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**Research Report in Mathematics, Number 32, 2020**

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Submitted to the School of Mathematics in partial fulfilment for a degree in Master of Science in Social Statistics

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Master Thesis

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# Abstract

Approximating the reduction level of STH infections is important in policy and decision making nationally as well as globally.This is to ensure the control measures put in place aligns with WHO recommendation of infections control and intervention.There have been various statistical models that have been utilised in studying infectious disease pattern toward arriving in informed decisions regarding mitigation and interventionn measures.in containing the spread of STH infections. However, majority of models have not given efficient guidelines for predicting the future course of epidemic.Unlike the previous study which experienced limitation due to lack of data of at least 200 individuals,this study aimed to apply the Markov model with baseline data of at least 1500 individual who tested positive of infections. This pre-post study was used the parasitological data collected during a deworming programme for school going children aged 1-15 years conducted in Mwea between 2004 and 2007 to calculate the prediction by calculating the transition probabilities of different states of intensity following the first year of annual MDA administration and subsequent three years with treatment done once per year.

The initial study done in 2004 involved a baseline parasitological survey on STH and schistosomiasis conducted in a total of 91 schools in Mwea.41 schools were selected as follow up sample at multiple points each year for four years and examined for intestinal helminths.The sample total was 3809 children who were then treated annually with albendazole (400mg) and praziquantel with the number assumed to remain the same. Treatment coverage between the years 2004 and 2009 was reported at approximately 40,000 school going children in Mwea . During the years 2012-2013, treatment coverage for Mwea was 48,602, while in 2013-2014, the coverage was at 46,999 . The annual treatment of the school going children has continued in all the schools in the area over the years, except for year 2010 and 2011 when the program stopped temporally.

Results:At baseline, the prevalence of any STH was 44.3% . Hookworm was at 12.1%, Ascaris lumbricoides was at 2.2%, and Trichuris trichiura was at 1.4%. The male prevalence was highest with 23.7% while that of women was at 20.6% at baseline. After treatment, prevalence of STH decreased to 11.5%, (T. trichiura 0.3%,A. lumbricoides 0.6%, and hookworm 1.2%). In conclusion,we recommend the Markov chain model technique as viable for modeling the transitional changes estimates of infections outcomes at discrete time steps for future predictions.

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# Declaration and Approval

I the undersigned declare that this dissertation is my original work and to the best of my knowledge, it has not been submitted in support of an award of a degree in any other university or institution of learning.

Signature Date

Beatrice Muchiru Kinyua
Reg No. I56/10865/2018

In my capacity as a supervisor of the candidate's dissertation, I certify that this dissertation has my approval for submission.

Signature Date

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# Dedication

This project is dedicated to me.

# Acknowledgments

The success and final outcome of this project required a lot of guidance and assistance from many people and I am extremely privileged to have got this all along the completion of my project. All that I have done is only due to such supervision and assistance and I would not forget to thank them.

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Secondly I would also like to thank my colleague students as well as my family who helped me a lot in finalizing this project within the limited time frame.Special thanks to my late Mum,Ann Wanjiku,first for giving birth to me and supporting me spiritually throughout my life.You remain my role model.

My heartfelt thanks. ....

Beatrice Muchiru Kinyua

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Nairobi, 2020.

# Contents

# 1 CHAPTER 1:INTRODUCTION

## 1.1 Introduction

The aim of the study is to assess the effectiveness of treatment by estimating the reduction in levels of prevalence of Soil-transmitted Helminths infections among school based primary school children in Mwea ,Kirinyaga County,kenya. This chapter includes background of the study, statement of the problem, general objective, specific objectives of the study, justification and significance of the study.

## 1.2 Background of the problem

It is estimated over a 5.3 billion people globally have been affected by soil infectious diseases which are grouped under neglected tropical diseases.They are resulting to a large adverse social and economic impact in the poorest region of the world especially sub-Saharan Africa, the Americas, China and East Asia.. The impact,including one billion school-aged children (SAC), live in areas of endemic infection have at least one of these soil-transmitted helminth (STH) species (Pullan and Brooker, 2012).They are identified in the World Health Organization (WHO) 2020 goals for neglected tropical diseases as a target for renewed effort to upgrade their global public health burden through mass drug administration (MDA) and water and hygiene improvement. The STH are the most prevalent under neglected tropical diseases (NTDs) and are caused by the intestinal parasitic nematodes.They are; Ascaris lumbricoides, Trichuris trichiura and the hookworm species, Ancylostoma duodenale and Necator americanus.In Kenya,over 10 million Kenyans are estimated to be infected with STHs and over 12 million people living in rural endemic areas in the country are at risk of infection with these parasites. Some of the factors previously studied such as access to safe water and sanitary related practices of caregivers and children have been reported to be associated with STH infection. Periodical treatment aims to reduce and maintain the intensity of infection, and to protect infected at-risk populations from morbidity.

The World Health Organization's (WHO) policy for STH control recommends periodic on mass drug administration (MDA)in endemic areas to contain and ultimately eliminate STHs.(Strunz et al., 2014). MDA strategies identify three groups, preschool-aged children (pre-SAC), SAC, and women of childbearing age, on the basis that heavy infection in these groups will have a detrimental impact on anaemia, child growth, and development.
Over the past several years, members of the NTD Modelling Consortium have published

papers on mathematical models of the transmission dynamics, control, and elimination of STH .A good understanding of the epidemic dynamic would greatly enhance the control and prevention of infectious diseases, while dynamic model is probably one of the oldest and best-known mathematical tools to study the law of epidemic development. Dynamic health policies make real-time recommendations in response to changing population characteristics (e.g. disease prevalence, proportion of individuals that are immune), disease characteristics (e.g. infectivity, antimicrobial resistance), and resource constraints (e.g. vaccines, antimicrobial drugs, personnel, and budget) (Wallinga et al., 2010; Merl et al., 2009; Ludkovski and Niemi, 2010) Most existing approaches for identifying optimal policies for infectious disease control use mathematical or simulation models of disease spread as a basis for comparing the performance of a number of pre-determined health policies (Dimitrov et al., 2009; Goldstein et al., 2010; Halloran et al., 2008). Currently, most of mathematical and epidemiological models have been proposed in identifying the prevalence of infections.However,most of these models are not able to generalize the transition estimates of disease outcomes at discrete time steps for future predictions as well as probability distribution of individual state. The objective of this study was to model the changes in prevalence and intensity of Soil Transmitted Helminths infection in response to treatment among school aged children in Mwea, Kirinyaga county, Central Kenya to assist dynamic decision making as real-time data on disease spread become available during an epidemic.

