UNIVERSITY OF GHANA

MODELING MATERNAL MORTALITY IN GHANA USING HIERARCHICAL MODELS (2010-2013)

BY

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DECLARATION

I hereby declare that this thesis is my own work towards the attainment of MPhil degree and that, to the best of my knowledge, it contains no material previously published by another person nor material which has been accepted for the award of any other degree of the University of Ghana, except where due acknowledgement has been made in the text.

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ABSTRACT

This thesis examined the appropriate model that best fit maternal mortality data in fifty six health facilities in the Central, Eastern, Greater Accra and Western regions of Ghana from 2010 to 2013 as well as factors contributing to this menace in the various health facilities. The study began with the application of a simple Poisson regression model which was extended to capture the hierarchical structure, overdispersion and zero-inflation. Expressions for the mean, variance and score equations were derived. All estimations were done in the maximum likelihood framework. In this thesis we show that all different extensions of the Poisson model is based on mixture of distributions. The overall best model showed that maternal mortality in the various health facilities in Ghana depends on the number of referrals (into and out of hospital facility), number of antenatal visits exceeding four, number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of medical doctors and number of midwives at the facility. We found that maternal mortality was significant in all four regions and for all years considered and that more pregnant women attend antenatal at clinics (Polyclinics, clinics, health centers and community health planning service centers) than in hospitals (general hospitals, regional hospitals and teaching hospitals) but more of them deliver in the hospitals than in the clinics. 2.3% and 12.9% of the pregnant women had HIV/AIDS and malaria respectively. Eclampsia and Pre-Eclampsia were the leading direct cause of maternal death while anaemia in pregnancy was second to a collection of other complications for the indirect cause. Finally, we estimated Ghana's maternal mortality ratio at 382 per 100000 live births.

Key words: Poisson regression model, hierarchical models, overdispersion, maternal mortality ratio, zero-inflated models.

DEDICATION

This piece of work is dedicated to the Almighty Jehovah God for giving me the strength and the will to make it happen. My sincere gratitude also goes to my mum, Miss Grace Amoah, my two kid sisters, Grace and Mercy for their immense support and contribution.

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R Codes for Maternal Mortality Data

LIST OF ABBREVIATIONS

AIC	Akaike Information Criterion
AIDS	Acquired Immuno Deficiency Syndrome
ARIMA	Auto Regressive Moving Average
BIC	Bayesian Information Criterion
CHAG	Christian Health Association of Ghana
DHMT	District Health Management Team
CHPS	Community Health Planning and Services
Cl	Clinics
CSO	Central Statistical Office
DIC	Disseminated Intra Coaqulation
EM	Expectation Maximization
EmOC	Emergency Obstetric Care
GDHS	Ghana Demographic and Health Survey
GH	General Hospitals
GHS	Ghana Health Service
GLM	Generalized Linear Models
GLMM	Generalized Linear Mixed Models
GSS	Ghana Statistical Service
HC	Health Center
HCC	Health Centers and Clinics
HD	Health Directorate
HFs	Health Facilities
HIMS	Health Information Management System
HIV	Human Immunodeficiency Virus

ICD-10	International Classification of Disease Tenth Revision
IMM	Institutional Maternal Mortality
KATH	Komfo Anokye Teaching Hospital
LGC	Latent Growth Curve
ll	log-likelihood
LM	Linear Model
LMM	Linear Mixed Model
MDG	Millennium Development Goal
ML	Maximum Likelihood
MMDAs	Metropolitan Municipal and District Assemblies
MMRates	Maternal Mortality Rates
MMR	Maternal Mortality Ratio
MOH	Ministry of Health
MPs	Members of Parliaments
NB	Negative Binomial Regression Model
NBG	Negative Binomial GLMM
P	Poisson Regression Model
PC	Polyclinics
pdf	Probability Density Function
PG	Poisson GLMM
PHC	Population and Housing Census
PID	Personal Identification
PHS	Public Health Services
RAMOS	Reproductive Age Mortality Survey
RH	Regional Hospitals

STATA	Statistics and Data
TH	Teaching Hospitals
TTH	Tamale Teaching Hospital
UNFPA	United Nations Population Fund
UNICEF	United Nations Children's Fund
UG	University of Ghana
US	United States
WHO	World Health Organization
WMD	Why Mothers Die
ZI	Zero Inflated Model
ZINB	Zero inflated Negative Binomial GLM
ZINB	Zero inflated Negative Binomial GLMM
ZIP	Zero inflated Poisson GLM
ZIPG	Zero inflated Poisson GLMM

CHAPTER 1

1.0 INTRODUCTION

This study aims at modeling maternal mortality and the associated factors in Ghana from 2010 to 2013 using hierarchical models. The study will investigate the factors related to maternal mortality in Ghana. This chapter takes a look at the background of the study, the general profile of the study area, the problem statement, research questions and objectives, research methodology, justification of the study as well as scope and limitations of the study are discussed.

1.1 BACKGROUND OF THE STUDY

Maternal mortality is widely considered as a sentinel indicator of the quality of a health care delivery system and as a key indicator of population health and social and economic development (Wilmoth *et al.,* 2012). Millennium Development Goal 5 (MDG 5) calls for a reduction in the maternal mortality ratio (MMR) by three quarters between 1990 and 2015. To measure progress, the World Health Organization (WHO), the United Nations Children's Fund (UNICEF), the United Nations Population Fund (UNFPA) and the World Bank published estimates of maternal mortality in 2012, referred to hereafter as the WHO estimates.

The world's attention was actually drifted to maternal mortality when in 1985; Rosenfield and Maine (1985) published a thought-provoking article in the Lancet, titled 'Maternal Mortality – a neglected tragedy - where is the M in MCH?' Rosenfield and Maine alerted the world to the fact that many developing countries were neglecting this important problem and that existing programs were unlikely to reduce the high maternal mortality rates in the developing world. The WHO publication, 'Maternal Mortality: helping women off the road to death' in 1986 threw more

light on this menace. This led to the Save Motherhood Initiative in 1987 and the addition of decreasing maternal mortality in the Millennium Development Goals (MDG 5). Since then maternal mortality has received special attention by various government worldwide.

As most maternal deaths occur within health facilities, the referrals from one facility to another may simply implied that no deaths are reported during a period of time, triggering a situation that appears often in count data collected in health services; the excessive number of zero count relative to Poisson distribution, a well-known member of the exponential family . Thus the Poisson model has to be extended to account for (1) the excess number of zeros (2) the hierarchical structures and correlated data and (3) the remaining sources of overdispersion.

In recent years there has been considerable interest in models for count data allowing for zeros particularly in the health sector. These models complement more conventional models for overdispersion that concentrate on modeling the variance-mean relationship accurately.

In this thesis we review and compare Poisson zero-inflated models with particular application to maternal mortality in health facilities in Ghana with emphasis on multilevel modeling.

1.2 PROFILE OF THE STUDY AREA

The Republic of Ghana lies almost in the center of the countries along the Gulf of Guinea (the West African coast). Its southern coast extends between latitudes 4½° North at Cape Three Points and 6½° North in the extreme east and is thus not far from the Equator. From the coast, the country extends inland to about latitude 11° North covering a distance of 672 kilometers from South to North. The distance across the widest part from east to west measures 536 kilometers. The country has a total land area of 239,460 square kilometers. The 2010 Population and Housing Census (PHC) organized by the Ghana Statistical Service (GSS) estimated Ghana's

population at 24,658,823 with 12,633,978 females and 12,024,845 males. Greater Accra and Ashanti region having the greater share of the population while Upper East and Upper West region had the smaller share.

Ghana is divided into 10 administrative regions, subdivided into a total of 216 Metropolitan Municipal and District Assemblies (MMDAs) whose work are supervised by a democratically elected Executive President with the help of his Vice and appointed Executive Ministers. The country also has two hundred and seventy five democratically elected Members of Parliaments (MPs) who make laws and pass important bills for national development.

1.3 HEALTH CARE DELIVERY

The Ministry of Health (MOH) headed by the Minister of Health in collaboration with the Ghana Health Service (GHS) headed by a Director oversees all health related matters through the various Health Directorate (HD) located in all the MMDAs. The HDs headed by their Health Directors supervise health activities at the MMDAs and report directly to the MOH. The Public Health Services (PHS) at this level is co-ordinated by the District Health Management Team (DHMT) headed by the Health Directors. The team focuses on providing support to sub-districts in disease prevention and control, health promotion and general education of the public on health issues. Information at various health facilities are coordinated by the team through the Health Information Management System (HIMS).

There are three thousand two hundred and seventeen health facilities (HFs) located all over the country to cater for various health needs of the populace. This is made up of four teaching hospitals, eight regional hospitals, three psychiatric hospitals, three hundred and forty three hospitals (fifty nine Christian Health Association of Ghana (CHAG), ten Islamic, ninety six government, one hundred and fifty six private and twenty two quasi government), two thousand

and eighty three health centers and clinics (HCC) (one hundred and sixty eight CHAG, eight Islamic, one thousand one hundred and six government, seven hundred and thirty two private and sixty nine quasi government), three hundred and eighty nine private maternity homes and three hundred and seventy nine Community Health Planning and Services(CHPS) (GHS. The Health Sector in Ghana, Facts and Figures 2010).

The hospitals are in the MMDA capitals, the HCC are located in cities and towns while the maternity homes and CHPS are mostly in the villages and small communities. Most of the health facilities are closer to the people except some interior villages and communities where the people walk long distances to access these facilities.

1.4 PROBLEM STATEMENT

The WHO states that worldwide 1500 women die each day, or one a minute, in pregnancy or due to childbirth related complications. It is estimated that fifty six percent of these deaths occur in sub-Saharan Africa, with maternal mortality ratio of 500 deaths per 100,000 live births and 350 per 100,000 live births in Ghana (WHO 2012, MDG Report 2012) whiles the annual health report 2012 by the Ghana Health Service (GHS) shows various regions exhibit high institutional maternal mortality (IMM) even though it showed impressive health records.

In Ghana, three quarters of all maternal deaths occur during birth and the immediate post-partum period (GDHS, 2008) and the factors contributing to this menace in the various health facilities remain unclear.

Most research on maternal mortality in Ghana has been based on a single health facility or a particular district and is mostly based on patterns and descriptive studies whereas those that model concentrate only on the number of maternal deaths without considering their related

factors. It is against this background that this thesis is undertaken to identify the best model as well as identify the main factors contributing to maternal mortality in various HFs in the country.

1.5 RESEARCH QUESTION

1. What is the most appropriate model that best describes maternal mortality in health facilities in Ghana?

2. What are the main contributing factors to maternal death in these health facilities?

1.6 OBJECTIVES OF THE STUDY

The study aims at developing a model that takes the inflation of zero, and overdispersion and longitudinal to maternal mortality at various HFs in the four regions of Ghana.

1.6.1 SPECIFIC OBJECTIVES

The study will focus on:

- Identifying the most appropriate model that best fit the data.
- Examining the main factors contributing to maternal mortality.

1.7 RESEARCH METHODOLOGY

Different models will be used to examine the number of maternal deaths. Maximum likelihood estimation will be used to estimate the parameters of the models. The data is assumed to be coming from a Poisson distribution since the response and the covariates are counts. The Poisson model will be extended to account for heterogeneity in the data as well as the excessive amount of zero counts.

1.8 DATA

The data available is from the Bio-Statistics/Health information Department and maternity wards of the various HFs for the period 2010 to 2013. The data involves:

- Total number of maternal deaths
- Total number of deliveries
- Total number of obstetric referrals from/to HF
- Total number of antenatal visits exceeding four
- Total number of obstetric cases with HIV/AIDS
- Total number of obstetric cases with malaria
- Total number of doctors at maternity ward
- Total number of midwives
- Total number of paramedical staff at maternity ward
- Type of HF
- Location of HF
- Existence of Emergency Obstetric Care (EmOC)
- Existence of a waiting house or room
- Cause-specific maternal deaths

1.9 STATISTICAL SOFTWARE TO BE USED

Data manipulations were done in excel and imported into R-studio for further manipulations.

1.10 SOURCE OF KNOWLEDGE

The main sources of knowledge would be the Hospital Library's, UG Balm library, the Regional Health Directorates Library, the Ministry of Health Research Center-Accra, Senior midwives, Obstetricians and Gynaecologists and other relevant health professionals as well as the internet.

1.11 JUSTIFICATION FOR THE STUDY

Since the inception of the Millennium Development Goals, (MDG 5) which states that: improve maternal health by targeting a reduction of seventy five percent in the 1990 MMR by the year 2015 and achieving a universal access to reproductive health by the same year, 2015, has increased interest in programs aimed at improving MMRates.

Using available empirical evidence, this study would seek to furnish decision makers and other stakeholders with vital information regarding the major cause-specific deaths and factors contributing to maternal mortality in the said regions for possible policy interventions. In addition, this study would also contribute to knowledge on the use of appropriate statistical models in the analysis of maternal health vis-à-vis stimulating further research.

1.12 SCOPE AND LIMITATION

The study is restricted to the Central, Eastern, Western and Greater Accra regions of Ghana due to time constraint and proximity to UG. Over seventy six hospitals were selected from these regions for data collection, but data from only fifty six such facilities were made available. For each hospital retrospective data is collected over a period of four years. The study would use medical autopsy results to assess maternal mortality causes. The study will suffer constraints of

time, resource inadequacy, unavailability of relevant literature and others of the like since it is structured within the confines of a thesis study matter.

1.13 THESIS ORGANIZATION

The thesis is in five chapters. Chapter 1 is the introductory to the entire study. It examines the general background of maternal mortality and the general profile of the study area. The problem statement, research questions and objectives, research methodology, justification of the study as well as scope and limitations of the study are discussed in this chapter. Chapter 2 reviews related literature based on the thesis objectives and preferred models to be used in achieving these objectives. Expected outcome of the study and other comparative results of similar studies are also discussed in this chapter. Chapter 3 describes the theory of the model to be used, model formulations and methods of estimation. Chapter 4 is dedicated to data collection, analysis and results. Chapter 5 concludes the entire study by stating specific recommendations to stakeholders based on the major findings made in the study.

CHAPTER 2

LITERATURE REVIEW

2.0 INTRODUCTION

This chapter discusses the literature available on maternal mortality as well as summary of abstracts on various literatures and the general working title.

2.1 THE SITUATION OF MATERNAL MORTALITY

Some maternal deaths are still unavoidable, and there are instances of outstanding medical and midwifery care provided in the face of overwhelming complications. However, more than half of women who die had some aspect of substandard clinical care. Some die because their condition was not diagnosed or they received ineffective care or the wrong treatment. Not all care is consistent with current national clinical guidelines or provided by experienced staff. Cardiac arrests are rare in maternity units but they can and do happen and their management is, in some cases, suboptimal (WMD, 2002).

Maternal mortality is often described as hard to measure and difficult to monitor. This statement contains some truth, but similar challenges also arise in measuring and monitoring other cause-specific deaths, such as those from AIDS, tuberculosis and malaria (AbouZahr, 1998). The WHOs International Classification of Disease Tenth Revision (ICD-10) estimate maternal mortality ratio (MMR) and maternal mortality rates (MMRates) from direct and indirect causes as $\text{MMR}=\frac{\text{Total Maternal Deaths}}{\text{Total live Births}}\times 100,000 \text{ live births}$ and

$$\text{MMRate} = \frac{\text{Total Maternal Deaths}}{\text{Total women of reproductive age}} \times 100,000 \text{ women of reproductive age}$$ respectively.

The WHO ICD-10 further estimate the proportion of maternal deaths among deaths of women of reproductive age as $\text{PM} = \frac{\text{Maternal Death}}{\text{Total death of women at ages 15 to 49}}$

Maternal mortality ratios are a function of both economic and social development. Of all the social indicators, one that clearly discriminates between developing and developed countries is maternal mortality ratio. Reducing maternal mortality is not just an issue of development, but also an issue of human rights (Hunt and De Mesquita, 2012). Nieburg (2012) emphasized that societies that have achieved the lowest levels of maternal mortality have done so by preventing pregnancies, by reducing the incidence of certain (pregnancy) complications, and by having adequate facilities and well-trained staff to treat the complications.

Sarpong (2012) found that both the mean number of occurrence and incidence of maternal death cases at the KATH were high for all the years considered and that the mean number of occurrence of maternal death cases did not significantly reduce over the period 2000 to 2010. He concluded that statistically, the mean rate of maternal death cases is not significant over the period of time under study. He stressed further that, although the ARIMA model adequately fits the data and is useful for predicting future mortality ratios, it is not recommended for medium and long term predictions.

Gumanga *et al*. (2011) reported that the absolute number of maternal deaths had declined from 74 in 2007 to 33 in 2010 at the TTH. They further emphasized that though there has been a significant decline in Maternal Mortality, the rate of decline is unacceptably low.

