AJMS
Asian Journal of Mathematical Sciences

REVIEW ARTICLE

ON THE USE OF BAYESIAN PROBABILITY NETWORKS WITH A REVIEW OF MALARIA CASE

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Received: 02-04-2025; Revised: 10-05-2025; Accepted: 03-06-2025

ABSTRACT

In spite of the versatile and general acceptability of estimation of disease cases from the various available methods in literature, incorporating model uncertainty remains an open issue. In this article, we derived a probability based graphical model using expert opinions in related studies on malaria and its hypothesized predictors with a Bayesian belief network (BBN). This approach is well applied in ecological studies and other environmental sciences in recent times for various estimations and predictions based on Bayesian reasoning. We gave a brief description of a BBN framework, its pros and cons, examine the principle of conditional independence. Also, we explore Markov Chain principles as it relates to a BBN formulation and useful guidelines for developing the preliminary structure of the network. We finally derived the topology of a BBN as a directed acyclic graph with malaria predictors as network nodes. We also illustrated the use of the network with an illustrative example.

Keywords: Bayesian Networks, Probability, Uncertainty, Malaria, DAG

INTRODUCTION

A Bayesian Belief Network (BBN) is a probabilistic graphical based model that represents connections between some set of related random variables. The variables are the network nodes and the edges are the dependencies between nodes. These dependencies among nodes are captured and quantified with computation of conditional probabilities in the directed acyclic graph with Bayes probability calculus [1, 2].

Studies have documented a quite number of tools or models for epidemic of vector-borne and other infectious diseases [3, 4]. For instance, the commonly used statistical methods like logistics regression and discriminant analysis methods were reviewed by [4] to model the distribution of species. The author identified issues relating to the needed number of predictors to be included in the models, selection of the right set of candidate models, problem of sparse datasets and introduction of spatial covariance and auto-covariance among others. The study noted that the ability to exclude some models from the set of identified models for any particular distribution problem is important to identify the best current model. Other notable models include hierarchical Bayesian models for force of infection discussed by [5], temporal and spatial heterogeneity in malaria infection patterns [6]; an application of a SIR compartment model to a childhood infectious disease like measles reported in [7], usage of a compartment model approach for the exploration of the patterns and the dynamics of disease outbreak documented in [8]. The Authors used a modified version of a SIR model; a Susceptible Exposed Infected Hospitalized and Recovered (SEIHR) espoused in [9] to model the dynamics of diphtheria in Nigeria. Likewise, [10] incorporate vaccination (which is essential to contain the disease spread) into the SIR model to model the waves of a Monkeypox epidemic. Other Researchers submitted that the growth rate of infection determines the total number of infections and that epidemic spread differently in different stages. These stages are defined by the structural breakpoints on the time series data. Thereby fitting different theoretical probability distributed such as Normal, Negative Binomial, Poisson, Gamma, Exponential, and Lognormal were suggested [11].

Despite existence of various methods documented in literature for modeling vector-borne diseases like dengue and malaria, estimation of the disease cases when limited data are available, incorporating different data into the same model and handling the uncertainties become an open problem. Also, the existing approaches rely heavily on statistical associations for determination of inter-relationships among variables rather than conceptual framework with different hierarchical levels [12, 13]. These and other inadequacies of the existing multivariable statistical procedures are overcome with an advent of a belief network in various fields of study. In recent times, a BBN has become one of the methods that handle such issues under different probability scenarios to model the uncertainty and form a unified estimation and prediction technique for hierarchical structure among covariates [14]. A Bayesian reasoning based on weighted likelihood (with a specified prior probability as the weight) forms the basis of a BBN as a decision support tool [15]. The availability of so many computer-based algorithms for learning the network and expert opinions enhance its usage across various disciplines [16, 17]. This method has been used widely over decades and various network proposed [18-20]. For example, [21] formulated a BBN template for modeling simple hierarchical- like structure as a unified alternative estimation and prediction techniques to multi-level analysis. The proposed method takes into account the interactions and uncertainty among the explanatory variables at different levels. The developed model was tested with a diarrhea example. Also, [14] proposed a Bayesian network approach for modeling risk and uncertainty for project cost analysis. The derived technique allows for the various dependencies in the cost items and trade-off scenarios between the response and the included project items. These unique features of BBNs are identified as lacking in the other known methods like regression and artificial neural networks (ANN).

