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A supervised machine learning approach for diagnosing Lassa fever and viral Hemorrhagic fever types reliant on observed signs

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Abstract

Lassa hemorrhagic fever is an infectious life-threatening fever characterized by bleeding caused by the single-stranded virus of the Arenaviridae virus family transmitted to humans via contact with blood, urine, food, or household items contaminated with rodent urine and/or feces, and other body secreted fluids from an infected person with the Lassa virus. The symptoms of this disease are fever, general weakness, malaise, headache, sore throat, chest pain, nausea, vomiting, bleeding from the mouth and nose just to name a few. In 2011, the World Health Organization (WHO) declared Lassa fever as an endemic and pandemic due to the spread of the Lassa virus in West African countries such as Benin, Ghana, Guinea, Liberia, Mali, Sierra Leone, and Nigeria respectively that has caused millions of death yearly due to a lack of early diagnosis of the ailment in this region. In the recent past, several systems have been developed to diagnose this endemic disease, but they generated a lot of false-negative during testing and were unable to detect Lassa fever, its overlapping symptoms, and Viral Hemorrhagic fever types. Hence, in this paper, we proposed and simulated a model to diagnose Lassa fever, and Viral Hemorrhagic fever types using a machine learning technique called Bayesian Belief Network. The model was designed using Bayes Server and tested with data collected from a Viral Hemorrhagic Fever medical repository. The model had 100% overall prediction accuracy based on test data; with 98.73% sensitivity of Lassa fever, and 98.98 sensitivity of Viral Hemorrhagic fever types in that order.

Keywords: Lassa fever, Viral hemorrhagic fevers, Prediction, Supervised machine Learning, Bayesian belief network

1. Introduction

Fever is described as an increment in body temperature which is usually higher than normal. It is otherwise called pyrexia and febrile response and can virtually affect all and sundry ranging from children to adults. On the other hand, a short-term increase in body temperature can help your body fend off illness. Nonetheless, a severe fever can be a symptom of a serious condition that requires immediate medical attention [1].

Be that as it may, it was stated that for an adult, a fever may be prickly, but usually is not a cause for concern unless it reaches 103 °F which is equivalent to 39.4 °C or even higher. In the case of infants and toddlers, a slightly amplified temperature may indicate a serious infection [2]. A fever can be caused by many medical conditions ranging from non-serious to life-threatening and are characterized by an increment in body temperature.

Conversely, there are two major types of fever namely non-serious and life-threatening. These aforesaid fevers differ based on its duration. For instance, continuous fever (a fever where the temperature remains above normal throughout the day); intermittent fever (temperature increase is present only for a certain period, later returning to normal) and quotidian fever (a fever that has a periodicity of 24 h) are categorized as Non-serious [3,4].

Life-threatening fevers tend to last over a longer period and can lead to death if no medical treatment is administered, examples of this class of fever are tertian fever (a fever with a period of 48 h); Quartan fever (a fever where high temperature persists over a 72 h) and remittent fever (a fever where the temperature stays

normal during the day to oscillate more than 1 °C in the space of 24 h); Pel–Ebstein fever (is a kind of fever associated with Hodgkin's lymphoma, being high for one week and low for the following week); Neutropenic fever (a fever in the absence of normal immune system function), yellow fever, malaria fever, typhoid fever, and viral hemorrhagic fever. Nevertheless, the aforementioned fevers are categorized as life-threatening due to their effect on humans [5,6,7]. Of all the above-mentioned life-threatening fever types, Viral Hemorrhagic fever is quite deadly owing to its hemorrhagic nature.

Viral Hemorrhagic fever (VHF) is a group of potentially life-threatening infections associated with fever and bleeding as defined by [8]. VHFs may be caused by five distinct families of RNA viruses namely the families of Arenaviridae, Filoviridae, Bunyaviridae, Flaviviridae, and Rhabdoviridae. All types of VHF are characterized by fever and bleeding disorders and all can progress to high fever, shock, and death in many cases. Examples of VHFs are Crimean Congo hemorrhagic fever, Ebola virus disease, Marburg virus disease, Omsk hemorrhagic fever, and Lassa fever just to name but a few.

However, in this paper, we intend to focus on Lassa fever due to the zoonotic and endemic nature of its virus which is transmitted from animal to human and human to human in a direct or indirect mode.

Lassa fever is a type of Viral Hemorrhagic fever caused by the infectious Lassa virus, which is a member of the Arenaviridae virus family, a single-stranded RNA virus that is zoonotic and transmitted to humans via contact with food or household items contaminated with rodent urine, feces, and other body secreted fluids from a Lassa virus-infected person. Furthermore, the Lassa virus has an incubation period of 2 to 21 days in humans after contact with the virus. Conversely, Lassa fever is quite predominant in Sub-Sahara Africa especially in the region of West Africa where the ailment was first discovered in 1969 when two missionary nurses died of the virus in a town called Lassa in Nigeria. Moreover, the virus was eventually named after the town in Nigeria because it was there the first outbreak occurred [9].

From the onset of the disease, it is symptomatic and usually gradual, starting with fever, general weakness, and malaise. After a few days, headache, sore throat, muscle pain, chest pain, nausea, vomiting, diarrhea, cough, and abdominal pain may follow. In severe and critical cases, facial swelling, fluid in the lung cavity, bleeding from the mouth, nose, vagina, or gastrointestinal tract, respiratory distress, and low blood pressure may develop. However, 80% of the mainstream Lassa fever infections in individuals have the aforementioned symptoms with severity level which tends to be non-existent (asymptomatic), mild and moderate; while the other 20% of infections in persons tend to advance to more severe and critical level with a distinctive feature of hemorrhaging to some vital parts of the body and neurological problems such as loss of hearing, tremors, and encephalitis. Nonetheless, deaths may be recorded within two weeks after symptom begins to manifest owing to the failure of several organs in the body as a result of excessive bleeding.

In West Africa, the number of Lassa fever infections yearly approximately stands at 100,000 to 300,000 confirmed cases with over 5,000 reported deaths and counting [10]. Furthermore, in some West African countries like Sierra Leone and Liberia, it was affirmed that yearly 10% to 16% of patients admitted in hospitals have the Lassa fever virus which signifies the severe impact of the virus on the population of this region.

In a similar report of the World Health Organization (WHO), Lassa fever was categorized as endemic and pandemic due to the spread of the Lassa virus in Benin, Ghana, Guinea, Liberia, Mali, Sierra Leone, and Nigeria, but almost certainly subsists in other West African countries as well [11].

Owing to the pandemic nature of the disease, diagnosis of Lassa fever required definitive testing that was only available in specific laboratories because laboratory specimens are sometimes perilous and must be handled with extreme care.

Lassa virus infections can only be diagnosed definitively in the laboratory using the following tests namely reverse transcriptase-polymerase chain reaction (RT-PCR) assay, antibody enzyme-linked immunosorbent assay (ELISA), antigen detection tests, and virus isolation by cell culture. Since the symptoms of Lassa fever vary and are non-specific, clinical diagnosis is often difficult and insidious especially early in the course of the disease. One distinctive feature of Lassa fever is that it is difficult to distinguish from other viral hemorrhagic fevers like Ebola virus disease and other disease causing-fever such as malaria, shigellosis, typhoid fever, and yellow fever due to the overlapping symptoms they share in common.

Owing to this aforesaid unique characteristic, the aforementioned diagnostic methods for diagnosing Lassa fever had the following issues such as usage of RT-PCR testing can lead to false results owing to the contamination of deoxyribonucleic acid (DNA), ELISA is labor-intensive and quite expensive to prepare antibody because it is a sophisticated technique that has some degree of antigen information concerns; cell culture method requires a lot of time for the viral stimulated transform to become visible, which sometimes takes weeks to months.

