# Project 2: Data Analysis on a Birth Weight Dataset

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# I. Introduction

# II. Data Exploration

# III. Analysis

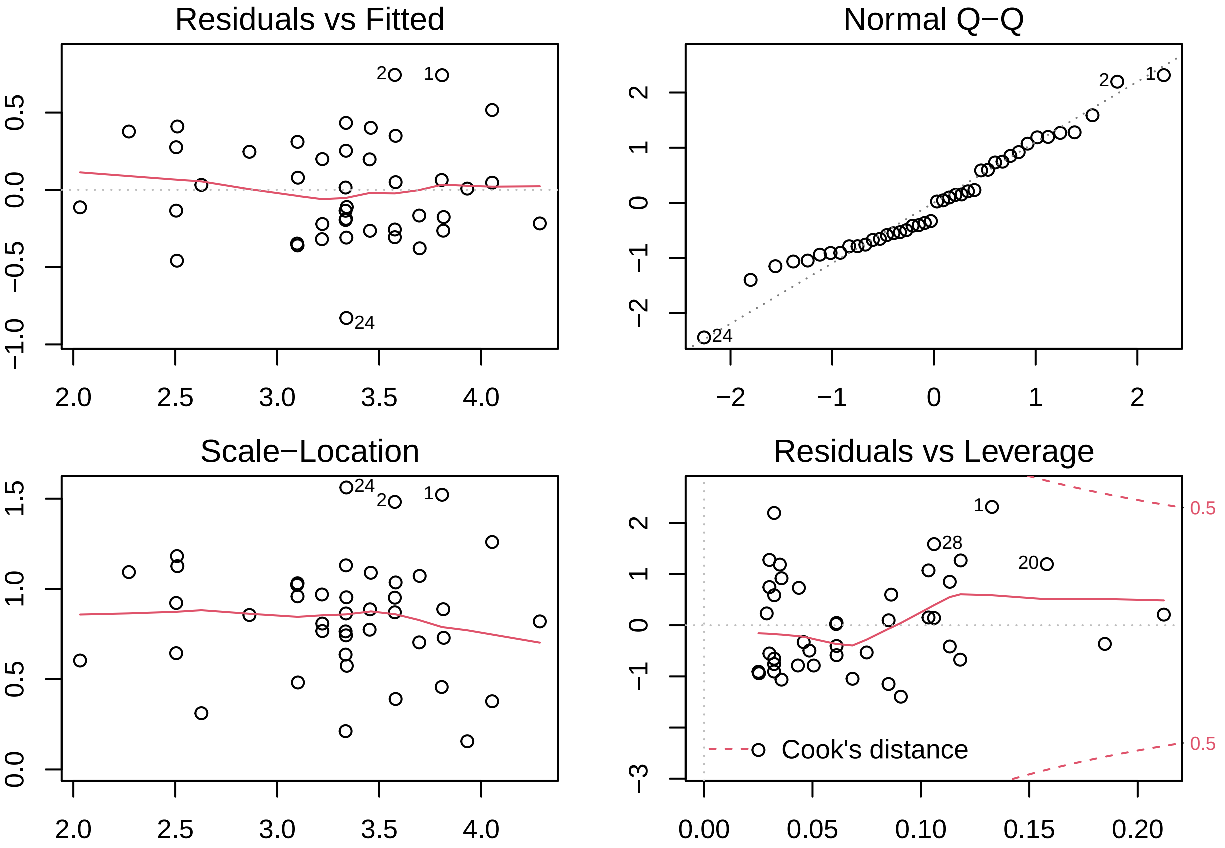
### i. Linear Model Fitting

Multiple linear regression attempts to model the relationship between two or more explanatory variables and a response variable by fitting a linear equation to observed data. In the given data, our response variable is the infant's birth weight and our explanatory variables are factors that supposedly effect birth weight. To get the reduced model, we looked at the full model's coefficients to determine if the predictor variable were significant. If it was significant, we can assume that changes in the predictor variable was significantly associated with changes in birth weight, and therefore its beta coefficient was not 0.

$$\text{Reduced Model: } Y = -5.45\beta_0 + .12\beta_2 + .118\beta_3$$

The reduced model involves the predictor variables: head circumference and gestation period.

