Funnel Plots for Assessing Institutional Performance

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Abstract

This thesis presents a comparison of maternal outcomes for births in New Zealand District Health Boards (DHBs). This is carried out through analysis of the National Minimum Dataset collected by the Ministry of Health for 2007.

The outcome compared is postpartum haemorrhage (PPH) the results are displayed using funnel plots, a useful tool for displaying unbiased information on performance outcomes when comparing institutions.

Exploration of the data found that there are differences in the demographics, maternal and birth characteristics among DHBs. The rates of PPH are different and the population mixes are made up of a range of different proportions of ethnic groups, ages and deprivation indexes. The exploratory analysis found that a large number of factors are associated with PPH. And that birth weight, parity and gestation had a large number of missing observations. These factors are not missing at random and require imputing prior to constructing the funnel plots.

Results show that there is divergence amongst DHBs in the postpartum haemorrhage rate. First a raw PPH rate was plotted and the results indicated there were differences among DHBs. As there are many potential predictors for PPH a logistic regression model was applied to find the most important factors related to PPH. This allows us to apply an adjusted rate for the funnel plot. The risk adjusted funnel plot also indicated differences among DHBs.

Two approaches are taken to account for the overdispersion. A winsorised estimate and a winsorised estimate with a random effects term are applied to the data. The approaches produced different results. The winsorised estimate widened the control limits and the random effects term narrowed the control limits. All four plots identified an extreme outlier and this was later removed from the analysis and the winsorisation funnel plots were rerun. The influential outlier made a difference and from this we can conclude that 2 out of 20 DHBs lie outside the 95% control limits. These two DHBs could be stated as having a very low rate of PPH.

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Contents

1	Introduction	1
1.1	Background	1
1.2	Structure of this Thesis	4
1.3	Research Objectives	5
1.4	Postpartum Haemorrhage	5
2	Literature Review	9
2.1	Literature Review on Funnel Plots	9
2.2	New Zealand Research	13
3	Data Description	17
3.1	Data Collection Procedure	17
3.2	Coding of Ethnicity	19
3.3	Data Quality Issues	20
3.4	Study Dataset	21
3.5	Data Cleaning	21
3.6	Derived Variables	22
4	Statistical Methods	27
4.1	Exploratory Data Analysis	27
4.2	Funnel Plots	28
4.2.1	Unadjusted Funnel Plot	30
4.2.2	Risk Adjusted Funnel Plot	31

4.2.3	Winsorised Funnel Plots	32
4.2.4	Winsorisation using general linear modelling	33
4.2.5	Winsorised Estimate using the Random Effects	34
4.3	Logistic Regression	35
4.3.1	Choice of Model	40
4.4	Imputation	41
4.4.1	Introduction	41
4.4.2	Mechanisms of Missingness	42
4.4.3	Related Studies	45
4.4.4	Methods of Imputation	46
4.4.5	Choice of Variables and Imputation Method	47
5	Exploratory Data Analysis	49
5.1	Data Description	49
5.2	Demographic Characteristics	53
5.2.1	Maternal and Birth Characteristics	58
5.2.2	Birth Interventions and mode of delivery	61
5.3	Potential Predictors for PPH	63
5.3.1	District Health Boards	63
5.3.2	Demographics	65
5.3.3	Maternal Birth Characteristics	66
5.3.4	Mode of Delivery and birth interventions	68
6	Unadjusted Comparison	71
6.1	DHB Comparisons	71
6.1.1	Ethnicity	72
6.1.2	Mother's Age	74
6.1.3	Gender	75
6.1.4	Parity	76
6.1.5	Deprivation Index	76
6.1.6	Summary	77
6.2	Unadjusted Funnel Plot	78

6.2.1	Unadjusted Funnel Plots Method	78
6.2.2	Unadjusted Funnel Plot Results	79
7	Risk Adjusted Comparisons	81
7.1	Imputation	81
7.1.1	Investigation of Variables to be Imputed	81
7.1.2	Imputation Method	87
7.1.3	Imputation Results	90
7.1.4	Summary	92
7.2	Logistic Regression Results	94
7.3	Risk Adjusted Funnel Plots	97
7.3.1	Risk Adjusted Funnel Plot Results	99
7.4	Winsorised Funnel Plots	101
7.4.1	Winsorised Estimates with Random Effects	104
7.4.2	Winsorisation Funnel Plot Results	106
7.4.3	Winsorisation Random Effects Funnel Plot Results	107
7.4.4	Winsorisation Results Excluding Auckland DHB	108
7.4.5	Winsorisation with Random Effects Results Exclud- ing Auckland DHB	110
8	Discussion	113
A	Glossary	121
B	Imputation Regression Results	123
B.1	Gestation	123
B.2	Parity	124
B.3	Birth Weight	125
C	Model Selection Results	129
C.1	Regression results for Adjusted Plot	133

List of Figures

5.1	Map of NZ DHBs	50
5.2	Frequency of Mother's Age	53
5.3	Percentage of mothers by Deprivation Index	55
5.4	Percentage of Mothers Ethnic Group by Age	56
5.5	Deprivation Index by Mothers Age	57
5.6	Deprivation Index by Mothers Ethnicity	57
5.7	Gestation	59
5.8	New borns birth weight	59
5.9	Age by Parity for all Mothers	61
5.10	Deprivation Index by Parity	62
5.11	Mother's Ethnicity for mothers who have had a PPH	66
6.1	PPH comparison across DHBs	72
6.2	DHB by Ethnicity	73
6.3	DHB by Median Age	75
6.4	DHB by Parity	76
6.5	DHB by NZ Deprivation Index	77
6.6	Unadjusted Funnel Plot	79
7.1	Age Distribution, for the whole dataset, data where gesta- tion is missing, data where parity is missing and data where birth weight is missing (as defined below)	82

7.2	Distribution of Ethnic Group (top) and Deprivation Index distribution (bottom) for the whole dataset, where gestation is missing, where parity is missing and where birth weight is missing	84
7.3	Distribution of birth weight, gestation and parity, before and after imputation	93
7.4	Matrix of Regression Variables for selection	96
7.5	Matrix of Regression Variables for that are chosen	97
7.6	Log Odds Ratio	98
7.7	Adjusted Rate	100
7.8	Winsorisation Funnel Plot	106
7.9	Winsorisation Random Effects Funnel Plot	108
7.10	Winsorisation Funnel Plot Excluding Auckland DHB	109
7.11	Winsorisation Random Effects excluding Auckland DHB . .	111

List of Tables

1.1	ICD10-AM Codes and definitions.	6
3.1	Standard prioritisation of ethnicity.	20
3.2	The numbers of records removed in the data clean step. . .	23
3.3	Mapping of Ethnicities	24
5.1	The Total Number of Births for each DHB.	51
5.2	The NZ Population for each DHB	52
5.3	The Total Number of Mothers Ethnicity	54
5.4	Frequency of Parity	60
5.5	Type of Births Procedures	63
5.6	The number of Mothers who have had a PPH by DHB	64
5.7	Mother's Age by PPH	65
5.8	Parity by PPH	67
5.9	New Born's birth weight for mothers who had a PPH	67
5.10	PPH by Gestation	68
5.11	Type of Birth by Postpartum Haemorrhage	69
7.1	The number of percentage of missing parity by PPH.	84
7.2	Percentage of missing records for Gestation, Birth Weight and Parity for each DHB.	85
7.3	Summary of Birth Weight Imputation	91
7.4	Summary of Gestation Imputation	91
7.5	Summary of Parity Imputation	92

Chapter 1

Introduction

1.1 Background

This thesis studies the rates of Postpartum Haemorrhage (PPH) in New Zealand district health boards (DHBs). Funnel plots will display and show divergence in PPH rates between each DHB. This thesis used data supplied from the Ministry of Health (MoH) National Minimum Dataset (NMDS) and Maternal and Newborn Information Systems (MNIS).

Apart from annual reports published by the Ministry of Health (Ministry of Health, 2004) there is very little research in New Zealand that looks at DHBs and their outcomes in a medical context. DHBs are mainly measured against each other for economic reasons using administrative data and not for the interest of health outcomes, such as mortality related events. This research will specifically look at the rate of PPH for each DHB.

This topic is unique in New Zealand because it will investigate a medical outcome (PPH). Most research in this area has previously been based on mortality or Myocardial infraction rates. Secondly this type of research is useful to inform hospitals, providers and their funders to identify areas that require further in-depth self monitoring and quality improvement for

health care in maternity.

Funnel Plots

A funnel plot is a way of displaying information visually for institutional comparison. It helps to identify institutions that are divergent from the average and those that are not (Spiegelhalter, 2005a). The funnel plot can be from a complex dataset and allows a visual comparison of data derived from multiple health care units such as hospitals, doctors and surgeons et cetera (Gale et al., 2006).

A funnel plot is a form of Statistical Process Control (SPC) Chart (Dover and Schopflocher, 2011) and can be used to study comparative performance measures (Gale et al., 2006). An SPC chart is also known as a Shewart chart or process-behaviour chart and is used to determine whether the process being monitored is in control or not. If a process being monitored is not in control then some observations from the process will be divergent from the rest. These charts are also useful in identifying variation amongst institutions. If variation has been identified, adjustments need to be made to bring the process back into control (Spiegelhalter, 2005b).

In a funnel plot a 'target' rate and an observed indicator for each institution are plotted against a precision measure. Control limits that are based on this precision measure are then added and form a 'funnel' around the target. The funnel is wider where precision is low and narrower as precision increases. This adds a visual line to the plot so we can see where the observations lie in relation to each other and the control limits. This identifies outliers, those who are performing well and those who are not (Spiegelhalter, 2005a). The control limits are similar to confidence intervals. When the control limits are plotted they can easily help interpret and identify the outlying institutions.

If an observation lies near the horizontal target line this indicates that the number of outcomes observed is similar to the expected outcome. If an observation is below the horizontal line then the outcome observed is lower than expected. If the observation is above the horizontal line then the observed outcome is greater than expected (Coory et al., 2007).

An important advantage of a funnel plot is that it displays variation among the units which can be adjusted for. If overdispersion around the target occurs there are many methods that can be applied to adjust for this. Previous research has used the funnel plot to look at hospital units or patients against a specific outcome (Coory et al., 2007; Spiegelhalter, 2005a; Richardson et al., 2009).

A funnel plot is a useful graphic aid to display and compare institutions against each other without ranking. It identifies the divergent units and the most extreme units as well as the units closest to the average (Spiegelhalter, 2005a).

Overdispersion

Overdispersion is the presence of greater variability than expected in the dataset (Berk and MacDonald, 2008). It cannot be accredited to just a few institutions or change. It can arise because there can be many factors that can contribute to the excess variability. If contributing factors are not accounted for then the majority of institutions can be incorrectly labeled as abnormal (Spiegelhalter, 2005b).

There are many methods for dealing with overdispersion such as using an adjustment method or a winsorisation random effects method (Spiegelhalter, 2005a). The risk adjustment method measures factors that are associated with the excessive variability and can bring the process in control. The random effects method adds a constant to the sampling variance

of each unit (Spiegelhalter, 2005a). Other methods include clustering the units into more homogeneous groups so that the comparisons can be made by comparing like with like. This is similar to benchmarking and can be considered as a form of risk stratification within the cluster (Spiegelhalter, 2005b).

1.2 Structure of this Thesis

Chapter Two is a literature review divided into two sections which discuss international and NZ based research. The research specifically looks at studies in a medical context using funnel plots and the performance of institutions, with specific examples that relate to this research analysis.

Chapter Three describes the National Minimum Dataset (NMDS) and examines how the data is collected, the coding of ethnicity and the quality issues with the dataset.

Chapter Four describes the methods that will be used in the following chapters or sections including Exploratory Data Analysis (EDA), Funnel Plots, Logistic Regression and Imputation.

Chapter Five presents the Exploratory Data Analysis (EDA) where demographic, maternal, type of birth, birth interventions and mode of delivery are explored. These explanatory variables are explored to identify relationships with PPH.

Chapter Six presents the unadjusted comparison results. Firstly DHB comparisons are explored. The relationship between the explanatory variables and the DHBs are analysed to identify differences among DHBs. The unadjusted funnel plot method and results are then presented.

Chapter Seven presents the choice of imputation method used and the results from imputation. The logistic regression results are presented which are used for the risk adjusted funnel plot. The risk adjusted, winsorised and winsorisation random effects funnel plots results are presented and examined.

Chapter Eight is a discussion on the findings of this research and a conclusion of the results.

1.3 Research Objectives

There are three key objectives in this body of research:

1. To determine if there is a difference among DHBs in their rates of PPH.
2. To model the factors that are associated with PPH.
3. To determine if risk adjustment reduces divergence in PPH rate among DHBs.

1.4 Postpartum Haemorrhage

This section describes the term Postpartum Haemorrhage (PPH) and the associated factors and outlines previous research about PPH. Throughout the chapter Postpartum Haemorrhage will be referred to as PPH (Ministry of Health, 2004).

PPH is the excessive bleeding of a genital tract following the birth of a baby. A primary PPH in more precise terms it is where the mother has

had a blood loss of more than 500ml from the genital tract within the first 24 hours following delivery (Ministry of Health, 2004). A secondary PPH is blood loss of 500ml or more after 24 hours of delivery. (Ministry of Health, 2004). For this work primary PPH is the main focus.

It is assumed, in this study, a mother who had a PPH had one of the following diagnosis ICD-10-AM (the 10th revision of the ICD10 Australian modification) codes in table 1.1.

Table 1.1: ICD10-AM Codes and definitions.

ICD10-AM Code	Description
16556700	Other management of postpartum haemorrhage
O720	Immediate postpartum haemorrhage, within the first 24 hours (following delivery of placenta)
O721	Delayed and secondary postpartum haemorrhage (after the first 24 hours following delivery)
O722	Postpartum haemorrhage due to coagulation defects

Definitions of PPH can vary. The main definition is classified as blood loss from the genital tract exceeding 500mls within 24 hours of delivery of the baby (Harrison, 1998; Mousa, 2007). In practical terms this is very difficult to measure and quantify. Blood loss can often be underestimated because of catchment of blood, as swabs and clothes are often used to contain the blood. Combs et al. (1991) states that primary PPH with a loss greater than 500ml occurs in 1-5% of deliveries in high-income families.

PPH is an associated risk factor for pregnancy. Excessive blood loss following birth can cause a severe drop in blood pressure leading to shock and death if not treated (University of Virginia Health System, 2010). Ma-

ternal death from postpartum haemorrhage is extremely rare. Mousa (2007) found that in the UK, 1/100,000 deliveries are at risk of maternal death. In developing countries the risk is greater at about 1/1000 (Mousa, 2007).

Taylor et al. (2005) found that PPH has a higher risk following a second pregnancy after a C-section and found that women who did not have a C-section were at lower risk of PPH.

Risk factors associated with PPH are placental abruption, multiple pregnancy, pregnancy induced hypertension, having many previous births, infections, obesity, induced labour, the use of forceps or vacuum assisted delivery, episiotomy, previous PPH, C-section, pre-eclampsia, race/ethnicity and many others (Combs et al., 1991; University of Virginia Health System, 2010; Harrison, 1998; Mousa, 2007; McCormic et al., 2002; Taylor et al., 2005; Waitemata District Health Board, 2006; Jacobs, 2012). Many symptoms can occur during PPH such as uncontrolled bleeding, decreased blood pressure, increased heart rate, decrease in the red blood cell count and swelling and pain in the tissues of the vaginal and perineal wall (Jacobs, 2012; Taylor et al., 2005; McCormic et al., 2002).

The reported incidence of PPH can vary. The incidence of PPH in the UK varies from 4% to 11%. National Womens Hospital reports a high incidence of PPH with 18% of all women suffering a primary PPH of 500mls to 1000mls and 4% suffering a primary blood loss of greater than 1000mls (National Womens Hospital, 1996). Knight et al. (2009) found in 2006 that in Australia 10% of mothers giving birth had a PPH. In Scotland the rate was 4 per 1000 women, Canada 5% and US 3%. University of Virginia Health System (2010) suggests that 4% of women have a PPH and it is more likely to occur with a caesarean birth. This shows measurement of blood loss for PPH can differ.

PPH can be treated and managed prior and after pregnancy. Management can consist of medication, procedures or therapies (University of Virginia Health System, 2010; Mousa, 2007). The main risks factors for PPH associated with this analysis are instrumental delivery, caesarean section, episiotomy, birth weight, parity and ethnicity.

Chapter 2

Literature Review

2.1 Literature Review on Funnel Plots

There are a number of international research publications that have looked at many outcomes for health care providers using funnel plots. Many studies have used mortality outcomes related to heart conditions for example myocardial infraction. This section will review previous international research using funnel plots in a medical context.

A study based in Queensland, Australia, (Coory et al., 2007) involved patients admitted to hospitals with Acute Myocardial Infraction (AMI). This study compares specific hospitals using cross-sectional analysis and sequential motoring based on control charts. The main issue that needed addressing is how to present such data in a meaningful way that is easy to interpret. As most hospitals data are collected for administration and funding use, it makes it difficult to have such measures for quality of care.

Control charts are used to display and detect unusual performance of hospitals. A crude rate of AMI can be misinterpreted, risk adjustment is required to take into account factors that are related to AMI. This is so that hospitals that treat higher risk patients are not unfairly penalised. There

are several methods for risk adjustment such as risk adjusted cumulative sum (CUSUM), risk adjusted expected minus observed, and Cumulative Risk-Adjusted Mortality (CRAM) plots. For this study the expected minus observed was used for a risk adjusted method.

With the use of league table type methods, a few outlying hospitals can be identified as either high or low outliers. This ignores the differing levels of precision across hospitals due to varying sample sizes. This method has many limitations and a more preferable way to display hospital outcomes would be the use of a funnel plot. This allows a hospital specific measure to be plotted against a precision measure with confidence limits that form the funnel around the average or target. From this graphical representation one can easily determine where each hospital sits in relation to each other.

A study based in the UK, Gale et al. (2006) used funnel plots to look at the performance of health care professionals using Myocardial infarction data. The purpose was to use funnel plots to demonstrate that data from the MINAP (Myocardial Infarction National Audit Project) can be used to allow more meaningful interpretations. This study investigated 230 hospitals, approximately 100,000 patients. Gale et al. (2006) found that the funnel plot is a useful aid to display institutional comparison. It was quickly identified how many hospitals fell outside the 95% control limits and how many were inside the control limits. Gale et al. (2006) concluded that funnel plots can be applied to complex data from multiple health care institutions, as it avoids such rankings as pass or fail for a hospitals' performance.

Dover and Schopflocher (2011) used funnel plots in public health surveillance. Dover and Schopflocher (2011) investigated the MVA (Motor Vehicle Accidents) death rate in 2007 in Alberta, Canada. The aim was to inves-

tigate how to display the analysis, so that it is in the best interest of planning, implementation and evaluation of the public health system. This will allow public health policies to be made after monitoring the health status of the population.

The first approach uses a simple model to construct the first funnel plot which uses a crude motor vehicle mortality rate. It was found that 23% of the sub regions fall outside the 95% confidence limits. As this first approach shows large overdispersion a second approach was taken where a risk adjusted rate is used to take into the account variables that may be associated with MVA, such as the use of the seat belts, drink driving and road type etc. The adjusted rate then becomes the product of the provincial crude rate and the ratio of observed to expected values from the relevant regression model. A step by step approach was used for the model where a small set of factors was added to the regression model and analysed. Pearson's goodness-of-fit statistics were used at each stage of the modelling process to assess whether the adjusted variables were significant. Once the regression model was finalised the risk adjustment funnel plot showed that the overdispersion had been taken into account.

Dover and Schopflocher (2011) concluded that funnel plots are a useful tool for displaying small area data in health surveillance and detecting anomalies. It is also important to consider relationships among other variables to deal with overdispersion. Using this information the public health decision makers can discuss the implications and use for routine monitoring.

Ohlssen et al. (2007) conducted a larger study using a modelling framework to identifying unusual performance in health care providers. Cross-sectional data were used from health care providers to detect unusual performance. The purpose was to create a structure for comparing methods,

focusing on the estimation and hypothesis testing approach.

