QUEUEING THEORY BASED MODEL AND NETWORK ANALYSIS FOR PREDICTING THE TRANSMISSION AND CONTROL OF EBOLA VIRUS DISEASE

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DEDICATION

Dedicated to

My darling husband, **Dr. Ikeme John Dike**, and my lovely children **Okey and Ike**
whose love, dream, sacrifice, support and encouragement;
My brother and wife, **Mr** and **Mrs Obiajulu Peter Nwofor**, whose hospitality,
And
My late lovely father, **Chief E. C. Nwofor** and my beloved mother **Mrs E. C. Nwofor**, who initiated the educational foundation;
Led to achieve my doctoral degree.

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ABSTRACT

Ebola Virus Disease (EVD) is a complex epidemic killer disease. Recently, the disease has caused serious loss of life, waste of economy and material resources in West Africa nations. Literature shows that mathematical theories and models such as agent-based model, models based on ordinary differential equation for assessment studies and intervention measures have been proposed by several researchers to handle the outbreak of the disease. But, agent-based model comes with high computational cost, and model based on ordinary differential equation describes reality with varying accuracy. Therefore, there is the need for a mathematical model that can describe the real nature of the disease, reduce computational cost and better prediction of its behaviour. This study presents the modelling and analysis of EVD transmission and control using queueing theory technique. Data collected from WHO Ebola Data and Statistics of the recent outbreak in Guinea, Liberia and Sierra Leone from December 2013 to July 2015 is used in the study. The SEI_LI_CDR (Susceptible, Exposed, Likely Infected, Confirmed Infected, Dead/Recovery) Ebola epidemic model is proposed to accommodate all the transmission phases and be able to explain EVD transmission and control reliably. The EVD transmission patterns and possible control measures are determined using the basic properties of queueing theory. The SEI_LI_CDR based compartmental model is obtained, where SEI_LI_CDR represent the compartments within the countries. In addition, the SEI_LI_CDR based network model is also developed to characterize every interpersonal contact that can potentially lead to disease transmission. Findings indicate that the spread of EVD follows an irregular and random pattern. Also, the SEI_LI_CDR model shows that the Quasi-Stationary Distribution approximation is better than the existing models for the description of EVD problems. Result of the application of queueing theory yielded that the developed model is a reasonable approximation, showing when Ebola Virus is controlled. While, result from network model indicates that the population is vulnerable to large scale epidemics before intervention in the three countries. The vulnerability decreased drastically after intervention. The researcher recommends that studies need to be conducted to include other continent of the world affected by Ebola Virus Disease. The underlying factors of the epidemic are changing rapidly with the increase in safety measures, researchers should develop model that can predict cases in such situation.

ABSTRAK

Penyakit Virus Ebola (EVD) adalah wabak penyakit pembunuh kompleks. Terkini, penyakit ini telah menyebabkan kehilangan nyawa yang serius, pembaziran ekonomi dan sumber bahan di negara-negara Afrika Barat. Literatur menunjukkan bahawa teori dan model matematik seperti model berasaskan ejen, model berdasarkan persamaan pembezaan biasa untuk kajian penilaian dan langkah intervensi telah dicadangkan oleh beberapa penyelidik untuk menangani penularan wabak penyakit ini. Tetapi, model berasaskan ejen memerlukan kos komputeran yang tinggi, dan model berdasarkan persamaan pembezaan biasa menggambarkan realiti dengan ketepatan yang berubah-ubah. Oleh itu, terdapat keperluan untuk model matematik yang dapat menggambarkan sifat sebenar penyakit ini, mengurangkan kos komputeran dan dapat meramalkan perilakunya dengan lebih tepat. Kajian ini membentangkan pemodelan dan analisis penyebaran dan kawalan EVD menggunakan teknik teori giliran. Data yang dikumpul daripada Data Ebola dan Statistik WHO untuk wabak terkini di Guinea, Liberia dan Sierra Leone dari Disember 2013 hingga Julai 2015 digunakan dalam kajian ini. Model wabak Ebola SEI_LI_CDR (Mudah terdedah, Terdedah, Dijangka dijangkiti, Disahkan dijangkiti, Mati/Pemulihan) adalah dicadangkan untuk mewakili semua fasa penyebaran dan dapat menjelaskan penyebaran dan kawalan EVD dengan pasti. Corak penjangkitan dan langkah-langkah kawalan EVD ditentukan dengan menggunakan sifat-sifat asas teori giliran. Model SEI_LI_CDR berasaskan petak diperolehi di mana SEI_LI_CDR mewakili petak dalam setiap negara. Sebagai tambahan, model rangkaian berasaskan SEI_LI_CDR juga dibangunkan untuk mencirikan setiap hubungan interpersonal yang berpotensi membawa kepada jangkitan penyakit. Dapatan kajian menunjukkan bahawa penyebaran EVD mengikut corak yang tidak seragam dan rawak. Model SEI_LI_CDR juga menunjukkan bahawa penghampiran *Quasi-Stationary Distribution* dapat menghuraikan masalah EVD dengan lebih baik daripada model yang sedia ada. Hasil aplikasi teori giliran menunjukkan bahawa model yang dihasilkan adalah penghampiran munasabah yang menunjukkan bila Virus Ebola dapat dikawal. Disamping itu, keputusan dari model rangkaian menunjukkan bahawa penduduk terdedah kepada wabak besar sebelum intervensi di ketiga-tiga negara. Kerentanan menurun secara drastik selepas intervensi. Penyelidik mengesyorkan kajian perlu dijalankan merangkumi benua lain di dunia yang terjejas oleh Penyakit Virus Ebola. Faktor-faktor yang mempengaruhi wabak ini berubah pesat dengan peningkatan langkah-langkah keselamatan, penyelidik harus membangunkan model yang dapat meramalkan kes-kes dalam keadaan sedemikian.