## 1.3 Problem Statement

Global commitment focuses on school based chemotherapy programmes to implement helminth control strategies. Evidence-based programs that use high quality infection data and appropriate statisticalapproaches are essential to provide recommendations for infectious disease control. However, application of such a model requires a large amount of empirical or experimental data to ensure accuracy of the prediction requiring data for at least for two consecutive years from at least 200 individuals. Since this amount of data is not often available from STH control programmes, the possible application of the model in control programme is limited. To overcome the above limitation ,we propose in the present study,application of a Markov chain with four data sets available and collected over a 5-year period during a control programme based on annual treatment .The study is aimed in assisting in decision-making by making projections regarding important issues such as intervention-induced changes in the spread of disease and observed patterns.The justification of using the model is that we have four set of data sets including baseline to estimate the transition probabilty ,as the model is stable over time.

## 1.4 Research objectives

### 1.4.1 Main objective

To model the changes in reduction of prevalence of soil-transmitted helminths infections in response to prazequantil treatment among school based children in Mwea, Kirinyaga County, Central Kenya

### 1.4.2 Specific Objectives

- To determine the prevalence of Soil transmitted infections before treatment among school based children in Mwea
- To identify reinfection pattern of prevalence of soil transmitted helminths infections state in response to prazequantil treatment using Markov Chain model among school based children in Mwea.
- To estimate kth step of transition matrix of probability to provide prediction about the number of individuals who are expected to be infected in future discrete time.

## 1.5 Justification and Significance of the Study

Mass de-worming and targeted sanitation improvements have the power to drastically reduce STH prevalence and associated morbidity. Regular delivery of benzimidazole-based anthelminthics toschool-aged children is considered the primary mitigation and intervention strategy with, involvement of teachers and communities at large, for both implementation of school-based treatment and for increased coverage to all those at risk. Yet effective reduction in STH-related morbidity is limited by a poor understanding of reinfection patterns in current infection risk and the future state of infection after treatment which may stem from untargeted mass drug roll-outs This modelling technique aims at predicting the expected changes in prevalence of any STH infections after treatment as a result of transitions between different states of intensity of infection defined by WHO which can be estimated using four data sets for future predictions.

## 1.6 Outline

The subsequent section of this project are organized as follows;chapter two ,literature review on reduction measures of STH;chapter three,describes the study methodology;chapter four provides the results and data analysis ;chapter five is on study conclusion and recommendations.

# 2 CHAPTER TWO:LITERATURE REVIEW

## 2.1 Introduction

Models of STH transmission under repeated rounds of community-wide MDA suggest that transmission interruption in a variety of transmission settings may be possible through chemotherapy alone .This chapter provides the review of works done by authors and other researchers that relate to the topic under the study.

## 2.2 Soil Transmitted Helminths Infections

Soil-transmitted helminthiasis (STH) is one of the commonest neglected tropical diseases (NTDs) worldwide and remains a public health problem in poor communities with enormous consequences for development (Tchuem Tchuenté et al. 2013). The four most common STHs are roundworm (Ascaris lumbricoides), whipworm (Trichuris trichiura), and the anthropophilic hookworms (Necator americanus and Ancylostoma duodenale). Recent estimates suggest that A. lumbricoides infects 1.221 billion people, T. trichiura 795 million, and hookworms 740 million (de Silva and others 2003) Anaemia is one of the most common side effects of infection with STH or schistosomes, due to blood loss in the intestine or urinary tract. Moreover there is a direct association between the intensity of STH infection, blood loss and consequent anaemia, especially for hookworms (Bundy et al., 1995;Chan, Medley, Jamison Bundy, 1994; Larocque, Casapia, Gotuzzo Gyorkos, 2005). Since the majority of those treated in MDA programs will either be uninfected or have only light intensity infections rather than the moderate to severe infections thought to account for the bulk of STH morbidity (De Silva et al. 2015, Montresor et al.2015), statistical power to pick up population-wide effects is typically limited (Bundy, Walson and Watkins, 2013). The morbidity caused by STH is directly related to the number of worms (intensity of infection) and the duration of infection. Infections of moderate to heavy intensity are mainly responsible for the morbidity due to STH. Infections by worms affect the nutritional status of children through various mechanisms, such as feeding on host tissue and interfering with absorption of nutrients (Hall, Hewitt et al . 2008).

## 2.3 Soil-transmitted helminth treatment

Regular treatment, despite re-infection, is able to control morbidity in high transmission areas (Savioli et al., 2002) because, even if prevalence of infection remains high, moderate to heavy infections (responsible for morbidity) decline over time. The main control strategies for STH infections are regular periodic MDA targeting pre-SAC and SAC using

anthelmintics (predominantly albendazole and mebendazole). STH control programmes, which originally used mobile teams to distribute the drugs, are now predominantly centred around school-based delivery systems (WHO, 2002; Hotez et al., 2006). There has been a growing recognition of the disease burden in and potential benefit of treating pre-SAC (Albonico et al., 2008) and more broadly the whole community especially for the control of hookworm with its predominance in adult age groups (Anderson et al., 2015). Although both albendazole and mebendazole have a good efficacy against A. lumbricoides, mebendazole fails to effectively clear hookworm infections, and neither drug has an adequate efficacy against T. trichiura (Keiser and Utzinger, 2008; Vercruysse et al., 2011) e with cure rates of 28 and 36%, respectively. Aside from SAC, WHO also recommends the treatment of pre-SAC, women of childbearing age, and adults in certain high-risk occupations (such as tea-pickers and miners) (WHO, 2006). The breakpoint of transmission defines the moment at which reproduction cannot occur any longer and the helminth population collapses without further treatment of remaining infections. Mathematical models can simulate this behavior and investigate the impact of MDA on the likelihood of transmission interruption.

