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Optimization of a hybrid forward chaining and certainty factor model for malaria diagnosis based on clinical and laboratory data

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ABSTRACT

Malaria remains a serious public health problem in Indonesia, particularly in Papua Province, which accounts for 89% of national malaria cases. The similarity of malaria symptoms with other infectious diseases and limited laboratory facilities often lead to delays and inaccuracies in diagnosis. The study proposes an optimized hybrid model that combines forward chaining and certainty factor (CF) by integrating clinical and laboratory data to improve the accuracy of malaria diagnosis. The research design includes acquiring knowledge from medical experts, developing a rule-based system using forward chaining, and applying CFs to overcome uncertainty in symptom interpretation. The system is implemented using Python with support from libraries such as NumPy and PyKnow. The test results showed that the integration of laboratory data significantly improved diagnostic performance, with accuracy increasing from 81% malaria-positive using clinical data alone to 98% malaria-positive after combining with laboratory data. Expert testing to validate the accuracy of clinical and laboratory data results compared to expert validation results in an accuracy score of 98%. These findings show that the optimization of the hybrid forward chaining model and CF for malaria diagnosis based on clinical and laboratory data as a recommendation tool for early diagnosis of malaria in endemic areas.

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1. INTRODUCTION

Malaria is an infectious disease with high morbidity and mortality rates in various endemic areas, including Indonesia [1]-[3]. Papua Province is the highest contributor to malaria cases in Indonesia, accounting for 89% of positive cases. This disease affects all age groups, caused by the bite of the Anopheles mosquito, which carries the Plasmodium parasite. The complexity of clinical symptoms, which often resemble other diseases, is compounded by limited laboratory testing facilities [4], [5], this causes the malaria diagnosis process to often experience delays or inaccuracies, which can ultimately reduce the effectiveness of therapy and worsen the patient's condition. The government's efforts to improve public health independence through free screening services need to be supported by technological innovation, particularly to accelerate early malaria diagnosis. Data from the Jayapura Regency Health Office in 2022 recorded 47,953 malaria cases, the highest number in the last five years. The diagnostic process at primary care facilities such as the

Elly Uyo Community Health Center generally begins with registration, anamnesis, physical examination, and laboratory confirmation through microscopic testing or a rapid diagnostic test (RDT). Although the clinical process is running relatively well, the main challenges are the availability of laboratory equipment and human resources. [6], [7].

In technological developments, artificial intelligence-based expert systems [8], [9]. These systems have been extensively applied to support the diagnosis of infectious diseases, including malaria. Nevertheless, the majority depend primarily on patients' subjective symptom data, which reduces their diagnostic accuracy. Prior studies, such as the 2023 fundamental research grant, have enhanced the diagnostic process for tertian and tropical malaria by integrating the forward chaining and certainty factor (CF) methods [10]. However, this study remains limited to clinical symptom data and has not yet incorporated laboratory results to achieve higher diagnostic accuracy. An expert system, in this context, refers to an information system that encapsulates the knowledge of specialists within a specific domain [11], [12]. The development of this system is intended to provide users with recommendations for appropriate problem-solving actions. Within the medical field, expert systems can be applied to analyze data and predict health conditions, such as identifying diseases based on patient symptoms. By leveraging a knowledge base and an inference engine composed of predefined rules, expert systems can effectively support the diagnostic process. The integration of the forward chaining approach with the CF method allows the system to process both clinical and laboratory data, thereby improving the accuracy of malaria diagnosis [13], [14].

Various previous studies have implemented forward chaining and CF in cases of infectious diseases and other infections. For example, research on the diagnosis of dengue hemorrhagic fever (DHF), malaria, and chikungunya showed 80%–98% accuracy for forward chaining and the superiority of CF in handling uncertainty. Another study on the diagnosis of ear infections produced 94% accuracy but was limited to one type of disease [15], while research in Mimika Regency recorded 98.2% accuracy for malaria diagnosis, but was only available for local access [16]. Another study detected three febrile diseases (DHF, malaria, typhoid) early with 95% accuracy, but the complexity of similar symptoms made the method less than optimal optimization [17].