Asamoah *et al*. (2011) found that haemorrhage was the highest cause of maternal mortality among different socioeconomic groups in Ghana.

A Retrospective Hospital-based Review of Maternal Mortality was undertaken by Qin Yi Lee (2010) at the Obstetrics and Gynaecology Department of KATH in Kumasi, Ghana using data from the biostatistics unit as well as all maternal deaths following admission from the period 1st January 2008 to 31st May 2010. His result revealed an estimated maternal mortality ratio of 1021.9 per 100 000 live births (95% CI: 906.6 - 1130.8).

Adamu *et al.* (2002) determined the incidence and causes of maternal mortality as well as its temporal distribution over a decade (1990–1999). They analyzed maternal deaths recorded within the study period in the State of Kano, Northern Nigeria and computed MMR using the Poisson assumption to derive confidence intervals around the estimates. They fitted a non-linear regression model to obtain the best temporal trajectory for MMR. Their study revealed that a total of 4154 maternal deaths occurred among 171621 deliveries, yielding a MMR of 2420 deaths per 100 000 live births. Eclampsia, ruptured uterus and anemia were responsible for about 50% of maternal deaths. They concluded that the area had one of the highest maternal mortality ratios in the world and suggested that maternal mortality could be reduced by half at study site with effective interventions targeted to prevent deaths from eclampsia, ruptured uterus and anaemia.

Yoko *et al.* (2011) did a study aimed at examining the quality of the data used for the estimates of MMR provided by the Trinidad and Tobago Central Statistical Office (CSO) using a retrospective reproductive age mortality survey (RAMOS) applied for 2000–06 to evaluate national estimates. They found that, data from CSO and external data sources yield conflicting

results. The CSO estimate of MMR in 2005 was 34·8, while those provided by UNICEF and the World Bank were 45.0 and 55.0, respectively. They recommended that specific maternal death review committee be established as the ideal maternal death review mechanism across all health jurisdictions in Trinidad and Tobago.

Razum *et al.* (1998) examined the impact of marital status on maternal mortality in the period before and the period after German reunification in the area covered by the former East Germany. They calculated the maternal mortality ratio by relating the number of maternal deaths among women resident in eastern Germany in 1980-96 to the respective number of live births, using national register data. They then investigated the effect of marital status, controlling for maternal age and year of death, in a Poisson regression model. Altogether, 413 maternal deaths and 2.99 million live births were reported, the overall maternal mortality ratio was stable before, and declined after, reunification. Before reunification, unmarried women had a risk of maternal death equal to that of married women; after reunification, they had 2.6 times the age adjusted risk of married women. Unmarried status thus became a significant risk factor for maternal mortality in eastern Germany after reunification.

Fernández *et al.* (2009) published a research report titled "Increase in maternal mortality associated with change in the reproductive pattern in Spain: 1996–2005". Their study aimed at analyzing the age-related trend in the maternal mortality ratio among mothers in Spain for the decade 1996–2005, and to describe the causes of death and associated socio-demographic factors for the years with highest mortality. An ecological study on trends, for the age-related trend in the maternal mortality ratio; an indirect standardization and Poisson regression model was used. They found that, prevalence of live births among mothers aged 35 years and over was 15% higher in Spain than in Europe. The maternal mortality rate increased by 20% (standardized

mortality ratio of 1.2, 95% CI 0.9 to 1.4) in 2005 with respect to 1996. The age-related risk of maternal mortality was three times higher among mothers aged 35–44 years versus those aged under 35 years. The highest mortality was detected during 2003–2004. The study therefore concluded that there was a change in the maternal mortality trend characterized by an increase in deaths, associated with advanced maternal age, as well as an increase in the prevalence of live births among mothers aged 35 years and over.

Worawan *et al.* (2010) undertook a study in Thailand aimed at using multiple sources of data to calculate the MMR in 2004–09, and to illustrate the difference between the official causes of death with the research findings. In their research individual data from civil registration and inpatient records from all public hospitals were used. The civil registration contains data about individual's personal identification (PID) etc. Their result shown that, the number of maternal deaths declined from 362 in 2004 to 269 in 2009. The country's MMR declined from 44·5 to 35·2, a 21% reduction. Their conclusion was that, using matching technique together with individual data, policy makers can get reliable information about the causes of maternal death.

Sullivan *et al.* (2003) determined the relationship between state-specific maternal mortality ratios and the density of maternal-fetal medicine specialists. State maternal mortality ratios from 1994 to 2001 were calculated from the Centers for Disease Control and Prevention WONDER database. Practitioner distribution data were obtained from professional associations. Demographic information regarding states was gathered from the 2000 US census data. Bivariable and multivariable analyses were conducted with the use of Spearman correlations and Poisson regression, respectively. The study showed that an increase of 5 maternal-fetal specialists per 10,000 live births results in a 27% reduction in the risk of maternal death. This risk reduction was based on a multivariable Poisson regression model that included the following

variables and their significant interactions: state-specific percentages of mothers in poverty, mothers without a high school diploma, minority mothers, and teenage mothers. The density of maternal-fetal medicine specialists is significantly and inversely associated with maternal mortality ratios, even after controlling for state-level measures of maternal poverty, education, race, age, and their significant interactions.

Mulu and Tilahun (2009) did a study that sort to analyze trends of and develop model for prediction of Health and Health related indicators of Ethiopia from the year 1987 to 2000. The determinants of the established trends were identified using ARIMA models in STATA. Among the mortality indicators considered in this study, it was only MMR that showed statistically significant decrement within the study period. The trends of Total Fertility Rate, physician per 100,000 population, skilled birth attendance and postnatal care coverage were found to have significant association with MMR trend. They concluded that current trend indicates the need to accelerate the progress of the indicators to achieve MDGs at or before 2015, particularly for Maternal Health and access to safe water supply.

Pillai, Maleku, and Wei (2013) stated that Latent growth curve (LGC) modeling approaches provide an excellent set of tools to examine the effects of female literacy longitudinally. In their application of LGC models, the unit of analysis was a country in the developing world. LGC models are essentially longitudinal models aiding explanations of levels and rate of change in outcome variables such as MMR.

Cutts *et al.*(1996) emphasized that lack of infrastructures and human resources are the main determinants of maternal mortality, which in many situations requires referrals of patients to better hospital facilities.

2.2 USE OF HIERARCHICAL ZERO-INFLATED MODELS

In the advanced world, the use of longitudinal model for maternal mortality data is wide spread. Clark, Hannan, and Raudenbush (2010) applied hierarchical model to estimate risk-adjusted mortality for hospitals not included in the reference sample and concluded that to allow independent verification, agencies using reference databases for hospital mortality ‘‘report cards’’ should publish their risk-adjustment equations. Similar hospitals not in the reference database may also use the published equations along with the approximations described to evaluate their own outcomes using their own data.

In the Special Issue on Longitudinal Methodology, Canadian Studies in Population, Kuate-Defo (2001) showed how conventional hazard models can be extended to handle multilevel data structures. He stressed the need to collect longitudinal data that are suited to benefit from the new tools of analysis, which are outpacing most available longitudinal data. Contextual longitudinal studies where observations are fully crossed (over time and context by multiple levels of observation units) and nested within larger clusters appear to be the proper venue. The observations within those clusters tend to be more similar than those in different clusters, and the paper showed how to estimate hazard models that take the clustering into account and model the various random parameters across individuals and groups. His article showed through a few illustrations that individual-level, family- level, community-level and area-level influences have independent effects on mortality and health processes, especially in the case of infant mortality and women’s reproductive health after childbirth. It should be admitted, however, multilevel failure-time models can become quite complex and there may be limitations of most computer programs for estimating such complex hierarchically clustered survival models, especially if some or all variables are time-dependent and context-dependent.

O.Loquiha *et al.* (2013) proposed hierarchical zero-inflated and overdispersed models with independent, correlated, and shared random effects for both components of the mixture model. They showed that all different extensions of the Poisson model can be based on the concept of mixture models, and that they can be combined to account for all different sources of heterogeneity. The models were applied to data on maternal mortality and related risk factors in health facilities in Mozambique.

Iddi and Molenberghs (2012) merged the attractive features of the so-called combined model of Molenberghs *et al.* (2010) and the marginalized model of Heagerty (1999) for hierarchical non-Gaussian data with overdispersion. In their model, the fixed-effect parameters retain their marginal interpretation. Lee *et al.* (2011) also developed an extension of Heagerty (1999) to handle zero-inflation from count data, using the hurdle model.

These studies recommended the use of appropriate models that takes into account the features of the data. However, such application of sophisticated models has not been applied to maternal mortality data from Ghana to the best of our knowledge. This study therefore seeks a first attempt by demonstrating how different conclusions from conversional approaches will be compared to the extended models.

CHAPTER 3

METHODOLOGY

3.0 INTRODUCTION

This chapter describes the methodologies used, their formulations and methods of analyzing the available data to satisfy the objectives of the study. Among the aspects that will come under discussion include the various methodologies used in modeling, the software specifications, and the features that are incorporated in the model. To help comprehend the extended and more sophisticated models, we review from the very basics and build up gradually to the most appropriate model. We begin with models for continuous outcome which form the basis and help in our understanding of nonnormal data. Extensions are treated in turn.

3.1 DATA SOURCE AND TYPE

The analysis is based on secondary data available from fifty six (56) health facilities including two teaching hospitals(TH), two regional hospitals (RH), twenty three general hospitals (GH), three polyclinics (PC), eighteen health centers(HC), three clinics (Cl) and five community health planning services(CHPS) selected from the Central, Eastern, Western and Greater Accra regions from 20010 to 2013. The response variable is the total number of maternal deaths at the health facility. The covariates includes; type of hospital facility (HF), location of the HF, existence of an emergency obstetric care (EmOC), number of doctors, number of midwives, number of paramedical staff at the maternity ward, number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of deliveries, number of obstetric

referrals from HF, number of obstetric referrals to HF. The total number of cause-specific maternal deaths was also recorded.

3.2 LINEAR MODEL

A linear model (LM) is a statistical model in which the independent variable or covariate has a linear relationship with the dependent or response variable. When a single covariate predicts the response variable in a LM, the model is referred to as a Simple Linear regression model otherwise it is referred to as a Multiple Linear regression model. We summarize linear models as proposed by Seber (1977) as well as Sen and Srivastava (1990).

The general linear model is of the form;

$$Y = \mathbf{X}\beta + \varepsilon \qquad (1)$$

Y and ε are random vectors whereas $\mathbf{X}$ is a matrix of known constants called the covariates and β is a vector of unknown parameters to be estimated, and σ^2 is the variance of the error term. where, $\varepsilon \sim N\left(0, \sigma^2 I\right)$ and $\operatorname{cov}\left(\varepsilon_i, \varepsilon_j\right) = 0$, for $i \neq j$. ε is iid. This implies that, $Y \sim N\left(\mathbf{X}\beta, \sigma^2 I\right)$ and $\operatorname{cov}\left(Y_i, Y_j\right) = 0$, for $i \neq j$. Y is iid.

3.2.1 Maximum likelihood estimation of β and σ^2

To estimate the unknown parameter β and σ^2, we know that

$$Y \sim N\left(\mathbf{X}\beta, \sigma^2 I\right)$$

Then the pdf of Y is

$$f\left(Y;\beta,\sigma^2\right) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left\{-\frac{1}{2}\left[\frac{\left(Y-\mathbf{X}\beta\right)'\left(Y-\mathbf{X}\beta\right)}{\sigma^2}\right]\right\}$$

The likelihood of the above density, is given by

$$L = \prod_{i=1}^{n} f\left(Y;\beta,\sigma^2\right)$$

$$= \left(2\pi\sigma^2\right)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2}\frac{\left(Y-\mathbf{X}\beta\right)'\left(Y-\mathbf{X}\beta\right)}{\sigma^2}\right\}$$

The $\log-$likelihood ℓ is

$$\ell = -\frac{n}{2}\ln\left(2\pi\sigma^2\right) - \frac{1}{2}\frac{\left(Y-\mathbf{X}\beta\right)'\left(Y-\mathbf{X}\beta\right)}{\sigma^2} \qquad (2)$$

Differentiating ℓ with respect to β yields

$$\frac{\partial \ell}{\partial \beta} = \frac{\mathbf{X}'\left(Y-\mathbf{X}\beta\right)}{\sigma^2}$$

Equating the *score statistic* above to zero and solving for β and replacing it with $\hat{\beta}$

yields the MLE

$$\hat{\beta} = \left(\mathbf{X}'\mathbf{X}\right)^{-1}\mathbf{X}'Y \qquad (3)$$

Also, differentiating (2) with respect to σ^2 yields

$$\frac{\partial \ell}{\partial \sigma^2} = -\frac{n}{2\sigma^2} + \frac{(Y - \mathbf{X}\beta)'(Y - \mathbf{X}\beta)}{2(\sigma^2)^2}$$

Equating the score statistic above to zero and solving for σ^2 and replacing it

with $\hat{\sigma^2}$ yields the MLE

$$\hat{\sigma^2} = \frac{(Y - \mathbf{X}\beta)'(Y - \mathbf{X}\beta)}{n} \qquad (4)$$

From (3), $\hat{\beta}$ is an unbiased estimator of β and has variance given as $\text{var}\left(\hat{\beta}\right) = \hat{\sigma^2}(\mathbf{X}'\mathbf{X})^{-1}$

From (4), $\hat{\sigma^2}$ is a biased estimator of σ^2 and has variance given by $\text{var}\left(\hat{\sigma^2}\right) = \frac{2\sigma^4}{n}$.

The variance of the score statistic is called the *information.*

3.3 LINEAR MIXED MODEL

Linear Mixed Models (LMMs) are statistical models for continuous outcome variables in which the residuals are normally distributed but may not be independent or have constant variance.

Since in LMs the residuals and the responses are homoscedastic and not correlated, they are modified to LMMs to accommodate heteroscedatisticity and correlation between the residuals as well as the responses taking into consideration the fixed and random effects.

We outline linear mixed effects models as proposed by Laird and Ware (1982) as well as Longford (1993).The general linear mixed model is of the form:

$$Y = \mathbf{X}\beta + \mathbf{Z}\mu + \varepsilon \qquad (5)$$

where, Y is a $n-$dimensional vector of responses. $Y \sim N\left(\mathbf{X}\beta,\ \mathbf{Z}D\mathbf{Z}' + \Sigma\right)$, μ is a $q-$dimensional vector of random effects. $\mu \sim N\left(0, D\right)$. ε is a $n-$dimensional vector of residuals. $\varepsilon \sim N\left(0, \Sigma\right)$. μ, ε independent. $\mathbf{X}$ is a $n \times p$ design matrix of known covariates. β is a $p-$dimensional vector of fixed$-$effect parameters. $\mathbf{Z}$ is the $n \times q$ design matrix of covariates. Where $q \leq p$. With $\mathbf{X}\beta$ being the fixed effect component and $\mathbf{Z}\mu + \varepsilon$ the random effect component. D and Σ are covariance matrices. Here the responses may not be independent. The fixed effect parameters describe the relationship of the covariates with the response variable for the entire population whereas the random effects are specific to subjects within the population.

3.3.1 Maximum Likelihood estimation β and V

From the above, we have

$$Y \sim N\left(\mathbf{X}\beta,\ \mathbf{V}\right)$$

where $\mathbf{V} = \mathbf{Z}D\mathbf{Z}' + \Sigma$

The pdf of Y is given by

$$f\left(Y; \beta, \sigma^2\right) = \frac{1}{\sqrt{2\pi|\mathbf{V}|}} \exp\left\{-\frac{1}{2}\left(Y - \mathbf{X}\beta\right)' \mathbf{V}^{-1}\left(Y - \mathbf{X}\beta\right)\right\}$$

The likelihood, L, of the pdf above is

$$L = \left(2\pi|\mathbf{V}|\right)^{-\frac{n}{2}} \exp\left\{-\frac{1}{2}\left(Y-\mathbf{X}\beta\right)' \mathbf{V}^{-1}\left(Y-\mathbf{X}\beta\right)\right\}$$

The log – likelikelood, ℓ, is given as

$$\ell = -\frac{n}{2}\ln\left(2\pi|\mathbf{V}|\right) - \frac{1}{2}\left(Y-\mathbf{X}\beta\right)' \mathbf{V}^{-1}\left(Y-\mathbf{X}\beta\right) \qquad (6)$$

When $\mathbf{V}$ is known, we obtain the optimal value of β by equatng the score statistic to zero and solving for β.

$$\frac{\partial \ell}{\partial \beta} = \frac{1}{2}\mathbf{X}'\mathbf{V}^{-1}\left(Y-\mathbf{X}\beta\right)$$

The ML estimator for β, $\hat{\beta}$ is

$$\hat{\beta} = \left(\mathbf{X}'\mathbf{V}^{-1}\mathbf{X}\right)^{-1}\mathbf{X}'\mathbf{V}^{-1}Y \qquad (7)$$

With $\hat{\beta}$ being an unbiased estimator of β and $\text{var}\left(\hat{\beta}\right) = \left(\mathbf{X}'\mathbf{V}^{-1}\mathbf{X}\right)^{-1}$

when $\mathbf{V}$ is unknown we replace β in (6) with $\hat{\beta}$ yielding

$$\ell = -\frac{n}{2}\ln\left(2\pi|\mathbf{V}|\right) - \frac{1}{2}\left(Y-\mathbf{X}\hat{\beta}\right)' \mathbf{V}^{-1}\left(Y-\mathbf{X}\hat{\beta}\right) \qquad (8)$$

In (8), however, there no closed form solution for the optimal value of $\mathbf{V}$, so $\mathbf{V}$ is estimated by performing computational iterations until convergence is obtained.

