

1. Executive Summary

2. Introduction

2.1. Background

The economic and social implications of low birth weights (LBW) amongst newborn babies are problematic (Walker *et al.*, 2009). According to the World Health Organisation (2012), LBW is defined as an infant mass of less than 2500 g (up to and including 2499 g) or five pounds 8.2 ounces. Such occurrences can lead to post-natal medical problems and even contribute to lower literacy levels (Walker *et al.*, 2009).

External factors, such as smoking, during pre-natal development have additionally raised concerns in the past. An American study by MacMahon *et al.*, (1965), proposed that cigarette smoke is a key genetic mutagen and can be detrimental to a smoking mother's foetus, resulting in neonatal LBW. This was a profound, yet unappreciated insight into human development. However, from the 786 individual infants in this study, it appeared that smoking lowered infant birthweight but with no subsequent affects to the baby were stated (MacMahon *et al.*, 1965). More recent studies have indicated contradictory views (Lawoyin, 2001; Adegboye *et al.*, 2010). Factors acquired maternally such as genetic endowment, particular medical (for example hypertension, anaemia, UTI), or even socio-cultural practices have indicated various significance in impacting progressive pre-natal development. Lawoyin, (2001) and Adegboye *et al.* (2010) stated that such maternal factors have led to the possibility of infant LBW, birth asphyxia or premature births – all concerns relating to increased infant mortality. Abrevaya (2006) also stated that both social and economic inequality can be detrimentally affected by low birthweights as mothers of a lower socio-economic backgrounds are more at risk of their baby having a low birth weight.

Primary studies have provided identification of key factors that contribute to LBW with aid from numerous retrospective studies. However, many social, economic and biological factors can contribute to lower birth weights, thus it has been difficult to isolate or identify unique factor as more important than others (Makhija *et al.*, 1998; Negi *et al.*, 2006). With large data sets available,

recording both births and information about the mothers health and background, it is important for studies to continue to examine the relationships between various social, economic and biological factors and low birth weights as finding causal factors could help alleviate the social and economic costs of low birth weights (Makhija *et al.*, 1989; Walker *et al.*, 2009). As with similar studies (e.g. Visscher *et al.*, 2003; Abrevaya, 2006) a linear models will most likely be extremely important for attempting to determine causal relationships, thus it is important that potential models are tested and one selected which works best with the variables.

2.2. Aims and Research Questions

Given the importance of understanding and assessing relationships between various social, economic and biological variables and birth weight, this study will use a data set from the Child Health and Development Studies (CHDS) containing such variables to assess relationships. Following initial data exploration for identify interesting relationships between variables, a linear model will be developed to assess potential drivers of low birth weight babies. Model selection tests will determine the best linear model to assess relationships within the data set. This report will provide an insight into the following research question:

What relationships are there between the measured variables and the birth weight of babies?

3. Methodology

All the statistical computing and analysis within this report was performed using the RStudio® V1.2.1335 (R Core Team, 2019). The following additional packages within R were used: dplyr (Wickham *et al.*, 2019), car (Fox and Weisberg, 2019), corrplot (Wei and Simko, 2017), ggplot2 (Wickham, 2016), tidyr (Wickham and Henry, 2019), tidyverse (Wickham, 2017), MuMIn (Barton, 2019), GGally (Schloerke *et al.*, 2018), effects (Fox, 2003), ggpubr (Kassambara, 2019), MLmetrics (Yan, 2016), caret (Kuhn *et al.*, 2019).

3.1. Cleaning the Data

The data set provided by the CHDS was initially checked for inconsistencies such as unknown values. Filtering the data helped to determine the number of unknown values present in the data for each variable. Once identified, unknown values had their values re-assigned to NA.

The way categorical variables had been assigned values within the data set meant that within the categories for variables such as race, for example, that 0-5 all represented white. Therefore, in categorical variables where this occurred, values were merged so that each category only had one value assigned to it. These values in the data set were then re-assigned to the name what they

represented, for example in the variable race, where 0 represented white, this was changed to white; this enabled categorical and numerical variables to be completely separated.

The value for the date was a single number and so the values were changed to standard date format. It was assumed based on the data that 0 was 1st January 1958. In addition, in order to ensure consistency in the units of measurement, all units were converted to kilograms as birth weight had been measured in ounces but the mother and fathers weights were measured in pounds. Finally, the increments for income were changed to increments of 2500 between the values 1 and 9.

3.2. *Exploratory Analysis*

To gain an overview of the data, the summary function was utilised in R which presented a series of summary statistics for each category (R Core Team, 2019). To determine relationships between numerical variables only, a subset of the main data set was created including only such variables. The correlations between the variables within this subset were initially explored by producing a correlation matrix using the corrplot package (Wei and Simko, 2016); correlations which were not significant to a 99% confidence level were excluded. The package ggplot2 (Wickham, 2016) was then used to create various point scatter plots of birth weight against age, height and weight of mother and father and the gestation length. Initially, these variables were plotted against baby weight and the points colour coded based on the categorical variables such as whether or not the mother smoked, the race of father and the race of the mother. Four further plots were then created of the numerical variables against baby weight. The data was filtered further to include plots which showed the number of cigarettes smoked by mums who continued to smoke through pregnancy, mums who had never smoked filtered by their race, the number of cigarettes smoked by mums who smoked until pregnancy and mums who used to smoke but not now colour coded by race.

3.3. *Partitioning the Data*

When developing a linear model, its ability to predict is important (Fushiki, 2012). Therefore, it is important the model is developed and followed by a series of validation tests to determine how accurately the model is at prediction (Kassambara, 2018). Following the method originally proposed by Shao (1993), the entire data set was split into subsets. In this study this was a 20% and an 80% subset based on the number of rows. The 80% subset was used to develop and fit the model and the 20% subset could be used to validate the models predictive abilities (Shao, 1993; Kassambara, 2018).

3.4. Creating the Linear Model

In order to create a suitable linear model to help describe the variables affecting birth weight, two models were created with the 80% subset of the data and two alternative model selection methods used and the best model selected (Benedetti and Brown, 1978; Shao, 1993; Kassambara, 2018).

3.4.1. Model One

Model one was created using the backwards variable elimination method for model selection (Austin, 2008). This involves beginning with a model which includes all variables within the data set and one by one eliminates variables from this starting model until a pre-determined significance level for each variable within the model is reached (Austin, 2008; Brusco and Steinley, 2015). The use of a linear model requires that two fundamental assumptions were met: Linearity and constant variance. A series of diagnostic tests were used to test the assumptions on all the covariates. In all tests, a significance level of 0.05 was used.

A two-tailed ANOVA test was first conducted to determine whether there was a significant difference between the means of the covariates in the model. The test used the following null (H_0) and alternative (H_a) hypotheses:

H_0 : There is no significant difference between the means of the covariables

H_a : There is a significant difference amongst the means of the covariables

To assess the extent of collinearity within the data, which is variables are very highly correlated with one another, a variance inflation factor (VIF) test was conducted to the extent of collinearity within the data. The residuals of the model should ideally be normally distributed. Hence, a Shapiro-Wilk test was conducted. The test had the following H_0 and H_a :

H_0 : The model residuals are normally distributed

H_a : The model residuals are not normally distributed

A non-constant error variance test was then undertaken to measure the spread of the error amongst the residuals as it is assumed in a linear model that the variance amongst the residuals are normally distributed. The test used the following H_0 and H_a :

H_0 : The error variance of the model residuals is constant

H_a : The error variance of the model residuals is not constant

The final test conducted was the Durbin-Watson (DW) test which is a measure of autocorrelation within the residuals. The test used the following H_0 and H_a :

H_0 : The model residuals are uncorrelated

H_a : There is autocorrelation present between the residuals of the model

Following testing the assumptions of the linear model, confidence intervals for the variables were produced and various plots were created to visualise the distribution of the residuals such as QQ-plots, this could be used as a visual support of the assumption tests. Finally, the residual distribution of the covariates and the partial residual distribution per covariate were plotted.

