Fixed Effects:
##             (Intr)
## AGE_BH_2006 -0.495
```

```
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=symbs[as.numeric(as.factor(plot
```

```
legend("bottomright", legend=c(blocks,sttypes),pch=c(22,22,22,symbs),pt.bg=c
```



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

summary(crownmod)#positive effect of age on crown, lsightly 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

```
#4. set expected effect sizes for simulating data
dens.b = 1#effect of pre-density
age.b = Bage.dens#age effect (older stands have lower post-density? use coef
trt.b = -1 #trt is amount removed (0,3 x predens)
sigma.bl =6.055#estimated block-level sigma from 2006 data
sigma.st =22.37#estimated stand-type sigma from 2006 data

sigma = .1#
b0 = int.dens# from model above

#use the effect sizes and predictors plus error to generate the y variable

block = x$block
nblock = length(unique(x$block))
nplot = 72

nstand = 3
blockeff = rep(rnorm(nblock, 0, sigma.bl), each = nplot)
standeff = rep(rnorm(nstand, 0, sigma.st), each = nplot)
ploteff = rnorm(nblock*nplot, 0, sigma)

ypred = b0 + dens.b*x$predens.z + age.b*x$age2006.z + trt.b*x$trt.z+ blockef

#lmer(ypred ~ predens.z + age2006.z + trt.z+ (1|block)+ (1|stand.code), data


#now lets write a for loop that uses different sample sizes to figure out hc
fulldat<-cbind(ypred,x)
nplots<-rep(c(5,10,15,20,25,30,35,40,45), times=10)
allplots<-c()
for(i in 1:length(nplots)){
  subsdatc<-sample_n(fulldat[fulldat$block=="C",], nplots[i])
  subsdatn<-sample_n(fulldat[fulldat$block=="N",], nplots[i])
  subsdats<-sample_n(fulldat[fulldat$block=="S",], nplots[i])
  subsdat<-rbind(subsdatc,subsdatn,subsdats)
```

```
  fit<-lmer(ypred ~ predens.z + age2006.z + trt.z+ (1|block)+ (1|stand.code)
  cis<-confint(fit)
  fit.sum<-c(nplots[i],fixef(fit),cis[3,],cis[4,],cis[5,],cis[6,])
  allplots<-rbind(allplots,fit.sum)
}
```

```
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decre
## profile: using minstep
```

```
## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decrea
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decrea
## profile: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decrea
## profile: using minstep

## Warning in profile.merMod(object, which = parm, signames = oldNames, .
## monotonic profile for (Intercept)

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit
## (Intercept): falling back to linear interpolation

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## Model failed to converge with max|grad| = 0.00487029 (tol = 0.002, comp

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
```

```
## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in zetafun(np, ns): slightly lower deviances (diff=-1.36424e-12
## detected

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in zetafun(np, ns): slightly lower deviances (diff=-5.57066e-12
## detected

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in zetafun(np, ns): slightly lower deviances (diff=-7.27596e-12
## detected

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in zetafun(np, ns): slightly lower deviances (diff=-7.27596e-12
## detected

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig02

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit
## for .sig02: falling back to linear interpolation

## Warning in regularize.values(x, y, ties, missing(ties)): collapsing to
## 'x' values

## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## Model failed to converge with max|grad| = 0.00251254 (tol = 0.002, comp

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
```

```
## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## Model failed to converge with max|grad| = 0.00309077 (tol = 0.002, comp

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig02

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit
## for .sig02: falling back to linear interpolation

## Warning in regularize.values(x, y, ties, missing(ties)): collapsing to
## 'x' values

## boundary (singular) fit: see ?isSingular
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular
```

```
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig02

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit
## for .sig02: falling back to linear interpolation

## Warning in regularize.values(x, y, ties, missing(ties)): collapsing to
## 'x' values

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular
```

```
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
```

```
## Model failed to converge with max|grad| = 0.00738056 (tol = 0.002, comp

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in zetafun(np, ns): slightly lower deviances (diff=-1.81899e-12
## detected

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): Last two rows hav
## identical or NA .zeta values: using minstep

## Warning in zetafun(np, ns): slightly lower deviances (diff=-1.93268e-12
## detected

## Warning in FUN(X[[i]], ...): non-monotonic profile for .sig02

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit
## for .sig02: falling back to linear interpolation

## Warning in regularize.values(x, y, ties, missing(ties)): collapsing to
## 'x' values

## boundary (singular) fit: see ?isSingular
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## Model failed to converge: degenerate Hessian with 1 negative eigenvalue

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
```

```
## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## Model failed to converge with max|grad| = 0.00268727 (tol = 0.002, comp

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$check
## Model failed to converge with max|grad| = 0.00815029 (tol = 0.002, comp

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decrea
## profile: using minstep

## Warning in profile.merMod(object, which = parm, signames = oldNames, .
## monotonic profile for (Intercept)

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit
## (Intercept): falling back to linear interpolation
```

```
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkCo
## Model failed to converge with max|grad| = 0.00575558 (tol = 0.002, compor

## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## Warning in nextpar(mat, cc, i, delta, lowcut, upcut): unexpected decrease
## profile: using minstep

## Warning in profile.merMod(object, which = parm, signames = oldNames, ...)
## monotonic profile for (Intercept)

## Warning in confint.thpr(pp, level = level, zeta = zeta): bad spline fit f
## (Intercept): falling back to linear interpolation

## boundary (singular) fit: see ?isSingular
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkCo
## Model failed to converge with max|grad| = 0.052424 (tol = 0.002, componer

## Computing profile confidence intervals ...

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkCo
## Model failed to converge with max|grad| = 0.0140444 (tol = 0.002, compone

## Computing profile confidence intervals ...
## Computing profile confidence intervals ...

## boundary (singular) fit: see ?isSingular

## Computing profile confidence intervals ...
```

```
allplots<-as.data.frame(allplots)
colnames(allplots)<-c("n","int","predens.b","age.b","trt.b","int.lc","int.uc


par(mfrow=c(1,3))
plot(allplots$n,allplots$predens.b,main="pre-density",ylim=c(0,7))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$predens.b.lc[i],allplots$n[i],allplots$prede
}
abline(h=dens.b, lwd=2, col="red")
plot(allplots$n,allplots$age.b,main="age",ylim=c(-1,0))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$age.b.lc[i],allplots$n[i],allplots$age.b.uc[
}
abline(h=age.b, lwd=2, col="red")
plot(allplots$n,allplots$trt.b,main="trt",ylim=c(-1.5,0))
for(i in 1:dim(allplots)[1]){
  arrows(allplots$n[i],allplots$trt.b.lc[i],allplots$n[i],allplots$trt.b.uc[
}
abline(h=trt.b, lwd=2, col="red")
```