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LIST OF ABBREVIATIONS

AIDS	-	Acquired Immunodeficiency Syndrome
ANS	-	Average Number in the System
AWTR	-	Average Waiting Time for Recovery
AWTS	-	Average Waiting Time in the System
B	-	Bcell- humoral immunity
BD	-	Birth Death
BD_{sa}	-	Birth Death Sampled Ancestors
BD_{ss}	-	Birth Death Super Spreader
BDEI	-	Birth Death Exposed Infected
BDSIR	-	Birth Death Susceptible Infected Removed
CDC	-	Centre for Disease and Control
CFR	-	Case Fatality Ratio
CI	-	Confidence Interval
CIA	-	Central Intelligence Agency
CNN	-	Cable News Network
CS/s	-	Compartmental Size per second
DFE	-	Disease Free Equilibrium
DRC	-	Democratic Republic of Congo
E	-	Exposed
EBOV	-	Ebola Virus
EFSA	-	European Food Safety Authority
EGARCH	-	Exponential Autoregressive Conditional Heteroskedatic
EHF	-	Ebola Haemorrhagic Fever
ENS	-	Expected Number in the System
ETUs	-	Ebola Treatment Units
EVD	-	Ebola Virus Disease

FCFS	-	First Come First Served
GI/M/S	-	General Independent/Memoryless/Server
HHCs	-	Household Contacts
HIV	-	Human Immunodeficiency Virus
HPD	-	Highest Posterior Density
I	-	Infected
IBT	-	International Business Times
IgG	-	Antibodies called Immunoglobulin
MATLAB	-	Matrix Laboratory
MCMC	-	Markov Chain Monte Carlo
MGARCH-DCC-		Multivariate Generalize Autoregressive Conditional Heteroskedatic-Dynamic Correlation Coefficient
M/G/1	-	Memoryless/General/1 (Number of Server is 1)
M/G/N	-	Memoryless/General/N (Number of Server is N)
M/M/./.	-	Memoryless/ Memoryless /. (Number of Server is .)/ Capacity (.)
M/M/1	-	Memoryless/ Memoryless /1 (Number of Server is 1)
M/M/1/K	-	Memoryless/ Memoryless /1 (Number of Server is 1)/Capacity (K)
M/M/S	-	Memoryless/ Memoryless /S (Number of Server is S)
M/M/s/K	-	Memoryless/ Memoryless /s (Number of Server is s)/Capacity (K)
PGF	-	Probability Generating Functions
PPR	-	Prevalence Proportion Ratios
QC	-	Quarantine Centre
QSD	-	Quasi-Stationary Distribution
REBOV	-	Reston Ebola Virus
RMSE	-	Root Mean Square Error
RR	-	Rate Ratio
S	-	Susceptible
SD	-	Standard Deviation
$SEID_bD_IR$	-	Susceptible Exposed Infected Dead Buried Dead Infected Removed

SEI_LI_CDR	-	Susceptible Exposed Likely Infected Confirmed Infected Dead Recovered
SEIHFR	-	Susceptible Exposed Infected Hospitalized Funeral Removed
SEIR	-	Susceptible Exposed Infected Removed
SEIS	-	Susceptible Exposed Infected Susceptible
SIR	-	Susceptible Infected Removed
SIIR	-	Susceptible Latent Infected Removed
SIS	-	Susceptible Infected Susceptible
SLLN	-	Strong Law of Large Numbers
T	-	Tcell-mediated immunity
USD	-	United States Dollar
UNICEF	-	United Nations of Children's Fund
WHO	-	World Health Organization
ZEBOV	-	Zaire Ebola Virus

LIST OF SYMBOLS

$	-	United States Dollar
R_o	-	Basic Reproduction Number
ρ	-	Probability of Infection
T	-	Time
$I(t)$	-	Number of Infective at time t
$S(t)$	-	Number of Susceptible at time t
Ω	-	States Space
λ	-	Infection/Transmission Rate
μ	-	Recovery rate
β	-	Effective Contact Rate
k	-	Infective Individual
R_c, R_e or R_t	-	Effective Reproduction Number
$1/k$	-	Average Incubation Period
N	-	Total Effective Population Size
I_C/N	-	Probability that Contact is made with Infectious Individual
CD4 T	-	Assist Other White Blood Cells in Immunologic Process
CD8 T	-	Destroy Virus Infected Cells and Tumour Cells
L*(t,.)	-	Joint Distribution of the Number of Jobs Present at time t
V_o(t,.)	-	Sojourn Time of a Tagged Job Placed in the System at t under various initial conditions in terms of the Laplace transform with respect to t
P	-	Probability

T_d	-	Total Delay in the System
T_m	-	Average Time an Individual that is Infected Spends in the System
T_r	-	Recovery Time
N	-	Number of Infected Individuals in the System
$E(N)$	-	Expectation of Number of Individuals Infected in the System at Time *t*
$E(T)$	-	Expectation of Total Delay in the System
$N(t)$	-	Number of Individuals Infected in the System at Time *t*
$N_A(t)$	-	Number of Individuals Infected that Arrives at the System up to Time *t*,
$N_D(t)$	-	Number of Individuals Infected that Departs from the System up to Time *t*
T_m	-	Mean Time an Infected Individual Spends in the System
$P(\beta_n)$	-	Inter-arrival Probability Density Function
$1/\lambda$	-	Mean of Inter-arrival Probability Density Function
$1/\lambda^2$	-	Variance of Inter-arrival Probability Density Function
Y_i	-	Sum of Poisson Random Variables for Independent Random Variables
P_{S_n}	-	Partial Sum
N_n	-	Number of Infected Individuals at Time n
Ω_1	-	System that Every Exposed Individual Enters
Ω_2	-	Each Infected Individual Leaves Ω_1 and Enters another System Ω_2
Hrs	-	Hours
Δ	-	Small Change
Q	-	Quasi-Stationary Distribution
$\pi_{m,n}$	-	Limiting Ratio of Time that there were m