Due to the shortfalls of the aforementioned diagnostic methods, there is the need to design a less difficult and faster method for diagnosing the disease. Hence, the use of machine learning technique to diagnose this disease will serve as an alternative which will help provide information that can be employed to safeguard against this kind of disease before its actual incubation.

However, Artificial Intelligence (AI) has been applied in diagnosing Lassa fever and Hemorrhagic fevers in the works of [12-25] respectively.

In this paper, a supervised machine learning technique called Bayesian Belief Network (BBN) was utilized in diagnosing Lassa fever with its symptoms. BBN is a multifaceted probabilistic network that merges expert knowledge and observed data sets. It maps out a route for cause and effect associations between variables and trains them with a probability that indicates the level at which one variable is likely to sway another.

Conversely, BBN was our method of choice on account of its ability to make a prescient inference. The chosen approach uses the Bayes theorem which is a statistical technique that guides high accuracy in terms of predicting, detecting events, and their occurrences based on data sets made available for training and testing of the model.

One significant feature our proposed model has over existing systems is its ability to diagnose Lassa fever just as the overlapping symptoms it has with other viral hemorrhagic fevers which will bring forth improvement in the following areas: the anticipation of Lassa fever, recognition of Lassa fever, and diagnosis of Viral Hemorrhagic fever with concluding outcomes identified with Lassa fever .

Furthermore, the abovementioned distinctive feature of our proposed model serves as a new contribution to knowledge in the area of detection, prediction of Lassa fever, Viral Hemorrhagic Fever types, and other forms of fevers using AI as an approach.

In any case, the rest of the paper is sorted out as follows: Section 2 contains the related works on Lassa fever and Viral Hemorrhagic Fever types diagnosis utilizing AI, Section 3 clarifies the chosen supervised AI method BBN used in diagnosing Lassa fever and Viral Hemorrhagic fever types, Section 4 contains the simulation, results and discussion and Section 5 finishes up research work with future directions.

2. Materials and methods

In the time past, several studies have been conducted on diagnosing Lassa fever using machine learning techniques.

Tunmibi et al. [12] presented a rule-based expert system called e-Diagnosis that diagnosed Lassa fever and other types of fever. The system results helped reduce overcrowding at the hospitals, cost-effective, reliable, and had a high-level of detection accuracy of various types of fever. Osigbemeh et al. [13] proposed an expert system that diagnosed contagious diseases using Fuzzy logic as an approach. The expert system detected contagious diseases such as Lassa fever and Ebola fever with 90% detection accuracy. Osaseri and Osaseri [14] developed an expert system that employed the Adaptive Neuro-Fuzzy Inference System (ANFIS) for the prediction of Lassa fever. The system predicted Lassa fever with high detection accuracy. Abiola et al. [15] designed a medical expert system for diagnosing Lassa fever based on rules. The system aimed to replace the manual method of diagnosing Lassa fever still been practiced by medical professionals, with an Expert System (ES) which had the capability of correcting all the limits associated with the manual method of diagnosing Lassa fever . The system detected Lassa fever with high detection accuracy. Ajenaghughrure et al. [16] proposed an integrated expert system that diagnosed several types of fever using Fuzzy Logic as an approach. Nevertheless, the expert system showed detected the symptom relationship between the various types of fevers namely Dengue Hemorrhagic fever, Malaria fever, Typhoid fever, Lassa fever , and Yellow fever respectively, with the fuzzy rules applied accurately determining the type of fever first, and then ascertained the level of infection to be either mild or severe. Aminu et al. [17] presented an expert system diagnosing Lassa fever and related ailments using Fuzzy Logic. The system diagnosed Lassa fever and related ailments with high detection accuracy. Nnebe et al. [18] proposed a Neuro-fuzzy system to detect Lassa fever based on observed symptoms. The system detected cases of Lassa fever with high detection accuracy based on the twenty-nine observed symptoms captured. Steur and Mueller [19] presented a system that classified Viral Hemorrhagic Fever (VHF) with emphasis on Ebola and Lassa fever using Neural Network (NN). The system detected Ebola and Lassa fever with high detection accuracy. Egwali and Obi [20] developed a Neuro-fuzzy system to identify Ebola Hemorrhagic fever (EHF). The system detected EHF with high detection accuracy based on symptoms using 29 clinical signs and indications which were classified into 5 levels. Govinda et al. [21] designed a multi-fever expert system to detect Dengue Hemorrhagic fever, Malaria fever, and Typhoid fever using a rule-based technique called Fuzzy Logic. The system was able to determine the level of infection ranging from mild to severe with high detection exactness, and also make recommendations where necessary on food and drugs to be administered to infected patients. Djam et al. [22] developed an expert system for handling malaria termed fuzzy expert system for the management of malaria (FESMM). The system detected malaria with high detection accuracy based on clinical observations, medical diagnosis, and expert knowledge. Besides, the system also served as a decision support system (DSS) for healthcare practitioners in malaria-endemic regions.

Alile and Bello [23] presented a model for detecting Dengue Haemorrhagic fever (DHF) using a machine learning technique called Bayesian Belief Network. The proposed model detected Dengue Haemorrhagic fever using data retrieved from Dengue Haemorrhagic fever medical repository and had 99.84% prediction precision

based on test data. Imanov and Asengi [24] proposed an expert system for diagnosing Lassa fever using Artificial Intelligence. The system diagnosed Lassa fever with high detection accuracy, with the system's outcomes authenticated and supported by specialized medical personnel based on his analysis. Furthermore, the system could analyze Lassa fever where the number of infected patients is high. On the other hand, the system also assists medical experts with speedy, precise determinations and can be used in situations where is a shortage or no medical expert available. Alile [25] presented a model for early diagnosis of cerebral malaria, multi-fever, and mosquito-borne diseases using a supervised machine learning approach called Bayesian Belief Networks. The proposed model detected cerebral malaria, mosquito-borne diseases, and other types of fevers such as Dengue Hemorrhagic Fever, Malaria Fever just to name but a couple with an overall prediction exactness of 99.98% based on test data. Notwithstanding, Table 1 below shows a summary of the existing systems discussed above showing the ailment type, the artificial intelligence (AI) Technique employed to diagnose the ailment type, aims, and objectives, as well as the strengths.

Table 1 A summary table of existing systems.

