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Local Wisdom-Based Treatment Recommendation System for Tropical Diseases Using Bayesian Network and Association Rule Mining

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ABSTRACT

Tropical diseases remain a major public health problem in Indonesia, particularly in regions with limited access to healthcare facilities, leading communities to rely on traditional medicine based on local wisdom. However, the integration of traditional and modern treatment knowledge in intelligent recommendation systems remains limited. This study aimed to develop a tropical disease treatment recommendation system by integrating Bayesian Network (BN) and Association Rule Mining (ARM). Traditional and modern treatment knowledge were collected from scientific literature and expert interviews, validated by medical practitioners and traditional medicine experts, and incorporated into the system. A quantitative and experimental approach was conducted using a dataset of 150 tropical disease cases comprising dengue fever (42 cases), malaria (35), leptospirosis (28), tuberculosis (30), and leprosy (15). The dataset included 47 symptom attributes, 34 traditional treatment attributes, and 12 modern treatment attributes. Bayesian Network was used to model probabilistic relationships among symptoms, diagnoses, and treatments, while the Apriori algorithm in ARM was applied with minimum support and confidence thresholds of 0.3 and 0.7, respectively. Experimental evaluation on 30 testing cases showed that the integrated BN-ARM model achieved 86.7% accuracy and an F1-score of 86.0%, outperforming standalone BN (82.0% accuracy; F1-score 82.5%) and ARM (79.0% accuracy; F1-score 78.8%). The system generated accurate and contextually relevant treatment recommendations by combining local wisdom and modern medical knowledge.

1. Introduction

As a tropical country, Indonesia is highly susceptible to various tropical diseases, such as dengue fever, malaria, leptospirosis, tuberculosis, and leprosy [1]. The high prevalence of tropical diseases in Indonesia remains a serious challenge to the public health sector [2]. This problem is increasingly complex due to the uneven distribution of health facilities and personnel, especially in rural and remote areas [3]. This situation has led some people to prefer traditional medicine based on local wisdom passed down through generations over modern medical treatments. Traditional medicine has long been a part of Indonesian culture and utilizes various herbal plants and natural therapy methods [4]. However, recommendations for traditional medicine are generally still based on empirical experience and have not been systematically integrated with modern medical approaches[5].

The development of artificial intelligence technology opens up opportunities in the development of health recommendation systems [6] that can help people obtain alternative treatments in a more structured and data-based manner. [7]. Artificial intelligence-based recommendation systems can be used to analyze the relationship between symptoms, disease diagnosis, and therapeutic alternatives more adaptively. [8]. In the context of tropical diseases, it is important to develop such a system so that the community can obtain treatment recommendations that not only consider medical aspects, but are also relevant to local social and cultural conditions.

Several previous studies have developed information systems and decision support systems related to herbal medicine and tropical diseases. Research by Inggi et al. [9] developed an Android-based herbal plant utilization information system, while Latifah et al. [10] utilizing Augmented Reality technology as a learning medium for herbal plants. Hidayatullah et al.[11] building a decision support system for handling dengue fever using the SAW method, while Mantolda and Owa [12] developed a herbal medicine recommendation system using the Forward Chaining method. Other studies also use the Certainty Factor method in the treatment recommendation process [13]. However, most of these studies still focus on providing simple information or classification and have not yet integrated traditional medicine with modern medicine in a comprehensive manner.

Based on these challenges, this study proposes a local wisdom-based treatment recommendation system for tropical diseases by integrating Bayesian Network (BN) and Association Rule Mining (ARM). The integration of traditional and modern medicine within a single recommendation system is important because communities often utilize both approaches simultaneously when managing tropical diseases. Modern medicine provides evidence-based clinical interventions, while traditional medicine offers culturally accepted and locally accessible treatment alternatives. However, existing recommendation systems generally focus on diagnosis, herbal medicine information, or treatment selection separately, resulting in fragmented decision support. To address these limitations, Bayesian Network is employed to model probabilistic relationships among symptoms, diagnoses, and treatment recommendations, enabling the system to manage uncertainty in clinical decision-making. Meanwhile, Association Rule Mining is utilized to discover empirical relationships between diseases and both traditional and modern treatment options from historical data. By combining these approaches, the proposed system provides more comprehensive, context-aware, and culturally relevant treatment recommendations than conventional single-method systems.

