

Using OCT Biomarkers to Predict Visual Acuity after One Year of VEGF Therapy

Brian Dang and Ethan Mai

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```
AMD <- as.data.frame(read.csv("~/Downloads/dataframev2.csv", header = TRUE, stringsAsFactors = FALSE))
library(ggplot2)
library(GGally)
library(knitr)
library(car)
library(MASS)
library(lmtest)
```

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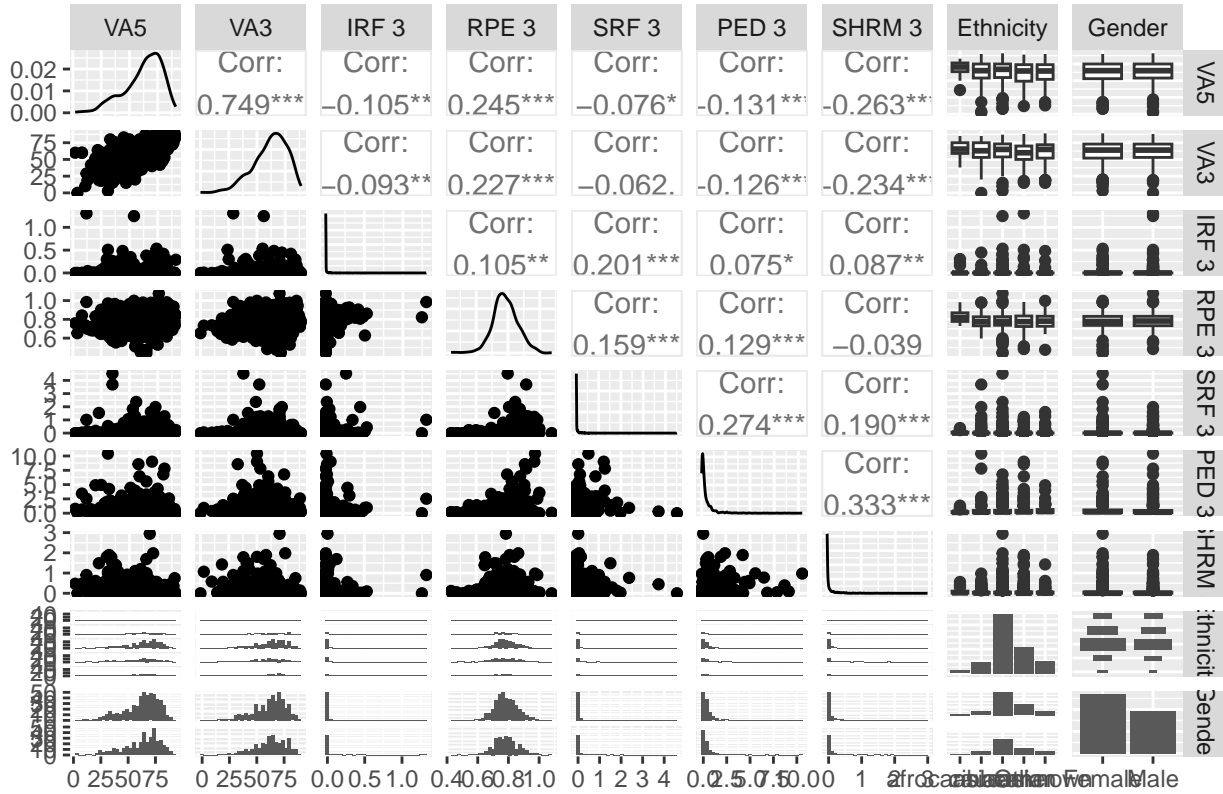
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Note that appropriate data transformations were applied after looking at initial model fits (i.e. transformations were applied in the ‘Model 2’ and ‘Model 3’ sections).

1. Model 1

```
ggpairs(AMD, columns = c(10,8,13,18,23,28,33,3,5), columnLabels = c("VA5", "VA3", "IRF 3", "RPE 3", "SRF 3"))
```

Fig 1. Pairs plot of our untransformed response and predictors



