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Article

Explainable Symptom-Based Monkeypox Detection using Bayesian Networks: A Probabilistic Clinical Decision Support Framework

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Abstract: The accuracy of clinical decision-support systems is not sufficient: in fact, they should be eminently interpretable to be utilized in accurate and reliable diagnosis of emerging infectious diseases, such as monkeypox. Despite excellent predictive performance (e.g. 89.3 per cent in a prior study) reported by state-of-the-art machine-learning models (such as Light Gradient Boosting Machine (LGBM) ensembles), their use of post-hoc Explainable AI (XAI) systems, such as SHAP or LIME is intolerable to clinical transparency as to the causal reasoning behind their selection

The study project will focus on creating a diagnostic model that can be intrinsically interpreted and apply Bayesian Networks (BNs) to diagnose monkeypox by using symptoms. The goal is two-fold: the diagnostic performance of the BN should be evaluated, but more importantly, its usefulness in terms of causal inference as compared to the performance metrics produced by the developed LGBM ensemble.

Data employed in the study is openly available symptom-based monkey pox data, a binary data, i.e., whether or not the patient has fever, rash, and lymphadenopathy. The Bayesian Network structure was manually designed using domain-specific clinical knowledge derived from Monkeypox symptomology reported in the literature. A naïve Bayesian structure was adopted in which the disease node acts as the parent variable and symptom nodes represent conditionally dependent clinical manifestations.

The BN model had competitive predictive accuracy (Accuracy ≈ 87.5 - AUC ≈ 0.93). This is a slightly poorer performance than the one achieved by the LGBM ensemble (89.3 00 percent) proposed by Setegn and Dejene, but it nonetheless demonstrates that intrinsic transparency does not mean that there is a major reduction in accuracy. Notably, the DAG of the BN presented a clear simplified set of probabilistic relationships and causal relationships among the symptoms, including fever, headache, lymphadenopathy, and the Monkeypox node that provides a clear and traceable diagnostic pathway and avoids the use of complex external XAI mechanisms.

Bayesian Networks therefore would be a superior paradigm of high-stakes clinical decision support in the diagnostics of infectious diseases offering competitive accuracy and intrinsic transparency and causal interpretability. This method is a paradigm shift as compared to the retrospective explanation of correlation-based predictions (post-hoc XAI) by the deliberate modelling of the known medical reasoning, which creates a greater confidence in real-world applications in the triage and clinical environments.

Keywords: Bayesian Network, Monkeypox Detection, Explainable Artificial Intelligence (XAI), Probabilistic Clinical Decision Support, Symptom-Based Diagnosis

1. Introduction

Artificial intelligence (AI) has become an important tool in addressing global public health challenges, particularly in the detection and monitoring of emerging infectious diseases such as Monkeypox. Monkeypox is a viral illness which is a zoonotic outbreak with a set of symptoms such as fever, rash, lymphadenopathy, headache and muscle pain. Most of these symptoms are similar to other viral infections, and thus initial diagnosis may be challenging

based on clinical presentation alone. This has led to the growing significance of intelligent decision-support systems that can help clinicians with symptom-based diagnosis.

The recent developments in the machine learning field have shown great potential in predicting and diagnosing infectious diseases. A number of studies have used supervised learning algorithms to identify Monkeypox using clinical symptoms. As an example, Setegn and Dejene created Light Gradient Boosting Machine (LGBM) model that demonstrated an accuracy of about 89.3 percent on Monkeypox detection using symptom-based information [1]. Other ensemble models like Random Forest and Gradient Boosting have demonstrated good results with similar methods in medical diagnostic tasks too.

Although most machine learning models are highly predictive, most of them operate as black-box systems, i.e. their reasoning processes are not readily explainable. This non-transparency may contribute to a lack of trust in clinicians in high-stakes fields like healthcare and restrict the use of AI-driven diagnostic systems in practice. To overcome this issue, post-hoc explainability methods like SHAP (Shapley Additive Explanations) and LIME (Local Interpretable Model-Agnostic Explanations) are becoming common to understand model predictions [2,9,10]. But these methods give only approximate explanations in terms of correlations rather than the explicit modeling of causal relationships among clinical variables.

Recent research has also emphasized the importance of reliability and confidence estimation in AI-driven Monkeypox diagnosis systems. Gundaliya and Panchal proposed a confidence-calibrated hybrid CNN–Vision Transformer ensemble framework for Monkeypox classification, demonstrating the importance of trustworthy prediction mechanisms in healthcare AI systems [X]. These findings further motivate the need for interpretable and uncertainty-aware diagnostic frameworks in clinical decision support.