3.4.2. Model Two

Model two was created using the forward model selection method. As with model one, model selection was undertaken on R, where the AIC value was used to select a suitable model. The same assumption testing and diagnostic plots were also undertaken for model two. The difference between the production of model one and model two lies in the use of either the forward or the backwards selection method. The H_0 and H_a were the same for the assumptions tests in model two. In addition, confidence intervals, QQ-plots and residual and partial distribution plots were also produced as with model one.

3.4.3. Selecting the Best Model

Once two models had been developed, it was important to select the model which was best at describing the relationship between birth weight and the other variables within the data set. In R, the AIC value was calculated for each model and this was the basis of selection. The model with the lowest AIC value was chosen as this shows the model has a better fit.

3.5. Model Validation

As previously stated, assessing the models predictive ability is important (Shao, 1993). Model validation tests assess this through determining the prediction error of the model

(Fushiki, 2011). There are a wide array of different validation methods, two were used in this study.

3.5.1. Cross-Validation Set Approach

In this method, the 20% subset is used to validate the data (Kassambara, 2018). The error in the prediction is stated as the root mean square error (RMSE) which can be used to compare the model and chose the model with the lowest RMSE (Kassambara, 2018)

3.5.2. Five-fold Cross-validation

This method involved splitting the data into 5 random subsets which in this case was 20% subsets. Then 80% was used to develop the model and 20% retained to evaluate the model. The model would be rested on one subset and then repeated on each subset which would allow an average prediction error to be calculated (Kassambara, 2018). This method is preferred to many others as it is less computationally intensive and is useful for larger data sets such as the one in the study (Fushiki, 2011).

3.5.3. Selecting the Best Model

Based on the cross-validation tests, the model with the lowest prediction error is typically chosen as this shows it has the greatest predictive ability (Shao, 1993; Ronchetti et al., 2012).

3.6. Bootstrapping

Bootstrapping allows the distribution of the sample population to be determined without making assumptions about the data (Fox, 2002; Reference, ???). This involves repeatedly re-sampling a sample of a specified size using the main data set as a sampling population (Fox, 2002). The re-sampled data is then fitted to the model, this is repeated 1000 times which will give 1000 estimators or the parameters. It is suggested by Efrom and Tibshirani (1993) that 1000 samples is more than satisfactory to provide accurate outputs. Finally, a quantile function will be used to get confidence intervals for 95% (Reference, ???).

4. Results

4.1. *Cleaning the Data*

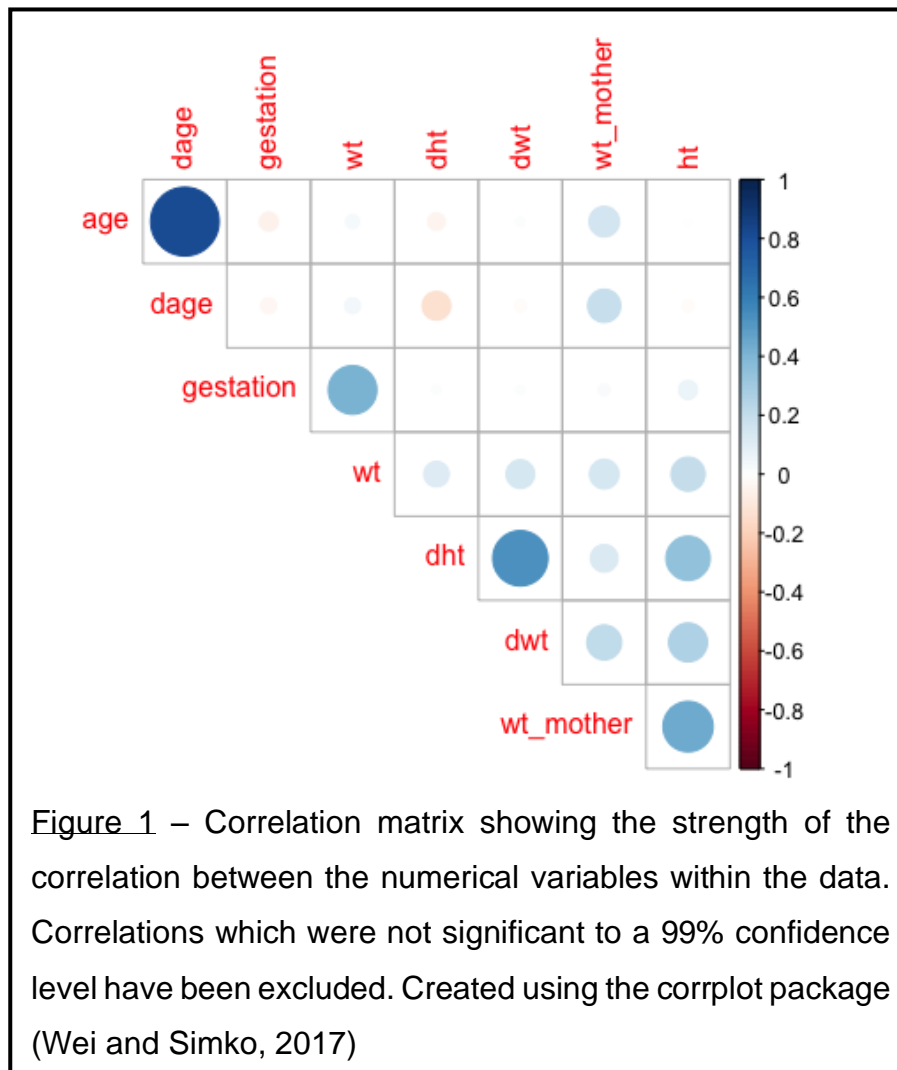
Table 1 presents the number of unknown values for each variable. The majority of variables had very few unknown values. The variables fathers height, fathers weight and income it can be seen all had a much higher frequency of unknown values.

Table 1 – Frequency of unknown values per variable out of a total of 1236 values for each variable

Variable	Unknown Values
Plurality	0
Outcome	0
Date	0
Gestation	13
Sex	0
Birth Weight	0
Parity	0
Mothers Race	13
Mothers Age	2
Mothers Education	1
Mothers Height	22
Mothers Pregnancy Weight	36
Fathers Race	15
Fathers Age	7
Fathers Education	13
Fathers Height	492
Fathers Weight	499
Marital	2
Income	124
Does Mother Smoke	10
If Mother Quite, how long ago?	9
Number of Cigarettes smoked per day	10

4.2. Exploratory Analysis

Figure 1 shows a correlation matrix for the numerical variables. There appears to be very little evidence of correlations between the variables in question. The two strongest relationships present are between the age of the mother and age of the father and the height of the dad and weight of the mother.



Figures 2, 3 and 4 show the 7 numerical variables against baby weight, with the points colour coded based on whether or not the mother smoked, the race of father and the race of the mother respectively. In figures 2, 3 and 4, there are very few relationships evident between the variables and birth weight. The only variable in which there is evidence of a relationship with birth weight is gestation and to a lesser extent the mothers weight. These relationships both appear to be positive with gestation time mothers weight increasing with birth weight. However, this relationship is still relatively weak as there are points spread over a wide area.

