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Implementation of Forward Chaining and Naive Bayes to Determine the Severity of Measles in Toddlers

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Abstract

This study aims to determine the severity level of measles in children using the Forward Chaining and Naive Bayes methods. Sixteen symptoms were analyzed through decision tables, weighted likelihood tables, and simulated patient data. Forward Chaining was applied to match symptoms with predefined diagnostic rules, while Naive Bayes calculated severity probabilities based on symptom likelihoods. All computations were carried out using Microsoft Excel to ensure traceability and accuracy. The results indicate that both methods produce generally consistent classifications, with minor variations in cases involving overlapping symptoms. Forward Chaining provides deterministic outputs, whereas Naive Bayes offers more detailed probabilistic assessments. Overall, the combination of both approaches is effective for supporting early identification of measles severity in children.

Introduction

Measles is one of the most contagious diseases that, up to now, has become a world health concern, especially in groups of toddlers who are more susceptible to viral infections (Arnap et al., 2024; Camilleri & Fileri, 2025; Misin et al., 2020; Senthilingam, 2020; Patel et al., 2020). Disease This is marked by the emergence of symptoms beginning in the form of fever, cough, runny nose, and red, then followed by a rash on the skin that spreads all over the body (World Health Organization, 2024). According to the WHO report, although the immunization program has been implemented globally, cases of measles still often appear, especially in areas with low and limited sanitation (Global Immunization Unit WHO, 2024; Duclos et al., 2009; Feldstein, 2017; Duclos et al., 2009; World Health Organization, 2019). This shows that disease measles still become threat Serious for health of children in various developing countries.

Severity level of measles can vary in each individual, starting from condition light until complications that threaten life, such as pneumonia, encephalitis, or seizures (World Health Organization, 2024; Global Immunization Unit WHO, 2024; Nickson, 2023; Sheikh & Hirsch, 2023; Meiring & Arscott-Mills, 2021; Kurdybacha et al., 2025). Therefore, identification level severity from an early is very important to speed up clinical and preventive occurrence worsening conditions. A systematic, symptom-based approach is needed to help

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medical personnel or researchers assess a patient's condition more objectively (Kroenke, 2014; Kalantar-Zadeh et al., 2022; Mueller et al., 2017; Pinheira et al., 2025).

With the development of information technology, various computational methods have begun to be applied in the medical world to support symptom-based diagnostic processes. One widely used method is Forward Chaining, a rule-based reasoning approach that works by matching a patient's condition to a previously formulated IF–THEN rule (Diva Aliyah et al., 2023; Faisal et al., 2024; Pangestu et al., 2024). This method is widely used in expert systems because it provides a structured, transparent, and easily verifiable reasoning process (Faisal et al., 2024; Sajida et al., 2024).

Another frequently used method is Naive Bayes, a probabilistic approach that predicts a condition based on the probability of certain symptoms occurring (Glaveli et al., 2023; Gregoriades et al., 2024; Bohra et al., 2017). Naive Bayes has been widely used in the diagnosis of various diseases, both infectious and non-infectious, due to its ability to process symptom weights and generate probabilities that reflect the level of confidence in a category (Gunawan & Kuswanto, 2024; Mutiara et al., 2020).

Several studies have shown that combining rule-based techniques such as Forward Chaining with probabilistic methods like Naive Bayes can improve analytical accuracy and overcome the weaknesses of each method (Kurniawan, 2025; Listiana & Nora, 2025). Forward Chaining excels in deterministic decisions, while Naive Bayes is effective in handling variations in symptoms with varying intensities.

Based on this background, this study was conducted to analyze the severity of measles in 20 toddlers using both methods. By mapping symptoms in a decision table and a weighting table, this study aimed to evaluate the level of agreement between the two methods, identify the symptoms most influential in determining the stage, and provide a more comprehensive picture of measles diagnosis patterns in children (Munir, 2023; Umroh et al., 2024).