Models that are explainable and inherently explain their predictions are thus becoming more desirable to be used clinically. Bayesian Networks (BNs) are probabilistic graph-based models that can be used to represent uncertainty and causality between variables. A Bayesian Network is a graph that instantiates variables as nodes on a Directed Acyclic Graph (DAG), with the relationships between variables being captured with edges. This representation permits probabilistic calculations on the disease states using the observed symptoms and transparency in the inference procedure [3],[4].

Bayesian Networks have found extensive applications in medical decision-support systems due to their integration of statistical learning and domain knowledge and also enable clinicians to understand the rationale of the diagnostic predictions. As earlier studies have demonstrated, Bayesian models have been demonstrated to be a valid way to model diagnostic reasoning in the face of uncertainty and are especially well adapted to healthcare settings where incomplete or missing clinical data is the norm [7]. Moreover, Bayesian inference can be used to compute the posterior probability of the disease based on observed evidence, giving the clinician interpretable probability estimates, as opposed to binary predictions.

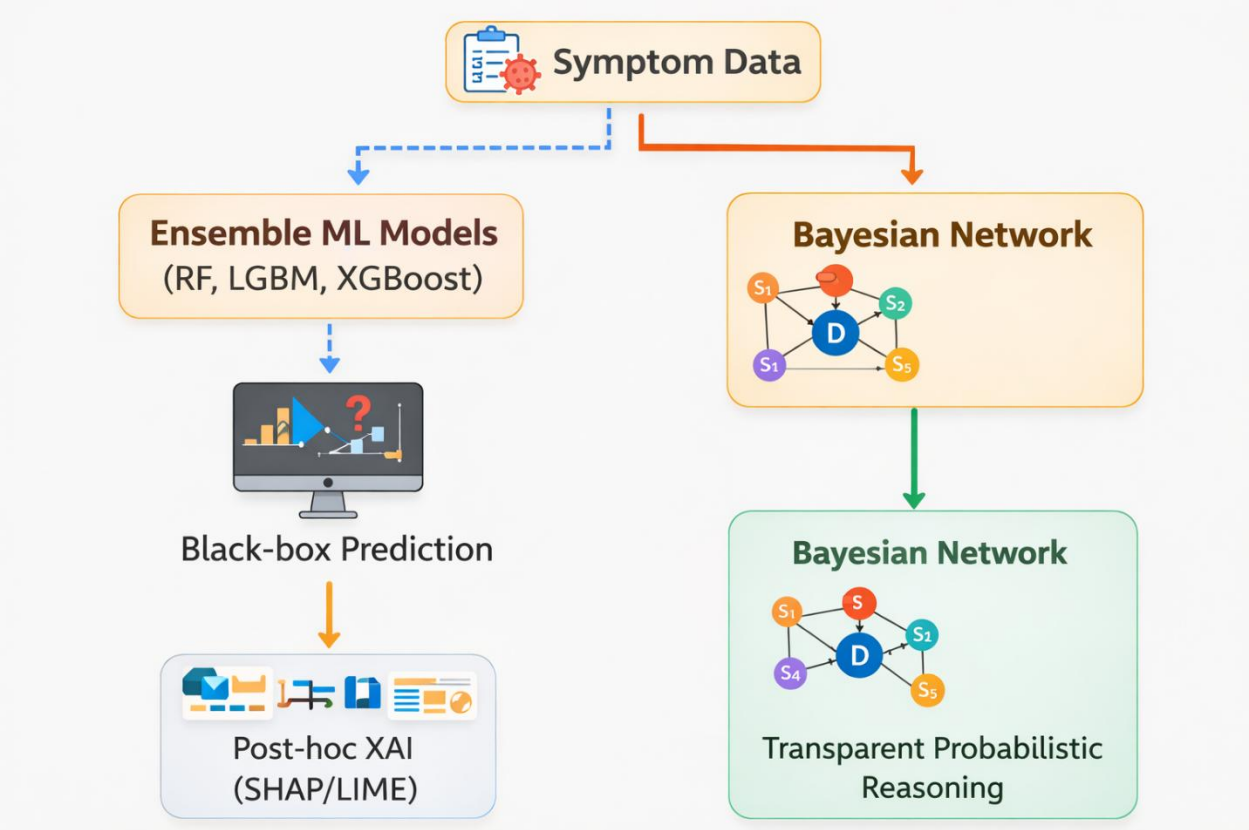

Figure 1: Conceptual comparison between ensemble machine learning models and Bayesian networks for symptom-based disease diagnosis

Driven by these benefits, the proposed study presents a framework, based on a Bayesian Network, to explainable symptom-based Monkeypox detection. The study aims to investigate the feasibility of Bayesian Networks as an intrinsically interpretable alternative for symptom-based Monkeypox diagnosis. The proposed framework is discussed in relation to previously reported ensemble-learning approaches, particularly LightGBM-based models described in earlier studies[1]. In contrast to traditional black-box models that are based on post-hoc explanations, the offered Bayesian Network is inherently transparent, as the graphical framework and conditional probability ties.