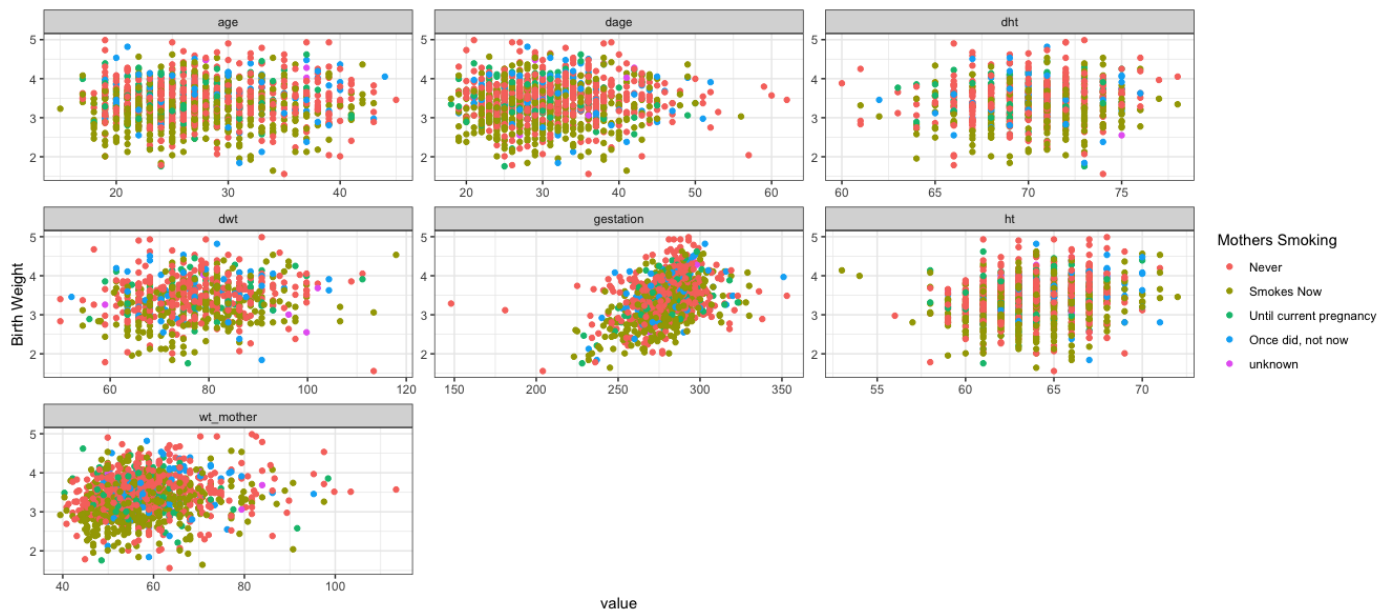


Figure 2 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight). The points are colour coded based on mothers smoking. Figure created using ggplot2 (Wickham, 2016).

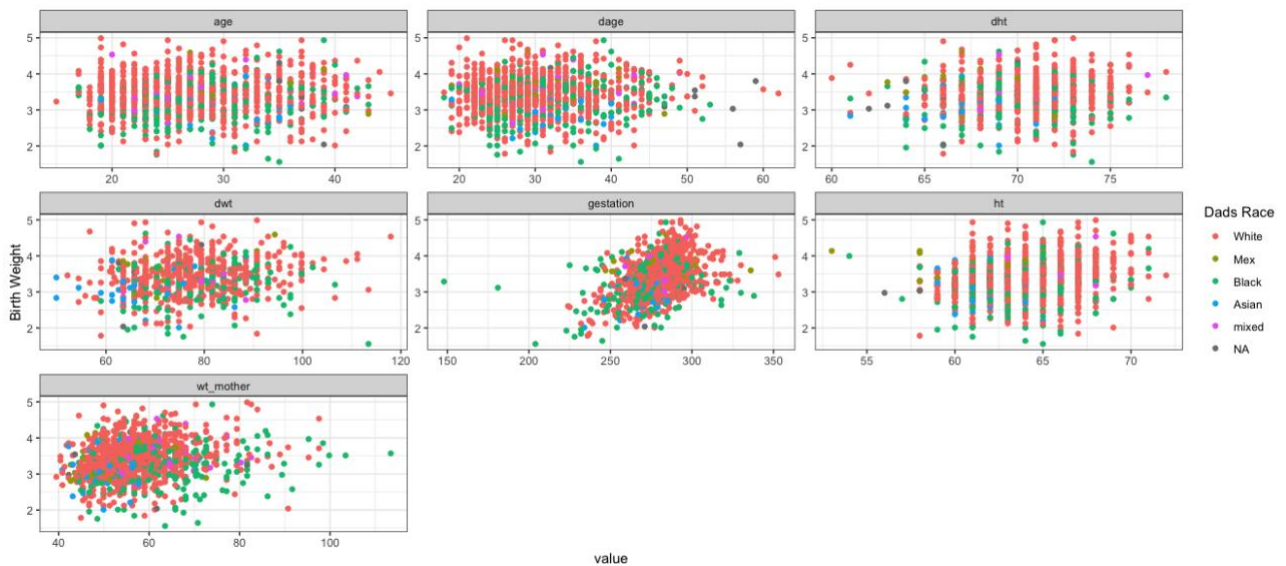


Figure 3 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight). The points are colour coded based on the dads race. Figure created using ggplot2 (Wickham, 2016).

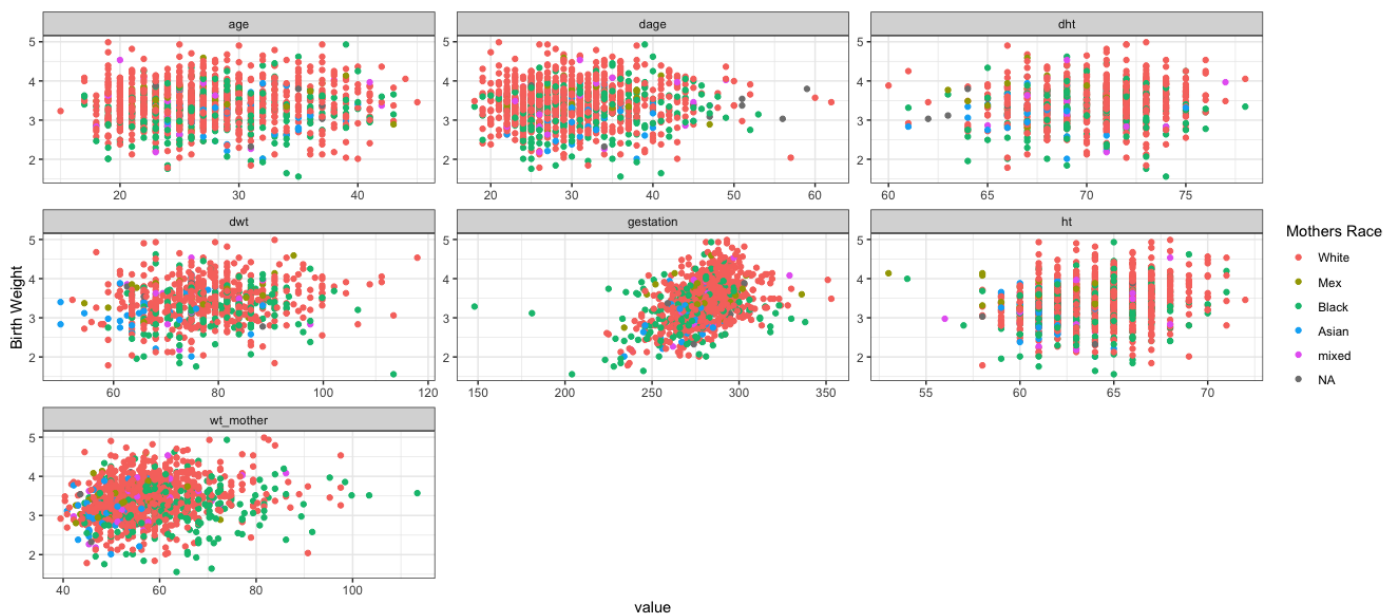


Figure 4 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight). The points are colour coded based on the mothers race. Figure created using ggplot2 (Wickham, 2016).

Figures 5-8 were filtered and so each contained less data. Similarly to figures 2-4, there was very little which could be inferred from these plots as there were very few relationships evident between the variables and the data was very widely spread. In all 4 figures, the plot for gestation against birth weight showed the most evidence for a relationship being present. There appeared to be a weak positive relationship between gestation and birth weight with gestation period increasing with increasing birth weight. The plots of birth weight and mothers weight also suggested a very weak positive relationship in figures 5 and 6, a negative relationship in figure 7 and no relationship in figure 8. However, none of the relationships can be seen as significant due to the large spread of the points.