After getting the reduced model, we must first check the model assumptions. If we do not check whether the model assumptions are true, it would lead to our model being imprecise due to possible outliers, non-constant variance, and nonlinearity of the outcome.



1) Linearity of Data
   For the Residual vs. Fitted plot, we can assume the linear assumption is reasonable because the line mostly lies on 0 and there are no patterns in the points.

2) Normality of Residuals
Looking the QQ Plot above, although the model seems a little left skewed, because it is relatively straight, we can assume the reduced model is normal. We can also check normality by also conducting a Shapiro-Wilks test. The result is that the p-value = 0.3, and therefore it fails to reject the normality null hypothesis. The reduced model's errors are normal.

3) Homogeneity of Residual Variance
For the Scale-Location plot, the red line is approximately horizontal and the residuals seems to be randomly scattered around the red line. This means that the spread of the residuals is roughly equal at all fitted values. We can assume that homoscedasticity is likely satisfied for the reduced model.

4) Outliers and High Leverage Points
Looking at the Residuals vs. Leverage plot, it highlights the top three extreme points (#1, #20, and #28). The most obvious outlier is point 20 at about 1.5 standard deviations above/below the mean. These outliers are, however, not influential because they are within the Cook's distance lines.

Overall, the reduced model appears to be adequate because it meets the model assumptions.

To test if our reduced model is correct in assuming that certain predictor variables are not significant, we can use the anova function to compare the full model against the reduced model to perform a partial F test.

$$H_0\text{: } \beta_1 = \beta_4 = \beta_5 = \beta_6 = \beta_7 = \beta_8 = \beta_9 = \beta_{10} = \beta_{11} = \beta_{12} = 0$$
$$H_A\text{: } \beta_i \neq 0 \text{ for at least one i}$$

Using the partial F test, the F-statistics is F = 1.236 and the p-value = 0.3106. This p-value is not significant at any $\alpha$ value, and therefore we fail to reject the null hypothesis. We can conclude that the other predictor variables do not statistically contribute significantly to an infant's birth weight. The most statistically significant variables in determining an infant's birth weight are: head circumference and gestation period.

### ii. LDA & MANOVA

We want to test if the two gropus are significantly different using MANOVA, meaning we want to see if $\mu_{smoker} = \mu_{notsmoker}$ for the two mean vectors. In this case the official test is:

$H_0 : \mu_{smoker} = \mu_{notsmoker}$

$H_a : \mu_{smoker} \neq \mu_{notsmoker}$

The mean vectors for each group are:

| smoker | Length | Birthweight | Headcirc | Gestation | mage | mnocig |
|---|---|---|---|---|---|---|
| 0 | 51.80000 | 3.509500 | 35.05000 | 39.45000 | 24.30000 | 0 |
| 1 | 50.90909 | 3.134091 | 34.18182 | 38.95455 | 26.68182 | 18 |

| mheight | mppwt | fage | fedyrs | fnocig | fheight |
|---|---|---|---|---|---|
| 164.4500 | 57.5 | 27.50000 | 13.70000 | 9.7 | 179.7000 |
| 164.4545 | 57.5 | 30.18182 | 13.63636 | 24.0 | 181.2273 |

For the one way MANOVA we can check to see the probability that the smoker variable affects the model. We can calculate 3 different statistics and measure them against their individual F-distributions to test the model.

As seen above, we can reject the null hypothesis for all three tests, thus there is sufficient evidence to indicate a difference among the means for the smoking status.