S/N	Diagnosed ailment type	Utilized AI technique	Aims and objectives	Strengths
1.	Fever [12].	Fuzzy Logic	To Detect Various Types of fevers Using Fuzzy Logic.	The system was cost-effective, reliable, and had a high-level of detection accuracy of various types of fever.
2.	Contagious Diseases [13].	Fuzzy Logic	To diagnose contagious diseases such as Lassa fever and Ebola Virus Using Fuzzy Logic.	The expert system detected contagious diseases such as Lassa fever and Ebola fever with 90% detection accuracy.
3.	Lassa fever [14].	Neuro-Fuzzy	To predict Lassa fever Using the Adaptive Neuro-Fuzzy Inference System (ANFIS).	The system predicted Lassa fever with high detection accuracy.
4.	Lassa fever [15].	Fuzzy Logic	To replace the manual method of diagnosing Lassa fever still been practiced by medical professionals by designing a medical expert system for diagnosing Lassa fever based on Fuzzy Logic rules.	The Expert System (ES) had the capability of correcting all the limits associated with the manual method of diagnosing Lassa fever. Also, the system detected Lassa fever with high detection accuracy.
5.	Multi-fever (Dengue Hemorrhagic fever, Malaria fever, Typhoid Fever, Lassa fever, and Yellow Fever) [16].	Fuzzy Logic	To develop an expert system that diagnosed several types of fever using Fuzzy Logic.	The system showed the relationship between the various types of fever and accurately determined the type of fever, then discovered the level of infection which was either mild or severe.
6.	Lassa fever [17].	Fuzzy Logic	To identify Lassa fever and related ailments Using Fuzzy Logic as an Approach.	The system diagnosed Lassa fever and related ailments with high detection accuracy.
7.	Lassa fever [18]	Neuro-Fuzzy	To detect Lassa fever based on observed manifestations	The system identified cases of Lassa fever with high detection accuracy based on the twenty-nine observed symptoms captured.
9.	Ebola Virus and Lassa fever [19].	Neural Networks	To classify Viral Hemorrhagic fever (VHF) with prominence on Ebola and Lassa fever	The system recognized Ebola and Lassa fever with high detection accuracy.
10	Ebola Hemorrhagic fever [20].	Neuro-Fuzzy	To detect Ebola Hemorrhagic fever (EHF)	The system identified Ebola Hemorrhagic Fever based on symptoms using 29 clinical signs and manifestations which were classified into 5 levels, hence resulting in high detection accuracy of EHF.
12.	Malaria Fever [22].	Fuzzy Logic	To detect Malaria fever	The system detected malaria with high detection accuracy based on clinical examinations, medical analysis, and expert knowledge. The system served as a decision support system (DSS) for healthcare practitioners.
13.	Dengue Hemorrhagic fever [23]	Bayesian Belief Network	To Detect Dengue Hemorrhagic fever (DHF)	The model detected DHF with 99.84% prediction accuracy. Also, the system identified their types of fever.
14.	Lassa fever [24]	Artificial Intelligence	To Diagnose Lassa fever	The proposed framework diagnosed Lassa fever in patients with high detection accuracy. Besides, the system assisted the health professionals with a swift, correct diagnosis, and can be employed where there is little or no expertise.
15.	Cerebral Malaria, Multi-fever, and Mosquito-Borne Diseases [25]	Bayesian Belief Network	To Diagnose Cerebral Malaria, Multi-fever, and Mosquito-Borne Diseases.	The proposed model detected Cerebral Malaria, Multi-fever, and Mosquito-Borne Diseases with 99.98% prediction precision.

2.1 Raw material

The data set whose snapshot is shown in Figure 2 was utilized by our chosen machine learning technique called BBN to predict Lassa fever and Hemorrhagic fever types which were retrieved from the Health data Machine Learning repository for Hemorrhagic fevers. The machine learning data set was trained, tested, and aided in the design of a model for predicting Lassa fever and Hemorrhagic fever types which are shown in Figure 3.

2.2 Methodology

In this paper, the method we intend to utilize in predicting Lassa fever, Viral Hemorrhagic fever, and the overlapping symptoms that exist amongst them is a non-invasive artificial intelligence (AI) method called Machine Learning.

Machine Learning is a branch of artificial intelligence that deals with the design of models and the development of algorithms that allows computers to make predictions via training and testing of data sets [26]. What is more, training is the process of making the system or model able to learn while testing is the process of establishing the correctness of forecasts made by the model after learning from data. More to the point, all machine learning algorithms have 3 components namely representation, evaluation, and optimization respectively. Representation is the pictorial depiction or physical structure of the designed machine learning model. For instance, machine learning techniques that depict models are in form of decision trees, graphical models (Bayes/Markov nets), neural networks, support vector machines (SVM), sets of rules/logic programs, instances, and model ensembles just to name but a few; Evaluation is the use of numerical expressions to calculate the designed model's prediction accuracy, the likelihood of instances occurring, cost, utility, and entropy just to name but a couple; and Optimization is a process of getting the best results from the designed model using different optimization techniques such as combinatorial optimization (Greedy search), convex optimization (Gradient descent), and Constrained optimization (Linear programming) respectively [26].

Nonetheless, there are four major approaches of machine learning that conform to the three (3) key aforesaid components of machine learning algorithms; they are namely Supervised Learning, Semi-Supervised Learning, Unsupervised Learning, and Reinforcement Learning.

Supervised Learning is a feature of pattern recognition that utilizes a set of named instances deemed as training data alongside the expected desired outcome. With the employment of the named instances, a predictive model is obtained during the training stage to categorize newly generated data sets. This process is realized by supplying the named instances into a definite machine learning algorithm. Examples of techniques that utilize this type of learning are BBN (Naïve Bayes), Neural Networks, Deep Learning, Decision Trees such as C4.5 and ID3 algorithms, Artificial Neural Network, K-Nearest Neighbor (KNN), Support Vector Machine (SVM), Hidden Markov Model (HMM), and so on; Unsupervised Learning unravels patterns in unnamed data set employed as training data with the sole aim of making accurate classification decisions in a set of newly formed instances. Also, it generally entails the application of clusters to recognize the classes each instance fits into. For example, Grouping and Dimensionality Reduction are techniques under this form of machine learning; Semi-Supervised Learning coalesces the merits of supervised and unsupervised learning techniques in the course of designing a model meant for classification of fresh instances of a data set; and Reinforcement Learning is a form of machine learning that permits a software agent, for instance, a sensor to gain and learn from series of activities such as interaction with its immediate environment. Examples of Reinforcement Learning techniques are Temporal Difference Learning and Q-learning just to name but a few [27].

Thus, in this paper, we intend to employ a supervised machine learning approach called BBN. BBN is a directed acyclic graphical model that utilizes probability to demonstrate conditional dependencies that prevail amongst nodes on a graph [28]. It is a complex probabilistic network that merges expert knowledge and observed data sets. It maps out the cause and effect relationships between variables and encodes them with a probability that signifies the amount in which one variable is probable to influence another. All the same, BBN is based on a probabilistic theorem called Bayes theorem, and is represented in the mathematical formula below:

$$P(a|b) = \frac{P(b|a)P(a)}{P(b)} \quad (1)$$

where, P(a) is the probability of the event "a" happening without any information about event "b". It is called the "Prior". P(a|b) is the conditional probability of the event "a" happening given that event "b" has already occurred. It is otherwise called the "Posterior".

P (b|a) is the conditional probability of event "b" happening given that event "a" has already occurred. It is called the "Likelihood".

P (b) is the probability of event "b" happening without any information about event "a". It is called the "Marginal Likelihood".

The Naive Bayes classifiers are often represented as a type of directed acyclic graph (DAG). The DAG comprises vertices representing random variables and arrows connecting pairs of nodes. Figure 1 shows a pictorial representation of a Bayesian Belief Network.

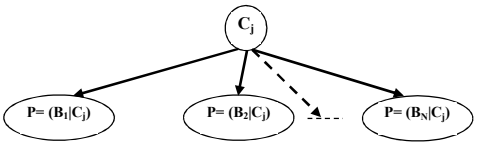

Figure 1 A Pictorial Representation of a Bayesian Belief Network.

Some advantages of this model are: it is quite quick in making inferences, the resulting probabilities are easy to interpret, the learning algorithm is quite easy to understand and the model adequately combines with utility functions to make optimal inferences. In this paper, we intend to detect Lassa fever, its symptoms, and Viral Hemorrhagic fever (VHF) disease types using a supervised machine learning technique called BBN. A model consisting of 88 nodes where some nodes represent a form of disease ailment or factors that influence the diagnosis of Lassa fever and its symptoms will be designed using Bayes Server. A Viral Hemorrhagic fever data set will be used to train and test the system. Using the Pareto Principle, 80% of the data set will be used to train the model while the remainder will be used in testing the model. The model aims to achieve a high level of detection accuracy with the use of the overlapping symptoms of Lassa fever and various types of Viral Hemorrhagic fevers.

3. Results and discussion

3.1 Data set

The data set utilized for predicting Lassa fever and Viral Hemorrhagic fevers was retrieved from [29]. The data set consists of Lassa fever, Viral Hemorrhagic fevers, types, features, and factors that aid prediction of the aforementioned diseases arranged in the order of 88 columns and 51 rows respectively. The Bayesian Belief Network model was designed using the data set below on the Bayes-Server platform. The values are between 0 and 1 because the probability of events occurring can be greater than 0 but less than 1. However, Figure 2 below shows a snapshot of the data set which contains ailments and factors that aids the diagnosis of Lassa fever, Viral Hemorrhagic fever, and types.