3.4 THE EXPONENTIAL FAMILY

In LMs and LMMs the response variables are assumed to be strictly from the normal distribution. The question then is what happens when the responses are not normally distributed? This led to the introduction of Generalized Linear Models (GLMs) and Generalized Linear Mixed Models (GLMMs).

In GLMs and GLMMs, we will assume that the observations come from a one parameter distribution in the exponential family with pdf

$$f(Y;\theta)=\begin{cases} a(\theta)b(y)\exp\left[c(\theta)s(y)\right] & y\in b, \\ 0 & \text{elsewhere.} \end{cases}$$

where $a(.), b(.), c(.)$ and $s(.)$ are suitable choice functions and $\theta(\theta\in\Omega)$ is a unidimensional parameter and Ω is the sample space such that $\Omega=\{\theta:\gamma<\theta<\delta\}$

To make the expression above easier to work with we rewrite it as

$$f(Y;\theta)=\begin{cases} \exp\left[s(y)c(\theta)+A(\theta)+B(y)\right] & y\in b, \\ 0 & \text{elsewhere.} \end{cases} \qquad (9)$$

where $A(\theta)=\log a(\theta)$ and $B(y)=\log b(y)$ in the above, such that

i. B, the support of Y, is independnt of θ,

ii. $c(\theta)$ is a continuous function of $\theta \in \Omega$,

iii. Finally,

(a) if Y is a continous random variable then each of $B'(y) \neq 0$ and $B(y)$ is a continous function of $y \in B$

(b) if Y is a discrete random variable then $B(y)$ is a function of $y \in B$

Also, for $s(y) = y$, the distribution is said to be in the *canonical* form and $c(\theta)$ is the *natural* parameter of the distribution. Other parameters apart from the parameter of interest, θ are called a *nuissance* parameter.

3.4.1 Properties of Distributions in the Exponential Family

The properties of this distribution are as follows,

$$\int f(Y;\theta)dy = 1 \qquad (10)$$

$$\int \frac{df(Y;\theta)}{d\theta}dy = 0 \qquad (11)$$

$$\int \frac{d^2 f(Y;\theta)}{d\theta^2}dy = 0 \qquad (12)$$

The integration is done over the range of the response variable and so depends on the type of response variable. For a discrete case the limit of the integration is from 0 to ∞, for a continuous case from $-\infty$ to ∞ and for binary 0 to 1.

From (9),

$$\frac{df(Y;\theta)}{d\theta} = \left[s(y)c'(\theta) + A'\right] f(Y;\theta)$$

Substituting this into (11), we have

$$\int \left[s(y)c'(\theta) + A'\right] f(Y;\theta) dy = 0$$

Rearranging the above yields,

$$E\left[s(y)\right] = -\frac{A'(\theta)}{c'(\theta)} \qquad (13)$$

since $\int s(y)\, f(Y;\theta)\, dy = E\left[s(y)\right]$.

Also,

$$\frac{d^2 f(Y;\theta)}{d\theta^2} = \left[s(y)c''(\theta) + A''\right] f(Y;\theta) + \left[s(y)c'(\theta) + A'(\theta)\right]^2 f(Y;\theta)$$

By simple algebra this can be written as

$$\frac{d^2 f(Y;\theta)}{d\theta^2} = \left[s(y)c''(\theta) + A''(\theta)\right] f(Y;\theta) + \left[c'(\theta)\right]^2 \left[s(y) - E\left[s(y)\right]\right]^2$$

Substituting this expression into (12), we have

$$\int \left\{ \left[s(y)c''(\theta) + A''(\theta)\right] f(Y;\theta) + \left[c'(\theta)\right]^2 \left[s(y) - E\left[s(y)\right]\right]^2 \right\} dy = 0$$

This can be simplified further as

$$c''(\theta) E\left[s(y)\right] + A''(\theta) + \left[c'(\theta)\right]^2 \operatorname{var}\left[s(y)\right] = 0$$

Since $\int\left[s(y)-E\left[s(y)\right]\right]^2 dy = \operatorname{var} s(y)$.

Rearranging the above yields,

$$\operatorname{var}\left[s(y)\right] = \frac{c''(\theta)A'(\theta) - A''(\theta)c'(\theta)}{\left[c'(\theta)\right]^3} \qquad (14)$$

3.4.2 Mean and Variance of the Score statistic

The log-likelihood for each Y of the exponential family is

$$\ell = s(y)c(\theta) + B(y) + A(\theta) \qquad (15)$$

Differentiating partially with respect to θ yields,

$$\frac{\partial \ell}{\partial \theta} = s(y)c'(\theta) + A'(\theta)$$

The score statistic above is regarded as a random variable.

Taking expectation of the score equation yields,

$$E\left(\frac{\partial \ell}{\partial \theta}\right) = c'(\theta)E\left[s(y)\right] + A'(\theta)$$

Substituting (13) and simplifying yields

$$E\left(\frac{\partial \ell}{\partial \theta}\right) = 0 \qquad (16)$$

The variance of the the score statistic is

$$\operatorname{var}\left(\frac{\partial \ell}{\partial \theta}\right)=\left[c'(\theta)\right]^2 \operatorname{var}\left[s(y)\right]$$

Substituting (14) and simplifying yields,

$$\operatorname{var}\left(\frac{\partial \ell}{\partial \theta}\right)=\frac{c''(\theta)A'(\theta)}{c'(\theta)}-A''(\theta) \qquad (17)$$

Which gives the information about θ.

The exponential family just defined includes the binomial, Poisson, exponential, gamma, inverse Gaussian distributions and as a special case the normal distribution.

We consider as special examples the Poisson, Bernoulli and Negative Binomial distributions respectively as members of the exponential family and determine their natural parameters.

3.4.3 Count Data

For count data $Y_i \sim Poi(\mu_i)$, where the Y_i's are independent.

The pdf of the Y_i is given by

$$f(Y_i;\mu_i)=\begin{cases}\dfrac{\mu_i^{y_i}e^{-\mu_i}}{y_i!} & y_i=0,1,2,\ldots \ , \mu_i>0\\ 0 & \text{otherwise}\end{cases} \qquad (18)$$

$$=\begin{cases}\exp\left[y_i\log\mu_i-\mu_i-\log\Gamma(y_i+1)\right] & y_i=0,1,2,\ldots \ , \mu_i>0\\ 0 & \text{otherwise}\end{cases}$$

Comparing the above to (9) gives

$$c(\mu_i) = \log \mu_i \ , A(\mu_i) = -\mu_i \text{ and } B(y_i) = -\log \Gamma(y_i + 1). \text{ Thus}$$

$$c'(\mu_i) = \frac{1}{\mu_i} \text{ and } A'(\mu_i) = -1 \qquad (19)$$

Substituting the (19) into (13) , we have

$$E(Y_i) = \mu_i$$

Also,

$$c''(\mu_i) = \frac{-1}{\mu_i^2} \text{ and } A''(\mu_i) = 0 \qquad (20)$$

When (19) and (20) are substituted into (14) we have

$$\text{var}(Y_i) = \mu_i$$

Thus for a Poisson distribution with parameter μ_i, the natural parameter is $\log \mu_i$

called the **log** function.

3.4.4 Binary Data

Let Y_i be *n* independent binary random variables with

$P(Y_i = 1) = \pi_i$ and $P(Y_i = 0) = 1 - \pi_i$. Then $Y_i \sim Bernoulli(\pi_i)$

The pdf of Y_i is given by

$$f\left(Y_i;\pi_i\right)=\begin{cases}\pi_i^{y_i}\left(1-\pi_i\right)^{1-y_i} & y_i=0,1. \quad 0<\pi_i<1\\ 0 & \text{otherwise.}\end{cases}$$

$$=\begin{cases}\exp\left[y_i\log\left(\dfrac{\pi_i}{1-\pi_i}\right)+\log\left(1-\pi_i\right)\right] & y_i=0,1. \quad \pi_i>0\\ 0 & \text{otherwise.}\end{cases}$$

comparing this with (9), we have

$$c\left(\pi_i\right)=\log\left(\frac{\pi_i}{1-\pi_i}\right),\ A\left(\pi_i\right)=\log\left(1-\pi_i\right) \text{ and } B\left(y_i\right)=0$$

which has derivatves

$$c'\left(\pi_i\right)=\frac{1}{\pi_i\left(1-\pi_i\right)} \text{ and } A'\left(\pi_i\right)=\frac{-1}{1-\pi_i} \qquad (21)$$

$$c''\left(\pi_i\right)=\frac{2\pi_i-1}{\left[\pi_i\left(1-\pi_i\right)\right]^2} \text{ and } A''\left(\pi_i\right)=\frac{-1}{\left(1-\pi_i\right)^2} \qquad (22)$$

Substituted (21) into (13) gives

$$E\left(Y_i\right)=\pi_i$$

Also, substituting both (21) and (22) into (14) and simplifying gives

$$\text{var}\left(Y_i\right)=\pi_i\left(1-\pi_i\right)$$

Thus the natural parameter of the binary random variable is $\log\left(\dfrac{\pi_i}{1-\pi_i}\right)$ which is called the **logit** function.

3.4.5 Overdispersed Count Data

For overdispersed count data we assume the responses $Y_i \sim Negative\ Binomial(r, \theta_i)$.

The $Y_i's$ are iid and r the overdispersed parameter. The pdf of the $Y_i's$ is

$$f(Y_i; r, \theta_i) = \begin{cases} \binom{r + y_i - 1}{y_i - 1} \theta_i^{y_i} (1-\theta_i)^r & y_i = 0,1,2,... \quad 0<\theta_i<1 \\ 0 & \text{Otherwise} \end{cases}$$

$$= \begin{cases} \exp\left\{ y_i \log\theta_i + r\log(1-\theta_i) + \log\binom{r + y_i - 1}{y_i - 1} \right\} & y_i = 0,1,2,... \quad 0<\theta_i<1 \\ 0 & \text{Otherwise} \end{cases}$$

comparing with (9), we have

$$c(\theta_i) = \log\theta_i \ , A(\theta_i) = r\log(1-\theta_i) \text{ and } B(y_i) = \log\binom{r + y_i - 1}{y_i - 1}$$

$$c'(\theta_i) = \frac{1}{\theta_i} \text{ and } A'(\theta_i) = \frac{-r}{1-\theta_i}$$

$$c''(\theta_i) = \frac{-1}{\theta_i^2} \text{ and } A''(\theta_i) = \frac{-r}{(1-\theta_i)^2}$$

Substituting these into (13) and (14) yields

$$E(Y_i) = \frac{r\theta_i}{1-\theta_i} \text{ and } \operatorname{var}(Y_i) = \frac{r\theta_i}{(1-\theta_i)^2}$$

Thus, the Negative Binomial distribution as a member of the exponential family has

natural parameter $\log\theta_i$

3.5 GENERALIZED LINEAR MODEL

LMs are extended to Generalized Linear Models (GLMs), for outcomes that are members of the exponential distribution because (1) the data may not necessarily be assumed to be normally distributed and (2) the mean may not necessarily be taken as a linear combination of parameters but that some functions of the mean is.

We describe the generalized linear model as formulated by Nelder and Wedderburn (1972).

The general component of a GLM includes:

1. A *random component,* Y, which is a distribution from the exponential family of distributions, with Y being a vector of responses.
2. A *systematic component* consisting of a linear combination of predictor variables.

$$\eta = \mathbf{X}\beta$$

with **X** being the design matrix of covariates and β a vector of unknown

fixed effect parameters.

3. A monotonic (and differentiable) *link function* that maps the mean of the response variable onto the systematic component.

$$g(\mu) = \eta$$

where $\mu = g^{-1}(\eta)$ is called the mean function and $E(Y) = \mu$

The function $g(\mu)$ is the *link function*.

Examples of link functions includes;

(i) the identity, $g(\mu) = \mu$;

(ii) the log, $g(\mu) = \log \mu$;

(iii) the logit, $g(\mu) = \log\left(\frac{\mu}{1-\mu}\right)$;

(iv) the probit $g(\mu) = \Phi^{-1}(\mu)$ and

(v) the complementary log – log, $g(\mu) = \log\left[-\log(1-\mu)\right]$

Let us now consider the Poisson and binary distributions as GLMs.

From our previous discussions, we know that the Poisson distribution with parameter μ_i has natural parameter of $\log \mu_i$. In the presence of observed covariates, $\log \mu_i = X_i\beta$.

When expressed in terms of μ_i yields

$$\mu_i = e^{X_i\beta} \qquad (23)$$

This is referred to as the **Poisson** regression model.

Similarly, for a bernoulli random variable the natural parameter is $\log\left(\frac{\pi_i}{1-\pi_i}\right)$

And so, $\log\left(\frac{\pi_i}{1-\pi_i}\right) = X_i\beta,$ expressing this in terms of π_i yields

$$\pi_i = \frac{e^{X_i\beta}}{1+e^{X_i\beta}} \qquad (24)$$

The expression in (24) is referred to as the **logistic** regression model.

For the Negative Binomial distribution we have $\log\theta_i$ as the natural parameter and so

$$\theta_i = e^{X_i\beta} \qquad (25)$$

known as the **Negative Binomial** regression model.

3.5.1 Maximum Likelihood Estimation in GLM

Consider independent random variables $Y_1,...,\ Y_n$ satisfying the properties of the GLM.

We wish to estimate parameters β which are related to the $Y_i's$ through $E(Y_i)=\mu_i$ and $g(\mu_i)=X_i\beta=\eta_i$. For each Y_i the log-likelihood function of the canonical form is formed by replacing $s(y)$ in (15) with y, yielding

$$\ell_i = y_i c(\theta_i) + B(y_i) + A(\theta_i) \qquad (26)$$

where $A(.),\ B(.)$ and $c(.)$ have their usual meanings.

From (13) and (14) we know that

$$\mu_i = -\frac{A'(\theta_i)}{c'(\theta_i)} \qquad (27)$$

$$\text{var}(Y_i) = \frac{c''(\theta_i)A'(\theta_i) - A''(\theta_i)c'(\theta_i)}{\left[c'(\theta_i)\right]^3}$$

from the definition of GLMs we have

$$g(\mu_i) = X_i\beta = \eta_i \qquad (28)$$

The log-likelihood for all the Y_i's is

$$\ell = \sum_{i=1}^{n} \ell_i = \sum_{i=1}^{n} y_i c(\theta_i) + \sum_{i=1}^{n} A(\theta_i) + \sum_{i=1}^{n} B(y_i)$$

To obtain the maximum likelihood estimator for the parameter β_j we need

$$\frac{\partial \ell_i}{\partial \beta_j} = \sum_{i=1}^{n} \left[\frac{\partial \ell_i}{\partial \theta_i} \bullet \frac{\partial \theta_i}{\partial \mu_i} \bullet \frac{\partial \mu_i}{\partial \beta_j} \right] \qquad (29)$$

using the chain rule of differentiation.We will consider each term on the right hand side of (29) separately. First

$$\frac{\partial \ell_i}{\partial \theta_i} = y_i c'(\theta_i) + A'(\theta_i)$$

Obtained by differentiating (26). By simplifying and substituting (27) we have

$$\frac{\partial \ell_i}{\partial \theta_i} = c'(\theta_i)[y_i - \mu_i]$$

Next, $$\frac{\partial \theta_i}{\partial \mu_i} = 1 \Big/ \left(\frac{\partial \mu_i}{\partial \theta_i} \right)$$

Diferentiating (27) gives

$$\frac{\partial \mu_i}{\partial \theta_i} = \frac{-c'(\theta_i) A''(\theta_i) + A'(\theta_i) c''(\theta_i)}{\left[c'(\theta_i) \right]^2}$$

Simplifying and substituting (14) we have

$$\frac{\partial \mu_i}{\partial \theta_i} = c'(\theta_i) \operatorname{var}(Y_i)$$

Finally, from (28) we have

$$\frac{\partial \mu_i}{\partial \beta_i} = \frac{\partial \mu_i}{\partial \eta_i} \bullet \frac{\partial \eta_i}{\partial \beta_i} = \frac{\partial \mu_i}{\partial \eta_i} y_i$$

Hence the score equation becomes

$$\mathrm{K}_i = \frac{\partial \ell}{\partial \beta_i} = \sum_{i=1}^{n} \left[\frac{(y_i - \mu_i)}{\operatorname{var}(Y_i)} y_i \left(\frac{\partial \mu_i}{\partial \eta_i} \right) \right] \qquad (30)$$

The variance-covariance matrix of the K_i's has term

$$\mathrm{T}_{ij} = E\left(\mathrm{K}_i \mathrm{K}_j\right)$$

which form the **information** matrix **T**.

$$\mathrm{T}_{ij} = E\left\{\sum_{i=1}^{n}\left[\frac{\left(y_i-\mu_i\right)}{\mathrm{var}\left(Y_i\right)} y_i\left(\frac{\partial\mu_i}{\partial\eta_i}\right)\right]\sum_{j=1}^{m}\left[\frac{\left(y_j-\mu_j\right)}{\mathrm{var}\left(Y_j\right)} y_j\left(\frac{\partial\mu_j}{\partial\eta_j}\right)\right]\right\}$$

$$\mathrm{T}_{ij} = \sum_{i=1}^{n}\frac{E\left(y_i-\mu_i\right)^2 y_i y_j}{\left[\mathrm{var}\left(Y_i\right)\right]^2}\left(\frac{\partial\mu_i}{\partial\eta_i}\right)^2 \qquad (31)$$

because $E\left[\left(y_i-\mu_i\right)\left(y_j-\mu_j\right)\right]=0,$ for $i \neq j$ since the Y_i's are iid. Using $E\left[\left(y_i-\mu_i\right)^2\right]=\mathrm{var}\left(Y_i\right)$.

$$\mathrm{T}_{ij} = \sum_{i=1}^{n}\frac{y_i y_j}{\mathrm{var}\left(Y_i\right)}\left(\frac{\partial\mu_i}{\partial\eta_i}\right)^2 \qquad (32)$$

Writtng (32) in matrix form gives

$$\mathbf{T} = \mathbf{Y}'\mathbf{W}\mathbf{Y} \qquad (33)$$

where **W** is the $n \times n$ matrix with diagonal elements $\frac{1}{\mathrm{var}\left(Y_i\right)}\left(\frac{\partial\mu_i}{\partial\eta_i}\right)^2$.

