Babies Birthweight

The file babies.csv contains data on baby birthweights. The variables are:

- bwt - birth weight (in ounces)
- gestation - length of the pregnancy (in days)
- parity - 1 if baby was first born, 0 otherwise
- age - mother's age (in years)
- height - mother's height (in inches)
- weight - mother's weight (in lbs.)
- smoke - 1 if the mother is a smoker, 0 otherwise

```
babyData = read.csv('http://people.hsc.edu/faculty-staff/blins/classes/spring17/mat
h222/data/babies.csv')
head(babyData)
```

```
##   case bwt gestation parity age height weight smoke
## 1    1 120       284      0  27     62    100     0
## 2    2 113       282      0  33     64    135     0
## 3    3 128       279      0  28     64    115     1
## 4    4 123        NA      0  36     69    190     0
## 5    5 108       282      0  23     67    125     1
## 6    6 136       286      0  25     62     93     0
```

```
dim(babyData)
```

```
## [1] 1236    8
```

Cleaning up the data

There are a lot of cells with NA (not available) entries, and these could mess up our analysis below. The `na.omit()` command is a fast way to remove these.

```
babyData = na.omit(babyData)
head(babyData)
```

```
##   case bwt gestation parity age height weight smoke
## 1    1 120       284      0  27     62    100     0
## 2    2 113       282      0  33     64    135     0
## 3    3 128       279      0  28     64    115     1
## 5    5 108       282      0  23     67    125     1
## 6    6 136       286      0  25     62     93     0
## 7    7 138       244      0  33     62    178     0
```

```
dim(babyData)
```