To date, no malaria diagnostic system has been found that specifically integrates clinical data (subjective symptoms) and laboratory data (objective results) in a hybrid forward chaining and CF model. Therefore, this study aims to develop and optimize a hybrid forward chaining and CF model that integrates clinical and laboratory data to improve the accuracy of malaria diagnosis [18], [19].

The novelty of this study lies in the integration of clinical symptoms with laboratory data, offering more comprehensive information and enhancing the accuracy of diagnosis. Optimization of the hybrid model allows for more flexible inference processing in the face of patient data uncertainty. System validation was conducted directly on field data in malaria-endemic areas in Papua, thus strengthening the system's effectiveness and acceptability in a real-world context and supporting community health independence programs. Furthermore, during the implementation phase, this research used the Python programming language. The system was implemented using Python with support from libraries such as NumPy and PyKnow, which served as the basis for system development [20], because it supports various artificial intelligence libraries and expert systems that facilitate the efficient implementation of forward chaining and CF methods.

2. METHOD

2.1. Research design

This research uses an expert system development approach based on the forward chaining and CF methods optimized for malaria diagnosis. The research process begins with field observations and literature review, followed by knowledge base design, inference rule formulation, uncertainty calculation using CF, and hybrid model optimization to improve the accuracy of malaria diagnosis based on clinical and laboratory data.

2.2. Research procedure

The research stages can be seen in Figure 1. Referring to Figure 1 which describes the stages of the research, this study applies an expert system development approach by combining the forward chaining and CF methods to improve the accuracy of malaria diagnosis. The research process begins with field observation at the *Puskesmas* and literature review to obtain the latest information and theoretical foundations. Furthermore, the identification of tertiana and tropical malaria types was carried out, then a knowledge base was compiled that contained the relationship between clinical symptoms and laboratory data. The forward chaining method is used to formulate diagnosis rules based on IF–THEN rules [21], while the CF is applied to deal with uncertainty by giving weight to the measure of belief (MB) and measure of disbelief (MD) values. The two data were combined to generate a level of confidence in the diagnosis.

The combination of these two methods was optimized into a hybrid model that was tested on 100 respondents with clinical data and 100 malaria cases using clinical and laboratory data. The data analyzed included clinical symptoms (fever, chills, headache, muscle pain, nausea, and vomiting) as well as laboratory test results (microscopic and RDT). Accuracy tests were conducted by comparing results from clinical data with combined clinical and laboratory data.