The current study demonstrates the practical application of a typical BBN for the estimation of model parameters in its simplest forms for both experts and non-experts to understand. The study also derives a probability-based networks as influence diagram for malaria epidemics.

Concepts and Theorems in BBNs

2.1 **Bayes Theorem of Probability Calculus**

Consider three probabilities of events given as X, Y and Z. The conditional probability of Y given Z has occurred (1), and its cross product from the fundamental law of probability calculus which represents the joint probability of Y and Z occurring (2). Equation 3 is the Bayes rule with the first term to the left of equation representing the posterior distribution of Y given Z. The numerator is the product of likelihood ($P(Z|Y)$) of event Z given event Y has occurred, the marginal probability (prior) of Y is written as $P(Y)$ and the normalizing term $P(Z)$ as the denominator. Bayes theorem serves as a pivot where the Bayesian statistics hangs. The inferences in belief networks operate with the application of the principles embedded in the Bayes rule of probability popularly known as Bayes theorem. Equation 3 becomes (4) using the concept of total probability. Hence, P(Y|Z) and P(Z|Y)P(Y). For all values of y, the denominator remains constant.

$$P(Y|Z)=\frac{P(YZ)}{P(Z)} \tag*{1}$$

$$P(YZ)=P(Y|Z).P(Z)=P(Z|Y)P(Y) \tag*{2}$$

$$P(Y|Z)=\frac{P(Z|Y)P(Y)}{P(Z)} \tag*{3}$$

$$P(Y|Z)=\frac{P(Z|Y)P(Y)}{P(Z|Y=y_1)P(Y=y_1)+...+P(Z|Y=y_n)P(Y=y_n)} \tag*{4}$$

2.2 Bayesian Belief Networks

A Bayesian Belief Network also referred to as a belief network or causal network, is a statistical technique that uses graphs to represent the topology of a set of connected random variables and their conditional independencies. It represents probability relationships between a set of variables. A typical BBN is a directed acyclic graph (DAG) which consists of nodes, edges and condition probability tables (CPTs) attached to the various nodes [20]. In network analysis, the set of random variables are the network nodes while edges (links) represent the dependencies among the linked nodes. The nodes are drawn by circles which represent the variables and the edges are displayed as arrows. The conditional probability tables are the probabilities at the various nodes conditioned on the parent nodes. The probabilities are thus represented by the CPTs. Each node in the network is associated with a known probability distribution which is used in the computation of the conditional probability of the nodes given the input from the parent. These probabilities constitute the parameter estimate for the nodes. Concisely, a DAG represents the joint distribution of the nodes (random variables) in the network [22].

Suppose there are two nodes E and M linked by an edge from E to M. The value assumed by M depends on the value taken by E. Node E is thus referred to as the parent node while node M is the child. Likewise, if node E is preceded and edged by another node say A, then node A influences node E. The node A is the parent of node E but an ancestor of node M. A BBN as an acyclic graph has the property that there is no node that can be its own ancestor, thus, it does not allow for the dynamism of feedback. The recursive property allows for ease of factorization of a set of nodes. Each of the node depends only on its own descendants but is conditionally independence of other nodes in the network given the states of its parent [23]. The principle of conditional independence of a BBN guarantees easy computation of the posterior probability given the evidence.

The computation of the joint probability distribution for any network in a DAG given the data requires the principles of Markov Chain. The conditional probability at any node is conditional independent of its descendants given the current states of the parent node. Hence, the network exhibits the Markovian property as the conditional probability of each node depends only on its parent [15].

If the nodes are set of discrete random variables in the topology of a Bayesian network, , then, the joint probability distribution of the structure of the network is thus given as the product of the conditional probabilities at various nodes given individual parent (5).

$$P(X=x_1,x_2,...,x_n)=\prod_{i=1}^{n}p(x_i\,|\,x_{i-1},x_{i-2},...,x_1)$$

$$P(X=x_1,x_2,...,x_n)=\prod_{i=1}^{n}p(x_i\,|\,parent(x_i)) \tag{5}$$

parent(X_i) is the parent to node X_i and equation 5 specify the probability model of X given the graphical structure of the network.