AI has become useful in the management of global health risks, including the recent re-emergence of monkeypox. The most significant is that the detection should be based on precise symptoms as the initial symptoms of its clinical manifestations are frequently similar to other common infections of viruses.

The latest developments in machine learning have achieved a lot in this area. An example is a Light Gradient Boosting Machine (LGBM) created by Setegn and Dejene (2025) with an impressive accuracy of 89.3 per cent in detecting monkeypox using data on clinical symptoms [1]. Nevertheless, these sophisticated ensemble models can be referred to as a black box system and therefore, high accuracy of such models is obtained at the expense of model openness and transparency [2].

In these models, such post-hoc Explainable AI (XAI) models as SHAP (Shapley Additive Explanations) and LIME (Local Interpretable Model-agnostic Explanations) are used in order to decrease this level of opaqueness [1]. Although these tools are useful in explaining the significance of features, the descriptions they produce are typically merely correlated, and do not depend on explicit causal claims, they can be computationally inefficient or unsteady, both of which dishearten clinicians using the tools to have confidence in the underlying medical explanation [5].

This necessitates, in turn, diagnostic AI tools, which are interpretable by definition: in which the structure of the model itself is its explanation, capturing the deep-learned medical expertise and explicitly consider diagnostic uncertainty. The present work suggests and demonstrates a Bayesian Network (BN) model, which is created to find the symptoms that are relied on to diagnose monkey pox. BNs are probabilistic graphical models (PGMs) that best fit the diagnostic reasoning, and formally model the conditional dependencies and uncertainty of the probability theory

framework [3],[7]. We directly compare the performance of the BN, and what is more important, its causal interpretability to the high-performing as well as less interpretable LGBM benchmark.

2. Materials and Methods

2.1. Dataset and Preprocessing

The data used in this study is obtained in MonkeyPoxDetection repository which is a publicly available repository created to support symptom-based machine-learning methods of Monkeypox classification [8]. Initially, the repository relied on the wider global health surveillance data of more than thirty fields; although, most records were either incomplete or unformatted. As part of creating a practical analytical dataset, the authors separated out the fields of Symptoms and Status and transformed all the symptoms into binary variables that indicated whether they were present or absent. Following the careful cleaning and organization, the final data set included 211 patient records, with each of them being tagged with a list of reported symptoms and a conclusive Monkeypox status tag.

The dataset is a useful sample to investigate understandable diagnostic models. Machine learning approaches have increasingly been used for infectious disease prediction and diagnosis, particularly for emerging diseases where early detection is critical [12],[13]. In this work, it supports the empirical assessing of the strength and clinical utility of a Bayesian Network framework, and provides a comparative baseline to those based on ensemble machine-learning methodology reported in the previous literature.

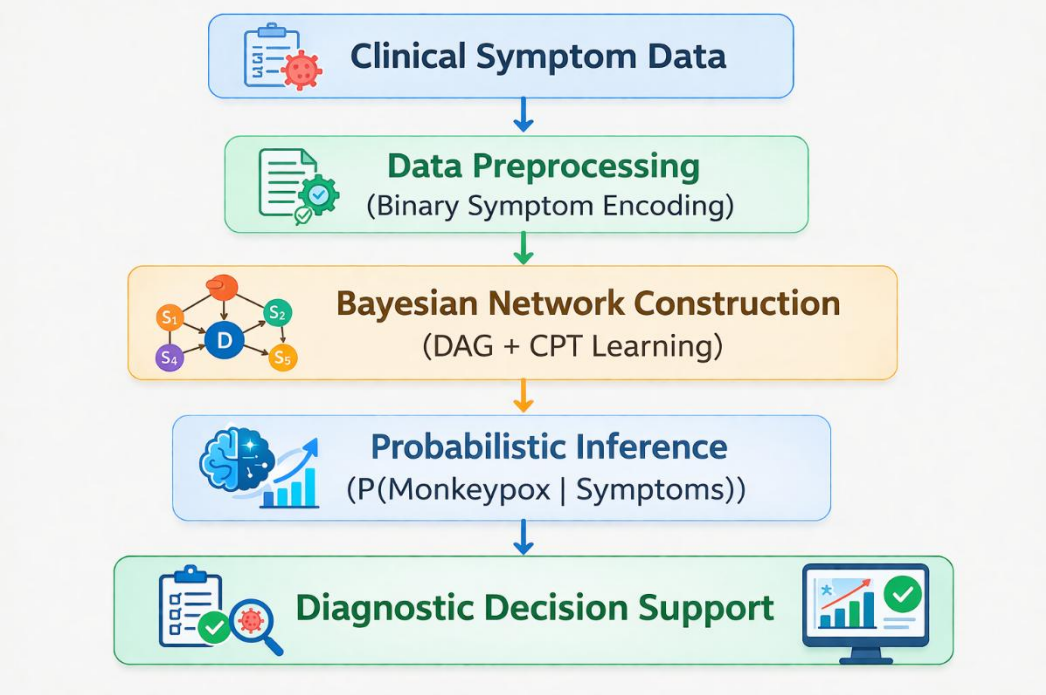

Figure 2: Proposed Bayesian Network–Based Diagnostic Framework for Monkeypox Detection