```
model1 <- lm(va3~vol_irf3 + vol_rpe3 + vol_srf3+ vol_ped3+vol_shrm3 + ethnicity+gender, data = AMD)

tab_1 <- data.frame(round(summary(model1)$coefficients,4))
kable(tab_1, caption = "OLS Coefficient Estimates for Model 1, $adj R^2=0.1149$", col.names = c("Estimate", "Std. Error", "t value", "P(>|t|)"))
```

Table 1: OLS Coefficient Estimates for Model 1, $adjR^2 = 0.1149$

| | Estimate | Std. Error | t value | P(> t) |
|--------------------|----------|------------|---------|---------|
| (Intercept) | 30.0106 | 5.7460 | 5.2229 | 0.0000 |
| vol_irf3 | -18.1565 | 6.1956 | -2.9306 | 0.0035 |
| vol_rpe3 | 45.6047 | 6.0287 | 7.5646 | 0.0000 |
| vol_srf3 | -1.4079 | 1.7843 | -0.7890 | 0.4303 |
| vol_ped3 | -1.2780 | 0.5620 | -2.2739 | 0.0232 |
| vol_shrm3 | -11.0385 | 2.0284 | -5.4420 | 0.0000 |
| ethnicityasian | -2.2534 | 3.2704 | -0.6890 | 0.4910 |
| ethnicitycaucasian | -1.4482 | 2.9783 | -0.4863 | 0.6269 |
| ethnicityOther | -3.9451 | 3.0666 | -1.2865 | 0.1986 |
| ethnicityunknown | -2.9883 | 3.2381 | -0.9229 | 0.3563 |
| genderMale | 0.4665 | 0.9505 | 0.4908 | 0.6237 |

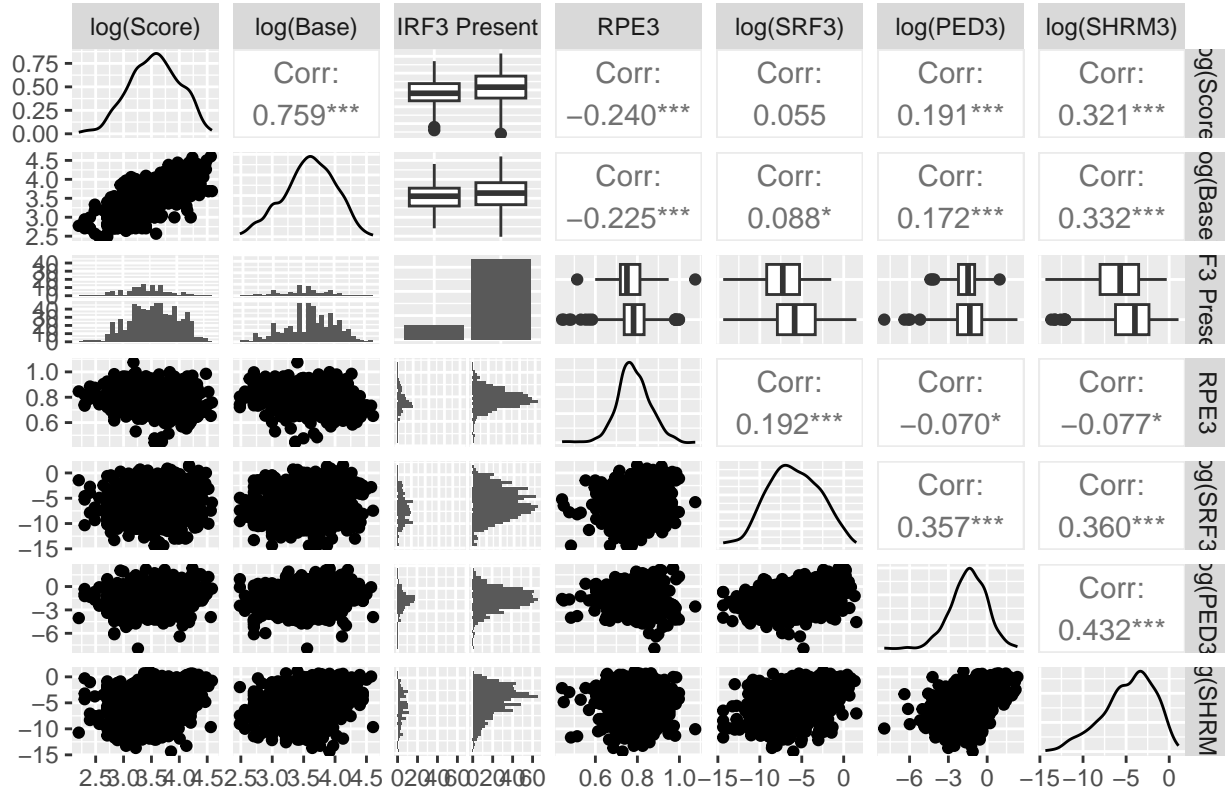
2. Model 2

```
AMD$score <- 100-AMD$va5
AMD$base <-100-AMD$va3
AMD <- transform(AMD, lscore = log(score), lbase=log(base), lsrf3=log(vol_srf3),lped3=log(vol_ped3), lshrm3=log(vol_shrm3))
```