		Exposed, n Infected Persons
m	-	Exposed
n	-	Infected Person
$E(t)$	-	Number of Exposed at Time t
$I^T(t)$	-	Total Number of Infected Persons at Time t
$P^T{}_k$	-	Total Probability for k^{th} Infective
$\{X_1, X_2, ...\}$	-	Series of Nonnegative, Independent and Identically Distributed Random Variable
∞	-	Infinity
$m(t)$	-	Mean-Value or the Renewal Function
ϕ	-	Probability that Specific Person is in Infectious State
$\lim_{t\to\infty}$	-	Limit as t tends to infinity
e	-	exponential
$\pi_{m,n_L n_C}$	-	Limiting Ratio of time in which there were m exposed, n_L Likely Infected and n_C Confirmed Infected Persons not being in the Absorbing State but Conditioning in the Process
π_k	-	Total Number of Infectious Persons for Quasi-Stationary Distribution
n_L	-	Number of Likely Infected
n_C	-	Number of Confirmed Infected
(E, I_L, I_C)	-	The State Space of Number of Exposed, Likely Infected and Confirmed Infected Persons
$I_L(t)$	-	Number of Likely Infected at Time t
$I_C(t)$	-	Number of Confirmed Infected at Time t
P_{m,n_L,n_C}	-	Probability of the Joint Quasi-Stationary Distribution
!	-	Factorial
$\lambda I_C / N$	-	Rate at which Individual in Contact with the Virus

		Enter the Exposed State
$1/k$	-	Average Incubation Period
ω_L	-	Rate at which Individual Move from Likely Infected to Confirmed Infected State
ω_C	-	Rate at which Individual Move from Confirmed Infected to Death or Recovery State
τ	-	Beginning of Intervention Time
α	-	Control of Rate of Transmission
t_0	-	Initial Outbreak Time
$f(x)$	-	Function of x
F	-	Rate of Appearance of New Infections in the Compartment
V	-	Rate of Transfer of Individuals into and out of Compartment
υ_1	-	Rate at which Individual Progress from Exposed to. Likely Infectious Individuals
υ_2	-	Rate at which Individual Progress from Likely Infected to Confirmed Infectious Individual
d	-	Death Rate
η_1	-	Control Rate for Exposed Individuals
η_2	-	Control Rate for Confirmed Infectious Individuals
q	-	Successful Control Infectious individuals
$(p=1-q)$	-	Unsuccessful Control Infectious Individuals
$\dot{E}$	-	Differential of Exposed
$\dot{I_L}$	-	Differential of Likely Infected
$\dot{I_C}$	-	Differential of Confirmed Infected
$\dot{S}$	-	Differential of Susceptible
$\dot{D}/\dot{R}$	-	Differential of Dead/Recovery
ρ	-	Spectral Radius of Matrix FV^{-1}

x_0	-	Jacobian Matrix
$Df(x_0)$	-	Derivative $[\partial f/\partial x]$ Evaluated at the Disease Free Equilibrium
P_E	-	Probability of Exposed
P_{I_L}	-	Probability of Likely Infected
P_{I_C}	-	Probability of Confirmed Infected
P_S	-	Probability of Susceptible
$P_{D/R}$	-	Probability of Dead/Recovery
T	-	Transmissibility
T_C	-	Critical Transmissibility or Epidemic Threshold
c	-	Mean Degree
c^2	-	Mean Square Degree
$G_0(h)$	-	Probability Generating Functions for a Degree
$\langle c-1 \rangle$	-	Excess Degree
$\langle c \rangle$	-	Mean Degree Absolute value
$\langle c_e \rangle$	-	Mean Excess Degree Absolute Value
$\langle e \rangle$	-	Average Size of an Outbreak Absolute Value
E	-	Probability of a Full-Blown Epidemic
l	-	Probability that the Person at the End of an Edge or Line Does Not Have the Disease
r_c	-	Probability that a Patient Zero with Degree c will Start an Epidemic or Probability that Transmission of the Disease Along at Least One of the Edges Originating from the New Node or Vertex will Lead to an Epidemic
$1-T$	-	Probability that the Disease Does Not Get Transmitted Along the Edge
Tl	-	Probability that Even if Disease is Transmitted to the Next Node or Vertex, it Does Not Proceed into

		a Full- Blown Epidemic, for Any One of its c Edges
$1-\prod_{i=1}^{N}\left(1-r_{c_i}\right)$	-	Probability that an Outbreak of Size N will Kindle an Epidemic
f_c	-	Probability that an Individual with Degree c will Become Infected During an Epidemic is Equal to One Minus the Probability that None of an Individual c Contact will Transmit the Disease to an Individual

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CHAPTER 1

INTRODUCTION

1.1 Overview of the Research Problem

Ebola Virus Disease (EVD) is a disease caused by infection with the virus of the family *Filoviridae*, genus Ebola virus (Feldmann *et al*., 2011). It is one of the greatest challenges mankind has faced since inception of the world. The toughness of the challenge might be linked to the ways the disease transmits from place to place and from person to person.