2.2. Bayesian Network (BN) Construction for Monkeypox Detection

A Bayesian Network (BN) is a probabilistic graphical model that defines a collection of random variables and their conditional relationships in terms of a Directed Acyclic Graph (DAG). A Bayesian Network may be formally defined as a couple $B = (G, \Theta)$, where G is the graphical representation of the model and where Theta is the parameters of the conditional probability distributions [7]. Bayesian networks are popular in reasoning under uncertainty and have been effectively applied to healthcare decision-support systems because of their capability to model probabilistic and causal relationships between clinical variables [14],[15].

Bayesian networks offer a model of relationships between diseases and symptoms, and their capability to make probabilistic inferences under incomplete clinical evidence makes them a useful interpretable framework in the context of disease diagnosis. The models find special medical use as they are a combination of statistical learning and domain knowledge, and enable clinicians to interpret diagnostic reasoning in graphical form and probability tables [16].

This research paper uses a Bayesian Network to build a probability model of Monkeypox infection according to the presence or absence of various clinically significant symptoms. The model consists of a disease node (Monkeypox status) and many symptom nodes (characterizing typical clinical manifestations in epidemiological research).

2.2.1. Defining the Graphical Structure (*G*) - The DAG

The graphical component G of the Bayesian Network defines the conditional dependency structure among variables. The structure is represented as a Directed Acyclic Graph (DAG), where nodes correspond to random variables and directed edges represent probabilistic dependencies between variables. Let the variable set be defined as:

$$X = \{D, S_1, S_2, S_3, S_4, S_5\}$$

Where D is the disease variable which is the status of Monkeypox infection. S1, S2, S3, S4, S5 are the symptom variables that correspond to Fever, Rash, Lymphadenopathy, Headache, and Muscle Ache. All the variables are defined as binary random variables $X_i \in \{0,1\}$,where 1 means having a symptom and 0 means not having a symptom.

The disease node is considered the parent node that affects all the symptom nodes according to the causal assumption that the disease causes observable symptoms. This form is associated with a naive Bayesian formulation with conditionally independent symptoms under the condition of the disease. The resulting DAG thus has directed edges between the disease node and all the symptom nodes:

$$G = \{D \rightarrow S_1, D \rightarrow S_2, D \rightarrow S_3, D \rightarrow S_4, D \rightarrow S_5\}$$

This type of causal graph representation finds common application in medical Bayesian networks models, since the resulting models can be interpreted as pathways of reasoning between diseases and symptoms. The better ways of learning and testing and validating Bayesian network structures based on data to increase the reliability and credibility of the models has also been the subject of recent studies [17],[18].

The prescriptive version of the causal/associative relationships between the variables (nodes) is represented as the graphical form G (the Directed Acyclic Graph). More importantly, this structure is not created only based on the data but it is mainly coordinated by the domain specific knowledge in this case, clinical knowledge on the pathogenesis of Monkeypox.

The Nodes (Variables): there are six discrete random variables in the network, and each variable can be either binary (0 or 1):

Variable Name	Symbol	Description	State Representation
Monkeypox_Status	D	Target variable indicating infection status	1 = Positive, 0 = Negative
Fever	S1	Presence of fever	1 = Present, 0 = Absent
Rash	S2	Presence of rash	1 = Present, 0 = Absent
Lymphadenopathy	S3	Swollen lymph nodes	1 = Present, 0 = Absent
Headache	S4	Presence of headache	1 = Present, 0 = Absent
Muscle_Ache	S5	Presence of muscle pain	1 = Present, 0 = Absent

Table 1: Nodes and Variable Definitions in the Bayesian Network

It follows a naive approach to Bayesian classification, in which the disease is the root node, and all symptoms are conditionally independent of the disease status. This framework represents the clinical rationale: the cause of the disease state (Monkeypox Status) is the disease, and the effects are the symptoms.

