Assignment_06 - STAT 689

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```
# import third-party modules
library("HRW")
library("tidyverse")
library("mgcv")
library("nlme")
```

Read in our data

```
fram <- read.csv("/Users/panders2/Documents/schools/tamu/stat_689/homework/semiparametric-regression/hw
names(fram) <- tolower(names(fram))
# check that we have 1615 observations
dim(fram)
```

```
## [1] 1615   10
```

Create new variables for the systolic blood pressure readings and the two cholesterol measurements.

```
# systolic blood pressure first
fram$lsbp <- log(((fram$sbp21 + fram$sbp22 + fram$sbp31 + fram$sbp32) / 4) - 50)
# cholesterol measurements second
fram$lcholest <- log((fram$cholest2 + fram$cholest3) / 2)
```

Keep only the variables that we will be working with directly and make sure everything seems reasonable.

```
fram2 <- fram %>%
  dplyr::select(chd, age, smoker, lsbp, lcholest)
head(fram2)
```

```
##   chd age smoker     lsbp lcholest
## 1   0  56      0 4.317488 5.654242
## 2   0  38      1 4.241327 5.451038
## 3   0  54      1 4.347047 5.654242
## 4   0  42      1 4.185860 5.541264
## 5   0  47      1 4.454347 5.583496
## 6   0  43      1 4.269697 5.298317
```

Question 1

Fit a multiple linear regression of LSBP on lcholest and smoker via "lm" function. Produce estimates, standard errors, and p-values.

```
# fit model
lin_mod <- lm(lsbp ~ smoker + lcholest
              , data=fram2
              )
# produce summary
summary(lin_mod)
```

```
##
```

```
## Call:
## lm(formula = lsbp ~ smoker + lcholest, data = fram2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.79148 -0.14009 -0.02043  0.10915  0.93289
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.55569    0.17029  20.880  < 2e-16 ***
## smoker      -0.03796    0.01251  -3.034  0.00246 **
## lcholest     0.15540    0.03140   4.949 8.22e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2107 on 1612 degrees of freedom
## Multiple R-squared:  0.02036,    Adjusted R-squared:  0.01915
## F-statistic: 16.75 on 2 and 1612 DF,  p-value: 6.299e-08
```

Question 2

Conduct web research on whether smokers have higher or lower blood pressure on average compared with non-smokers.

WebMD indicates that individuals who smoke tend to have higher blood pressure than those who do not. This is not consistent with my findings from Question 1, which indicate that participants who smoke have lower blood pressure than those who do not, conditional on our transformed cholesterol variable. There is nothing in the documentation to indicate that smoker is not encoded with '1' as the positive class. This result is suspicious, and suggests that we need to check our data or revisit our model specification.

Question 3

The model produces the expectation of LSBP given smoking status *conditional on* cholesterol.

Question 4

Recreate the same model as in Question 1, but also include an interaction amongst the independent variables.

```
lin_mod2 <- lm(lsbp ~ smoker + lcholest + smoker:lcholest
               , data=fram2
               )

summary(lin_mod2)
```

```
##
## Call:
## lm(formula = lsbp ~ smoker + lcholest + smoker:lcholest, data = fram2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -0.79151 -0.14039 -0.02046  0.10916  0.93280
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.55075    0.33525  10.591   <2e-16 ***
## smoker          -0.03130    0.38907  -0.080   0.9359
## lcholest         0.15632    0.06191   2.525   0.0117 *
## smoker:lcholest -0.00123    0.07184  -0.017   0.9863
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2108 on 1611 degrees of freedom
## Multiple R-squared:  0.02036,    Adjusted R-squared:  0.01854
## F-statistic: 11.16 on 3 and 1611 DF,  p-value: 2.993e-07
```

The smoking indicator is still negatively associated with our blood pressure variable, but is no longer significant in the presence of the interaction term.

Question 5

Run a semiparametric ANCOVA with mgcv, the semiparametric version of an ANCOVA without an interaction.