Infectious &	Intermittent	Irritability	KFD	Lassa Fever	LCM	Life-Threatening	Liver Failure	Loss of Appetite	Loss of Hearing	Low Blood	Low Platelet	LUHF
1.1	0.739	-0.744	0.822	1.08	-0.488	0.556	1.91	1.01	-1.58	0.388	0.701	-0.0899
0.389	0.129	-0.203	-0.59	0.06	-1.59	-1.72	-0.887	-3.41	0.871	-1.49	-1.68	-2.17
0.213	-0.669	0.312	-0.683	-0.185	-0.363	0.516	-0.861	-0.523	-1.54	-1.28	0.523	0.623
-0.766	0.649	1.7	-0.052	-1.01	-0.867	1.37	-0.0859	2.41	0.493	0.988	0.412	-1.04
1.59	1.08	1.6	0.319	-2.27	-1.42	0.232	-0.362	-0.234	-2.02	-2.02	1.09	-0.179
0.105	0.583	0.482	1.08	1.08	-0.921	-0.128	-1.25	1.49	1.37	-0.358	-2.17	-0.261
-0.758	-0.0178	-0.278	-1.61	1.53	-0.311	-0.23	-1.27	0.906	0.39	0.336	-1.61	1.09
1.03	0.946	0.0543	-0.455	-0.163	0.105	-0.627	1.52	-0.0199	-0.0491	0.199	-0.442	-0.0821
-0.219	-0.223	0.143	1.76	1.18	0.306	0.799	-0.25	-0.397	-1.35	0.49	0.976	-1.19
-1.85	-0.902	0.462	1.61	-0.00333	-1.61	-0.738	-1.6	0.26	-0.371	-0.396	-0.0826	1.12
-1.44	-1.21	-0.795	0.501	-0.679	-0.609	1.12	-1.95	0.658	0.896	0.249	-0.605	-0.456
1.8	0.44	-0.562	-0.689	0.739	-0.265	0.168	-0.274	0.436	-0.911	1.16	-0.311	-0.782
-1.74	0.907	-0.0126	-0.00522	-1.41	0.224	1.25	0.529	-1.15	0.578	0.451	-0.212	-2.66
0.155	0.0914	-0.707	-0.254	0.0428	-1.16	-0.0388	-0.191	-0.166	0.505	-0.926	-0.134	1.48
-0.338	-1.03	-0.381	-0.379	-1.21	0.506	-1.03	0.453	0.191	0.159	1.02	0.674	2.27
-3.14	0.517	1.23	0.307	-1.75	-1.39	1.46	1.09	-0.11	-0.658	0.6	-0.555	-0.763
-0.833	1.11	0.603	-0.002	0.36	-0.934	-0.787	-0.00569	-0.268	-0.256	1.46	-1.47	-0.638
-1.3	-1.02	-0.312	-0.629	1.44	-1.12	0.481	1.25	-1.01	0.857	0.238	-0.359	0.968
-0.413	-0.513	-0.774	-1.68	0.462	-0.339	0.423	-1.72	-0.648	-0.0258	0.631	1.09	0.801
0.516	-0.888	-0.333	0.326	0.599	-0.706	0.0288	2.12	0.56	-0.294	2.83	0.157	-0.707
-1.56	-0.914	0.488	0.613	2.29	-1.07	0.206	0.504	-1.16	-0.826	0.88	-1.23	-0.283
0.259	-0.412	1.11	1.47	-0.15	1.94	1.33	1.22	-1.31	1.67	-1.63	0.672	0.214
0.876	-0.741	2.1	0.498	-0.906	0.776	-0.61	1.27	-0.124	2.03	-1.75	0.471	-0.351
-0.271	-0.201	1.03	-0.43	0.829	-0.894	0.0931	-0.428	0.243	-2.17	-0.343	-0.0257	-0.702

Figure 2 Snapshot of data set.

3.2 Simulation

The simulation was conducted using the data set in Figure 2 in training, testing, and predicting Lassa fever, and Viral hemorrhagic fever. Be that as it may, previews of the used data set, designed BBN model for predicting Lassa fever, Viral Hemorrhagic fever and their manifestations, BBN model convergence chart, loglikelihood batch query chart, likelihood plots of ailments being the cause of Lassa fever and Viral Hemorrhagic fever, loglikelihood graph for detecting Lassa fever; likelihood against loglikelihood plot for predicting Lassa fever, Viral Hemorrhagic fever and symptoms, and the proposed BBN model prediction accuracy via confusion matrix were taken during the simulation process and appear beneath in figures

2,3,4,5,6,7,8,9, and 10 respectively with simulation results tabulated and analyzed for easy understanding just before the diagrams.

The data set consists of a mixture of disease ailments, and factors that are taken into consideration in the detection of Lassa fever (LHF) amounting to 88 with each ailment and factor having a value that represents the probability of such disease ailment and factor causing Lassa fever. The ailments and factors are shown in Table 2 below**.**

Table 2 Ailments and factors that are taken into consideration in the detection of Lassa fever and Viral Hemorrhagic fever types**.**

Ailments		Factors
Abdominal Pain	Acute Kidney Failure	Arenaviridae Virus
Alkhurma Hemorrhagic Fever (AHF)	Back Pain	Incubation Period (2 to 21)
Bleeding	Bleeding of the Privates	
Blurred Vision	Chapare Hemorrhagic Fever (CHHF)	
Chest Pain	Cold	
Confusion	Continuous Fever	
Cough	Delirium	
Diarrhea	Dizziness	
Drowsiness	Ebola Virus Disease (EVD)	
Eyes Pain	Facial Swelling	
Fatigue	Fever	
Gastrointestinal Tract Bleeding	Headache	
Hemorrhagic Fever with Renal Syndrome (HFRS)	Intermittent Fever	
Irritability	Joint Pain	
Kyasanur Forest Disease (KFD)	Lassa fever	
Life-Threatening Fever	Liver Failure	
Loss of Hearing	Low Blood Platelet	
Low Blood Pressure	Lujo Hemorrhagic Fever (LUHF)	
Lymphocytic Choriomeningitis (LCM)	Maculopapular Rash	
Malaise	Malaria Fever	
Marburg Hemorrhagic Fever (MarburgHF)	Measles	
Meningitis	Meningoencephalitis	
Mental Disturbances	Mild Jaundice	
Motor Abnormalities	Mouth Bleeding	
Multi-Organ Dysfunction	Muscle Pain	
Nausea	Neck Swelling	
Neurological Problems	Neutropenic Fever	
Non-Serious Fever	Nose Bleeding	
Paralysis	Pel-Ebstein Fever	
Quartan Fever	Quotidian Fever	
Rash	Red Blood Cell Count	
Redness of Eyes	Remittent Fever	
Respiratory Distress	Rift Valley Fever (RVF)	
Salivary Gland Pain	Sensory Disturbances	
Shock	Sore Throat	
Stiff Neck	Stomach Pain	
Swollen Pancreas	Tertian Fever	
Testicular Pain	Tick-Borne Encephalitis (TBE)	
Tremors	Typhoid Fever	
Vascular Leakage	Viral Hemorrhagic Fever (VHF)	
Vomiting	Weakness	
Weight Loss	White Blood Cell Count	
Yellow Fever		

3.3 BBN model for diagnosing Lassa fever, viral hemorrhagic fever types, and their symptoms

BBN for predicting Lassa fever, its symptoms, and Viral Hemorrhagic Fever types were designed such that the nodes on the network are linked based on the probability of a disease resulting in another and factor influencing another factor. In our model for a case to be denoted as a Lassa fever, the ailments, disease-causing agents, and other factors taken into cognizance in the diagnosis of Lassa fever are shown in Table 3 below.