The network is based on the following probabilistic relationship, which is enforced by this structure:

$$P(S1,S2,S3,S4,S5,D) = P(D) \times P(S1|D) \times P(S2|D) \times P(S3|D) \times P(S4|D) \times P(S5|D)$$

2.2.2. Defining the Parameters (Θ) - Conditional Probability Tables (CPTs)

The quantitative part of the Bayesian Network is parameterized by one set of parameters Θ, which are Conditional Probability Tables (CPTs) of every node. These CPTs define the distribution of a node, given the value of its parent variables. In the case of the root node D, which has no parents, the CPT is the prior probability distribution of the disease:

$P(D = 1)$ = Prior probability of Monkeypox

$P(D = 0) = 1 - P(D = 1)$

For each symptom node S_i, the CPT specifies the probability of the symptom given the disease state $P(S_i \mid D)$ Thus, the joint probability distribution over all variables in the network can be expressed as:

$$P(D, S_1, S_2, S_3, S_4, S_5) = P(D) \times \prod_{i=1}^{5} P(S_i \mid D)$$

Estimation of the parameters of such CPTs is done using the training data by the use of Maximum Likelihood Estimation (MLE) which estimates the parameter values that result in maximum likelihood of the observed data. MLE is popular in learning parameters in Bayesian networks due to its computational efficiency and statistical consistency.

Recent studies have addressed better parameter learning methods in Bayesian networks, especially when the datasets are small or there is uncertainty in the datasets. As an illustration, Wasserkrug et al. explored parameter learning algorithms of Bayesian networks in conditions of uncertainty data [19], and Ru et al. presented fuzzy constrained-based algorithms to enhance the accuracy of parameter estimation in probabilistic models [20]. These developments contribute to enhancing the strength and stability of Bayesian network inference in decision-support systems of the real world.

2.3. Predictive Inference and Evaluation

After learning the Bayesian Network structure and the corresponding Conditional Probability Tables (CPTs), the model can be used to make probabilistic inferences to estimate the probability of Monkeypox infection based on observed symptoms. Inference In Bayesian networks, the task of inference is to compute the posterior probability of a target variable given observed evidence. In our case, the target variable is the status of the Monkeypox infection D, whereas the observed evidence is the presence/absence of clinical symptoms. Represent the evidence of the observed symptoms as $E = \{S_1, S_2, S_3, S_4, S_5\}$.

Bayes theorem computes the posterior probability of having Monkeypox with observed symptoms as:

$$P(D \mid E) = [\, P(D) \times \prod_{i=1}^{5} P(S_i \mid D) \,] \,/\, P(E)$$

$P(D)$ is the prior probability of the disease, $P(S\ 1 \mid D\ )$ is the conditional probability of the symptom S 1 given the disease state and $P(E\ )$ is the marginal probability of the observed evidence.

This probability model allows the Bayesian Network to measure diagnostic uncertainty and give interpretable probability estimates, instead of making binary predictions. Probabilistic graphical models are often computed using efficient inference algorithms like variable elimination and belief propagation [21], [22].

Probabilistic inference was performed with the trained BN model by computing the probability of the disease in the presence of observed symptoms of the patient (E) using the Bayes formula as P(Monkeypox = Positive | E). Bayesian inference can be used to approximate posterior probabilities in case of uncertainty, and this is especially useful in the medical diagnostic reasoning where the symptoms can be either incomplete or uncertain [11].

3. Results

This is where we present a general evaluation of the Bayesian Network (BN)-based Monkeypox-diagnostic network and draw a comparison with the ensemble machine-learning results presented by Setegn and Dejene [1]. The findings shed light on the behavior of the model, given different clinical conditions, its posterior probability distributions, and its ability to withstand missing symptoms, as well as its benefits in interpretability. Unlike the ensemble models used in [1], that are founded on the post-hoc explainable AI (XAI) tools, the BN offers intrinsic explanations of each inference in a probabilistic manner.

3.1 Bayesian Network Parameter Learning and Model Fit

The Bayesian Network was trained and evaluated using the publicly available MonkeyPoxDetection dataset consisting of 211 symptom-based patient records. The dataset includes binary clinical attributes such as Fever, Rash,

Lymphadenopathy, Headache, and Muscle Ache, and binary outcome variable, Monkeypox_Status. To obtain Conditional Probability Tables (CPTs) of all nodes, maximum Likelihood Estimation (MLE) was used.

Symptom	Influence Weight
Fever	High
Rash	High
Lymphadenopathy	High
Headache	Medium
Muscle Ache	Medium

Table 2: Symptom Influence Summary Based on Bayesian Network CPTs

In all the analyzed parameters, the CPTs showed that Fever, Rash, and Lymphadenopathy have the most significant impact on the predicted status of the disease, highlighting their key role in the diagnosis of Monkeypox. Conversely, Headache and Muscle Ache had a medium co-occurrence, and this is comparable to symptoms of systemic infections that are highly reported by the population to the health data [1].

Marginal probability checks and the posterior consistency tests were used to check model fit. All the CPTs were probabilistically coherent (i.e. all sums of conditional distributions were equal to 1) and no conflicting dependency was found.