## 2.4 Mathematical Model

Deterministic models have commonly been used as tools for studying epidemic behavior (Anderson and May, 1992; Hethcote, 2000).They have been very useful in understanding the dynamics of infectious disease, estimating important epidemiologic parameters (e.g. basic reproductive numbers), and determining targets for disease control (e.g. critical proportions of the population to immunize). Model-free approaches calculate ERRs directly from data using simple arithmetic operations, without invocation of distributional (modelling) assumptions. Many stochastic models of infectious diseases utilize non-negative integer-valued Markov processes in continuous or discrete time. In these Markov models, the state of the process is defined as the number of individuals that are susceptible, infected, etc. Mathematical models can be particularly useful tools for investigating the cost-effectiveness of interventions because models can be used to make projections over long time horizons and can, therefore, capture the long-term benefits of interventions. In a recent systematic review on this area (Turner et al., 2015), only two studies (Guyatt et al., 1993, 1995) were identified that investigated the cost effectiveness of alternative STH treatment strategies using a dynamic model.

## 2.5 Mapping Modelling

Mapping disease transmission risk is crucial in public health for evidence based decision-making as well as understanding the disease occurrence linking disease cases with environmental features in spatial perspective (Koch and Denike, 2009). Geospatial analyses of recent large-scale epidemiological studies of STH prevalence11 show that prevalence heterogeneity is considerable within PC implementation units. Understanding and an-

ticipating the “where” of an outbreak may be a valuable tool for effective public health interventions (Frieden, 2013) as well as for animal health. Thus, disease mapping is key in understanding and anticipating disease occurrence and generating visual tools for decision makers. In addition to the study of parasites, epidemiologists could be interested also in the vectors and reservoirs (Estrada-Peña et al., 2014) to understand how the parasites are dispersed and maintained in the landscape, respectively. Earlier studies have shown that the prevalence of STHs may vary considerably between countries, and also between rural and urban communities. Furthermore, since treatment efficacy and reinfection rates are different for each species of STH, in regions with ongoing MDA programs, this would also influence the prevalence and species distribution.In the past 20 years, progress in geographical information system (GIS) and remote sensing techniques, coupled with spatial modelling, enabled a better understanding of helminth ecology and mapping at high spatial resolution.

Ecological niche and biology-driven models have been used in assessing the distribution of helminth infections . Bayesian geostatistical models offer a robust methodology for identifying determinants of the disease distribution and for predicting infection risk and burden at high spatial scales . These models have been widely used in assessing the relationship between helminth infection with demographic, environmental, and socioeconomic predictors, at sub-national , national, or regional scales. In the Americas, high resolution, geostatistical, model-based risk estimates have been obtained for the whole continent as well as for Brazil. A key issue in geostatistical modelling is the selection of the predictors. Most of the variable selection methods in geostatistical applications rely on standard methods, such as stepwise regression or bivariate associations that are appropriate for non-spatial data. However, ignoring spatial correlation leads to incorrect estimates of the statistical significance of the predictors included in the model. Furthermore, biotic interactions are important only when studying diseases at very fine spatial scales such as when studying transmission dynamics within a population (Peterson et al., 2011). This series of evidence and assumptions supports the idea of mapping diseases based on climatic variables or other environmental features.

## 2.6 Other Preventive Measures

### 2.6.1 Sanitation and Hygiene

Sustainable long-term STH control is expected to require improved access to water, sanitation, and hygiene(WASH) . Despite 15 years of concerted efforts under the framework established by the Millennium Development Goals (MDGs), the global sanitation crisis persists. Over 2.5 billion people still lack access to improved sanitation facilities, and 1 billion people practice open defecation (OD) in fields, bushes, or other open spaces (WHO and UNICEF, 2014). Although global sanitation targets under the MDGs are included in the environmental sustainability goals (Goal 7), a key reason for increasing sanitation coverage is to reduce exposure to human fecal pathogens, reducing enteric disease burden among children under five (Ahmed et al., 2012; Cairncross et al., 2010; Wolf et al., 2014) and improving child growth and development (Dangour et al., 2013; Spears et al., 2013). The integration of STH control with the provision of water, sanitation and hygiene education interventions (WASH) is thus been promoted as a complementary strategy for the elimination of STH (Freeman et al. 2013). WASH resource programming includes access to safe water, improved sanitation and good hygiene practices and education (Freeman et al. 2013).
Sanitation is composed by two elements which are complementary: “hardware” such as toilets, latrines, sewage treatments, and “software” such as personal hygiene and legislation. Because STHs are transmitted through poor sanitation and hygiene, school-aged children are typically at increased risk resulting in high prevalence and intensity of infection due to high level of exposure (Montresor et al., 1998; WHO, 2002). In the Americas, for example, there has been a precipitous decline in prevalence and in absolute numbers since the 1960s, a change largely attributable to national treatment programmes coincidental with social and economic development which have brought about improved access to clean water and proper sanitation (PAHO, 2000; Ehrenberg et al. 2003). By reducing contact with fecally contaminated soil or water, improvements in sanitation and access to clean water decrease transmission of STH infections(Corrales et al., 2006; Mara et al., 2010; Soares Magalhaes et al., 2011; WHO, 2006; Ziegelbauer et al., 2012).

