

Multi-Agent Bayesian Framework For Parametric Selection In The Detection And Diagnosis of Tuberculosis Contagion In Nigeria

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Abstract

Decision making has become quite a critical factor in our everyday living. The provision of data alongside its consequent processing has further sought to extend and expand our reasoning faculties as well as effectively aid proper decision making. But data is daily, produced at an exponential rapid rate and the volume in amount of data churned out to be processed even more so that we now require data storage optimization techniques to process such humongous volume of data. These have today, necessitated the need for advancement in data mining process. With the tremendous advances made in data mining, machine learning, storage virtualization and optimization – amongst other fields of computing – researchers now seek a new paradigm and platform called data science. This field today has become quite imperative as it seeks to provide beneficial support in constructing models and algorithms that can effectively assist domain experts and practitioners to make comprehensive and sound decisions regarding potential problematic cases. We focus on modeling social graph using implicit suggest algorithm in medical diagnosis to effectively respond to problematic cases of Tuberculosis (TB) in Nigeria. We introduce spectral clustering and Bayesian Network, construct algorithms cum models for predicting potential problematic cases in Tuberculosis as well as compare the algorithms based on data samples collected from an Epidemiology laboratory at the Federal Medical Center Asaba in Delta State of Nigeria. The volume of data was collated and divided into two data sets which are the training dataset and the investigation dataset. The model constructed by this study has shown a high predictive capability strength compared to other models presented on similar studies.

Keywords: tuberculosis, Bayesian Network, epidemiology, Nigeria, deep learning, contagion, reinforcement algorithm

1. Introduction

Tuberculosis has remained a leading cause of death from a single infectious agent. While, it propagates as an infectious disease and thrives as a contagion, tuberculosis is curable. The disease caused by Mycobacterium tuberculosis mainly – and occasionally by the Mycobacterium tuberculosis complex (Cruz et al, 2014; Marais et al; 2004; Chiang et al, 2015). The World Health Organization (WHO) has since declared tuberculosis (TB) an epidemic. TB is most commonly, transmitted by inhalation of infected droplet nuclei that are discharged in the air when an infected patient with untreated sputum-positive pulmonary TB coughs, sneezes, talks and/or spits. Furthermore, consumption of raw milk containing Mycobacterium bovis, is also a plausible means of being infected with TB (WHO, 2008; 2015). Smear positive TB patients are responsible for up to 90% of transmission occurring in the community (Zar et al, 2005; Starke, 2014; American Academy of Pediatrics, 2015). Its negative impact on the society at an increased alarming rate can be attributed to the various forms of living standards, social habits and other factors that includes poverty and living habits, migration, population growth and HIV/AIDS. A significant problem and challenge to the society thus, is the fact that many instances of TB remains undetected, undiagnosed and even unreported either due to the non-provision of medical aid, late reach to medical facility, lack of finance to get adequate medical care etc – to mention a few.

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Machine learning algorithm requires gathering of necessary dataset as cases, examples, and instances of all possible object classes. This is because in order to effectively train the adopted and adapted model, instances of dataset must be appropriately labelled in order to minimize the error rate in the classification (Ojugo and Eboka, 2019; 2020). These errors discern cum determine how effective and efficient the model progressed and is able to mine the data features of interest. Also, these errors can be resultant of the fact that in grouping cum labelling the data, some data points – even when not in the same class or group, can have lots of similarities under the unsupervised learning, or as they are used to predict new objects in a class under supervised learning. Also, the dataset must also be formatted appropriately to be used by the model; Else, it will result in data-type mismatch as the users tries to encode the data (via pre-processing stages) so that model is adequately trained to classify the data points into their corresponding classes (Ojugo and Otakore, 2020; Ojugo and Yoro, 2020).

1.1. Tuberculosis In Nigeria

Tuberculosis has been and will remain an epidemic and major health challenge that requires quick medical attention in Africa and the sub-Saharan countries. It is easily transmitted when an infected patient (with the pulmonary tuberculosis) coughs, spits or sneezes, they leave droplets of the tubercle bacilli in the air – so that an exposed person that inhales only a few of the droplet gets infected. WHO in 2015, reported that a third of the world’s population is infected with latent tuberculosis (i.e. persons are infected with the tubercle bacilli but they are not sick and cannot transmit the disease). Also, in furtherance to this – it has been confirmed that throughout their lives – infected patients have a 10-percent chance of developing the disease (WHO, 2015; Stockdale et al, 2010; Pfyffer, 2015).

Even with the often reported high prevalence of tuberculosis, its high rate of mortality, high development of anti-TB drugs as well as reported high incidences – there has also been seen and reported, a high rate in morbidity resulting from TB infection as tuberculosis continues to threaten public health worldwide. A major reason has been attributed to improper diagnosis and treatment, poor adherence to medication from experts, presence of multi-resistant TB, underlying medical conditions, increased migration pattern and HIV pandemic (Sun et al, 2011; Parasha et al, 2013).