Thus for GLM, ML estimators are obtained by iterative weighted least squares$\left(\text{Charnes } et\ al.,1957\right)$.

3.5.2 Fisher Scoring Agorithm

Nelder and Wedderbum (1972) estimated $\hat{\beta}$ in GLMs using the Fisher Scoring algorithm which is a Newton – Raphson method for evaluating maximum likelihood equations numerically. For Poisson and Negative Binomial regression models with log link, we shall model it as;

$$g(\mu) = \log \mu$$

Then differentiating the link function with respect to μ gives

$$g'(\mu) = \frac{1}{\mu}$$

Given an initial estimates, the algorithm updates it to β^N by

$$\beta^N = \beta + \left\{ E\left(-\frac{\partial^2 \ell}{\partial \beta \partial \beta'} \right)^{-1} \right\} \frac{\partial \ell}{\partial \beta}$$

Where both derivatives, if they exist, are evaluated at β, and the expectation evaluated as if β were the true parameter values. β is then replaced by β^N and the updating is repeated until convergence. It can be shown that for GLM, the updating equation is

$$E\left(\frac{\partial^r \ell}{\partial \beta_j \partial \beta_l \ldots \partial \beta_r} \right) = -\sum_{i=1}^{n} \left[X_{ij} X_{il} \ldots X_{ir} e^{X_i \beta} \right]$$

Which can be written as, by substituting (33)

$$\beta^N = \beta + (\mathbf{X}'\mathbf{W}\mathbf{X})^{-1}\mathbf{X}'\mathbf{W}\mathbf{Z}$$

Where

$\mathbf{W}=e^{X_i\beta}$ is an $n\times n$ diagonal matrix

$$\mathbf{Z}=\left(Y_i - e^{X_i\beta}\right)\frac{1}{e^{X_i\beta}} = Y_i e^{-X_i\beta} - I$$

is the n vector with i^{th} component and I is a n vector of ones.

If $T(\beta)$ is Fisher informaton, then the standard errors of the parameter estimates is

$$se\left(\hat{\beta},\hat{\gamma}\right) = \sqrt{diag\left[T(\beta)^{-1}\right]}$$

3.5.3 The Poisson Regression Model

The Poisson regression model (P) is a model used to describe count data as a function of a set of predictor variables from the Poisson distribution. To model the observed count based on the covariate using the Poisson model, we assume

$$Y_i \sim Poi(\mu_i)$$

From (18) the pdf is

$$f(Y_i;\mu_i) = \begin{cases} \dfrac{\mu_i^{y_i}e^{-\mu_i}}{y_i!} & y_i = 0,1,2,\ldots \ , \mu_i > 0 \\ 0 & \text{otherwise} \end{cases} \qquad (34)$$

with $\mathrm{E}(Y_i) = \mathrm{var}(Y_i) = \mu_i$ and from (24), $\mu_i = e^{X_i\beta}$

3.5.3.1 Maximum Likelihood Estimation of β

The log – likelihood of the distribution above is

$$\ell = \sum_{i=1}^{n} y_i \ln \mu_i - n\mu_i - \sum_{i=1}^{n} \ln \Gamma(y_i + 1) \qquad (35)$$

Substituting (23) we have

$$\ell = \sum_{i=1}^{n} y_i X_i \beta - n e^{X_i \beta} - \sum_{i=1}^{n} \ln \Gamma(y_i + 1)$$

From (29) the score equation is

$$K_j = \frac{\partial l}{\partial \beta_i} = \sum_{i=1}^{n} \left(y_i - e^{X_i \beta} \right) X_i$$

The Hessian is thus given by

$$\frac{\partial^2 l}{\partial \beta_i \partial \beta_j} = -\sum_{i=1}^{n} e^{X_i \beta} X_i X_j \;\Rightarrow E\left(\frac{\partial^2 l}{\partial \beta_i \partial \beta_j} \right) = -\sum_{i=1}^{n} e^{X_i \beta} X_i X_j$$

From (33) the variance covariance matrix of the $K_j's$

$$T_{jm} = \sum_{i=1}^{n} e^{X_i \beta} X_i X_j$$

which can be written in matrix form as

$$\mathbf{T} = \mathbf{X'WX}$$

where $\mathbf{W}=e^{X_i \beta}$

Thus β is obtained by the Fisher Scoring Algorithm described in Section 3.5.2.

3.5.4 The Negative Binomial Regression Model

The Poisson model above is restrictive due to its mean-variance relationship. To model the observed count Poisson data based on the covariates, using the Negative Binomial (NB) model, we assume

$$y_i \mid \mu_i \sim Poi(\mu_i)$$

$$\mu_i \sim \Gamma(\alpha, \lambda)$$

where α is the shape parameter and λ the scale parameter.

Thus

$$f(\mu_i) = \frac{\lambda^{\alpha}}{\Gamma(\alpha)} \mu_i^{\alpha-1} e^{-\frac{\mu_i}{\lambda}}$$

Which implies that

$$f(y_i \mid \mu_i) = \frac{\mu_i^{y} e^{-\mu_i}}{y!}$$

Then from Ridout, Dime`trio and Hinde (1998), $E(y_i \mid \mu_i) = \mu_i$ and $\text{var}(y_i \mid \mu_i) = \mu_i + \mu_i^2 \varepsilon$

where the overdspersion parameter ε is not related to any observed specific cause or structure.

Thus the marginal distribution is given by

$$f(y_i) = \int_0^{\infty} \frac{\lambda^{\alpha}}{\Gamma(\alpha)} \mu_i^{\alpha-1} e^{-\lambda\mu_i} \frac{\mu_i^{y_i} e^{-\mu_i}}{y_i!} \, d\mu_i$$

$$= \binom{\alpha + y_i - 1}{y_i - 1} \left(\frac{1}{1+\lambda}\right)^{y_i} \left(\frac{\lambda}{1+\lambda}\right)^{\alpha}$$

with $E(y_i)=\frac{\alpha}{\lambda}$, $\text{var}(y_i)=\frac{\alpha}{\lambda^2}$.

For the sake of convinience let $E(y_i)=\psi=\frac{\alpha}{\lambda}$ and $k=\frac{1}{\alpha}$

Then the marginal distribution becomes

$$f(y_i;\psi)=\begin{cases}\binom{\frac{1}{k}+y_i-1}{y_i-1}\left(1-\frac{1}{1+k\psi}\right)^{y_i}\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}} & y_i=0,1,2,.. \text{ and } \quad \psi>0 \\ 0 & \text{Otherwise}\end{cases} \qquad (36)$$

$f(y_i;\psi)$ above is here by referred to as the hierarchical gamma-Poisson mixture distribution and also known as the NB distribution which satisfies the overdispersion requirement.

3.5.4.1 Maximum Likelihood Estimation of β

The log-likelihood of NB distribution is given as

$$\ell=\sum_{i=1}^{n}\ln\Gamma\left(\frac{1}{k}+y_i\right)-n\ln\Gamma\left(\frac{1}{k}\right)-\sum_{i=1}^{n}\ln\Gamma(y_i)+\sum_{i=1}^{n}y_i\ln k\psi-\sum_{i=1}^{n}y\ln(1+k\psi)$$

$$-\frac{n}{k}\ln(1+k\psi) \qquad (37)$$

From (25), we have $\psi=e^{X_i\beta}$. Substituting this into the log – loglkelihood, we have

$$\ell=\sum_{i=1}^{n}\ln\Gamma\left(\frac{1}{k}+y_i\right)-n\ln\Gamma\left(\frac{1}{k}\right)-\sum_{i=1}^{n}\ln\Gamma(y_i)+\sum_{i=1}^{n}y_i\ln k+\sum_{i=1}^{n}y_iX_i\beta$$

$$-\sum_{i=1}^{n}y_i\ln\left(1+ke^{X_i\beta}\right)-\frac{n}{k}\ln\left(1+ke^{X_i\beta}\right)$$

The score equation is given by

$$\frac{\partial \ell}{\partial \beta} = \sum_{i=1}^{n} y_i X_i - \sum_{i=1}^{n} y_i X_i k e^{X_i\beta}\left(1+ke^{X_i\beta}\right)^{-1} - nX_i e^{X_i\beta}\left(1+ke^{X_i\beta}\right)^{-1}$$

$$= \sum_{i=1}^{n} y_i X_i - \left(k\sum_{i=1}^{n} y_i + n\right) X_i e^{X_i\beta}\left(1+ke^{X_i\beta}\right)^{-1}$$

The Hessian is given by

$$\frac{\partial^2 \ell}{\partial \beta_i \partial \beta_j} = -\left(k\sum_{i=1}^{n} y_i + n\right)\left[1-k\left(1+ke^{X_i\beta}\right)^{-1}\right]\left[X_i X_j e^{X_i\beta}\left(1+ke^{X_i\beta}\right)^{-1}\right]$$

Thus,

$$E\left(\frac{\partial^2 \ell}{\partial \beta_i \partial \beta_j}\right) = -\left(k\sum_{i=1}^{n} y_i + n\right)\left[1-k\left(1+ke^{X_i\beta}\right)^{-1}\right]\left[X_i X_j e^{X_i\beta}\left(1+ke^{X_i\beta}\right)^{-1}\right]$$

And so we use the Fisher Scoring Algorithm as described in Section 3.5.2 to estimate β taking into consideration overdispersion.

3.6 GENERALIZED LINEAR MIXED MODELS

LLMs are extended to Generalized Linear Mixed Models (GLMMs) because (1) the data may not necessarily be assumed to be normally distributed and (2) the mean may not necessarily be taken as a linear combination of parameters but that some functions of the mean is.

A generalized linear mixed model (GLMM) is also a GLM with fixed and random effects in the linear predictor. The term "mixed" in GLMM comes from the fact that both fixed effects and random effects are included in the model. The fixed effects are viewed as constant in the population; whereas, random effects are considered stochastic. The fixed effects convey

systematic and structural differences in responses. The random effects convey stochastic differences between subjects. The addition of random effects permits generalizations to the population from which subjects have been (randomly) sampled, accounts for differences between subjects, and accounts for within subjects' dependency.

The general components of a GLMM include;

I. A *random component*, Y, which is a distribution from the exponential family of distributions.

II. A *systematic component* consisting of a linear combination of predictor variables.

$$\eta = \mathbf{X}\beta + \mathbf{Z}\upsilon$$

with $\mathbf{X}$ being the design matrix of covariates, β a vector of unknown fixed effect parameters, $\mathbf{Z}$ a design matrix of covariates and υ a vector of random effects.

$\upsilon \sim f(\upsilon)$, where $f(\upsilon)$ is also a distribution from the exponential family.

III. A monotonic (and differentiable) *link function* that maps the mean of the response variable onto the systematic component.

$$g(\mu) = \eta = \mathbf{X}\beta + \mathbf{Z}\upsilon$$

where $\mu = g^{-1}(\mathbf{X}\beta + \mathbf{Z}\upsilon)$ is called the mean function and $E(Y) = \mu$ and υ is a vector of random effects.

In the case of count data, we have $Y \sim Poi(\mu)$. With the mean μ modelled as

$$\mu = e^{(\mathbf{X}\beta + \mathbf{Z}\upsilon)} \qquad (38)$$

For binary data we have $Y \sim Bernoulli(\pi)$. With the mean π modelled as

$$\pi = \frac{e^{(\mathbf{X}\beta+\mathbf{Z}\upsilon)}}{1+e^{(\mathbf{X}\beta+\mathbf{Z}\upsilon)}} \qquad (39)$$

Whereas for $Y \sim Negative\ Binomial(r,\theta)$, we have

$$\theta = e^{(\mathbf{X}\beta+\mathbf{Z}\upsilon)} \qquad (40)$$

3.6.1 Maximum Likelihood Estimation in GLMMs

Let $Y|\upsilon \sim f(Y|\upsilon)$ and $\upsilon \sim f(\upsilon)$

Then the likelihood is given by

$$L = \int \prod_i f(Y|\upsilon) f(\upsilon) d\upsilon$$

Where the integral is over the distribution of υ.

The log-likelihood is given by

$$\ell = \log \int f(Y|\upsilon) f(\upsilon) d\upsilon \qquad (41)$$

With the likelihood above, when the random effect is in the linear form, the integral can be solved in closed form and the resulting likelihood maximized directly.

However, when the random effect enters a nonlinear form, the integral has no closed form solution except in special cases. In such a situation the solution is categorized as methods based on computerized *integral approximations* and *linearization* programmed in statistical software.

Integral approximation methods approximate the log likelihood function of the GLMM and numerically optimize the approximated function. These methods provide an actual objective function for optimization and enable you to compare nested models with true likelihood ratio tests. However, these methods are not suited to accommodate a large number of random effects, crossed random effects, and multiple subject effects.

Linearization methods employ expansions to approximate the model by one based on pseudo-data with fewer nonlinear components. The process of computing the linear approximation must be repeated several times until some criterion stabilizes. The fitting methods based on linearizations are usually doubly iterative. The GLMM is approximated by a linear mixed model based on current values of the covariance parameter estimates. The resulting linear mixed model is then fit, which is itself an iterative process. On convergence, the new parameter estimates are used to update the linearization, which results in a new linear mixed model. The process stops when parameter estimates between successive linear mixed model fits change within a specified tolerance only.

3.6.1.1 A Monte Carlo Expectation Maximization $(\mathbf{EM})$ Algorithm

For a GLMM we know that $g(\mu) = \mathbf{X}\beta + \mathbf{Z}\upsilon$. We further assume that $\upsilon \sim iid\ N\left(0, \sigma^2 I_{m_r}\right)$ and $\varepsilon \sim iid\ N\left(0, \tau^2 I_n\right)$, where ε is the error associated with the response variable, $\mathbf{X}$ and $\mathbf{Z}$ are $n \times p$ and $n \times q$ matrices of known covariates respectively such that $q \leq p$. We wish to estimate the parameters β, σ^2 and τ^2 in the log-likelihood described in (41). A key element of the EM algorithm as proposed by McCulloch(1994) is the so called 'complete data', denoted by Y and some unobserved random variables υ. The idea is to choose υ appropriately so that the ML becomes trivial for the complete data.

Let $w = (y, \upsilon)$ denote the complete data which are assumed to have a pdf $f\left(w|\theta\right)$, from the exponential family, depending on a vector θ of unknown parameters.

In the E-step of the algorithm, one computes the conditional expectaion

$$Q\left[\theta\middle|\theta^{(k)}\right] = E\left[\log f\left(w|\theta\right)\middle|y, \theta^{(k)}\right]$$

where $\theta^{(k)}$ is the estimated θ at the step k(the current step) and Q a function of θ..