### 2.6.2 Health Education

Health awareness is usually increased when communication strategies of proven efficacy are adopted (Kinzie, 2005). Lack of knowledge about disease transmission and prevention can greatly contribute to low uptake of health care interventions. Studies have shown that respondents who are knowledgeable about the risks to health and methods of preventing parasitic infections were more likely to comply with mass treatment. Health education aims to increase health and hygiene awareness and to change health behaviour in the population. These findings highlight the fact that the public health implications of STH infection are much greater than previously realized and that STH infection may in-

directly contribute to significant mortality worldwide (DCPP,2008). By increasing health education, creating awareness and addressing people's behaviours, health and hygiene promotion reduce transmission and reinfection (Aiello et al., 2008; Asaolu and Ofoezie, 2003; Ekpo et al., 2008; Fewtrell et al., 2005; WHO, 2006).

## 2.7 Research Gap

Eliminating soil-transmitted helminthiasis as a public health problem has to go beyond preventive chemotherapy for SAC alone, as other groups at risk also serve as a reservoir of infection, e.g., hookworm infections frequently predominate in adult populations. Coverage of preventive chemotherapy for PSAC continues to lag behind the coverage for SAC; to date, there is no regular preventive chemotherapy program against soil-transmitted helminthiasis for community especially non-school going children in addition to Inadequate information about population dynamics and rumors about side effects of MDA drugs adversely affected the compliance of the intervention.

# 3 CHAPTER THREE:METHODOLOGY

## 3.1 Introduction

This chapter will include: research design, selection and description of the study area, study population, data collection method and model formulation.

## 3.2 Research design

The study used Transition Probabilty Matrix Markov in modelling the changes in reduction of STH infections after treatment among school based children in Mwea. For each worm , four states of intensity infection were included: none, light, moderatem and heavy. Kato-Katz was the only method used to collect parasitological data which was recorded in excel for further analysis.

## 3.3 Description of the study area

This study was conducted in the Mwea Division of Kirinyaga South district in Kirinyaga County, central Kenya (00°4054S, 037°2036E) and has a population of 237,382 (census, 2019). Mwea is situated in the lower altitude zone (approx. 1150mASL) of the district in an expansive flat land mainly characterized by black cotton and red volcanic soils. The main agricultural activity is rice farming which is grown under flood irrigation. The specific area (survey area) of study was Mwea Tebere Rice Irrigation,largely rural population, which comprises Thiba,Mutithi and Murinduko educational zones.

## 3.4 Study Population

The study involved all the school based children from Nursery to standard 8 who were included in the initial treatment in 2003. There were 92 primary schools both public and private, out of which 41 schools were sampled for follow up. The sample set for this study was N= 3809 which is assumed to stay constant over 4 years on population level.

## 3.5 Data Collection

Treatment was administered to a total of 4000 pupils in one day. Overnight Stool Samples were collected in laboratory test tubes in the morning before classes . Each child was provided with a stool sample collection test tube with unique identifiers to take home and bring first morning stool as per instructions from the ESACIPAC team and the assistance

of the teacher.
The specimen were examined at Kimbimbi Hospital with the assistance of the Vector Born Laboratory staff.No questionnaire were introduced to the children but the head teachers and the class teachers were important to provide some health related issues about the school but without questionnaires

## 3.6 Model formulation

This part explains the Markov Chain model which will be used in this project as well as estimating the transition probability of the infectious states for nth step

### 3.6.1 Discrete Time Markov Chain Model

Definition:A Markov chain is essentially a conditional probability process $X0, X1, X2, ...$ where $X_t$ is the state at time $t.X_{t+1}$ depends only on $X_t$ but it does not depend upon $X_{t1}, ..., X_1, X_0$.
This is represented mathematically as:

$$P(X_{t+1} = s|X_t = s_t, X_{t1} = s_{t1}, ..., X_0 = s_0) = P(X_{t+1} = s|X_t = s_t), \quad \textbf{(1)}$$

for all $t = 1, 2, 3, ...$ and for all states $s_0, s_1, ..., s_t, s$.

### 3.6.2 Markov Chain in relation to Infection dynamics

The study will adopt the work of Arnoldo and Bernd who modeled Infectious diseases using Markov chain with four possible states. Their work has been modified into five possible states to suit the purpose of this study. Arnoldo and Bernd (2015) modeled infectious diseases with four possible states.This study will assume that modeling intensity of infectious diseases involves four possible states.The possible states are Susceptible (CS1), light Intensity (CS2), moderate intensity (CS3), heavy intensity (CS3).

Consider four discrete states: Susceptible (0), light Intensity (1), moderate intensity (2), heavy intensity (3) states. If$(X_i, i = 0, 1, 2)$ represent the number of individuals at any state from the underlying infection at any time t.
Thus, the first-order time-homogeneous Markov dependency can statistically be modeled as ;

$$P(X_n = i_n|X_{n-1} = i_1, X_0 = i_0) = P(X_n = i_n|X_{n-1} = i_{n-1}) \quad \textbf{(2)}$$

In mathematical terms, the baseline prevalence of an STH infection can be described by 4 condition states (CS), and the changes in the prevalence of infection occurring every year

as a result of a treatment intervention can be represented by the transition probability (TP) through discrete condition states $i\varepsilon I, I = 0,1,2,3$, where 0,1,2 and 3 represent states of no infection, light, moderate and heavy intensity infections, respectively.
A symmetrical $IxI$ matrix is produced for a time period of 1 year, called the TP matrix (P) and can be described in cardinal form as:

$$P = \begin{bmatrix} p_{00} & p_{01} & \cdots & p_{03} \\ p_{10} & p_{11} & \cdots & p_{13} \\ : & : & \ldots & : \\ p_{I0} & p_{i1} & \cdots & p_{II} \end{bmatrix}, \tag{3}$$

where $p_{ij}$ is the probability that an individual will move from state i to state j after discrete period interval.
In the transition matrix P:

1.The transition matrix P must list all possible states in the state space S.
2.P is a square matrix $(N)$, because $X_{t+1}$ and $X_t$ both take values in the same state space S (of size N).
3.The rows of P should each sum to 1:

$$\sum_{i=1}^{N} p_{ij} = \sum_{i=1}^{N} \mathbb{P}(X_{t+1} = j | X_t = i) = 1 \tag{4}$$

This simply states that $X_{t+1}$ must take one of the listed values.
4.The columns of P do not in general sum to 1.