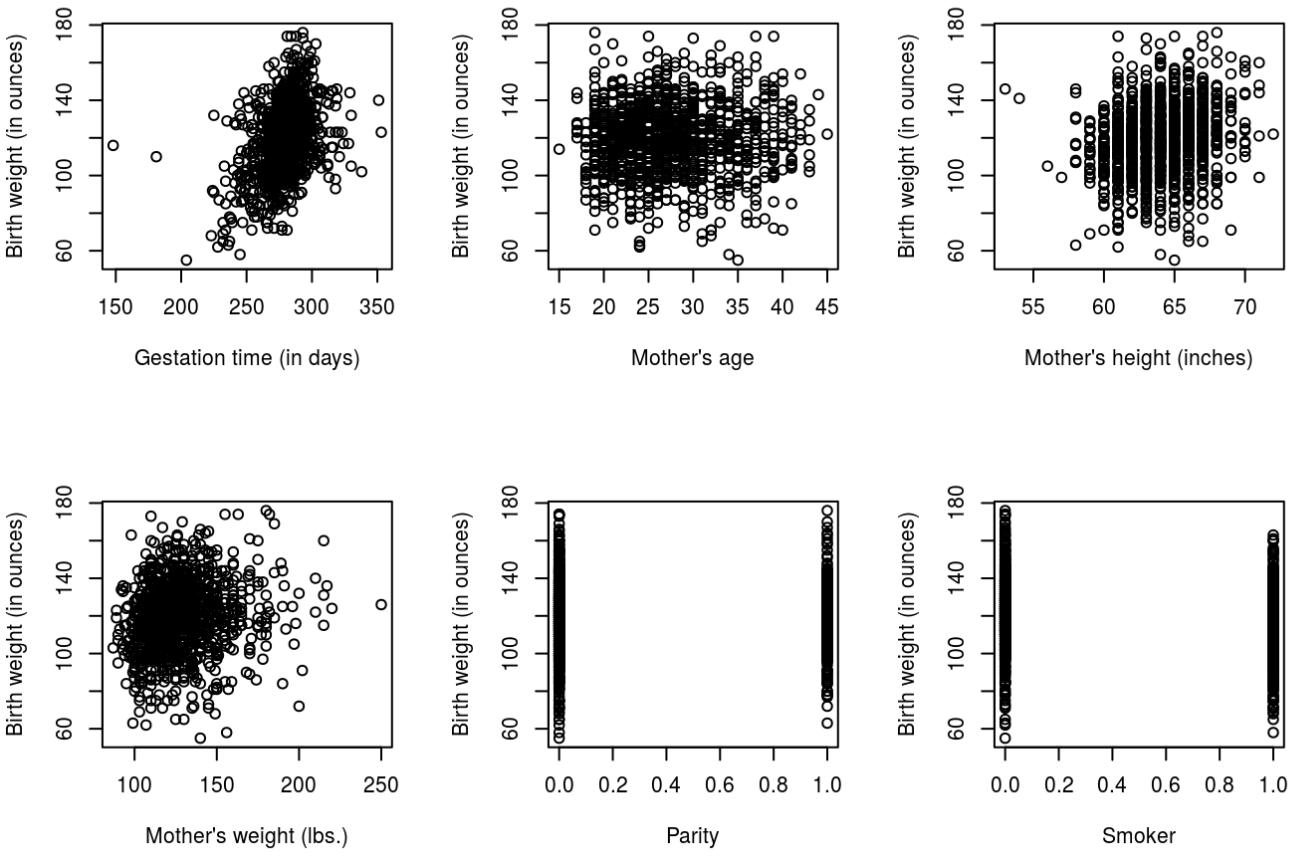
```
## [1] 1174    8
```

Whenever you omit data, you should make sure that you aren't omitting a large percentage of the sample, and you might also want to check the way that the data was collected to make sure that individuals with missing data are not systematically different from other individuals in the sample. In this example, we are omitting 62 rows of data (out of 1236). That's only about 5% of the data, so we probably aren't affecting our results too much.

Checking the linear relationship

We need to check that there is a roughly linear relationship between each of the explanatory variables and the response variable. The `par()` command below lets us arrange the graphs in a 3-by-2 matrix.

```
par(mfrow=c(2,3))
plot(babyData$gestation,babyData$bwt,xlab='Gestation time (in days)',ylab='Birth we
ight (in ounces)')
plot(babyData$age,babyData$bwt,xlab="Mother's age",ylab='Birth weight (in ounces)')
plot(babyData$height,babyData$bwt,xlab="Mother's height (inches)",ylab='Birth weigh
t (in ounces)')
plot(babyData$weight,babyData$bwt,xlab="Mother's weight (lbs.)",ylab='Birth weight
(in ounces)')
plot(babyData$parity,babyData$bwt,xlab="Parity",ylab='Birth weight (in ounces)')
plot(babyData$smoke,babyData$bwt,xlab="Smoker",ylab='Birth weight (in ounces)')
```



There are no major departures from linearity here. Gestation time vs. Birthweight has few outliers with low gestation time, but they aren't a huge concern given the large sample size. Notice that Mother's weight is skewed right, but I'm not sure that making the model more complicated to try to correct the issue is worth the trouble.