```
ind <- which(AMD$vol_srf3 < 0.0000001)
AMD.sub <- AMD[-ind,]
ind2<- which(AMD.sub$vol_shrm3 < 0.0000001)
AMD.sub <- AMD.sub[-ind2,]
AMD.sub$irf3 <- factor(ifelse(AMD.sub$vol_irf3 < 0.0000001, "No", "Yes"))
model2 <- lm(lscore~ lbase+as.factor(irf3) + vol_rpe3 + lsrf3+ lped3+lshrm3,data = AMD.sub)

ggpairs(AMD.sub, columns = c(44,45,49,18,46,47,48), columnLabels = c("log(Score)", "log(Base)", "IRF3 Present", "RPE3", "log(SRF3)", "log(PED3)", "log(SHRM3)"), rowLabels = c("log(Score)", "log(Base)", "IRF3 Present", "RPE3", "log(SRF3)", "log(PED3)", "log(SHRM3)"), diag = "density", lower = "points", upper = "correlation")
```

Fig 2. Pairs plot of our transformed response and predictors



```
tab_2 <- data.frame(round(summary(model2)$coefficients,4))
kable(tab_2, caption = "OLS Coefficient Estimates for Model 2, $adj R^2=0.5907$", col.names = c("Estimate", "Std. Error", "t value", "P(>|t|)"))
```

Table 2: OLS Coefficient Estimates for Model 2, $adjR^2 = 0.5907$

| | Estimate | Std. Error | t value | P(> t) |
|--------------------|----------|------------|---------|---------|
| (Intercept) | 1.0103 | 0.1660 | 6.0847 | 0.0000 |
| lbase | 0.7793 | 0.0271 | 28.7220 | 0.0000 |
| as.factor(irf3)Yes | 0.0866 | 0.0289 | 3.0009 | 0.0028 |
| vol_rpe3 | -0.3861 | 0.1358 | -2.8437 | 0.0046 |
| lsrf3 | -0.0067 | 0.0038 | -1.7364 | 0.0829 |
| lped3 | 0.0161 | 0.0085 | 1.8918 | 0.0589 |
| lshrm3 | 0.0093 | 0.0041 | 2.2431 | 0.0252 |

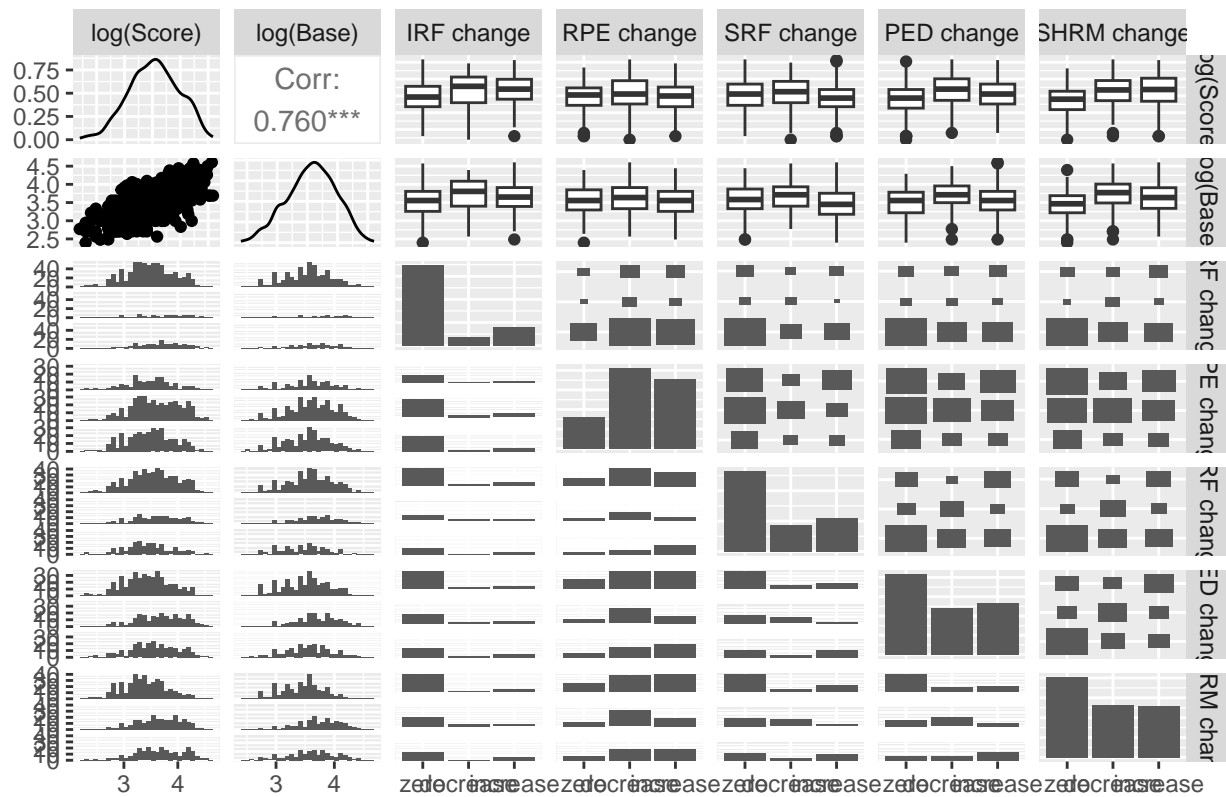
3. Model 3 (Final Model):