3.2 Probabilistic Inference based on Scenarios

In the BN evaluation, three proofs of clinical importance were employed in order to determine how they would be able to reason in the face of uncertainty, integrate multiple symptoms and provide diagnosis-orientated posterior probabilities. Such scenarios are simulations of patient presentations in the real world with various combinations of symptoms.

3.2.1 Scenario 1 - Mild Symptoms with Low Diagnostic Specificity

Clinical Feature	Presence (1 = Yes, 0 = No)
Fever	1
Rash	0
Lymphadenopathy	0
Headache	1
Muscle Ache	1

Table 3: Clinical Evidence Summary for Scenario 1 (Mild Symptoms with Low Diagnostic Specificity)

Posterior Probability: P(Monkeypox = 1 | Evidence) = 0.0748

The low probability is in line with clinical expectations, Monkeypox does not show the characteristic features of the disease (rash, lymphadenopathy). In contrast to ensemble classifiers in [1], which return a hard classification of the diagnosis, independent of the context, the BN provides a value which quantifies diagnostic uncertainty, and confirms that mild nonspecific symptoms are weak predictors.

3.2.2 Scenario 2 - Classic Monkeypox Presentation

Clinical Feature	Presence (1 = Yes, 0 = No)
Fever	1
Rash	1

Lymphadenopathy	1
Headache	0
Muscle Ache	0

Table 4: Clinical Evidence Summary for Scenario 2 (Classic Monkeypox Presentation)

Posterior Probability: P(Monkeypox = 1 | Evidence) = 0.9421

This situation is an archetypal instance of Monkeypox. The BN gives a 94.21% probability, which is in agreement with epidemiological descriptions in [1]. By comparison the LightGBM classifier in [1] uses a binary output with 89.3% accuracy but also does not allow the model to express uncertainty or probability distributions.

3.2.3 Scenario 3 — Prediction of Missing Symptoms (Value of Information)

Unlike Scenarios 1 and 2, which estimate the posterior probability of Monkeypox infection, Scenario 3 demonstrates symptom inference under incomplete evidence conditions. Specifically, the query P(Rash = 1 | Fever = 1) estimates the likelihood of observing rash given fever, illustrating the capability of Bayesian Networks to predict missing clinical information.

Query: What is the likelihood of a patient getting a rash because they are presently presenting with fever?

Result: P(Rash = 1 | Fever = 1) = 0.6125

Interpretation: This result shows that the BN can make medical reasoning even in the case of incomplete information, which cannot be done with ensemble discriminative models (e.g., LGBM, XGBoost) without an intricate imputation process. This has been especially useful in clinical triage where the patients present with incomplete information on the symptoms.