Table 3 Ailments, disease-causing agents and factors taken into cognizance in the diagnosis of Lassa fever.

Ailments		Disease-Causing Agents	Other Factors
Abdominal Pain	Acute Kidney Failure	Arenaviridae Virus	Incubation Period (2 to 21)
Alkhurma Hemorrhagic Fever (AHF)	Back Pain		
Bleeding	Bleeding of the Privates		
Blurred Vision	Chapare Hemorrhagic Fever (CHHF)		
Chest Pain	Cold		
Confusion	Continuous Fever		
Cough	Delirium		
Diarrhea	Dizziness		
Drowsiness	Ebola Virus Disease (EVD)		
Eyes Pain	Facial Swelling		
Fatigue	Fever		
Gastrointestinal Tract Bleeding	Headache		
Hemorrhagic Fever with Renal Syndrome (HFRS)	Intermittent Fever		
Irritability	Joint Pain		
Kyasanur Forest Disease (KFD)	Lassa fever		
Life-Threatening Fever	Liver Failure		
Loss of Hearing	Low Blood Platelet		
Low Blood Pressure	Lujo Hemorrhagic Fever (LUHF)		
Lymphocytic Choriomeningitis (LCM)	Maculopapular Rash		
Malaise	Malaria Fever		
Marburg Hemorrhagic Fever (MarburgHF)	Measles		
Meningitis	Meningoencephalitis		
Mental Disturbances	Mild Jaundice		
Motor Abnormalities	Mouth Bleeding		
Multi-Organ Dysfunction	Muscle Pain		
Nausea Neck Swelling			
Neurological Problems	Neutropenic Fever		
Non-Serious Fever	Nose Bleeding		
Paralysis	Pel-Ebstein Fever		
Quartan Fever	Quotidian Fever		
Rash	Red Blood Cell Count		
Redness of Eyes	Remittent Fever		
Respiratory Distress	Rift Valley Fever (RVF)		
Salivary Gland Pain	Sensory Disturbances		
Shock	Sore Throat		
Stiff Neck	Stomach Pain		
Swollen Pancreas	Tertian Fever		
Testicular Pain	Tick-Borne Encephalitis (TBE)		
Tremors	Typhoid Fever		
Vascular Leakage	Viral Hemorrhagic Fever (VHF)		
Vomiting	Weakness		
Weight Loss	White Blood Cell Count		
Yellow Fever			

Furthermore, Figure 3 below shows the BBN model for detecting Lassa fever, Viral Hemorrhagic Fevers (VHFs), and their symptoms.

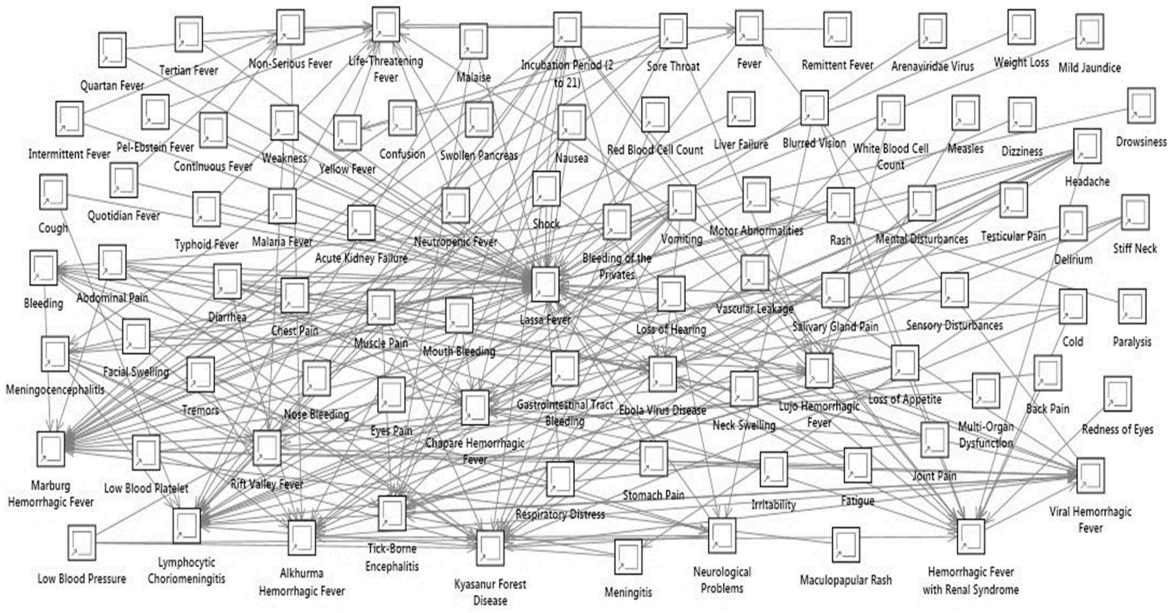

Figure 3 Bayesian belief network model for diagnosing Lassa fever, Viral Hemorrhagic fever types, and their symptoms.

So, to mathematically represent our model we have:

$$\text{Lassa fever} = \prod_{i=1}^{88} P\,(\text{Disease}_i|\text{Parents}(\text{Disease}_i)) \quad (2)$$

where,
$\prod$ is Capital pi. where the range is from number 1 to number 88
Disease: Node with a Disease Ailment
Parents (Disease_i) = Nodes that converge on Disease Ailment_i
The data set was used to train and test the model. Upon completion of training and testing the BBN model, the test data converged at time series 2. The log-likelihood value for each case was recorded.

3.4 Convergence chart of Lassa fever, viral hemorrhagic fever types, and symptoms at iteration count 2

The Convergence chart for the BBN model in Figure 3 shows the time the model was created, Convergence checkbox ticked to show that the model converged at iteration count 2, a loglikelihood value of -646.501995256 689, and Bayesian Information Criterion (BIC) value of 1934.57576340359.

Nevertheless, Figure 4 below shows the BBN model convergence of Lassa fever and its symptoms at Iteration Count 2.

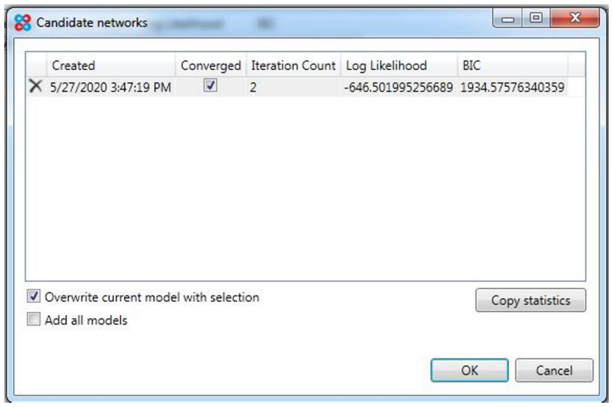

Figure 4 Bayesian Belief Network Model for Diagnosing Lassa fever, Viral Hemorrhagic Fevers, and Their Symptoms Converging at Time Series 2.

3.5 Simulation results

The simulation conducted in Figure 3 produced results in form of charts which can be seen in Figures 5, 6, 7, 8, 9, and 10 respectively. The charts produced during the simulation process are loglikelihood batch query chart for predicting Lassa fever, Viral Hemorrhagic Fever types, and their symptoms; the likelihood plot showing the relation of combined Arenaviridae and Viral Hemorrhagic Fever leading to Lassa fever infection case and its probabilities; the likelihood plot showing the relation of Viral Hemorrhagic Fever types leading to an infectious and pandemic disease infection and its probabilities; the loglikelihood graph for detecting Lassa fever, its symptoms and VHFs; the likelihood against loglikelihood graph for predicting Lassa fever with its symptoms, and the proposed BBN model prediction accuracy via confusion matrix respectively. The result generated from the simulation indicated that the network was able to predict >99% of Lassa fever on the data set accurately, and it had a loglikelihood of 92.45 on the test data set.