```
semi_mod <- mgcv::gam(lsbp ~ factor(smoker) +
                        s(lcholest, k=23, bs="cr")
                      , data=fram2
                      , method="REML"
                     )
summary(semi_mod)
```

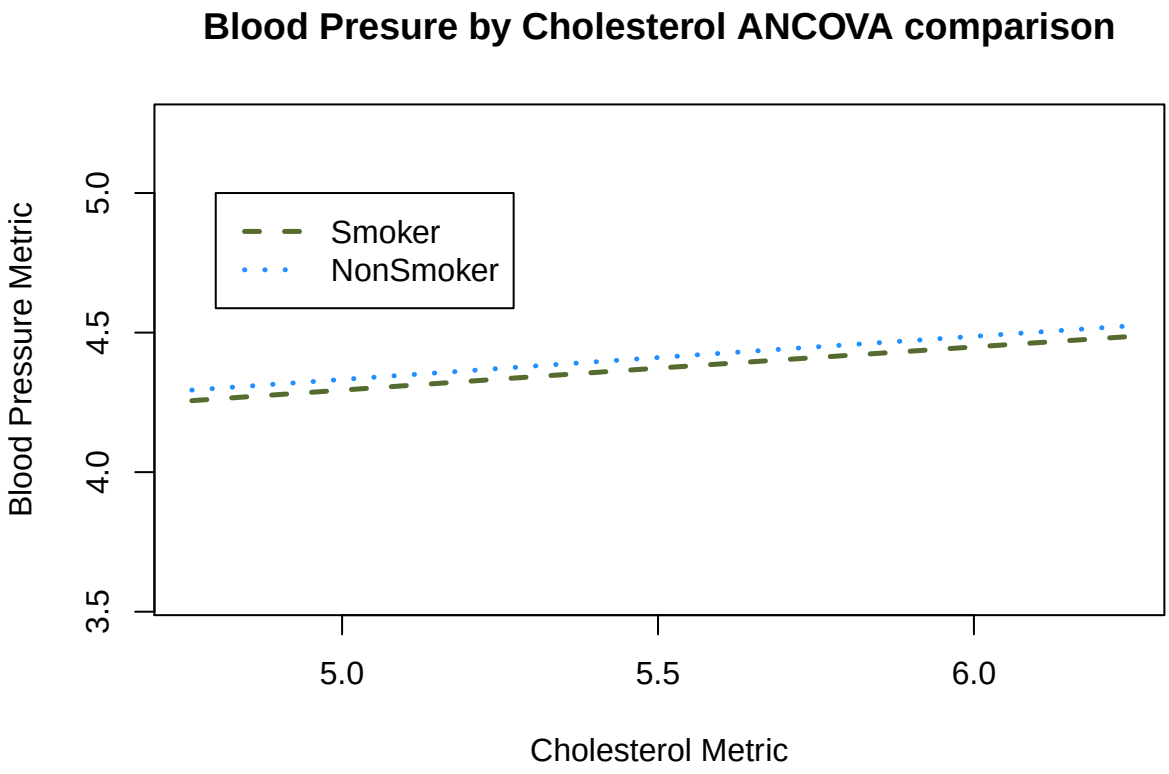
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## lsbp ~ factor(smoker) + s(lcholest, k = 23, bs = "cr")
##
## Parametric coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.39713    0.01100 399.735  < 2e-16 ***
## factor(smoker)1 -0.03799    0.01251  -3.036  0.00244 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##               edf Ref.df     F  p-value
## s(lcholest) 1.064  1.126 22.27 1.73e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0192   Deviance explained = 2.04%
## -REML = -214.85  Scale est. = 0.044402  n = 1615
```

Question 6

For the data in part 5, display a plot of the two lines, but without the data

```
# first, generate the data required for plotting
ng <- 1000
# x var
x_var <- seq(from=min(fram2$lcholest)
             , to=max(fram2$lcholest)
             , len=ng
             )
# y prediction variables
f_hat_smoker <- predict(semi_mod
                        , newdata=data.frame(
                         smoker=rep('1', ng)
                         , lcholest=x_var
                        )
                        , se.fit=TRUE
                        )

f_hat_nosmoke <- predict(semi_mod
                         , newdata=data.frame(
                            smoker=rep('0', ng)
                            , lcholest=x_var
                           )
                         , se.fit=TRUE
                         )
```

```
lineColors <- c("darkolivegreen", "dodgerblue")

plot(fram2$lcholest, fram2$lsbp, type="n"
     , xlab="Cholesterol Metric"
     , ylab = "Blood Pressure Metric"
     , main="Blood Presure by Cholesterol ANCOVA comparison"
       )

lines(x_var, f_hat_smoker$fit, lty=2, lwd=2.5, col=lineColors[1])
lines(x_var, f_hat_nosmoke$fit, lty=3, lwd=2.5, col=lineColors[2])

legend(4.8, 5
       , c("Smoker", "NonSmoker")
       , lty=c(2,3)
       , lwd=rep(2.5, 2)
       , col=c(lineColors[1], lineColors[2])
       )
```