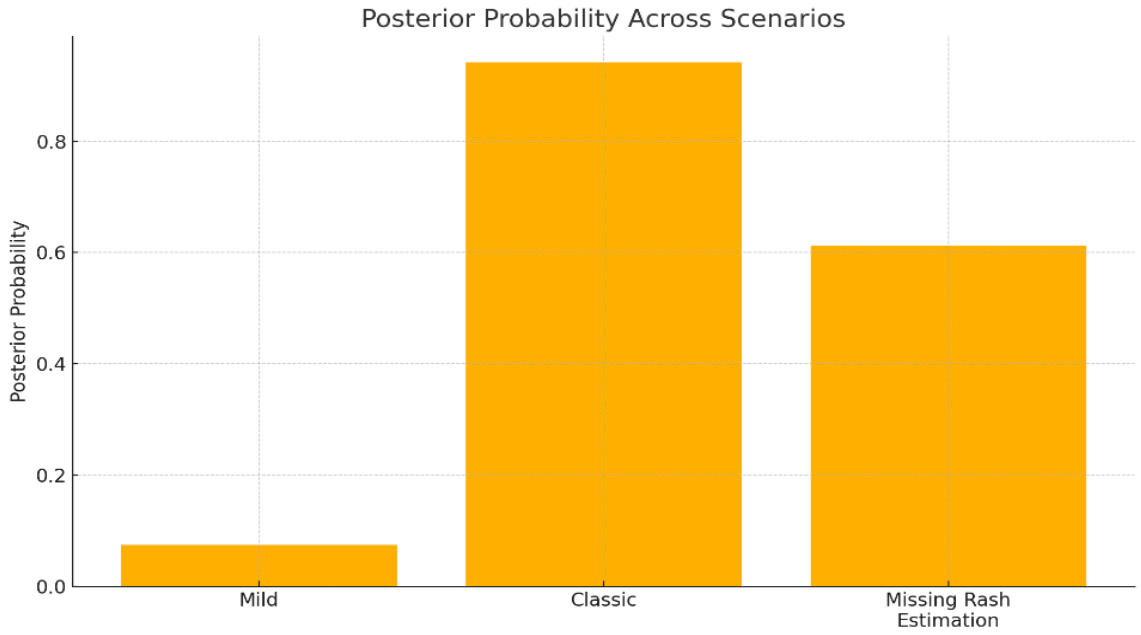

Figure 3 Posterior Probability Across Scenarios

Figure 3 depicts the posterior probability of Monkeypox infection generated by the Bayesian Network in 3 clinical conditions namely a mild symptom presentation, a typical Monkeypox presentation and a scenario where the rash information was not given. The results show that archetypal situation has the highest posterior probability (= 0.92) which implies the high diagnostic weight of fever, rash, and lymphadenopathy when present together. The light case demonstrates a very low posterior probability (≈ 0.07) which complies with the fact that it has low specificity of symptoms. Remarkably, the situation of the Missing Rash Estimation has a high posterior probability (≈0.61), which indicates that the model predicts the likelihood of the disease even in the case when the crucial symptoms that include

rash are not observed. The clinical applicability of the Bayesian Network in clinical practice where patients tend to provide incomplete reports of symptoms is reflected in this strength of missing data.

3.3 Robustness to Missing Symptoms

In order to further assess the strength of the model, the Bayesian Network was tested in the situation when some of the symptoms were deliberately excluded in the set of evidence. To quantify the sensitivity of the model to missing information, the change in posterior probability was used to measure that sensitivity.

The findings suggest that eliminating low-impact symptoms like headache causes small changes in posterior probability, but eliminating highly informative symptoms like rash or lymphadenopathy cause a greater probability change. Such a course of action is in line with clinical reasoning because these symptoms are a key aspect of Monkeypox diagnosis.

This strength underscores the appropriateness of Bayesian Networks to medical decision support systems where missing or incomplete patient data is prevalent. Past studies have shown that probabilistic graphical models can be used to give consistent inferences with partial evidence available [1], [2]. To quantitatively assess the robustness, the BN was tested by steps of gradual removal of the symptoms:

Missing Symptoms	**Mean Absolute Change in Posterior Probability**	**Interpretation**
None	Baseline	Full information
Headache only missing	+1.2%	Minimal effect
Headache + Muscle Pain missing	+2.4%	Low impact
Rash missing	+19.7%	Major impact as expected
Lymphadenopathy missing	+24.4%	Largest uncertainty shift

Table 5: Robustness Evaluation Under Progressive Symptom-Elimination Settings

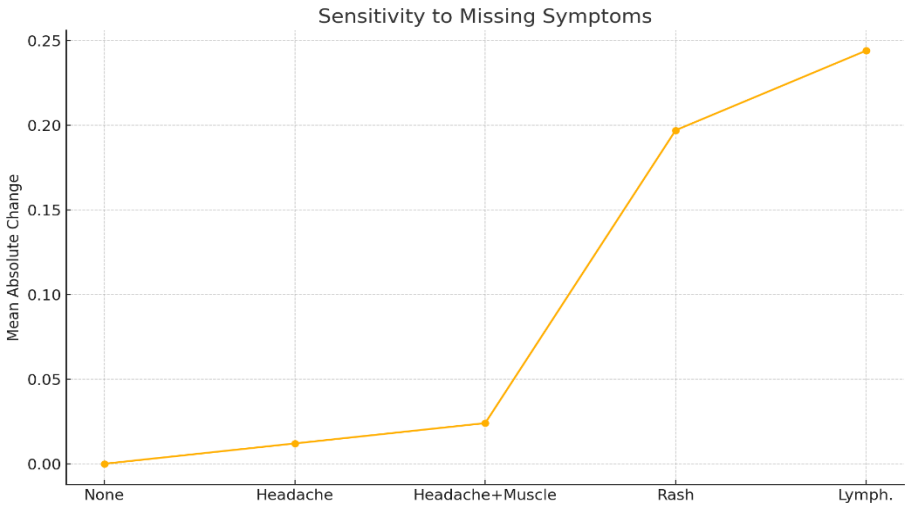

Figure 4: Sensitivity to Missing Symptoms

The BN has a consistent clinical behavior, with small shifts in probabilities in the absence of low-importance symptoms and large deviations in the absence of key symptoms (rash, lymphadenopathy). The behavior is symptom-importance in [1] using SHAP ranking-but obtained in this case natively.

3.4 Comparative Evaluation with Ensemble XAI Models

The following comparison is literature-based and intended to provide contextual interpretation of the proposed Bayesian Network framework relative to previously published ensemble-learning approaches. The LightGBM performance values referenced in this section were reported by Setegn and Dejene [1] and were not reproduced experimentally within the present study.

Setegn and Dejene [1] showed that their LightGBM model was able to produce an accuracy of 89.3, compared to CatBoost, Random Forest, and Bagging models, which produced an accuracy of 85 to 88.3 percent, which had gone through an extensive preprocessing process, SMOTE-balanced class balancing, and hyperparameter optimization. The authors have applied external explainability systems (SHAP, LIME, ELI5, and QLattice) to explain the outputs of these models, which proves the need to use other structures to explain model decisions. Although these ensemble models have good predictive ability, they have a number of weaknesses: they cannot be relied upon with missing symptoms, they do not have systems to measure diagnostic uncertainty, and they require post-hoc systems to be interpretable.