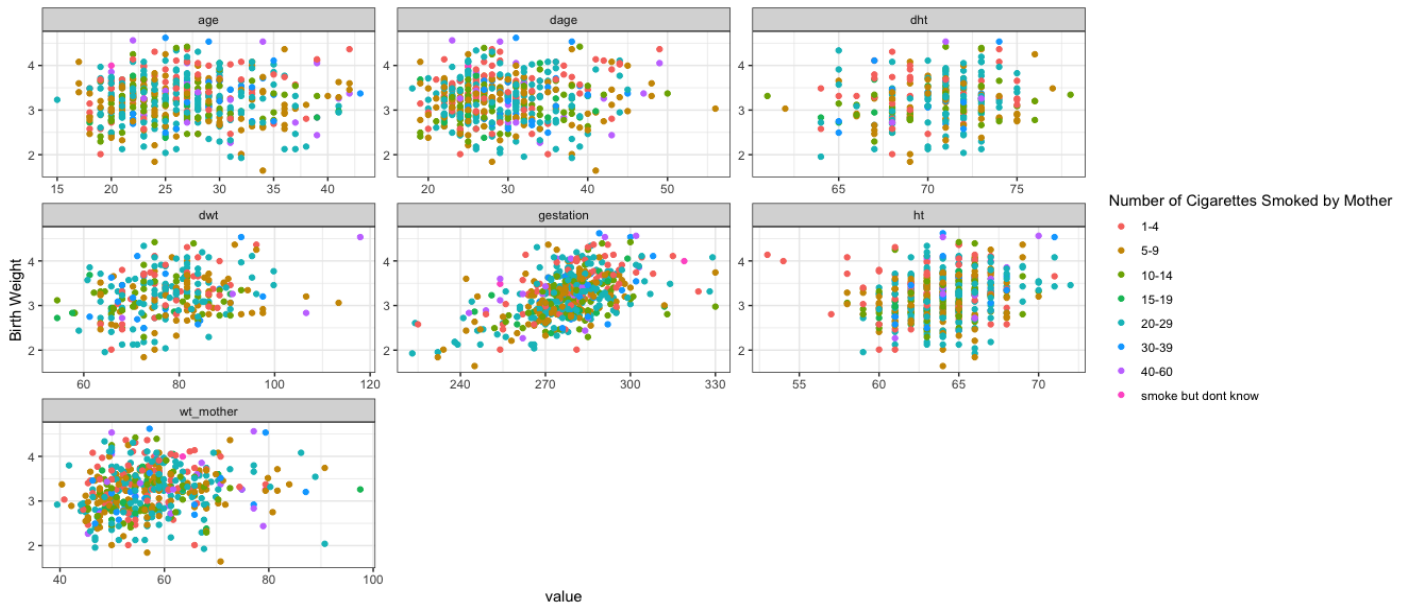


Figure 5 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight). The points are colour coded based on the number of cigarettes smoked by the mother during pregnancy. Figure created using ggplot2 (Wickham, 2016).

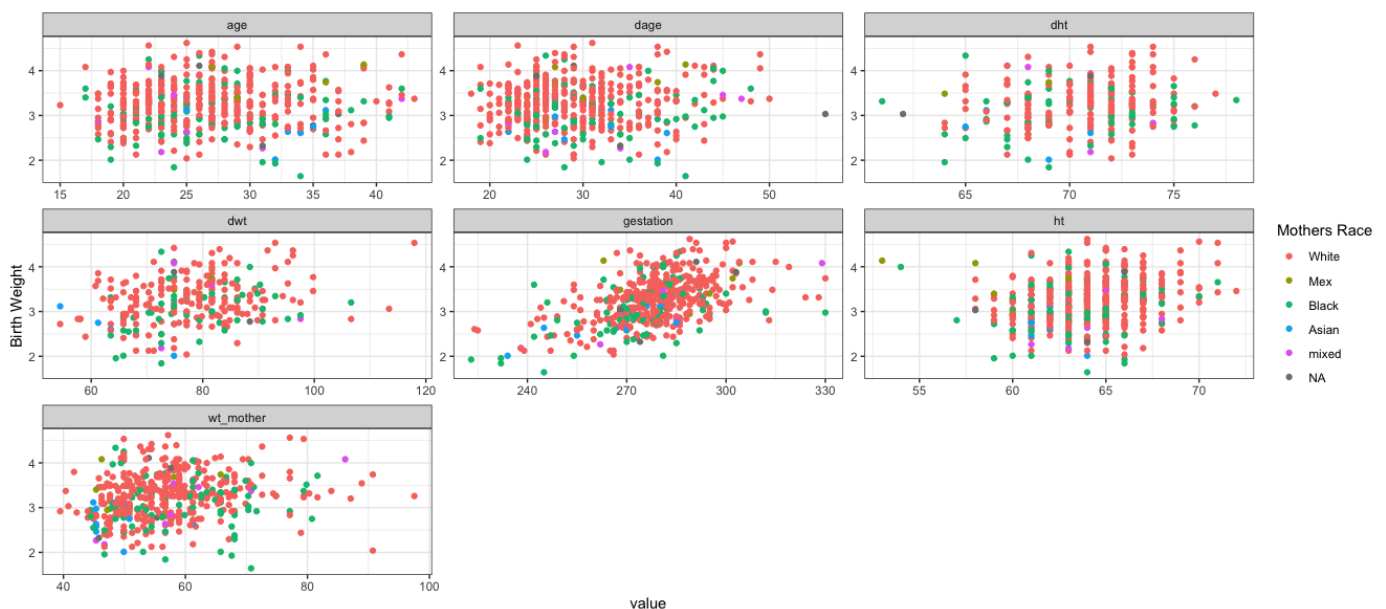


Figure 6 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight) for mothers who had never smoked. The points are colour coded based on the race of the mother. Figure created using ggplot2 (Wickham, 2016).

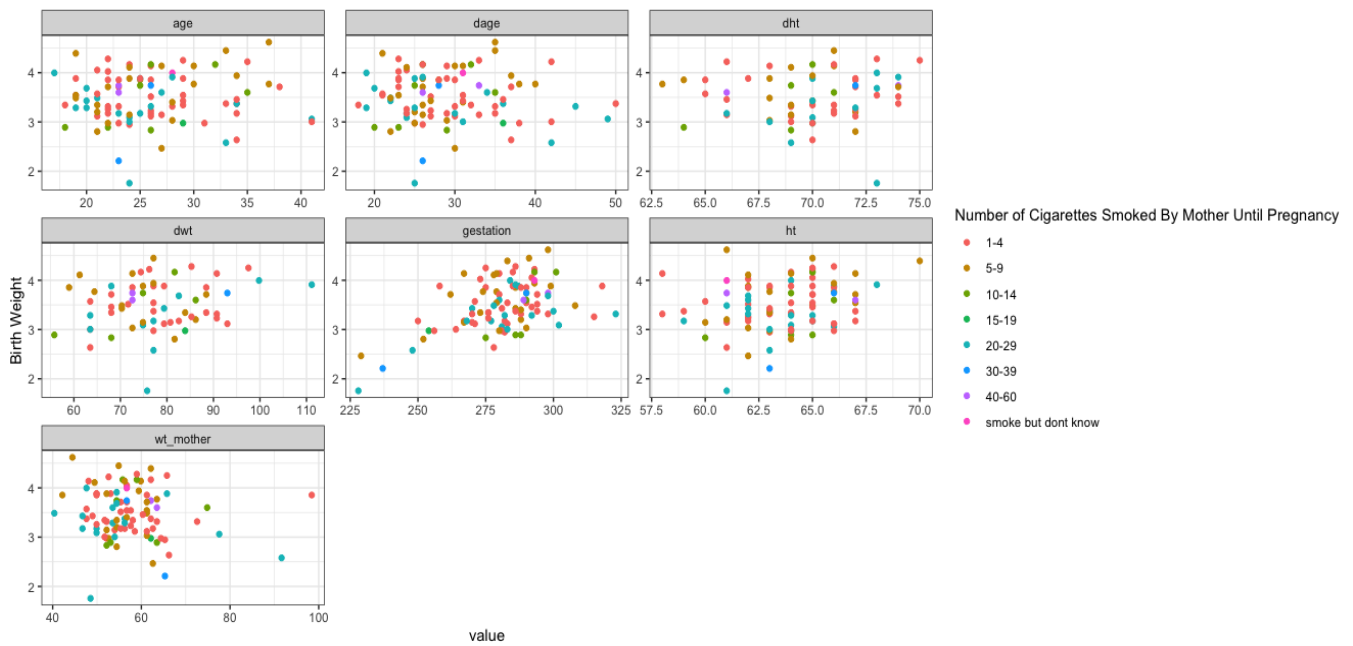


Figure 7 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight) for mothers who smoked until pregnancy. The points are colour coded based on the number of cigarettes smoked by the mother until pregnancy. Figure created using ggplot2 (Wickham, 2016).