In mathematical terms, a belief network B can be defined as follows:

Let B be a BBN with nodes V, a belief network can be given succinctly as $B=(X,G,P)$ for some given set of random variables for all $X_1,X_2,...X_n$.

$G=(V,E)$ is an acyclic directed graph with nodes $V=V_1,V_2,...,V_n$ and links $E=E_1,E_2,...E_n$. Each node in G represents the random variable $X_v \in X$ with a finite set of mutually exclusive states and the directed link E is the (conditional) dependence and independence of the nodes given the parent(s) for all $E \subseteq V x V$ of the probability P in the network G between the random variables according to the d-separation criterion.
$P(X_v \mid parent(X_v))$ is the conditional probability of the child given the parent for each node in the probability network.

In recent times, there is a gain in popularity and application of probability networks in a range of areas. Such applications include customer satisfaction [23], risk assessment [24], stock returns [25, 26], fire service [20, 27], ecology [28] and disease epidemiology of malaria and dengue fever [19, 29].

2.3 Strengths and Weaknesses of BBNs

The application of a BBN offers so many advantages in ecological and environmental sciences [2, 14]. A causal probability network allows combination of dataset from different locations and time with published information. It also describes both direct and indirect variables interactions and influences via the causal structure of the network.

It allows usage of probability theory to take care of the uncertainty in the estimation process. Though the computations may sometimes rigorous, but are easily understandable based on the simple algebraic simplifications and intuitive statistical principles.

Bayesian networks are flexible in input modifications (addition and removal of variables not affecting the significant of others) as well as in providing output.

Additionally, it allows for inferences from a network with several nodes simultaneously. Also, trade-off scenarios are allowed in a BBN inferences based on different values of evidence. It shows how much a specific node is influenced by other nodes via sensitivity of the constructed network topology [30].

In a BBN, missing data constitute no problem to handle by expert. It incorporates expert opinion (inform of prior knowledge) in the network structure and missing data situations [31].

Despite numerous advantages in application of a BBN, it has some weaknesses as a graphical model. The BBN is recursive in nature, hence no provision for feedback in the causal flow on the network topology. This serves as a hitch to the network especially if a dynamic system with feedback is involved. Similarly, exclusive use of discrete variables as input in BBNs applications serve as another form of limitation.

Also, when large number of variables are involved in the structure of the network with quite number of discrete states, a BBN computation becomes complex as the network grows exponentially and computation time increases. Sometimes, if most of the variables in the network are conditionally independent of one another, this setback may be eliminated.

In situation of non-availability of data, expert subjective judgment can set in and introduce uncertainty in the estimates of the conditional probability in the network nodes.

3. Application of BBNs in Malaria Modeling

A BBN provides a robust method of visualizing and Modelling a complex real life phenomenon as it combines causal relationships between variables graphically and offer a probability framework to handle the embedded uncertainty in the model [12, 18]. The use of a BBN to depict the influence of malaria predictors on disease cases is illustrated in this study.

We give two examples of a BBN for the study. The first example is a simple network aimed at illustrating the probability relations between the nodes of the network topology while the second example is a BBN derived for malaria epidemic spanning demographic, socio-economic, climatic, land use, control intervention measures, vector control and abundance, and entomological inoculation rate (EIR).

3.1 Illustrative Example of A BBN

Figure 1 shows a BBN with three nodes connected by arrows showing dependencies of the three discrete random variables in the network. The variables and their states are as given: (G)ood and (P)oor for (K)AP node, Yes and No for (I)ntervention measure node and Yes and No for (C)ases node. The probability tables (PTs) for the nodes in the network are displayed in Tables 1-3. The probability distribution of the variables included in the model shows the relationships between the nodes (Table 4). The calculations are based on the assigned probabilities at all the three levels of the model.