Transmission is the unbroken sequence of event by a system. According to Lahm *et al*. (2007) and Walsh *et al.* (2003), Ebola outbreaks and transmission among humans has been associated with direct exposure to fruit bats and mortality among other wild animals, which tend to succumb to the infection. Once there is an outbreak, it can easily be transmitted from person to person. Subsequently, humans need to adopt some control measures to avoid further transmission and possible eradication of the disease. The quest to provide some control measures has attracted some researchers to develop various EVD transmission and control models.

A model is a physical, mathematical, or logical representation of a system, entity, phenomenon, or process. EVD models such as SIR (Susceptible, Infected, Removed), and others such as SEIR (Susceptible, Exposed, Infected, Removed), $SEID_bD_IR$ (Susceptible, Exposed, Infected, Dead Buried, Dead Infected, Removed), SEIHFR (Susceptible, Exposed, Infected, Hospitalized, Funeral, Removed) were

derived from basic epidemiological model SIR, were used by researchers. Researchers use Removed to mean those who recuperate or die from the illness. In the proposed research there is provision for Death and Recovery phases. However, these models are not suitable to be used because they do not accommodate the transmission phases of Ebola. Thus, model that would accommodate the transmission phases and be able to explain EVD transmission and control reliably in the real world is needed. According to WHO (2014a), WHO (2014b), WHO (2015a), CDC (2014a), Goeijenbier *el al.* (2014), Hass (2014), Alan (2013) and Singh (2014), EVD transmission phases are: Susceptible, Exposed, Likely Infected, Confirmed Infected, Dead, Recovery (SEI_LI_CDR). Therefore, in this study, the SEI_LI_CDR model of EVD transmission is proposed through queueing theory. Queueing theory is the mathematical study of waiting lines, or queues (Sztrik, 2012). It deals with the analysis of serving customers arriving to a facility with a fixed number of servers (Hernandez-Suarez *et al.*, 2010). M/M/1 queueing model is applied which refers to the way the disease is transmitted, that is, infection is from one stage to another. For example, in SEI_LI_CDR model an infected individual has to pass through the $S \longrightarrow E \longrightarrow I_L \longrightarrow I_C \longrightarrow D/R$ stages one after the other. The characteristics of queueing theory is that it has Poisson arrival, exponential service times and number of server (capacity). Through applying Poisson and exponential distributions assists to model complex phenomenon of waiting of infected individual in a queue as simple mathematical equation thereby reducing coputational cost (quantification of the difficulty of a computational problem in terms of the computer resources such as computational time or amount of memory required for its solution). These equations are analyzed to describe the real nature of the disease, better prediction of its behaviour and helps in capacity planning decision. That is, it assists in determining the number of EVD Quarantine Centres (QC) with respect to infected EVD patients. The application of queueing theory in the transmission dynamics and control of EVD assists in the development of a reliable EVD model. The theory monitors the outbreak of the disease, the trend of the disease and the eradication of the disease.

1.2 Motivation

Ebola Virus Disease currently has no known effective treatment or vaccine. Stadler *et al.* (2014) argued that supportive care and disease containment is the only available focus of relief efforts in bringing down the case fatality in case of any outbreak. Ebola outbreak has affected adversely the economy of the affected West African countries. Nwaoga (2014) revealed that Nigeria government spent USD11.875 million (United States Dollar) on the fight against EVD as of August 2014. Furthermore, United State government has committed USD175 million, partnering with the United Nations and other international partners to help the government of Guinea, Liberia, Sierra Leone, Nigeria, and Senegal. On the other hand, World Health Organisation (WHO) has spent USD1 billion so far (WHO, 2014c). The United Nations of Children's Fund (UNICEF) spent USD65 million in Liberia, USD61 million in Sierra Leone, and USD55 million in Guinea (UNICEF, 2014a, b). Additional USD10 million was also mapped out to the neighbouring countries to get them prepared for potential spread of the disease within their borders, with the remaining USD9 million required for regional coordination efforts (WHO, 2014c; UNICEF, 2014a,b). Table 1.1 shows expenses of countries and organisations on combating Ebola Virus Disease.

Table 1.1 : Country/Organisation Expenditure on Ebola Virus Disease

Country/Organisation	**Amount $(USD)**
Nigeria	11.875million
United State, United Nations, and other partners	175 million
WHO	1 billion
UNICEF	65 million (Liberia) 61 million (Sierra Leone) 65 million (Guinea) 10 million (neighbouring countries) 9 million (regional coordinators)

The high death rate is another worry. Information gathered from WHO (2014a) and WHO (2015a) Ebola Data and Statistics showed that in February 2015 there were 3155 total cases and 2091 total death. In March 2015, there were 3429 total cases and 2263 total death and in April, there were 3548 total cases and 2346 total death for Guinea as shown in Figure 1.1.