Methods

This research focuses on the conceptual and computational analysis of the Forward Chaining and Naive Bayes methods without developing any application or expert system. The study emphasizes methodological exploration rather than system implementation. Decision tables, weight tables, and decision trees are employed as analytical tools to support the reasoning and classification processes. All calculations are conducted using Microsoft Excel to ensure transparency, traceability, and ease of replication. This approach simplifies the calculation process and facilitates structured data management (Arnap et al., 2024; Diva Aliyah et al., 2023). Data-driven computational approaches have been widely applied in the prediction and classification of infectious diseases by identifying patterns from historical and clinical data. Machine learning models are capable of handling uncertainty in medical data and providing probabilistic predictions that are more adaptive compared to purely rule-based methods (Lee & Chen, 2022).

Data Collection and Preparation

The research data were obtained through literature studies from scientific journals, reports from international health organizations, and references discussing measles symptoms and reasoning techniques in expert systems (Camilleri & Fileri, 2025; World Health Organization, 2024; Mutiara et al., 2020). The application of artificial intelligence methods in this study focused on the toddler population because this age group has different clinical characteristics compared to other age groups. Previous research has shown that machine learning-based approaches are effective when used on pediatric clinical data and are able to adjust for variations in symptoms based on patient age (Kumar et al., 2024; Nur Rahmaha et al., 2024).

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The selection of symptoms in this study was based on a literature review specifically discussing the clinical manifestations of measles in the toddler age group (0–5 years). This focus was chosen because toddlers have different physiological characteristics and levels of vulnerability compared to school-age children or adults. The literature used was selected from WHO reports and pediatric journals that emphasize the typical symptoms of measles in early childhood, ensuring the data remains relevant to the research context. The data used includes:

The G01–G16 symptom list, which represents the clinical phases of measles from initial symptoms to complications, also includes a stage list to indicate severity.

Table 1. Symptoms

Code	Symptom	Description Clinical
G01	Fever mild (37.5–38.4°C)	A mild increase in body temperature in the early phase of infection
G02	Mild cough	A dry cough is common appear before a rash
G03	Runny nose watery	Nasal secretions due to irritation of the upper respiratory tract
G04	Pain/irritation in the throat	Mild inflammation due to viral infection
G05	Watery eyes (conjunctivitis), light)	Irritation light on the conjunctiva
G06	Red skin without rash	Erythema light before the emergence of rash
G07	Lust Eat decreases	Decline in intake, Eat consequence condition general child
G08	Tired and lethargic	Fatigue general consequence response to infection
G09	Koplik's spots	Spots with white, grayish discoloration of the mucosa cavity of the mouth, typical of measles
G10	Red rash comprehensive	Maculopapular rash spreading from the face to the body
G11	Fever high (>39°C)	Indication progressiveness disease
G12	Severe cough / rapid breathing	Signs of involvement system breathing
G13	Conjunctivitis heavy	Inflammation eye level carry on
G14	Duration fever > 5 days	Indication infection persistent
G15	Seizures or disturbance neurological	Manifestation complications system nerve
G16	Saturation oxygen < 95%	Indication of disturbance: breathing heavy

Sixteen symptoms were used in the study. These symptoms were chosen to represent the entire clinical journey of measles, starting from the prodromal phase, the eruptive phase, and the convalescent phase. Symptoms that are infrequent, nonspecific, or difficult to consistently observe in toddlers are excluded to ensure the analysis remains focused and stable. This approach aims to maintain a balance between clinical completeness and the feasibility of the analysis.

Four severity stages were defined:

Table 2. Stadiums

Disease Code	Disease Stage	Description
P01	Mild	Initial symptoms are mild, without complications
P02	Moderate	Symptoms are, needs observation

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P03	Severe	Symptoms are heavy, and necessary care is intensive
P04	Very Severe (critical)	Complications systematic risk tall

Symptom weight table (0–1) to describe the probability of symptoms appearing in each severity category, based on expert input.