This paper discusses two alternative approaches that correspond to different interpretations of the word 'unusual'. The two approaches used were an estimation approach and a hypothesis based approach. The estimation approach is based on a single complex model in which the 'extreme' cases are identified. The hypothesis testing approach attempts to find a simple model to describe the cases which are of interest and that are divergent.

There are two study examples that are used in this paper by Ohlssen et al. (2007). The first is a patient-specific risk score that looks at coronary artery bypass graft patients, where the measure is 30 day morality rates for patients for each surgeon. Ohlssen et al. (2007) found that one surgeon was an outlier but could be treated as an over performer rather than an under performer. The second study contains routine data that are used in central monitoring of health services. It was based on data from the health care commission and looks at provider performance against emergency readmissions to hospital with 28 days of discharge.

This study by Ohlssen et al. (2007) concludes that there are three possible approaches to cross-sectional studies of unusual performance. The first, estimation of provider effects, requires flexible modelling assumptions and that the provider effects can be assessed using ranking or a set of external targets. The second, the hypothesis testing approach of each provider's outcome with an estimated null model using a classical p-value with no explicative alternative. And thirdly, a fully Bayesian hypothesis testing approach with an explicit alternative and calculation of posterior probabilities of the providers. The recommended approach is to use the hypothesis testing approach with no specific alternative and the use of p-values to quantify unusual performance.

This suggests that there are some key points that need to be considered. First, deciding on the null model for acceptable variation between providers. Secondly how to remove the influential providers that are potentially not in the null distribution or down weigh them (ie winsorisation). Thirdly, how to adjust for multiple comparisons.

2.2 New Zealand Research

A New Zealand based study by Richardson et al. (2009) looks at the ethnic and social-economic inequalities in mortality rates across regions. Using a hierarchical Bayesian approach, it uses posterior mortality rates from the models to calculate standardised rate ratios with credible intervals.

There are three main objectives that this study explores. Firstly to examine the mortality differences across regions in NZ by looking at income and ethnical inequalities. Secondly, to demonstrate the use of hierarchical Bayesian methods compared against simple empirical methods. Lastly, to investigate across regions the mortality rate for such factors as ethnicity, income, age and sex and to see how they differ among regions. The data used is the 2001 Census combined with the 2001-2004 mortality data in the New Zealand Census Mortality Study (NZCMS).

(Richardson et al., 2009) uses a hierarchical Bayesian regression approach to model the mortality rates in the 2001-2004 cohort, Richardson et al. (2009) found evidence of varying mortality rates among ethnic groups across NZ regions. There was no evidence for divergence among income groups in mortality across regions. If routine data were used it would report similar variability in NZ European mortality rates across DHBs but much greater variability in Māori mortality rates and in Māori:European rate ratios.

Richardson et al. (2009) concluded this is an interesting paper for the health service. They concluded that there are differences among regions in mortality rates and perhaps this should be considered when funding specific regions or DHBs. It is recommended that hierarchical Bayesian methods play an important role in prediction capabilities and displaying regional variation. This application allows more definite conclusions than routine empirical methods when comparing small populations.

Another NZ based study which has been recently published by Graham et al. (2012) looks at the variation among hospital outcomes using hierarchical Bayesian modelling and propensity scores to assess hospital performance. The study goes into great detail about how to adjust for comparing hospital performance with propensity scores methods to control case-mix factors. With the use of a Bayesian model this will allow assessment of performance on multiple outcomes. The sample population used is that of NZ public hospitals for patients that have been treated for AMI, pneumonia or stroke and the 30 day post admission mortality rate.

There are two main concerns that arise with the data and are addressed. Firstly, how to manage random variation and secondly the influence of case-mix adjustment. These are both important aspects of measuring performance as an incorrect measure could classify hospitals as having 'good' performance when it is actually 'poor' performance.

(Graham et al., 2012) shows how a hierarchical Bayesian method can improve the precision of the target and can control for any variation that may occur. Propensity scores are used here to obtain population standardised risk rates for each hospital and then the standardised risk rates are then modelled using hierarchical Bayesian method.

Although there are specific limitations of this study were identified Graham et al. (2012) found the Bayesian method and propensity scores for assessing hospital performance for treatment against AMI, pneumonia or stroke is a valuable and practical method to measure and compare the performance of each hospital.

Chapter 3

Data Description

The Ministry of Health's New Zealand Health Information Services collects and holds two datasets that contain information on hospital births. These are the National Minimum Dataset (NMDS) and the Maternal and Newborn Information Systems (MNIS). Data for this study were extracted from these two datasets. This chapter describes the data collection procedure, coding and quality issues for these two datasets (Ministry of Health, 2012a).

3.1 Data Collection Procedure

There are two sources which the MoH have provided and are used in this study. The NMDS and the MNIS both are described in more detail.

The NMDS provides unit record data about hospital events, including births. This information is provided by both publicly funded and private hospitals (Ministry of Health, 2012a) and includes information about health conditions and procedures used.

All hospitals whether public or private, must follow and use the interna-

tional standard classifications of diseases and health problems, or ICD-10-AM, the 10th revision of the ICD10 Australian modification codes. All records must also have a valid National Health Index (NHI) number. This is to match the hospital admissions data from NMDS (Ministry of Health, 2012a). Records are then sent to New Zealand Health Information Service (NZHIS) for validation and checking and then are loaded into the NMDS. Publicly funded hospitals have 21 days after the month of discharge to lodge the event. For public hospitals the files are electronic and these are processed daily. For paper and private hospital electronic records NZHIS has a team that manually processes these.

MNIS is data collected by services provided by Lead Maternity Caregivers (LMCs). It contains information and data on antenatal, birth and postnatal maternal services.

There are two sources where information is obtained from: the HealthPAC (health payment, agreements and compliances) and NMDS Systems. HealthPAC (health payment, agreements and compliances) previously known as Health Benefits Limited, collects information from claim forms submitted by LMCs. The main purpose of this system is to collect information about payments of LMCs for their services to pregnant women, mothers and babies. The payment information identifies services used and care given to the recipient (the mother and or baby). This information is then submitted to HealthPAC via a claim form (Ministry of Health, 2012a).

These claim forms are then forwarded to MoH and then in turn, entered into the co-payments database operated by HealthPAC. LMC claims are mainly used to provide primary information about payments and caregivers to facilitate payment of the LMCs. Therefore clinical and demographic information is of secondary nature and these areas of interest and have less scrutiny about the quality of information given. This informa-

tion is supplemented once extracted from hospital records from the NMDS (Ministry of Health, 2012a).

MNIS was established in 2001. The MNIS contains information from 1999 onwards. The coverage of this information has improved over the years from 68% in 1999, for all births, deaths and marriages to 83% in 2003 and 77% in 2004. The MNIS and NMDS are linked together through the women's NHI number which is matched to hospital admissions data from NMDS (Ministry of Health, 2012a).

3.2 Coding of Ethnicity

Ethnicity is the ethnic group or groups that people identify with or feel they belong to. Ethnicity is a measure of cultural affiliation, as opposed to race, ancestry, nationality or citizenship. Ethnicity is self perceived and people can belong to more than one ethnic group.

A person's ethnicity can change over time. MoH can record up to three ethnic groups for a person. Ethnic group is defined by MoH as "a group of people who have culture, language, history of traditions in common. Ethnicity is not the same as race, ancestry, or country of birth." (Ministry of Health, 2012b)

Collecting ethnicity can be problematic as providers or health care users are unwilling to divulge the information. Some can be unwilling to label themselves and some can be confused about the difference between ethnicity, nationality, race or citizenship. MoH collects ethnicity data in the same way the NZ census ethnicity data are collected (Ministry of Health, 2012b; Statistics New Zealand, 2012). This is essential because hospitalisation rates are calculated by comparing the two datasets to determine pro-

portions of the population hospitalised. MoH uses prioritised ethnicity according to Statistics NZ (Statistics New Zealand, 2012) by using specific algorithms that prioritised ethnic codes. Prioritised ethnicity is a hierarchical classification of ethnic group. For simpler analysis multiple records of ethnic groups per individual are prioritised using a standard by the NZHIS see table 3.1

Table 3.1: Standard prioritisation of ethnicity.

Ethnicity	Prioritisation order
Māori	1
Pacific peoples	2
South East Asian	3
Indian	4
Chinese	5
Other Asian	6
Other	7
Other European	8
European	9
Not Reported	10

3.3 Data Quality Issues

There are some known quality issues with the data which are described below. This information has been sourced from Ministry of Health (2004) and with personal communication from Information Analysts at MoH. The quality issues are:

1. Incorrect reporting of parity as very little data quality work was done on this in the HealthPAC source system. This led to limited completeness and quality of parity data.
2. Incorrect reporting of Estimated delivery date (EDD). EDD was accepted if in an incorrect date format.

3. The pregnancy identifier EDD field sometimes contained the provider ID instead of EDD.

Projects are underway to improve the quality and completeness of maternal and infant data in the MNIS National collection.

3.4 Study Dataset

The data used, has separate datasets for mothers and babies. These were then linked using the mother's NHI number and delivery date. The dates used to extract data are the babies' date of birth from 1/1/2007 to 31/12/2007. Several ICD-10-AM codes are used to identify where a mother has given birth. These include outcome of delivery, delivery code or a delivery procedure code. To identify birth events there will be one record per baby using the diagnosis of ICD-10-AM of live born infants.

3.5 Data Cleaning

In this section we describe the data cleaning that is required to prepare the data for the EDA and analysis presented in the next few chapters. As the dataset contained birth information from years 2004-2008 and there were separate tables for mothers and babies. Data processing and cleaning was necessary prior to the analysis.

1. Select 2007 year.
2. Selected matched mothers and babies only, otherwise not all variables are available for analysis (removed where match index is equal to B or M)

3. Remove cases where any DHB birth is overseas (as we are not interested in comparing overseas hospitals, only DHBs in NZ).
4. Removed cases where birth location of the hospital is not private or public (coded as 1 or 2).
5. Removed cases where mother's plurality is not recorded (ie missing value).
6. Remove mothers where plurality is 2 or 3, as this is recorded where the mother gave birth to twins or triplets. To restrict to single births.
7. Removed records where the deprivation index cannot be identified, this is where DHB of residence is overseas or not identified.
8. Remove multiple mothers that are not identified in the above steps. Removed mothers where mother's ID and babies DoB (Date of Birth) are the same as this indicates twins.
9. Removed multiple mothers second births because a mother may have had two births in 2007. Here we kept only the first birth. However this may cause a small bias if PPH is more (or less) likely the more children a mother has.

Table 3.2 shows the number of records removed in the data clean for each step.

3.6 Derived Variables

PPH

PPH is recorded as an ICD-10-AM code as based on V4 (April 09) FINAL ICD-10-AM 6th Edition Clinical Code Table. The codes descriptions are other management of postpartum haemorrhage, third-stage haemorrhage,

Table 3.2: The numbers of records removed in the data clean step.

Total Number	Difference	Description
65,784		In the 2007 Year, total number of records
57,478	8,306	Selected matched mothers and babies only, so removed where matched index is B or M
57,427	51	Removed where DHB birth is 999 or xxx. Where DHB is overseas.
57,426	1	Removed cases where birth location is not private or public
57,426	0	Removed where any cases where gender of the baby is unknown
57,419	7	Removed cases where mothers plurality is NA
55,907	1,512	Removed mothers where plurality is 2 or 3, so if plurality was recorded with a 2 or 3, that is twins or triplets, these records are removed from the analysis
55,890	17	Remove where DHB residence is 999 or xxx
55,840	50	Removed multiple mothers that were not identified in the above steps. Removed mothers where their ID and babies DoB birth are the same this indicators twins
55,811	29	Removed multiple mothers second births. As a mother may have had two births in 2007, here we kept only the first birth.
	55,811	Total

other immediate postpartum haemorrhage and delayed and secondary postpartum haemorrhage. The codes are 1656700, O720, O721, O722 respectively. If any four of these diagnosis codes was assigned to the mother then PPH was set to 1, if a mother did not have anyone of these diagnosis codes then PPH was set to 0 for no PPH.

Mother's Age

The age of the mother when giving birth. For the EDA this was grouped into the following age bands: 19 and Under, 20-24, 25-29, 30-34, 35-39 and 40+. For the risk adjusted comparison age bands were not used and the mothers age was used.

Ethnicity

Ethnicity is recorded as 26 different ethnic groups. In this research the ethnicity groups were classed as one of the five groups: European, Māori, Pacific, Asian, Other or Non Response. Table 3.3 shows the grouping of ethnicity used for this research.

Table 3.3: Mapping of Ethnicities

European	Māori	Pacific
European not further defined	Māori	Pacific Peoples not further defined
New Zealand European		Samoan
Pakeha		
Other European		Cook Island Māori
		Tongan
		Niuean
		Tokelauan
		Fijian
		Other Pacific Peoples
Asian	Other	NR
Asian not further defined	Middle Eastern	Don't know
Southeast Asian	Latin American/Hispanic	Refused to answer
Chinese	African (or cultural group of African origin)	Response unidentifiable
Indian	Other (retired 01/07/2009)	Not stated
Other Asian	Other ethnicity	

Gestation

Is recorded in weeks. For the EDA has been grouped into the following categories: 0-37 weeks pre-term, 38-42 weeks normal, 42+ weeks post term.

Parity

Parity is the number of times a mother has previously given birth and this is recorded from 0 to 14 times. For analysis work parity has been grouped into two categories: 1 for mothers who have never given birth before and 0 for mothers who have given birth at least once before.

Breech

This indicates if the mother has had a breech birth. Five different types of breech have been recorded. These are, an assisted breech delivery, assisted breech delivery with forceps, a breech extraction, a breech extraction with forceps and a spontaneous breech delivery. As breech birth numbers are very low these have been combined into one category called breech.

Birth weight

Birth weight is recorded in grams and for the EDA has been grouped into the following categories: $\leq 2499\text{g}$, 2500-4499g and 4500g+.

Chapter 4

Statistical Methods

In this chapter the statistical methods that are used in this thesis are described. This includes a description of the data that are investigated in the Exploratory Data Analysis (EDA) and an explanation of the funnel plots that will be analysed and displayed. The funnel plots include the unadjusted, risk adjusted and the winsorised funnel plots. Logistic regression and imputation methods are then presented.

4.1 Exploratory Data Analysis

The Exploratory Data Analysis (EDA) presents a summary overview of DHBs and their populations. It explores demographic characteristics such as age, ethnicity, deprivation index and the relationships between these characteristics. Maternal and birth characteristics including gestation, newborn's birth weight and parity are examined. Birth interventions and mode of delivery are explored. Potentially important predictors of PPH are presented and the relationships among the variables are investigated. Lastly, comparisons among DHBs are presented and the differences between DHBs in terms of demographic, maternal and birth characteristics and PPH are investigated. The EDA is a purely exploratory analysis where results are presented in tables and graphs.

4.2 Funnel Plots

This section introduces components, functions and advantages of the funnel plot in the context of health related studies. A funnel plot is useful for providing a graphical representation of outcomes or health indicators across different providers (Spiegelhalter, 2005a). It is a scatter plot of an outcome against a measure of precision. An institution can be defined as a health provider, hospital, surgeon etc. In particular the funnel plot draws attention to the important relationships between the outcomes and volume of cases and can easily identify the outliers. (Sterne and Egger, 2001; Spiegelhalter, 2005a)

In the funnel plot the observed indicator for each institution is plotted against a precision measure. A 'target' indicator value is determined and a line is drawn as this value. The target can be the average across all institutions or a pre-specified value. Control limits are calculated as functions of the precision measure and then added to the plot to form a funnel around the target. This aids the understanding of where the observations lie in relation to each other and the control limits and identifies outliers, those who are performing well and those who are not (Spiegelhalter, 2005a).

With the aid of confidence limits it makes it easy to identify the outlying units. DHBs are used in this analysis however any unit of analysis could be used. Other analysis in the health sector have used hospitals, surgical teams, General Practitioners, or individual surgeons (Coory et al., 2007; Gale et al., 2006).

An advantage of funnel plots is that there are no false rankings of institutions compared to league tables where there must be rank order (Spiegel-

halter, 2005a). For example in a league table one hospital must be at the top and one must be at the bottom. Another important aspect of a funnel plot is that it can allow for additional variation. If a funnel plot is over-dispersed then adjustments for this can be included, such as using winsorisation or adjustment for additional variables that are important to predict the outcome (Spiegelhalter, 2005a).

The funnel plot for proportions has four components

1. An indicator Y . In this study Y is the proportion of births in which PPH occurs.
2. A target θ_0 for Y which denotes the expectation, so that $\mathbb{E}(Y|\theta_0) = \theta_0$ for the providers considered 'in control'.
3. A precision parameter ρ , which determines accuracy of the indicator. So for a given DHB that is in control and the target being achieved is the null distribution of Y is taken as $p(y|\theta_0, \rho)$, where ρ is proportional to the inverse of the variance of Y where n is the sample size. Since Y is a proportion we have $\mathbb{E}(Y|\theta_0) = \theta_0$ and $\text{Var}(Y|\theta_0) = \theta_0(1 - \theta_0)/n$

Given that the first two moments of rate p are

$$\begin{aligned} E[Y|\theta_0] &= \theta_0 \\ \text{Var}(Y|\theta_0) &= \theta_0(1 - \theta_0)/n \end{aligned}$$

we can parameterise these using a location θ_0 and precision ρ where

$$\begin{aligned}\rho &= \frac{g(\theta_0)}{\text{Var}(Y|\theta_0)} \\ &= \frac{g(\theta_0)}{\theta_0(1 - \theta_0)/n}\end{aligned}$$

for some arbitrary function $g(\cdot)$. The precision parameter can be made independent of θ_0 by setting $g(\theta_0) = \theta_0(1 - \theta_0)$, in which case $\rho = n$.

4. Control Limits $y_p(\theta_0, \rho)$ for a P-value p , where the chance of exceeding these limits for an in control unit is p . The control limits can then be calculated as

$$Y_p(\theta_0, \rho) = \theta_0 \pm Z_p \sqrt{\text{Var}(Y|\theta_0)} = \theta_0 \pm Z_p \sqrt{\frac{\theta_0(1 - \theta_0)}{n}} \quad (4.1)$$

Given a series of I observations, Y_i is associated with the precision parameter ρ_i . A funnel plot then can be constructed as a plot of Y_i against ρ_i , with θ_0 as the target which can be shown as a horizontal line and the control limits are superimposed on the plot as a function of the parameter ρ .

The above section describes the general form of the funnel plot. This now can be applied to the NMDS where the rate of PPH will be plotted against each DHB.

4.2.1 Unadjusted Funnel Plot

An unadjusted funnel plot uses the unadjusted rate, Y_i and plots this against the population size $\rho_i = n_i$. The unadjusted plot is the first step to investigating and displaying the raw rates of PPH for each DHB. This approach does not take into account that each DHB is made up of different popula-

tion mixes which would need to be adjusted for.

4.2.2 Risk Adjusted Funnel Plot

Funnel plots are not limited to a single rate but can be used for more complex models to estimate the rate of interest. An risk adjusted funnel plot takes into account factors that may have influenced the outcome of interest. The risk adjustment is carried out using a judgment based modelling procedure where the choice of covariates are based on variation in patient mix that occurs between units (DHBs). This is to allow a for a fair comparison between DHBs to occur.

The target θ_0 is still the national rate of PPH this is displayed as the centre-line. A logistic regression model is used for the risk adjustment to calculate the expected number of events. The logistic model is used to derive a probability of an event occurring (say PPH) for individuals with a particular set of covariates. The predicted values for each DHB are summed over the set of individuals that have given birth in each DHB to give the expected number of events. This can be contrasted with the observed number of events O to give a standardised event ratio where this can be calculated by:

$E = \sum_i^n \hat{p}_i$, where $\hat{p}_i$ is the predicted probability of the PPH individual i ,

$O = \sum_i^n x_i$, where $x_i = 1$ if PPH occurs and $x_i = 0$ otherwise.