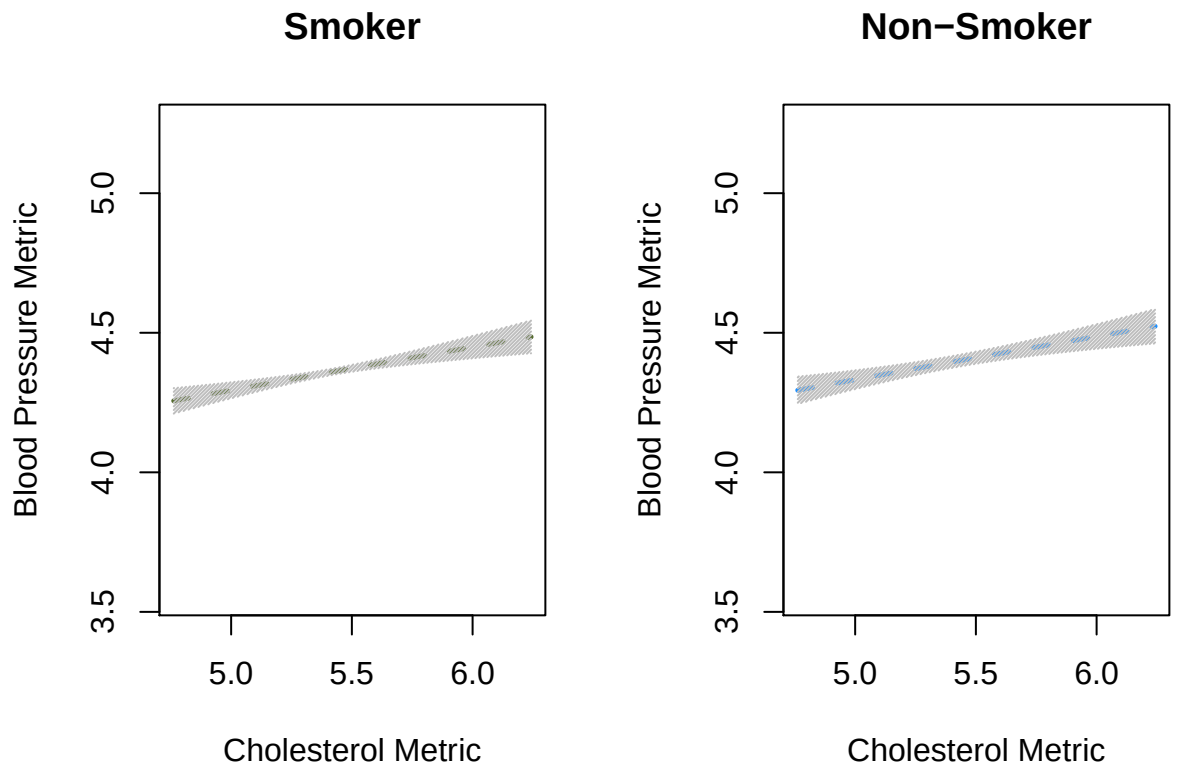


Question 7

Display a plot of the two lines, but split into two separate graphics, and with pointwise 95% confidence intervals.

```
plot_with_bands <- function(mod_pred, range_var, color_vec, color_idx, lty, title="NULL") {
  # create a regression fit with 95% pointwise confidence intervals for the line
  upper <- mod_pred$fit + (1.96 * mod_pred$se.fit)
  lower <- mod_pred$fit - (1.96 * mod_pred$se.fit)
  fit <- mod_pred$fit

  plot(fram2$lcholest, fram2$lsbp, type="n"
       , xlab="Cholesterol Metric"
       , ylab = "Blood Pressure Metric"
       , main=title
        )

  lines(range_var, fit, lty=2, lwd=2.5, col=color_vec[color_idx])

  polygon(x=c(range_var,rev(range_var))
        , y=c(upper
        , rev(lower))
        , col="gray"
        , border=NA
        , density=75
        )

                  }
```

```r
# execute the function
par(mfrow=c(1,2))
plot_with_bands(mod_pred=f_hat_smoker, range_var=x_var, color_vec=lineColors, color_idx=1, lty=2
                , title="Smoker")
plot_with_bands(mod_pred=f_hat_nosmoke, range_var=x_var, color_vec=lineColors, color_idx=2, lty=3
                , title="Non-Smoker")
```




```r
par(mfrow=c(1,1)) # reset
```