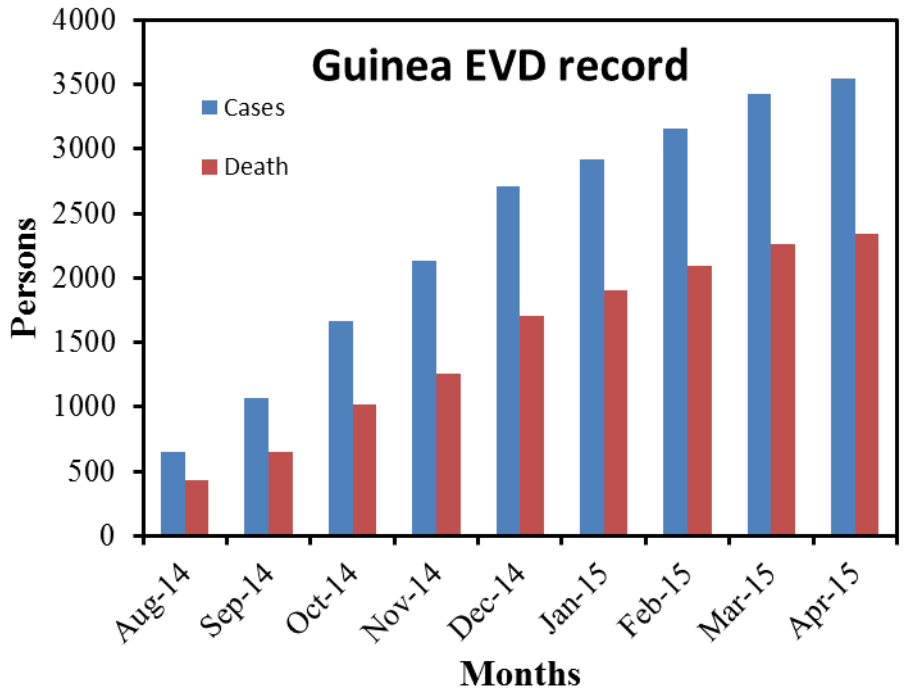

Figure 1.1 : Record of EVD in Guinea.

Subsequently, in February 2015 there were 9238 total cases and 4037 total death; in March 2015 there were 9602 total cases and 4301 total death, in April there were 10042 total cases and 4486 total death for Liberia as in shown Figure 1.2.

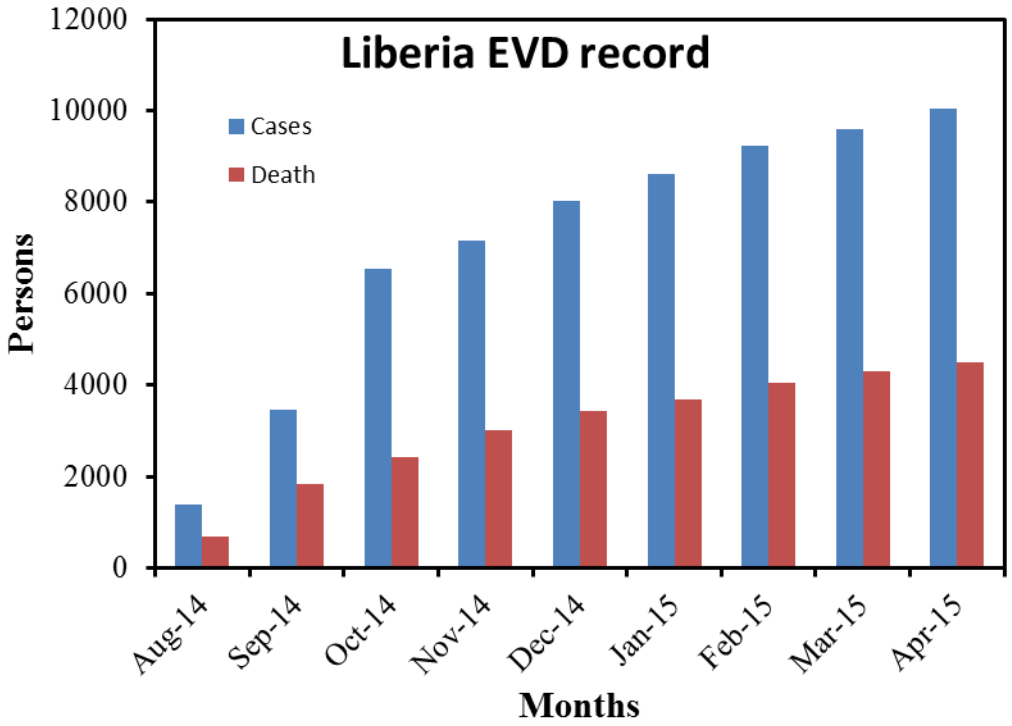

Figure 1.2: Record of EVD in Liberia.

As for Sierra Leone, in February 2015 there were 11301 total cases and 3461 total death; in March 2015 there were 11841 total cases and 3747 total death, in April there were 12201 total cases and 3857 total death as shown in Figure 1.3.

