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A Bayesian belief network modelling of household factors influencing the risk of malaria: A study of parasitaemia in children under five years of age in sub-Saharan Africa



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ABSTRACT

Studies that focus on integrated modelling of household factors and the risk for malaria parasitaemia among children in sub-Saharan Africa (SSA) are scarce. By using Malaria Indicator Survey, Demographic Health Survey, AIDS Indicator Survey datasets, expert knowledge and existing literature on malaria, a Bayesian belief network (BBN) model was developed to bridge this gap. Results of sensitivity analysis indicate that drinking water sources, household wealth, nature of toilet facilities, mother's educational attainment, types of main wall, and roofing materials, were significant factors causing the largest entropy reduction in malaria parasitaemia. Cattle rearing and residence type had less influence. Model accuracy was 86.39% with an area under the receiver-operating characteristic curve of 0.82. The model's spherical payoff was 0.80 with the logarithmic and quadratic losses of 0.53 and 0.35 respectively indicating a strong predictive power. The study demonstrated how BBN modelling can be used in determining key interventions for malaria control.

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Software availability

Name: Netica version 5.12 Developer: Norsys Software Corporation Address: 3512 West 23rd Avenue, Vancouver, BC, Canada, V6S1K5 Tel: +1 604 221 2223 Fax: +1 604 221 2238 E-mail: info@norsys.com Availability: www.norsys.com

1. Introduction

Malaria is one of the leading causes of morbidity and mortality in Africa. It is mainly reported among children under the age five years, pregnant women, elderly persons, and people with compromised immune systems. In 2013, over 430,000 child deaths

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occurred in Africa and about 128 million people were infected with malaria in sub-Saharan Africa (SSA) (World Health Organisation, 2014). Malaria transmission depends on favourable conditions for vector survival, parasite development and opportunities of human exposure to mosquito bites (Enayati and Hemingway, 2010). Given this complexity, robust models predicting factors that enhance mosquito propagation and mediate between malaria transmission are urgently required to facilitate rational decisions in malaria control.

The risk for malaria parasitaemia can be modelled at both large spatial scale and household level. At large spatial scale, geographical information system, remote sensing and Bayesian geostatistics have been comprehensively used to predict factors contributing to the risk for malaria parasitaemia. For example, it has been predicted that climate change is likely to increase malaria burden in densely populated highlands of Africa if no appropriate interventions are put in place (Siraj et al., 2014). Other studies have shown that high rainfall intensities, increased surface temperatures, land use changes, variations in surface water, humidity and vegetation have spatial-temporal influence on the breeding, survival and dispersal of adult mosquitoes (Raso et al., 2012; Riedel et al., 2010; Stefani et al., 2013; Stensgaard et al., 2011; Vanessa et al., 2011). At

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household level, malaria risk factors are largely identified and modelled using logistic regression models. In these studies, it has been predicted that households without toilet facilities, protected water sources as well as those with thatch/mud walls, earth floors and thatch roofs are at a higher malaria risk (Wanzirah et al., 2015; Liu et al., 2014; Ayele et al., 2012; Yamamoto et al., 2010). Other household risk factors including the inadequate use of insecticide treated nets (ITNs), living at lower altitudes and household poverty have also been predicted (Graves et al., 2009).

However, one of the primary challenge of logistic regression models is their inability to represent conceptual reasoning (Christakos, 2003) about malaria risk factors which are characterised by uncertainties and at the same time, they are not capable of handling complex causal relationships (Aguilera et al., 2011). Additionally, multiple factors influencing the risk for malaria parasitaemia at household level do not act in isolation, but rather in an aggregated format. Thus, integrated modelling approaches (Laniak et al., 2013) that provide insight into holistic interactions between the risk for malaria parasitaemia and household level factors are needed to aid rational decision making in malaria control programs. The commonly used modelling types that integrate multiple factors, values, scales, uncertainties and stakeholder participation include systems dynamics, Bayesian networks, coupled component models, agent-based models and knowledge-based models (Kelly et al., 2013). Given the range of dynamics and uncertainties of household malaria risk factors, this study purposively used the Bayesian belief network modelling approach.