Question 8

Run the semiparametric version of ANCOVA but with an interaction.

```r
semi_mod2 <- mgcv::gam(lsbp ~ factor(smoker)*lcholest +
                         s(lcholest, k=23, bs="cr")
                       , data=fram2
#                        , method="REML"
                      )
summary(semi_mod2)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## lsbp ~ factor(smoker) * lcholest + s(lcholest, k = 23, bs = "cr")
##
## Parametric coefficients:
```

```
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 0.3664545  0.0218837  16.746   <2e-16 ***
## factor(smoker)1            -0.0330055  0.3891394  -0.085    0.932
## lcholest                    0.7444406  0.0044560 167.063   <2e-16 ***
## factor(smoker)1:lcholest -0.0009226  0.0718517  -0.013    0.990
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df     F p-value
## s(lcholest) 1.015  1.091 94.01  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Rank: 25/26
## R-sq.(adj) =  0.0186   Deviance explained = 2.05%
## GCV = 0.044542  Scale est. = 0.044429  n = 1615
```

From the above results, it does appear that there is an interaction present between *smoker* and *lcholest*. While the p-value for the interaction term itself is not anywhere close to indicating significance, the coefficient for the *smoker* factor is no longer significant, which was more in line with my prior expectations.

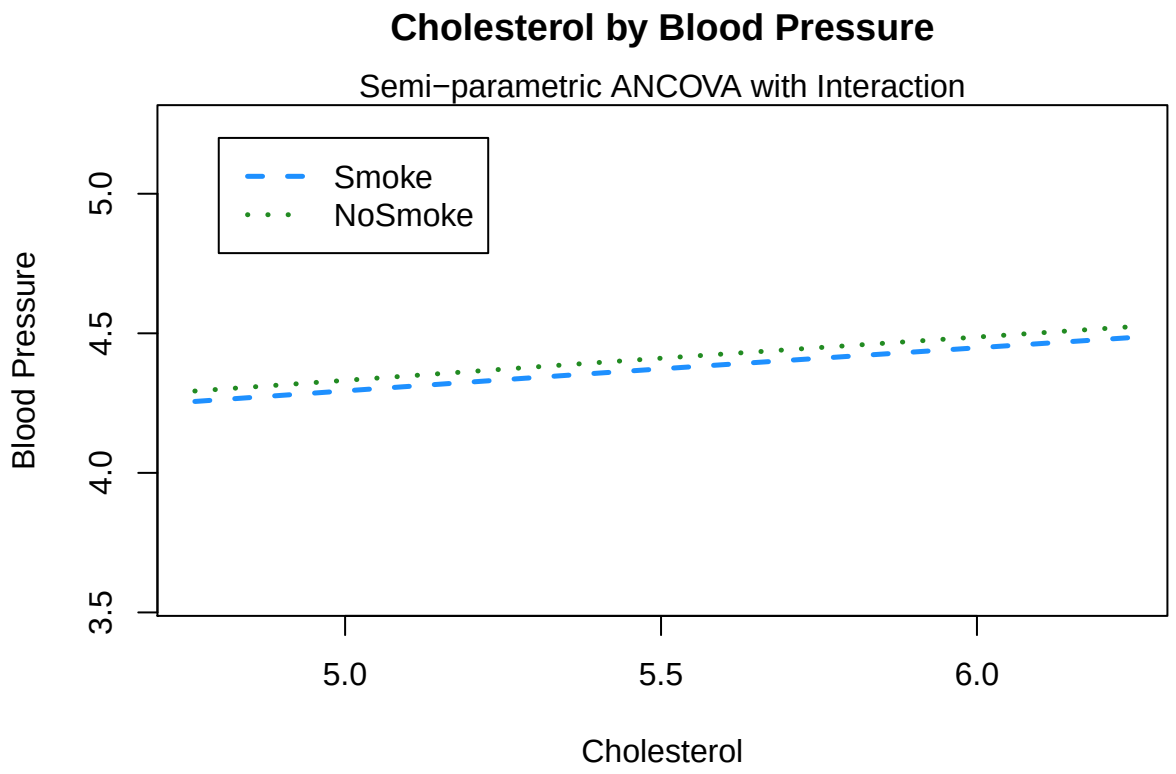
Question 9

Display the fits of the above regressions, but without the data points.

```
ng <- 1000
x_vec <- seq(from=min(fram2$lcholest), to=max(fram2$lcholest), len=ng)
fHat_smoke <- predict(semi_mod2, newdata=data.frame(
                      lcholest=x_vec
                      , smoker=rep('1', ng)
                       )
                     )

fHat_nosmoke <- predict(semi_mod2, newdata=data.frame(
                      lcholest=x_vec
                      , smoker=rep('0', ng)
                       )
                     )
```

```