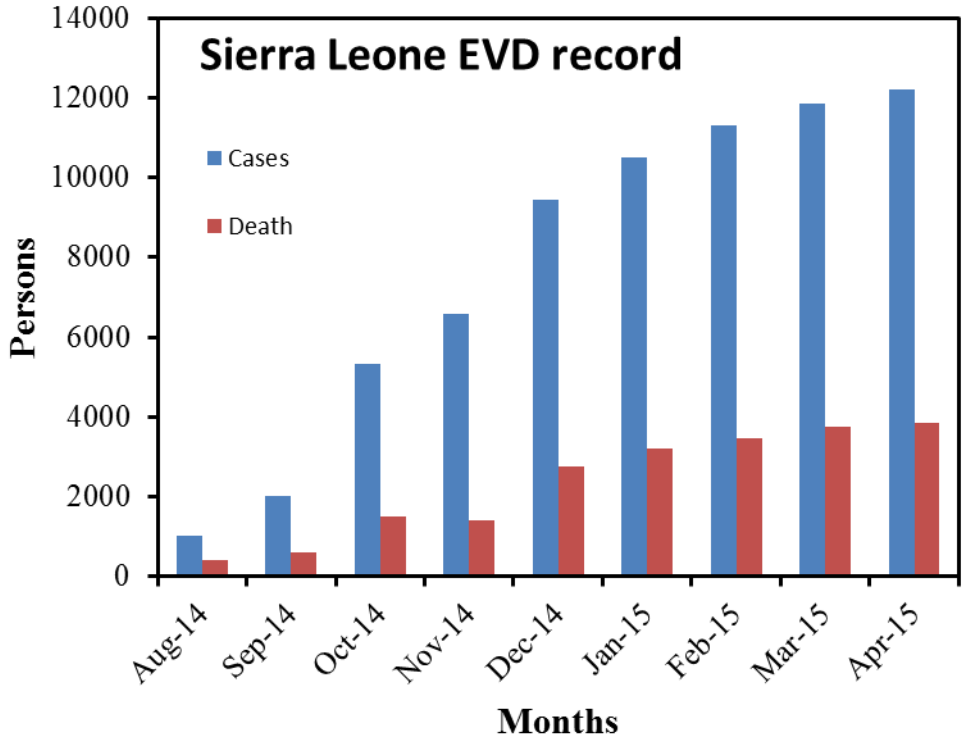

Figure 1.3 : Record of EVD in Sierra Leone.

Therefore, it has been shown in Table 1.1, Figures 1.1, 1.2, and 1.3 that a study for evident transmission of EVD is extremely important in order to find out the best ways to minimise the disaster caused by the disease. For example, in Figure 1.3 Sierra Leone has smaller number of death/cases compared to Guinea in Figure 1.1 and Liberia in Figure 1.2 because the outbreak started later which is May 2014 in Sierra Leone, December 2013 in Guinea and March 2014 in Liberia.

However the trend was on the increase for the three countries-Guinea, Liberia and Sierra Leone. Guinea was declared Ebola free on December 2015, Liberia on 9 May 2015 and Sierra Leone on November 2015. Guinea and Sierra Leone both had much larger outbreaks and it took a little longer. Liberia has been the most affected, with 4809 death, 3955 death in Sierra Leone and 2536 death in Guinea. Liberia Ebola epidemic that was declared free on 9 May re-emerged seven weeks later when a 17 year old man died from the disease and more cases was reported. The same happened in September, which is why the latest declaration of Liberia being Ebola free, while welcome one should be treated with caution (WHO, 2015a; BBC, 2016).

1.3 Background of the Research

As a result of the above mentioned problems, some researchers have carried out studies in finding possible means of eradicating EVD transmission in the affected areas. The studies can be divided into three criteria.

1.3.1 Outbreak, Transmission and Control

Siettos *et al*. (2015) developed an agent-based model to study the 2014 Ebola virus epidemic outbreak, transmission and control in Liberia and Sierra Leone. They employed equation free approach to assign estimates to key epidemiological variables. Their data was derived from WHO Ebola Data and Statistics. The proposed model was found reliable for future EVD prediction in Liberia and Sierra Leone. However, equation free algorithms are generally not accurately expressed. In addition, all agent-based approach comes with high computational cost (Kelso & Milne, 2011).

Gomes *et al*. (2014) assessed the international spreading risk associated with the 2014 West African Ebola outbreak. They used the global epidemic and mobility model to generate stochastic individual based simulation. They found out that the extension of the outbreak is more likely occurring in African countries, increasing the risk of international dissemination on a longer time scale. However, it is difficult to use the approach for complex simulation and as such Gomes *et al.* (2014) used short term data only in their study.

1.3.2 Intervention

Rivers *et al*. (2014) modelled the impact of interventions on Ebola in Sierra Leone and Liberia using ordinary differential equations and simulations. They

forecasted the progression of Ebola. The researchers also looked at the effectiveness of numerous interventions such as increased contact tracing, improved infections control practices and the use of a hypothetical pharmaceutical intervention to improve survival of hospitalized patients. They found out that there is increasingly severe epidemic with no sign of having reached the peak as at 31st December 2014. However, ordinary differential equation based models describe reality with varying accuracy (Isberg, 2012).

1.3.3 Queueing Analysis

The theory of queues and its analysis by the method of imbedded Markov chain was proposed by Kendall (1953). He used the technique to show the relationship between M/G/1 queues and; birth and death process. Subsequently, Kitaev (1993) proposed a processor-sharing model to find the relation between birth and death processes and the M/G/1 queues with processor sharing. Furthermore, Ball and Donnelly (1995) used M/G/1 theory to find total cost of the epidemic. Hernandez-Suarez *et al*. (2010) applied queueing theory to SIS (Susceptible, Infected, Susceptible) and SEIS (Susceptible, Exposed, Infected, Susceptible) epidemic models. However, their concern was on general epidemic. It is good to mention that each epidemic has its own special characteristics.

As can be seen, researchers have developed various epidemic based model of Ebola virus, mainly for Liberia and Sierra Leone. Their models were derived from the original SIR model proposed in 1932 as cited in Bashar *et al.* (2015). Some of the researchers extended the model to accommodate latent property of the Ebola virus during incubation period. But their models did not cover all the necessary EVD transmission phases.

Furthermore, the way Ebola Virus Disease invade countries differ due to socio-cultural and population behavioural differences. Hence, there is a need to study the way Ebola Virus Disease invaded different affected West African countries and measures taken to address the spread. In order to minimise the spread of the disease,

a mathematical model that can determine the real nature of EVD transmission in a better way is deemed necessary. The scenario leading to the research problem is summarized in Figure 1.4.