3.5.1 Loglikelihood batch query chart for predicting Lassa fever, viral hemorrhagic fever types, and their side-effects

This loglikelihood batch query chart shows the result of the test data. Here, 50 experimental cases were conducted and the analysis of the results generated from the test data is shown in Table 4 below.

Table 4 Loglikelihood batch query chart for predicting Lassa fever, Viral Hemorrhagic fever types, and their side-effects simulation results.

S/N	Predict(Lassa fever)	Predict (VHF)	(Arenaviridae Virus)	Predict(Incubation Period (2 to21 days))
Experiment 1	0.267	0.444	0.705	0.85
ORIGINAL DATA SET				
Test Data	0.267001161	0.443601342	0.7048121	0.85001244
Sensitivity	26.7%	44.4%	70.5%	85%
Experiment 2	0.268	0.916	0.234	0.884
ORIGINAL DATA SET				
Test Data	0.2680021321	0.915810001	0.233601124	0.88391311
Sensitivity	26.8%	91.6%	23.4%	88.4%
Experiment 3	0.323	0.342	0.304	0.267
ORIGINAL DATA SET				
Test Data	0.322711423	0.3418016215	0.303910583	0.267022200
Sensitivity	32.3%	34.2%	30.4%	26.7%

Be that as it may, Figure 5 below shows a pictorial representation of the loglikelihood batch query chart for predicting Lassa fever, Viral Hemorrhagic fever types, and their side-effects.

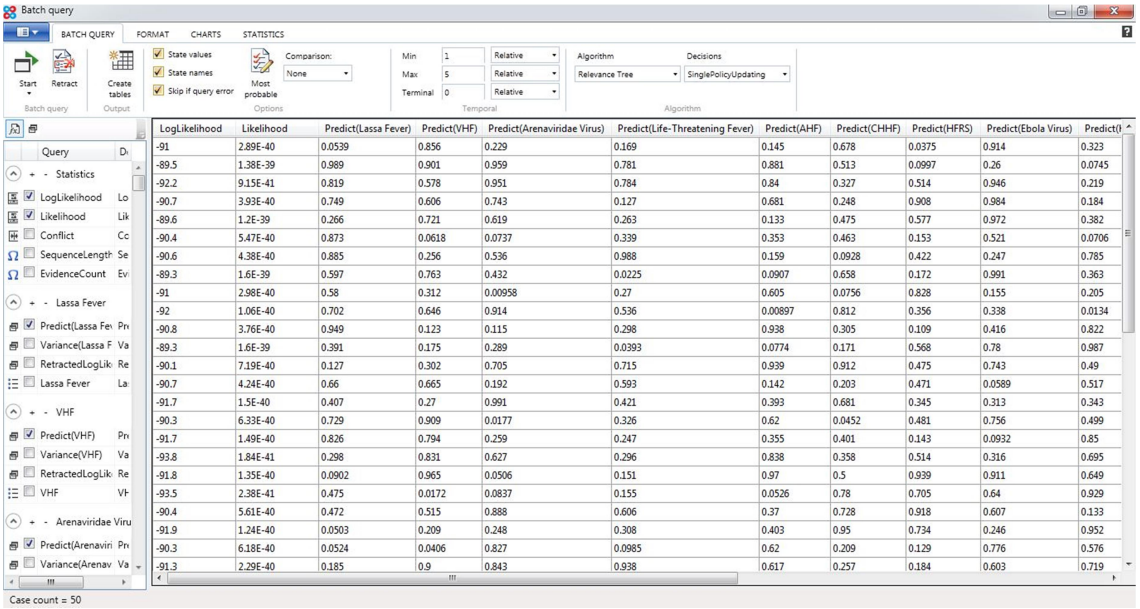

Figure 5 Loglikelihood chart batch query for predicting Lassa fever, Viral Hemorrhagic Fever types, and their symptoms.

3.5.2 Likelihood plot showing relation of combined viral hemorrhagic fever and arenaviridae virus as the cause of Lassa fever and its probabilities in the BBN model

The likelihood plot shows the possibility of Viral Hemorrhagic Fever and Arenaviridae virus(Combined) being the cause of Lassa fever Infection. In this plot, 50 experimental cases were taken into consideration with each colored point in the graph classified as a case (instance) and assigned a probability that is stationed on the right of the graph. The Viral Hemorrhagic Fever and Arenaviridae virus(Combined) on the Y-axis is plotted against Lassa fever on the X-axis. However, from this graph, there are five diagnostic classes of combined Viral Hemorrhagic Fever and Arenavirida virus infection which our system was able to detect; they are asymptomatic, mild, moderate, severe, and critical classes respectively.

Table 5 below shows the summary of the likelihood plot for combined Viral Hemorrhagic Fever and Arenaviridae Virus as the cause of Lassa fever and its probabilities in the BBN model in Figure 3.

Table 5 Results of likelihood plot for combined Viral Hemorrhagic Fever and Arenaviridae Virus as the cause of Lassa fever, and its probabilities

Class of Infection	Probabilistic Interval on Y-axis	Probabilistic Interval on X-axis	Number of Detected Cases	Prediction Status
Asymptomatic	0 to 0.2	0.000193 to 1.002	12	Asymptomatic
Mild	0.2 to 0.4	0.000193 to 1.002	8	Mild
Moderate	0.4 to 0.6	0.000193 to 1.002	8	Moderate
Severe	0.6 to 8	0.000193 to 1.002	10	Severe
Critical	0.8 to 1	0.000193 to 1.002	12	Critical

- Total Number of Cases Highest Probability Value Attained 50 0.987268157559792.
- Overall Probability Value That Can be Reached 1.The Sensitivity of Combined Viral Hemorrhagic Fever and Arenaviridae Virus as the Cause of Lassa fever = 98.73%.

Besides, Figure 6 showcases the likelihood plot showing the relation of combined Viral Hemorrhagic Fever and Arenaviridae virus as the cause of Lassa fever and its probabilities In The BBN Model.

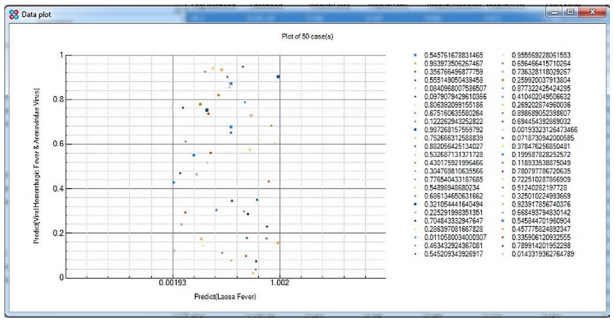

Figure 6 The Likelihood Plot of Viral Hemorrhagic fever and Arenaviridae Virus (Combined) as the Cause of Lassa fever and Its Probabilities In the BBN Model.

3.5.3 Likelihood plot showing relation of viral hemorrhagic fever types as the cause of infectious and pandemic disease (Lassa fever) and its probabilities in the BBN model

The likelihood plot shows the possibility of how contact with Viral Hemorrhagic Fever types leads to an infectious and pandemic disease infection case. In this plot, 50 experimental cases were taken into consideration with each colored point in the graph classified as an instance (case) and assigned a probability that is stationed on the right of the graph. The Predict (Viral Hemorrhagic Fever Types) on the Y-axis is plotted against Predict (Infectious and Pandemic Disease) on the X-axis. However, from this graph, there are five diagnostic classes of Viral Hemorrhagic fever type cases that our system was able to detect; they are asymptomatic, mild, moderate, severe, and critical classes respectively. Table 6 below shows the summary of the likelihood plot for Viral Hemorrhagic fever types as the cause of infectious and pandemic disease (Lassa fever) and its probabilities in the BBN model in Figure 3.