The state of a Markov chain at time $t$ is the value of $X_t$ while the state space of a Markov chain, S, is the set of values that each $X_t$ can take.

### 3.6.3 Definition of States:

State 0(CS1) : it comprised of individuals who have not been identified with infections
State 1(CS2) : it comprised of infected individuals with light intensity infection
State 2(CS3) : it comprised of infected individuals with moderate intensity infection
State 3(CS4) : it comprised of infected individuals with heavy intensity infection.

### 3.6.4 Parameters of the Markov Chain (Probabilities of Transition)

$P_{ii}$ : probability of remaining in a state i
$P_{ij}$ : transition probability from state $i$ to state $j$, i$\neq j$

### 3.6.5 Model Assumptions

•It assumes stationarity based on.
•The intervention did not reduce significantly the faecal contamination of soil in short term.
•The current state of an individual is dependent only on the state of the individuals at the previous time step.
•No individual at the removed state can be susceptible or infected.
•The population is constant throughout the observed time of the disease outbreak.

## 3.7 Estimation of Transition Probabilities

TPMS were measured from baseline data and three-year follow-up data.
Consider four discrete states: Susceptible (0), light Intensity (1), moderate intensity (2), heavy intensity (3) states.The changes between these four CS are defined as transition probabilities (TP).
If$(X_i, i = 0,1,2,3)$ represent the number of individuals at any state from the underlying infection at any time t.
Then one year transition probability is estimated using following equation.

$$p_{ij} = \frac{n_{ij}}{\sum_{k=1}^{i} n_{ik}} \tag{5}$$

where,$n_{ij}$ is the number of individuals who transition from state $i$ to state $j$ in one cycle.

The probability that a susceptible individual first becomes infected after two time steps is simply the probability that it remained susceptible for exactly one time step and then became infected during the next time step:

$$Pr(X_{n+2} = 1, X_{n+1} = 0 | X_n = 0) = p_{00}p_{01} \tag{6}$$

Consequently, the probability that a susceptible individual becomes infected for the first time between the $m1$ and m time steps would be:

$$f_{01}^{(m)} = Pr(X_{n+m} = 1, X_{n+m-1}, ..., X_{n+1} = 0 | X_n = 0) = p_{00}^{m-1} p_{01} \tag{7}$$

for $1 \leqslant m < \infty$,
The same logic follows for calculating the probability that an infected individual first

recovers between the $m1$ and m time steps:

$$f_{10}^{(m)} = Pr(X_{n+m} = 0, X_{n+m-1} = 1, ..., X_{n+1} = 1 | X_n = 1) = p_{11}^{m-1} p_{10} \tag{8}$$

As $m$ gets large ($m \to \infty$), the probability of initial infection (or recovery) approaches zero, which implies that the total probability of becoming infected (or recovering) approaches a limit (a value between 0% and 100%).
In our four-state model, the overall probability that an individual transitions from state i to j (as $m \to \infty$) has a simple closed form solution:

$$Pr(i \to j) = \frac{p_{ij}}{1 - p_{ii}} \tag{9}$$

### 3.7.1 Estimation Method

Using the maximum-likelihood estimation (MLE) for each infection,the likelihood of the transition probability, $p_{ij}$, is that of a binomial model:

$$L(p_{ij}|N, y) = \binom{N_i}{x_{ij}} p_{ij}^{x_{ij}} (1 - p_{ij})^{N_i - x_{ij}} \tag{10}$$

given the data (N and x), where $N_i$ is the number of observed transitions that start in state $i$ and $x_{ij}$ is the number of transitions from i specifically to j.

And,

$$\sum_i p_{ij} = 1 \tag{11}$$

Generally, if $X(0) = x_0, X(1) = x_1, ..., X(n) = x_n$ are independent random variables and have a joint density function of $P[X(0), X(1), ..., X(n)|\theta]$, the likelihood function is a function of $\theta$.
It is given by,

$$L(\theta) = L(\theta|x_0, x_1, ..., x_n) = p(x_0, x_1, ..., x_n|\theta) = \prod_{i=0}^{n} p(x_i|\theta). \tag{12}$$

For some observed data,$x_n' = (x_0, x_1, ..., x_n)$, the likelihood function of the Markov process is the product of the transition conditional probabilities and is given by;

$$L(\theta) = L(\theta|x_n') = p(x_0) \prod_{i=1}^{n} p(x_i|x_{i-1} = p(x_0) \prod_{i=0}^{n} \prod_{i=0}^{n} p_{j \leftarrow i}^{n_{ji}} \tag{13}$$

where $n_{ji}$ is the count of transitions from $i$ to $j$.

### 3.7.2 Estimating $P^n$ Transition Matrix

The n -step transition probability for a Markov chain is;

$$p_{ij}^n = Pr(X_{k+1} = j | X_k = 1) \tag{14}$$

Given the one-step transition probabilities, it is straightforward to calculate higher order transition probabilities using the following result.

$$P_{ij}^n = \sum p_{i,k}^m p_{k,j}^{n-m} \tag{15}$$

for m= 0,1,2,... n (**Chapman–Kolmogorov Equation**)

**Proof**
Using the principle of total probability

$$Pr(X_{l+n} = j | X_l = i) = \sum_k Pr(X_{l+n} = j | X_l = k, X_{l+m} = k) Pr(X_{l+m} = k | X_k = i) \tag{16}$$

Using the Markov property,the expression reduces to the desired form

$$Pr(X_{l+n} = j | X_l = i) = \sum_k Pr(X_{l+n} = j | X_{l+m} = k) Pr(X_{l+m} = k | X_k = i) \tag{17}$$