```
AMD$irf_change <- round(AMD$vol_irf5-AMD$vol_irf3,4)
AMD$rpe_change <- round(AMD$vol_rpe5-AMD$vol_rpe3,4)
AMD$srf_change <- round(AMD$vol_srf5-AMD$vol_srf3,4)
AMD$ped_change <- round(AMD$vol_ped5-AMD$vol_ped3,4)
AMD$shrm_change <- round(AMD$vol_shrm5-AMD$vol_shrm3,4)

AMD$irfcat <-cut(AMD$irf_change, breaks = c(-Inf,-.005,.005,Inf), labels = c("decrease","zero","increase"))
AMD$rpecat <-cut(AMD$rpe_change, breaks = c(-Inf,-.01,.01,Inf), labels = c("decrease","zero","increase"))
AMD$srfcat <-cut(AMD$srf_change, breaks = c(-Inf,-.01,.01,Inf), labels = c("decrease","zero","increase"))
AMD$pedcat <-cut(AMD$ped_change, breaks = c(-Inf,-.05,.05,Inf), labels = c("decrease","zero","increase"))
AMD$shrmcat <-cut(AMD$shrm_change, breaks = c(-Inf,-.005,.005,Inf), labels = c("decrease","zero","increase"))
AMD$irfcat<- relevel(AMD$irfcat,"zero")
AMD$rpecat<- relevel(AMD$rpecat,"zero")
AMD$srfcat<- relevel(AMD$srfcat,"zero")
AMD$pedcat<- relevel(AMD$pedcat,"zero")
AMD$shrmcat<- relevel(AMD$shrmcat,"zero")

ggpairs(AMD, columns = c(44,45,54,55,56,57,58), columnLabels = c("log(Score)", "log(Base)", "IRF change", "RPE change", "SRF change", "PED change", "SHRM change"))
```

Fig 3 Pairs plot of our response and predictors after factorizing the OCT biomarkers



