UNIVERSITY OF NAIROBI
COLLEGE OF BIOLOGICAL AND PHYSICAL SCIENCES
CENTRE FOR BIOTECHNOLOGY AND BIOINFORMATICS (CEBIB)

POSTGRADUATE PROPOSAL PRESENTATION SCHEDULE

DATE: March 31, 2021
VENUE: ONLINE (Google Meet)

S/No.	NAME	Degree	Project Title	Supervisor(s)	Time
1.	Murungi Hellen Mwaura (I80/57474/2020)	PhD (Bioinformatics)	Exploiting Statistical Models to Predict Risk Factors and Appropriate Corrective Intervention Outcomes that Improve Maternal, Neonatal And Child Health (NMCH) in Kenya.	Dr. Benard Kulahoma Dr. Timothy Kamanu	12.00pm – 12.20am
2.	Cherono Brenda Terer I56/83486/2015	MSc (Biotechnology)	An Assessment of Tick-borne Viruses and Infection Profiles in Isiolo and Turkana Counties.	Dr. Christine Adhiambo Dr. Rosemary Sang Dr. David Tchouassi	12.20pm – 12.35pm

PhD RESEARCH PROPOSAL

Topic:

EXPLOITING STATISTICAL MODELS TO PREDICT RISK FACTORS AND APPROPRIATE CORRECTIVE INTERVENTION OUTCOMES THAT IMPROVE MATERNAL, NEONATAL AND CHILD HEALTH (NMCH) IN KENYA

ABSTRACT

The topic of the proposal is '**exploiting statistical models to predict risk factors and appropriate corrective intervention outcomes that improve maternal, neonatal and child health in kenya'**. The sustainable development goal number three of the vision 2030 aims to increase health and well-being for people of all ages and therefore save lives and increase life expectancy. Achieving the SDG target calls for improvement in goal centered interventions. Multiple interrelated conditions that are preventable, for example, malnutrition, birth complications, and infectious diseases contribute to extremely high neonatal, child under five years, and maternal mortality rates in middle and low-income countries. it is imperative to analyze existing data for example those from the Africa-Ki data repository and the Kenya National Data Archive (KeNADA) using statistical models to predict risk factors and intervention outcomes that improve maternal, neonatal and child health (MNCH). This will highlight specific areas of the SDG 3 indicators requiring improvement for certain demographic groups, thereby enabling focused interventions and resource use. The main objective of this study is to use mathematical models to generate quantitative predictions on etiological risk factors that are indiscernible solely by intuition and highly targeted interventions that significantly improve MNCH, thereby fast-tracking SDG target attainment. Generalized linear models with or without mixed-effects shall be used. Subsets of the entire data sets alongside simulated datasets will be used as training, validation, and test sets. The effects of heterogeneity in data sets will be analyzed to establish how intrinsic and extrinsic factors among sub-populations from different regions in the country account for deviation from the anticipated SDG targets under evaluation. Bayesian spatial models and supervised machine learning methods that merge descriptive statistics and spatial relationships will be used to establish intrinsic attributes and correlation of variables in complex data structures that characterize health-related meta-data from different surveys. Expected results include development of a computational algorithms and a graphical user-interphase. The findings will improve policy planning and interventions targeting at-risk populations by adapting customized interventions for each demographic group. This evidence-based approach will provide policymakers and program implementers with an optimal mix of interventions that improve MNCH, which enable quantification of inequalities and identification of successes and failures of programs and policies at the local level.

AN ASSESSMENT OF TICK-BORNE VIRUSES AND INFECTION PROFILES IN ISIOLO AND TURKANA COUNTIES

Ticks are obligate hematophagus parasites of livestock and wildlife. Ticks infect animals and human with viral pathogens causing illness ranging from asymptomatic to infectious, severe and virulent diseases such as Crimean-Congo Hemorrhagic Fever Virus (CCHFV). Febrile illness are major onset symptoms of tick-borne viral infections are similar to of malaria, typhoid, measles among others leading to misdiagnosis and unreported of tick-borne viral infections. CCHFV is of great concern in this study due to the virulent nature and high case mortality rate with no known therapy or vaccine effective against the disease. Tick-borne viruses control pose a challenge due to the tick resistance to acaricides which is the most control method used. Targeting these arboviruses pose a challenge due to the ability to undergo genetic modifications such as recombination and re-assortment that results in viral re-emergence and emergence of new viruses. Circulating arboviruses in Isiolo and Turkana counties will be assessed by CCHFV pre-screening in *Hyalomma* ticks, isolation of tick-borne virus in cell culture, PCR based molecular techniques and automated Sanger sequencing. CCHF antibodies in human sera will be assayed by use of IgG and IgM ELISA to identify present and previous exposures to CCHFV infection. R Programming open source software will be used with Excel database and pivot tables to carry out statistical analysis as Chi Square, Analysis of Variance(ANOVA) and Logistic regression model. Software and search tools such as BLAST and MEGA will be used to perform phylogenetic analysis to confirm specific identity of the virus present in the tick samples. Tick-borne viruses prevalence resulting from this study will inform on health and economic risks associated with the exposure of tick and tick-borne viruses.