This result can be written in a more compact form using transition probability matrices. It is easily seen that the **Chapman–Kolmogorov** equations can be written in terms of the n -step transition probability matrices as;

$$P^n = P^m P^{n-m} \tag{18}$$

Then, noting that $P^{(1)} = P$, it follows that $P^{(2)} = p^{(1)} p^{(1)} = p^{(2)}$, and using induction, it is established that

$$P^{(n)} = P^n \tag{19}$$

The above is obtained through matrix multiplication.
That is,we can examine the n-step transition probabilities of the Markov process by raising the matrix to $n^{th} power$,$P^n$ where the probability that a process initially in state i will be in state j after exactly n time steps is simply the elements of matrix $P^n$, denoted as $p_{ij}^n$

# 4 CHAPTER FOUR:DATA ANALYSIS AND RESULTS

## 4.1 Data

The sample set for this study was N= 3809 which is assumed to stay constant over 4 years on population level. The STH prevalence before the introduction of MDA in 2004 (baseline prevalence) was obtained that determined the total STH prevalence for each worm type in 4000 SAC. The number of eggs per gram of faeces was calculated by adding the egg counts in all fields together then multiply the total by 24 to give the EPG of faeces.We then subdivided this into no infection, light, moderate and heavy infection intensity according to the WHO classification listed in Table 1(saved in graphics) and tabulated prevalence by STH type and severity as shown in Table 1.

Table 1:WHO classification table for STH Intensity

| | Condition State 1 | Condition State 2 | Condition State 3 | Condition State 4 |
|---|---|---|---|---|
| STH species | Zero eggs (epg) | Infections of light intensity (epg) | Infections of moderate intensity (epg) | Infections of heavy intensity (epg) |
| *A. lumbricoides* | 0 | 1–4999 | 5000–49 999 | > 50 000 |
| *T. trichiura* | 0 | 1–999 | 1000–9999 | > 10 000 |
| Hookworms | 0 | 1–1999 | 2000–3999 | > 4000 |

epg = eggs per gram of faeces.

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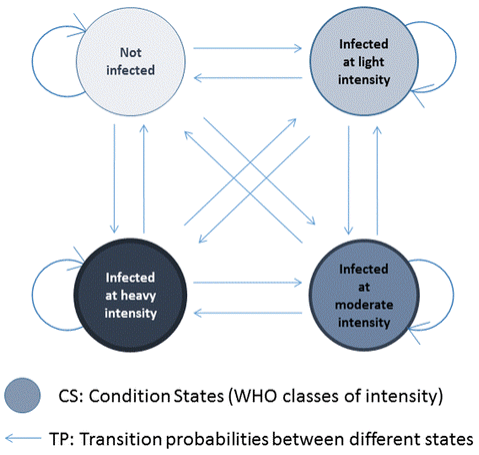
Transition diagram illustrating a Markov transition probability matrix



## 4.2 Prevalence and Observed Reduction of Infections over 4 years

### 4.2.1 Analysis

The results of the soil transmitted helminth survey at baseline was as follows, 461(12.1%) individuals were positive for hookworms, of whom 231 (6.1%) were positive with low intensity, 83 (2.1%) with moderate intensity and 148(3.9%) with high intensity. For T. trichiura, 54/3809(1.4%) were positive of whom 18(0.4%) with low intensity and 33 (0.9%) with moderate intensity and 3(0.1%) with heavy intensity. For A. lumbricoides, 85/3809 (2.2%) were positive of whom 45 (1.2%) with light intensity, 23 (0.6%) with moderate intensity and 17(0.4%) with heavy intensity (Table 3). In total, 294/1687(17%) individuals had a soil helminth infection of light intensity, 139/1687 (8%) with infection of moderate intensity, and 168/1687(10%) with infection of heavy intensity. During the administration period of mass drug administration, the prevalence of any STH infection was reduced from 44.3% (sample positive 1687 individuals) to 15.1% after 1year (sample positive 577 individuals),to 13.9% after 24months (sample positive 529 individuals),13.4% after 36 months (sample positive 510 individuals)(Table 3)

### 4.2.2 Results

Table 2.Soil-transmitted helminthiases (STH) prevalence S.Mansoni subdivided in light, moderate and heavy infection before mebendazole MDA

| | Total Prevalence | | Light Infection | | Moderate Infection | | Heavy Infection | |
|---|---|---|---|---|---|---|---|---|
| | Positive | % | Positive | % | Positive | % | Positive | % |
| Hookworm | 461 | 12.1 | 231 | 13.7 | 83 | 4.9 | 148 | 8.7 |
| A.Lumbricoides | 84 | 2.2 | 45 | 2.7 | 23 | 1.4 | 17 | 1 |
| T.Trichiura | 54 | 1.4 | 18 | 1.1 | 33 | 2 | 3 | 0.2 |
| S.Mansoni | 1371 | 36 | 0 | 0 | 0 | 0 | 1371 | 36 |

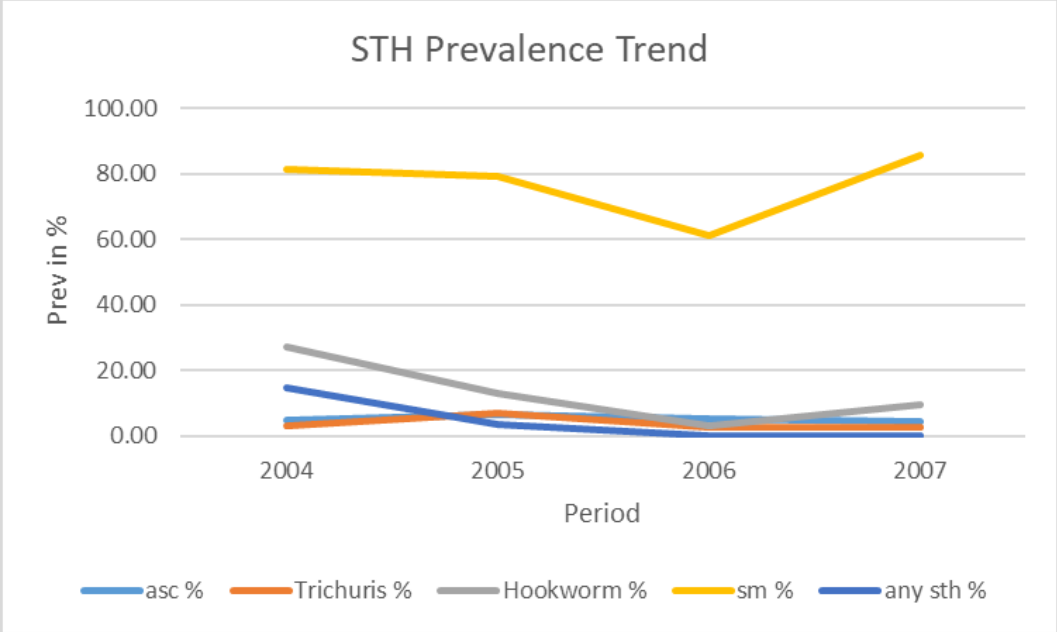
Table 3: The prevalence of STH of four years mebendazole MDA compared to the baseline.