Table 3. Symptom Weight

Code	Symptom	Mild	Moderate	Severe	Very Severe
G01	Fever mild (37.5–38.4°C)	0.80	0.50	0.20	0.05
G02	Mild cough	0.70	0.50	0.30	0.10
G03	Runny nose watery	0.55	0.75	0.25	0.07
G04	Pain / irritation throat	0.65	0.50	0.30	0.10
G05	Conjunctivitis light	0.50	0.65	0.50	0.15
G06	Red skin without rash	0.65	0.50	0.30	0.10
G07	Lust Eat decrease	0.40	0.75	0.65	0.40
G08	Tired and lethargic	0.45	0.80	0.65	0.50
G09	Koplik's spots	0.20	0.85	0.60	0.60
G10	Red rash comprehensive	0.15	0.90	0.65	0.75
G11	Fever high (>39°C)	0.05	0.45	0.95	0.05
G12	Severe cough / rapid breathing	0.05	0.40	0.95	0.85
G13	Conjunctivitis heavy	0.05	0.35	0.90	0.80
G14	Duration fever > 5 days	0.05	0.40	0.95	0.80
G15	Seizures / disturbances neurological	0.01	0.05	0.60	0.95
G16	saturation < 95%	0.01	0.10	0.70	0.98

Symptom weights are determined based on expert judgment, referring to the degree of association between each symptom and the clinical severity of measles in toddlers, as reported in the medical literature. These weights are used as an initial probabilistic representation (expert-based weighting) to support the Naive Bayes method calculations and are not intended to represent absolute clinical values. This approach is commonly used in expert system research when large-scale empirical data are not yet available.

Decision tables and decision trees, which map the relationship between symptoms and severity categories.

Table 4. expert decisions

Code	Symptom	Mild (0–1)	Moderate (0–1)	Severe (0–1)	Very Severe (1-0)
G01	Fever mild (37.5–38.4°C)	✔	✔	-	-
G02	Mild cough	✔	✔	-	-
G03	Runny nose watery	✔	✔	-	-
G04	Sore throat	✔	✔	-	-
G05	Watery eyes/conjunctivitis light	✔	✔	✔	-
G06	Red skin without rash	✔	✔	-	-
G07	Lust eat decrease	-	✔	✔	-
G08	Tired and lethargic	-	✔	✔	-
G09	Koplik's spots	-	✔	✔	✔
G10	Red rash comprehensive	-	✔	-	✔

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G11	Fever high (>39°C)	-	✔	✔	-
G12	Severe cough / rapid breathing	-	-	✔	✔
G13	Red eye critical	-	-	✔	✔
G14	Duration fever > 5 days	-	-	✔	✔
G15	Seizures/signs neurological	-	-	✔	✔
G16	saturation < 95%	-	-	✔	✔

The expert decision table is used as the basis for developing forward-chaining rules by showing the relationship between each symptom and disease severity. A check mark (✔) indicates that a symptom is clinically relevant to appear at a specific severity level. This table is not intended to provide quantitative weighting, but rather to represent expert logic in grouping symptoms based on the progression of measles in toddlers.

Patient data (20 patients) was used as the basis for calculation and validation tests.

Table 5. Patient Data Summary

Severity Stage	Amount Patient	Percentage
Mild	5	25%
Moderate	5	25%
Severe	6	30%
Very Severe	4	20%
Total	**20**	**100%**

Of the 20 patients analyzed, measles severity was categorized as mild (5 patients) with mild disease, moderate (5 patients) with moderate disease, severe (6 patients) with severe disease, and very severe (4 patients) with very severe disease. This composition indicates that the data used covered a fairly balanced variation in severity, thus providing adequate representation for the classification method. All data were compiled in a Microsoft Excel table to facilitate data processing and analysis.

Forward Chaining Method

The Forward Chaining method is used as a rule-based reasoning mechanism to determine the initial severity of measles in toddlers based on the combination of symptoms they present. This method operates data-driven, starting with initial facts in the form of patient symptoms, then matching them with predefined IF–THEN rules to arrive at a conclusion on the severity level.