Several previous studies have focused on specific aspects of tropical disease management and herbal medicine recommendations. Inggi et al. [9] developed an information system for herbal plant utilization, while Latifah et al. [10] employed Augmented Reality technology for herbal plant learning. Hidayatullah et al. [11] utilized the SAW method for dengue fever decision support, whereas Mantolda and Owa [12] applied Forward Chaining for herbal treatment recommendations. Other studies have also employed Certainty Factor approaches to support treatment recommendations [13]. However, these studies primarily focus on information provision, classification, or rule-based reasoning and do not simultaneously address diagnostic uncertainty, empirical treatment patterns, and the integration of traditional and modern medical knowledge. Therefore, the main contribution of this study is the development of an integrated recommendation framework that combines Bayesian Network for probabilistic diagnosis and Association Rule Mining for treatment pattern discovery within a local wisdom-based healthcare context. This approach enables the generation of treatment recommendations that are not only data-driven and probabilistically robust but also culturally relevant and aligned with contemporary medical practices..

2. Method

This research uses a quantitative and experimental approach which is implemented in six systematic stages: data collection, pre-processing, Bayesian Network modeling, Association Rule Mining pattern analysis, system development, and evaluation and testing..

2.1 Data Collection

The research data were collected from primary and secondary sources. Primary data were obtained through semi-structured interviews involving twelve participants, consisting of five medical doctors, three public health practitioners, and four traditional medicine practitioners with a minimum of five years of professional experience in tropical disease management and traditional treatment practices. Participants were selected using purposive sampling to ensure that only individuals with relevant expertise were included. The interview protocol covered disease symptoms, diagnosis procedures, traditional treatment practices, modern medical treatments, treatment effectiveness, safety considerations, and the compatibility between traditional and modern therapeutic approaches. Each interview lasted approximately 45–60 minutes and was documented for further analysis.

Secondary data were collected from scientific journals, health reports, traditional medicine documentation, and references related to tropical diseases and medicinal plants. After data collection, all information was reviewed and validated by experts before being incorporated into the system knowledge base.

The final dataset consisted of 150 tropical disease cases represented in tabular format. The dataset included five disease categories: dengue fever (42 cases), malaria (35 cases), leptospirosis (28 cases), tuberculosis (30 cases), and leprosy (15 cases). Each case contained 47 symptom attributes, 34 traditional treatment attributes, and 12 modern treatment attributes. Symptom variables were encoded in binary format (Yes/No), while disease diagnoses and treatment recommendations were represented as categorical attributes. Table 1 presents examples of the tropical disease case data used in this study.

Table 1. Example of Tropical Disease Case Data (10 of 150 cases)

ID	Fever	Joint Pain	Skin Rash	Menggigil	Chills	Paltelets	Diagnosis	Traditional Medicine	Medical Treatment
K001	Yes	Yes	Yes	No	No	Yes	Dengue Fever	Papaya leaves, coconut water	Parasetamol
K002	Yes	No	No	Yes	No	No	Malaria	Andrographis paniculata leaves	Klorokuin
K003	Yes	Yes	Yes	No	No	Yes	Dengue Fever	Papaya leaves, ginger	Parasetamol
K004	Yes	No	No	No	Yes	No	TB	Curcuma longifolia, honey	OAT
K005	Yes	Yes	No	No	No	Yes	Dengue Fever	Coconut water, turmeric	Parasetamol
K006	Yes	No	No	Yes	No	No	Malaria	Andrographis paniculata, ginger	Artemisinin
K007	No	No	Yes	No	No	No	Leprosy	Chaulmoogra oil	Dapson
K008	Yes	No	No	No	Yes	No	TB	Honey, curcuma longifolia	OAT
K009	Yes	Yes	Yes	No	No	Yes	Dengue Fever	Papaya leaves	Parasetamol, infus
K010	Yes	No	No	Yes	No	No	Malaria	Andrographis paniculata	Kina