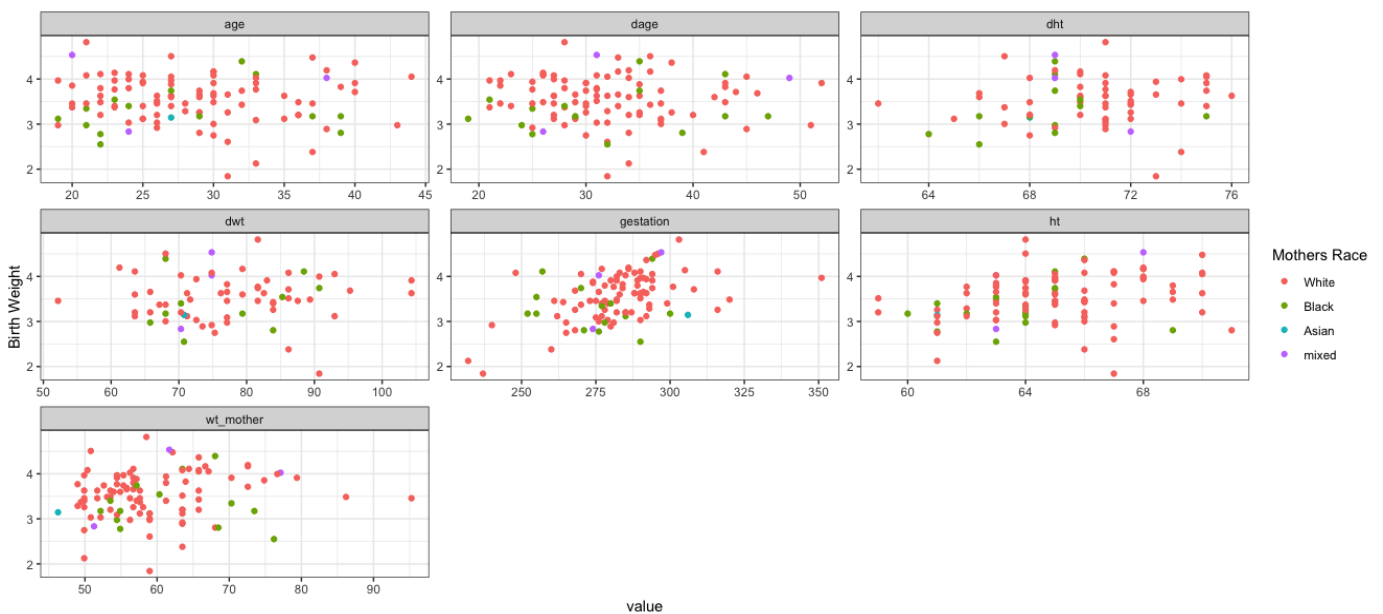


Figure 8 – Scatter plot for birth weight against 7 numerical variables age (mothers age), dage (dads age), dht (dads height), dwt (dads weight), gestation, ht (height), wt_mother (Mothers weight) for mothers who once smoked but not now. The points are colour coded based on the mothers race. Figure created using ggplot2 (Wickham, 2016).

4.3. Creating a Linear Model

4.3.1. Model One

The step wise backward model selection led to the selection of model which included the variables: gestation, parity, mothers race, mothers height, dads height and number of cigarettes smoked. Table 2 shows the results of the ANOVA test on model 1. When a significance value of 0.05 is used, the p-value for gestation, parity, race, mothers height and the number of cigarettes smoked are less than 0.05. Therefore, the null hypothesis can be rejected here and it is considered plausible that there is a significant difference between the means of the covariates. Therefore, if these variables are included in the model, it significantly changes the results of the model. The p-value for the variable Dads Height is greater than 0.05 and hence the null hypothesis is accepted and it is considered plausible there is no significant difference between the means of the covariates, this variable is less likely to make a significant difference to the model.

Table 2 – ANOVA results for model one. F-values have been rounded to 2 decimal places

Factors	Degrees of Freedom	F-value	P-value
Gestation	1	97.75	< 2.2 e-16
Parity	1	8.92	0.0029728
Race	4	6.51	4.16 e-05
Mothers Height	1	19.24	1.421e -05
Dads Height	1	2.20	0.1390217
Number of cigarettes smoked	9	3.75	0.001415

The VIF test results (table 3) show the values are all low (less than 5), there is likely no collinearity within the variables, each variable is predicting something different (reference ???).

Table 3 – VIF test results for model one.

Factors	Degrees of Freedom	GVIF	GVIF ^{1/(2*DF)}
Gestation	1	1.058771	1.028966
Parity	1	1.100260	1.048933
Race	4	1.376156	1.040719
Mothers Height	1	1.206111	1.098231
Dads Height	1	1.199174	1.095068
Number of cigarettes smoked	9	1.245428	1.012268

The p-value for the Shapiro-Wilk test (table 4) is greater than the 0.05 significance level, hence the null hypothesis is accepted and it considered plausible the model residuals are normally distributed.

Table 4 – Shapiro-Wilk p-value

Model	p-value
1	0.2149

The NCV test produced a p-value (table 4) which was greater than the 0.05 significance level and hence the null hypothesis must be accepted suggesting the error variance of the residuals is constant.

Table 4 – NCV test results

Model	Chi Square	Degrees of Freedom	p-value
1	0.2927551	1	0.58846

The DW test statistic (table 5) was less than 2 suggesting a small amount of positive autocorrelation present (reference ???). The p-value was greater than 0.05 and so the null hypothesis is accepted it suggests there is no correlation between the residuals.

Table 5 – Durbin-Watson test output

Model	Autocorrelation	D-W statistic	p-value
1	0.07329175	1.850598	0.098

Table 6 shows the confidence intervals for each variable included in model one.

Table 6 – 2.5% and 97.5% confidence intervals. Values have been rounded to 2 decimal places.

Factors	2.5%	97.5%
Intercept	-4.93	-2.01
Gestation	0.01	0.016
Parity	0.01	0.05
Race Mexican	0.11	0.57
Race Black	-0.24	-0.04
Race Asian	-0.36	0.08
Race Mixed	0.08	0.73
Mothers Height	0.02	0.05
Dads Height	-0.00	0.03
Numbers 1-4	-0.13	0.12
Numbers 5-9	-0.20	0.07
Numbers 10-14	-0.43	-0.10
Numbers 15-19	-0.55	0.01
Numbers 20-29	-0.38	-0.15
Numbers 30-39	-0.56	-0.08
Numbers 40-60	-0.40	0.32
Numbers who smoke but don't know	-0.45	0.26
Number unknown	-0.64	0.14

Figure 9 shows a series of plots of the residuals. Figure 9a shows the fitted residuals. The line fitted through the points is straight which suggests the model is capturing the signal of the model. Figure 9b and 9c show Q-Q plots for the residuals. The residuals fit well with the straight line and therefore suggest the residuals are normally distributed, this is also supported by the histogram in figure 9d.