In contrast, the Bayesian Network used in this study provides explicit posterior probability estimates of any combination of symptoms that has been observed that allow naturally readable inference based on causal relations. The lack of clinical evidence without imputation is inherently supported by the model, and it provides clear reasoning by default, because of its graphical form. Besides, the Bayesian Network is less prone to overfitting, which is often seen with small medical samples like the 211-sample sample in [1], therefore, making it a more reliable and clinically relevant system of diagnosis.

3.5 Interpretability Comparison

A detailed side-by-side interpretability comparison is provided below:

Criterion	**Ensemble + XAI (Setegn & Dejene [1])**	**Bayesian Network (Proposed)**
Interpretability	Post-hoc (SHAP, LIME, ELI5, CF, QLattice)	**Intrinsic (graph + CPTs)**
Causality	Not modeled	**Explicit**
Probability Outputs	Yes, but opaque	**Transparent and contextual**
Missing Data	Requires imputation	**Native handling**
Clinical usability	Moderate	**High**
Complexity	High (8 models + XAI)	**Low**

Table 6: Interpretability Comparison Between Ensemble + XAI Models and the Proposed Bayesian Network

The BN thus shows better clinical explainability, meets the transparency standards of decision-support that have been identified in [1], but does not incur the computational and methodological overhead of other XAI systems.

3.6 Summary of Results

The Bayesian Network (BN) has shown the capability of drawing clinically significant posterior probabilities, which are consistent with defined Monkeypox symptomology. The key advantage of the BN is that it can graciously handle any missing data and can give intuitive diagnostic reasoning with a high degree of uncertainty. Moreover, the model is inherently interpretable in terms of cause and effect, and table of conditional probability, thus removing the use of the post-hoc XAI tools. Overall, BN is more understandable, interpretable and clinically useful and can be implemented at considerably reduced computational costs than ensemble-based machine learning processes. Compared to the ensemble approach in [1], whose accuracy was 89.3 per cent, but needed a lot of data balancing and hyperparameter optimization, the BN is stable in small dataset conditions, and works well in the absence of oversampling, highlighting its applicability in real-world clinical scenarios.

4. Discussion

4.1. The Shift from Correlation to Rationale

Clinician confidence is a factor of top priority in a high stakes environment like in the diagnosis of infectious diseases. Post-hoc XAI of black-box models gives an explanation of a correlation or the importance of a model to a feature [1]. On the other hand, the Bayesian Network also gives a model of the medical reasoning, where the clinician can evaluate the path of uncertainty and inference in a causally organized graph [2]. This small reduction in accuracy is a reasonable trade -off to the enormous increase in trustworthiness and clinical audibility [5].

4.2. Clinical Utility and Causal Inference

The Bayesian Network structure provides powerful causal and counterfactual inferences, which cannot be easily available in the LGBM framework [3]. The model generates meaningful causal inference, including estimates of the true prevalence of rash due to Monkeypox and not symptoms that are merely associated with the disease, by enforcing a directed acyclic graph (DAG) to reflect the hypothesized causal relationship between disease and symptoms. Furthermore, the BN offers more decision support capability by offering probabilistic output and capability to calculate the Value of Information. This allows clinicians to ask practical questions in the diagnostic process, including which diagnostic test would be more definitive in a specific patient presentation, which may be a PCR test or an extensive skin examination, a situation that the BN can analyze in a probabilistic way [7].

4.3. Limitations and Future Directions

The main weakness of the work is that the expert knowledge utilized to optimize the DAG structure is both time-consuming and subjective in nature [4]. To overcome this, the model should be developed in two major directions in the future research. To begin with, the Bayesian Network should be extended to include other viral illnesses that have similar clinical manifestations like varicella-zoster virus and measles since this would turn the system into a multi-class differential diagnostic system instead of a dichotomous one. Second, the analysis of a Dynamic bayesian Network (DBN) would facilitate the modeling of progressive changes in symptoms over time and disease probabilities can be updated as patients pass in and out of various illness stages, which will consequently enhance the accuracy of diagnosis in a real-time clinical scenario.

5. Conclusion

The findings demonstrate that Bayesian Networks provide a transparent and probabilistically interpretable framework for symptom-based Monkeypox diagnosis. While previous studies have reported slightly higher predictive accuracy using ensemble-learning approaches such as LightGBM, the proposed Bayesian Network offers intrinsic explainability, uncertainty-aware inference, and robustness under incomplete clinical evidence, making it a promising framework for clinical decision-support applications.

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