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))
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 a 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 to 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 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 add in 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)
```

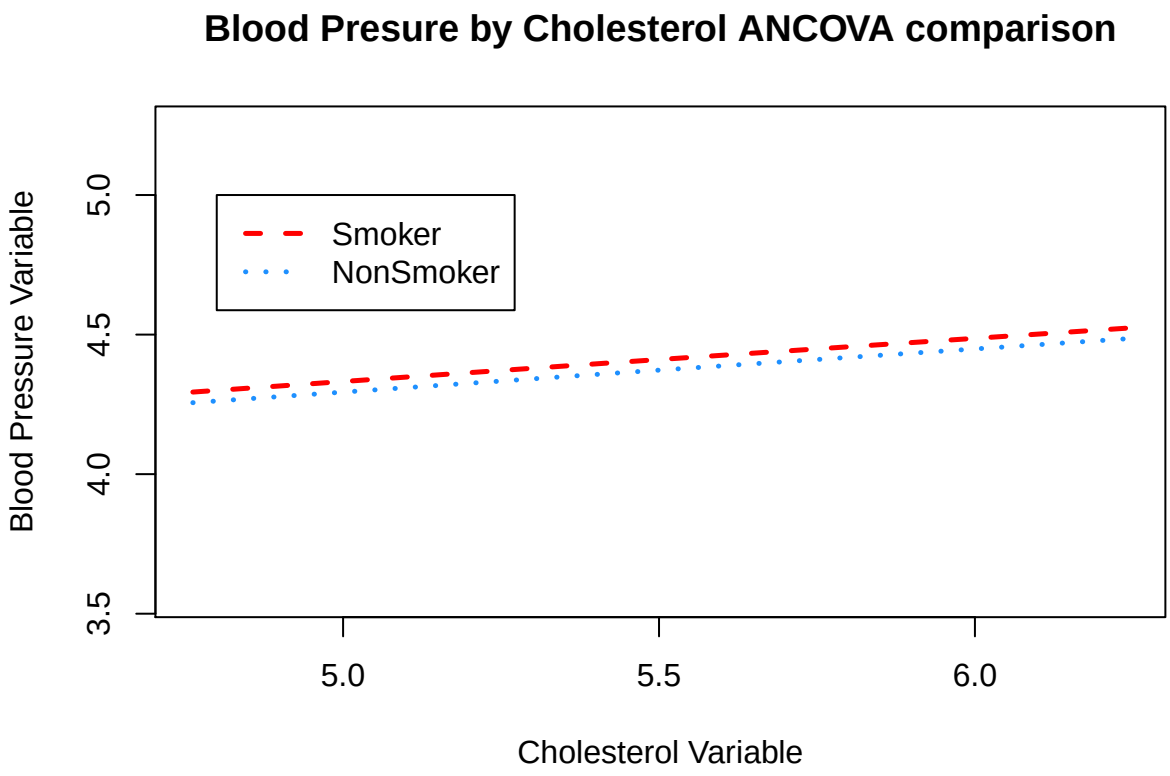
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## lsbp ~ factor(smoker) + s(lcholest, k = 23, bs = "cr")
##
## Parametric coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.39713    0.01100 399.735  < 2e-16 ***
## factor(smoker)1 -0.03799    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

x_var <- seq(from=min(fram2$lcholest)
             , to=max(fram2$lcholest)
             , len=1000
             )
f_hat_smoker <- predict(semi_mod
                        , newdata=data.frame(
                         smoker=rep('0', 1000)
                         , lcholest=x_var
                        )
                        )

f_hat_nosmoke <- predict(semi_mod
                         , newdata=data.frame(
                            smoker=rep('1', 1000)
                            , lcholest=x_var
                          )
                         )
```

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

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

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

Skipping for now

Question 8

Run the semiparametric version of ANCOVA but with an interaction.

```
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
```

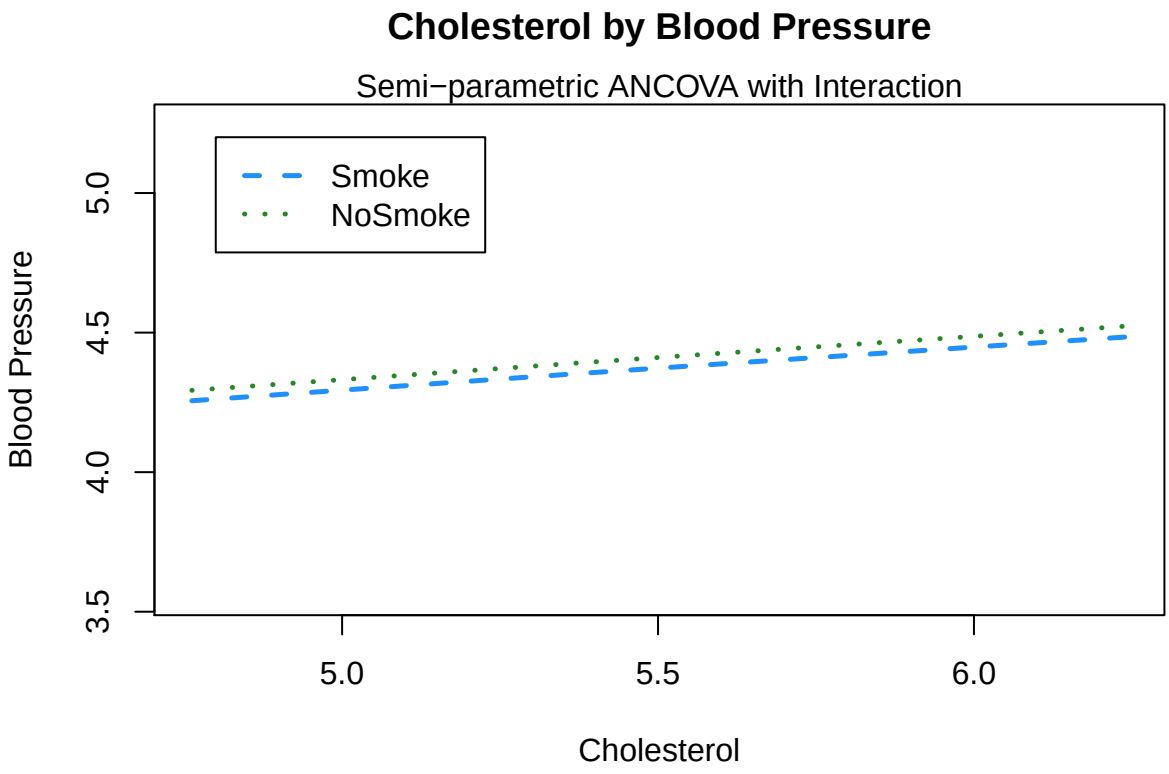
From the above results, it does not appear that there is any sort of interaction present, as the p-value on the interaction term between *smoker* and *lcholest* is not significant.

Question 9

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

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

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

```
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.

Question 11

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

```
# First, fit the null model
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)

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

Run native code using lme to fit LSBP vs. age

```
#mixed_mod <- nlme::lme(fixed=lsbp ~ age, data=fram2)
```

```
#summary(fram2)
```