We then calculate the standardised ratio as $O/E \times N$, where N is the national rate.

This is the risk adjusted rate which can then be plotted against each DHBs population. The control limits use the same formula as the unadjusted funnel plot, now with the adjusted rate (Spiegelhalter, 2005a). For more details on this approach and logistic regression, this is explained in more

detail in section 4.3.

4.2.3 Winsorised Funnel Plots

The previous two funnel plots methods unadjusted and risk adjusted are based on the assumption that the null target distribution, $f(y|\theta_0, \rho)$, fully expresses the variability of the in control units. However this may not be the case as the data could actually be ‘overdispersed’. Overdispersion is the presence of greater variability than is expected in the dataset (Berk and MacDonald, 2008).

As the data becomes overdispersed it becomes increasingly necessary to take this overdispersion into consideration. If the above assumption is violated then this would suggest that the data is overdispersed (around the target). This may occur because of a larger number of unmeasured co-variates that have not been accounted for in the risk adjusted method. The winsorisation approach attempts to adjust for this overdispersion (Spiegelhalter, 2005a)

There are two approaches to winsorisation

1. A standard GLM approach
2. Winsorisation using a random effects model

The GLM approach adds a factor ϕ that inflates the null variance and limits the extreme values and draws them into the mean. The GLM approach reduces the effect of large outliers (Spiegelhalter, 2005b). The random effects model adds a constant term to the sampling variance of each DHB unit. These methods are described in more detail in the next sections.

4.2.4 Winsorisation using general linear modelling

The standard GLM approach will add a factor ϕ , that inflates the null variance by a certain percentage factor k . This changes the extreme Z – score values bringing them closer to the mean and the target. Which in turn reduces the treatment effect.

The precision parameter ρ , is calculated by

$$\rho = g(\theta_0)/\mathbb{V}_0(Y|\theta_0, \rho) \quad (4.2)$$

where the subscript on $\mathbb{V}_0$ has now been introduced to indicate this situation with no allowance for over-dispersion.

Here a multiplicative approach is used. This introduces a over-dispersion factor of ϕ that inflates the null variance, so that

$$\mathbb{V}(Y|\theta_0, \rho, \phi) = \phi \mathbb{V}_0(Y|\theta_0, \rho) = \frac{\phi g(\theta_0)}{\rho} \quad (4.3)$$

Note the previous equation used $g(\theta_0)\rho = \theta_0(1 - \theta_0)/n$ to specify the variance. If all sample units I are assumed to be in control then ϕ can be estimated by:

$$\hat{\phi} = \frac{1}{I} \sum_i \frac{(y_i - \theta_0)^2 \rho_i}{g(\theta_0)} = \frac{1}{I} \sum_i z_i^2 \quad (4.4)$$

where z_i is the standardized Pearson residual given by

$$Z_i = \frac{Y_i - \theta_0}{\sqrt{V_0(Y_i|\theta_0, \rho_i)}} \quad (4.5)$$

The current control limits can then be inflated by a factor $\sqrt{\hat{\phi}}$ around θ_0 based on the previous control limits. Over-dispersed control limits can be calculated as in equation 4.1 which also include the inflated factor $\hat{\phi}$ (Spiegelhalter, 2005a).

$$y_p(\theta_0, \rho) = \theta_0 \pm z_p \sqrt{\hat{\phi}g(\theta_0)/\rho} \quad (4.6)$$

4.2.5 Winsorised Estimate using the Random Effects

The second approach for adjusting for overdispersion is using the winsorised estimate as calculated above and adding a random effects term τ . This is an additive variance model, so for each DHB the variance is increased by the same amount.

The random effects model assumes that Y_i has an expected value of $E(Y_i) = \theta_i$ and a variance of $V(Y_i) = \sigma_i^2$. For ‘on target’ DHBs it is assumed that θ_i is drawn from a distribution and i is for each DHB, distributed with a mean θ_0 and standard deviation τ . A standard ‘methods of moments’ estimator can be used to calculate τ (Spiegelhalter, 2005a). The null hypothesis is now represented by a distribution rather than a single point.

In general

$$E(Y_i) = \theta_i \quad (4.7)$$

then

$$Var(Y_i) = \frac{\theta_i(1 - \theta_i)}{n_i} \quad (4.8)$$

where n_i is the sample size from each Y_i that is observed.

To adjust for overdispersion using a random-effects approach it is assumed that

$$\theta_i \sim G[\theta_0, \tau^2] \quad (4.9)$$

where $G[\theta_0, \tau^2]$ is a distribution with a mean θ_0 and variance τ^2 .

We therefore estimate θ_i by p_i the observed rate for each DHB in this case

$$Var[Y_i] = \theta_i(1 - \theta_i)/n_i \sim p_i(1 - p_i)/n_i = s_i^2 \quad (4.10)$$

The method of moments estimate can be calculated as:

$$\hat{\tau}^2 = \frac{I\hat{\phi} - (I - 1)}{\sum_i w_i - \sum_i w_i^2 / \sum_i w_i} \quad (4.11)$$

where $w_i = 1/s_i^2$,

s_i^2 is the variance for each DHB proportion $p_i(1 - p_i)/n_i$ and $\hat{\phi}$ is the test for heterogeneity if $\hat{\phi} < (I - 1)/I$ then $\hat{\tau}^2$ is to be set to 0 and complete homogeneity is assumed.

The funnel plot confidence limits are given by:

$$\theta_0 \pm Z_p \sqrt{V_0(Y|\theta_0, \rho) + \tau^2} \quad (4.12)$$

4.3 Logistic Regression

A common method for regression applications is the analysis of binary data in the use of a Logistic Regression Model. Binary responses are a common outcome that are studied in medical research. For example the death of a patient due to disease, the presence of disease and treatment outcomes after surgery or occurrence of PPH. For this research it is of interest to look at a response variable Y and see how a set of predictor variables X are related to Y . For example these predictors could be demographic characteristics, type of treatment and risk factors etc. The outcome variable, known as the response, can take the value of 0 or 1 where $Y=1$ denotes where the event has occurred (Harrell, 2001).

First let's look at a linear regression model that is denoted by:

$$E(Y|X) = x^T \beta$$

For binary outcomes we wish to model $P(Y_i = 1|X)$, where i indexes an

individual patient if not a hospital, there are many predictors let X denote a vector of X 's $(X_1, X_2, \dots, X_k)$. If a linear regression model is used to model binary outcomes the predictions of $P(Y = 1|X)$ may not be constrained between 0 and 1. Hence a generalized linear model is preferred for the analysis of binary response (Harrell, 2001).

A generalized linear model is made up of a linear predictor

$$\eta_i = \beta_0 + \beta_1 x_{1i} + \dots + \beta_p x_{pi}$$

and two functions a link function and a variance function. The link function describes how the mean, $E(Y_i) = \mu_i$, depends on the linear predictor using $g(\mu_i) = \eta_i$. The variance function describes how the variance, $var(Y_i)$ depends on the mean. $var(Y_i) = \phi V(\mu_i)$, where ϕ is the dispersion parameter.

For binary data the distribution is

$$Y_i \sim \text{Binomial}(1, \mu_i) = \text{Bernoulli}(\mu_i)$$

Where $\mu_i = P(Y_i = 1)$

Then

$$E(Y_i) = \mu_i$$

and

$$var(Y_i) = \mu_i(1 - \mu_i)$$

Therefore the variance function is given by

$$V(\mu_i) = \mu_i(1 - \mu_i)$$

The link function $g(u_i)$ must map μ_i from (0,1) to the range $(-\infty, \infty)$ where,

$$g(\mu_i) = \text{logit}(\mu_i) = \log \left(\frac{\mu_i}{1 - \mu_i} \right)$$

The logistic regression model links the mean $\mu_i = P(Y = 1|X)$ to the linear predictor using

$$\begin{aligned} \text{logit}(\mu_i) &= \log \frac{\mu_i}{1 - \mu_i} \\ &= X_i^T \beta \end{aligned}$$

If the factors are additive then this model will assume that for every predictors X_j

$$\begin{aligned} \text{logit}(\mu_i) &= \text{logit}(P(Y_i = 1|X)) = \beta_0 + \beta_1 X_{i1} + \dots + \beta_j X_{ij} + \dots + \beta_k X_{ik} \\ &= \beta_j X_{ij} + C \end{aligned}$$

where if all other factors are held constant, C is defined

$$C = \beta_0 + \beta_1 X_1 + \dots + \beta_{j-1} X_{j-1} + \beta_{j+1} X_{j+1} + \dots + \beta_k X_k$$

The parameter β_j can be interpreted as the change in log odds for a unit change in X_j , if X_j represents a single factor and all other factors remain constant. This can also be written in the terms of odds ratio:

$$\begin{aligned} \frac{\text{odds}(Y = 1|X_1, X_2, \dots, X_j + 1, \dots, X_k)}{\text{odds}(Y = 1|X_1, X_2, \dots, X_j, \dots, X_k)} &= \exp[\beta_j X_j + \beta_j - \beta_j X_j] \\ &= \exp(\beta_j) \end{aligned}$$

Therefore, a one unit increase in X_j increases the odds that $Y = 1$ by a

factor of $\exp(\beta_j)$. To demonstrate only one predictor X will be used that has a binary outcome of 0 or 1. The model can be written as:

$$\begin{aligned}\text{logit}(Y = 1|X = 0) &= \beta_0 \\ \text{logit}(Y = 1|X = 1) &= \beta_0 + \beta_1\end{aligned}$$

β_0 is the log odds where $Y = 1$ and $X = 0$. The difference between these two equations is β_1 . This can be seen as the difference when $X = 0$ and when $X = 1$. Therefore the regression parameters can be interpreted by:

$$\begin{aligned}\beta_0 &= \text{logit}(P^0) = \log(P^0/(1 - P^0)) \\ \beta_1 &= \text{logit}(P^1) - \text{logit}(P^0)\end{aligned}$$

where P^0 is $P(Y = 1|X = 0)$ and P^1 is $P(Y = 1|X = 1)$. If we add a continuous predictor X the regression equation becomes

$$\text{logit}(Y = 1|X) = \beta_0 + \beta_1 X_1$$

where this model assumes a straight line in the log odds and that for one unit increase in X will increase the odds by a factor of $\exp(\beta_1)$.

This can be simplified to an odds ratio for each estimate as

$$\frac{\text{odds}(X = 1)}{\text{odds}(X = 0)} = \exp(\beta_1)$$

where $X=0$ is the reference level and for large samples the odds ratio has the 95% confidence interval:

$$\exp(\hat{\beta}) \pm 1.95\sqrt{\text{Var}(\hat{\beta})}$$

Goodness of fit

The goodness of fit test describes how well the model fits the data. There are few measures to assess the goodness of fit for logistic regression models. Pearson and Deviance residuals are calculated for logistic regression models and these measures can be assessed. Residual plots using the Deviance and Pearson residuals are used to check influential outliers and systematic trends.

The deviance can be used for unweighted data and is used to compare the maximised values of the log likelihood function for the maximal and the model of interest. The deviance is defined as:

$$D = 2[\log L_{max} - \log L]$$

where L_{max} is the likelihood for the saturated model and L is the likelihood for the model of interest. In both cases the likelihood is evaluated at the maximum likelihood estimates of the parameters.

In large samples the deviance follows an approximate chi-square distribution $D \sim \chi^2_{n-p}$ where n is the number of observations and p is the number of parameters. The Pearson residuals can be tested using chi-square test. This compares the observed and expected values, using a chi-square distribution χ^2_{n-p} .

A Hosmer-Lemeshow test can also be used to assess the goodness of fit for a binary logistic model. It tests whether or not the observed event rates match the expected event rates and follows a chi-square distribution with $n - 2$ df.

4.3.1 Choice of Model

As there are a large number of possible explanatory variables to apply to the risk adjustment funnel plot, choosing the 'most appropriate' model can be a tedious task (Harrell, 2001).

An advantage with logistic regression and any regression model, is you can apply three different methods to identify the most 'appropriate model'. These methods are forward, backward and stepwise elimination. Below is a explanation about each choice of model selection. (Harrell, 2001)

Backwards Elimination:

This method starts with a model containing all the explanatory variables and eliminates variables one by one, at each stage choosing the variables for exclusion as the one leading to the smallest decrease in the AIC value. The AIC value is used to judge when further exclusions would represent a significant deterioration in the model.

Forward Selection:

This method starts with a model containing none of the exploratory variables and then considers variables one by one for inclusion, at each step the variable added is one that results in the biggest increase in AIC. An AIC value is used to judge whether further additions would represent a significant improvement in the model.

Stepwise Regression:

This method is essentially a combination of forward selection and backward elimination. It starts with no variables in the model and variables are added using the forward selection method. With each addition of a variable, a backward elimination process is considered to assess where the variables entered earlier might now be removed because they no longer contribute significantly to the model. The AIC value is used to detect vari-

ables to be kept or removed, a entry and exit value can be used.

The stepwise logistic regression procedure considers a number of possible multiple regression models and selects subsets of parameters to test for possible addition to the model or elimination from the model. This is the most preferable method as it has the ability to add and remove covariates. The stepwise method is used to select the best model. This model is then applied to the imputation method used.

4.4 Imputation

This section presents approaches and methods for imputation. In detail it describes imputation, missing data mechanisms, the choice of variables and the most suitable imputation approach.

4.4.1 Introduction

Imputation is the substitution of a particular value for a missing value. It uses a set of methods, rules or a set of conditions that compute a value to be imputed for a missing value (Gelman and Hill, 2007).

As potential predictors for the model can have large numbers of missing values it is an essential step to impute these values. Without substituting these missing values the results will become biased. It can also severely reduce power and produce biased estimates (Arnold and Kronmal, 2003). There are many imputation methods for dealing with missing data and a selected few will be described below.

Imputation is used to prevent data becoming misleading of the population and non-representative of real world data. It is useful to impute values to allow the data to become more representative and help deal with missing

data. One variable may be more susceptible to missingness than any other variable. It is sensible to fill the gaps (missing values) with sensible values which results in the imputation being unbiased (Gelman and Hill, 2007).

In R, a language and environment for statistical computing and graphics, missing values are denoted by NAs. If values are missing the regression automatically excludes them and therefore can limit the amount of information available for analysis. These factors that could be removed can be potentially good predictors of the data model and if missing, biased estimates and results will be produced.

It is best to use imputation when there are small item non-response or missing values for critical variables, so that we can be confident that the effect of imputation is minimal, and that the methods used are strongly informed by the data. It is best to first evaluate variables and to identify what type of missingness there is prior to imputing values.

4.4.2 Mechanisms of Missingness

As there are many different imputation methods first useful to know why the data is missing and learn the pattern of missingness. This can help determine the most appropriate imputation method. There are four general conceptions of missing data which are known as missing data mechanisms. These are missingness completely at random (MCAR), missing at random (MAR), missing not at random (MNAR) and missing that depends on the missing value itself (not ignorable)(Gelman and Hill, 2007).

MCAR (Missing Completely at Random)

MCAR missingness means that the units with missing data can be treated as a simple random sample of the total sample: and in particular that miss-

ingness does not depend on either the covariates or the outcome variable of interest. (Scheffer, 2002; Rubin, 1976).

MAR (Missing at Random)

Here the probability that an individual value will be missing is independent of $Y^{(m)}$ (but may depend on $Y^{(o)}$). If this assumption holds likelihood based inferences are valid. For example if gender, ethnicity and age are provided but gestation is missing at random, then the probability of a non-response to this variable depends on these others being fully recorded variables. Here it is acceptable to exclude the missing cases, as long as the regression controls for all variables that affect the probability of missingness (Little and Rubin, 1989; Scheffer, 2002).

MNAR (Missing Not at Random)

Missingness that depends on unobserved predictors. When the probability that an individual value will be missing depends on $Y^{(m)}$ (Arnold and Kronmal, 2003).

Missingness that depends on the value itself

When the probability of missingness depends on the potentially missing variable itself. So for example one DHB could be more likely to not respond to a question for some reason, this could be to do with training, quality etc. If the observations with these missing values are discarded it can lead to results that are not truly representative of the DHB. Complete cases only could be a solution. However this would discard cases that are not complete cases and can lead to the above problem of biased estimates (Gelman and Hill, 2007). Bias is the biggest problem associated with NMAR missingness, and it cannot be corrected for. It cannot be tested for, since we lack the ability to detect the correlation between the response indicator and the unobserved outcome.

4.4.3 Related Studies

A study by Schenker et al. (2006) on NHIS (National Health Interview Survey) health and income data describes and evaluates the methods and approaches of multiple regression imputation. The data is from the 2005 NHIS from the National Health Centre for Health. It is based on the National Health and Income Survey which contains a large proportion of non response for total family income and personal earnings from employment. The study uses multiple imputation which is similar to the approach that will be used with the NMDS. The method used takes the form; let X denote the fully observed variables and let $Y^{(1)}, Y^{(2)}, \dots, Y^{(k)}$ denote the k variables with missing values, ordered by the amount for missingness from least to most. The process then follows for $Y^{(1)}, Y^{(2)}, \dots, Y^{(k)}$ in c rounds. In the first instance the regression of $Y^{(1)}$ on X is fitted to the cases with $Y^{(1)}$ and the missing values of $Y^{(1)}$ are randomly imputed from the fitted model. Then the regression of $Y^{(2)}$ on X and $Y^{(1)}$ is fitted with the $Y^{(2)}$ observed and then the $Y^{(2)}$ values are imputed and so forth. It is a continuous loop until all missing values for the variables listed are imputed. The main findings of this study found was that multiple imputation usually results in lower estimated standard errors than data that does not have any imputation.

Another study by Arnold and Kronmal (2003), describes the experience of using cardiovascular health study of imputing missing data on a large number of variables that were collected at baseline. The data used in this study was designed to identify risk factors for cardiovascular disease in individuals aged 65 years and over. When participants were first examined (this is the baseline measure) an extensive clinical examination was conducted. Multiple imputation was applied to missing data where an iterative approach is used on these variables.

When it comes to the choice of predictors in the imputation model it is

important to include a large number of predictors and is also necessary to use such variables that will be used in further analysis (Rubin, 1996; Meng, 1994; Schenker et al., 2006).

4.4.4 Methods of Imputation

There are many different methods for imputing values. It is important to choose the most sensible approach for the type of data that will be imputed. Some methods of imputation which potentially could be used for this data are described below.

Mean Imputation

Mean imputation imputes the mean value for all missing values. It takes the mean of observed values of the variable for complete data and imputes this value into all missing values. It gives a sensible overall mean, assuming the data is MAR. This approach can only be done for continuous outcome variables. However it can distort the distribution. This approach also ignores the relationships among variables.

Hot Deck Imputation - within classes

This approach divides data into imputation classes then replaces each missing value with the data from a randomly chosen donor in the same class. This method assumes MAR (where X =imputation class), it preserves distributions within the classes and it works well with moderately large classes (30+). This method finds it difficult to deal with multivariate (X,Y) relationships.

Hot Deck Imputation - Distance based

Chooses values from the most similar donors available and is based on a multivariate distance. This method can choose the best match or randomly

from k best. As it is multivariate distance it is possible to limit the donor usage by including a penalty for heavy use of using values further away. This model is more robust as it allows for multivariate ($\mathbf{X}, \mathbf{Y}$) relationships, though it can be less efficient to run.

Regression Imputation

In this approach, missing values are estimated based on predicted values generated by a regression model. The regression model is based on known variables for the missing unit of observation and requires that all values used as predictors are complete cases for the variables used in the regression.

Multiple Imputation

Rubin (1987) describes multiple imputation as a technique used that replaces each missing value with two or more values representing a distribution of possibilities. In summary the method of multiple imputation involves firstly imputing data under an appropriate model of choice and repeating this step to ensure the data is filled in. Secondly, analyse each dataset and or variable separately to identify and obtain desired parameter estimates and standard errors. And lastly combine all results from above to form a full dataset (Fox, 2008; Arnold and Kronmal, 2003).