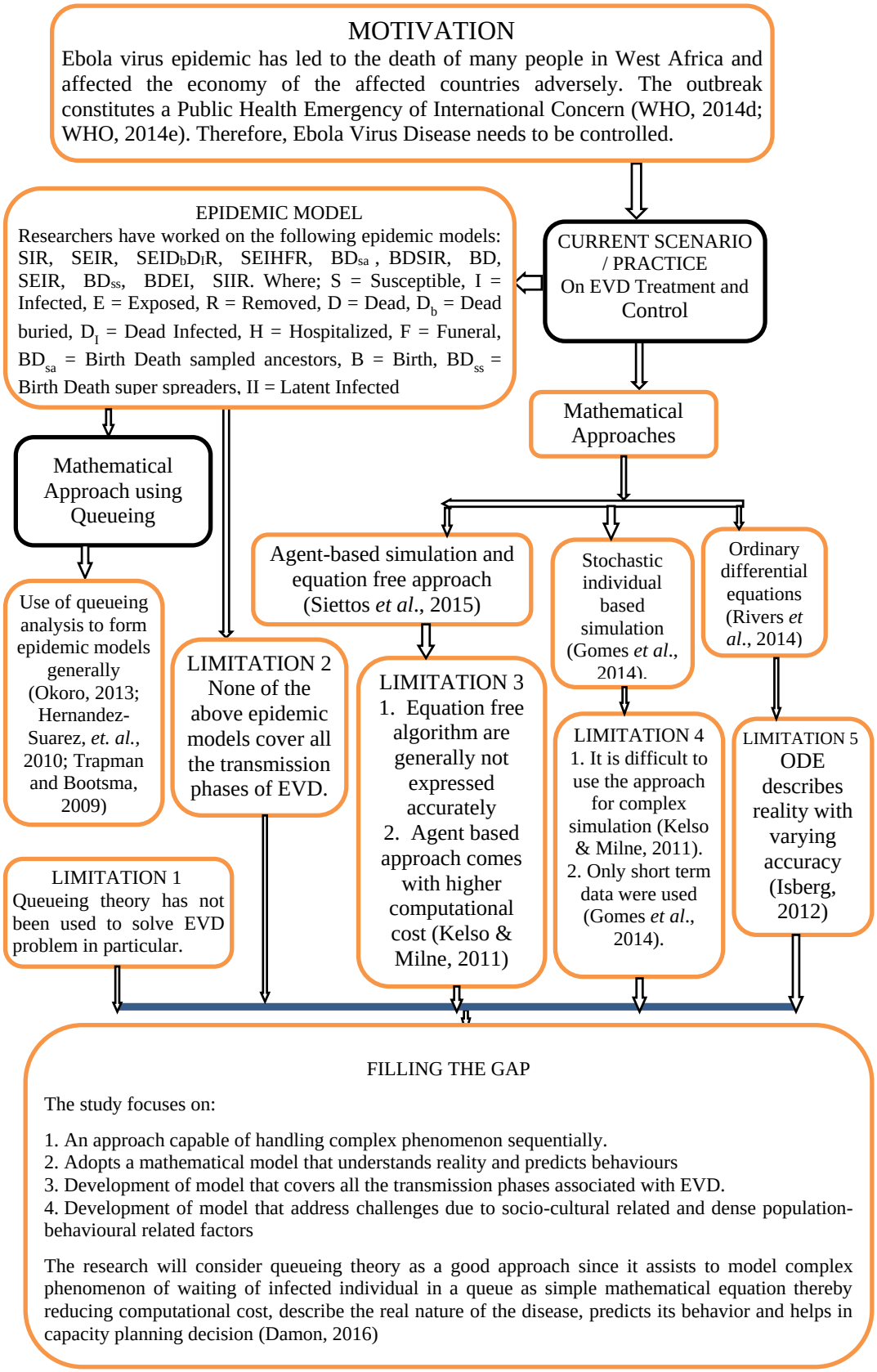

Figure 1.4 : Scenarios Leading to Research Problem

1.4 Statement of the Problem

Ebola Virus Disease is a complex and unprecedented epidemic killer disease. Recently, the disease has caused serious loss of life, waste of economy and material resources in West African nations like Nigeria, Senegal, Liberia, Sierra Leone and Guinea (WHO, 2014d). A lot of mathematical theories and models such as agent-based model, model based on ordinary differential equation for necessary assessment studies and intervention measures have been proposed by several researchers on ways to handle outbreak of the disease (Chowell and Nishiura, 2014). The researcher is of the opinion, that if EVD and its effects are not carefully studied and managed, it will claim immeasurable number of lives and properties within West Africa and her neighbours in no distant time. Therefore, a model that is capable of explaining the real nature of EVD transmission is needed.

As a result of the transmission mode and deadly nature of the disease, this study proposes an EVD transmission and control model based on queueing theory that considers all the transmission phases in order to understand the real nature of the disease and predict its behaviour. A queueing theory based compartmental model that explains individual queues of EVD and a queueing theory based network model to explain network of EVD queues in the three most affected countries are developed. Compartmental model is based on subdividing the population under consideration into various sections, while queueing network model is an interconnected collection of stations and contact network is applied. Therefore contact exist in designated stations which involves use of urban contact network such as household, shopping centre, religious centre, schools, workplaces and hospitals in a given community.

1.5 Research Questions

The problem statement raised several research challenges. These challenges will be addressed by providing answers to the following questions:

1. How would queueing theory be applied to determine Ebola Virus Disease transmission pattern?
2. How would all transmission phases and behaviours of EVD be described through developed queueing theory based SEI_LI_CDR (Susceptible, Exposed, Likely Infected, Confirmed Infected, Dead, Recovery) model?
3. How would SEI_LI_CDR based compartmental model using the queueing theory approach be obtained for EVD analysis?
4. How would SEI_LI_CDR based network model using the queueing theory approach be obtained for EVD analysis?