Table 6 Results of likelihood plot for Viral Hemorrhagic Fever types as the cause of infectious and pandemic disease (Lassa fever), and its probabilities.

Class of Infection	Probabilistic Interval on Y-axis	Probabilistic Interval on X-axis	Number of Detected Cases	Prediction Status
Asymptomatic	0 to 0.2	0.009982 to 1.01	10	Asymptomatic
Mild	0.2 to 0.4	0.009982 to 1.01	11	Mild
Moderate	0.4 to 0.6	0.009982 to 1.01	9	Moderate
Severe	0.8 to 1	0.009982 to 1.01	9	Severe
Critical	0.6 to 0.8	0.009982 to 1.01	11	Critical

- The Sensitivity of Viral Hemorrhagic fever Types as the Cause of Infectious and Pandemic Disease (Lassa fever) = 98.98%.

Notwithstanding, Figure 7 below shows the likelihood plot showing the relation of Viral Hemorrhagic Fever types as a cause of infectious and pandemic disease and Its Probabilities In The BBN model.

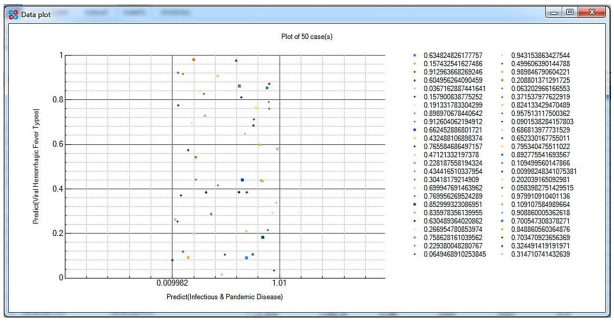

Figure 7 The Likelihood Plot Showing Relation of How Contact with Viral Hemorrhagic Fever Types Leading to an Infectious and Pandemic Disease Infection Case and Its Probabilities In The BBN Model.

3.5.4 The loglikelihood graph for detecting Lassa fever , viral hemorrhagic fever types, and symptoms

This loglikelihood graph for detecting Lassa fever shows the residual values on the vertical axis plotted against the loglikelihood values on the horizontal axis. A residual value is an appraisal of how much a

regression line vertically misses a data point. Regression lines are the superlative fit of a set of data. The lines are classified as average with a few data points fitting the line while others miss the line.

In this graph, 50 experimental cases were conducted which resulted in the values, which are shown in Table 7 below.

Table 7 Results of loglikelihood graph for detecting Lassa fever, Viral Hemorrhagic fever types, and their symptoms.

Number of Plotted Cases	Residual Values	Loglikelihood Values	Resulting Values
50	94	-91.87	92.45
	93	-90.87	92.10
	92	-89.87	92.05
	91	-88.87	91.95
	90	-87.87	91.23
	89	-86.87	91.20
	88	-85.87	91
	87		90
	86		86.02

- Loglikelihood Value For Detecting Lassa fever, Viral Hemorrhagic Fever Types, and Their Symptoms = 92.45.

Conversely, residual values should be evenly and randomly spaced around the horizontal lines. Critically, observing the system' experimental results values obtained from the horizontal lines on the graph, it can be seen that the point where the highest residual value and the loglikelihood independent variable attained meets at -91.87 on X-axis and 92.45 on Y-axis, with 94 being the maximum value that can be attained by the system. Hence, the Loglikelihood value of detecting Lassa fever with its Symptoms is 92.45.

On the other hand, Figure 8 shows the loglikelihood graph for detecting Lassa fever, Viral Hemorrhagic fever types, and symptoms.

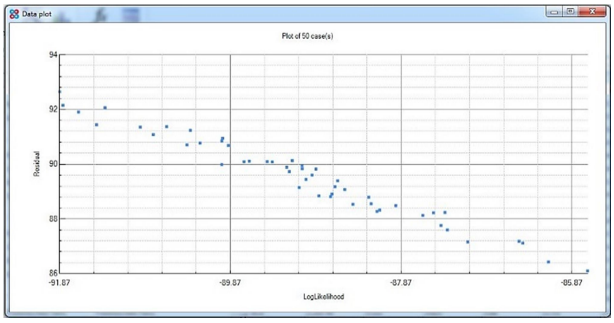

Figure 8 Loglikelihood Graph for Detecting Lassa fever, Viral Hemorrhagic fever types, and their symptoms.

3.5.5 The likelihood against loglikelihood for predicting Lassa fever, viral hemorrhagic fever types, and symptoms

This likelihood against loglikelihood graph for predicting Lassa fever shows the residual values (Likelihood) on the vertical axis plotted against the loglikelihood values (independent variables) on the horizontal axis.

A residual (Likelihood) value is an appraisal of how much a regression line vertically misses a data point. It shows the probability of an event (Lassa fever) occurring with probabilistic values between 0 and 1.

Regression lines are the superlative fit of a set of data. The lines are classified as average with a few data points fitting the line while others miss the line.

In this graph, 50 experimental cases were conducted which resulted in the values that are shown in Table 8 below.

Table 8 Results of likelihood against loglikelihood plot for detecting Lassa fever, Viral Hemorrhagic fever types, and their symptoms.

Number of plotted cases	Residual values (Likelihood values)	Loglikelihood values	Resulting probabilistic values
50	1	-91.16	0.9999
	0.9	-90.16	0.9998
	0.8	-89.16	0.9995
	0.7	-88.16	0.9994
	0.6	-87.16	0.9994
	0.5	-86.16	0.9990
	0.4	-85.16	0.8999
	0.3		0.8995
	0.2		0.7095
	0.1		0.0004
	0		0.0002

- Maximum Likelihood That Can be Reached Highest Loglikelihood Independent Prediction Value Attained Maximum Probabilistic Value Reached By The System 1 -91.16, 0.9999.
- Likelihood Against Loglikelihood Plot Probabilistic Value For Detecting Lassa fever , Viral Hemorrhagic fever Types and Their Symptoms = 0.9999.

Preferably, residual (likelihood) values should be evenly and randomly spaced around the horizontal lines. Critically, observing the system's experimental results values obtained from the horizontal lines on the graph, it can be seen that the probability likelihood value obtained is 0.9999, and the loglikelihood independent prediction value is -91.16.

Be that as it may, Figure 9 shows a snapshot of the likelihood against loglikelihood plot for predicting Lassa fever, Viral Hemorrhagic Fever types and symptoms.

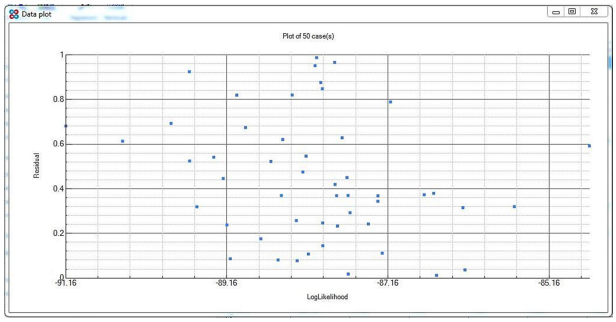

Figure 9 The Likelihood against the Loglikelihood Graph for Predicting Lassa fever, Viral Hemorrhagic fever types, and their symptoms.

3.6 Proposed BBN model prediction accuracy via confusion matrix

A confusion matrix shows the number of exact and/or imprecise predictions made by a classification model, for instance, a Bayesian Belief Network Model. More to the point, the diagonals elements of the confusion matrix display the number of exact prediction positioned from top left to bottom right, while the elements that are off the diagonal range illustrates the incorrect predictions. Conversely, the confusion matrix for the proposed BBN model in Figure 10 showed an overall prediction accuracy of 100% based on test data. Nonetheless, Figure 10 shows the proposed BBN model prediction accuracy via confusion matrix.