4.4.5 Choice of Variables and Imputation Method

As there are a variety of imputation methods to choose from how do we know which is the most appropriate to use?

If mean imputation were to be used it assumes that the data is MAR. However this could severely distort the distribution as there are several variables that require imputation that are continuous. It would not make

much sense to impute via this method. If hot deck imputation was chosen, donors of similar characteristics are chosen which allows for multivariate relationships. This is a more preferable method. For the NMDS we may want to impute through matching. For example each unit of Y that is missing, find a unit with the same values for a set of predictors, X in the observed data and copies the Y value. This would be a sensible approach as it would not distort the data. The best approach would be to use a multiple imputation regression approach.

The advantage of regression imputation approach is that you can use a separate set of regression models for each Y and is easier to fit a more reasonable model. The disadvantage is that you have to be careful in ensuring that the separate regression models are consistent with each other so that all regression models should be fairly similar (Gelman and Hill, 2007).

There are several variables that have a large number of missing values that are important predictors of PPH. These are gestation, parity and birth weight. First these three variables need to be investigated and explored to determine the pattern of missingness.

Chapter 5

Exploratory Data Analysis

In this section the population of interest is defined and then explored. The Exploratory Data Analysis (EDA) presents a summary overview of DHBs and their population demographic characteristics such as age, ethnicity, deprivation index and their relationships. Maternal and birth characteristics are then presented. These include gestation, newborns birth weight and parity. Birth interventions and model of delivery are explored and lastly the potential predictors of PPH are presented and relationships among variables are explored. This establishes our expectations about relationships among the variables of interest. EDA is a purely an exploratory analysis where table and graphs are presented displaying but not quantifying relationships among two or three variables at a time.

5.1 Data Description

In 2007 New Zealand was divided into 21 DHBs. See Figure 5.1 for a map of NZ DHBs.

In the 2007 data there were 56,681 distinct mothers who gave birth to 57,478 babies. For this analysis we are interested in single births therefore

Figure 5.1: Map of NZ DHBs

mothers who gave birth to more than one baby were excluded. Mothers who gave birth overseas or who are overseas residents are also excluded from the analysis. See section 3.5 for a more detailed description of exclusions from the dataset. The analysis in this section will only look at singleton births. There are 55,811 mothers who gave birth to 55,811 babies. This is the total number of mothers that will be used in the analysis.

Table 5.1: The Total Number of Births for each DHB.

District Health Board	Total Number of Births (%)
Counties Manukau	7,986 (14.13%)
Waitemata	6,797 (12.18%)
Auckland	6,091 (10.91%)
Canterbury	6,039 (10.82%)
Waikato	4,757 (8.52%)
Capital and Coast	3,511 (6.29%)
Bay of Plenty	2,616 (4.69%)
MidCentral	2,004 (3.59%)
Hawke's Bay	1,986 (3.56%)
Hutt	1,918 (3.44%)
Otago	1,876 (3.36%)
Northland	1,850 (3.31%)
Nelson Marlborough	1,482 (2.66%)
Taranaki	1,430 (2.56%)
Lakes	1,380 (2.47%)
Southland	1,359 (2.44%)
Whanganui	783 (1.40%)
Tairāwhiti	649 (1.16%)
South Canterbury	602 (1.08%)
Wairarapa	455 (0.82%)
West Coast	340 (0.61%)
Total	55,811 (100%)

Table 5.1 shows the number of births in each DHB in 2007 in rank order. Counties Manukau has the largest proportion of births at 14.13% and West Coast has the smallest proportion of births in NZ at 0.61%.

It is not surprising that the first four DHBs listed in table 5.1 have the highest proportion of births, (Counties Manukau, Waitemata, Auckland and Canterbury, 14.13%,12.18%,10.91% and 10.82% respectively) as these are the largest populated areas in New Zealand (Statistics New Zealand, 2012). Table 5.2 shows Waitemata, Canterbury, Counties Manukau and Auckland have 10-12% of the population and therefore should be expected

to have the highest number of births. Likewise that South Canterbury, Wairarapa and West Coast (1.08%, 0.82% and 0.61% respectively) have the smallest number of births in New Zealand as these are small populated areas. This can be compared to table 5.2 where West Coast, Wairarapa and South Canterbury only have 1% of the NZ population each. From this table 5.1 also demonstrates that there is a large variation in numbers of births per DHB. Some DHBs have a very small number of births compared to other DHBs which report a very large number of births.

Table 5.2: The NZ Population for each DHB

District Health Board	Population (%)
Waitemata	481,611 (11.96%)
Canterbury	466,407 (11.58)%
Counties Manukau	433,086 (10.75)%
Auckland	404,619 (10.05%)
Waikato	339,192 (8.42%)
Capital and Coast	266,658 (6.62%)
Bay of Plenty	194,931 (4.84)%
Otago	179,397 (4.45%)
MidCentral	158,841 (3.94%)
Northland	148,440 (3.69%)
Hawkes Bay	148,248 (3.68%)
Hutt	136,101 (3.38%)
Nelson Marlborough	130,062 (3.23%)
Southland	106,827 (2.65%)
Taranaki	104,277 (2.59%)
Lakes	98,319 (2.44%)
Whanganui	62,211 (1.54%)
South Canterbury	53,877 (1.34%)
Tairāwhiti	44,463 (1.10%)
Wairarapa	38,613 (0.96%)
West Coast	31,326 (0.78%)
Total	4,027,506 (100%)

5.2 Demographic Characteristics

In this section the demographic characteristics of the 2007 NMDS investigates age, ethnicity, deprivation index, gender of the baby and their relationships are explored.

Mother's Age

Figure 5.2 shows the percentage of mothers by age. This distribution shows the age of mothers range from 13 to 51 years. Most mothers giving birth in 2007 are aged 32 and 33 years. The average age of the mother is 29 years. There are smaller proportions of mothers aged under 19 years and over 40 years.

Figure 5.2: Frequency of Mother's Age

Mother's Ethnicity

The largest proportion of mothers are of European ethnicity (58%), as shown in table 5.3 followed by Māori, (19%), Pacific (10%) and Asian (9%) ethnicity. Other and Unknown are very small proportions (3% and 1% respectively) of mothers who gave birth in 2007. There are 398 missing ethnicity

values.

Table 5.3: The Total Number of Mothers Ethnicity

European	Māori	Pacific	Asian	Other	Unknown	Total
32,204 (58%)	10,804 (19%)	5,712 (10%)	5,276 (9%)	1,417 (3%)	398 (1%)	55,811

Deprivation Index

Deprivation Index is an index of socioeconomic deprivation based on the 2006 census data, and calculated for each meshblock from Statistics NZ (Statistics New Zealand, 2012). The ordinal scale ranges from 1 to 10, where 1 represents the areas with the least deprived and 10 the most deprived areas. The deprivation index is derived from nine factors from the 2006 census and combined into a score for each meshblock, reflecting 10 different deprivation scores. A meshblock is defined as a geographical unit defined by Statistics New Zealand, for 2006 it contains a median of approximately 87 people (Statistics New Zealand, 2012).

As shown in Figure 5.3 a large proportion of mothers live in the most deprived areas. There are smaller proportions of mothers who live in the least deprived areas. 14.61% of mothers are situated in the deprived index of 9, and 13.81% in the deprived index of 10. At the least deprived indices of 1, 2 and 3. There are 7% of mothers in each of these areas. There are 37 missing values for this variable.

Gender

Of the 55,811 babies born 48% of births are female and 52% are male.

Mother's Ethnicity by Mother's Age

Figure 5.4 shows mother's ethnic group by age. European is the largest ethnic group for all age groups over 20 years. In the 19 years and under age group, 48% of mothers are Māori and 37% are European. This age group

Figure 5.3: Percentage of mothers by Deprivation Index

has the largest proportion of Māori ethnicity compared to any other age group. Given that Māori mothers are 19% of all births in 2007, and Māori are 15% of the NZ population they are over-represented in the 19 and Under and 20-24 age group (Statistics New Zealand, 2012). For the 20-24 age group there are 32% Māori and 43% are European. For the Asian Ethnicity group the largest proportion of mothers are in the 25-29 age group at 12% and also in the 30-34 age group at 11%. Pacific People have large proportions of mothers in the 20-24 age group at 15% and at the 25-29 age group at 12%. A chi-squared test shows that there is an association between age group and ethnicity ($\chi^2 = 5967$, $df = 20$, $p\text{-value} < 0.0001$).

Mother's age by Deprivation Index

Large proportions of women aged 30-34 years are in the least deprived areas of 1-4, with approximately 35% in each index and small proportions of these mothers in the most deprived area 10 at 20%. For the younger women in the 19 and under age group, 14% of mothers are based in the

Figure 5.4: Percentage of Mothers Ethnic Group by Age

most deprived areas of 10 and 2.9% based in the least deprived area of 1. Also mothers who are in the age group 20-24 years have large proportions of mothers in the most deprived areas, compared to the least deprived areas, 26% to 6%. For the 25-29 age group there are even proportions of mothers across each deprivation index, see figure 5.5. A Chi-square test shows that there is an association between deprivation index and mothers age ($\chi^2 = 3754$, $df = 45$, $p\text{-value} < 0.0001$).

Deprivation Index by Mothers Ethnic Group

There is an association between mother's ethnic group and deprivation index ($\chi^2 = 11398$, $df = 36$, $p\text{-value} < 0.0001$). There are large proportions of European ethnicity in deprivation index 1-8, and smaller proportions in deprived deciles 9 and 10, see figure 5.6. In the deprivation index 10, there are large proportions of Māori, 40%, Pacific 31% and 20% European. In the deprivation index of 9, 29% are Māori, 44% European and 13% Pacific. This shows these two deprivation areas are made up of different proportions of ethnic groups. The Asian ethnic group is a constant

Figure 5.5: Deprivation Index by Mothers Age

proportion across the indices, approximately 10% in each area. The most deprived area is the only exception here with only 6% being Asian in this group.

Figure 5.6: Deprivation Index by Mothers Ethnicity

5.2.1 Maternal and Birth Characteristics

This section presents some key maternal and birth characteristics. These include gestation, birth weight, parity and PPH. These factors and their relationships are explored.

Postpartum Haemorrhage

There are 55,811 mothers who gave birth in NZ in 2007. Of these 5,249 (9.40%) had a PPH and 50,562 (90.60%) mothers did not have a PPH.

Gestation

Gestation is recorded in weeks and shows the length of pregnancy until a mother gives birth. A normal pregnancy can range from 37 to 42 weeks. If an infant is born before 37 weeks this is considered pre-term and infants born after 42 weeks are considered a post-term birth. We would expect to see in 2007, NMDS the majority of births occurring between 37 to 42 weeks (Ministry of Health, 2012b).

Figure 5.7 shows there are very small proportions of mothers who have given birth between 14-34 weeks. At 37 weeks this number increases dramatically to a large peak at around 40 weeks. This then drops just as steadily as it rose at 42 weeks. This variable has 1,009 (1.84%) missing values.

Birth weight

The average full term baby weighs 3500g (seven and a half pounds, (Ministry of Health, 2012a). Around 95% of babies weigh between 2500g and 4250g. If a baby weighs less than 2500g, this is considered a low birth weight. In the NMDS, birth weight ranges from 225g to 7000g, with an average weight of 3466g. The data shows a left-skewed distribution of birth weight, with the highest proportion of birth weights at around 3600g as seen in figure 5.8. There are 448 missing values for this variable.

Figure 5.7: Gestation

Figure 5.8: New borns birth weight

Parity

There are 19,014 (34.07%) new mothers, who had never given birth before

and 5,774 (10.35%) mothers have previously given birth once before, the most extreme is a mother who has given birth 14 times. This variable has 26,083 (46.73%) missing values (see Table 5.4). This is a very large number of missing values (near 50%). Most of these values are likely to be zero. As this is a key explanatory variable imputation will be carried out for parity in Chapter 7. For further analysis work parity has been grouped into two categories, one for mothers who have never given birth before and the second for mothers who have given birth at least once before.

Table 5.4: Frequency of Parity

Parity	Number of Mothers
0	19,014 (34.07%)
1	5,774 (10.35%)
2	2,950 (5.29%)
3	1,115 (2.00%)
4	484 (0.87%)
5	212 (0.38%)
6	104 (0.19%)
7	39 (0.07%)
8	21 (0.04%)
9	8 (0.01%)
10+	7 (0.01%)
Missing	26,083 (46.73%)
Total	55,811 (100%)

Parity by Age Group

For mothers with known parity, age by parity in figure 5.9 shows 98% of mothers who have only given birth once for age group 19 and under. 93% of mothers aged 20-24 have only given birth once. There are more mothers in the older age groups, 35-39 and 40+ that have given birth more than once. A test of association shows that there is a relationship between parity and mothers age ($\chi^2 = 4002$, $df = 5$, $p\text{-value} < 0.0001$).

Figure 5.9: Age by Parity for all Mothers

Parity by Deprivation Index

Parity by Deprivation Index shows for all deprivation indices excluding index 10, over 60% of mothers with known parity are first time mothers. Deprivation Index 2 only reports 57% of mothers giving birth for their first time and correspondingly a higher proportion of mothers who have previously given birth at 43%, see figure 5.10. The findings of higher rates of one or more prior births at higher deprivation indices is consistent with the earlier finding that birth rates are higher at higher deprivation indices. A test of association shows that there is a relationship between parity and deprivation index ($\chi^2 = 114$, $df = 9$, $p\text{-value} < 0.0001$).

5.2.2 Birth Interventions and mode of delivery

Birth Interventions

There are some common birth interventions that are used during child birth. These can include induction, epidural, episiotomy and manual removal of

Figure 5.10: Deprivation Index by Parity

the placenta. Episiotomy and manual removal of the placenta are two important factors for PPH (University of Virginia Health System, 2010; Harrison, 1998). In the NMDS 5,553 (9.95%) of mothers had episiotomy and 810 (1.45%) had a manual removal of the placenta.

Mode of Delivery

There are many medical tools that can assist the mother with delivery. Not all mothers require these procedures and are therefore classified as a 'normal birth'. There are large numbers of emergency Caesarean sections (7,732) and Elective Caesarean Sections (5,732, see Table 5.5). There are small proportions of other assisted births such as breech, the use of forceps or vacuum extraction. 66.46% (37,093) of mothers had a normal birth. Caesarean sections accounted for 24.12%, the remaining are breech births (0.25%), forceps (3.17%) and vacuum extraction (6.00%), (see Table 5.5). There are 5 different categories of breech births these are: an assisted breech delivery, assisted breech delivery with forceps to after-coming head, a breech extraction, a breech extraction with forceps to after-

coming head and a spontaneous breech delivery. As birth numbers are very low, these have been combined to one category called breech.

Table 5.5: Type of Births Procedures

Type of Birth	Number of Births
Emergency Caesarean Section	7,732(13.85%)
Elective Caesarean Section	5,732 (10.27%)
Breech	137 (0.25%)
Forceps	1,768 (3.17%)
Vacuum Extraction	3,349 (6.00%)
Normal Birth	37,093 (66.46%)
Total	55,811(100%)

5.3 Potential Predictors for PPH

This section looks at potential factors that can be related to PPH. As this dataset does not contain all factors that are associated a few variables have been selected to be investigated. These variables are most likely to have potential impacts on PPH. First a summary of the number of PPH for each DHB will be presented, then demographic, maternal, birth characteristics and birth interventions are explored.

5.3.1 District Health Boards

Table 5.6 shows in order of highest proportion of PPH for each DHB. This shows Auckland DHB has the highest proportion of PPH at 14.02%, followed by Otago with the next highest proportion at 11.19%. Tairāwhiti at 11.09%, Northland at 11.32%, Mid Central, Counties Manukau and Waikato at 10%. Nelson Marlborough and Southland DHBs have very small proportions 4.25% and 3.90% respectively. The national rate of PPH is 9.40%.

This table 5.6 shows where DHBs sit amongst the national rate of PPH. It shows that there are some much higher rates (14.02%) than the national rate and some very low rates (3.90%). Even though Tairāwhiti has a very low number of births, it has a high rate of PPH at 11.09%, compared to the national rate. Whereas Waitemata has a high number of births (6,797) but a lower rate of PPH at 7.55%. A test of association shows that there is a relationship between PPH and DHBs ($\chi^2 = 369$, $df = 20$, $p\text{-value} < 0.0001$).

Table 5.6: The number of Mothers who have had a PPH by DHB

DHB	Postpartum Haemorrhage			
	Yes	No	Total	(%)
Auckland	854	5,237	6,091	14.02
Otago	210	1,666	1,876	11.19
Tairāwhiti	72	577	649	11.09
Northland	204	1,646	1,850	11.03
Counties Manukau	835	7,051	7,886	10.59
MidCentral	211	1,793	2,004	10.53
Waikato	488	4,269	4,757	10.26
Canterbury	593	5,446	6,039	9.82
West Coast	30	310	340	8.82
Taranaki	118	1,312	1,430	8.25
Capital and Coast	284	3,227	3,511	8.09
Hutt	155	1,763	1,918	8.08
Lakes	110	1,270	1,380	7.97
Waitemata	513	6,284	6,797	7.55
Hawkes Bay	149	1,837	1,986	7.50
Bay of Plenty	186	2,430	2,616	7.11
Wairarapa	31	424	455	6.81
South Canterbury	41	561	602	6.81
Whanganui	49	734	783	6.26
Nelson Marlborough	63	1,419	1,482	4.25
Southland	53	1,306	1,359	3.90
Total	5,249	50,562	55,811	9.40

5.3.2 Demographics

This sections investigates mothers' demographic characteristics such as age and ethnicity against PPH.

Mother's Age

Table 5.7 shows the percentage of PPH by each age group. This shows the age group 40+ years has the highest percentage of PPH at 10.87%. This is approximately 2% higher than the 19 and under age group which has the lowest percentage of PPH at 8.67%. All other age groups have a rate which is close to the PPH national rate of 9.40%. A chi-square test shows there is no relationship between age and PPH ($\chi^2 = 8.46$, $df = 5$, $p\text{-value} = 0.1324$).

Table 5.7: Mother's Age by PPH

Age	Postpartum Haemorrhage			
	Yes	No	Total	(%)
19 and Under	387	4,075	4,462	8.67%
20-24	933	8,793	9,726	9.59%
25-29	1,263	12,274	13,537	9.33%
30-34	1,505	14,527	16,032	9.39%
35-39	939	9,073	10,012	9.38%
40+	222	1,820	2,042	10.87%
Total	5,249	50,562	55,811	9.40%

Mother's Ethnicity

Figure 5.11 shows the percentage of mothers ethnic groups for mothers who have had a PPH. The European group shows that 8.52% of mothers had a PPH. The Pacific ethnic group has the highest percentage of mothers who have had a PPH at 13.62%. Even though Pacific ethnicity makes up a total of 10.23% of the population of mothers who gave birth in 2007, a high proportion of these mothers had a PPH.

Even though European is the biggest ethnic group (58%, see table, 5.3) the

number of mothers have a lower rate of PPH at 8.52% compare this to 13.62% for the Pacific group. The Asian ethnicity have the second highest rate of PPH at 10.84%, and Māori at 9.14%. For a test of association there is a relationship between PPH and ethnicity ($\chi^2 = 162$, $df = 4$, $p\text{-value} < 0.0001$).

Figure 5.11: Mother's Ethnicity for mothers who have had a PPH

5.3.3 Maternal Birth Characteristics

This section investigates maternal birth characteristics such as parity, birth weight, gestation, episiotomy and removal of placenta against PPH.

Parity

Looking at parity against PPH there seem to be more first time mothers that have had a PPH, (11.07%) compared to mothers who have given birth at least once before (8.81%, see table 5.8). Note that there are 26,083 missing values for this variable. If all observations were complete, this may change

the percentage of mothers who have a PPH. A test of association shows a relationship between parity and PPH ($\chi^2 = 38.02$, $df = 1$, $p\text{-value} < 0.0001$).