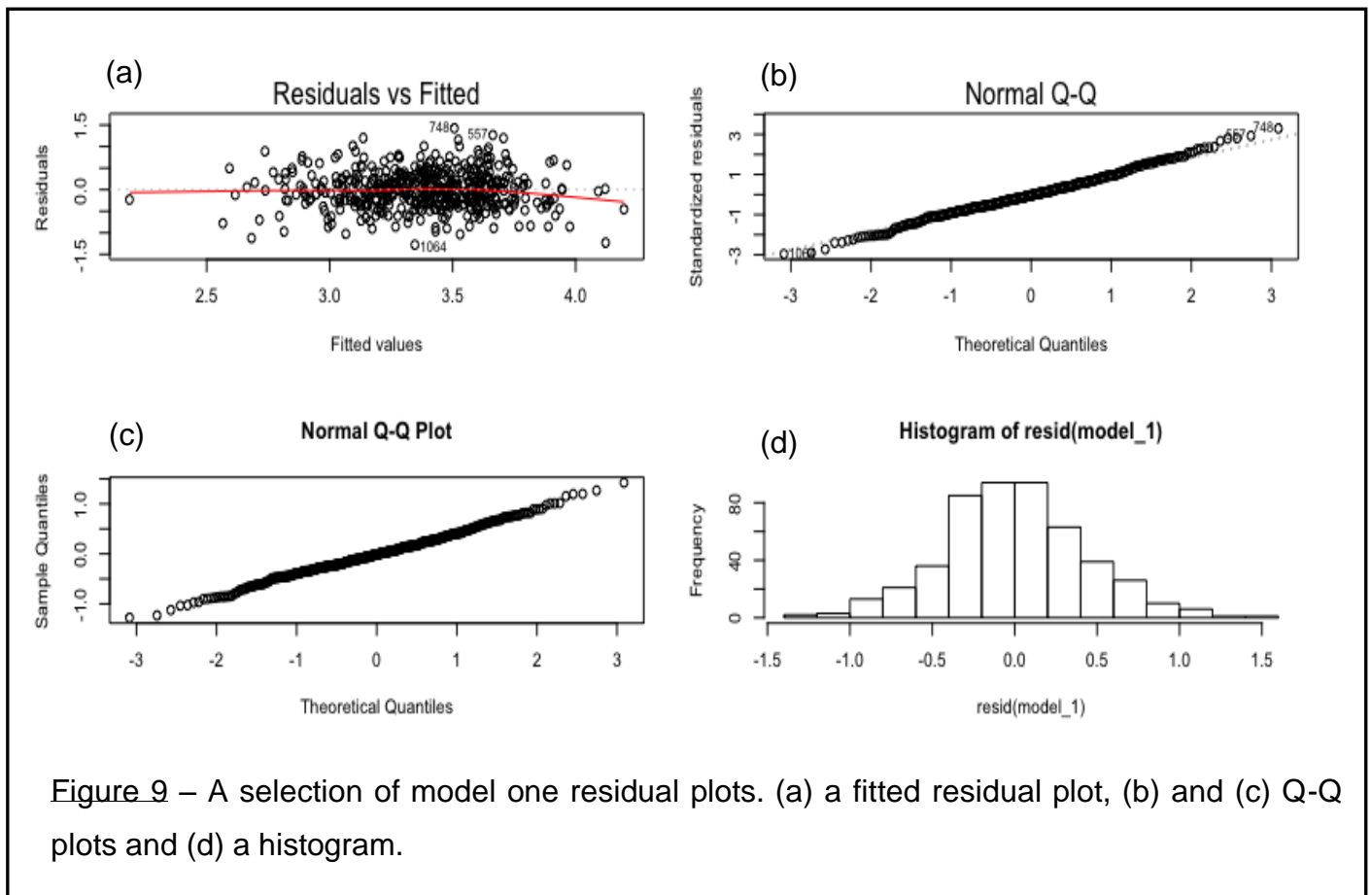


Figure 10a and 10b show the partial residual plots for the model one covariates including the distribution of the covariates.

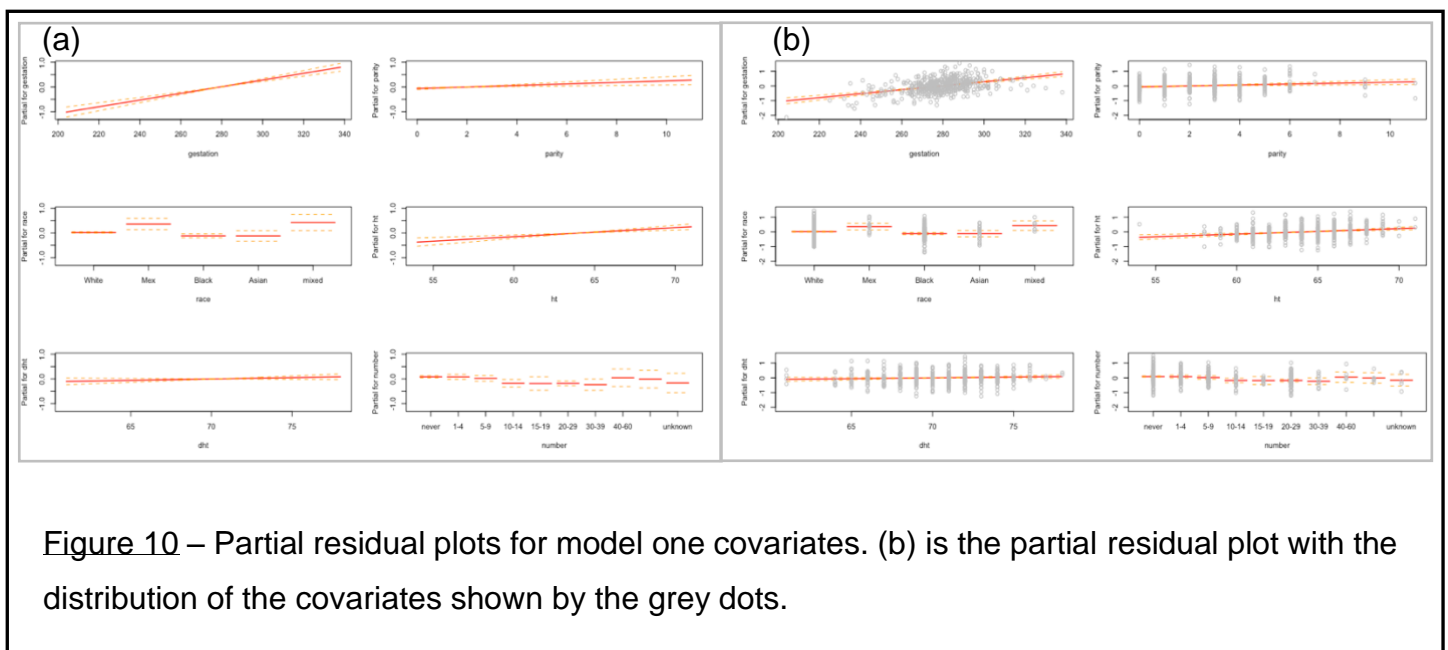


Figure 11 shows the relationship between gestation and birth weight. The p-value and R value are shown in the top left corner. The p-value of less than 0.05 means the null hypothesis that there is no relationship between gestation and birth weight would be rejected. In addition, the fact the slope is not 0 also presents plausible evidence to make the null hypothesis plausible.