```
model3 <- lm(lscore~lbase+irfcat+rpecat+srfcat+pedcat+shrmcat,data = AMD)
tab_3 <- data.frame(round(summary(model3)$coefficients,4))
kable(tab_3, caption = "OLS Coefficient Estimates for Model 3, $adj R^2=0.6076$", col.names = c("Estimate", "Std. Error", "t value", "Pr(>|t|)"))
```

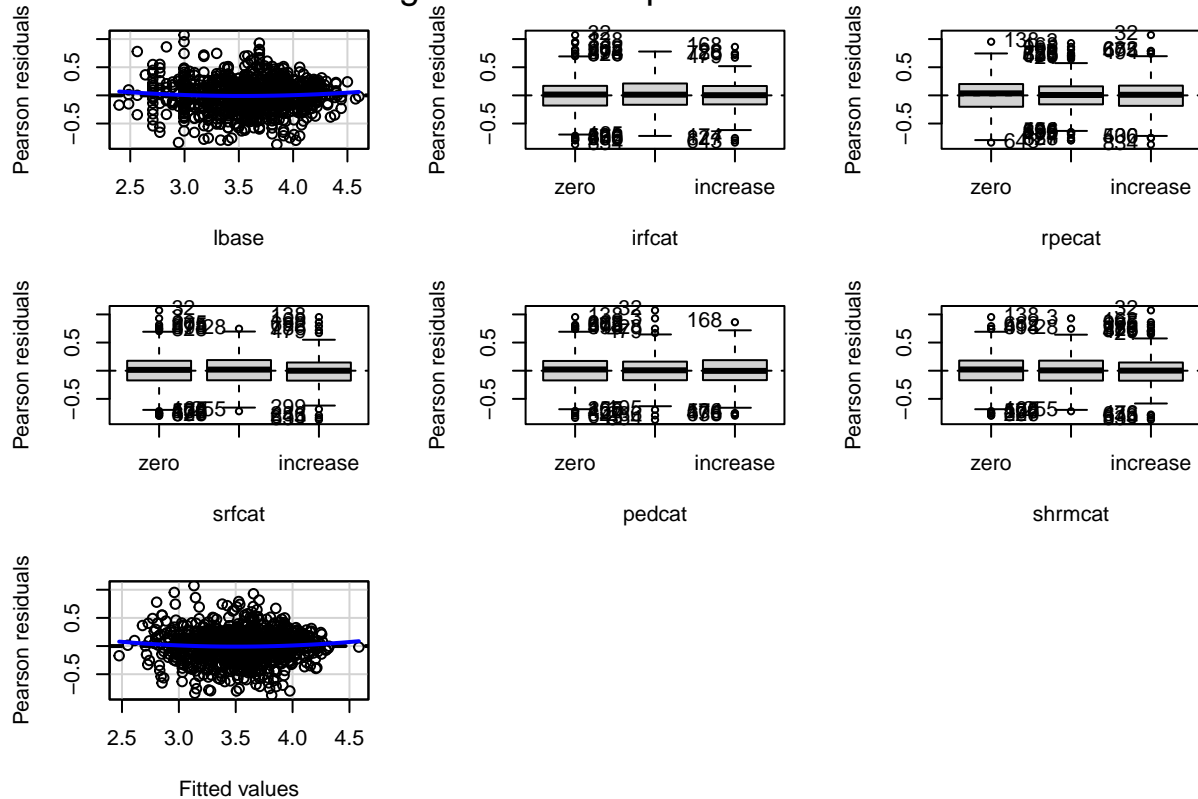
Table 3: OLS Coefficient Estimates for Model 3, $adjR^2 = 0.6076$

| | Estimate | Std. Error | t value | P(> t) |
|------------------|----------|------------|---------|---------|
| (Intercept) | 0.5404 | 0.0879 | 6.1495 | 0.0000 |
| lbase | 0.8107 | 0.0245 | 33.1292 | 0.0000 |
| irfcatsdecrease | 0.0673 | 0.0350 | 1.9219 | 0.0549 |
| irfcatsincrease | 0.1096 | 0.0253 | 4.3259 | 0.0000 |
| rpecatsdecrease | 0.0621 | 0.0261 | 2.3794 | 0.0175 |
| rpecatsincrease | 0.0048 | 0.0266 | 0.1809 | 0.8565 |
| srfcatsdecrease | -0.0654 | 0.0261 | -2.5118 | 0.0122 |
| srfcatsincrease | -0.0094 | 0.0239 | -0.3932 | 0.6942 |
| pedcatsdecrease | 0.0463 | 0.0244 | 1.8943 | 0.0585 |
| pedcatsincrease | 0.0339 | 0.0236 | 1.4348 | 0.1517 |
| shrmcatsdecrease | 0.0166 | 0.0252 | 0.6605 | 0.5091 |
| shrmcatsincrease | 0.1126 | 0.0244 | 4.6225 | 0.0000 |

4. Model Diagnostics on Model 3

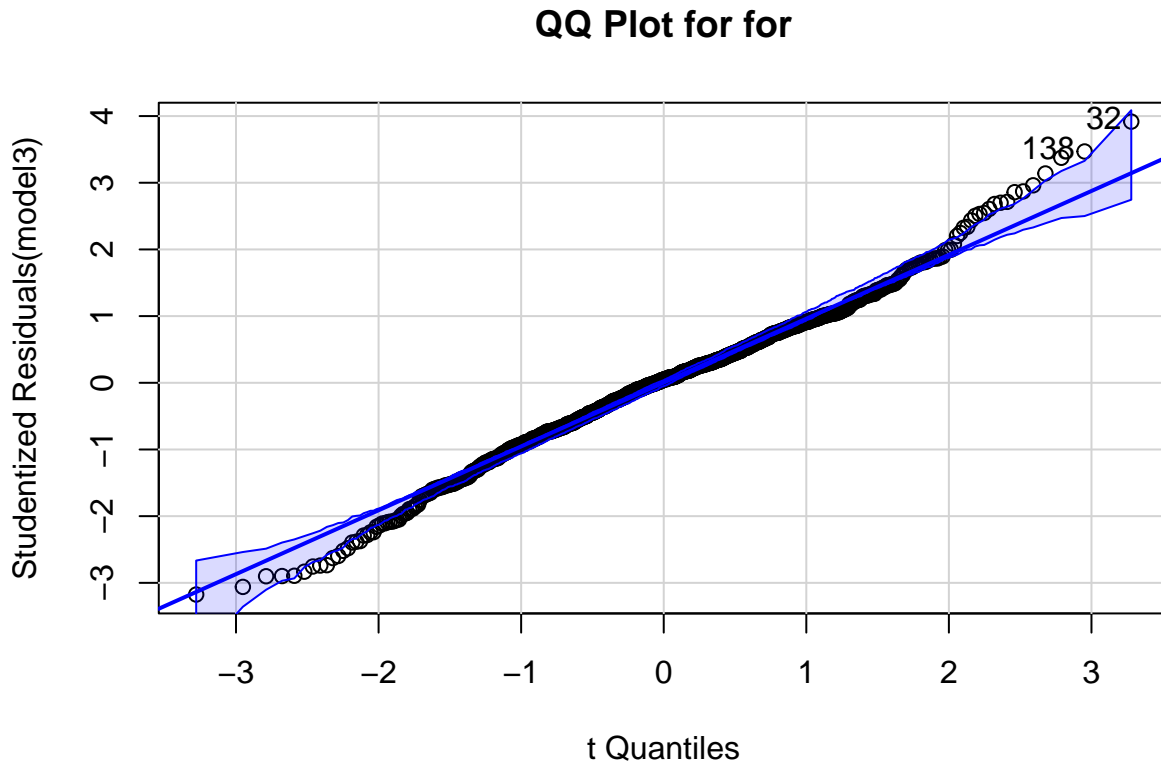
```
residualPlots(model3,main="Fig 4. Residuals plot of Model 3")
```

Fig 4. Residuals plot of Model 3