The node KAP has no parent; therefore, the node is not influenced by any other node. The probability is the same as the assigned probability in Table 1. The Intervention measure node is a child of the first node (KAP-node) with PT in Table 2. The table shows the assigned conditional probability of the intervention node conditioned on KAP node. Likewise, Cases-node follows similar pattern of calculation with intervention node. The third node (Cases-node) PT is conditional probability of Cases given joint probabilities of Intervention and KAP nodes. This is true because both nodes (Intervention and KAP) are parent to node

Cases of BBN:

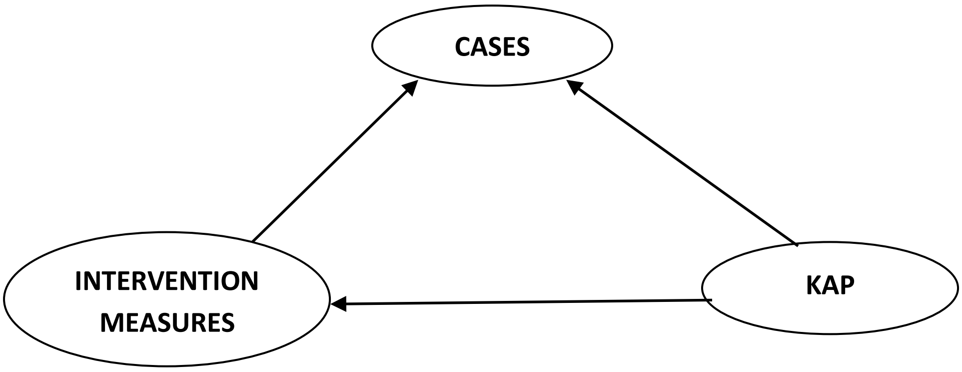

Figure 1: An Illustration of a Bayesian Belief Network

Table 1. Node Probability Table: KAP

KAP-node	
G	P
0.65	0.35

Table 2: Node Probability Table: INTERVENTION

	KAP-node	
Intervention measure	G	P
Yes	0.7	0.25
No	0.3	0.75

Table 3: Node Probability Table: CASES

	KAP-node			
	G		**P**	
Intervention Measure-node	Yes	No	Yes	No
Cases-node				
Yes	0.3	0.65	0.4	0.9
No	0.7	0.35	0.60	0.1

The various calculations of the probability distributions at the nodes are as given below:

$$P(I=Yes)=P(I=Yes\,|\,KAP=G).P(G)+P(I=Yes\,|\,KAP=P).P(P)=0.5425$$

$$P(I=No)=P(I=No\,|\,KAP=G).P(G)+P(I=No\,|\,KAP=P).P(P)=0.4575$$

$$P(KAP,I)=PT(KAP).diagPT(I)=\begin{pmatrix}0.7 & 0.25\\ 0.3 & 0.75\end{pmatrix}\begin{pmatrix}0.65 & 0\\ 0 & 0.35\end{pmatrix}=\begin{pmatrix}0.455 & 0.0875\\ 0.195 & 0.2625\end{pmatrix}$$

$$P(Cases)=PT(Cases).VectorP(KAP,I)=\begin{pmatrix}0.3 & 0.65 & 0.4 & 0.9\\ 0.7 & 0.35 & 0.6 & 0.1\end{pmatrix}=\begin{pmatrix}0.455\\ 0.195\\ 0.0875\\ 0.2625\end{pmatrix}=\begin{pmatrix}0.5343\\ 0.4650\end{pmatrix}$$

Table 4: Probability Distributions of the Network Nodes

Node	Probability
KAP	
G	0.65
P	0.35
Intervention measure	
Yes	0.54
No	0.46
Cases	
Yes	0.53
No	0.47

A typical BBN allows flexibility and manipulations of the nodes. For example, if there is scenario that the assigned probability in the PT of KAP-node for state G changes from 0.65 to 1.0 in Figure 1. Then, this influences the probability distributions of the other node PTs with the application of Bayes rule to the affected node. The probabilities in node KAP becomes P(KAP=G) =1 and P(KAP=P) =0. The new distribution for node Intervention, P(I=Yes) =0.7, P(I=No) =0.3, and node Cases, P(Cases=Yes) =0.405, P(Cases=No) = 0.595.