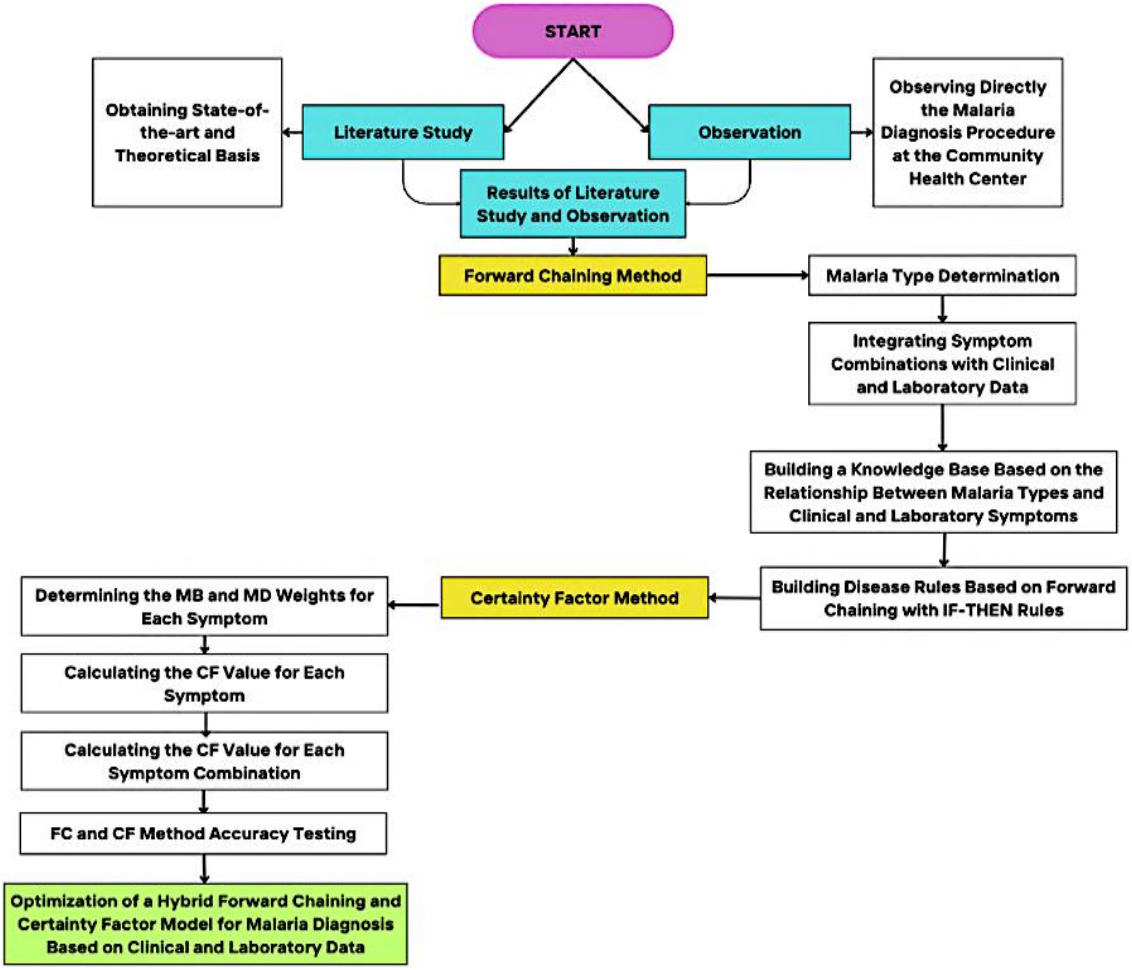

Figure 1. Research stages

In this study, the integration of clinical and laboratory data is a crucial foundation for generating more accurate decisions. This system relies not only on forward chaining-based expert rules but also strengthens the reasoning results with a CF method to measure the certainty of the hypotheses formed. This approach allows the combination of patient clinical symptoms and laboratory test results, allowing the system to provide more comprehensive recommendations. To clarify the model's position within the research pipeline, Figure 2 provides a conceptual diagram depicting the relationships between the main components.

2.3. Data

The research data was obtained from the medical records of malaria patients at the Elly Uyo Community Health Center, Jayapura Office. The clinical data used included the basic symptoms of tertian and tropical malaria, as described by dr. Nurul Amirah Sudirman:

i). Tertian malaria, characterized by a fever pattern that recurs every 48 hours, high fever accompanied by chills and sweating, with chills present (early fever), profuse sweating after the fever phase, general headache, muscle/joint pain, moderate nausea/vomiting, mild to moderate anemia, frequent diarrhea, and very frequent loss of appetite.

ii). Tropical malaria, characterized by an irregular fever pattern that recurs every 24 hours, high fever that is continuous and irregular, chills that are often more severe, sweating that may occur frequently, severe

headache, muscle/joint pain that is more severe, frequent nausea/vomiting, severe anemia, occasional diarrhea, and frequent loss of appetite.