Forward Chaining rules are developed based on expert knowledge and medical literature, taking into account the relationship between clinical symptoms and measles severity. In this study, Forward Chaining serves as an initial filter to group patients into candidate severity levels before probabilistic analysis using the Naive Bayes method is performed.

The Forward Chaining rules used are as follows:

Rule 1 (Mild)

If a patient experiences a mild fever (G01) accompanied by prodromal symptoms such as a mild cough (G02), runny nose (G03), or sore throat (G04), and is not accompanied by severe symptoms such as seizures (G15) or low oxygen saturation (G16), then the patient is classified as Mild (R).

Rule 2 (Moderate)

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If a patient exhibits Koplik spots (G09) and a red rash (G10), accompanied by decreased appetite (G07) or weakness (G08), but has not experienced serious complications, then the patient is classified as Moderate (S).

Rule 3 (Severe)

If the patient experiences a high fever (G11), respiratory distress (G12), severe conjunctivitis (G13), or a fever that persists for more than five days (G14), without seizures or hypoxia, then the patient is classified as Severe (B).

Rule 4 (Very Severe)

If the patient experiences seizures or neurological disorders (G15) or oxygen saturation below 95% (G16), then the patient is immediately classified as Very Severe (SB).

The results of Forward Chaining are candidate severity levels, which are then further analyzed using the Naive Bayes method to reach a final probabilistic decision.

Naive Bayes Method

The next stage of this study applies the Naive Bayes method to calculate the probability of measles severity levels based on the observed patient symptoms. Naive Bayes is a probabilistic classification approach derived from Bayes' theorem and assumes conditional independence among symptoms given a particular severity class. In this research, symptom weights are treated as conditional likelihood values, while prior probabilities are obtained from the class distribution in the dataset or assumed to be equal when data are limited (Jamil et al., 2024).

Based on Bayes' theorem, the posterior probability of a severity class K given a set of observed symptoms $G = \{g_1, g_2, \dots, g_n\}$ is formulated as:

$$P(K \mid G) = \frac{P(K) \prod_{i=1}^{n} P(g_i \mid K)}{P(G)}$$

Since the denominator $P(G)$ is constant for all severity classes, the comparison among classes is performed using the unnormalized posterior probability:

$$P(K \mid G) = P(K) \prod_{i=1}^{n} P(g_i \mid K)$$

The severity category with the highest posterior probability is selected as the final classification result. All probability calculations, including likelihood multiplication, prior estimation, and normalization, were performed manually using Microsoft Excel to ensure transparency, traceability, and ease of validation (Glavei et al., 2023; Mutiara et al., 2020; Listiana & Nora, 2025).

Compiling a Decision Tree

A decision tree is created to illustrate the flow of determining severity based on the sequence of symptoms. This representation facilitates visualization of the analysis logic without depicting the application structure or flowchart. This technique is often used in rule-based diagnostic research (Gregoriades et al., 2023; Kurniawan, 2025).

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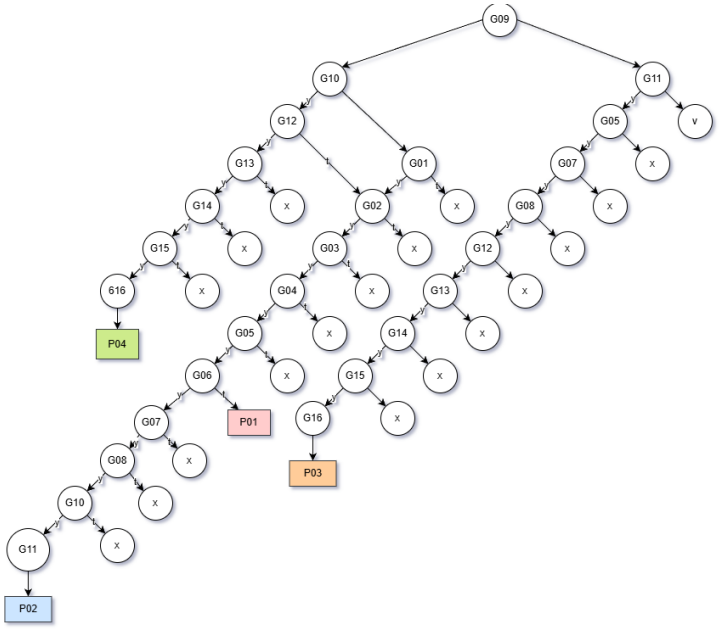