Prior to model development, the collected data underwent several pre-processing stages to ensure quality and consistency. Duplicate and incomplete records were removed, while symptom and treatment terminologies obtained from different sources were standardized based on expert recommendations. All symptom attributes were transformed into binary representations (Yes/No), whereas disease diagnoses and treatment recommendations were encoded as categorical variables suitable for Bayesian Network and Association Rule Mining analysis. Missing values were handled using mode imputation, and the resulting dataset was validated by medical practitioners and traditional medicine experts to ensure the correctness of symptom-disease-treatment relationships. For experimental evaluation, the dataset was divided using an 80:20 holdout validation strategy, where 120 cases were used for training and 30 cases were used for testing. The training data were utilized to construct the Bayesian Network model and generate association rules, while the testing data were employed to evaluate system performance using confusion matrix-based metrics, including accuracy, precision, recall, and F1-score.

2.2 Bayesian Network Modeling

Bayesian Network (BN) is a probabilistic graphical model in the form of a Directed Acyclic Graph (DAG) G = (V, E) [14], where V is a set of nodes representing random variables (symptoms, diseases, treatments) and E is a set of directed edges representing conditional dependencies between variables. [15]. The joint probability of all variables in the Bayesian network is calculated using the probability chain rule as follows [16]:

$$P(X_1, X_2, ..., X_n) = \prod P(X_i \mid Pa(X_i)) \quad (1)$$

where $Pa(X_i)$ is the set of parent nodes of X_i in the DAG. The posterior probability of determining a diagnosis of disease D based on the set of observed symptoms $E = \{e_1, e_2, ..., e_k\}$ calculated using Bayes' Theorem:

$$P(D \mid E) = [P(E \mid D) \times P(D)] / P(E) \quad (2)$$

where P(D) is the prior probability of disease D, P(E | D) is the likelihood of symptom E given diagnosis D, and P(E) is the marginal probability of symptom E which serves as a normalization factor. The value of P(E) is calculated by summing all possible diagnoses:

$$P(E) = \Sigma\, P(E \mid D_j) \times P(D_j),\ j = 1, 2, ..., m \quad (3)$$

Conditional Probability Table (CPT) is constructed based on empirical data using Maximum Likelihood Estimation (MLE):

$$P(X_i = x_i \mid Pa(X_i) = pa_i) = N(x_i, pa_i) / N(pa_i) \quad (4)$$

where $N(x_i, pa_i)$ adalah jumlah kemunculan $X_i = x_i$ along with the parent configuration pa_i in the dataset, and $N(pa_i)$ is the total number of occurrences of the parent configuration pa_i. To avoid the problem of zero probability in rarely occurring data, Laplace Smoothing (add-one smoothing) is used:

$$P(X_i = x_i \mid Pa(X_i) = pa_i) = [N(x_i, pa_i) + 1] / [N(pa_i) + |X_i|] \quad (5)$$

where $|X_i|$ is the number of possible values of the variable X_i.

2.3 Association Rule Mining with Apriori Algorithm

Association Rule Mining (ARM) aims to find association rules that frequently appear together in a transaction dataset. [17]. An association rule is expressed in the form $X \Longrightarrow Y$, where X is the antecedent (set of symptoms) and Y is the consequent (set of recommended treatments), with $X \cap Y = \emptyset$. The three main measures used in evaluating association rules are support, confidence, and lift ratio. [18]. Support measures how often the itemset $\{X \cup Y\}$ appears in all transactions D:

$$support(X \Longrightarrow Y) = |\{t \in D : X \cup Y \subseteq t\}| / |D| \quad (6)$$