The tubercle bacilli particularly, has a high risk propagation arte in overcrowded scenarios without adequate ventilation and light as the bacilli can survive in the stale conditions for long periods of time. This implies that exposure and its transmission can also effectively occur indoors. Also, casual cum random contact, mass public transport and genetic susceptibility are the main factors for the epidemics of TB in recent years. Over-crowding that is ever present in mass public transport plays a primary role for close contact or overcrowded conditions which can facilitate the transmission of PTB. Awareness campaigns among other means about TB transmission can act as preventive measures and practices especially in high risky or overcrowded conditions were one of the major stop TB strategy to achieve the Millennium Development Goals – MDGs (Brittle et al, 2009; Sanchini et al, 2014).

1.2. Problem Formulation With Dataset Encoding

Disease propagation as contagion is not left behind in these scenes as relevant phenomenon, paradigms and theories emerge when investigating biological theories and social impacts on many of such tasks or events (Ojugo and Otakore, 2020a; 2020b; 2021). For this study, we retrieved the data from the Federal Medical Centre Epidemiology laboratory (Epi-lab) of the various Medical Centres in Akwa-Ibom, Cross-Rivers, Delta, Edo, Rivers and Imo States of Nigeria – for the period 2010 to May 2020. Dataset contains about 4687 instances and cases with about 34-attributes, including patient’s personal data, symptoms the patient suffers from, HIV and other tests, history of the disease, diagnostic tools used, treatment that includes regimens for the type of the disease and doses given, with its drug reaction, the follow-up results for the whole treatment period, also costs and hospitalization paid. Also, attributes that are likely to affect the patient behaviour towards treatment includes: chemotherapy completed, treatment failed, treatment discontinued, death, and transferred out (Ojugo and Eboka, 2020; 2021).

2. Materials and Methods

2.1. Study Area and Sample Gathering

We employ a cross-sectional study involving the analysis of secondary data from various unit TB registers in urban areas. Nigeria ranks within the 20 high-TB-burden countries; Its diagnostic and treatment services are provided in health centers and hospitals. Various strategies to end TB in the country has been adopted and committed to reaching missed TB cases in the vulnerable population. The Niger Delta is an urban region, responsible for the oil-rich deposits of the country. It has a population of over 46million people. Health service coverage has reached to 95% of the population. There are over 345 health facilities to include (and not limited to) public hospital, public health centres, private health centers and non-governmental organization (NGO) clinics to provide health services to the population in the area. All public and private health facilities provide TB screening services for patients. 98% of the health facilities provide diagnostic and treatment services; while 97% provide diagnostic services. The TB case finding and treatment outcome data were obtained from the TB registers of facilities at the capital of the states to include Akwa-Ibom, Cross-Rivers, Delta, Edo, Rivers and some parts of Imo for the period within 2010 to May 2020. All TB patients that were registered and received treatment in the selected health facilities were included in the study.

2.2. Study Design

The dataset contains about 54 attributes and 24,687 instances, including personal data of the patient, symptoms the patient suffers from, HIV/AIDS and other tests, history of the disease, diagnostic tools used, treatment that includes regimens for the type of the disease and doses given, with its drug reaction, the follow-up results for the whole treatment period, also costs and hospitalization paid. However, attributes that are likely to affect the patient behaviour towards the treatment (treatment outcome is one of the following: cured, treatment completed, treatment failed, treatment discontinued, death, and transferred out). The dataset was further categorized into:

1. Attributes related to particular patient (age, sex, etc)
2. Attributes related to regimen TB classification and category
3. Attributes that are related to proximity to health center
4. Attribute related to treatment's side effect (social or clinical)
5. Attributes that are related to duration of treatment

For the implicit suggest algorithm, we employ a graph-based model to process the dataset. We also study interesting statistics about the attributes concerning the class distribution over the values of each attribute as well as present cum discuss the results therein. The usually steps in data mining includes: (a) data gathering, (b) data pre-processing to ensure the dataset to be used is appropriately formatted, (c) selection of features of interest, (d) data analysis involves knowing which operations with attributes selected to encode into the model as well as what data transformations is required etc, (e) data-mining involves learning of the relationship between the overall attributes and probability of underlying feats of interest with target algorithm deployed and implemented in order to construct the prediction model, (f) evaluate our model by domain expert, comparing the results with other researchers, or by sensitivity analysis, and an optional, (g) if the model achieves the acceptable accuracy then the process will terminate; Else, items (c) to (f) is repeated.