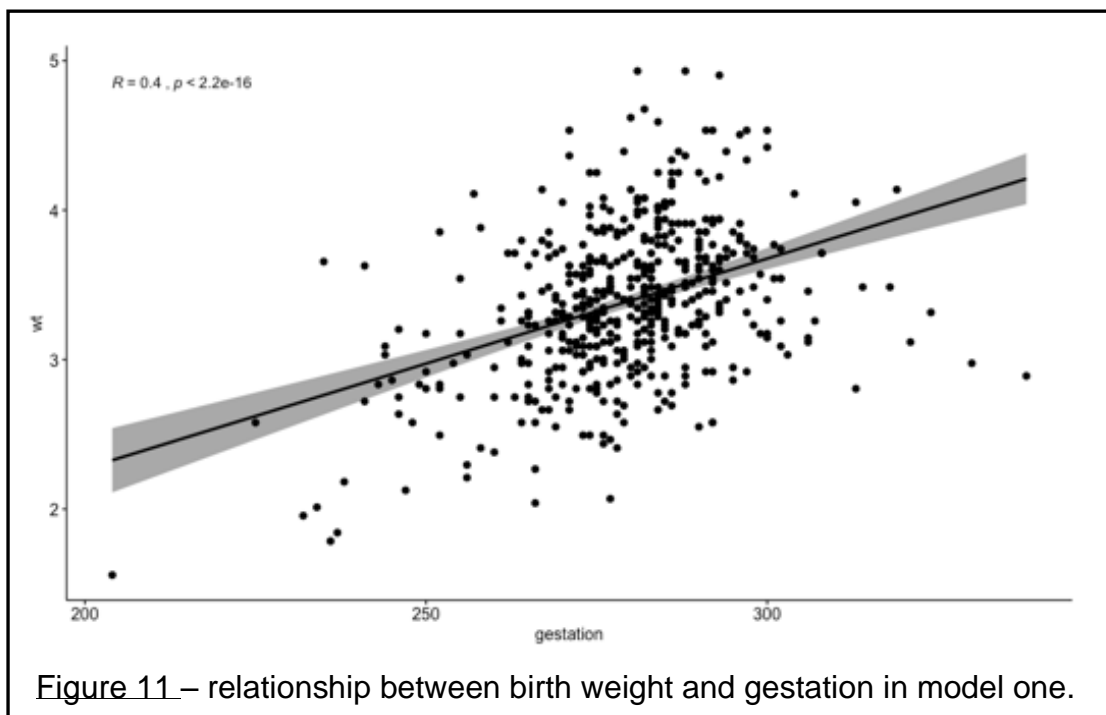


Figure 11 – relationship between birth weight and gestation in model one.

4.3.2. Model Two

Table 7 shows the results of the ANOVA test on model two. The p-value for race, smoke, gestation, parity and mothers height are less than 0.05 so the null hypothesis can be rejected. It can therefore be considered plausible that there is a significant difference between the means of the covariates. The p-values for the weight of mother and weight of dad were greater than 0.05 so the null hypothesis is accepted and it is considered plausible there is no significant difference between the means of covariates; these variables are less likely to make a significant difference to the model.

Table 7 – ANOVA results for model two. F-values have been rounded to 2 decimal places

Factors	Degrees of Freedom	F-value	P-value
Race	4	6.27	6.379 e-05
Weight of Mother	1	2.12	0.1460778
Weight of Dad	1	3.02	0.0826929
Smoke	4	6.95	1.899 e-05
Gestation	1	93.99	< 2.2 e-16
Parity	1	6.61	0.0104455
Mothers Height	1	12.25	0.005097

Similarly to model one, the VIF test results for model two (table 8) show the values are all low (less than 5), there is likely no collinearity within the variables, each variable is predicting something different (reference ????).

Table 8 – VIF test results for model two

Factors	Degrees of Freedom	GVIF	GVIF ^{1/(2*DF)}
Race	4	1.348022	1.038035
Weight of Mother	1	1.383816	1.176357
Dads Weight	1	1.131438	1.063691
Smoke	4	1.140104	1.016525
Gestation	1	1.045863	1.022675
Parity	1	1.133581	1.064698
Mothers Height	1	1.376836	1.173386

Similarly to model one, the Shapiro-Wilk test value for model one (table 9) is greater than the 0.05 significance level, hence the null hypothesis is accepted and it considered plausible the model residuals are normally distributed.

Table 9 – Shapiro-Wilk p-value

Model	p-value
2	0.09212

The NCV test produced a p-value (table 10) which was greater than the 0.05 significance level and hence the null hypothesis must be accepted suggesting the error variance of the residuals is constant.

Table 10 – NCV test results

Model	Chi Square	Degrees of Freedom	p-value
2	0.1664701	1	0.68327

The DW test statistic (table 11) was only very slightly less than 2 suggesting a small amount of positive autocorrelation present (reference ???). The p-value was greater than 0.05 and so the null hypothesis is accepted it suggests there is no correlation between the residuals.

Table 11 – Durbin-Watson test output

Model	Autocorrelation	D-W statistic	p-value
2	0.04839412	1.900212	0.23

Table 12 shows the confidence intervals for all of the variables in model 2

Figure 12 shows a series of plots of the residuals from model two. Figure 11a shows the fitted residuals. Similarly to model one the fitted line through the points is straight suggesting the model is capturing the signal of the model. The Q-Q plots in figure 9b and 9c show Q-Q for the residuals show that the residuals fit well with the straight line and therefore suggest the residuals are normally distributed, this is also supported by the histogram in figure 9d which shows a normal distribution.

Table 12 – 2.5% and 97.5% confidence intervals. Values have been rounded to 2 decimal places.

Factors	2.5%	97.5%
Intercept	-3.99	-1.45
Race Mexican	0.13	0.59
Race Black	-0.23	-0.03
Race Asian	-0.33	0.12
Race Mixed	0.05	0.71
Mothers Weight	-0.00	0.01
Dads Weight	-0.00	0.01
Smokes Now	-0.31	-0.13
Smoked Until Pregnant	-0.13	0.17
Smoked once, not now	-0.17	0.10
Smoke Unknown	-0.68	0.10
Gestation	0.01	-0.02
Parity	0.01	0.05
Mothers Height	-0.01	-0.05