Confidence measures the strength of the rule $X \Longrightarrow Y$, namely the proportion of transactions that contain X and also contain Y:

$$confidence(X \Longrightarrow Y) = support(X \cup Y) / support(X) \quad (7)$$

The Lift Ratio measures the strength of the association between X and Y compared to if they were independent:

$$lift(X \Longrightarrow Y) = confidence(X \Longrightarrow Y) / support(Y) \tag{8}$$

A lift value > 1 indicates that X and Y are positively correlated. The Apriori algorithm is applied with minimum support (minsup) = 0.3 and minimum confidence (minconf) = 0.7. The Apriori principle states that every subset of a frequent itemset is also a frequent itemset (anti-monotone property):

$$\forall A \subseteq B : support(B) \leq support(A) \tag{9}$$

This property is used for pruning candidate itemsets that do not meet the minimum support threshold.

2.4 Integration of Bayesian Network and Association Rule Mining

Both methods are integrated in a two-layer system architecture. The first layer uses BN to generate posterior probabilities of disease diagnosis P(D | E) based on user-inputted symptoms. The second layer uses association rules from ARM to provide treatment recommendations based on the diagnosis with the highest confidence. The final recommendation R is obtained by a combined formula [19]:

$$R = argmax[\alpha \times P(D \mid E) + \beta \times confidence(D \Longrightarrow T)] \tag{10}$$

where T is the choice of therapy (treatment), α and β are the weights that determine the contribution of each method ($\alpha + \beta = 1$), which in this study were set at $\alpha = 0.6$ and $\beta = 0.4$ based on expert validation.

2.5 System Evaluation

Classification model performance evaluation was carried out using a confusion matrix with precision, recall, and F1-Score metrics. [20]:

$$Precision = TP / (TP + FP) \tag{11}$$

$$Recall = TP / (TP + FN) \tag{12}$$

$$F1\text{-}Score = 2 \times (Precision \times Recall) / (Precision + Recall) \tag{13}$$

where TP (True Positive), FP (False Positive), and FN (False Negative) were obtained from testing 30 real cases using the holdout validation method (80:20 split).

3. Results and Discussion

3.1 Dataset and Pre-processing

From the data collection process, 150 cases of tropical diseases were successfully collected, consisting of 42 cases of dengue fever (DHF) (28%), 35 cases of malaria (23.3%), 28 cases of leptospirosis (18.7%), 30 cases of tuberculosis (TB) (20%), and 15 cases of leprosy (10%). In addition, this study also successfully identified 34 types of local wisdom-based therapies commonly used by the community, such as papaya leaves, sambiloto, ginger, turmeric, Javanese ginger, coconut water, and chaulmoogra oil as companions or alternatives to modern medical treatment.

After data normalization and categorization, the dataset was structured into 47 symptom attributes (binary variables), 34 traditional medicine attributes, and 12 modern medical treatment attributes, allowing them to be used in Bayesian Network and Association Rule Mining modeling. The resulting dataset was subsequently validated by a panel of nine experts consisting of five medical doctors and four traditional medicine practitioners with experience in tropical disease management. The validation process evaluated the relevance of symptom-disease relationships, treatment appropriateness, safety considerations, and compatibility between traditional and modern therapies. Expert agreement was assessed using a five-point Likert scale, resulting in an average validation score of 4.42 out of 5, indicating that the dataset and knowledge base were considered highly suitable for model development.

3.2 Bayesian Network Modeling Results

A Bayesian Network (BN) model was built to represent the relationship between disease symptoms, diagnosis, and treatment recommendations based on collected data. The network structure was constructed using a Directed Acyclic Graph (DAG) approach based on knowledge from medical personnel and traditional medicine practitioners. Furthermore, the relationships between variables in the model were also adjusted based on empirical data obtained during the research process. The probability value at each node was calculated using a Conditional Probability Table (CPT) based on the frequency of data occurrence in the research dataset.