Because the null hypothesis is rejected, it is of interest to determine what caused the rejection using one way ANOVA. For this we iterate through all of the variables (besides of course our dependent variable "smoker"), and run single factor ANOVA on each. Below are shown the outputs of each one way ANOVA for each.

| | Wilks | Pillai | Roy |
|---|---|---|---|
| statistic | 0.3500588 | 0.6499412 | 1.8566629 |
| approx F | 4.4869352 | 4.4869352 | 4.4869352 |
| num Df | 12.0000000 | 12.0000000 | 12.0000000 |
| den Df | 29.0000000 | 29.0000000 | 29.0000000 |
| Pr(>F) | 0.0004592 | 0.0004592 | 0.0004592 |

| | Df | Sum.Sq | Mean.Sq | F.value | Pr..F. |
|---|---|---|---|---|---|
| Length | 1 | 8.3151515 | 8.3151515 | 0.9640247 | 0.3320766 |
| **Birthweight** | **1** | **1.4764303** | **1.4764303** | **4.3824556** | **0.0426962** |
| Headcirc | 1 | 7.8963203 | 7.8963203 | 1.3839674 | 0.2463803 |
| Gestation | 1 | 2.5716450 | 2.5716450 | 0.3623253 | 0.5506145 |
| mage | 1 | 59.4320346 | 59.4320346 | 1.8912752 | 0.1767120 |
| **mnocig** | **1** | **3394.2857143** | **3394.2857143** | **44.8979592** | **0.0000000** |
| mheight | 1 | 0.0002165 | 0.0002165 | 0.0000050 | 0.9982284 |
| mppwt | 1 | 0.0000000 | 0.0000000 | 0.0000000 | 1.0000000 |
| fage | 1 | 75.3463203 | 75.3463203 | 1.6236045 | 0.2099434 |
| fedyrs | 1 | 0.0424242 | 0.0424242 | 0.0088711 | 0.9254310 |
| **fnocig** | **1** | **2142.2761905** | **2142.2761905** | **8.4506270** | **0.0059251** |
| fheight | 1 | 24.4363636 | 24.4363636 | 0.4956506 | 0.4854961 |

Based on this, we can see that the mother's and father's respective number of cigarettes are likely the primary mean difference that causes the models for smoker and non-smoker to be different in the MANOVA analysis. We can also see that Birthweight has a low p-value, which fits with earlier analysis suggesting that smoking affects birthweight.

For a new child with the following qualities, we want to determine using LDA if the mother was a smoker or not.

| length | birthweight | headcirc | gestation | smoker | motherage | mnocig | mheight | mppwt | fage | fedyrs | fnocig | fheight |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 61 | 5.1 | 36 | 43 | ? | 43 | 7 | 165 | 64 | 38 | 19 | 45 | 189 |

To do this we will calculate with Mahalanobis distance to classify a new observation. We calculate the distance from the centroid of the non-smoker and smoker groups as $D0$ and $D1$ respectively. Whichever value is less is the group that the observation falls closer to. When we do this we see the following:

| D0 | D1 |
|---|---|
| **53.10848** | 64.4205 |

Based on the LDA, we would conclude that the mother is NOT a smoker based on $D0 < D1$, implying that the baby would belong in group 0. This is interesting because mnocig $= 7$ which logically would imply the mother is a smoker, however the baby's birthweight is larger than any other birthweights we have seen in our data. Since we saw in single factor ANOVA that smoking has a strong effect on birthweight, the birthweight being so high is likely what placed the baby in the non-smoker group against intuition. This is an interesting example where we see the shortcomings of LDA in prediction power when faced with an outlier.

# IV. Conclusion

Linear Regression - two most significant variables in predicting birth weight were head circumference and gestation period and this is proven by our partial F test (rest are insignificant); reduced model is good bc we checked the 4 assumptions