| Deworming | Positive STH(%) | A.Lubricoides(%) | T.Trichiura(%) | Hookworm(%) | S.Mansoni(% |
|---|---|---|---|---|---|
| Before | 1687(44.3) | 84(2.2) | 54(1.4) | 461(12.1) | 1371(36) |
| Post-2005 | 577(15.1) | 38(1) | 41(1.1) | 76(2) | 422(11.1) |
| Post-2006 | 529(13.9) | 27(0.7) | 13(0.3) | 34(0.9) | 455(12) |
| Post-2007 | 510(13.4) | 23(0.6) | 14(0.3) | 49(1.3) | 424(11.1) |

Table 4:The prevalence of STH based on intensity of infection pre(2004) and post MDA(2007).

| Infection Intensity | **A.Lubricoides(%):BP=2.2** | | **T.Trichiura(%):BP=1.4** | | **Hookworm(%):BP=12.1** | |
|---|---|---|---|---|---|---|
| | Before | After | Before | After | Before | After |
| Light | 45(1.2) | 18(3.5) | 18(0.4) | 14(0.4) | 231(6.1) | 49(1.3) |
| Moderate | 23(0.6) | 5(1) | 33(0.9) | - | 83(2.1) | - |
| Heavy | 17(0.4) | - | 3(0.1) | - | 148(3.9) | - |

Graph 1: STH Prevalence as a result of treatment over 4 years.




## 4.3 Transition probabilities Matrix

The model,Transition Probability Matrix Set(TPMS) was adopted to represent the treatment of 3809 school-aged children with mebendazole every 12 months.The worm prevalence was calculated for each year and split up in no infection, light, moderate and heavy infection intensity.

### 4.3.1 Analysis

Generally,the infections after treatment decreased over three years, while the infection for the *hookworm* and *T.Trichuris* showed some slight increase in infection for the fouth year. Overall reduction was 1177(69.7%) for the thre worms combined attributed to 61(72.6% reduction) for *A.lumbricoides* , 40(74.1% reduction) for *T.trichiura* ,412(89.3% reduction ) for *hookworm* compared to the initial baseline values before treatment. The treatment

effect was the most pronounced in the first year. After an initial drop in disability the values stabilized over time.The prevalence of heavy infection in all three worms reached 0% after one year of treatment.

### 4.3.2 Results

Table 5.Distribution in regards to intensity of infection over four years.

| | | ***Hookworm(%)*** | ***T.Trichuris(%)*** | ***A.Lumbricoides(%)*** | ***S.Mansoni(%)*** |
|---|---|---|---|---|---|
| **Baseline** | **Light** | 231(6.1) | 18(0.5) | 45(1.2) | 0 |
| | **Moderate** | 83(2.2) | 33(0.8) | 23(0.6) | 0 |
| | **Heavy** | 148(3.9) | 3(0.1) | 17(0.4) | 1372(36) |
| | **Total** | **462(12.2)** | **54(1.4)** | **85(2.2)** | **1372(36)** |
| **2005** | **Light** | 75(2) | 41(1.1) | 30(0.8) | 314(8.2) |
| | **Moderate** | 1(0) | 0 | 8(0.2) | 114(3) |
| | **Heavy** | 0 | 0 | 0 | 28(0.7) |
| | **Total** | **76(2)** | **41(1.1)** | **38(1)** | **456(11.9)** |
| **2006** | **Light** | 32(0.8) | 12(0.3) | 23(0.6) | 294(7.7) |
| | **Moderate** | 0 | 0 | 6(0.1) | 103(2.7) |
| | **Heavy** | 0 | 0 | 0 | 53(1.4) |
| | **Total** | **32(0.8)** | **12(0.3)** | **29(0.7)** | **450(11.8)** |
| **2007** | **Light** | 49(1.2) | 14(0.3) | 18(0.5) | 295(7.7) |
| | **Moderate** | 0 | 0 | 5(0.1) | 96(2.5) |
| | **Heavy** | 0 | 0 | 0 | 47(1.2) |
| | **Total** | **49(1.2)** | **14(0.3)** | **23(0.6)** | **438(11.4)** |

The transition probability matrices for the three worms infections are presented as;

$$\mathrm{P}_{Hk} = \begin{pmatrix} 0.88 & 0.06 & 0.02 & 0.04 \\ 0.98 & 0.02 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \end{pmatrix}, P_{Tt} = \begin{pmatrix} 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}, P_{Al} = \begin{pmatrix} 0.98 & 0.01 & 0.01 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}$$

## 4.4 Estimating the $P^n$ Transition Probability Matrix

Recall, the Chapman–Kolmogorov equations 19:ie $P^{(1)} = P$, it follows that $P^{(2)} = P^{(1)}P^{(1)} = P^{(2)}$ , and by induction, $P^{(n)} = P^n$

### 4.4.1 Results

Then,it follows for infections;