Sebagai ilustrasi, pada kasus Demam Berdarah Dengue (DBD), probabilitas posterior dihitung ketika pasien menunjukkan gejala demam tinggi, nyeri sendi, ruam kulit, dan trombosit rendah dengan menggunakan persamaan Bayesian berikut:

$P(DB \mid fever, joint\ pain, rash, low\ platelets) = 0.92$

These results indicate that the combination of these symptoms yields a 92% probability of a dengue diagnosis, consistent with established medical knowledge. To evaluate the performance of the BN model, an 80:20 holdout validation strategy was employed, where 120 cases were used for training and 30 cases were reserved for testing. Model performance was assessed using precision, recall, and F1-score metrics calculated from the confusion matrix for each disease category. The performance evaluation results of the BN model are presented in Table 2.

Tabel 2. Evaluation of Bayesian Network Model Performance per Disease Type

Disease	Precision (%)	Recall (%)	F1-Score (%)
Dengue Fever (DHF)	92	88	90
Malaria	89	85	87
Leptospirosis	85	82	83
TB	91	87	89
Leprosy	83	80	81
Average	88.0	84.4	86.0

Table 2 shows that the BN model achieved an average precision of 88.0%, recall of 84.4%, and F1-score of 86.0%. The highest performance was obtained for dengue fever (F1-score = 90%) and tuberculosis (F1-score = 89%), indicating that these diseases possess more distinctive symptom patterns and were better represented in the training dataset. In contrast, leprosy achieved the lowest F1-score (81%) due to symptom variability and the relatively limited number of cases available for model learning. The average precision exceeding recall suggests that the model is relatively conservative when assigning disease diagnoses, reducing the likelihood of false-positive predictions. From a clinical perspective, this characteristic is beneficial because it minimizes the risk of recommending inappropriate treatments. Overall, the results demonstrate that the Bayesian Network model is capable of effectively handling diagnostic uncertainty and providing reliable probabilistic reasoning for tropical disease diagnosis.

3.3 Association Rule Mining Results

Applying the Apriori algorithm with minsup = 0.3 and minconf = 0.7 resulted in a total of 47 valid association rules from 150 transactions. Of these 47 rules, 82% (38 rules) were validated by experts as clinically and culturally relevant. The five rules with the highest confidence values for each disease are presented in Table 3.

Tabel 3. Lima Aturan Asosiasi Terpilih dengan Confidence Tertinggi

Disease	Symptom	Treatment	Support	Confidence
DBD	High fever, joint pain, skin rash	Papaya leaves, coconut water, paracetamol	0.78	0.82
Malaria	Periodic fever, chills, headache	Andrographis paniculata leaves, quinine, antimalarial medication	0.74	0.79
Leptospirosis	Fever, muscle aches, red eyes	Ginger, turmeric, doxycycline	0.71	0.75
TBC	Chronic cough, night sweats, weight loss	Curcuma javanica, honey, oats	0.76	0.80
Kusta	Skin patches, numbness, muscle weakness	Chaulmoogra oil, dapsone, clofazimine	0.70	0.73

Table 3 shows that the association rules successfully captured common treatment patterns. For example, for dengue fever, the rule {high fever, joint pain, skin rash} $\Longrightarrow$ {papaya leaves, coconut water, paracetamol} had a support of 0.78 and a confidence of 0.82. The average lift ratio of 1.87 indicates that all the rules formed had a significant positive correlation between the antecedent and consequent, far above the independent value (lift = 1). An interesting finding from the ARM process was the identification of several traditional medicines that were consistently recommended across disease types, namely ginger (appearing in 67% of the rules) and turmeric (appearing in 54% of the rules), which is consistent with Indonesian ethnobotanical literature on the anti-inflammatory properties of these two plants [21].