Figure 1. Decision Tree

A decision tree is constructed based on a decision table and Forward Chaining rules to depict a hierarchical inference flow. The tree structure shows that severe symptoms, such as respiratory and neurological disorders, are placed on the final branch, leading directly to the high severity category. Thus, the decision tree serves as an analytical tool to visualize the expert logic used in this study.

Rule Forward Chaining

Rule Forward Chaining is arranged based on a combination of dominant symptoms that represent the severity of the disease.

R1:
If G09 And G10 And G12 And G01 And G02 And G03 And G04 And G05 And G06 Then P01 (Mild)

R2:
If G09 And G10 And G12 And G01 And G02 And G03 And G04 And G05 And G06 And G07 And G08 And G10 And G11 Then P02 (Moderate)

R3:
If G09 And G10 And G12 And G01 And G02 And G03 And G04 And G15 And G16 Then P03 (Severe)

R4:
If G09 And G10 And G12 And G13 And G14 And G15 And G16 Then P04 (Very Severe)

The Forward Chaining rule is based on a combination of dominant symptoms representing each level of measles severity. The rule takes into account the order of clinical progression, with severe symptoms playing a more decisive role than early symptoms.

Validation Stage

The results of the analysis using Forward Chaining and Naive Bayes were compared with manual diagnosis on simulated patient data. This validation was used to assess the consistency of the results and the accuracy of both methods compared to clinical references (Umroh et al., 2024; Ar-Rayyan et al., 2024). The entire comparison process was conducted using Excel to ensure easy and accurate retesting of the results.

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This approach was chosen to provide clarity of the inference process and allow for separate evaluation of the methods without being influenced by the complexity of the system implementation.

Results and Discussion

The results obtained need to be understood in the context that Forward Chaining acts as a rule-based deterministic inference mechanism, while Naive Bayes is used to provide a probabilistic assessment that considers the weight of symptoms more comprehensively.

This study implemented the Forward Chaining (FC) and Naive Bayes (NB) methods to determine the severity of measles in toddlers. The implementation was carried out analytically using simulated data, without building an expert system. The data used consisted of 20 patients, 16 symptoms, and four severity classes: Mild (R), Moderate (S), Severe (B), and Very Severe (SB).

Forward Chaining is used to determine the initial class based on expert rules, while Naive Bayes is used for validation and probabilistic decision strengthening.

Diagnostic process flow:

Patient Data → Forward Chaining → Candidate Class → Naive Bayes → Final Diagnosis

Implementation of the Naive Bayes Method

The Naive Bayes method was employed to determine the probability of measles severity levels based on combinations of patient symptoms. This method applies Bayes' theorem, assuming conditional independence among symptoms. The general formula is:

$$P(C \mid G) = P(C) \times \prod P(G_i \mid C)$$

where:

$P(C \mid G)$= posterior probability of severity class given symptoms

$P(C)$= prior probability of each severity class derived from the dataset distribution

$P(G_i \mid C)$= likelihood of symptom occurrence in class C

The final diagnosis corresponds to the class with the highest posterior probability.

Example Calculation

Assume a patient presents the following symptoms:

G10, G15, G08, G09, and G04

Posterior probabilities were computed for each severity class.