So in the M-step, one maxmizes $Q\left[\theta\middle|\theta^{(k)}\right]$ with respect to θ to obtain the next step estimator $\theta^{(k+1)}$. The process is then iterated until convergence.

The log-likelihood based on the complete data has the expression

$$\ell = c - \frac{1}{2}\left[n\ln\left(\tau^2\right) + \sum_{r=1}^{q} m_r \ln\left(\sigma_r^2\right) + \sum_{r=1}^{r} \frac{\upsilon_r'\upsilon}{\sigma_r^2} + \frac{1}{\tau^2}\left(y - X\beta - \sum_{r=1}^{q} Z_r\upsilon_r \right)'\left(y - X\beta - \sum_{r=1}^{r} Z_r\upsilon_r \right)\right]$$

where c does not depend on the data or parameters.

Thus to complete the E-step we estimate

$$E\left(\upsilon_r \middle| y\right) = \sigma_r^2 Z_r' V^{-1}\left(y - X\beta\right)$$

$$E\left(\upsilon_r'\upsilon_r \middle| y\right) = \sigma_r^4\left(y - X\beta\right)' V^{-1} Z_r Z_r' V^{-1}\left(y - X\beta\right) + \sigma_r^2 m_r - \sigma_r^4 tr\left(Z_r' V^{-1} Z_r\right)$$

where $V = \mathrm{var}\left(y\right) = \tau^2 I_n + \sum_{r=1}^{q} \sigma_r^2 Z_r Z_r'$, $1 \le r \le q$

Once the E-step is completed, the M-step is straight forward because

$$\left(\sigma_r^2\right)^{(k+1)} = m_r^{-1} E\left(\upsilon_i'\upsilon_r \middle| y\right)\Big|_{\beta=\beta^{(k)},\sigma^2=\left(\sigma^2\right)^{(k)}}$$

and

$$\beta^{(k+1)} = \left(X'X\right)^{-1}\left[y - \sum_{t=1}^{q} Z_t E\left(\upsilon_t \middle| y\right)\Big|_{\beta=\beta^{(k)},\sigma^2=\left(\sigma^2\right)^{(k)}} \right]$$

where $\sigma^2 = \left(\sigma_j^2\right)$

3.6.2 Poisson GLMM with normal random effect

For the Poisson GLMM (PG) we assume

$$y_i \,|\upsilon_i \sim ind.Poi\left(\mu_i\right)$$

$$\upsilon_i \sim iid\ N\left(0,\sigma^2 I\right)$$

and from (23) $\mu_i = e^{X_i\beta+\upsilon_i}$

With a further assumption that each of Z_i has a single entry equal to 1. So

$$E\left(Y\right)=e^{X_i\beta+\frac{\sigma^2}{2}} \text{ and } \operatorname{var}\left(Y\right)=\omega\left[1+\omega\left(e^{\sigma^2}-1\right)\right]$$

where ω=$e^{X_i\beta+\frac{\sigma^2}{2}}$.

Then from (41) the log-likelihood of the Poisson GLMM is

$$\ell = \log\left(\prod_{i=1}^{m}\int_{-\infty}^{\infty}\prod_{j=1}^{n}\frac{\mu_i^{y_i}e^{-\mu_i}}{y_i\,!}\frac{1}{\sqrt{2\pi\sigma^2}}e^{-\frac{1}{2\sigma^2}\upsilon_i^2}d\upsilon_i\right)$$

$$= \mathbf{YX}\beta-\sum_{i,j}y_i\,!+\sum_i\log\int_{-\infty}^{\infty}e^{\left\{y_i\upsilon_i-\sum_j e^{X_i\beta+\upsilon_i}\right\}}\frac{1}{\sqrt{2\pi\sigma^2}}e^{-\frac{1}{2\sigma^2}\upsilon_i^2}d\upsilon_i$$

The parameters in the log-likelihood above are evaluated using the EM algorithm described above with a statistical software.

3.6.3 Negative Binomial GLMM with normal random effect

For the Negative Binomial GLMM (NBG) we assume

$$y_i \mid \upsilon_i \sim ind.\ \ Negative\ Binomial\ \left(\tfrac{1}{k}, \psi\right)$$

$$\upsilon_i \sim iid\ N\left(0, \sigma^2 I\right)$$

and from (40) $\psi = e^{X_i\beta+\upsilon_i}$

With the same assumption in the Poisson case

$$E\left(Y\right) = e^{X_i\beta+\frac{\sigma^2}{2}} \text{ and } \operatorname{var}\left(Y\right) = \omega\left[1+\omega\left(e^{\sigma^2}-1\right)\right]$$

where $\omega = e^{X_i\beta+\frac{\sigma^2}{2}}$.

Then from (41) the log-likelihood of the NB GLMM is

$$\ell = \log\left(\prod_{i=1}^{m}\int_{-\infty}^{\infty}\prod_{j=1}^{n}\binom{\frac{1}{k}+y_i-1}{y_i-1}\left(\frac{k\psi}{1+k\psi}\right)^{y_i}\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}}\frac{1}{\sqrt{2\pi\sigma^2}}e^{-\frac{1}{2\sigma^2}\upsilon_i^2}d\upsilon_i\right)$$

The parameters in log-likelihood above are evaluated using the EM algorithm described above with a statistical software.

3.7 OVERDISPERSION

Practically many types of outcomes using standard models within the GLMs and GLMMs for their analysis, such as binomial and count observations, often exhibit variability exceeding what is predicted by the binomial or Poisson distribution (Molenberghs *et al.*, 2010).

Let y_{ij} denote the $j^{th}\left(j=1,2,...,k_i\right)$ maternal death count from the hospital $i=1,2,...,K.$ We assume that the $y_{ij} \sim Poi\left(\mu_{ij}\right)$ where $E\left(y_{ij}\right)=\text{var}\left(y_{ij}\right)=\mu_{ij}$ with

$$\log\left(\mu_{ij}\right)=\beta_0+\beta_1 X_{ij}$$

A key assumption of the Poisson model as a member of the exponential family from the GLM and GLMMs is that the variance is equal to the mean. However, in many applications with count data, the observed variance is higher than the mean, leading to overdispersion (Agresti, 2002). Overdispersion $\left(E\left(y_{ij}\left|x_{ij}\right.\right)<\text{var}\left(y_{ij}\left|x_{ij}\right.\right)\right)$ can have many causes and different modeling concepts.

3.7.1 Causes of Overdispersion

There are many different possible causes of overdispersion and in any modeling situation a number of these could be involved. Some possibilities are:

- Variability of experimental material – this can be thought of as individual variability of the experimental units(i.e. type of hospital facility) and may give an additional component of variability which is not accounted for by the basic model;
- Correlation between individual responses – for example in various health facilities we expect pregnant mothers to have services from experienced health professionals with correlated training;
- Cluster sampling;
- Aggregate level data – the aggregation process can lead to compound distributions;
- Omitted unobserved variables – in some sense the other categories are all special cases of this, but generally in a rather complex way.

In some circumstances the cause of the overdispersion may be apparent from the nature of the data collection process, although it should be noted that different explanations of the overdispersion process can lead to the same model so in general it is difficult to infer the precise cause, or underlying process, leading to the overdispersion.

3.7.2 Consequences of Overdispersion

When we identify the possible presence of overdispersion, what are the consequences of failing to take it into account? Firstly, the standard errors obtained from the model will be incorrect and may be seriously underestimated and consequently we may incorrectly assess the significance of individual regression parameters. Also, changes in deviance associated with model terms will also be too large and this will lead to the selection of overly complex models. Finally, our interpretation of the model will be incorrect and any predictions will be too precise.

3.8 OVERDISPERSION MODEL WITH RANDOM-EFFECTS

Both overdispersion and correlation can happen together, and this led Molenberghs *et al.* (2010) to formulate a flexible and unified modeling framework, which they termed the combined model, to simultaneously capture overdispersion and correlation for a wide range of clustered data, including count, binary and time-to-event.

From Section (3.7) above, the Poisson model with normal and gamma random effects can be specified as

$$Y \sim Poi\left(\mu = \phi\upsilon\right)$$

with the conditional mean μ modelled as $\phi\upsilon$ and

$$\upsilon = e^{(\mathbf{X}\beta + \mathbf{Z}\omega)}$$

where $\omega \sim N(0, D)$, $\mathbf{X}$ and $\mathbf{Z}$ are known matrix of covariate and β is a vector of unknown fixed regression coefficients (Kassahun *et al.*, 2012).

Molenberghs *et al.* (2007) and Molenberghs *et al.* (2010) marginalized the combined model analytically over the gamma random effect.

3.9 ZERO-INFLATED MODEL

As maternal mortality occur within health facilities, the referrals from one facility to another may imply that no deaths are reported within a particular time, hence triggering a phenomenon that appears in many health services: the excessive number of zero count, more than expected relative to a Poisson distribution. Such data are fitted as a zero-inflated model (ZI) (Lambert, 1992).

In a zero-inflated model we assume that the zeros come from two processes. The first process generates only zeros with probability, π_i for observation i, and the second process generates counts with probability, $(1-\pi_i)$. Thus for a zero-inflated model the probability distribution is given by

$$P(Y_i = y_i) = \begin{cases} \pi_i + (1-\pi_i) f_i(0|\mu_i) & \text{if } y = 0, \\ (1-\pi_i) f_i(y_i|\mu_i) & \text{if } y > 0. \end{cases} \qquad (42)$$

With π_i and μ_i functions of covariates. Link functions, such as logit or probit, can be used for π_i, and the common log link is used for μ_i. In our setting, the parameter π_i is known as the

eligibility probability, and hence a random variable Y can be viewed as an "eligibility" indicator taking the value 1 if maternal death occurred in a HF and 0 otherwise.

These zero-inflated count model described above has specific forms namely, the zero-inflated Poisson model and the zero-inflated Negative Binomial model.

3.9.1 Zero-Inflated Poisson GLM

The zero-inflated Poisson GLM (ZIP) extends the Poisson model by addressing inflation of zeros in the data.

The pdf of the ZIP is given by

$$P(Y_i = y_i) = \begin{cases} \pi_i + (1-\pi_i)\mathrm{e}^{-\mu_i} & \text{if } y_i = 0, \\ (1-\pi_i)\dfrac{\mu_i^{y} e^{-\mu_i}}{y!} & \text{if } y_i > 0. \end{cases} \qquad (43)$$

Which is achieved by substituting (34) into (42).

From (23) and (24) we have

$$\pi_i = \frac{e^{X_i\gamma}}{1+e^{X_i\gamma}} \quad \text{and} \quad \mu_i = e^{Z_i\beta}$$

where γ and β are vector of fixed parameters associated with the excess zeros and X_i and Z_i known matrices of covariates for the i^{th} individual for excess zero.

Apparently, the parameters γ and β are such that γ_i is the odds ratio of a unit increase in the j^{th} element of X_i on the probability of being excess zero and β_i is the incidence ratio of a unit increase in the j^{th} element of Z_i on the mean of the population.

Further,

$$E(y_i) = \sum 0.P(y_i = 0) + \sum y_i.P(y_i > 0)$$

Sustituting expressions for $P(y_i > 0)$ yields

$$E(y_i) = (1-\pi_i)\mu_i \qquad (44)$$

When we substitute expressions for π_i and μ_i into (44) we have,

$$E(y_i) = \frac{e^{Z_i\beta}}{1+e^{X_i\gamma}} \qquad (45)$$

Here the population mean is a function of all covariates and parameters from both parts of the model.

From the above, if $Z=X$ as is usually specified, an increase from the j^{th} to the $(j+1)^{th}$ covariates yields the incidence ratio

$$\frac{E\left(y_{ij}\left|x_{ij}=j+1,\overline{x_i}=\overline{x_i}\right.\right)}{E\left(y_{ij}\left|x_{ij}=j,\overline{x_i}=\overline{x_i}\right.\right)}=e^{\beta_j}\frac{1+e^{\left(j\vartheta_j+\overline{x}'\overline{\vartheta}\right)}}{1+e^{\left((j+1)\vartheta_j+\overline{x}'\overline{\vartheta}\right)}}$$

Where $\overline{x_i}$ indicates all covariates except x_{ij} and $\overline{\vartheta}$ is created by removing ϑ_j from ϑ.

In the ratio above, if $\vartheta_j=0,\ e^{\beta_j}$ is constant across all levels of the covariates, otherwise it is not constant across all levels of the covariates including extraneous ones in the logistic portion of the ZIP model.

Also the variance of the ZIP can be obtained by simple computations as

$$\text{var}\left(y_i\right)=\mu_i+\left(\frac{\pi_i}{1-\pi_i}\right)\mu_i^2 \qquad (46)$$

The likelihood for this ZIP model is

$$L\left(\pi,\mu\left|y\right.\right)=\prod_{y_i=0}\left[\pi_i+\left(1-\pi_i\right)\mathrm{e}^{-\mu_{ij}}\right]\times\prod_{y_i>0}\left[\left(1-\pi_i\right)\frac{\mu_{ij}^{y}e^{-\mu_{ij}}}{y!}\right]$$

We find the likelihood of the expected value μ given the data and k which allows for overdispersion.

This is expressed as a log-likelihood denoted by ℓ:

$$\ell=\sum_{i=1}^{n}I\left(y_i=0\right)\ln\left[\pi_i+\left(1-\pi_i\right)\mathrm{e}^{-\mu_i}\right]+\sum_{i=1}^{n}I\left(y_i>0\right)\ln\left[\left(1-\pi_i\right)\frac{\mu_i^{y_i}e^{-\mu_i}}{y_i!}\right]$$

$$\ell = \sum_{i=1}^{n} \begin{cases} \ln\left[\pi_i + (1-\pi_i)\mathrm{e}^{-\mu_i}\right] & if\ y_i = 0 \\ y_i \ln \mu_i + \ln(1-\pi_i) - \mu_i - \ln\Gamma(y_i+1) & if\ y_i > 0 \end{cases} \quad (47)$$

The log-likelihood above is represented in the form of ZIP GLM by substituting $\mu_{ij} = e^{X_{ij}\beta}$ and $\pi_i = \frac{e^{Z_i\gamma}}{1+e^{Z_i\gamma}}$. Thus yielding

$$\ell = \sum_{i=1}^{n} \begin{cases} \ln\left[\frac{e^{Z_i\gamma}}{1+e^{Z_i\gamma}} + \left(\frac{1}{1+e^{Z_i\gamma}}\right)e^{-e^{X_i\beta}}\right] & if\ y_i = 0 \\ y_i X_i\beta - \ln\left(1+e^{Z_i\gamma}\right) - e^{X_i\beta} - \ln\Gamma(y_i+1) & if\ y_i > 0 \end{cases}$$

The score equations are given by

$$G_i = \left[\frac{\partial \ell}{\partial \beta} \qquad \frac{\partial \ell}{\partial \gamma}\right]' \quad (48)$$

where

$$\frac{\partial \ell}{\partial \beta} = \sum_{i=1}^{n} \begin{cases} \left(-X_i e^{X_i\beta - e^{X_i\beta}}\right)\left(1+e^{Z_i\gamma}\right)^{-1}\left[\frac{e^{Z_i\gamma}}{1+e^{Z_i\gamma}} + \left(\frac{1}{1+e^{Z_i\gamma}}\right)e^{-e^{X_i\beta}}\right]^{-1} & if\ y_i = 0 \\ y_i X_i - X_i e^{X_i\beta} & if\ y_i > 0 \end{cases}$$

and

$$\frac{\partial \ell}{\partial \gamma} = \sum_{i=1}^{n} \begin{cases} \left(1-e^{-e^{X_i\beta}}\right)\left[Z_i\left(1+e^{Z_i\gamma}\right)^{-2}\right]\left[\frac{e^{Z_i\gamma}}{1+e^{Z_i\gamma}} + \left(\frac{1}{1+e^{Z_i\gamma}}\right)e^{-e^{X_i\beta}}\right]^{-1} & if\ y_i = 0 \\ -X_i e^{Z_i\gamma} & if\ y_i > 0 \end{cases}$$

The matrix of the second derivative is given as

$$\begin{bmatrix} \frac{\partial^2 \ell}{\partial\beta\partial\beta'} & \frac{\partial^2 \ell}{\partial\gamma\partial\beta} \\ \frac{\partial^2 \ell}{\partial\beta\partial\gamma} & \frac{\partial^2 \ell}{\partial\gamma\partial\gamma'} \end{bmatrix}' \qquad (49)$$

Parameter estimates are obtained using the Fisher scoring algorithm described in Section 3.5.2 only that here we have two parameters.