Table 5.8: Parity by PPH

Parity	Postpartum Haemorrhage			
	Yes	No	Total	(%)
0	2,105	16,909	19,014	11.07
1+	944	9,770	10,714	8.81
Missing	2,200	23,883	26,083	8.43
Total	5,249	50,562	55,811	9.40

Birth Weight

The average birth weight for the NMDS for 2007 is 3466g. Any weight under 2500g is considered a low birth weight. For mothers who have had a PPH, 88% of birth weights range between 2500g to 4499g. There are smaller percentage of babies weighing 2499g or less (5%) and 7% weight over 4500g. see table 5.9 A Chi-Square test of association shows that there is a difference between PPH and babies' birth weights ($\chi^2 = 144.12$, $df = 2$, $p\text{-value} < 0.0001$).

Table 5.9: New Born's birth weight for mothers who had a PPH

Birth weight	Frequency
<2499	256 (5%)
2500-4499	4,660 (88%)
4500+	292 (7%)
Total	5,208 (100%)

Gestation

The proportion of pre-term mothers who have a PPH is 9.38% and the proportion of post-term mothers who have a PPH is higher at 15.71%. See table 5.10. A test of association shows that there is no difference between

gestation and PPH ($\chi^2 = 3.25$, $df = 2$, $p\text{-value} = 0.1960$).

Table 5.10: PPH by Gestation

Gestation	Yes	No	Total	(%)
Pre term (<37 weeks)	556	5,369	5,925	9.38
Normal (37-42)	4,596	44,211	48,807	9.42
Post-term (42+ weeks)	11	59	70	15.71
Missing	86	923	1,009	8.52
Total	5,249	50,562	55,811	9.4

Episiotomy and Removal of Placenta

A test of association shows us that there is an association between episiotomy and PPH ($\chi^2 = 152.31$, $df = 1$, $p\text{-value} < 0.0001$). Of the 5,553 mothers who had episiotomy 777 of these had a PPH (14.8%). For mothers who had the procedure to remove the placenta (810) 574 of these mothers had a PPH (70.8%). A chi-square test shows that there is an association between removal of the placenta and PPH ($\chi^2 = 3643.74$, $df = 1$, $p\text{-value} < 0.0001$).

5.3.4 Mode of Delivery and birth interventions

This section explores mode of delivery and birth interventions against PPH.

Table 5.11 shows the percentage of mothers who have had a PPH for the different types of birth. The use of forceps has a high percentage of PPH at 16.91% and for Emergency Caesarean Sections the rate is 15.11%. 14.27% of mothers who have a Vacuum Extraction have a PPH. 7.43% of mothers who had a normal birth have a PPH. This is a lower rate than the national average (9.40%). A chi-square test for a test of association shows that there is an relationship between the type of birth and PPH ($\chi^2 = 676.45$, $df = 9$,

p-value < 0.0001).

Table 5.11: Type of Birth by Postpartum Haemorrhage

Type of Birth	Postpartum Haemorrhage			
	Yes	No	Total	(%)
Emergency Caesarean Section	1,168	6,564	7,732	15.11
Elective Caesarean Section	533	5,199	5,732	9.30
Breech	14	123	137	10.22
Forceps	299	1,469	1,768	16.91
Vacuum Extraction	478	2,871	3,349	14.27
Normal Birth	2,757	34,336	37,093	7.43
Total	5,249	50,562	55,811	9.40

Chapter 6

Unadjusted Comparison

In this chapter we explore the DHB characteristics, PPH rates, ethnicity, age, gender of the baby, parity and deprivation index. The second section of this chapter presents the method and results for the unadjusted funnel plot.

6.1 DHB Comparisons

From the EDA we already know that DHBs have different population sizes, birth rates and PPH rates (see figure 6.1). As DHBs are an important part of this analysis the following section explores demographic and maternal characteristics of DHBs.

These figures are presented in geographical order from the top of the North Island to the bottom of the South Island. If the figures were to be presented in alphabetical order, the pattern of similarities and differences between adjacent DHBs would be lost. Therefore representing these figures in a geographical order helps gain a clearer understanding of the relationships between DHBs (see figure 5.1).

Figure 6.1: PPH comparison across DHBs

First we look at the PPH rate for each DHB and their 95% confidence intervals (see figure 6.1). The confidence intervals are calculated as: $\hat{\theta}_i \pm Z \sqrt{\frac{\hat{\theta}_i(1-\hat{\theta}_i)}{n_i}}$ where $\hat{\theta}_i = X_i/n_i$, and X_i = the number of PPH for DHB i and n_i = the total number of births for DHB i and $Z = 1.96$.

The PPH rate differs amongst DHBs. Auckland DHB has the highest rate at 14%, with very narrow confidence limits. Whereas Tairāwhiti and the West Coast have very wide confidence limits due to their smaller populations. Nelson Marlborough and Southland DHBs have the lowest PPH rate at 0.038 and 0.042 respectively.

6.1.1 Ethnicity

From figure 6.2 shows that Northland, Lakes and Tairāwhiti DHBs have the largest proportions of Māori ethnicity at 46%, Lakes 45% and Tairāwhiti 59%. Whanganui (35%), Hawke's Bay (34%), Bay of Plenty (32%) and Waikato (28%) have the next largest proportions of Māori. Auckland at

Figure 6.2: DHB by Ethnicity

9%, Canterbury, South Canterbury and Otago at 8% have the smallest proportions of Māori.

West Coast (87%), South Canterbury (86%), Otago (84%) and Nelson Marlborough (81%) have the highest proportion of European ethnicity. Counties Manukau (27%) and Tairāwhiti (36%) have the smallest proportion of European ethnicity.

Counties Manukau has the largest proportion of Pacific ethnicity at 31% followed by Pacific ethnicity are Auckland (19%), Waitemata (12%), Capital & Coast and Hutt (10%). Taranaki, West Coast and South Canterbury have the lowest proportions of Pacific ethnicity at 1%.

Auckland has the highest proportion of Asian ethnicity at 22%, followed by Waitemata and Counties Manukau at 15% and Capital & Coast at 10%. Wairarapa and West Coast have the lowest proportions of Asian ethnicity at 1%.

Overall we can see that the top of the North Island is largely made up of European, Māori, Pacific and Asian ethnicities. The middle of the North Island has the highest proportion of Māori (this area includes Lakes, Bay of Plenty, Tairāwhiti, Hawke's Bay, Taranaki and MidCentral). The lower part of the North Island is predominately made up of European ethnicity and approximately 18% Māori. This area consists of Whanganui, Wairarapa, Hutt and Capital & Coast DHBs. The South Island DHBs are largely made up of European ethnicity (80%). Visually we can see that the DHBs are made up of different proportions of ethnic groups. A test of association shows that there is a relationship between DHBs and ethnicity, ($\chi^2 = 14617$, $df = 80$, $p\text{-value} < 0.0001$).

6.1.2 Mother's Age

Tairāwhiti, Lakes and Whanganui DHBs have the youngest median age of mothers giving birth at 27 years. Capital & Coast have the highest median age at 32 years. Waitemata, Auckland and Canterbury have the next highest median age of 31 years, (see figure 6.3). The rest of the DHBs have a median of 28, 29 or 30 years.

The median has been used here to identify the 'middle' age, rather than the average. The median is used as a measure of location in the skewed distributions. For example if one DHB had extremely low values then the mean would move towards these values. This would skew the mean and would produce biased results.

Figure 6.3: DHB by Median Age

For a test of association age has been categorised into age groups. The age groups used here are <19, 20-24, 25-29, 30-34, 35-39 and 40+. A test of association shows that there is a relationship between DHB and age ($\chi^2 = 1979$, $df = 100$, $p\text{-value} < 0.0001$).

6.1.3 Gender

There are 51.5% male babies and 48.5% female babies. Auckland (52.52%), Bay of Plenty (52.14%), Capital & Coast (52.49%) and South Canterbury (53.32%) have the highest proportion of male births. A test of association shows no relationship between gender and DHB ($\chi^2 = 15$, $df = 20$, $p\text{-value} = 0.7498$).

Figure 6.4: DHB by Parity

6.1.4 Parity

Figure 6.4 shows there are more first time mothers for all DHBs. South Canterbury (72.70%), Southland (68.92%), Auckland (68.88%), Canterbury (66.77%) and Otago (66.70%) have the highest percentage of first time mothers. There are high proportions of mothers who have had previous births in West Coast (43.89%), Tairāwhiti (43.70%) and Northland (41.35%). This is using the raw data and not the imputed values. There are approximately 26,083 missing values. A test of association shows that there is a relationship between parity and DHB ($\chi^2 = 158$, $df = 20$, $p\text{-value} < 0.0001$).

6.1.5 Deprivation Index

Figure 6.5 shows the median deprivation index for Northland, Counties Manukau, Lakes, Tairāwhiti and Hawke's Bay DHB is 9. The least deprived areas with an index of 4 is Capital & Coast. Waitemata, Canterbury, Otago and Southland have a median deprivation index of 5. A chi-square test shows an association between deprivation index and DHB ($\chi^2 = 19484$, $df = 180$, $p\text{-value} < 0.0001$).

Figure 6.5: DHB by NZ Deprivation Index

6.1.6 Summary

Results from the EDA show a variety of characteristics of key explanatory factors between DHBs. DHBs have different population mixes, ethnic groups, deprivation indexes and birth characteristics. Northland DHB has the largest Māori population (46%) with 41.35% of mothers having previously given birth. Northland DHB is also one of the most deprived areas with a median index of 9. Tairāwhiti DHB also has one of the largest Māori population (46%), with median age of mothers giving birth of 27 years and 43.7% of mothers who have previously given birth. Tairāwhiti DHB also has a deprivation index of 9. Capital & Coast has the highest median age of mothers giving birth at 32 years and is the lowest deprived area at index 4. South Canterbury has the largest European ethnic group at 86% and 73% are first time mothers. This shows us that DHBs differ in populations mix across NZ. These differences must be adjusted for when comparing PPH rates across DHBs since some of these demographic and birth characteristics are related to PPH. We will start considering a comparison with no adjustment.

6.2 Unadjusted Funnel Plot

For the unadjusted funnel plot the rate of PPH for each DHB is calculated as the total number of women who have had a PPH divided by the total population of mothers for that DHB. This is the PPH rate. Each DHB has their own specific rate of PPH. This PPH rate is then plotted against the number of women who gave birth in 2007 for the DHB. The rate θ is the NZ national rate of PPH and θ_0 is the target rate. The control limits are calculated for each DHB and superimposed onto the graph. The 95% and 99.8% control limits are calculated for each DHB and these are then plotted as the control limits.

6.2.1 Unadjusted Funnel Plots Method

The unadjusted funnel plot is constructed using the follow method described below.

1. Calculate the unadjusted rate $\hat{\theta}_i = X_i/n_i$ where X_i is the total number of women who have had a PPH in DHB i and n_i is the total number of women who gave birth in DHB n_i . This is the proportion of women that have had a PPH in each DHB.
2. Calculate the variance using the equation $var_i = \hat{\theta}_0(1 - \hat{\theta}_0)/n_i$ where $\hat{\theta}_0 = y_i/n_i$ where $\hat{\theta}_0 = \sum_i X_i / \sum_i n_i$ is the national rate and n_i is the total number of women who give birth in DHB i .
3. The confidence interval can be calculated as $\hat{\theta}_0 \pm Z_p\sqrt{var_i}$
4. To plot the unadjusted funnel plot. Plot $\hat{\theta}_0 = \frac{Y_i}{n_i}$ against the precision parameter n_i , with the target $\hat{\theta}_0 = p$ shown as a horizontal line and superimpose the control limits on the plot as function of the parameter n_i . The national rate is $\theta_0 = 5249/55811 = 0.09405$. The horizontal

axis is the DHB population and the vertical axis the PPH rate. Each DHB's unadjusted PPH rate is then plotted and the control limits superimposed on top of this.

6.2.2 Unadjusted Funnel Plot Results

Figure 6.6: Unadjusted Funnel Plot

Figure 6.6 shows the unadjusted funnel plot for the rate of PPH for each DHB and the control limits. Of the 21 DHBs, 7 are within the 95% control limits and 14 are outside these control limits. There are 11 DHBs that are within the 99.8% confidence limits, with two of these DHBs on the boarder of the 95% confidence limits. Those DHBs that sit above the upper control limits are underperforming, with a higher than expected proportion of PPH. Those that sit below the lower control limits have significantly lower

PPH rates than that seen at the national level. The funnel plot show there are some extreme outliers at both ends of the spectrum. In the upper right of the funnel plot one DHB that has an unadjusted rate over 0.125 and is far beyond the control limits. The lower right hand of the figure shows two DHBs that have an unadjusted rate under 0.05 and are well outside the control limits, even when the control limits here are wider at this point.

The funnel plot shows large variation between the PPH rates across DHBs. This variability shown in figure 6.6 could be because of unmeasured covariates. As the funnel plot shows extensive overdispersion, the next step would be to adjust for covariates. This would include demographics, maternal and birth characteristics.

Chapter 7

Risk Adjusted Comparisons

In this chapter the imputation method and results are presented. The choice of model for the logistic regression is shown. The risk adjusted and winsorised funnel plots methods and results are presented.

7.1 Imputation

This section explores the variables to impute, describes the method used and the results of the imputation are presented.

7.1.1 Investigation of Variables to be Imputed

To investigate if imputation is a valid procedure we look at the distributions of the variables to be imputed. This is to identify how they differ from the rest of the sample. The three variables to be investigated are gestation, parity and birth weight. These have been identified as important predictors of PPH (University of Virginia Health System (2010); Taylor et al. (2005); Waitemata District Health Board (2006); Jacobs (2012); Combs et al. (1991)) and also have a large number of missing values as seen in the EDA. Gestation has 1.84% (1,009) missing values, Birth weight has 0.8%

(448) missing values and parity has 46.74% (26,083) missing values. Ideally we should not see any difference in distributions for the predictors against the outcome (except for the data size generated difference). If the data is MAR then these distributions should look relatively similar.

First we look at the variables and their distributions against age, ethnic group and deprivation index. Then the missing values are investigated against PPH and DHBs to see how they differ. For example, a distribution of mothers age for all mothers who gave birth in 2007 will be shown and this will be compared against mothers who have a missing recorded value for gestation.

Figure 7.1: Age Distribution, for the whole dataset, data where gestation is missing, data where parity is missing and data where birth weight is missing (as defined below)

The first investigation shows the distributions of age, ethnic group and deprivation index against gestation, parity and birth weight. There are four data sets used for the first comparison against age. In figure 7.1 the 'all' distribution shows mothers age for all mothers who gave birth in 2007. The 'gestation' distribution shows gestation by mothers age for mothers that have a missing value for gestation. The 'Parity' histogram shows the distribution of mothers age for mothers who have a missing value for parity. The 'birth weight' histogram shows mothers age by birth weight for mothers who have a missing value for birth weight.

For the age distribution against the missing variables (see figure 7.1) the distributions of parity displays a similar pattern to the whole dataset. Gestation is more 'flat' between the ages of 18-26 years rather than a gradual increased step by step to the peak age of 30 years. Birth weight also has a more 'flat' distribution of ages between 15-25 years. The peak here is 30 years which is the same for all mothers age. Even though gestation and birth weight show a slightly different pattern of ages in the younger years from 15-25, the overall pattern is still similar to the entire dataset.

Figure 7.2 shows the distribution of ethnic group and deprivation index for the entire dataset and where gestation, parity and birth weight values are missing. Ethnic group is coded as 1 for European, 2 for Māori, 3 for Pacific, 4 for Asian and 5 for Other ethnicity. The trend for the ethnicity is similar for all four histograms. It shows the largest group is European, followed by Māori. Where gestation has a missing value the Māori ethnic group have a higher number missing values proportionally to the other ethnic groups. The birth weight figure also shows a similar pattern. However the pattern for ethnicity is relatively similar for gestation, parity and birth weight against the entire dataset. This shows that the missingness is not related to these characteristics.

In the deprivation index comparison (see figure 7.2), all three distributions of gestation, parity and birth weight have a similar pattern to the entire dataset. There are fewer mothers in the least deprived areas and more mothers in the most deprived areas. The gestation and birth weight histograms have a smaller amount of mothers in the least deprived areas compared to the entire dataset.

The second investigation looks at PPH and DHB and their distribution of missingness. PPH and DHBs are important measures in this study. It is therefore essential to explore the pattern of missingness for gestation, par-

Figure 7.2: Distribution of Ethnic Group (top) and Deprivation Index distribution (bottom) for the whole dataset, where gestation is missing, where parity is missing and where birth weight is missing

ity and birth weight against PPH and DHBs.

Table 7.1: The number of percentage of missing parity by PPH.

Parity				
PPH	Observed	Missing	Total	Missing Rate
Yes	3,049	2,200	5,249	41.9%
No	26,729	23,833	50,562	47.1%
Total	29,778	26,033	55,811	46.6%

Birth Weight				
PPH	Observed	Missing	Total	Missing Rate
Yes	5,206	43	5249	0.82%
No	50,157	405	50,562	0.80%
Total	55,363	448	55,811	0.80%

Table 7.1 shows the missingness rate for each variable by PPH. We would expect to see the same amount of missingness against each variable for PPH and no PPH. Table 7.1 shows this that there are some differences

PPH	Gestation			Missing Rate
	Observed	Missing	Total	
Yes	5,163	86	5249	1.64%
No	46,639	923	50,562	1.83%
Total	54,082	1,009	55,811	1.84%

with the missing rate for Parity. The missing rate for parity by no PPH is 47.1% and for a PPH is 41.9% these two rates are different. Birth weight missing rate for No PPH and for a PPH are similar at 0.80% and 0.82% respectively. Gestation missing rate is differs by 0.2%.

Table 7.2: Percentage of missing records for Gestation, Birth Weight and Parity for each DHB.

DHB	Total Observed	Parity %	Gestation %	Birth Weight %
Northland	1,850	45.89	0.22	0.22
Waitemata	6,797	47.15	0.03	0.13
Auckland	6,091	42.32	0.16	0.21
Counties Manukau	7,886	45.27	0.77	0.77
Waikato	4,757	43.73	1.64	1.43
Lakes	1,380	47.03	0.14	0.14
Bay of Plenty	2,616	43.08	3.52	0.46
Tairāwhiti	649	58.40	0.31	0.15
Hawke's Bay	1,986	45.27	27.09	2.87
Taranaki	1,430	43.92	2.10	1.61
MidCentral	2,004	48.95	0.50	0.40
Whanganui	783	47.77	0.51	0.51
Capital and Coast	3,511	43.58	3.28	3.28
Hutt	1,918	45.78	1.25	1.15
Wairarapa	455	52.53	0.44	0.22
Nelson Marlborough	1,482	48.65	0.27	0.27
West Coast	340	47.06	0.59	0.59
Canterbury	6,039	54.69	0.10	0.23
South Canterbury	602	38.54	0.66	0.66
Otago	1,876	53.57	0.16	0.43
Southland	1,359	51.21	1.18	1.18

Table 7.2 shows the percentage of missing values for parity, gestation and birth weight for each DHB. 47% of parity is missing, this has the largest number of missing values. Tairāwhiti DHB has the largest number of miss-

ing parity (58%). Canterbury, Otago and Wairarapa have over half of the values of parity missing (54%, 53%, 52% respectively). South Canterbury has the lowest number of missing values for parity (38%). In general the DHBs have a similar proportion of missing values for parity and there are only a few DHBs that stand out as being different to the other DHBs. Almost half the data values are missing for this variable and therefore is not ignorable. Parity is the number of times a mother has given birth. The values can range from 0-14 with 0 being the most frequent. The median is 0 and mean is 0.6468. We will most likely want to impute this value in the range of 0-2.

Gestation has 1.8% of missing values. In table 7.2 there is one noticeable DHB that has a larger number of missing values for gestation. This is the Hawke's Bay DHB with 27% (538) missing values for gestation are missing. Capital & Coast have the next largest proportion of missing values for gestation (3.25%). There are a total of 1,009 missing values for gestation period and hence not ignorable because a large number of missing values come from one DHB (see table 7.2).