Mild Class

$$\mathrm{P(Mild \mid G)} = 0.15 \times (0.15 \times 0.01 \times 0.45 \times 0.20 \times 0.65)$$
$$\mathrm{P(Mild \mid G)} \approx 0.000013$$

Moderate Class

$$\mathrm{P(Moderate \mid G)} = 0.15 \times (0.90 \times 0.05 \times 0.80 \times 0.85 \times 0.50)$$
$$\mathrm{P(Moderate \mid G)} \approx 0.00230$$

Severe Class

$$\mathrm{P(Severe \mid G)} = 0.40 \times (0.65 \times 0.60 \times 0.65 \times 0.60 \times 0.30)$$
$$\mathrm{P(Severe \mid G)} = 0.0182$$

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Very Severe Class

$P(\text{VerySevere} \mid G) = 0.30 \times (0.75 \times 0.95 \times 0.50 \times 0.60 \times 0.10)$
$P(\text{VerySevere} \mid G) \approx 0.00641$

The posterior probabilities obtained are:

Table 6. Posterior Probability

Severity Class	Probability
Mild	0.000013
Moderate	0.00230
Severe	0.0182
Very Severe	0.00641

Since the Severe class has the highest posterior probability, the patient is classified as having Severe measles severity.

Table 7. Patient classification

No	Symptoms (Codes)	Manual Class	Predicted Class	P(R)	P(S)	P(B)	P(SB)
1	G01, G14, G15, G04, G10, G07, G02	Very Severe	Moderate	0.4019	0.5351	0.0399	0.0231
2	G11, G16, G05, G08, G13, G01	Very Severe	Severe	0.0179	0.1082	0.8621	0.0118
3	G10, G15, G08, G09, G04	Severe	Moderate	0.0293	0.7076	0.0034	0.2597
4	G11, G03, G07, G13, G12, G08	Severe	Moderate	0.0293	0.7076	0.0034	0.2597
5	G10, G15, G08, G09, G04	Severe	Moderate	0.0293	0.7076	0.0034	0.2597
6	G05, G14, G11, G13	Severe	Severe	0.0019	0.0106	0.9864	0.0012
7	G08, G03, G01, G10, G02	Moderate	Mild	0.9092	0.0908	0.0000	0.0000
8	G16, G07, G03, G14, G13	Very Severe	Very Severe	0.0007	0.0175	0.1879	0.7939
9	G15, G06, G12, G10, G05	Moderate	Very Severe	0.0311	0.1592	0.0963	0.7134
10	G10, G11, G15, G08, G09	Mild	Moderate	0.0010	0.6773	0.1778	0.1439
11	G13, G14, G02, G06, G09, G08	Mild	Moderate	0.1434	0.7239	0.1217	0.0109
12	G15, G02, G12, G13, G08, G16	Very Severe	Very Severe	0.0000	0.0000	0.0076	0.9924
13	G09, G14, G16, G12	Moderate	Very Severe	0.0000	0.0004	0.0278	0.9718
14	G05, G03, G12, G06, G16	Severe	Mild	0.5374	0.2800	0.0672	0.1153
15	G13, G07, G16, G15, G10, G06	Severe	Very Severe	0.0000	0.0002	0.0021	0.9976

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16	G14, G12, G09, G05, G11, G15, G13	Mild	Severe	0.0000	0.0000	0.9954	0.0046
17	G05, G13, G10, G01, G02, G14, G06	Very Severe	Moderate	0.4716	0.5088	0.0193	0.0002
18	G01, G02, G16, G06, G12, G03	Severe	Mild	0.9688	0.0291	0.0014	0.0007
19	G04, G09, G01, G02, G15, G12, G11	Very Severe	Severe	0.0961	0.1965	0.7046	0.0028
20	G16, G12, G07, G11	Severe	Severe	0.0004	0.0063	0.8524	0.1408

Naive Bayes Classification Results

The Naive Bayes method was applied to 20 patient cases. The classification results showed:

Correct predictions: 16 patients

Incorrect predictions: 4 patients

Naive Bayes Accuracy

$$\text{Accuracy}_{\text{NB}} = \frac{16}{20} \times 100\% = 80\%$$

This result indicates that Naive Bayes provides strong predictive capability when symptom probability distributions are considered.