Assuming the Fisher informaton $T(\beta,\gamma)$, the standard errors of the parameter estimates are

$$se\left(\hat{\beta},\hat{\gamma}\right) = \sqrt{diag\left[T(\beta,\gamma)^{-1}\right]} \qquad (50)$$

3.9.2 The Zero-Inflated Negative Binomial GLM

The zero-inflated Negative Binomial model (ZINB) corrects both overdspersion and presence of excessive zero count. The pdf of the ZINB is given by

$$P(Y_i = y_i) = \begin{cases} \pi_i + (1-\pi_i)\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}} & \text{if } y = 0, \\ (1-\pi_i)\binom{\frac{1}{k}+y-1}{y-1}\left(1-\frac{1}{1+k\psi}\right)^{y}\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}} & \text{if } y > 0. \end{cases} \quad (51)$$

where $\psi = \frac{\alpha}{\lambda}$ and $k = \frac{1}{\alpha}$ from the NB distribution above.

Which is achieved by substituting (36) into (42).

From (24) and (25) we have

$$\pi_i = \frac{e^{X_i\gamma}}{1+e^{X_i\gamma}} \quad \text{and} \quad \psi = e^{Z_i\beta}$$

where γ and β are vector of fixed parameters associated with the excess zeros and

X_i and Z_i known matrices of covariates for the i^{th} individual for excess zero.

Thus the expectation of y_i is

$$E(y_i) = (1-\pi_i)\psi_i \quad (52)$$

When we substitute expressions for π_i and ψ_i into (43) we have,

$$E(y_i) = \frac{e^{Z_i\beta}}{1+e^{X_i\gamma}}$$

Here the population mean is a function of all covariates and parameters from both parts of the model.

From the above, if $Z=X$ as is usually specified, an increase from the j^{th} to the $(j+1)^{th}$ covariates yields the incidence ratio

$$\frac{E\left(y_{ij}\left|x_{ij}=j+1,\overline{x_i}=\overline{x_i}\right.\right)}{E\left(y_{ij}\left|x_{ij}=j,\overline{x_i}=\overline{x_i}\right.\right)}=e^{\beta_j}\frac{1+e^{\left(j\vartheta_j+\overline{x}'\overline{\vartheta}\right)}}{1+e^{\left((j+1)\vartheta_j+\overline{x}'\overline{\vartheta}\right)}}$$

where $\overline{x_i}$ indicates all covariates except x_{ij} and $\overline{\vartheta}$ is created by removing ϑ_j from ϑ.

In the ratio above, if $\vartheta_j=0,\ e^{\beta_j}$ is constant across all levels of the covariates, otherwise it is not constant across all levels of the covariates including extraneous ones in the logistic portion of the ZINB model.

By similar computations as in the ZIP model, the variance of the ZINB model is

$$\text{var}\left(y_i\right)=\psi_i+\left(\frac{\pi_i+k}{1-\pi_i}\right)\psi_i^2 \qquad (53)$$

The likelihood of the ZINB model is

$$L\left(\psi;y,\pi_i\right)=\prod_{y=0}\left[\pi_i+\left(1-\pi_i\right)\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}}\right]\times\prod_{y>0}\left(1-\pi_i\right)\binom{\frac{1}{k}+y-1}{y-1}\left(1-\frac{1}{1+k\psi}\right)^{y}\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}}$$

Here we find the likelihood of the expected value ψ given the data and k which allows overdispersion. Typcally this is expressed as a log-likelihood denoted by ℓ:

$$\ell = \sum_{i=1}^{n} I\left(y_i = 0\right) \ln\left[\pi_i + \left(1-\pi_i\right)\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}}\right]$$
$$+\sum_{i=1}^{n} I\left(y_i > 0\right) \ln\left[\left(1-\pi_i\right)\binom{\frac{1}{k}+y_i-1}{y_i-1}\left(1-\frac{1}{1+k\psi}\right)^{y}\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}}\right]$$

which can be simplified as

$$\ell = \sum_{i=1}^{n} \begin{cases} \ln\left[\pi_i + \left(1-\pi_i\right)\left(\frac{1}{1+k\psi}\right)^{\frac{1}{k}}\right] & if\ y = 0 \\ y_i \ln\left(\frac{k\psi}{1+k\psi}\right) + \frac{1}{k}\ln\left(\frac{1}{1+k\psi}\right) + \ln\left(1-\pi_i\right) & \\ \quad + \ln\Gamma\left(\frac{1}{k}+y_i\right) - \ln\Gamma\left(\frac{1}{k}\right) - \ln\Gamma\left(y_i\right) & if\ y_i > 0 \end{cases} \tag{54}$$

Arguably, this can be expressed in terms of our ZINB GLM by substitutng $\psi = e^{X_i\beta}$ and

$\pi_i = \frac{e^{Z_i\gamma}}{1+e^{Z_i\gamma}}$ into the log-likelihood above

$$\ell = \sum_{i=1}^{n} \begin{cases} \ln\left[\frac{e^{Z_i\gamma}}{1+e^{Z_i\gamma}} + \left(\frac{1}{1+e^{Z_i\gamma}}\right)\left(\frac{1}{1+ke^{X_i\beta}}\right)^{\frac{1}{k}}\right] & if\ y = 0 \\ y_i \ln\left(\frac{ke^{X_i\beta}}{1+ke^{X_i\beta}}\right) + \frac{1}{k}\ln\left(\frac{1}{1+ke^{X_i\beta}}\right) - \ln\left(1+e^{Z_i\gamma}\right) & \\ \quad + \ln\Gamma\left(\frac{1}{k}+y\right) - \ln\Gamma\left(\frac{1}{k}\right) - \ln\Gamma\left(y_i\right) & if\ y_i > 0 \end{cases}$$

The score equations is same as that given in (48) except that here the overdispersion parameter is present. Thus,

$$\frac{\partial \ell}{\partial \beta}=\sum_{i=1}^{n}\begin{cases}-X_i e^{X_i\beta}\left(1+e^{Z_i\gamma}\right)\left(1+ke^{X_i\beta}\right)^{-\frac{1}{k}-1}\left[e^{Z_i\gamma}\left(1+e^{Z_i\gamma}\right)^{-1}+\left(1+e^{Z_i\gamma}\right)\left(1+ke^{X_i\beta}\right)^{-\frac{1}{k}}\right]^{-1} & if\ \ y_i=0,\\ kX_i e^{X_i\beta}-(k+1)X_i e^{X_i\beta}\left(1+ke^{X_i\beta}\right)^{-1} & if\ \ y_i>0.\end{cases}$$

and

$$\frac{\partial \ell}{\partial \gamma}=\sum_{i=1}^{n}\begin{cases}\left[e^{Z_i\gamma}-\left(1+ke^{X_i\beta}\right)^{-\frac{1}{k}}\right]Z_i e^{Z_i\gamma}\left(1+e^{Z_i\gamma}\right)^{-2} & if\ \ y_i=0,\\ -Z_i e^{Z_i\gamma}\left(1+e^{Z_i\gamma}\right)^{-2} & if\ \ y_i>0.\end{cases}$$

From which we can obtain the Hessian. The matrix of second derivative is the same as that in (49) except that here overdispersion i taken care of. Here also parameters are estimated same as that in the Poisson case with similar standard errors except that overdispersion is accounted for.

3.9.3 Zero Inflated Poisson GLMM

The ZIP or the ZINB are not suitable for correlated data. They are further extended to correct for dependncy in the data. The zero-inflated Poisson GLMM (ZIPG) has a pdf

same as that in (43) except that $\mu_i=e^{X_i\beta+\frac{\sigma^2}{2}}$ and $\pi_i=\dfrac{e^{Z_i\gamma+\frac{\sigma^2}{2}}}{1+e^{Z_i\gamma+\frac{\sigma^2}{2}}}$.

The mean and variance of the ZIPG is obtained by substituting expressions for μ_i and π_i into (44) and (46) respectively.

Similarly, for the log-likelihood we substitute the expressions for μ_{ij} and π_i into (47) yielding

$$\ell = \sum_{i=1}^{n} \begin{cases} \ln\left[\left(e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)\left(\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}+\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}e^{-e^{X_i\gamma+\frac{\sigma^2}{2}}}\right)\right] & if\ y_i=0 \\ y_i\left(X_i\beta+\frac{\sigma^2}{2}\right)-\ln\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)-e^{X_i\gamma+\frac{\sigma^2}{2}} & if\ y_i>0 \end{cases}$$

The score equations are given by

$$G_i = \left[\frac{\partial\ell}{\partial\beta} \quad \frac{\partial\ell}{\partial\gamma} \quad \frac{\partial\ell}{\partial\sigma^2}\right]' \qquad (55)$$

where

$$\frac{\partial\ell}{\partial\beta} = \sum_{i=1}^{n} \begin{cases} -X_i e^{X_i\beta+\frac{\sigma^2}{2}}\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} & \\ \left[\left(e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}+\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}e^{-e^{X_i\beta+\frac{\sigma^2}{2}}}\right]^{-1} & if\ y_i=0 \\ \left(y_i-e^{X_i\beta+\frac{\sigma^2}{2}}\right)X_i & if\ y_i>0 \end{cases}$$

$$\frac{\partial\ell}{\partial\gamma} = \sum_{i=1}^{n} \begin{cases} Z_i\left[1-e^{-e^{X_i\beta+\frac{\sigma^2}{2}}}\right]e^{Z_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-2} & \\ \left[\left(e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}+\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}e^{-e^{X_{ij}\beta+\frac{\sigma^2}{2}}}\right]^{-1} & if\ y_i=0 \\ -Z_i e^{X_i\beta+\frac{\sigma^2}{2}}\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} & if\ y_i>0 \end{cases}$$

and

$$\frac{\partial \ell}{\partial \sigma^2} = \sum_{i=1}^{n} \begin{cases} \frac{1}{2}\left\{1-\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)+e^{Z_i\gamma+\frac{\sigma^2}{2}}-\left[1+\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)e^{X_i\gamma+\frac{\sigma^2}{2}}\right]e^{-e^{X_i\beta+\frac{\sigma^2}{2}}}\right\} & \\ \left[\left(e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}+\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}e^{-e^{X_i\beta+\frac{\sigma^2}{2}}}\right]^{-1} & \text{if } y_i = 0, \\ \frac{1}{2}\left[y_i - e^{Z_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}-e^{X_i\gamma+\frac{\sigma^2}{2}}\right] & \text{if } y_i > 0. \end{cases}$$

From which the Hessian can be obtained. The matrix of the second derivatives is given by

$$\begin{bmatrix} \frac{\partial^2 \ell}{\partial\beta\partial\beta'} & \frac{\partial^2 \ell}{\partial\gamma\partial\beta} & \frac{\partial^2 \ell}{\partial\sigma^2\partial\beta} \\ \frac{\partial^2 \ell}{\partial\beta\partial\gamma} & \frac{\partial^2 \ell}{\partial\gamma\partial\gamma'} & \frac{\partial^2 \ell}{\partial\sigma^2\partial\gamma} \\ \frac{\partial^2 \ell}{\partial\beta\partial\sigma^2} & \frac{\partial^2 \ell}{\partial\gamma\partial\sigma^2} & \frac{\partial^2 \ell}{\partial\sigma^2\partial\sigma^{2\prime}} \end{bmatrix}' \qquad (56)$$

Thus the EM algorithm implemented in statistical packages is used to estimate the parameters as well as their standard errors.

3.9.4 Zero Inflated Negative Binomial GLMM

The zero-inflated Negative Binomial GLMM (ZINBG) has the same pdf as in (51) except that

$\psi = e^{Z_i\beta+\frac{\sigma^2}{2}}$ and $\pi_i = \frac{e^{X_i\gamma+\frac{\sigma^2}{2}}}{1+e^{X_i\gamma+\frac{\sigma^2}{2}}}$.

The mean and variance of the ZINBG is obtained by substituting expressions

for ψ and π_i into (52) and (53) respectively.

Similarly, for the log-likelihood we substitute the expressions for ψ and π_i into (54) yielding

$$\ell = \sum_{i=1}^{n} \begin{cases} \ln\left[e^{X_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} + \left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}}\right] & if\ y_i = 0 \\ y_i \ln ke^{Z_i\beta+\frac{\sigma^2}{2}} - y_i \ln\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right) - \frac{1}{k}\ln\left(1+e^{Z_i\beta+\frac{\sigma^2}{2}}\right) - \ln\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right) & \\ \quad + \ln\Gamma\left(\frac{1}{k}+y_i\right) - \ln\Gamma\left(\frac{1}{k}\right) - \ln\Gamma\left(y_i\right) & if\ y_i > 0 \end{cases}$$

With the score equation given same as that given in (55), where

$$\frac{\partial \ell}{\partial \beta} = \sum_{i=1}^{n} \begin{cases} -Z_i e^{Z_i\beta+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}-1} & \\ \qquad \left[e^{X_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} + \left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}}\right]^{-1} & if\ y_i = 0, \\ y_i Z_i - \left(1+ky_i\right) Z_i e^{Z_i\beta+\frac{\sigma^2}{2}}\left(1+e^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-1} & if\ y_i > 0. \end{cases}$$

$$\frac{\partial \ell}{\partial \gamma} = \sum_{i=1}^{n} \begin{cases} \left[e^{X_i\gamma+\frac{\sigma^2}{2}} - \left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}}\right] X_i e^{X_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-2} & \\ \qquad \left[e^{X_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} + \left(e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}}\right]^{-1} & if\ y_i = 0, \\ -X_i e^{X_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} & if\ y_i > 0. \end{cases}$$

and

$$\frac{\partial \ell}{\partial \sigma^2} = \sum_{i=1}^{n} \begin{cases} \frac{1}{2}\left\{\left[1-\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}}\right]\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-2} - e^{Z_i\beta+\frac{\sigma^2}{2}}\left(1+e^{X_i\gamma+\frac{\sigma^2}{2}}\right)^{-1}\left(1+ke^{Z_i\beta+\frac{\sigma^2}{2}}\right)^{-\frac{1}{k}-1}\right\} & \\ \left[\left(e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} + \left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} e^{-e^{X_i\beta+\frac{\sigma^2}{2}}}\right]^{-1} & \text{if } y_i = 0, \\ \frac{1}{2}\left[y_i - e^{Z_i\gamma+\frac{\sigma^2}{2}}\left(1+e^{Z_i\gamma+\frac{\sigma^2}{2}}\right)^{-1} - e^{X_i\beta+\frac{\sigma^2}{2}}\right] & \text{if } y_i > 0. \end{cases}$$

From which the Hessian can be obtained. The matrix of second derivatives is given in (56).

Here also parameters are estimated using the EM algorithm described earlier implemented in statistical software.

However, it should be noted that the EM algorithm is a natural contender for zero-inflated models (Lambert,1992) by formulating the model in terms of an unobserved binary indicator Z of whether the observation is a structural or sampling zero.

Interestingly, analysis will be done using complete cases of maternal death with the assumption that the data is missing completely at random. However methods of dealing with nonignorable missing-ness in zero-inflated models are provided in Hasan *et al.*(2009) and Maroutti(2011).

For our data there was no clear indication why some observations where missing, but expectations where that it is as a result of a random process.

Lee *et al*.(2006) and Yau *et al*.(2003) used independent random effects in the ZIPG and the ZINBG, whiles O. Loquiha *et al*.(2013) used correlated random effects for only the ZINBG, we propose a correlated random effect for both the ZIPG and the ZINBG.

3.10 AKAIKE INFORMATION CRITERION AND BAYESIAN INFORMATION CRITERION

In order to compare and choose an appropriate model, values of the penalized function statistics such as Akaike Information Criterion (AIC; Akaike 1994, 1973) and Bayesian Information Criterion (BIC, Burnham and Anderson, 2004) also known as Schwarz Criterion (Schwarz ,1978) will be used. AIC and BIC are referred to as "penalized" criteria because they combine a measure of model fit, typically twice the negative log-likelihood, with a penalty for model complexity, expressed as a function of the number of parameters. Smaller values of AIC and BIC are considered preferable. The AIC and BIC are estimated respectively by the formula:

$$\text{AIC} = 2k - 2\log(\text{likelihood})$$

OR

$$\text{AIC} = 2k + n\log(\text{residual sum of squares}) - n\log n$$

and

$$\text{BIC} = k \log n - 2 \log(\text{likelihood})$$

OR

$$\text{BIC} = \log\left(\text{error variance}\right) + \frac{k}{n} \log n$$

where k is the number of parameters in the model and and n the sample size.

3.11 STATISTICAL SOFTWARE TO BE USED

The models will be fitted within the maximum likelihood framework using the *gamlss, glmmADMB, lm4, MASS* and *pscl* packages in R statistical software. The *MASS* package will be used to fit the Poisson and Negative Binomial GLMs, the *lm4* for the Poisson GLMM, the *gamlss* for the Negative Binomial GLMM, the *pscl* for the zero-inflated GLMs and the *glmmADMB* for the zero-inflated GLMMs respectively.

CHAPTER 4

RESULTS AND DISCUSSION

4.0 DATA EXPLORATION

We commence with some preliminary analysis. Figure 1, shows the histogram of the number of maternal death indicates a higher proportion of excess zeros accounting for 75% of the data. A simple descriptive statistics shows a very high variance of 203.78 as compared to the mean of 4.01 indicating evidence of overdispersion. Thus there exist overdispersion and zero-inflation in our data.