**Hookworm**

$$\mathrm{P}_{Hk}^{(1)} = \begin{pmatrix} 0.88 & 0.06 & 0.02 & 0.04 \\ 0.98 & 0.02 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \end{pmatrix}$$

$$\mathrm{P}_{Hk}^{(2)} = (P_{Hk}^{(1)}) \times (P_{Hk}^{(1)})$$

$$\mathrm{P}_{Hk}^{(2)} = \begin{pmatrix} 0.88 & 0.06 & 0.02 & 0.04 \\ 0.98 & 0.02 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \end{pmatrix} \times \begin{pmatrix} 0.88 & 0.06 & 0.02 & 0.04 \\ 0.98 & 0.02 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \end{pmatrix} = \begin{pmatrix} 0.89 & 0.06 & 0.02 & 0.03 \\ 0.88 & 0.06 & 0.02 & 0.04 \\ 0.88 & 0.06 & 0.02 & 0.04 \\ 0.88 & 0.06 & 0.02 & 0.04 \end{pmatrix}$$

$The same logic follow for \mathrm{P}_{Hk}^{(3)}$ and $P_{Hk}^{(4)}$
i.e,

$$\mathrm{P}_{Hk}^{(3)} = \begin{pmatrix} 0.89 & 0.06 & 0.02 & 0.03 \\ 0.89 & 0.06 & 0.02 & 0.03 \\ 0.89 & 0.06 & 0.02 & 0.03 \\ 0.89 & 0.06 & 0.02 & 0.03 \end{pmatrix}, P_{Hk}^{(4)} = \begin{pmatrix} 0.89 & 0.06 & 0.02 & 0.03 \\ 0.89 & 0.06 & 0.02 & 0.03 \\ 0.89 & 0.06 & 0.02 & 0.03 \\ 0.89 & 0.06 & 0.02 & 0.03 \end{pmatrix}$$

In the long run,with large $n$, the system approaches its steady state of equilibirium. Hence, by matrix multiplication, the $n$-step transition probability matrix would be arrived by raising the matrix $P$ to nth power.

$$\mathrm{P}_{Hk}^{(n)} = \begin{pmatrix} 0.88 & 0.06 & 0.02 & 0.04 \\ 0.98 & 0.02 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \end{pmatrix}^{n}$$

**T.Trichuris**

The $n^{th}$ transition probability matrix for T.Trichuris presented below;

$$\mathrm{P}_{Tt}^{(1)} = \begin{pmatrix} 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}, P_{Tt}^{(2)} = \begin{pmatrix} 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0 & 0.01 & 0 \end{pmatrix}, P_{Tt}^{(3)} = \begin{pmatrix} 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0 & 0.01 & 0 \end{pmatrix}.$$

$$Consequently, P_{Tt}^{(n)} = \begin{pmatrix} 0.99 & 0 & 0.01 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}^n$$

**A.Lumbricoides**

The $n^{th}$ transition probability matrix for A.Lubricoides is presented below;

$$\mathrm{P}_{Al}^{(1)} = \begin{pmatrix} 0.98 & 0.01 & 0.01 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}, P_{Al}^{(2)} = \begin{pmatrix} 0.98 & 0.01 & 0.01 & 0 \\ 0.98 & 0.01 & 0.01 & 0 \\ 0.98 & 0.01 & 0.01 & 0 \\ 0.98 & 0.01 & 0.01 & 0 \end{pmatrix}, P_{Al}^{(3)} = \begin{pmatrix} 0.98 & 0.01 & 0.01 & 0 \\ 0.98 & 0.01 & 0.01 & 0 \\ 0.98 & 0.01 & 0.01 & 0 \\ 0.98 & 0.01 & 0.01 & 0 \end{pmatrix}$$

$$Consequently, P_{Al}^{(n)} = \begin{pmatrix} 0.98 & 0.01 & 0.01 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 0.99 & 0.01 & 0 & 0 \\ 1 & 0 & 0 & 0 \end{pmatrix}^n$$

Let $P$ be the transition matrix of a Markov chain, and let $U$ be the probability vector which represents the starting distribution.
Then the probability that the chain is in state $s_i$ after $n$ steps is the $i^{th}$ entry in the vector $u_{(n)} = uP^n$.

The $U_n$ is a vector probability that describe the percentage distribution in $n^{th}$ state of the system.
The initial distribution for the infectiosn are;
$\mathrm{U}_{Hk} = (0.88, 0.06, 0.02, 0.04)$
$U_{Tt} = (0.99, 0, 0.01, 0)$
$U_{Al} = (0.98, 0.01, 0.01, 0)$

# 5 CHAPTER FIVE:SUMMARY,CONCLUSION AND RECOMMENDATION

## 5.1 Summary

The Markov model,using transition probabilities matrix,showed a significant decrease in STH prevalence despite the occurrence of reinfection. The infection intensity was significantly reduced by 72.7% for STH combination infection, 89.4% for hookworm, 72.6% for A. lumbricoides, and T. trichiura for 74.1%.The heavy intensity was reduced to 0% within the first dose of MDA.

## 5.2 Conclusion

The analysis with Markov model have helped to identify the infection progress after treatment and predicted future distribution pattern by estimating nth transition probability matrix with initial distribution. The predicted future distribution pattern is significant measure of prevalence to policy makers of STH intervention programmes as it alert in case of unfavourable dynamic patterns in prevalence.
Previous studies demonstrate that children with adequate access to improved WASH conditions and knowledge in STH infections were positively associated with a higher impact of anthelmintic treatment. In line with the WHO strategy for controlling STH infections in endemic countries, the Kenya national school-based deworming program currently provides annual delivery of albendazole to school children forming part of intervention measure.

## 5.3 Recommendation

We recommend the model as resourceful tool of information to policy makers of STH control measures .We note however, most of the studies that have been carried out in this area have focused on school going children with no proper geographical mapping of infections. For the future researchers in this study,I recommend additional data to include women of reproductive age as well as adults who have been overlooked in this study. Enhancing the model predictability by linking spatio-temporal patterns geographical epidemiological infections spread including the said additional group will go a long way in analyzing mitigation and containment measures.

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