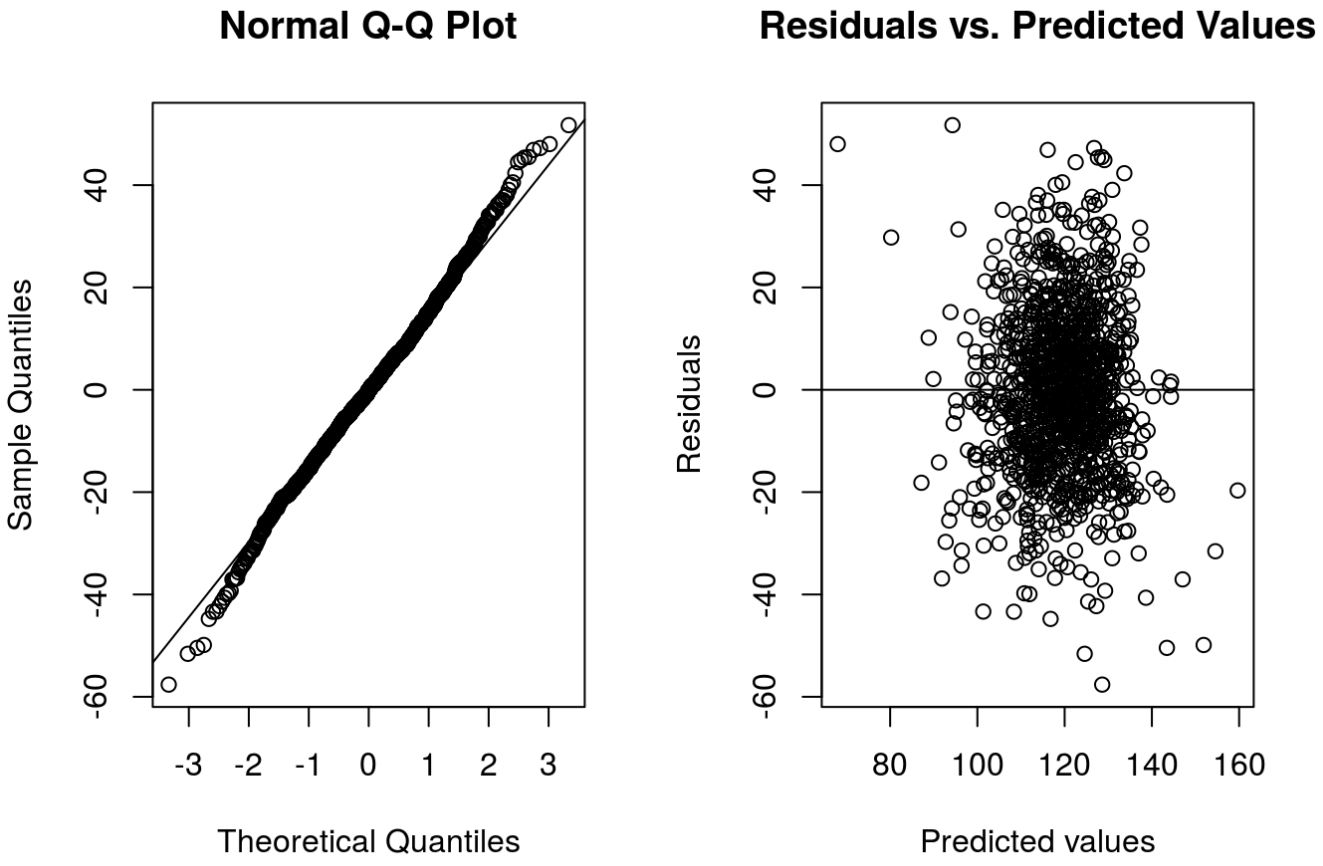
Checking the residuals

Just like in single variable regression, we need to check the residuals to see that they are roughly normally distributed with the same variance. This is much harder to do with so many variables. So here are some of the most important cases to check:

- residuals -vs- predicted values ($\hat{y}$)
- residuals -vs- each explanatory variable
- A normal quantile plot of residuals (to check for normality)

```
myLM = lm(bwt~gestation+age+height+weight+parity+smoke,data=babyData)
```

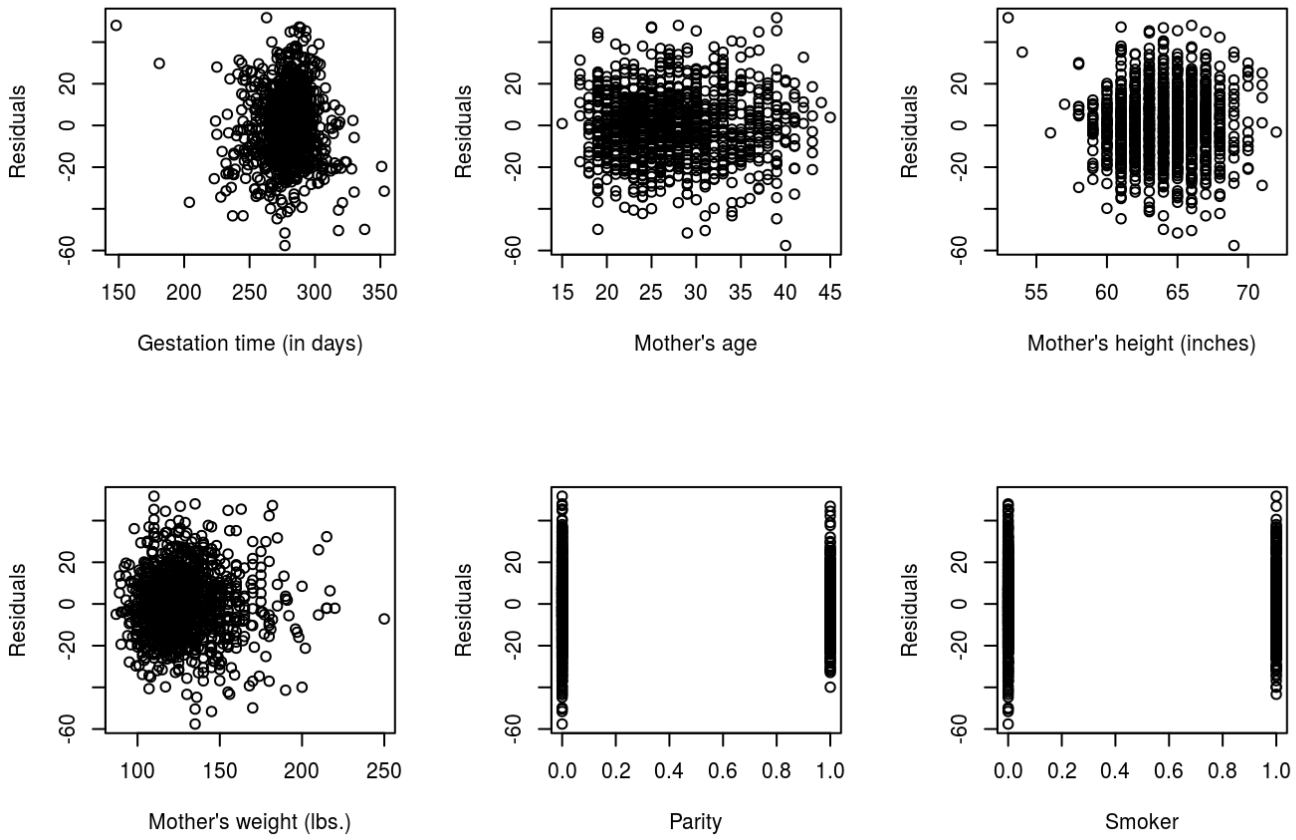
```
par(mfrow=c(1,2))
qqnorm(resid(myLM))
qqline(resid(myLM))
plot(fitted(myLM),resid(myLM),xlab='Predicted values',ylab='Residuals',main='Residuals vs. Predicted Values')
abline(0,0)
```