Gestation period is defined as the period in weeks that the mother carries the baby before giving birth. This can range from 0-42 weeks, the normal range of gestation is 37-42 weeks. In this data gestation period ranges from 14-45, with a large number of observations from 37-40 weeks (see figure 5.7). The median is 39 and lower quartile 37 and upper quartile 39. This would be a reasonable range 37-39, to impute for the missing values. This data is continuous.

There are 448 missing values for birth weight. Birth weight is recorded when the baby is first born and is measured in grams. 3.28% (115) of missing values for birth weight come from Capital & Coast DHB. 2.87% of missing values come from Hawke's Bay DHB and 1.43% from Waikato

DHB. Since this is not a random pattern of missingness, as such a large proportion come from a few DHBs.

The first investigation for mothers age, ethnic group and deprivation index shows the variables have missing values (gestation, parity and birth weight) all have similar distributions. The second investigation for gestation, parity and birth weight against PPH and DHB shows the pattern of missingness is not random. Some DHBs have a larger number of missing values than others. This illustrates the pattern of missingness is not ignorable and is therefore essential these variables gestation, parity and birth weight are imputed.

In order to prepare the data for imputation, it is important to consider the distributional assumptions of the method that will be used and the selection of variables that are imputed together (Arnold and Kronmal, 2003). As a multiple regression imputation method will be used it is essential to identify the covariates that will be used and to consider the model assumptions. It is also necessary to have consistency with the regression model used for each variable gestation, parity and birth weight. If related variables are not imputed together and then later utilised for analysis this will affect the relationship among them, by that the newly imputed variables will now not be related (Arnold and Kronmal, 2003).

7.1.2 Imputation Method

Set up of Data

Variables used in the regression are required to be formatted to numeric and binary form. This is necessary to allow the regression model to run to calculate the predictors and coefficients of the model. Below is a detailed step of which variables required transformation before the imputa-

tion function was run.

- Deprivation Index has been formatted into numeric
- Hospital Type is recorded as values 1 and 2 and this is changed to a binary variable which takes the values 0 and 1.
- Caesarean Section is formatted as binary (0,1) where 1 denotes for an event, that the mother has had a Caesarean section.
- Gender of the baby is in character form M and F and is formatted into binary 0 and 1 where Male=1 and Female=0.
- As ethnic group is a categorical variable, a set of dummy variables are created to incorporate ethnicity into the model. A binary variable is created for each ethnic group, where 1 is for an event, that the mother is in that ethnic group and 0 is for not in that ethnic group. Five different ethnic variables are created for Māori, Pacific, Asian, Other and NA, where the European ethnic group is the reference group.
- Gestation and DHB are turned into numeric. Birth weight is set to NA if recorded at 9999.

Method

This method of imputation is based on a similar method as described by Gelman and Hill (2007), Chapter 25.

1. Create a random imputation function in R.
Run a simple random imputation, for the three variables that have missing values, based on the observed data.

A simple random imputation is used to impute missing values of X based on the observed data for these values. This is used first as an interim step. This allows the next steps in the imputation to use all available observations.

As this part does not include information based on other observations it may not make much sense to use this. However it is a convenient starting point to the next step, where all observations are required.

2. Use a multiple regression imputation method that states, if the missing variables are a matrix Y with columns $Y_1, \dots, Y_k$ and full observed predictors are X , this first imputes all missing Y values using a crude approach (as in the first step) and then imputes Y_1 given $Y_2, \dots, Y_k$ and X , then Y_2 given $Y_1, Y_3, \dots, Y_k$ and X , using the newly imputed values for Y_1 and continuing this loop until all values are imputed.
3. A function in R is set up to run a simulation 20 times where a linear model is used for birth weight which is predicted with the variables of parity, mothers age, ethnic groups, plurality, gestation, hospital type, deprivation index, gender, DHB and PPH. The imputed value is obtained by taking the last predicted values from the simulation and is used to impute a value for birth weight where missing.

Gestation also has a linear model and predicted values are used to impute for the missing values of gestation. The same variables are used as in the birth weight model, however gestation has now been substituted with birth weight.

For parity a GLM with a logit link function is used. The fitted values are used for the prediction of missing values. Again the same variables are used as in the birth weight model, however parity has not been substituted with birth weight.

4. As these models are separate, all variables need to be added back into the full dataset.

Once the imputation method is run the relationships and distributions amongst the variables are explored. The data is scrutinised for outliers and any errors.

7.1.3 Imputation Results

Once the imputation has been run, checks need to be made. This will ensure that any imputation that has been made has not greatly altered the distribution of the variables. This section will go through each variable individually to check the distribution and summary statistics prior to and after imputation. Figure 7.3 shows histograms of the variables to be imputed.

Results of Birth Weight Imputation

Table 7.3 compares the summary statistics of the variable birth weight prior to and after imputation. The minimum birth weight has changed from 225 to 119.2. The median and mean has remained the same. The change in the minimum is expected because when imputing such values the imputation method has no restrictions on the minimum and maximum values. All missing values now have a value which fits well with the distribution of birth weight prior to imputation.

Figure 7.3 shows the distribution of birth weight values of all babies. Prior to imputation the graph shows a normal distribution with a minimum

weight of 225g and maximum weight of 7000g. On average most new born babies weigh in the range of 3500-4000g, here the birth weight mean is 3466g which is just a little lower than average. After imputation the distribution is similar, with the range is from 119.2g to 7000g. Looking at the imputed values there are larger proportions of imputed values in the range of 3000-4500g. This suggest this imputation is a satisfactory approach to imputing birth weight as we would expect a large number to be imputed around this range. The linear regression model gives an Adjusted R-squared of 0.3897 which means the explained variance from this regression is only 39% of the total variance. (See Appendix B.3)

Table 7.3: Summary of Birth Weight Imputation

	Min	1st Quarter	Median	Mean	3rd Quarter	Max	NA
Prior Imputation	225	3140	3490	3466	3830	7000	448
After Imputation	119.2	3140	3490	3466	3830	7000	0

Results of Gestation Imputation

Table 7.4 compares the summary statistics for gestation prior to and after imputation. There is no change to any of the statistics when all values are imputed for. All NA's now have a value after imputation. Figure 7.3 shows prior to and after imputation the distribution of gestation is relatively similar. The linear regression model gives an Adjusted R-squared of 0.3858, that is only 38.5% of the variation is explained in this model, and a $p - value < 0.0001$. (See Appendix B.1).

Table 7.4: Summary of Gestation Imputation

	Min	1st Quarter	Median	Mean	3rd Quarter	Max	NA
Prior Imputation	14	38	40	39.20	40	45	1,009
After Imputation	14	38	40	39.20	40	45	0

Results of Parity Imputation

For parity prior to imputation there are more mothers who have not given

birth before. After imputation this still remains true. Note that this variable is recorded as 0 or 1 where, 0 means the mother has not given birth before and 1 that the mother has given birth at least once before. Table 7.5 shows the summary statistics of parity prior to and after imputation. The minimum and maximum values remain the same as expected and the mean only changes slightly from 0.3600 to 0.3611 (see figure 7.3). To assess the measure of fit the binomial logistic regression model gives AIC of 31,233 and Residual deviance of 31,165 on 29,462 degrees of freedom (See Appendix B.2).

Table 7.5: Summary of Parity Imputation

	Min	1st Quarter	Median	Mean	3rd Quarter	Max	NA
Prior Imputation	0	0	1	0.3600	1	1	26,083
After Imputation	0	0	1	0.3611	1	1	0

7.1.4 Summary

Using an multiple imputation seems to be a reasonable approach to this data. It does not influence the variables imputed in anyway. It is important for these variables to be imputed as they are potential predictors for PPH. It is also essential to choose the most appropriate imputation method. If this is not done then this could severely impact the results and analysis.

When identifying and investigating the variables of interest for imputing, it is important to examine the distribution of missingness of the variables (Rubin, 1976; Scheffer, 2002). In particular exploring what is missing, how much is missing and the type and pattern of missingness (e.g. MCAR, MAR, not ignorable). If it is non-ignorable then imputation methods will need to be selected and used to fill in the missing data. If left missing, the data can cause bias and lead to incorrect inferences from our conclusions.

Figure 7.3: Distribution of birth weight, gestation and parity, before and after imputation

An imputation method needs to be carefully chosen depending on the characteristics of the data. Here gestation and birth weight are treated as continuous variables and parity is binary variable. These characteristics need to be taken into account.

A Multiple regression approach was chosen as this would give the most appropriate results. They would be unbiased, specific to the variables of

choice and produce reliable values. This imputation approach was carried out simultaneously for all three variables, to make sure the relationships among variables are not ignored. If they were ignored then the final dataset would be misleading and these relationships ignored.

The imputation process involved detailed explorations of the data in order to select which variables to impute. This involved investigating which variables should be imputed together, distributional assumptions and identification of outliers and extreme values.

Looking at complete case distributions and imputed values showed distributions are similar for gestation, parity and birth weight. Different distributional analysis were considered for gestation, results found a general linear model was preferred over a Poisson model. Many imputation methods were considered, however multiple random regression was the preferred approach.

7.2 Logistic Regression Results

Applying the Logistic Model to the data

The aim for this regression is to assess the probability of PPH occurring based on explanatory variables and their relationships (for example birth weight, gestation, ethnicity etc). As there are a large number of potential predictors to choose from, it is important to identify those that are useful. The first step in the risk adjusted funnel plot is to identify the important variables significant to the outcome of PPH. Once we identify these variables adjustments can be made by using the predicted probabilities from the model.

In a ideal world we would want to include every explanatory variable

available that may be useful in predicting the response, however this task would be too onerous and would be very difficult to interpret. It is preferable to use a selection of steps to make the model as simple as possible and therefore easier to interpret. Choosing the appropriate model for our data to fully explain the outcome PPH, requires iterations of logistic regression to help identify the 'important' variables. A selection of backwards elimination, forward selection and stepwise regression model methods are used to determine the best model.

Following consultation with an expert in this area (Sibanda T, personal communication) and literature (Waitemata District Health Board, 2006; University of Virginia Health System, 2010; Jacobs, 2012; Combs et al., 1991) it was determined that the variable and interactions in figure 7.4 (the gray shaded areas) are the most important to investigate. These variables and their interactions are chosen in the logistic regression method, to help choose the most appropriate model for the risk adjustment method. This leaves us with a choice of 13 main effects and 36 possible interactions to look at.

Once the stepwise regression has run, a logistic regression is run using the variables and their interaction identified in the stepwise method. This is to obtain the predicted probabilities and apply these to the risk adjusted method.

Method

To first identify the important factors the following procedure is used to fit the model using `proc logistic` in SAS.

In all models the response variable is PPH. The predictors include the main effects and some two way interactions. Figure 7.4 shows the main effects and interactions that could be potential predictors of PPH, these

	DHB Birth	Mothers Age	Ethnic Group of the Mother	Gestation (with imputation)	Deprivation Index	Parity (with imputation)	Episiotomy	Birth Weight (Log/imputed)	C-Section	Breech	Vaccum	Induction	Removal of Placenta
DHB Birth													
Mothers Age													
Ethnic Group of the Mother													
Gestation (with imputation)													
Deprivation Index													
Parity (with imputation)													
Episiotomy													
Birth Weight (with imputation and log)													
C-Section													
Breech													
Vaccum													
Induction													
Removal of Placenta													

Figure 7.4: Matrix of Regression Variables for selection

are shaded in gray. I used significant level 0.05 (5%) to identify the variables that are to remain or be removed in the regression model. Any variable that had a p-value of 0.05 or greater were eliminated from the model. PPH=1 is defined as an event has occurred. Even though a stepwise logistic regression method is the preferred option, both forward and backwards elimination were run to be used as a comparison against the stepwise method. This was to see if both or one of these methods produced the same results. The forward selection produced the same results as the stepwise (see Appendix C). The backwards elimination method added some extra factors including mothers age and the interaction between mothers age ethnic group, mothers age and birth weight, mothers age and C-section.

The stepwise method is the chosen method for the choice of variables to predict PPH. It shows 10 main effects and 9 interactions are significant factors in predicting PPH. Figure 7.5 shows the matrix of the variables considered potential factors, in gray and those in blue that have been chosen (see Appendix C.1).

The goodness of fit for the stepwise regression for selection of model shows the R-Square is 0.0538 which shows this model only explains 5% of the variation. The Hosmer and Lemeshow Goodness of Fit Test indicates the quality of model fit $p\text{-value} = 0.0023$

The next model is the final model to use for the risk adjusted funnel plot. This takes the variables and their interactions as identified in the stepwise regression as significant. This model is used to obtain the predicted probabilities to apply to the risk adjusted funnel plot.

	DHB Birth	Mothers Age	Ethnic Group of the Mother	Gestation (with imputation)	Deprivation Index	Parity (with imputation)	Episiotomy	Birth Weight (Log, Imputed)	C-Section	Breech	Vacuum	Induction	Removal of Placenta
DHB Birth													
Mothers Age													
Ethnic Group of the Mother													
Gestation (with imputation)													
Deprivation Index													
Parity (with imputation)													
Episiotomy													
Birth Weight (with imputation and log)													
C-Section													
Breech													
Vacuum													
Induction													
Removal of Placenta													

Figure 7.5: Matrix of Regression Variables for that are chosen

Figure 7.6 displays the log odds ratio and the 95% confidence interval for each factor. Asian and Pacific ethnic groups compared to European have a lower risk of PPH if all other factors are held constant. Ethnic groups Māori and Other have a higher risk for PPH compared to the European group, if all other factors are held constant. An increase in the baby's birth weight has a decrease in the risk of PPH, if all other factors remain constant. Parity and C-section have a increased risk for PPH, where all other factors are held constant.

7.3 Risk Adjusted Funnel Plots

The following method describes how the risk adjusted funnel plot is constructed.

1. Run a logistic regression using PPH as the event where the probability that PPH has occurred, event occurred = 1, where $P(pph = 1)$

Figure 7.6: Log Odds Ratio

The covariates chosen here are from the previous stepwise logistic regression in section 7.2. This will obtain the predicted values for each individual mother.

2. Calculate the sum of predicted values for each DHB i

This is the expected number of PPH, $E_i = \sum j \hat{y}_{ij}$ for each i

where,

$E_i = \sum \hat{p}_i j$, for each $i \dots \hat{p}_i j$ is the predicted probability of PPH for

mother j in the DHB i .

3. Calculate the risk adjusted rate y_i

$$\text{Risk Adjusted rate} = \frac{O_i}{E_i} \times \hat{\theta}$$

where

$\hat{\theta}_0$ is the national rate of PPH.

O_i is the number of mothers with PPH in DHB i

E_i is the expected number of PPH for DHB i

Therefore the risk adjusted rate is

$$= \frac{O_i}{\sum \hat{p}_{ij}} \times \hat{\theta}_0 \quad (7.1)$$

$\hat{p}_{ij}$ is the predicted values for each mother j in DHB i

4. To plot the adjusted funnel plot. Plot Y_i against the precision parameter n_i , with the target θ_0 shown as a horizontal line and superimpose the control limits on the plot as function of the parameter n_i .

7.3.1 Risk Adjusted Funnel Plot Results

After adjusting for variables as described in section 7.2, figure 7.7 shows the adjusted funnel plot and its control limits. From a quick glance there are many DHBs that still remain outside the control limits. There are now 10 DHBs that are out of control, compared to figure 6.6 there were 7 DHB's that sit outside the control limits. Ten of the 21 DHBs lie outside the 99.8% control limits, with one of these on the cusp of the limits. Eight DHBs lie with the 95% control limits. From the adjusted funnel plot (figure 7.7) it is very difficult to draw any conclusions because many DHBs are divergent from one another. Over half of the DHBs fall outside the 95% control limits.

Figure 7.7: Adjusted Rate

Looking at figure 7.7 in more detail, some DHBs that have shifted more considerably than others compared to the unadjusted funnel plot. In figure 6.6 Auckland DHB was at the point on the top right of the figure, the most extreme outlier (with an unadjusted rate of 0.140). In the adjusted funnel plot (see figure 7.7) Auckland maintains the same position at the top right of the funnel plot but now has moved closer towards the control limits (with a rate of 0.125). Nelson Marlborough and Southland DHBs still remain well outside the control limits. Nelson Marlborough and Southland are the two points close to each other at the bottom left of the graph. Their rates have moved from 0.043, 0.038 to 0.045, 0.043 respectively. Waitemata is the point at the right of the graph outside the lower control limits. After adjustment Waitemata still remains well outside the control limits. Northland, Otago, MidCentral and Waikato have

now moved from being inside the confidence limits to outside the confidence limits after the adjustment has been made. These DHBs are above the upper confidence limits. Bay of Plenty has moved inside the 99.8% confidence limits. Capital & Coast have moved just outside the lower 99.8% confidence limit. In the unadjusted funnel plot Capital & Coast were on the cusp of the 99.8% confidence limit.

This shows us that some DHBs have moved outside the control limits and some inside the limits. These DHBs rates have moved closer to the natural rate as expected (Counties Manukau and Lakes District).

Using an adjustment method the variables available, it is noticeable that some DHBs move closer to mean and some move further away. Suggesting there are still population differences between the DHBs and furthermore there are other factors that are not measured and available for us to use, that may need to be considered when adjusting for PPH. This model shows larger variability between DHBs as many DHBs fall outside the 95% and 99.8% control limits, indicating overdispersion around the target. This can occur because of unmeasured covariates not available or have not been measured or recorded. It may be more appropriate to use a Winsorisation approach to adjust for the overdispersion.

7.4 Winsorised Funnel Plots

Winsorised Estimate

An approach for this over-dispersion would be to use a standard GLM approach. This introduces a factor ϕ that will inflate the null variance by a certain percentage. This is a multiplicative variance model where each DHB's variance will change by a different amount, but through a common ϕ . It is expected that DHBs with larger variances will be affected more.

Method

1. Calculate the naive Z-scores for each DHB

$$Z_i = \frac{Y_i - \theta_o}{\sigma} \quad (7.2)$$

where

p_i = unadjusted rate of PPH for each DHB

θ_o = NZ national rate of PPH

$\sigma = \sqrt{(\theta_o(1 - \theta_o)/n_i)}$

where n_i = sample size of each DHB

2. Rank these Z-scores from largest to smallest
3. Identify Z_q and Z_{1-q} the 100_q percentiles, the largest and lowest naive Z-scores, where $q = 0.1$. Take the top and bottom 10% of the Z_i DHBs. This would be $21 \times 10\% = 2.1$. Identify the bottom two and top two DHBs. Take the second highest Z-score and assign this to the top two DHBs Z-scores. For the lowest two DHB Z-scores take the second to lowest Z-score and assign this to the two lowest DHB Z-scores. Leave the rest of the Z-scores unchanged. These are newly calculated Z-scores, Z^w that have been pulled in by the 'winsorised' 10%. From this, new confidence limits can be calculated.
4. Calculate the estimate $\hat{\phi}$ in (4.4) using Z^w .

$$\hat{\phi}^w = \frac{1}{I} \sum_i Z_i^w(q)^2 \quad (7.3)$$

where I = the total number of DHBs.

$\sum_i Z_i^w(q)^2$ = is the sum of the Z-scores new, squared.

The estimate $\hat{\phi}^w$ can also be multiplied by a debiasing factor $w(q)$ if all DHBs are in control and the only variability is due to over-dispersion. If this is the case, the variance of the winsorised Z-statistics

will tend to be less than ϕ . If it is assumed that $Z^W(q)$ is from a q -Winsorised standard normal distribution, then the variance can be calculated as in ?? paper:

$$\mathbb{V}[Z^W(q)] = 1 + 2q(z_q^2 - 1) - 2z_q e^{-z_q^2/2}/\sqrt{2\pi} = 1/w(q) \quad (7.4)$$

so $\hat{\phi} = w(q)\hat{\phi}^W$, where $z_q = \Phi^{-1}(1 - q)$.

where $\Phi^{-1}(1 - q)$ is the 100(1- q)% percentile of the standard normal distribution.