1.6 Objectives of the Study

The aim of the study is to develop queueing theory based EVD transmission and control model. The specific objectives are:

1. To determine Ebola Virus Disease transmission patterns and possible control measures using the basic properties of queueing theory.
2. To develop SEI_LI_CDR (Susceptible, Exposed, Likely Infected, Confirmed Infected, Dead, Recovery) model, for adequate description of all transmission phases and behaviours of EVD using queueing theory.
3. To obtain SEI_LI_CDR based compartmental model using the queueing theory approach for EVD analysis.
4. To obtain SEI_LI_CDR based network model using the queueing theory approach for EVD analysis.

1.7 Scope of the Research

Ebola Virus Disease transmission patterns and possible control measures will be determined using the basic properties of queueing theory. A three dimensional model of SEI_LI_CDR Ebola epidemic will be developed, solved and analysed to accommodate necessary EVD transmission phases. Queueing theory is used to

develop, solve and analyse the compartmental model and network model in determining the EVD transmission dynamics and control measures. The study considered the three most affected countries in West Africa (Guinea, Liberia and Sierra Leone). The EVD data documented by the World Health Organisation was trusted in finding the input parameters of the model.

1.8 Significance of the Research

Previous researchers applied models on one and two dimensional approach, on the other hand this study developed SEI_LI_CDR model which is three dimensional. Likewise other studies applied an agent-based model and equation free approach, the global epidemic and mobility model, and ordinary differential equations which cannot understand the real nature of the Ebola Virus Disease and predict its behaviour. Alternatively, this study adopted queueing theory which can make better predictions.

The real nature of the disease was understood through the use of the developed model and its behaviour was predicted. It also determined the Ebola Virus Disease transmission patterns. These findings will be of benefit to the World Health Organisation, institutions of higher learning, nations of the world especially West African nations.

The research findings will form part of essential EVD database for World Health Organisation. The organisations will refer to the information provided in the research findings in taking decisions concerning future EVD outbreak whenever it occurs.

The institutions of higher learning also will benefit from the findings of the research. Suggestions for further study provided in the research will form pedestal for future research.

Nations of the world, especially West African nations will utilize the model to combat EVD outbreak anytime it occurs. They will use the model to predict possible transmission pattern of the disease and also proffers controlling measures to address the outbreak.

1.9 Thesis Organisation

The thesis is classified into eight chapters. The organisation is as follows:

Chapter 1 consists of overview of the research problem, motivation, background of the research, statement of the problem, research questions, objectives of the study, scope of the research and significance of the research. This chapter gives understanding on the research work under consideration.

Chapter 2 provides comprehensive literature review based on the research topic. The literature reviewed covers the general overviews on Ebola Virus Disease transmission and control. The chapter further describes the brief history of Ebola Virus Disease, outlined possible effects of Ebola Virus Disease, control measures and other epidemic diseases. This chapter provides a description, summary, and critical evaluation of surveys books, scholarly article, and any other sources relevant to a particular issue about the study, area of research, or theory in relation to research problem being investigated.

Chapter 3 covers the research methodology adopted to perform this research work. The research design and procedure serves as the road map to achieve the research objectives. These include research plan, research design and procedure which is made up of ten steps-(framing of questions, structure the problem, data collection/data presentation, queueing analysis, development of Mathematical model, compartmental epidemiological model, network epidemiological model, running and testing the model, model validation and interpreting the results), operational framework as well as theoretical framework. This chapter offers the systematic, theoretical analysis of the methods applied to field of study.

Chapter 4 discusses the generation of the basic properties of queueing process from EVD data (Guinea, Liberia and Sierra Leone) using M/M/1 queueing model, test of exponentiality, queueing theory governing equation, application of queueing technique to EVD problem and analysis of Guinea, Liberia and Sierra Leone 2014 EVD outbreak. This chapter determines Ebola Virus Disease transmission patterns and possible control measures using the basic properties of queueing theory.

Chapter 5 covers the development of SEI_LI_CDR model, SIS and SEIS based Quasi-Stationary Distribution; Quasi-Stationary Distribution of the proposed SEI_LI_CDR model; SEI_LI_CDR model of the number of Exposed, Likely Infected and Confirmed Infected persons for marginal joint Quasi-Stationary Distributions; analysis of the developed SEI_LI_CDR model for adequate description of all transmission phases and behaviours of EVD using queueing theory and validation of the proposed SEI_LI_CDR model.

Chapter 6 discusses the development of the SEI_LI_CDR compartmental model; application of the SEI_LI_CDR compartmental model in EVD cases using Guinea, Liberia, and Sierra Leone as case studies; and application of queueing theory approach to SEI_LI_CDR compartmental model. This model explains traditional epidemiological analysis that is based on subdividing the population under consideration into various sections. Application of compartmental model to Ebola Virus Disease (EVD) will result in estimating of the fundamental quantity called the basic reproduction number, R_0 which is the number of secondary infections produced by a typical cases of an infection in a population that is totally Susceptible. The value above one means outbreak should flicker to large-scale epidemic. The model is validated using Chi-Square.

Chapter 7 highlights SEI_LI_CDR queueing networks, multiple channel open Jackson queueing networks, contact network, urban contact network (households, shopping centre, religious centre, schools, workplaces and hospital), transmissibility of EVD and epidemiological analysis of EVD. This model explains that contagious disease like Ebola transmits through networks, made by bodily interactions among

persons. The model is validated using urban contact network analysis, since it offers a high degree of realism.

Chapter 8 provides the summary of the research work and conclusion of the entire research work based on the results obtained in Chapters 4, 5, 6 and 7. It also discusses the contributions, limitations of the study and recommendations for future research work.

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