2.3. Experimental Bayesian Belief Network

Bayesian network (BN) is a directed acyclic graph commonly used in many domains which includes software reliability assessment and prediction, medical diagnosis. With Bayes theorem of conditional probabilities of random events, BN is a probabilistic model that uses a directed cycle graph to represent the random variables by nodes, which are connected by edges. The edge connect nodes A to B, where A as a parent node, represents a conditional probability $P(B, A)$ (Singh et al, 2001). Selection of algorithms depends on various factors, which includes availability of data (as an important feature that impacts on an algorithm's performance). A crucial feat of BN is its tolerance for noisy, incomplete data as it seeks to achieve good performance when the attribute is large (Ojugo and Otakore, 2021; Ojugo et al, 2015).

BN has been successfully applied to fields such as machine learning, medicine etc. BN represents knowledge and exploits data via a mathematical structure with simplified visual display cum representations of graphic probability relations between a set of variables under domain of uncertainty. BN is structured as a directed graph and conditional probability tables (CPTs) given the occurrence of its parent nodes (Ojugo and Eboka, 2018; 2021). BN probability is related to the degree of belief – measuring plausibility of an event given incomplete knowledge. It states the probability of an event A conditional on another event B denoted as $P(A|B)$ (Ojugo and Otakore, 2021b); And it is generally different from probability of B conditional on A written as $P(B|A)$. It implies that: (a) there is a definite relation between events $P(A|B)$ and $P(B|A)$, and Bayes theorem is the statement of such relations, (b) it computes $P(A|B)$ given the data about $P(B|A)$, and lastly, (c) its result employs new data to update the conditional probability of an event (Ojugo and Eboka, 2020). Given a sample space s , with a set of mutually exclusive events (A_1, A_2, \dots, A_n) from $s - B$ is any event from s whose probability is denoted as $P(B) > 0$. Using Bayes theorem, BN is described via Equation 1 and 2 (Ojugo and Okobah, 2018):

$$P(A_k|B) = \frac{P(A_k \cap B)}{P(A_1 \cap B) + P(A_2 \cap B) + \dots + P(A_n \cap B)} \quad (1)$$

Invoking: $P(A_k|B) = P(A_k) \cdot P(B|A_k)$ – probability becomes:

$$P(A_k|B) = \frac{P(A_k) \cdot P(B|A_k)}{P(A_1) \cdot P(B|A_1) + P(A_2) \cdot P(B|A_2) + \dots + P(A_n) \cdot P(B|A_n)} \quad (2)$$

For the BN classifier, we built the model to train the dataset via a conditional probability table (CPT) so that the algorithm first seeks to learn the structure of the BN. After which, it learns the train-dataset labels (and data points based on parameter(s) or feats of interest). It then builds the probability distribution tables for each nodal relationship in the network. It achieves this via two learning processes namely: (a) structured learning or casual discovery in which the Bayesian network learns the structure and parameters provided with the input dataset. The causal discovery is learned via using either of K_2 , Hill climbing and Tabu-Search, and (b) it achieves probability distribution learning with algorithms like BN estimator and multinomial estimator. Once, parameter learning is complete and the structure for CPT for each feat in the BN is also learned and completed, investigation cum testing of the model can commence. To apply BN for detection of the tuberculosis treatment, we adopt selected parameters whose probability distribution will yield the appropriate stochastic outcomes for the underlying feats of interest. To classify the data-points, we use the supervised learning model for the Bayesian network designed as in figure 1.

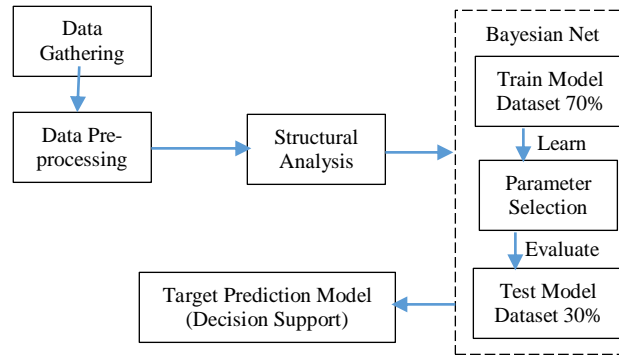


Fig. 1. Target Prediction Model Construction

3. Result Findings and Discussion

3.1. Presentation of Result Findings

Applying the Bayesian model with 5-fold retraining and/or cross validation in evaluating the prediction model based on the correctly classified instances, the model has produced 93.7563 percent accuracy rate (Table 1) showing confusion matrix with the five classes (a,b,c,d,e) representing the various treatment outcome groups.