MANOVA and LDA -

## Appendix: R Script

```
knitr::opts_chunk$set(echo = F, warning = F, message = F)
library(knitr)
library(dplyr)
library(kableExtra)
smok = read.csv("data/Birthweight_reduced_kg_R.csv")
smok = smok[,2:14]
fmodel = lm(Birthweight ~., data = smok)

#stepwise
#step(fmodel)
#rmodel = lm(Birthweight ~ Headcirc + Gestation + smoker + mppwt,
#data = smok)
#summary(rmodel)

#Under the coefficient method for selecting reduced model, RSE is higher than using the step fcn
summary(fmodel)$coefficient
nmodel = lm(Birthweight ~ Headcirc + Gestation, data = smok)
summary(nmodel)
par(mfrow=c(2,2))
par(mar=c(2, 2, 2, 2))
plot(nmodel)

#normality test
ei <- nmodel$residuals
the.SWtest = shapiro.test(ei)

anova(fmodel,nmodel)
save.means<-aggregate(formula = cbind(Length, Birthweight, Headcirc, Gestation, mage, mnocig, mheight, 

kable(save.means[1:7]) %>% kable_styling(latex_options = "hold_position") %>% row_spec(0,bold=TRUE, bac
kable(save.means[8:13]) %>% kable_styling(latex_options = "hold_position") %>% row_spec(0,bold=TRUE, ba
save = manova(formula = cbind(Length, Birthweight, Headcirc, Gestation, mage, mnocig, mheight, mppwt, f
Wilks = summary(save, test = "Wilks")$stats[1,2:6]
Roy = summary(save, test = "Roy")$stats[1,2:6]
Pillai = summary(save, test = "Pillai")$stats[1,2:6]
names(Wilks) = c("statistic", names(Wilks)[2:5])
names(Pillai) = c("statistic", names(Pillai)[2:5])
names(Roy) = c("statistic", names(Roy)[2:5])
kable(data.frame(Wilks, Pillai, Roy)) %>% kable_styling(latex_options = "hold_position") %>% row_spec(0
df = data.frame()
for(i in 1:13){
  if(i != 5) {
    data = data.frame(smok[,i], smok[,5])
    names(data) = c(names(smok[1,])[i], "smoker")
    mod.fit<-aov(formula = data[,1] ~ smoker, data = data)
    s = summary(mod.fit)
    df = rbind(df, data.frame(s[[1]][1,]))
  }
}
row.names(df) = names(smok[1,])[-5]
df %>% kable() %>% kable_styling(latex_options = "hold_position") %>% row_spec(which(df$Pr..F. < 0.05),
kable(matrix(c(61, 5.1, 36, 43,'?', 43, 7, 165, 64, 38), ncol = 10),  col.names = c("length", "birthwei
kable(matrix(c( 19, 45, 189), ncol = 3), col.names = c("fedyrs", "fnocig", "fheight")) %>% kable_stylin

new_baby = c(61, 5.1, 36, 43, 0, 43, 7, 165, 64, 38, 19, 45, 189)
names(new_baby) = c("length", "birthweight", "headcirc", "gestation", "smoker", "motherage", "mnocig",
obs = as.matrix(new_baby[-5])
pop0<-smok[smok$smoker == 0,-5]
pop1<-smok[smok$smoker == 1,-5]
N0<-nrow(pop0)
N1<-nrow(pop1)
#head(pop1)
sigma.hat0<-cov(pop0)
sigma.hat1<-cov(pop1)
sigma.hat.p<-((N0 - 1)*sigma.hat0 + (N1 - 1)*sigma.hat1)/(N0 + N1 - 2)
mu.hat0<-as.matrix(colMeans(pop0)) #Force it to be an actual column vector
mu.hat1<-as.matrix(colMeans(pop1))
b<-solve(sigma.hat.p) %*% (mu.hat0 - mu.hat1)
k<-0.5*t(mu.hat0 - mu.hat1) %*% solve(sigma.hat.p) %*% (mu.hat0 + mu.hat1)

D0<-t(obs - mu.hat0) %*% solve(sigma.hat.p) %*% (obs - mu.hat0)
D1<-t(obs - mu.hat1) %*% solve(sigma.hat.p) %*% (obs - mu.hat1)
data.frame(D0, D1) %>% kable() %>% kable_styling(latex_options = "hold_position") %>% column_spec(1, bol
```