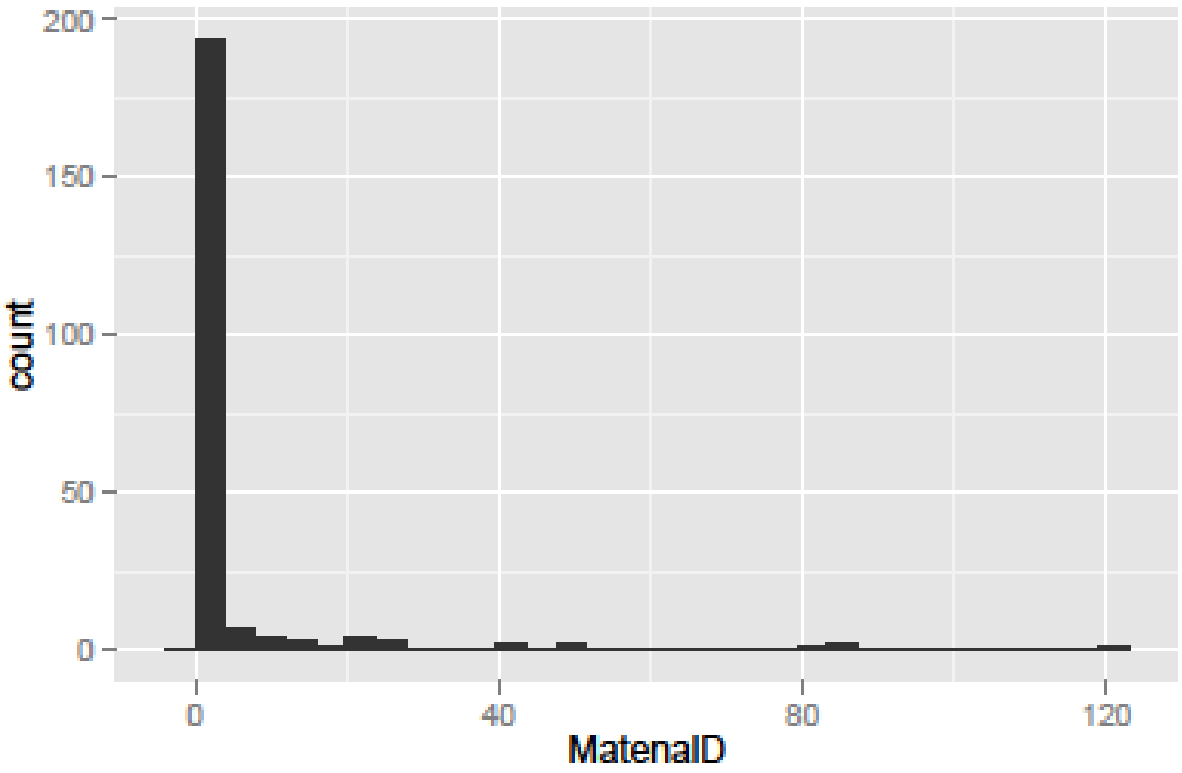

Figure 1: ***Maternal Mortality Data. Histogram. MatenalD represent Maternal Death.***

In Figure 2, the individual hospital profiles with fitted mean showed higher variability between clinics (HC, Cl, CHPS and PC) and hospitals (GH, RH and TH) as compared to within hospital variability. An indication of correlation inherent in the data. All clinics recorded zero maternal death for the entire period (i.e. from 2010 to 2013) contributing to the zero-nflation in our response whiles the hospitals recorded over 95% non-zero maternal death with the RH and TH recording the highest deaths.

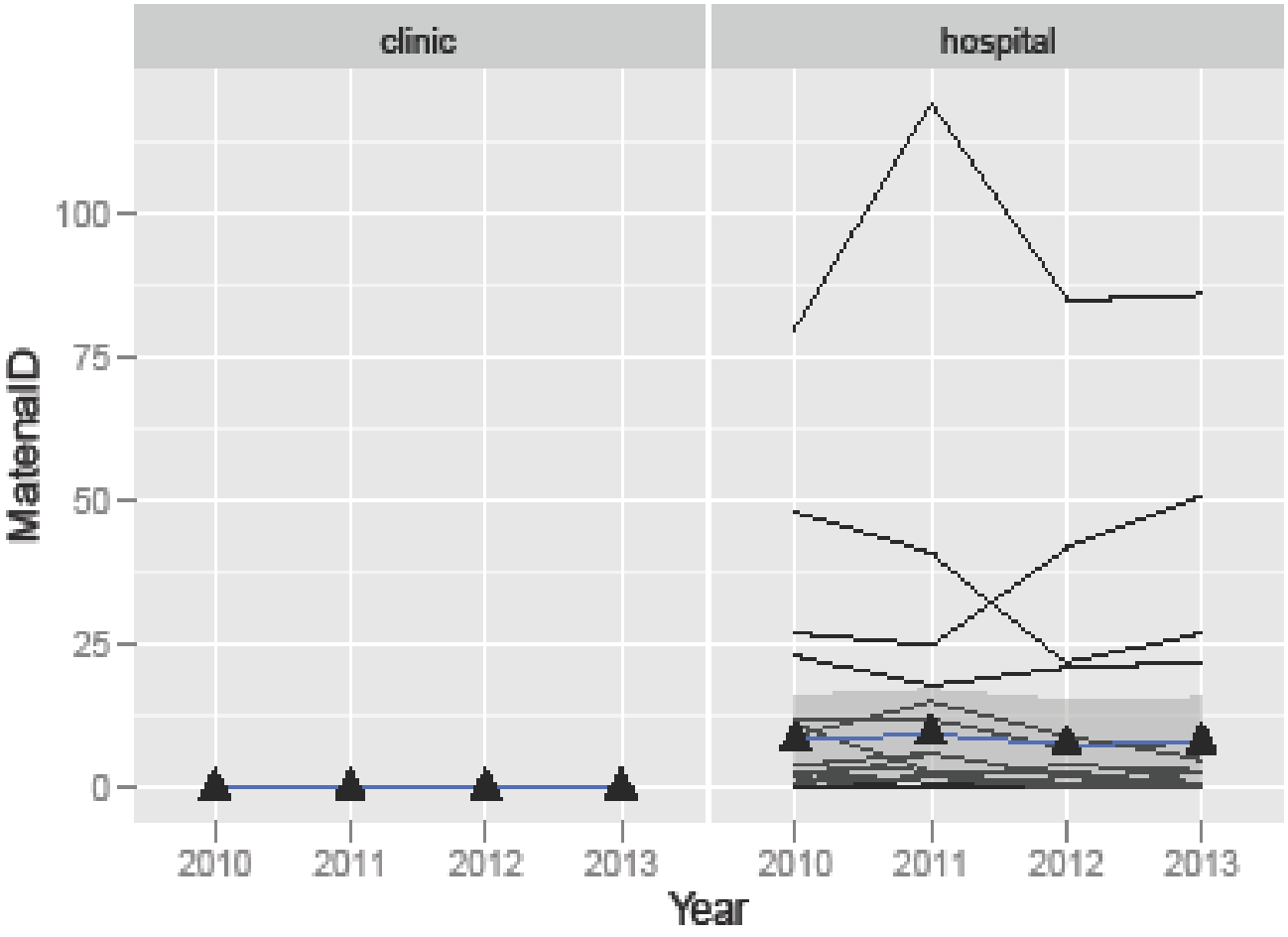

Figure 2:*Maternal Mortality Data. Hospital Facility Profiles with fitted mean.*

4.1 MODELLING

The number of deliveries at a hospital facility was assumed to be a measure of the women at risk. Thus our starting model was a Poisson regression model with mean μ_i related to covariates in the following way

$$\log \mu_i = \mathbf{X}\beta$$

We investigated the main effect and some two way interaction effect of all covariates using Poisson regression model (P), Poisson GLMM (PG), zero-inflated Poisson GLM (ZIP), zero-inflated Poisson GLMM (ZIPG), Negative Binomial regression model (NB), Negative Binomial GLMM (NBG), zero-inflated Negative Binomial GLM (ZINB) and zero-inflated Negative Binomial GLMM (ZINBG). The *MASS* package was used to fit the P and NB models, the *lm4* for the PG, the *gamlss* for the NBG, the *pscl* for the ZI GLMs and the *glmmADMB* for the zero-inflated GLMMs respectively. Interestingly the *glmmADMB* package in R does not allow covariates in the binary part of the ZI GLMMs. The Negative Binomial models and the Poisson GLMM and their ZIMs are referred in here as our so called hierarchical models. The GLMMs were assumed to have normal random effects. The models were selected using the stepwise deletion procedure implemented in the Drop1function in R with our significance level for removal set at 0.20. The stepwise deletion procedure, however, did not work for some of the hierarchical. The final best model was selected using values of AIC, BIC and negative two log-likelihood (-2ll).

The modeling began with a simple Poisson regression model. Using the stepwise deletion procedure non-significant covariates were eliminated and the best model obtained. The covariate of this model was used as the covariates for the proceeded models. These covariates included

Year, Region, number of antenatal visits exceeding four, number of referral into hospital facility, number of referral out of hospital facility, number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of medical doctors and number of midwives at the hospital facility. The Poisson model was extended to NB, PG, NBG, ZIP, ZINB, ZIPG and ZINBG respectively to cater for the overdispersion, correlation or zero-inflation or all. But our prime interest was on all. All two way interaction between these covariates were also checked.

Table 1, shows the various models and their AIC, BIC and -2ll. The smaller their value the better the fit.

Table 1: *Maternal Mortality Data. Poisson regression model fit and it extensions with their corresponding AIC, BIC and -2×log-likelihood (-2ll).*

Models	AIC	BIC	-2ll
P	806.09	864.08	772.09
PG	610.10	647.50	588.20
ZIP	744.56	738.08	720.60
ZIPG	708.20	732.29	688.19
NB	499.63	564.46	469.63
NBG	497.96	492.31	431.96
ZINB	492.33	483.88	426.40
ZINBG	519.70	557.20	497.67

Generally the Negative Binomial models performed better than their Poisson counterparts with respect to their fitted values. The table values also show how poorly the Poisson regression model performed relative to all other models. This shows the shortcomings of the Poisson regression model. The AIC, BIC and -2ll values for the Poisson model drops sharply (AIC from 806.09 to 610.10, BIC from 864.08 to 647.50 and -2ll from 772.09 to 588.20) from P to PG with the -2ll indicating the least change. The value fit then increases as we move to the ZIP and drops again for the ZIPG. For the Negative Binomial distribution the AIC, BIC and -2ll values dropped

from the NB through the NBG to the ZIPG and then increases for the ZINBG. In all the ZINB showed the least fit value in terms of AIC, BIC and -2ll. Hence on the basis of these values the ZINB is considered the best model this data.

Table 2 shows parameter estimates, standard errors and p-values for the zero-inflated GLMs and their extensions.

The dispersion parameter for the ZINB and ZINBG were 1.475 and 1.094 respectively.

Generally speaking, the Negative Binomial distribution had larger standard errors than the Poisson distribution for all models as expected. This confirms that the Poisson regression underestimate the standard error of estimates when the data is overdispersed. Specifically, both the ZINB and ZINBG models led to the same results.

Considering the zero-inflated part of our models, the ZIP had the following significant covariates: number of referrals (into and out of HF) and number of doctors. Number of obstetric cases with HIV/AIDS and number of obstetric cases with malaria was not significant. However the ZINB had only number of obstetric cases with malaria not being significant but all others were. The zero-inflated GLMMs showed no covariates for the zero-inflated part of our model.

Switching to the count part of our models, the ZIP had the following significant covariates; number of referrals (into and out of HF), number of doctors and number of midwives at the HF. Number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of antenatal visits exceeding four was not significant. Interestingly, number of obstetric cases with HIV/AIDS was significant in all regions but number of obstetric cases with malaria was not. For

Table 2. Maternal Mortality Data. Parameter estimates, standard errors(s.e.) and p-values(p) for the zero-inflated Poisson GLM (ZIP), zero-inflated Poisson GLMM (ZIPG), zero-inflated Negative Binomial GLM (ZINB), zero-inflated Negative Binomial GLMM (ZINBG).

	ZIP	ZIPG	ZINB	ZINBG
Effects	Estimates(s.e., p)	Estimates(s.e., p)	Estimates(s.e., p)	Estimates(s.e., p)
		Zero-inflated Part		
Intercept	3.142(0.505, 0.000)		3.284(0.531, 0.000)	
Referral in	-0.077(0.029, 0.008)		-0.075(0.026, 0.004)	
Referral out	0.017(0.013, 0.002)		0.019(0.019, 0.018)	
Malaria	-0.001(0.008, 0.283)		-0.011(0.008, 0.226)	
HIV/AIDS	-0.008(0.008, 0.336)		-0.012(0.001, 0.023)	
Doctors	-0.748(0.240, 0.002)		-0.677(0.248, 0.006)	
Overdispersion			1.475(0.393)	1.094(0.453)
Variance			0.467(0.050)	0.364(0.082)
		Count Part		
Intercept	2.591(0.070, 0.061)	-7.954(7.319, 0.232)	3.262(0.622, 0.454)	-8.740(7.60, 0.250)
Referral in	0.001	0.003(0.001, 0.000)	0.002	0.001(0.001, 0.110)
Referral out	-0.022(0.004, 0.002)	-0.015(0.004, 0.002)	-0.012(0.004, 0.072)	-0.002(0.006, 0.002)
Malaria	-0.003(0.000, 0.654)	-0.010(0.007, 0.338)	0.007(0.012, 0.039)	-0.014(0.007, 0.055)
HIV/AIDS	0.005(0.002, 0.407)	-0.024(0.012, 0.066)	-0.016(0.015, 0.077)	0.004(0.002, 0.798)
ANC	-0.002(0.003, 0.475)	-0.001(0.001, 0.558)	-0.006(0.004, 0.118)	0.000(0.000, 0.779)
Region				
Central	-2.197(0.336, 0.220)	-2.257(0.355, 0.085)	-1.880(0.619, 0.028)	-2.351(0.839, 0.005)
Greater Accra	-2.435(0.881, 0.062)	-3.109(1.250, 0.068)	-3.325(0.961, 0.023)	-4.461(0.102, 0.000)
Western	-2.109(0.318, 0.200)	-1.935(0.367, 0.110)	-2.228(0.561, 0.103)	-3.654(0.848, 0.000)
Eastern	-2.181(0.348, 0.190)	-3.071(1.680, 0.030)	-3.592(0.458, 0.080)	-1.064(0.194, 0.001)
Year				
2011	0.364(0.226, 0.156)	-0.371(0.383, 0.091)	0.659(0.427, 0.180)	0.356(0.511, 0.122)
2012	-0.123(0.239, 0.225)	-1.208(0.417, 0.135)	-0.099(0.443, 0.099)	-0.302(0.471, 0.807)
2013	-0.309(0.268, 0.394)	-1.781(0.538, 0.198)	-0.080(0.443, 0.108)	-0.115(0.515, 0.857)
Doctors	-0.067(0.003, 0.000)	-0.225(0.040, 0.000)	-0.258(0.038, 0.000)	-0.298(0.048, 0.000)
Midwives	0.014(0.003, 0.000)	0.035(0.009, 0.000)	0.043(0.008, 0.000)	0.054(0.012, 0.000)
Year × Malaria				
2011|Malaria	0.001(0.001, 0.168)	-0.000(0.001, 0.108)	-0.001(0.004, 0.003)	-0.003(0.002, 0.443)
2012|Malaria	0.001(0.001, 0.335)	0.001(0.001, 0.223)	-0.000(0.001, 0.005)	-0.001(0.002, 0.541)
2013|Malaria	0.014(0.001, 0.552)	0.002(0.001, 0.315)	-0.006(0.005, 0.011)	-0.000(0.001, 0.881)
Year × HIV/AIDS				
2011|HIV/AIDS	-0.010(0.005, 0.123)	0.014(0.010, 0.081)	-0.010(0.006, 0.008)	-0.003(0.008, 0.703)
2012|HIV/AIDS	-0.012(0.004, 0.070)	0.017(0.109, 0.011)	-0.008(0.008, 0.030)	-0.008(0.007, 0.282)
2013|HIV/AIDS	-0.007(0.003, 0.006)	0.024(0.012, 0.001)	-0.006(0.005, 0.011)	-0.005(0.007, 0.497)
Region × Malaria				
Central|Malaria	0.006(0.006, 0.629)	0.018(0.007, 0.809)	-0.001(0.012, 0.096)	0.024(0.009, 0.006)
Eastern|Malaria	-0.001(0.012, 0.220)	0.039(0.008, 0.145)	-0.001(0.019, 0.139)	0.011(0.009, 0.009)
G.Accra|Malaria	-0.002(0.006, 0.890)	0.013(0.007, 0.623)	-0.003(0.011, 0.067)	0.019(0.007, 0.010)
Western|Malaria	-0.006(0.006, 0.325)	0.005(0.007, 0.101)	-0.011(0.011, 0.022)	0.012(0.008, 0.110)
Region × HIV/AIDS				
Central|HIV/AIDS	0.026(0.014, 0.004)	0.017(0.017, 0.005)	0.037(0.025, 0.019)	0.007(0.030, 0.823)
Eastern|HIV/AIDS	-0.042(0.009, 0.000)	0.011(0.002, 0.004)	0.042(0.009, 0.040)	0.007(0.021, 0.113)
G.Accra|HIV/AIDS	-0.002(0.014, 0.000)	0.006(0.017, 0.293)	0.015(0.019, 0.012)	-0.016(0.020, 0.935)
Western|HIV/AIDS	0.031(0.010, 0.001)	0.029(0.011, 0.000)	0.041(0.018, 0.006)	0.037(0.018, 0.042)

all years maternal mortality was a major factor only in 2011. For the ZIPG, number of referrals (into and out of HF), number of obstetric cases with HIV/AIDS, number of doctors and number of midwives were significant but number of antenatal visits exceeding four and number of obstetric cases with malaria was not. Also number of obstetric cases with HIV/AIDS was significant in the Central, Eastern and Western regions but not in Greater Accra region whiles number of obstetric cases with malaria was significant only in the Eastern and Western regions. Maternal mortality was significant for all years for the ZIPG but was not for all years in the ZIP.