The residuals aren't perfectly normally distributed, it looks like the tails are too fat. But given the large sample size (over 1000), that probably isn't too big of a problem. In particular, it doesn't look like there is much of a pattern in which residuals or large or small based on the predicted birth weight.

Residuals vs. Each Explanatory Variable

```
par(mfrow=c(2,3))
plot(babyData$gestation,resid(myLM),xlab='Gestation time (in days)',ylab='Residuals
')
plot(babyData$age,resid(myLM),xlab="Mother's age",ylab='Residuals')
plot(babyData$height,resid(myLM),xlab="Mother's height (inches)",ylab='Residuals')
plot(babyData$weight,resid(myLM),xlab="Mother's weight (lbs.)",ylab='Residuals')
plot(babyData$parity,resid(myLM),xlab="Parity",ylab='Residuals')
plot(babyData$smoke,resid(myLM),xlab="Smoker",ylab='Residuals')
```



The residuals mostly seem to have the same variance throughout, there is no clear trend in the scatterplots above.

Inference Results

```
summary(myLM)
```

```
##
## Call:
## lm(formula = bwt ~ gestation + age + height + weight + parity +
##     smoke, data = babyData)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -57.613 -10.189  -0.135   9.683  51.713
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -80.41085   14.34657  -5.605 2.60e-08 ***
## gestation     0.44398    0.02910  15.258  < 2e-16 ***
## age          -0.00895    0.08582  -0.104  0.91696
## height        1.15402    0.20502   5.629 2.27e-08 ***
## weight        0.05017    0.02524   1.987  0.04711 *
## parity       -3.32720    1.12895  -2.947  0.00327 **
## smoke        -8.40073    0.95382  -8.807  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.83 on 1167 degrees of freedom
## Multiple R-squared:  0.258,  Adjusted R-squared:  0.2541
## F-statistic: 67.61 on 6 and 1167 DF,  p-value: < 2.2e-16
```

Choosing the best model

We will now remove variables from the full model to get the model with the best adjusted R-squared.

```
adjustedLM = lm(bwt~gestation+height+weight+parity+smoke,data=babyData)
summary(adjustedLM)
```

```
##
## Call:
## lm(formula = bwt ~ gestation + height + weight + parity + smoke,
##     data = babyData)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -57.716 -10.150  -0.159   9.689  51.620
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -80.71321   14.04465  -5.747 1.16e-08 ***
## gestation     0.44408    0.02907  15.276  < 2e-16 ***
## height        1.15497    0.20473   5.641 2.11e-08 ***
## weight        0.04983    0.02503   1.991  0.04672 *
## parity       -3.28762    1.06281  -3.093  0.00203 **
## smoke        -8.39390    0.95117  -8.825  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.82 on 1168 degrees of freedom
## Multiple R-squared:  0.2579, Adjusted R-squared:  0.2548
## F-statistic:  81.2 on 5 and 1168 DF,  p-value: < 2.2e-16
```

Prediction intervals and confidence intervals for parameters

These work exactly the same as the single variable case.

```
confint(adjustedLM)
```

```
##                     2.5 %       97.5 %
## (Intercept) -1.082688e+02 -53.15765131
## gestation    3.870403e-01   0.50111208
## height       7.532930e-01   1.55664866
## weight       7.247590e-04   0.09894223
## parity      -5.372856e+00  -1.20239124
## smoke       -1.026009e+01  -6.52771691
```

```
predict(adjustedLM,data.frame(gestation = 240,height=70,weight=120,age=25,parity=1,
smoke=0),interval='prediction')
```

```
##        fit      lwr      upr
## 1 109.4054 78.10146 140.7094
```