Bayesian belief networks (BBNs) are increasingly becoming popular robust probabilistic methods for modelling uncertainties and complex environmental domains (Uusitalo, 2007). BBNs exploit the Bayes' theorem and consist of a directed acyclic graph (DAG) with variables represented as nodes while edges between the interacting variables used to represent the causal linkages (Jensen and Nielsen, 2001). All nodes (i.e. "parent" and "child" nodes) contain mutually exclusive states (i.e. categorical, boolean, continuous or discrete) and are linked by probabilities to describe a network of complex interactions (Kjærulff, and Madsen, 2013; Korb and Nicholson, 2004). For example, "parent" nodes contain prior or unconditional probabilities of their states determined from actual existing conditions and these are then linked to the "child" or intermediate nodes with conditional probabilities obtained from empirical data, expert knowledge and model approximation results or in combination. Output nodes consist of posterior probabilities reflecting an updating of the entire chain of conditional probabilities of all states connected to nodes. The exercise of updating BBN model continuously, can give the model a longer life span than other traditional statistical models (Chen and Pollino, 2012).

BBNs have several advantages over traditional statistical models. They represent concise probabilistic relationships, integrate multiple factors, utilise both quantitative and qualitative data, and can handle uncertainties as well as missing data (Aguilera et al., 2011; Chen and Pollino, 2012; Uusitalo, 2007). Importantly, BBNs can improve the ease of communicating model results to stake-holders and can continuously be updated when new knowledge becomes available (Kelly et al., 2013; Uusitalo, 2007). Because of their versatility, BBNs have been extensively used in modelling the trends and impacts of climate change (Richards et al., 2013), disease dynamics and health care (Birrell et al., 2011; Ceccon et al., 2014; Velikovaa et al., 2014) and water resource management (Carriger and Barron, 2011) among others.

Although BBNs have been used to understand protein functions in malaria parasites (Mitrofanova et al., 2010) and asymptomatic malaria diagnosis (Barros et al., 2010), they have hitherto not been used in household malaria risk modelling. We thus developed a BBN model based on evidence from Malaria Indicator Survey (MIS), Demographic Health Survey (DHS) and AIDS Indicator Survey (AIS) datasets of purposively selected countries from SSA (MeasureDHS program, 2015a). The objectives of the study were: 1) to develop a BBN model from a set of household factors to predict the risk for malaria parasitaemia among children under the age of five years in an integrated approach; 2) to assess the model's accuracy; and 3) to identify significant household factors influencing the risk of malaria parasitaemia among children under the age of five years.

2. Materials and methods

The procedure used in this study was based on guidelines previously published by Chen and Pollino (2012), while integrating BBN modelling protocols used in natural resource management proposed by Cain (2001) and Marcot et al. (2006).

2.1. Review of existing knowledge on malaria risk factors

The initial step before constructing a BBN model is to either use subject-matter experts or review literature or both to identify key correlates or explanatory variables that influence an outcome of interest (Chen and Pollino, 2012; Marcot et al., 2006). Then, the identified factors can be arranged into an influence diagram for further BBN model building. In this study, the outcome of interest was to predict the probability of testing positive for malaria parasitaemia among children under the age of five years. Based on our outcome of interest, a comprehensive survey of relevant scientific literature on malaria risk factors was conducted. Keywords (e.g. 'household malaria risk factors') were used to guide the literature searching process within an appropriate scope.

Resultantly, 22 closely relevant peer-reviewed malaria articles were purposively selected and this was followed by an in-depth review to identify key household variables associated with malaria parasitaemia. According to the criteria proposed by Chen and Pollino (2012) and Borsuk et al. (2004), 10 key explanatory variables that were manageable, predictable, observable and highly associated with malaria parasitaemia were finally selected as shown in Table 1. Regional spatial factors like temperature, precipitation, land cover, and elevation among others (Weiss et al., 2015), were all excluded from the modelling exercise because they were beyond the household scope of this study.

Based on the identified key household factors (Table 1) together with online consultations and feedbacks from two experts, we developed an influence diagram (Fig. 1) to illustrate the impact of multiple interactions of household factors on the potential risk for malaria parasitaemia. The arrows illustrate a general direction of the cause-effect relationships among the factors.

2.2. Survey datasets with variables for model building

Three popular parasitaemia surveys of MIS, DHS and AIS conducted using standardised research procedure in SSA were used in this study (MeasureDHS program, 2015a). During these surveys, representative samples were obtained using probability sampling techniques consisting of a two-stage cluster sampling method while using a probability proportional method to estimate cluster size and sampling errors. Questionnaires were designed to collect background information on the social, economic and environmental aspects of the surveyed households. Methods of both Rapid Diagnostic Test (RDT) and the Blood Smear Test (BST) were used to test malaria parasitaemia among children under the age five years after getting consent from household heads. Detailed explanations of the different surveys, data collection techniques, coding and analysis of results among others are available on the DHS program website (MeasureDHS program, 2015a). Download English Version:

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