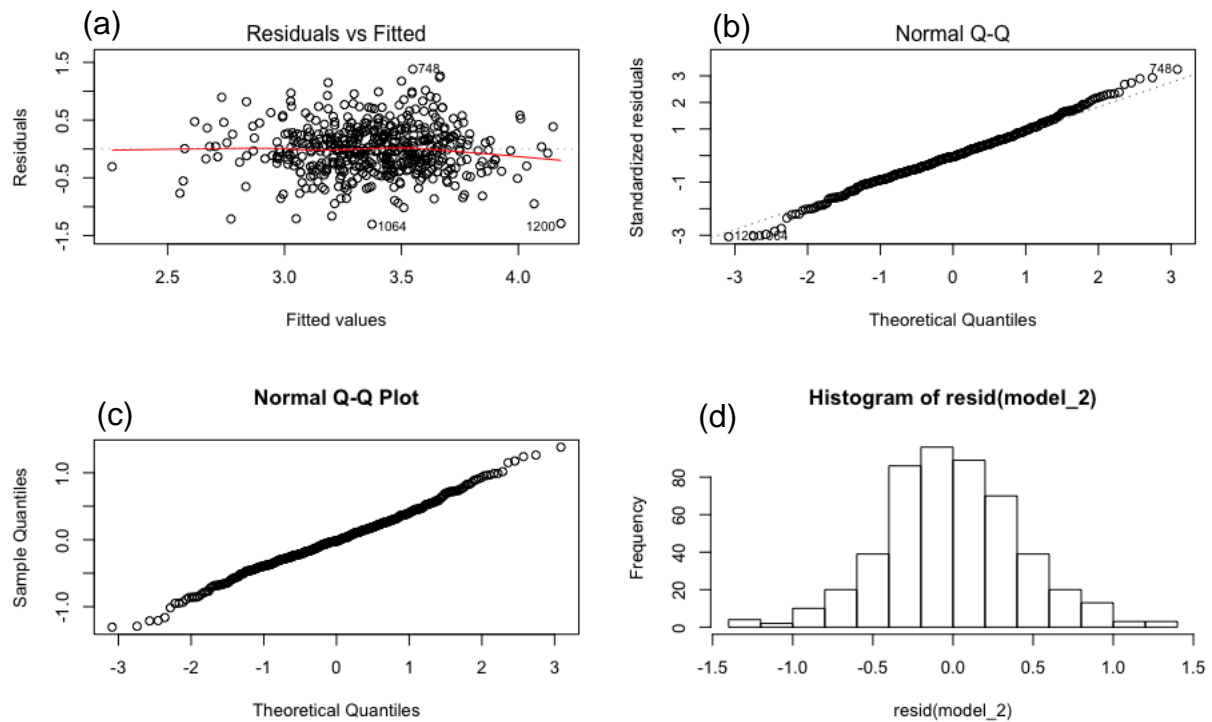
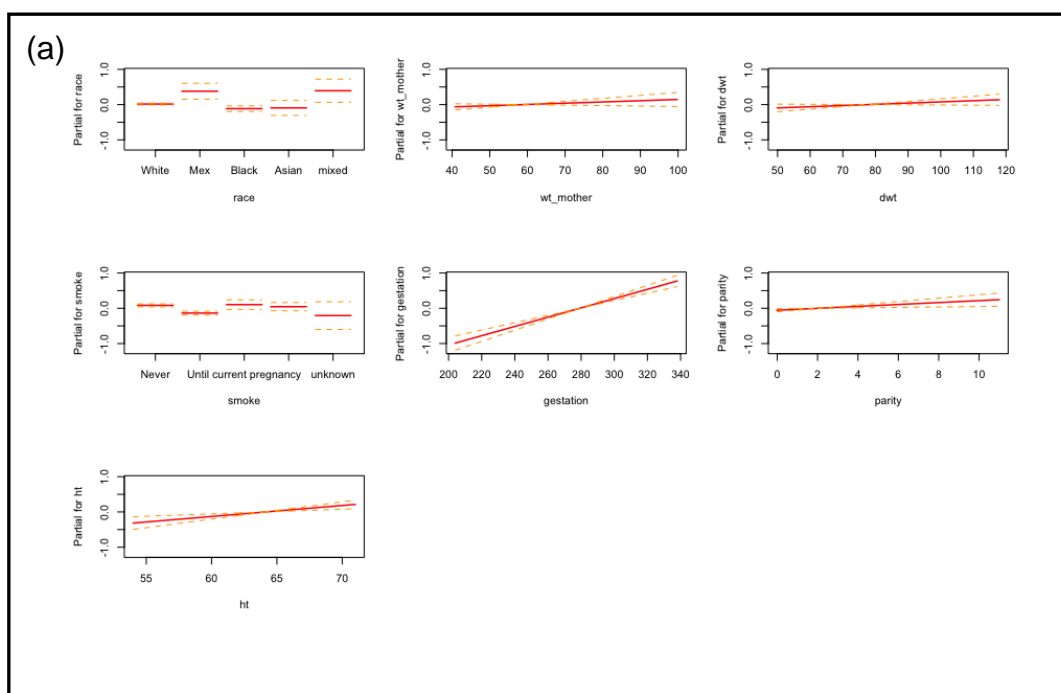
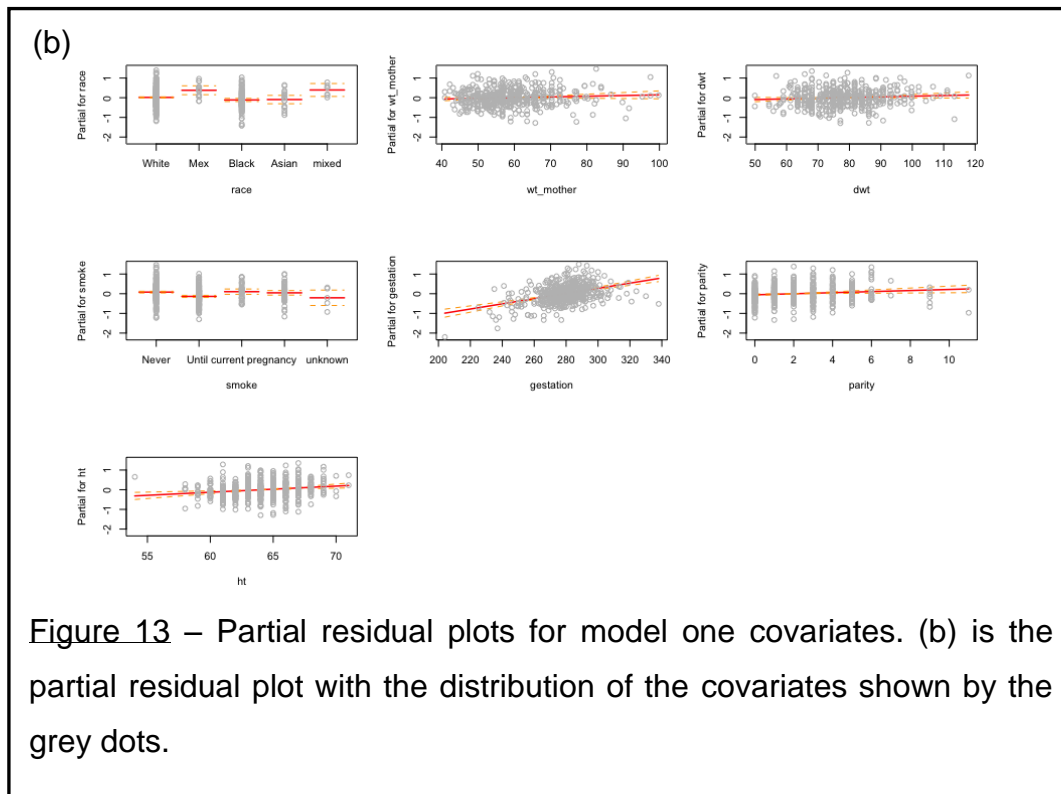


Figure 12 – A selection of model two residual plots. (a) a fitted residual plot, (b) and (c) Q-Q plots and (d) a histogram.

Figure 13a and 13b show the partial residual plots for the model one covariates including the distribution of the covariates.





4.3.3. Selecting the Best Model

The AIC values for each model were very similar, however, the AIC for model two is lower than for model one and hence based on this, model two would be selected.

Table 13– AIC values used to choose between model 1 and 2

Model	AIC Value
1	598.2940
2	592.8881

4.4. Model Validation

4.4.1. Validation the Set Approach

Table 14 shows the Mean Square Error (MSE) results from the set approach validation test. Model 2 showed the lowest MSE value and hence, from this test would be considered the best model (Kassambara, 2018).

Table 14 – MSE values from the validation set approach method

Model	MSE
1	0.2134067
2	0.2075065

4.4.2. 5-fold Cross-Validation

Table 14 shows the Root MSE (RMSE), R squared value and Mean Absolute Error (MAE) values from the 5-fold Cross-validation. The RMSE and MAE values for the models are very similar, however the values for model two are lower than for model one which suggests model two is a better model. The R-squared value for model two is higher which again suggests it is a better model.

Table 15 – RMSE, R-Squared and MAE values from the 5-fold Cross-Validation

Model	RMSE	R-Squared	MAE
1	0.4499902	0.2568768	0.3545067
2	0.4493301	0.2615274	0.3527888

4.5. Bootstrapping

Table 16 shows the confidence intervals from the bootstrapping undertaken on model two. In comparison to the confidence intervals from model 2 in table 12, they are very similar.

Table 16 – 2.5% and 97.5% confidence intervals for the bootstrapping of model two

Factors	2.5%	97.5%
Intercept	-4.10	-1.37
Race Mexican	0.16	0.57
Race Black	-0.23	-0.02
Race Asian	-0.33	0.11
Race Mixed	0.15	0.62
Mothers Weight	-0.00	0.01
Dads Weight	-0.00	0.01
Smokes Now	-0.31	-0.13
Smoked Until Pregnant	-0.12	0.16
Smoked once, not now	-0.19	0.10
Smoke Unknown	-0.80	0.18
Gestation	0.01	0.02
Parity	0.01	0.05
Mothers Height	-0.01	-0.05

5. Discussion

References

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