```
##          Test stat Pr(>|Test stat|)
## lbase          1.3768          0.1689
## irfcats
## rpecats
## srfcats
## pedcats
```

```
## shrmcat
## Tukey test      1.4106      0.1584
qqPlot(model3,main = "QQ Plot for for")
```



```
## [1] 32 138
ncvTest(model3)

## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 9.647212, Df = 1, p = 0.0018964
```

5. ANOVA

```
model31 <- lm(lscore~lbase,data = AMD)
anova(model31,model3)

## Analysis of Variance Table
##
## Model 1: lscore ~ lbase
## Model 2: lscore ~ lbase + irfcats + rpecats + srfcats + pedcats + shrmcats
##   Res.Df    RSS Df Sum of Sq    F    Pr(>F)
## 1     924 76.920
## 2     914 70.645 10     6.2748 8.1183 1.174e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Anova(model3)

## Anova Table (Type II tests)
```

```
##
## Response: lscore
##          Sum Sq Df    F value    Pr(>F)
## lbase      84.832  1 1097.5448 < 2.2e-16 ***
## irfcat      1.577  2   10.2009 4.155e-05 ***
## rpecat      0.746  2    4.8277 0.00821 **
## srfcats     0.488  2    3.1595 0.04291 *
## pedcat      0.326  2    2.1066 0.12224
## shrmcat     1.824  2   11.7965 8.747e-06 ***
## Residuals 70.645 914
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6. Variable Selection

```
stepAIC(model3, direction = "backward")
```