Misclassification mainly occurred between moderate and severe categories due to overlapping clinical symptoms such as fever intensity, rash spread, and respiratory involvement.

Diagnosis Using Forward Chaining

Forward Chaining is a rule-based inference method derived from expert clinical knowledge. Diagnosis is determined through IF–THEN rules based on symptom combinations.

Example rule:

IF:

High fever

Generalized rash

Neurological disturbances

THEN: Diagnosis: Very Severe measles.

This approach does not involve probability calculations but relies on deterministic expert-defined rules.

Forward Chaining Classification Results

When applied to the same dataset:

Correct predictions: 14 patients

Incorrect predictions: 6 patients

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Forward Chaining Accuracy

$$\text{Accuracy}_{\text{FC}} = \frac{14}{20} \times 100\% = 70\%$$

Although Forward Chaining performs well when symptoms clearly match predefined rules, it is less adaptable when symptoms vary or overlap across severity levels.

Comparative Analysis of Naive Bayes and Forward Chaining

The experimental results demonstrate that:

Naive Bayes achieved higher accuracy (80%) compared to Forward Chaining (70%).

Table 8. Accuracy Comparison of Naive Bayes and Forward Chaining Methods Based on Patient Data

Method	Amount of Data	Correct Diagnosis	Incorrect Diagnosis	Accuracy (%)
Naive Bayes	20	16	4	80%
Forward Chaining	20	14	6	70%

The probabilistic nature of Naive Bayes allows better handling of uncertain and varied symptom combinations.

Forward Chaining depends heavily on fixed expert rules, making it less flexible when patient symptoms do not exactly match predefined patterns.

Symptom overlap between moderate and severe measles cases contributes to classification discrepancies in both methods.

The higher performance of Naive Bayes in this study is primarily influenced by data characteristics rather than methodological superiority alone. The dataset contains variability in symptom combinations and unequal class distribution, conditions that favor probabilistic classification approaches.

Naive Bayes incorporates prior probabilities derived from actual patient data, improving model realism. Additionally, it can still generate predictions even with incomplete symptom information.

Forward Chaining remains valuable because it reflects expert clinical reasoning and ensures interpretability. However, its deterministic structure limits adaptability to diverse clinical presentations.

Therefore, combining both approaches may produce a more reliable clinical decision support system. Naive Bayes can provide probabilistic estimation, while Forward Chaining can serve as rule-based validation grounded in medical expertise.

Conclusion

Based on the results of applying the Forward Chaining (FC) and Naive Bayes (NB) methods to real-life measles patient data, it can be concluded that the Forward Chaining method has limitations because it relies heavily on the completeness and accuracy of the expert rules used. As a result, the variety of symptoms that appear in patients cannot be fully accommodated by the available rules. Meanwhile, the Naive Bayes method demonstrated better classification performance because it uses a probabilistic approach that can handle uncertainty and symptom variation between patients, resulting in a higher level of accuracy compared to the Forward Chaining method. The combination of the Forward Chaining and Naive Bayes methods results in a more systematic and consistent inference process than using each method separately. By

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utilizing real-life patient data, the results of this study are expected to better represent the actual clinical conditions, thus demonstrating the potential of applying this combined method to assist in more objectively analyzing measles severity in toddlers.

Although this study used real-life patient data, several limitations remain, including the relatively simple use of Forward Chaining rules and the adoption of uniform prior probability assumptions in the Naive Bayes method. Therefore, further research is recommended to develop more detailed and hierarchical Forward Chaining rules to more comprehensively describe the complexity of symptoms. Furthermore, future research can expand the amount and variety of patient data to improve the reliability of the evaluation results. Method development can also be carried out through the application of symptom weighting, the use of more realistic prior probability distributions, and the implementation and testing of the system in a computer-based environment so that the proposed method can be more optimally applied in clinical practice.

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