3.2 Malaria Probability Network

After an initial review of related literature, expert opinion and practice over time, a list of key environmental covariates were identified and use in the construction of influence diagram which serves as the first step in the building of a Bayesian network [32]. The initial network displays graphically the causal influence of the key malaria indicators on the disease cases (Figure 2). It shows interconnectivity and influences among related variables. The framework is the hierarchical paradigm which shows relationships at various levels in the network. The response in the network topology is predicting of probability of the disease cases at a particular random field. The malaria disease cases directly depend only on EIR, size of the family and place of abode of individual subject, hence the leaf node in the network has only those three parent nodes. While the EIR is a function of man biting and sporozoite rates, both family size and residence are function of individual level of education. Man biting rates (MBRs) are shown to be dependent on vector abundance, how well an individual acquire and use intervention and control measures [33] and also depends on the number of people or occupants of the house [34]. The root nodes include: climate variables (temperature, humidity and rainfall) [35, 36], land use (agriculture practices, topology and altitude) [29, 37, 38] and vector control determines the abundance of vectors around homes, offices and sites. Also, the root nodes (socio-economic status, age and gender) influence education which invariably affects KAP regarding malaria [39, 40] and occupation. Likewise, education dictates the type of occupation, family sizes and nature of residence of subjects [41-44]. In essence, the parent nodes feed child nodes in the network. The child nodes now become the parent nodes in the intermediate nodes in the network which finally affect the leaf nodes.

Based on the foregoing, we developed a BBN which can easily be explored with relevance data on vector-borne diseases like malaria. Figure 2 displays the developed BBN template for malaria and other vector-borne diseases with similar characteristics. The identification of the significant factors for the construction of the network topology need be carefully done and the cause, intermediate and effect nodes need be rightly connected. The parsimony in the network is achieved by making it as simple as possible, the parent-child node edges be as fewer as possible. A maximum of five parents to a child is recommended while other studies limit it to three parents [2, 32]. Likewise, all variables in the network should be observable, quantifiable and have a minimum number of discrete states while continuous variables can be discretized for easy computation and manipulations. The optimal network can be attained via blacklisting and whitelisting some nodes and learning the network severally until the desire network characteristics and certain statistical criteria (like obtaining network score with highest Bayesian information criterion and with smallest number of nodes) are met [21]. These and others steps can serve as additional guidelines for developing the structure of any Bayesian network.

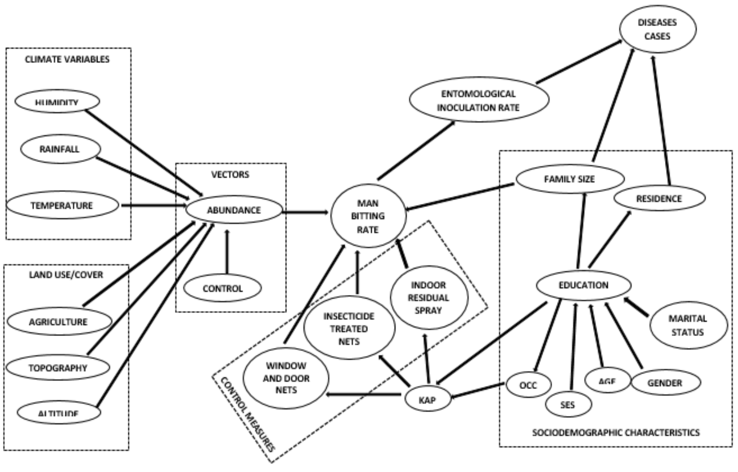

Figure 2: A Derived Bayesian Belief Network for Malaria Epidemic

Conclusion

The study demonstrated how to estimate disease cases with a modest BBN typical example. We also derived a BBN template for malaria epidemic modeling which can also be useful for other vector-borne diseases with similar characteristics. A BBN is a flexible graphical model which is handy in handling uncertainty under different scenarios. Parameters can easily be blacklisted or whitelisted to achieve the desire network parsimony. The example given is basically for demonstration purposes for the concepts underlying BBNs. The network learning can easily be achieved with algorithms available in computer software. Also, the developed malaria network need be validated with data in future. This we hope to achieve in the course of our research.

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