Figure 10 The Proposed BBN Model Prediction Accuracy via Confusion Matrix.

What is more, the likelihood graph results in Figure 6, 7 showed all classes of severity status of combined Arenaviridae and Viral Hemorrhagic Fever leading to Lassa fever infection; Viral Hemorrhagic Fever types leading to an infectious and pandemic disease cases ranging from asymptomatic, mild, moderate, severe, and critical classes with their probabilities; Figure 8 showed the system loglikelihood value of 92.45 for detecting Lassa fever, Viral Hemorrhagic fever types and their symptoms, the likelihood against loglikelihood prediction graph of Lassa fever, Viral Hemorrhagic fever and their side-effects in Figure 9, and Figure 10 showed the 100% prediction accuracy of the system.

Then again, with the accuracy of our BBN model derived; we intend to denote the sensitivity of Lassa fever and Viral Hemorrhagic Fever which is shown below using the Probability (P) of (Event Occuring|Given Evidence) denotation.

Thus, the probability of Viral Hemorrhagic Fever types leading to an infectious and pandemic disease case given there is evidence of ailments and factors that influence the diagnosis of the aforesaid disease types is denoted and shown in Table 9 below.

Table 9 Probability of Viral Hemorrhagic Fever types leading to an infectious and pandemic disease case given there is evidence of ailments and factors.

P (Viral Hemorrhagic fever types)	Alkhurma Hemorrhagic Fever (AHF), Arenaviridae Virus, Lassa fever, Chapare Hemorrhagic Fever (CHHF), Ebola Virus Disease (EVD), Hemorrhagic Fever with Renal Syndrome (HFRS), Kyasanur Forest Disease (KFD), Lassa fever , Life-Threatening Fever, Lujo Hemorrhagic Fever (LUHF), Lymphocytic Choriomeningitis (LCM), Marburg Hemorrhagic Fever (Marburg HF), Meningitis, Meningocencephalitis, Measles, Rift Valley fever (RVF), Tick-Borne Encephalitis (TBE) = 0.989846790604221

- The sensitivity of Viral Hemorrhagic fever types = 98.98%.

Furthermore, the probability of having Lassa fever infection given there is evidence of ailments and factors that influence the diagnosis of the aforesaid disease is denoted and shown in Table 10 below.

Table 10 Probability of a Lassa fever infection given there is evidence of ailments and factors.

P (Lassa fever)	Abdominal Pain, Acute Kidney Failure, Arenaviridae Virus, Back Pain, Bleeding, Bleeding of the Privates, Blurred Vision, Chest Pain, Cold, Confusion, Continuous Fever, Cough, Delirium, Diarrhea, Dizziness, Drowsiness, Eyes Pain, Fatigue, Facial Swelling, Fever, Gastrointestinal Tract Bleeding, Headache, Incubation Period (2 to 21), Intermittent Fever, Irritability, Joint Pain, Life-Threatening Fever, Liver Failure, Loss of Hearing , Low Blood Pressure, Low Blood Platelet, Maculopapular Rash, Malaise, Malaria Fever, Meningitis, Meningocencephalitis, Mental Disturbances, Measles, Mild Jaundice, Motor Abnormalities, Mouth Bleeding, Multi-Organ Dysfunction, Muscle Pain, Nausea, Neck Swelling, Neurological Problems, Neutropenic Fever, Non-Serious Fever, Nose Bleeding, Paralysis, Pel-Ebstein Fever, Quartan Fever, Quotidian Fever, Rash, Red Blood Cell Count, Redness of Eyes, Remittent Fever, Respiratory Distress, Salivary Gland Pain, Sensory Disturbances, Shock, Sore Throat, Stiff Neck, Stomach Pain, Swollen Pancreas, Tertian Fever, Testicular Pain, Tremors, Typhoid Fever, Yellow Fever, Vascular Leakage, Viral Hemorrhagic Fever, Vomiting, Weight Loss, Weakness and White Blood Cell Count = 0.987268157559792

- The sensitivity of Lassa fever = 98.73%.

3.7 Comparison of proposed model with existing systems

Our proposed model had an overall accuracy of 100% in predicting Lassa fever, its symptoms, and Viral Hemorrhagic Fever types; with 98.73% and 98.98% sensitivity of Lassa fever, Viral Hemorrhagic fever types in that order. Table 11 below shows a comparison of our proposed model with existing systems.

Table 11 Comparison of results with existing systems.

Existing Systems	Detection Accuracy	Proposed Model	Detection Accuracy	Ailments	Sensitivity
Osigbemeh et al. [13]	90%				
Osaeseri and Osaseri [14]	<= 99.84%				
Abiola et al [15]	<= 99.84%	A Supervised Machine Learning			
Ajenaghughrure et al. [16]	<= 99.84%	Model For Diagnosing Lassa fever	100%	Lassa fever	98.73%
Aminu et al. [16]	<= 99.84%	and Viral Hemorrhagic Fever			
Steur and Mueller [19]	<= 99.84%	Types Reliant on Observed Signs		Viral	98.98%
Egwali and Obi [20]	<= 99.84%			Hemorrhagic	
Govinda et al. [21]	<= 99.84%			Fever Types	
Djam et al [22]	99.84%				
Alile and Bello [23]	<= 99.84%				
Imanov and Asengi [24]	<= 99.84%				
Alile [25]	99.98%				

Comparing the 100% prediction accuracy of our model with the experiments conducted by [12-14,16-25] which has <= 99.98% prediction accuracy respectively, it is obvious our model has a better prediction accuracy. The higher prediction accuracy achieved by our model could be due to the range of the data set used in training and testing the model as well as its ability to predict the Lassa fever, its symptoms, Viral Hemorrhagic fever types, and overlapping symptoms Lassa fever shares with Viral Hemorrhagic fever types, hence aiding the high detection accuracy of the aforesaid disease.

4. Conclusion

Lassa fever is a contagious life-threatening disease caused by the Lassa virus, which belongs to the Arenaviridae virus family whose idiosyncratic attribute is its method of spread to humans which can be direct or indirect through contact with food and household items contaminated with rodents urine, feces, and secreted body fluids from a Lassa virus-infected person.

Nevertheless, the Lassa virus has an incubation period of 2 to 21 days in humans after contact before manifestations begin to show in the newly infected persons. Due to the aforesaid distinctive feature, it is quite difficult to detect owing to the overlapping symptoms the disease shares with other viral hemorrhagic fevers. In the recent past, numerous clinical and machine learning techniques have been employed to diagnose Lassa fever with the intent of curbing the untimely deaths of patients an area medical and IT professionals are making frantic efforts to improve on. Hence, there was the need to proffer a solution to curb this anomaly. Thus, in this paper, we utilized a supervised machine learning approach called Bayesian Belief Network to predict Lassa fever, its symptoms, and Viral Hemorrhagic Fever types. The network had 88 nodes with each node representing an exclusive ailment and factor that influence the diagnosis of Lassa fever and Viral Hemorrhagic fever types. The model was trained and tested and had an overall accuracy of 100% in predicting Lassa fever, its symptoms, and Viral Hemorrhagic Fever types; with 98.73% and 98.98% sensitivity of Lassa fever, Viral Hemorrhagic Fever types in that order.

Also, the system can be deployed in health facilities to help provide information that will be used to detect Lassa fever, its symptoms, and Viral Hemorrhagic Fever types. It will also bring about improvement in the following areas: Prediction of Lassa fever and Viral Hemorrhagic Fever types, detection of Lassa fever, and diagnosis of infectious and pandemic diseases with similar symptoms as Lassa fever.

5. Acknowledgements

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