So if we are to use a winsorised estimate of 10% then $w(0.10) = 1.47$ and the variance would then be $\mathbb{V}[Z^W(q)] = 1/1.47 = 0.68$. This will underestimate the variance by 32%.

5. The boundaries can then be calculated by

$$\theta_0 \pm z_p \sqrt{\hat{\phi}g(\theta_0)/n_i} \quad (7.5)$$

where

θ_0 = Target NZ rate $\hat{p}$

Z_p = 95% confidence interval limits at 1.96

$\hat{\phi}$ = winsorised estimate

$g(\theta_0) = \theta_0(1 - \theta_0)$

n_i = precision parameter = sample size

If the data has no true over-dispersion, then we can check for this. It can be assumed that $I\hat{\phi}$ has approximately a χ_I^2 distribution, which means the expected value $\mathbb{E}(\hat{\phi}) = 1/I$, and that the $\mathbb{V}(\hat{\phi}) = 2/I$. As the above is an assumption, one must test this assumption before applying this to the data. There are two points to check: (Spiegelhalter, 2005a)

1. That if $\hat{\phi} < 1 + 2\sqrt{2/I}$ assume that $\phi = 1$;
2. If the estimated is $\hat{\phi} > 1 + 2\sqrt{2/I}$ assume there is overdispersion.

Here the estimate $\hat{\phi}$ is 10.85 and $1 + 2\sqrt{2/I} = 1.13$ where $I = 21$. Therefore $10.85 > 1.13$ and $\hat{\phi}$ is not less than 1. This concludes there is overdispersion and adjustments can be made for overdispersion.

7.4.1 Winsorised Estimates with Random Effects

The other approach for adjusting for over-dispersion is using the win-sorised estimate as calculated above and adding a random effects term.

In this approach we assume that each DHB has its own distribution for the PPH rate, that is $\mathbb{E}(p_i) = \theta_i$ and $\mathbb{V}(Y_i) = s_i^2$ (Spiegelhalter, 2005a). For DHBs whose rates are on target θ_i is distributed with mean θ_0 and standard deviation τ . The null hypothesis will therefore be a distribution, (for example $\theta_i \sim N(\theta_0, \tau)$) rather than a point ($\theta_i = \theta_0$). The standard deviation τ can be estimated using the methods of moments estimator.

Method of moments estimate

$$\hat{\tau}^2 = \frac{I\hat{\phi} - (I - 1)}{\sum_i w_i - \sum_i w_i^2 / \sum_i w_i} \quad (7.6)$$

where $w_i = 1/s_i^2$

s_i^2 = is the variance for each DHB proportion $p_i(1 - p_i)/n_i$

$\hat{\phi}$ is the test for heterogeneity if $\hat{\phi} < (I - 1)/I$ then τ is to be set to 0 and complete homogeneity is assumed.

The funnel plot boundaries are given by

$$\theta_0 \pm z_p \sqrt{\mathbb{V}(Y|\theta_0, n_i) + \hat{\tau}^2} \quad (7.7)$$

Method

To apply this to the data the following steps below are used.

1. Calculate $\hat{\tau}^2$ as in equation 7.6

where

$\hat{\phi}$ = winsorised estimate

I = number of DHBs

2. Calculate the control limits

$$\theta_0 \pm z_p \sqrt{\mathbb{V}(Y|\theta_0, n_i) + \tau^2} \quad (7.8)$$

where

θ_0 = Target of NZ Rate p

Z_p = 95% confidence limits

$$V(Y|\theta_0, n_i) = \frac{g(\theta_0)}{n_i} = \frac{\theta_0(1-\theta)}{n_i}$$

where,

n_i = precision parameter

$\hat{\tau}^2$ can be calculated as

$$\hat{\tau}^2 = \frac{I\hat{\phi} - (I - 1)}{\sum_i w_i - \sum_i w_i^2 / \sum_i w_i} \quad (7.9)$$

where,

I = number of DHBs

$\hat{\phi}$ = winsorised estimate

$$w_i = 1/s_i^2$$

$Var(p_i) = s_i^2$ variance of proportion of each DHB $p_i(1 - p_i)/n_i$

p_i = unadjusted rate of PPH for each DHB i .

7.4.2 Winsorisation Funnel Plot Results

Figure 7.8: Winsorisation Funnel Plot

When estimating the inflation factor using residuals subject to 10% winsorisation, the winsorised estimate, 19 DHBs in figure 7.8 appear to be well within the 95% control limits. Two DHBs are on the cusp of the 95% control limits at the population mark about 1600. These are Southland and Nelson Marlborough. One DHB is outside the 99.8% control limits, at the population mark of approximately 6000. This is Auckland DHB. This has moved closer to the 99.8% limits where as in the previous funnel plots Auckland was situated well outside the limits. With the use of the 10% winsorised estimate has caused the control limits to widen, causing nearly all DHBs to be inside these limits.

When examining the previous two figures 6.6 and 7.7 these funnel plots have identified a few outliers. One in particular was very extreme compared the rest. This is Auckland DHB. As this was such an extreme outlier this one DHB could cause the results to shrink and conceal the true meaning of the funnel plot.

Sometimes when there are particular large estimates for a DHB it can cause an increase in the estimate ϕ , which can widen the funnel limits and make it very difficult to determine cases that are of interest. A more robust approach could be to use an random effects term in the winsorisation. And secondly remove Auckland DHB and their observations from the data and rerun the analysis. To see if this makes any difference to the divergence among DHBs (Marshall et al., 2004).

7.4.3 Winsorisation Random Effects Funnel Plot Results

The adjustment of adding a constant random effects term to the model, makes a large difference. The confidence limits are narrowed compared to the winsoriation funnel plot (see figure 7.8). There are a large number of DHBs outside the confidence limits. $\hat{\tau}^2$ is 0.00032, a very small value and hence why this funnel plots looks very similar to the unadjusted funnel plot, the random effects adjustment is making almost no difference.

Figure 7.9 shows the funnel plot of the winsoristed estimates using the random effects approach. This shows the PPH rate with a constant term added against the DHB population. Of the 21 DHBs, 8 DHBs fall outside the 99.8% control limits and 13 DHBs fall outside the 95% confidence limits. Auckland DHB is the extreme outlier, the point at the top right of the graph. Other DHBs who were outliers in the unadjusted plot remain out-

Figure 7.9: Winsorisation Random Effects Funnel Plot

liers in this funnel plot to.

As Auckland DHB seems to be an extreme outlier and could potentially be influencing the results the next step would be to remove Auckland DHB and rerun the analysis, to see if this makes any difference to the control limits.

7.4.4 Winsorisation Results Excluding Auckland DHB

As identified in figures (see 7.7, 7.8, 7.9) there was one extreme outlier observed, Auckland DHB. Auckland DHB has the highest rate of PPH of 14%.

Figure 7.10 is a funnel plot using the winsorisation method excluding

Figure 7.10: Winsorisation Funnel Plot Excluding Auckland DHB

Auckland DHB and their observations. A new national PPH rate (p) is calculated. This is now 8.8%. Using the same winsorisation method as in section 7.4, equation 7.5 is used to calculate a new set of control limits. p_i is plotted against the precision parameter n_i , with the target θ_0 as the horizontal line and the control limits superimposed on the plot as a function of the parameter n_i .

Figure 7.10 uses the standard approach excluding Auckland DHB. There are 2 DHBs that lie outside the 95% confidence limits and one on the cusp. All other DHBs are situated inside the control limits. The two DHBs that sit outside the 95% confidence limits are Southland and Nelson Marlborough with rates of 0.0389 and 0.0425 respectively. The other DHB that sits on the cusp of the 95% confidence limit is situated to the far left of the graph and this is Counties Manukau DHB at a rate of 0.1058.

Compare this to figure 7.8 which is the winsorisation approach inclusive of Auckland. Excluding Auckland has not made much difference to the funnel plot results.

7.4.5 Winsorisation with Random Effects Results Excluding Auckland DHB

This section uses the winsorisation with random effects method as described in section 7.4.1. The only difference here is that Auckland DHB and their observations are removed from the dataset. A new method of moments estimate is calculated using equation 7.6 and new funnel plot boundaries are also calculated using equation 7.8. The PPH rate is then plotted against each DHBs population with the 95% and 99.8% control limits superimposed on the plot.

Figure 7.11 shows the funnel plot for winsorisation method with a random effects term added, excluding Auckland DHB. The funnel plot limits narrow and many more DHBs sit outside the confidence limits. There are now 13 DHBs that lie outside the 95% confidence limits and 9 DHBs that lie outside the 99.8% confidence limits.

Figure 7.11: Winsorisation Random Effects excluding Auckland DHB

Chapter 8

Discussion

In this thesis the work carried out shows a useful comparison of DHBs performance against PPH rates for the 2007 year in NMDS. The thesis uses a range of methods to demonstrate the use of funnel plots for measuring performance of institutions. This analysis has established a picture of performance across NZ DHBs regions in relation to each other and their PPH rates. The work itself is unique as the focus is on DHBs in NZ in a medical context where previously very little research has been carried out in the subject area the variation in outcomes of mothers and births across DHBs.

In the EDA we found there are differences in PPH among the demographics, maternal and birth characteristics. There are also differences among the DHBs and their characteristics. The rates of PPH are different, the population mixes of DHBs are made up of a varying range of ethnic groups, ages and deprivation indexes. We also found in the EDA there are a lot of factors associated with PPH. This indicates the need for adjustment.

Following the EDA we found some important predictors of PPH had a large number of missing values and that these values were not missing completely at random. These predictors were gestation, parity and birth weight. Several DHBs had more missing data than other DHBs for some

variables. Imputation was then carried out to impute values for the missing values. A multiple regression imputation approach was used and the results from the imputation process were analysed. The variables imputed for are parity, birth weight and gestation.

Once the imputation had been run, the first funnel plot was constructed. This is the unadjusted funnel plot where the raw rate of PPH is plotted against each DHB. The unadjusted rate shows large variability among the rates of PPH for each DHB's population. It shows there are some extreme outliers at both ends of the population spectrum. Some DHBs with smaller numbers of births have a low rate of PPH and some DHBs with large rate of PPH. The large variation among the DHBs suggests there is overdispersion among the DHBs consequently factors need to be taken into account for PPH and a risk adjusted funnel plot is constructed.

This risk adjusted funnel plot attempts to take into account factors that are good predictive measures for PPH. A logistic regression model is run to identify these covariates and then an adjustment is made to the PPH rate. This risk adjusted funnel plot shows some DHBs rates move away and others adjust considerably closer to the target. This suggests there are potentially some factors that are not adjusted for because large overdispersion around the target still remains. Further methods are used to adjust the control limits of the plot.

First a winsorised estimate is calculated which shows shrinkage of the adjusted PPH rate and a widening of the control limits. This is because a multiplicative factor has been added to the control limits and adjustments made. A 10% winsorised estimate is added which inflates the control limits. It shows the larger DHBs with the higher Z-scores have moved the control limits outwards. It is from this point that you can really identify a few outliers that could be causing the change in the control limits. As

there are such large estimates for one DHB this can cause an increase in the estimate ϕ , which can widen the funnel limits and make it difficult to determine cases that are of interest. A more robust approach may be to include a random effects term.

With the addition of the random effects term causes the control limits to narrow. Using a winsorised estimate with a random effects term adds a constant term to the equation and appears to make a large difference to the control limits. The funnel plot, figure 7.9 shows no real difference compared to figure 6.6 as there are still a large number of DHBs outside the control limits. However there remains one outlier which could still cause shrinkage of the control limits of the DHB rate around the target.

On four funnel plots displayed one DHB stands out from the rest (see figures 6.6, 7.7, 7.8, 7.9). This is Auckland DHB. This DHB could have a large influence on the control limits produced. It was decided to remove Auckland DHB and its observations from the data and the analysis to be run again for the winsorised and random effects funnel plots.

With the exclusion of Auckland DHB the winsorisation funnel plot shows that nearly all DHBs are now within the 95% control limits and two DHBs are just outside these limits. This shows that Auckland DHB has a strong influence on this funnel plot. The results from the winsorisation with random effects term added shows variability among DHBs as many DHBs sit outside the 95% control limits. With this additive model the control limits have now shrunk.

Future work based on this research could involve obtaining more factors associated with PPH. There were a few variables unavailable to predict PPH such measures may include: who the baby was delivered by (obstetrician or midwife), where the baby was delivered (home birth or hospital), the

mothers previous medical history (previous PPH, C-section etc) these measures could be important to include in future analysis. Other such useful information that was not recorded is the mother's weight, infections and other medical details also could be useful measures of PPH.

Other work could involve an improved measure on the target rate θ . A Bayesian hierarchical method can be used to improve the precision of the target and can control for variation that can occur. This would be an interesting piece of analysis to conduct and to compare the Bayesian method to the methods used in this research.

This analysis will provide useful information to health care providers for funding, quality of care and administrative processes. These set of funnel plots are a useful way to provide a visual analysis of providers against a outcome and can be used in any context. This research is a practical approach for hospitals, providers and their funders to identify areas for more in-depth self monitoring and quality improvement for health care.

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Appendix A

Glossary

Assisted vaginal birth - A vaginal birth that requires assistance, for example, forceps.

Assisted vaginal birth, forceps - A vaginal birth requiring assistance with the use of a metallic obstetric instrument.

Assisted vaginal birth, vacuum extraction - A vaginal birth requiring assistance with the use of a suction cap that can be applied to the baby's head.

Assisted vaginal birth, vaginal breech birth - An vaginal birth requiring assistance because of the birth of a baby by the buttocks or lower limbs first rather than the head.

Birthweight - The first weight of the baby obtained after birth, usually to the nearest 5g.

Caesarean section - An operative birth through an abdominal incision.

Caesarean section, acute - also known as an Emergency Caesarean, a cae-

sarean section performed urgently for clinical reasons once labour has started. For the health of the baby and/or mother.

Caesarean section, elective - A Caesarean section performed as planned.

DHB - District Health Board, An organisation established by section 19 of the NZ Public Health and Disability Act 2000.

Episiotomy - A small incision of the perineal tissue surrounding the vagina at the time of birth.

Gestation - The duration of pregnancy in completed weeks, calculated from the date of the first day of a woman's last menstrual period and her infant's date of birth, or derived from a clinical assessment during pregnancy, or derived from an examination of the infant after birth.

Induction - A medical intervention to stimulate the onset of labour.

Parity - The number of previous pregnancies a mother has had that have resulted in a live birth or still births.

Postpartum Haemorrhage (PPH) - Abnormal bleeding experienced by the mother soon after labour or childbirth.

Postpartum Haemorrhage, primary - A blood loss of more than 500ml from the genital tract within 24 hours of childbirth.

Postpartum Haemorrhage, secondary - A blood loss of more than 500ml from the genital tract after 24 hours of childbirth up until 6 weeks after delivery.

Appendix B

Imputation Regression Results

B.1 Gestation

summary(lm.2)

Call:

```
lm(formula = gest ~ mothers_age + ethnicgp_MAO + ethnicgp_PCI + ethnicgp_ASN + ethnicgp_OTH + ethnicgp_NA + as.factor(parity_bin.imp) + C_section + hosp_type + as.numeric(res_dep01) + sex + factor(dhb_birth) + birth_weight.imp + pp_haem)
```

Residuals:

Min	1Q	Median	3Q	Max
-20.84	-0.78	0.11	0.93	6.69

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.503 on 54732 degrees of freedom
(1045 observations deleted due to missingness)

Multiple R-squared: 0.3862, Adjusted R-squared: 0.3858

F-statistic: 1044 on 33 and 54732 DF, p-value: $< 2.2e - 16$

Coefficients:	Estimate	Std. Error	t value	$Pr(> t)$	
(Intercept)	32.88	0.07	496.18	$< 2e - 16$	***
mothers_age	-0.01	0.00	-9.47	$< 2e - 16$	***
ethnicgp_MAO	-0.01	0.02	-0.34	0.73	
ethnicgp_PCI	-0.21	0.02	-8.32	$< 2e - 16$	***
ethnicgp_ASN	0.26	0.02	11.02	$< 2e - 16$	***
ethnicgp_OTH	0.15	0.04	3.70	0.00	***
ethnicgp_NA	0.09	0.08	1.12	0.26	
as.factor(parity_bin.imp)1	-0.16	0.01	-11.63	$< 2e - 16$	***
C_section	-0.47	0.02	-30.49	$< 2e - 16$	***
hosp_type	0.17	0.03	5.51	0.00	***
as.numeric(res_dep01)	0.00	0.00	-0.08	0.93	
sex	-0.28	0.01	-21.56	$< 2e - 16$	***
factor(dhb_birth)10	0.01	0.05	0.26	0.79	
factor(dhb_birth)11	-0.05	0.05	-0.99	0.32	
factor(dhb_birth)12	-0.13	0.06	-2.06	0.04	*
factor(dhb_birth)13	-0.14	0.04	-3.16	0.00	**
factor(dhb_birth)14	-0.11	0.05	-2.28	0.02	*
factor(dhb_birth)15	-0.12	0.08	-1.53	0.13	
factor(dhb_birth)16	-0.07	0.05	-1.25	0.21	
factor(dhb_birth)17	-0.28	0.09	-3.11	0.00	**
factor(dhb_birth)18	-0.06	0.04	-1.37	0.17	
factor(dhb_birth)19	-0.18	0.07	-2.58	0.01	*
factor(dhb_birth)2	-0.14	0.04	-3.53	0.00	***
factor(dhb_birth)20	-0.11	0.05	-2.24	0.02	*
factor(dhb_birth)21	-0.08	0.05	-1.43	0.15	
factor(dhb_birth)3	-0.09	0.04	-2.12	0.03	*
factor(dhb_birth)4	-0.11	0.04	-2.78	0.01	**
factor(dhb_birth)5	-0.05	0.04	-1.15	0.25	
factor(dhb_birth)6	-0.06	0.05	-1.05	0.29	
factor(dhb_birth)7	-0.08	0.05	-1.71	0.09	.
factor(dhb_birth)8	-0.16	0.07	-2.32	0.02	*
factor(dhb_birth)9	0.05	0.05	0.94	0.35	
birth_weight.imp	0.00	0.00	179.80	$< 2e - 16$	***
pp_haem	-0.14	0.02	-6.33	0.00	***

B.2 Parity

Summary(lm.3)

Call:

```
glm(formula = as.factor(parity_bin) ~ mothers_age + ethnicgp_MAO + ethnicgp_PCI + ethnicgp_ASN + ethnicgp_OTH + ethnicgp_NA + as.numeric(gest.imp)
```

```
+ C_section + hosp_type + as.numeric(res_dep01) + sex + as.factor(dhb_birth)
+ p_haem + birth_weight.imp, family = binomial(logit))
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.71	-0.83	-0.50	0.93	2.89

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 38552 on 29495 degrees of freedom

Residual deviance: 31165 on 29462 degrees of freedom

(26315 observations deleted due to missingness)

AIC: 31233

Number of Fisher Scoring iterations: 4

B.3 Birth Weight

```
summary(lm.1)
```

Call:

```
lm(formula = birth_weight ~ mothers_age + ethnicgp_MAO + ethnicgp_PCI
+ ethnicgp_ASN + ethnicgp_OTH + ethnicgp_NA + as.factor(parity_bin.imp)
+ C_section + hosp_type + as.numeric(res_dep01) + sex + factor(dhb_birth)
+ gest.imp + pp_haem)
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 454 on 55292 degrees of freedom