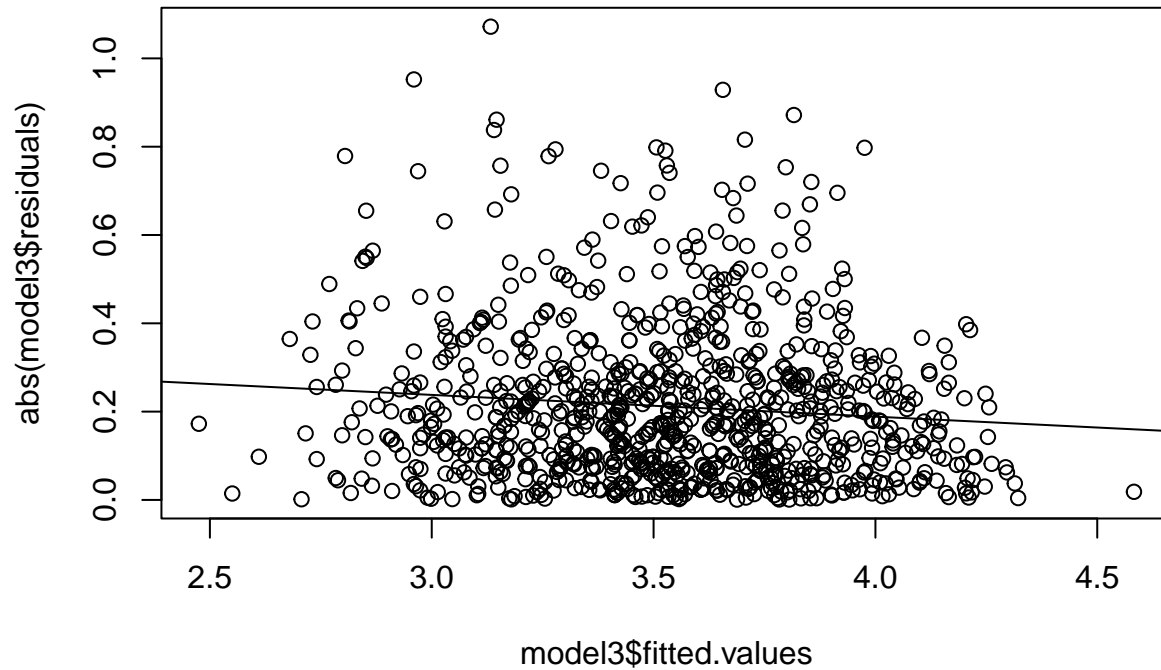
```
## Start:  AIC=-2358.79
## lscore ~ lbase + irfcat + rpecat + srfcats + pedcat + shrmcat
##
##          Df Sum of Sq    RSS    AIC
## <none>                70.645 -2358.8
## - pedcat    2      0.326  70.971 -2358.5
## - srfcats   2      0.488  71.134 -2356.4
## - rpecat    2      0.746  71.391 -2353.1
## - irfcat    2      1.577  72.222 -2342.3
## - shrmcat   2      1.824  72.469 -2339.2
## - lbase     1     84.832 155.477 -1630.3
##
## Call:
## lm(formula = lscore ~ lbase + irfcat + rpecat + srfcats + pedcat +
##     shrmcat, data = AMD)
##
## Coefficients:
##      (Intercept)          lbase  irfcatdecrease  irfcatincrease
##      0.540425      0.810726      0.067257      0.109575
##  rpecatdecrease  rpecatincrease  srfcatsdecrease  srfcatincrease
##      0.062142      0.004817     -0.065444     -0.009389
##  pedcatdecrease  pedcatincrease  shrmcatsdecrease  shrmcatincrease
##      0.046310      0.033859      0.016629      0.112622
```

7. Addressing Heteroscedasticity

7.a. Weighted Least Squares

7.b. Choosing Weights

```
emodel<- lm(abs(model3$residuals)~model3$fitted.values)
plot(abs(model3$residuals) ~ model3$fitted.values)
abline(emodel)
```



7.c. Fitting WLS

```
wt <- 1/emodel$fitted.values^2
wmodel3 <- lm(log(score)~log(base)+irfcats+rpecats+srfcats+pedcats+shrmcats,data = AMD,weights = wt)
tab_3w <- data.frame(round(summary(wmodel3)$coefficients,4))
kable(tab_3w, caption = "Weighted Least Squares Estimates for Model 3", col.names = c("Estimate","Std. Error","t value","P(>|t|)"))
```

Table 4: Weighted Least Squares Estimates for Model 3

| | Estimate | Std. Error | t value | P(> t) |
|------------------|----------|------------|---------|---------|
| (Intercept) | 0.5222 | 0.0892 | 5.8546 | 0.0000 |
| log(base) | 0.8146 | 0.0246 | 33.1785 | 0.0000 |
| irfcatsdecrease | 0.0699 | 0.0336 | 2.0820 | 0.0376 |
| irfcatsincrease | 0.1060 | 0.0244 | 4.3534 | 0.0000 |
| rpecatsdecrease | 0.0703 | 0.0259 | 2.7167 | 0.0067 |
| rpecatsincrease | 0.0083 | 0.0266 | 0.3101 | 0.7565 |
| srfcatsdecrease | -0.0643 | 0.0253 | -2.5375 | 0.0113 |
| srfcatsincrease | -0.0129 | 0.0238 | -0.5430 | 0.5873 |
| pedcatsdecrease | 0.0488 | 0.0239 | 2.0431 | 0.0413 |
| pedcatsincrease | 0.0330 | 0.0234 | 1.4096 | 0.1590 |
| shrmcatsdecrease | 0.0148 | 0.0249 | 0.5947 | 0.5522 |
| shrmcatsincrease | 0.1143 | 0.0241 | 4.7460 | 0.0000 |

```
ncvTest(wmodel3)
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.01799714, Df = 1, p = 0.89328
```