For the ZINB however, number of antenatal visits exceeding four, number of referrals (into and out of HF), number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of doctors and number midwives were found to be significant. Number of obstetric cases with HIV/AIDS and number of obstetric cases with malaria was significant in all regions as well as for all years. In the ZINBG only number of referrals (into and out of HF), number of obstetric cases with malaria, number of medical doctors and midwives at the HF were significant. Number of obstetric cases with HIV/AIDS and malaria was not significant. Both were not significant for all years as well. Also number of HIV/AIDS was a major factor in the Eastern and Western regions but not in the Central and Greater Accra regions. Malaria was a contributing in all regions.

Maternal mortality was significant in all regions for our model.

To sum up, we say number of referrals(into and out of HF), number of antenatal visits exceeding four, number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of doctors (Gynaecologist) and number of midwives at a HF play a major role in the number of maternal deaths at HFs in Ghana .

To conclude our analysis we do some basic statistics. 2.3% of all obstetric cases had HIV/AIDS and 12.9% had malaria. A bit over 60% of all pregnant women had their antenatal at clinics (HC, CHPS, Cl and PC) while over 70% of all deliveries occurred at the hospitals (GH, RH and TH).

Table three shows the cause-specific deaths. Eclampsia and Pre-eclampsia are the leading direct cause of maternal death followed by haemorrhage and unsafe abortion respectively. For the indirect causes, anaemia was second to others with HIV/AIDS being the third leading cause of death and malaria being fourth with a minimal contribution.

Table 3. Maternal Mortality Data. Cause-specific maternal deaths with percentage death contribution.

Cause-specific Maternal Deaths

	Percentage(%)		**Percentage(%)**
Direct Cause	74	**Indirect Cause**	26
Haemorrhage	36	Anaemia	26
Eclampsia and Pre-Eclampsia	41	Ectopic Pregnancy	4
DIC	3	HIV/AIDS	12
Sepsis	6	Malaria	2
Unsafe Abortion	11	Others	56
Others	3		

Though malaria is high among pregnant women it does not contribute much to maternal death.

Maternal mortality for the entire period of the study was 382 per 100000 live births.

CHAPTER 5

CONCLUSION AND RECOMMENDATION

5.0 CONCLUSION

This thesis investigated the best model that describes maternal mortality in health facilities in four regions of Ghana albeit the main factors that contributes to the menace in the health facilities in the country.

The data used was collected from fifty six HFs in the Central, Eastern, Greater Accra and Western regions and we assumed that the data was completely missing at random. The response of interest, the number of maternal death, is a count outcome.

We extended the Poisson regression model (P) to the Negative Binomial regression model (NB), Poisson GLMM (PG), Negative Binomial GLMM (NBG), zero-inflated Poisson GLM (ZIP), zero-inflated Negative Binomial GLM (ZINB), zero-inflated Poisson GLMM (ZIPG) and zero-inflated Negative Binomial GLMM (ZINBG). The final best model, ZINB, was selected based on AIC, BIC and -2ll values.

Mathematical expressions for the mean, variance, log-likelihood and the score equations for all models were derived. All estimations were done within the maximum likelihood framework.

The analysis was done in R statistical software using the *MASS* package for the P and NB, the *lm4* for the PG, the *gamlss* for the NBG, the *pscl* for the ZI GLMs and the *glmmADMB* for the zero-inflated GLMMs respectively.

We found that maternal mortality in HFs in Ghana depended on the number of referrals (into and out of HF), number of antenatal visits exceeding four, number of obstetric cases with HIV/AIDS, number of obstetric cases with malaria, number of medical doctors (Gynaecologist) and number of midwives at the HF. Existence of emergency obstetric care (EmoC), location of the HF and existence of a waiting house played no major roles. Maternal mortality was significant for all years (i.e. from 2010 to 2013). HIV/AIDS in pregnancy was a major significant in the Central, Eastern and Western regions but not in the Greater Accra region. Malaria in pregnancy was significant in all regions. Even though the Poisson regression model and the Negative Binomial regression model had malaria as a factor all extensions did not.

With the exception of Polyclinics with a single medical doctor, all other clinics have no medical doctors.

Maternal mortality was significant in all regions.

Furthermore, 2.3% of pregnant women had HIV/AIDS and 12.9% had malaria. More pregnant women attend antenatal in clinics (HC, CHIPS, Cl and PC) than in hospitals (GH, RH and TH) but more of them deliver in hospitals than in clinics.

Maternal mortality was estimated to be 382 per 100000 live births.

Eclampsia and Pre-eclampsia are the leading direct cause of maternal death followed by haemorrhage. For the indirect cause of maternal death, others are the leading cause with anaemia and HIV/AIDS following in order.

5.1 RECOMMENDATION

The Ministry of Health (MOH) must furnish clinics with the necessary infrastructure and well-trained medical doctors (Gynaecologist) so as to diagnose and deal with pregnancy complications at the early stages of pregnancy. The MOH must provide clinics with three or more midwives since about 98% of such clinics have only one midwife. It must also embark on a massive campaign on the importance of antennal visits for expectant mothers and save sex.

For further studies, a more comprehensive model to deal with overdispersion must be considered.

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APPENDIX

R Codes for Maternal Mortality Data

```
setwd("C:/Users/kassim/Desktop/workshop/Datasets")
myKT <- read.table("MaternalMortalityData.txt",header=T)
myKT
myKT<-within(myKT,{
  Region<-factor(Region)
  Year<-factor(Year)
  TypeHF<-factor(TypeHF)
  LocinDist<-factor(LocinDist)
  EmoC<-factor(EmoC)
  WaitnHse<-factor(WaitnHse)
  HospID<-factor(HospID)
  HospCat<-factor(HospCat)
})
summary(myKT)
var(myKT$MatenalD)
sd(myKT$MatenalD)
mean(myKT$MatenalD)
ggplot(myKT,aes(MatenalD)+geom_histogram()
       plot(myKT$MatenalD)
       pairs(myKT[,-6])

      #Calculating maternal mortality
       sum(myKT$MatenalD)/sum(myKT$Delivaries)*100000
```

```
sum(myKT$Delivaries)

sum(myKT$MatenalD)


#Percentage of pregnant women with HIV.AIDS

sum(myKT$HIV.AIDS)/sum(myKT$ANC)*100


# Percentage of women with malaria

sum(myKT$Malaria)/sum(myKT$ANC)*100


# Total maternal death

count(myKT$MatenalD)


#Percentage of zero maternal death

168/224*100



#Logitudinal plots

p<-ggplot(data=myKT, aes(x=Year, y=MatenalD, group=HospID))

p+geom_point()

p+geom_line()

p+geom_line()+facet_grid(.~HospCat)

p+geom_line()+stat_smooth(aes(group = 1))+stat_summary(aes(group=1), geom="point",
fun.y=mean,

                                    shape=17, size=3)+facet_grid(.~HospCat)
```

```
#GLMs

#the Poisson GLM

M1<-
glm(MatenalD~Region+HospCat+Year+ANC+LocinDist+EmoC+WaitnHse+Refin+Refout+

      Malaria+HIV.AIDS+Doctors+Midwives,

    family=poisson,data=myKT)

summary(M1)

BIC(M1)

logLik(M1)


#Stepwise deletion of non-contributing covariates

drop1(M1,test="Chisq")

M2<-update(M1, .~. -WaitnHse)

summary(M2)


drop1(M2,test="Chisq")

M3<-update(M2, .~. -LocinDist)

summary(M3)


drop1(M3,test="Chisq")

M4<-update(M3, .~. -EmoC)

summary(M4)


#Compare models

anova(M1,M2,M3,M4)
```

```
BIC(M4)

#Model with interaction
M5<-glm(MatenalD~Region+HospCat+Year+Refin+Refout+
        Malaria+HIV.AIDS+Doctors+Midwives+
(Region+HospCat+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives)*Year+(ANC+HIV.
AIDS+Malaria)*Region,
        family=poisson,
        data=myKT)

summary(M5)

BIC(M5)

#The Negative Bnomial GLM
M6<-
glm.nb(MatenalD~Region+Year+HospCat+LocinDist+EmoC+WaitnHse+ANC+Refin+Refout+
Malaria+HIV.AIDS+Doctors+Midwives, link="log", data=myKT)
summary(M6)
BIC(M6)

#Stepwise deletion of non-contributing covariates
drop1(M6,test="Chisq")
M7<-update(M6, .~. -WaitnHse)
summary(M7)
```

```
drop1(M7,test="Chisq")
M8<-update(M7, .~. -EmoC)
summary(M8)

drop1(M8,test="Chisq")
M9<-update(M8, .~. -LocinDist)
summary(M9)

drop1(M9,test="Chisq")
M10<-update(M9, .~. -ANC)
summary(M10)

drop1(M10,test="Chisq")
M11<-update(M10, .~.-HIV.AIDs)
summary(M11)

BIC(M11)

#Compare models
anova(M6,M7,M8,M9,M10,M11)



#Model with interaction
M12<-glm.nb(MatenalD~Region+HospCat+Year+Refin+Refout+
            Malaria+Doctors+Midwives+
```

```
(Region+HospCat+Refin+Refout+Malaria+Doctors+Midwives)*Year+(ANC+HIV.AIDS+Malar
ia)*Region,
            data=myKT)

    summary(M12)

    BIC(M12)

    #GLMMs
    #Poisson GLMM
    myKT$over<-1:nrow(myKT)
    contrasts(myKT$Region)
    contrasts(myKT$Year)
    contrasts(myKT$TypeHF)
    contrasts(myKT$LocinDist)
    contrasts(myKT$EmoC)
    contrasts(myKT$WaitnHse)
    contrasts(myKT$HospCat)
    contrasts(myKT$HospID)

    #HospID as random effects without overdispersion
    M17<-
glmer(MatenalD~Region+HospCat+ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwiv
es+
            (1|HospID),
          verbose=FALSE,
```

```
        family=poisson,
        data=myKT)
summary(M17)


#Stepwise deletion of non-contributing covariates(use of stepAIC is also accepted)
drop1(M17,test="Chisq")
M18<-update(M17, .~. -HospCat)
summary(M18)

drop1(M18,test="Chisq")
M19<-update(M18, .~. -Midwives)
summary(M19)

drop1(M19,test="Chisq")
M20<-update(M19, .~. -Refout)
summary(M20)

drop1(M20,test="Chisq")
M21<-update(M20, .~. -ANC)
summary(M21)

drop1(M21,test="Chisq")
M22<-update(M21, .~. -Malaria)
summary(M22)
```

```
#Comparison of models
anova(M17,M18,M19,M20,M21,M22)

# Model with interaction
M23<-
glmer(MatenalD~Region+Refin+HIV.AIDS+Doctors+Malaria+ANC+(Region+Refin+HIV.AIDS+Doctors+Malaria+ANC)*Year+
        (ANC+HIV.AIDS+Malaria)*Region+(1|HospID),
      verbose=FALSE,
      family=poisson,
      data=myKT)
summary(M23)

drop1(M23,test="Chisq")
M24<-update(M23, .~. -HIV.AIDS)
summary(M24)

drop1(M24,test="Chisq")
M25<-update(M24, .~. -ANC)
summary(M25)

#Negative Binomial GLMM

#with HospID as random effect
M26<-
gamlssNP(MatenalD~Region+EmoC+ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives+Year,
```

```
            random=~1|HospID,
            family=NBI,
            mixture="gq",k=20,
            data=myKT)
    summary(M26)
    logLik(M26)

    stepAIC(M26)

    #Model with interaction
    M27<-
gamlssNP(MatenalD~ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives+
              ANC*Year+Refin*Year+Refout*Year+Malaria*Year+HIV.AIDS*Year+

Doctors*Year+Midwives*Year+Region*ANC+Region*HIV.AIDS+Region*Malaria,
            random=~1|HospID,
            family=NBI,
            mixture="gq",k=20,
            data=myKT)
    summary(M27)

    #only interaction model
    M28<-
gamlssNP(MatenalD~ANC*Year+Refin*Year+Refout*Year+Malaria*Year+HIV.AIDS*Year+

Doctors*Year+Midwives*Year+Region*ANC+Region*HIV.AIDS+Region*Malaria,
            random=~1|HospID,
```

```
        family=NBI,
        mixture="gq",k=20,
        data=myKT)
summary(M28)

#Zero Inflated Models

#Poisson ZI GLM
M30<-
zeroinfl(MatenalD~Refin+Refout+Malaria+HIV.AIDS+Midwives+Doctors|Refin+Refout+Mala
ria+HIV.AIDS+Doctors,data=myKT)
summary(M30)
AIC(M29)
BIC(M29)

#Model with interaction
M31<-
zeroinfl(MatenalD~Year+Refin+Refout+Malaria+HIV.AIDS+Midwives+Doctors+Year*Malari
a+Year*HIV.AIDS+Region*HIV.AIDS+Region*Malaria|Refin+Refout+Malaria+HIV.AIDS+D
octors,data=myKT)
summary(M31)
AIC(M31)
BIC(M30)

#Negative Binomial ZI GLM
M32<-
zeroinfl(MatenalD~Refin+Refout+Malaria+HIV.AIDS+Midwives+Doctors|Refin+Refout+Mala
ria+HIV.AIDS+Doctors,data=myKT,dist="negbin",EM=TRUE)
```

```
summary(M32)

AIC(M31)

BIC(M31)


#Model with interaction

M33<-
zeroinfl(MatenalD~Year+Refin+Refout+Malaria+HIV.AIDS+Midwives+Doctors+Year*Malari
a+Year*HIV.AIDS+Region*HIV.AIDS+Region*Malaria|Refin+Refout+Malaria+HIV.AIDS+D
octors,data=myKT,dist="negbin",EM=TRUE)

summary(M33)

AIC(M32)

BIC(M32)


#Poisson ZI GLMM

M34<-glmmadmb(MatenalD
~Region++Year+ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives+

                (1|HospCat),

              data = myKT,

              family = "poisson",

              zeroInflation = TRUE,

              verbose = FALSE)

summary(M34)

BIC(M33)


#Model with interaction

M36<-glmmadmb(MatenalD
~Region+Year+ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives+
```

```
                (HIV.AIDS+Malaria)*Region+(HIV.AIDS+Malaria)*Year +(1|HospCat),
              data = myKT,
              family = "poisson",
              zeroInflation = TRUE,
              verbose = FALSE)
    summary(M36)
    BIC(M34)



    #Negative Binomial ZI GLMM
    M37<-glmmadmb(MatenalD
~ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives+
                (1|HospCat),
              data = myKT,
              family = "nbinom",
              zeroInflation = TRUE,
              verbose = FALSE)
    summary(M37)
    BIC(M35)


    drop1(M35,test="Chisq")
    M36<-update(M35, .~. -HIV.AIDS)
    summary(M36)


    drop1(M36,test="Chisq")
```

```
M37<-update(M36, .~. -Malaria)
summary(M37)

BIC(M37)

#Model with interaction
M38<-glmmadmb(MatenalD
~Region+Year+ANC+Refin+Refout+Malaria+HIV.AIDS+Doctors+Midwives+
                (HIV.AIDS+Malaria)*Region +(HIV.AIDS+Malaria)*Year+(1|HospCat),
              data = myKT,
              family = "nbinom",
              zeroInflation = TRUE,
              verbose = FALSE)
summary(M38)
BIC(M38)
```