plot(fram2$lcholest, fram2$lsbp, type='n'
     , xlab="Cholesterol"
     , ylab="Blood Pressure"
     , main="Cholesterol by Blood Pressure"
     )
mtext("Semi-parametric ANCOVA with Interaction")

col_vec <- c("dodgerblue", "forestgreen")
lines(x_vec, fHat_smoke, col=col_vec[1], lwd=2.5, lty=2)
lines(x_vec, fHat_nosmoke, col=col_vec[2], lwd=2.5, lty=3)

legend(4.8, 5.2, c("Smoke", "NoSmoke")
       , col=col_vec
       , lwd=rep(2.5, 2)
```

```
      , lty=c(2,3)
    )
```



Question 10

What does the interaction mean in the case when the factors are binary?

When we have a binary factor for our ANCOVA model, this indicates that the interaction term's coefficient is reflecting what happens to our outcome variable for that factor's non-reference class only. In this case, we are seeing the results of *smoker*=1 interacting with *lcholest*.

Question 11

Run an analysis of whether our two regression lines are significantly different.

```
# First, fit the null model - this is run on both the smokers and non-smokers
contrast_mod1 <- mgcv::gam(lsbp ~ s(lcholest), data=fram2)

# indicator of the smoke varible taking positive class
smoke_ind <- as.numeric(fram2$smoker==1)
# now, fit the alternative model
contrast_mod2 <- mgcv::gam(lsbp ~ s(lcholest, smoke_ind), data=fram2)

# run the final test
anova(contrast_mod1, contrast_mod2, test="F")
```

```
## Analysis of Deviance Table
```

```
##
## Model 1: lsbp ~ s(lcholest)
## Model 2: lsbp ~ s(lcholest, smoke_ind)
##   Resid. Df Resid. Dev Df Deviance      F   Pr(>F)
## 1      1613     71.988
## 2      1612     71.579  1  0.40861 9.2021 0.002456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

It appears that there is a significant difference between the two fits, for smoker and non-smoker.

Question 12

Ignore the smokers, and run native code using lme to fit LSBP vs. age.

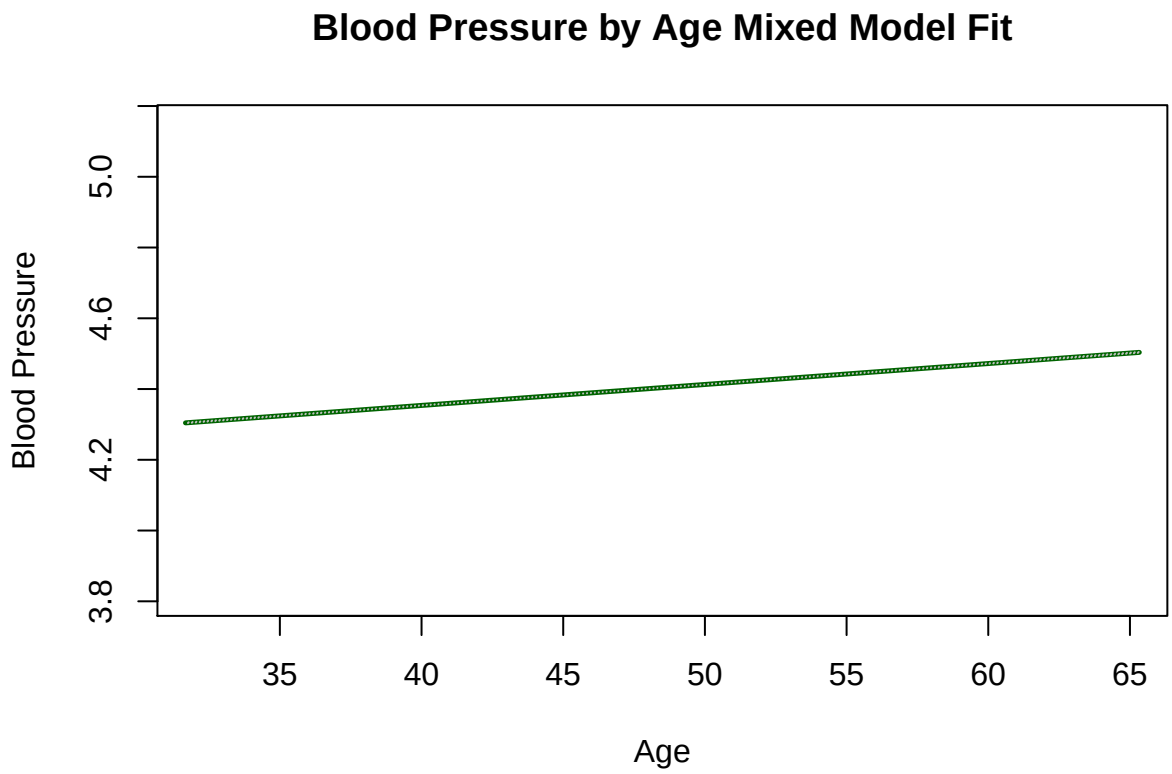
```
fram_ns <- fram2[which(fram2$smoker==0), ]
x <- fram_ns$age
y <- fram_ns$lsbp