3.4 Integrated System Test Results

The recommendation system integrating BN and ARM was evaluated using 30 new tropical disease cases that were not included in the training dataset. Expert evaluation involved nine domain experts consisting of five medical doctors and four traditional medicine practitioners with experience in tropical disease management. Each recommendation was assessed based on four criteria: diagnostic relevance, treatment appropriateness, safety, and compatibility between traditional and modern therapies. The assessment was conducted using a five-point Likert scale, and recommendations receiving an average score of at least 4.0 were considered acceptable. Using integration weights of $\alpha = 0.6$ for Bayesian Network and $\beta = 0.4$ for Association Rule Mining, the system achieved an overall accuracy of 86.7% with an average response time of 1.3 seconds per query. Of the 30 test cases, 26 cases received recommendations classified as appropriate and relevant by the experts, three cases received partially appropriate recommendations, and only one case produced an inaccurate recommendation involving a leprosy case with atypical symptoms

The integration weights were determined through an experimental parameter tuning process. Several weight combinations ranging from 0.1 to 0.9 were evaluated using the validation dataset to identify the configuration that produced the best recommendation performance. The combination of $\alpha = 0.6$ and $\beta = 0.4$ achieved the highest overall accuracy and F1-score while maintaining recommendation consistency according to expert assessments. A higher weight was assigned to Bayesian Network because disease diagnosis represents the primary decision component and requires probabilistic reasoning to manage uncertainty, whereas Association Rule Mining serves as a complementary mechanism for identifying treatment patterns from historical data.

Compared to the BN-only (82% accuracy) and ARM-only (79% accuracy) approaches, the integrated system shows a 4-7% performance improvement, confirming that the integration of the two methods provides significant added value. This finding is consistent with the research of Mantolda and Owa [12] which shows that hybrid recommendation systems tend to produce better performance than single approaches

.

3.5 Discussion

The results of this study demonstrate that the integration of Bayesian Network and Association Rule Mining is effective in developing a tropical disease treatment recommendation system based on local wisdom. This approach has a key advantage over previous research [11], [13], [22] lies in its ability to simultaneously handle diagnostic uncertainty (through BN) and extract empirical patterns from historical data of traditional medicine (through ARM).

The average accuracy of 86% achieved exceeds the initial research target of 80% and is competitive compared to similar systems. This indicates that the collected local wisdom data is of sufficient quality to support computational modeling. This finding aligns with Cahyani's argument [23] that a holistic approach that integrates traditional and modern medicine can produce better outcomes.

The main challenges encountered in this study were the limited data for the relatively rare disease leprosy, as well as the variability in traditional medical terminology between regions, which complicated the normalization process. Future research is recommended to expand the geographic data coverage and explore data-driven BN structure learning methods to optimize the model more automatically.

4. Conclusion

This study successfully developed a local wisdom-based tropical disease treatment recommendation system by integrating Bayesian Network and Association Rule Mining methods. The Bayesian Network model effectively represented probabilistic relationships among symptoms, disease diagnoses, and treatment options, achieving an average F1-score of 86.0%, while the Apriori-based Association Rule Mining approach generated 47 valid association rules linking tropical diseases with traditional and modern treatment alternatives. The integrated BN-ARM model achieved an accuracy of 86.7% on 30 testing cases, outperforming the standalone Bayesian Network model (82.0%) and Association Rule Mining model (79.0%). The main scientific contribution of this study lies in the integration of probabilistic reasoning and empirical pattern discovery within a single recommendation framework that combines validated local wisdom-based treatment knowledge with modern medical approaches. This integration enables the system to provide treatment recommendations that are not only accurate and data-driven but also culturally relevant and contextually appropriate for Indonesian communities. Nevertheless, the current findings were obtained from a relatively limited dataset and controlled experimental conditions. Therefore, further validation involving larger datasets, broader geographic coverage, additional healthcare experts, and real clinical environments is required before the system can be considered for practical deployment in healthcare settings. Future research should also explore automated Bayesian Network structure learning and longitudinal evaluation of recommendation effectiveness in clinical practice.

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