7.d. Sandwich Estimator

```
model3.sandwich = coeftest(model3,vcov. = hccm(model3, type="hc3"))
sandwich.se = round(sqrt(diag(hccm(model3, type="hc3"))), 4)
coef_est = data.frame(round(cbind(coef(model3),coef(wmodel3),model3.sandwich[,1]),4))
se_est = data.frame(round(cbind(sqrt(diag(vcov(model3))),sqrt(diag(vcov(wmodel3))),sandwich.se),4))
colnames(coef_est) = colnames(se_est) = c("OLS","WLS","Sandwich")
se_est2 = data.frame(round(cbind(sqrt(diag(vcov(model3))),sqrt(diag(vcov(wmodel3)))),4))

kable(se_est2, caption = "Comparison of SE for OLS and WLS estimation for Model 3", col.names = c("OLS"
```

Table 5: Comparison of SE for OLS and WLS estimation for Model 3

| | OLS | WLS |
|------------------|--------|--------|
| (Intercept) | 0.0879 | 0.0892 |
| lbase | 0.0245 | 0.0246 |
| irfcatsdecrease | 0.0350 | 0.0336 |
| irfcatsincrease | 0.0253 | 0.0244 |
| rpecatsdecrease | 0.0261 | 0.0259 |
| rpecatsincrease | 0.0266 | 0.0266 |
| srfcatsdecrease | 0.0261 | 0.0253 |
| srfcatsincrease | 0.0239 | 0.0238 |
| pedcatsdecrease | 0.0244 | 0.0239 |
| pedcatsincrease | 0.0236 | 0.0234 |
| shrmcatsdecrease | 0.0252 | 0.0249 |
| shrmcatsincrease | 0.0244 | 0.0241 |

7.e. Bootstrap

```
set.seed(123)
nboot = 1000
n=nrow(AMD)
dat.boot <- matrix(0,nboot,12)
for (i in 1:nboot){
  indices <- sample(seq(1,n), replace=T)
  m.boot <- lm(log(score)~log(base)+irfcats+rpecats+srfcats+pedcats+shrmcats,data = AMD[indices,])
  dat.boot[i,] <- m.boot$coefficients
}
mean.boot <- round(apply(dat.boot, 2, mean),4)
se.boot<-round(apply(dat.boot, 2, sd),4)
coef_est$Bootstrap = mean.boot
se_est$Bootstrap = se.boot

print(se_est)
```

```
##          OLS      WLS Sandwich Bootstrap
## (Intercept) 0.0879 0.0892  0.0927  0.0922
## lbase       0.0245 0.0246  0.0257  0.0258
## irfcatsdecrease 0.0350 0.0336  0.0344  0.0331
## irfcatsincrease 0.0253 0.0244  0.0260  0.0261
## rpecatsdecrease 0.0261 0.0259  0.0271  0.0264
## rpecatsincrease 0.0266 0.0266  0.0277  0.0271
```

```
## srfcatsdecrease 0.0261 0.0253 0.0263 0.0265
## srfcatsincrease 0.0239 0.0238 0.0244 0.0248
## pedcatsdecrease 0.0244 0.0239 0.0249 0.0246
## pedcatsincrease 0.0236 0.0234 0.0234 0.0228
## shrmcatsdecrease 0.0252 0.0249 0.0244 0.0238
## shrmcatsincrease 0.0244 0.0241 0.0256 0.0264
```

8. Cross Validation

```
k <- 10
n.obs <- nrow(AMD)
random.order <- sample(seq(1,n.obs),n.obs, replace=F)
cv.size <- rep(floor(n.obs/k),k)
cum.size <- c(0, cumsum(cv.size[-length(cv.size)]))
error.reduced <- rep(0,k)
error.full <- rep(0,k)
for (i in 1:k) {
  inds <- (cum.size[i]+1):(cum.size[i]+cv.size[i])
  AMD.subset <- AMD[-random.order[inds],]
  lm.reduced <- lm(lscore ~ log(base), data=AMD.subset)
  lm.full <- lm(lscore~lbase+irfcats+rpecats+srfcats+pedcats+shrmcats,data = AMD.subset)
  test.data <- AMD[random.order[inds],]
  predict.full <- predict.lm(lm.full,test.data)
  error.full[i] <- sqrt(mean((test.data$lscore - predict.full)^2))
  predict.reduced <- predict.lm(lm.reduced,test.data)
  error.reduced[i] <- sqrt(mean((test.data$lscore - predict.reduced)^2))
}

RMSPE.full = mean(error.full)
RMSPE.reduced = mean(error.reduced)
RMSPE.full

## [1] 0.279869
RMSPE.reduced

## [1] 0.2886124
plot(error.full, ylim=c(0,0.4), pch=16,ylab="Prediction Error")
points(error.reduced, col='blue', pch=4) #generally black points are below blue points
abline(h=mean(error.full), lty=2, col='black')
abline(h=mean(error.reduced), lty=3, col='blue')
legend('topright', legend=c('full','reduced'), pch=c(16,4), col=c('black','blue'))
```