Coefficients:	Estimate	Std. Error	z value	$Pr(> z)$	
(Intercept)	-2.20	0.34	-6.39	0.00	***
mothers_age	0.19	0.00	67.65	$< 2e - 16$	***
ethnicgp_MAO	1.21	0.04	28.65	$< 2e - 16$	***
ethnicgp_PCI	1.12	0.05	20.55	$< 2e - 16$	***
ethnicgp_ASN	0.33	0.05	6.99	0.00	***
ethnicgp_OTH	0.35	0.08	4.29	0.00	***
ethnicgp_NA	-0.93	0.19	-4.95	0.00	***
as.numeric(gest.imp)	-0.16	0.01	-17.33	$< 2e - 16$	***
C_section	-0.56	0.03	-16.63	$< 2e - 16$	***
hosp_type	0.58	0.07	8.35	$< 2e - 16$	***
as.numeric(res_dep01)	0.05	0.01	9.65	$< 2e - 16$	***
sex	-0.08	0.03	-2.85	0.00	**
as.factor(dhb_birth)10	-0.01	0.11	-0.07	0.94	
as.factor(dhb_birth)11	0.12	0.11	1.13	0.26	
as.factor(dhb_birth)12	-0.01	0.14	-0.06	0.96	
as.factor(dhb_birth)13	-0.54	0.10	-5.65	0.00	***
as.factor(dhb_birth)14	-0.11	0.11	-1.07	0.29	
as.factor(dhb_birth)15	0.18	0.18	1.01	0.31	
as.factor(dhb_birth)16	0.09	0.11	0.81	0.42	
as.factor(dhb_birth)17	0.39	0.19	2.05	0.04	*
as.factor(dhb_birth)18	-0.26	0.09	-2.91	0.00	**
as.factor(dhb_birth)19	-0.38	0.15	-2.49	0.01	*
as.factor(dhb_birth)2	-0.38	0.09	-4.30	0.00	***
as.factor(dhb_birth)20	-0.17	0.11	-1.52	0.13	
as.factor(dhb_birth)21	-0.23	0.12	-1.88	0.06	.
as.factor(dhb_birth)3	-0.78	0.09	-8.81	$< 2e - 16$	***
as.factor(dhb_birth)4	-0.15	0.09	-1.74	0.08	.
as.factor(dhb_birth)5	-0.18	0.09	-2.01	0.04	*
as.factor(dhb_birth)6	-0.13	0.12	-1.14	0.25	
as.factor(dhb_birth)7	-0.02	0.10	-0.19	0.85	
as.factor(dhb_birth)8	-0.05	0.16	-0.29	0.77	
as.factor(dhb_birth)9	0.10	0.10	1.00	0.32	
pp_haem	-0.38	0.05	-8.06	0.00	***
birth_weight.imp	0.00	0.00	21.29	$< 2e - 16$	***

Residuals:

Min	1Q	Median	3Q	Max
-3092.7	-299.4	-14.3	281.6	3800.1

(485 observations deleted due to missingness)

Multiple R-squared: 0.3901, Adjusted R-squared: 0.3897

F-statistic: 1071 on 33 and 55292 DF, p-value: $< 2.2e - 16$

Coefficients:	Estimate	Std. Error	t value	$Pr(> t)$	
(Intercept)	-3850.39	43.71	-88.09	$< 2e-16$	***
mothers_age	4.02	0.34	11.77	$< 2e-16$	***
ethnicgp_MAO	-59.61	5.65	-10.55	$< 2e-16$	***
ethnicgp_PCI	85.62	7.43	11.52	$< 2e-16$	***
ethnicgp_ASN	-204.40	7.03	-29.06	$< 2e-16$	***
ethnicgp_OTH	-80.25	12.44	-6.45	0.00	***
ethnicgp_NA	-42.51	23.08	-1.84	0.07	.
as.factor(parity_bin.imp)1	53.25	4.15	12.83	$< 2e-16$	***
C_section	48.43	4.65	10.41	$< 2e-16$	***
hosp_type	31.31	9.28	3.37	0.00	***
as.numeric(res_dep01)	-2.25	0.78	-2.87	0.00	**
sex	115.96	3.86	30.01	$< 2e-16$	***
factor(dhb_birth)10	-0.31	16.15	-0.02	0.98	
factor(dhb_birth)11	-0.84	14.76	-0.06	0.95	
factor(dhb_birth)12	20.63	19.42	1.06	0.29	
factor(dhb_birth)13	27.71	13.46	2.06	0.04	*
factor(dhb_birth)14	13.55	15.01	0.90	0.37	
factor(dhb_birth)15	45.65	23.85	1.91	0.06	.
factor(dhb_birth)16	16.28	16.04	1.02	0.31	
factor(dhb_birth)17	32.51	26.95	1.21	0.23	
factor(dhb_birth)18	-13.71	12.41	-1.11	0.27	
factor(dhb_birth)19	41.17	21.55	1.91	0.06	.
factor(dhb_birth)2	26.85	12.28	2.19	0.03	*
factor(dhb_birth)20	1.87	15.15	0.12	0.90	
factor(dhb_birth)21	-15.64	16.52	-0.95	0.34	
factor(dhb_birth)3	-1.10	12.42	-0.09	0.93	
factor(dhb_birth)4	8.30	12.06	0.69	0.49	
factor(dhb_birth)5	-3.91	12.77	-0.31	0.76	
factor(dhb_birth)6	10.33	16.19	0.64	0.52	
factor(dhb_birth)7	1.18	13.86	0.09	0.93	
factor(dhb_birth)8	17.65	20.75	0.85	0.40	
factor(dhb_birth)9	-14.91	14.83	-1.01	0.31	
gest.imp	181.87	1.02	178.29	$< 2e-16$	***
pp_haem	110.30	6.67	16.53	$< 2e-16$	***

Appendix C

Model Selection Results

The follow SAS code is used for the logistic regression stepwise method:

```
PROC LOGISTIC DATA=data2;
  CLASS induction (PARAM=EFFECT) ethnicgp (PARAM=EFFECT) res_dep01 (PARAM=EFFECT);
  MODEL pp_haem (Event = '1')=gest_imp mothers_age
    parity_bin_imp C_section breech rem_placenta birth_weight_imp_log
    episiotomy vacuum induction ethnicgp res_dep01 mothers_age*ethnicgp
    mothers_age*birth_weight_imp_log birth_weight_imp_log*ethnicgp
    mothers_age*parity_bin_imp parity_bin_imp*ethnicgp
    parity_bin_imp*birth_weight_imp_log episiotomy*ethnicgp
    birth_weight_imp_log*episiotomy mothers_age*C_section
    C_section*ethnicgp C_section*birth_weight_imp_log C_section*episiotomy
    C_section*gest_imp breech*episiotomy gest_imp*breech C_section*breech
    mothers_age*vacuum vacuum*ethnicgp birth_weight_imp_log*vacuum
    episiotomy*vacuum gest_imp*vacuum C_section*vacuum breech*vacuum
    mothers_age*induction birth_weight_imp_log*induction episiotomy*induction
    gest_imp*induction C_section*induction breech*induction vacuum*induction
    rem_placenta*ethnicgp C_section*rem_placenta rem_placenta*vacuum
    gest_imp*birth_weight_imp_log induction*ethnicgp /
  SELECTION=STEPWISE
  SLE=0.025
  SLS=0.05
  LINK=LOGIT
;
RUN;
```

The SAS output gives:

Type 3 Analysis of Effects			
Effect	DF	Square	Pr > ChiSq
gest_imp	1	96.72	<.0001
parity_bin_imp	1	6.18	0.01
C_section	1	16.33	<.0001
rem_placenta	1	1727.54	<.0001
birth_weight_imp_log	1	40.26	<.0001
episiotomy	1	146.58	<.0001
vacuum	1	25.50	<.0001
induction	3	42.76	<.0001
ethnicgp	4	13.16	0.01
res_dep01	9	26.92	0.00
birth_weigh*ethnicgp	4	14.97	0.00
parity_bi*birth_weig	1	6.60	0.01
C_section*birth_weig	1	10.43	0.00
vacuum*ethnicgp	4	11.07	0.03
episiotomy*vacuum	1	14.04	0.00
rem_placenta*vacuum	1	18.90	<.0001
gest_imp*birth_weigh	1	92.60	<.0001
induction*ethnicgp	12	23.58	0.02

Odds Ratio Estimates			
Effect	Point Estimate	95% Wald Confidence Limits	
res_dep01 1 vs 9	0.77	0.66	0.89
res_dep01 10 vs 9	1.02	0.91	1.13
res_dep01 2 vs 9	0.89	0.77	1.02
res_dep01 3 vs 9	0.83	0.72	0.95
res_dep01 4 vs 9	0.90	0.79	1.02
res_dep01 5 vs 9	0.85	0.75	0.97
res_dep01 6 vs 9	1.00	0.88	1.12
res_dep01 7 vs 9	0.88	0.78	1.00
res_dep01 8 vs 9	0.88	0.79	0.99

Association of Predicted Probabilities and Observed			
Percent Concordant	68.3	Somers' D	0.38
Percent Discordant	30.4	Gamma	0.38
Percent Tied	1.3	Tau-a	0.07
Pairs	2.62E+08	c	0.69

SAS output continued:

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Square	Pr > ChiSq
Intercept		1	19.02	3.32	32.78	<.0001
gest_imp		1	-0.85	0.09	96.72	<.0001
parity_bin_imp		1	2.71	1.09	6.18	0.01
C_section		1	4.32	1.07	16.33	<.0001
rem_placenta		1	3.70	0.09	1727.54	<.0001
birth_weight_imp_log		1	-2.77	0.44	40.26	<.0001
episiotomy		1	0.69	0.06	146.58	<.0001
vacuum		1	0.57	0.11	25.50	<.0001
induction	BN	1	-0.16	0.06	7.58	0.01
induction	M	1	-0.16	0.08	3.61	0.06
induction	MS	1	0.31	0.07	18.91	<.0001
ethnicgp	11	1	1.19	0.96	1.52	0.22
ethnicgp	12	1	-3.09	1.26	6.02	0.01
ethnicgp	13	1	-2.47	1.40	3.11	0.08
ethnicgp	14	1	1.59	1.43	1.25	0.26
res_dep01	1	1	-0.16	0.06	7.58	0.01
res_dep01	10	1	0.12	0.04	8.50	0.00
res_dep01	2	1	-0.01	0.05	0.03	0.85
res_dep01	3	1	-0.08	0.05	2.03	0.15
res_dep01	4	1	0.00	0.05	0.00	0.99
res_dep01	5	1	-0.05	0.05	1.17	0.28
res_dep01	6	1	0.10	0.04	5.38	0.02
res_dep01	7	1	-0.02	0.05	0.16	0.69
res_dep01	8	1	-0.02	0.04	0.17	0.68
birth_weight*ethnicgp	11	1	-0.18	0.12	2.39	0.12
birth_weight*ethnicgp	12	1	0.37	0.16	5.52	0.02
birth_weight*ethnicgp	13	1	0.35	0.17	4.13	0.04
birth_weight*ethnicgp	14	1	-0.20	0.18	1.30	0.25
parity_bi*birth_weig		1	-0.35	0.13	6.60	0.01
C_section*birth_weig		1	-0.43	0.13	10.43	0.00
vacuum*ethnicgp	11	1	0.19	0.11	3.14	0.08
vacuum*ethnicgp	12	1	-0.02	0.16	0.02	0.90
vacuum*ethnicgp	13	1	-0.30	0.19	2.53	0.11
vacuum*ethnicgp	14	1	0.40	0.14	8.42	0.00
episiotomy*vacuum		1	-0.44	0.12	14.04	0.00
rem_placenta*vacuum		1	-1.06	0.24	18.90	<.0001
gest_imp*birth_weigh		1	0.11	0.01	92.60	<.0001
induction*ethnicgp	BN 11	1	0.05	0.07	0.61	0.44
induction*ethnicgp	BN 12	1	0.17	0.09	3.55	0.06
induction*ethnicgp	BN 13	1	0.01	0.10	0.00	0.95
induction*ethnicgp	BN 14	1	0.05	0.12	0.15	0.70
induction*ethnicgp	M 11	1	0.24	0.10	5.69	0.02
induction*ethnicgp	M 12	1	-0.08	0.14	0.34	0.56
induction*ethnicgp	M 13	1	-0.13	0.15	0.81	0.37
induction*ethnicgp	M 14	1	0.22	0.16	1.83	0.18
induction*ethnicgp	MS 11	1	-0.24	0.09	7.62	0.01
induction*ethnicgp	MS 12	1	0.02	0.11	0.04	0.84
induction*ethnicgp	MS 13	1	-0.01	0.12	0.01	0.94
induction*ethnicgp	MS 14	1	0.12	0.14	0.75	0.39

Goodness of Fit

Partition for the Hosmer and Lemeshow Test					
Group	Total	pp_haem = 1		pp_haem = 0	
		Observed	Expected	Observed	Expected
1	5561	225	203.89	5336	5357.11
2	5537	209	258.62	5328	5278.38
3	5550	272	290.11	5278	5259.89
4	5539	311	324.83	5228	5214.17
5	5538	384	373.8	5154	5164.2
6	5535	468	455.62	5067	5079.38
7	5538	538	540.55	5000	4997.45
8	5539	573	617.09	4966	4921.91
9	5534	775	719.34	4759	4814.66
10	5504	1459	1430.13	4045	4073.87

Hosmer and Lemeshow Goodness-of-Fit		
Test		
Chi-Square	DF	Pr > ChiSq
24.0328	8	0.0023

Deviance and Pearson Goodness-of-Fit Statistics				
Criterion	Value	DF	Value/DF	q
Deviance	12978.85	1.60E+04	0.8128	1
Pearson	18028.06	1.60E+04	1.129	<.0001

Model Fit Statistics		
Criterion	Intercept Only	Intercept and Covariates
AIC	34561.96	31593.434
SC	34570.88	32030.607
-2 Log L	34559.962	31495.434

R-Square	0.0538	Max-rescal	0.116
----------	--------	------------	-------

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood	3064.527	48	<.0001
Score	4814.224	48	<.0001
Wald	2676.975	48	<.0001

C.1 Regression results for Adjusted Plot

The follow SAS code is used for the logistic regression method:

```
PROC LOGISTIC DATA=data2
;
  CLASS ethnicgp      (PARAM=EFFECT) induction(PARAM=EFFECT) res_dep01
(PARAM=EFFECT);
  MODEL pp_haem (Event = '1')=gest_imp parity_bin_imp C_section
rem_placenta birth_weight_imp_log vacuum episiotomy ethnicgp induction
res_dep01 birth_weight_imp_log*ethnicgp
parity_bin_imp*birth_weight_imp_log
C_section*birth_weight_imp_log vacuum*ethnicgp vacuum*episiotomy
rem_placenta*vacuum gest_imp*birth_weight_imp_log ethnicgp*induction
/

  LINK=LOGIT clodds=wald lackfit
;output out=pprobs p=pred xbeta=xbeta predicted=p u=uppercl l=lowercl
resdev=resdev lower=lowerci upper=upperci prob=prob h=h
;
RUN;
```

The SAS output gives:

Model Fit Statistics		
Criterion	Intercept	Intercept
	Only	and
		Covariates
AIC	34561.96	31593.434
SC	34570.88	32030.607
-2 Log L	34559.962	31495.434

Testing Global Null Hypothesis: BETA=0			
Test	Chi-Square	DF	Pr > ChiSq
Likelihood	3064.527	48	<.0001
Score	4814.224	48	<.0001
Wald	2676.975	48	<.0001

Responses			
Percent Concordant	68.3	Somers' D	0.378
Percent Discordant	30.4	Gamma	0.383
Percent Tied	1.3	Tau-a	0.065
Pairs	261539454	c	0.689

Hosmer and Lemeshow Goodness-of-Fit		
Test		
Chi-Square	DF	Pr > ChiSq
24.0328	8	0.0023

Type 3 Analysis of Effects			
Effect	DF	Wald Chi-Square	Pr > ChiSq
gest_imp	1	96.7217	<.0001
parity_bin_imp	1	6.1813	0.0129
C_section	1	16.3346	<.0001
rem_placenta	1	1727.541	<.0001
birth_weight_imp_log	1	40.2573	<.0001
vacuum	1	25.5044	<.0001
episiotomy	1	146.5798	<.0001
ethnicgp	4	13.1602	0.0105
induction	3	42.7636	<.0001
res_dep01	9	26.9201	0.0014
birth_weigh*ethnicgp	4	14.9698	0.0048
parity_bi*birth_weig	1	6.6014	0.0102
C_section*birth_weig	1	10.4318	0.0012
vacuum*ethnicgp	4	11.0685	0.0258
vacuum*episiotomy	1	14.0375	0.0002
rem_placenta*vacuum	1	18.9003	<.0001
gest_imp*birth_weigh	1	92.6004	<.0001
ethnicgp*induction	12	23.5845	0.0232

Analysis of Maximum Likelihood Estimates						
Parameter		DF	Estimate	Standard Error	Wald Chi-Square	Pr > ChiSq
Intercept		1	19.02	3.32	32.78	<.0001
gest_imp		1	-0.85	0.09	96.72	<.0001
parity_bin_imp		1	2.71	1.09	6.18	0.01
C_section		1	4.32	1.07	16.33	<.0001
rem_placenta		1	3.70	0.09	1727.54	<.0001
birth_weight_imp_log		1	-2.77	0.44	40.26	<.0001
vacuum		1	0.57	0.11	25.50	<.0001
episiotomy		1	0.69	0.06	146.58	<.0001
ethnicgp	11	1	1.19	0.96	1.52	0.22
ethnicgp	12	1	-3.09	1.26	6.02	0.01
ethnicgp	13	1	-2.47	1.40	3.11	0.08
ethnicgp	14	1	1.59	1.43	1.25	0.26
induction	BN	1	-0.16	0.06	7.58	0.01
induction	M	1	-0.16	0.08	3.61	0.06
induction	MS	1	0.31	0.07	18.91	<.0001
res_dep01	1	1	-0.16	0.06	7.58	0.01
res_dep01	10	1	0.12	0.04	8.50	0.00
res_dep01	2	1	-0.01	0.05	0.03	0.85
res_dep01	3	1	-0.08	0.05	2.03	0.15
res_dep01	4	1	0.00	0.05	0.00	0.99
res_dep01	5	1	-0.05	0.05	1.17	0.28
res_dep01	6	1	0.10	0.04	5.38	0.02
res_dep01	7	1	-0.02	0.05	0.16	0.69
res_dep01	8	1	-0.02	0.04	0.17	0.68
birth_weigh*ethnicgp	11	1	-0.18	0.12	2.39	0.12
birth_weigh*ethnicgp	12	1	0.37	0.16	5.52	0.02
birth_weigh*ethnicgp	13	1	0.35	0.17	4.13	0.04
birth_weigh*ethnicgp	14	1	-0.20	0.18	1.30	0.25
parity_bi*birth_weig		1	-0.35	0.13	6.60	0.01
C_section*birth_weig		1	-0.43	0.13	10.43	0.00
vacuum*ethnicgp	11	1	0.19	0.11	3.14	0.08
vacuum*ethnicgp	12	1	-0.02	0.16	0.02	0.90
vacuum*ethnicgp	13	1	-0.30	0.19	2.53	0.11
vacuum*ethnicgp	14	1	0.40	0.14	8.42	0.00
vacuum*episiotomy		1	-0.44	0.12	14.04	0.00
rem_placenta*vacuum		1	-1.06	0.24	18.90	<.0001
gest_imp*birth_weigh		1	0.11	0.01	92.60	<.0001
ethnicgp*induction	11 BN	1	0.05	0.07	0.61	0.44
ethnicgp*induction	11 M	1	0.24	0.10	5.69	0.02
ethnicgp*induction	11 MS	1	-0.24	0.09	7.62	0.01
ethnicgp*induction	12 BN	1	0.17	0.09	3.55	0.06
ethnicgp*induction	12 M	1	-0.08	0.14	0.34	0.56
ethnicgp*induction	12 MS	1	0.02	0.11	0.04	0.84
ethnicgp*induction	13 BN	1	0.01	0.10	0.00	0.95
ethnicgp*induction	13 M	1	-0.13	0.15	0.81	0.37
ethnicgp*induction	13 MS	1	-0.01	0.12	0.01	0.94
ethnicgp*induction	14 BN	1	0.05	0.12	0.15	0.70
ethnicgp*induction	14 M	1	0.22	0.16	1.83	0.18
ethnicgp*induction	14 MS	1	0.12	0.14	0.75	0.39