Table 1. Confusion Matrix and Percentage Achieved by Model

Class	A	B	C	D	E
a=Confirmed	568	1	0	0	0
b=Discharged	134	0	1	0	1
c=Death	20	0	3	5	0
d=Active	409	0	2	1	2
e=Absconded	2	0	0	1	0

A confusion matrix represents per true and false classes correct classification. Table 2 shows that confirmed class of 568 cases. Then the discharged class of 134 cases correctly classified as *true* as in class (a); while, 2 others (from b-to-e) classified as false. Classes (a) and (b) respectively shows no significant difference between them. Thus, the error in the classification do not have significant effect. But, the general percentage obtained from software (correctly classified instances) for proposed Bayesian model is 93.7563 percent.

3.2. Discussion of Result Findings

Table 2 shows the variable(s) relationship for the probabilities of the underlying feats. We note, that discharge class is dependent upon variable (piw) by 0.962 probabilities. Thus, we can violate the independent assumption “no more than one parent”. This is expressed by the set (maxNrOfParents=1) with which this process leads to achieve 94-percent accuracy. And the graphical model changes as in Figure 5 that describes how the probability distribution effect on model representation. The relations between attributes and their affection to the prediction result in accordance with the Bayesian belief network.

Table 2. Probability Distribution of (piw) Variable

Class	Yes	No
a=Confirmed	0.999	0.001
b=Discharged	0.962	0.038
c=Death	0.107	0.893
d=Active	0.01	0.99
e=Absconded	0.136	0.864

From figure 1, some assumption(s) made thus includes that: (a) all variables are statistically independent, and (b) all variables are completely independent in accordance with the independent assumptions. Figure 2 shows the data loading for the target prediction model.

4. Summary and Conclusion

With graph-based model, there are still a lot more variance to understand such as predictive variables and “behind-the-scenes” data. Though, the addition of more data to the task at hand may not solve it – but, we have aimed to define some parameters that helps predict social graph. There is the need to standardize parameters for social-graph models, which in turn raises new questions for the theory. In modelling ties, it is important to know: (a) what feats and parameters are necessary predictors to be used in predicting threshold, and (b) what limits are to be set for behavioural evolution. We believe our work makes some important contributions to the theory as thus: (a) extending tie-strength dimension as manifested in all social-graphs, (b) defining network structure dimension as a function of probability distribution of agents in problem space, (c) all dimensions modelled as a continuous value, (d) our result extends the realization of how structural dimension in predictive variables used in task help modulates other dimensions within, by filtering agent relationships via cliques and clusters, and (e) previous works assumed either the presence or absence of a link in the graph without recourse to the properties of the link itself.

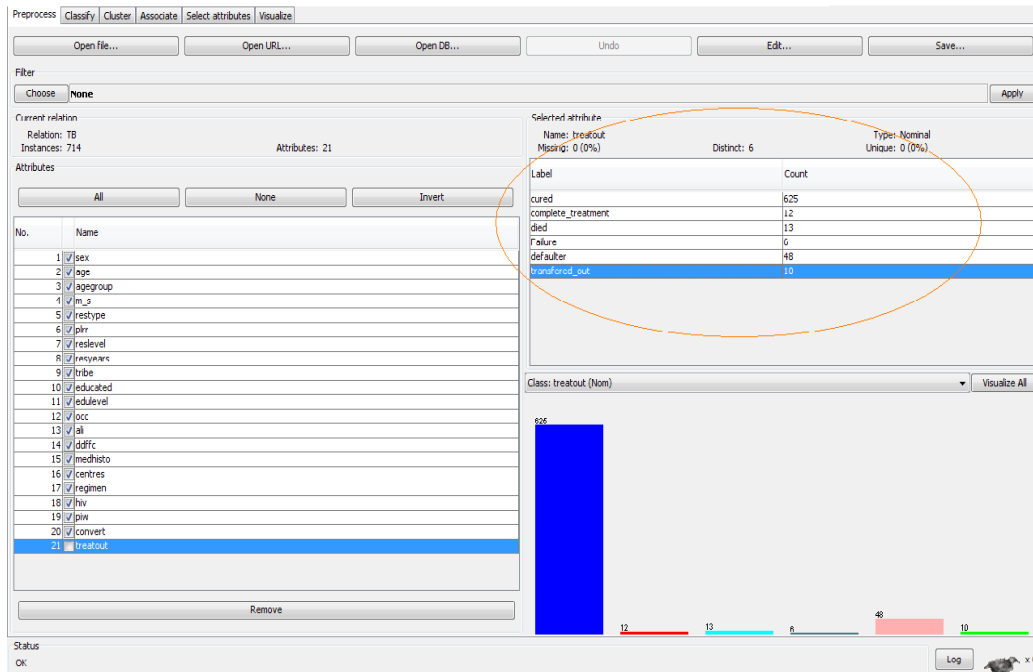


Fig. 2. Data Loading unto the Target Prediction Model

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