numIntKnots <- 23
intKnots <- quantile(unique(x), seq(0, 1, length=numIntKnots+2))[-c(1, numIntKnots+2)]

a <- 1.01 * min(x) - 0.01*max(x)
b <- 1.01 * max(x) - 0.01*min(x)
Z <- HRW::ZOSull(x, range.x=c(a, b), intKnots=intKnots)

dummyID <- factor(rep(1, length(x)))

# prep is finally over - run the model
mm_fit <- nlme::lme(y ~ x, random=list(dummyID=pdIdent(~ -1 + Z)))
```

Question 13

Display the fit without data points. Also provide a confidence band.

```
# extract our model coefficients
betaHat <- mm_fit$coefficients$fixed
uHat <- unlist(mm_fit$coefficients$random)
# create plotting parameters
ng <- 1001
xg <- seq(a, b, length.out=ng)
Xg <- cbind(rep(1, ng), xg)
Zg <- HRW::ZOSull(xg, range.x=c(a,b), intKnots=intKnots)
fHatg <- as.vector(Xg %*% betaHat + Zg %*% uHat)
plot(x, y, type='n'
     , xlab="Age"
     , ylab="Blood Pressure"
     , main='Blood Pressure by Age Mixed Model Fit'
     )
# plot the main line
lines(xg, fHatg, col="darkgreen", lwd=2.5)
```

```
# grab the standard error estimates
se_pred <- diag(Xg %*% mm_fit$varFix %*% t(Xg))
SE <- sqrt(se_pred)
# lower and upper bounds
upper <- fHatg + (1.96 * se_pred)
lower <- fHatg - (1.96 * se_pred)
# plot the confidence polygons
polygon(x=c(xg,rev(xg))
      , y=c(upper
      , rev(lower))
      , col="gray"
      , border=NA
      , density=75
      )
```



Pointwise 95% confidence interval is there, but very narrow and difficult to see.

Question 14

Is the fit of our mixed model statistically significant?

```
anova(mm_fit)
```

```
##             numDF denDF   F-value p-value
## (Intercept)     1   365 151345.51  <.0001
## x               1   365     22.13  <.0001
```

The F-test indicates that the fit of our model is significant.

Question 15

Test whether the fit is linear or quadratic vs. the need to do a semiparametric fit.

```
mm_fit <- nlme::lme(y ~ x, random=list(dummyID=pdIdent(~ -1 + Z)))
lin_fit <- lm(y ~ x)
quad_fit <- lm(y ~ x + x**2)
# conduct main test
anova(mm_fit, lin_fit, quad_fit)
```

```
##          Model df      AIC       BIC   logLik   Test      L.Ratio p-value
## mm_fit       1  4 -56.9505 -41.35091 32.47525
## lin_fit      2  3 -58.9505 -47.25080 32.47525 1 vs 2 9.982959e-08  0.9997
## quad_fit     3  3 -58.9505 -47.25080 32.47525
```

It does not appear that there is any statistical difference between the linear fit, quadratic fit, or the mixed_model semiparametric fit.