Laboratory data based on blood results obtained by Mrs. Sukmawati's Laboratory Technician were as follows:

i). Tertian malaria with positive RDT data for P. vivax/ovale, microscopically typical schizonts/trophozoites, few parasites, low parasitemia (<1%), normal/slightly decreased hemoglobin, and normal blood sugar.

ii). Tropical malaria with positive RDT data for P. falciparum, microscopically multiple ringed trophozoites, sickled gametocytes, high parasitemia (>5%, can be >20%), sharply decreased hemoglobin (severe anemia), and low blood sugar (hypoglycemia).

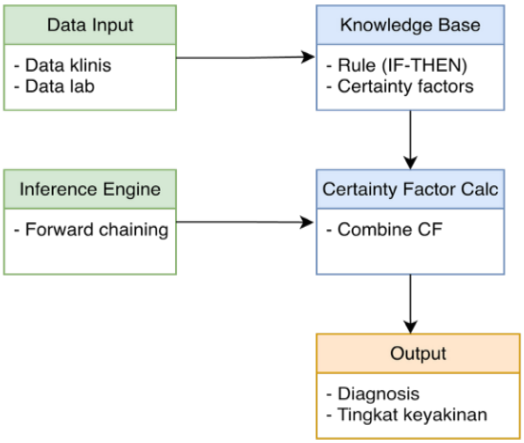

Figure 2. Conceptual diagram

2.4. Forward chaining method

The forward chaining method functions as a rule-based inference mechanism in which existing facts are compared with the *IF* component of an IF–THEN rule. When a fact corresponds to the IF condition, the rule is triggered, and its outcome (THEN part) is stored as a new fact in the knowledge base. The process begins with the top-level rule, and each rule is executed only once. Figure 3 is the inference process continues until no additional rules can be applied, at which point the matching process terminates [22].

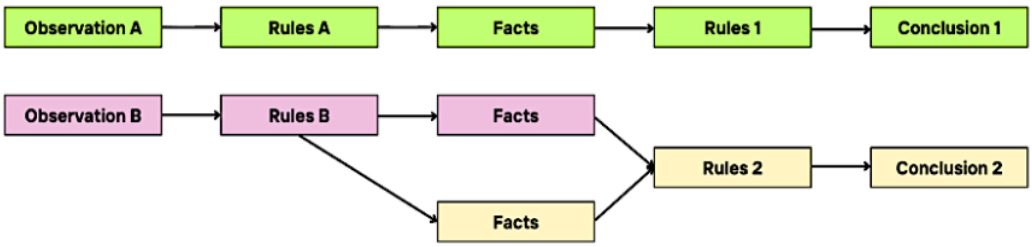

Figure 3. Forward chaining stage

2.5. Certainty factor method

The CF method is an approach used to manage uncertainty in decision-making. A CF represents the degree of confidence associated with a particular fact. The CF value ranges from +1.0 (completely certain) to –1.0 (completely uncertain). Positive values reflect the level of belief, whereas negative values indicate the degree of disbelief. The implementation of this method can be expressed mathematically through the following formula [23]-[25]:

a. The net belief method proposed by E.H. Shortliffe and B.G. Buchanan:

$$CF[H, E] = MB[H, E] - MD[H, E] \quad (1)$$

b. Combining CF values
CF for rules with similarly concluded rules:

$$CFcombine = CF[H, E]\ old + CF[H, E]\ gejala * (1 - CF[H, E]\ old) \quad (2)$$

3. RESULTS AND DISCUSSION

The analysis results are based on data compiled together with medical experts (doctors and laboratory personnel) to obtain a knowledge base from integrated symptom data + lab results.

3.1. Knowledge base

The knowledge base (rule base) was developed with a representation of the relationship between symptoms, laboratory results, and the types of malaria studied, namely tertian malaria and tropical malaria. The weights for MB and MD were determined based on expert validation. These values were used to calculate the CF per symptom. The knowledge base is shown in Table 1.

Table 1. Knowledge base

Disease code	Types of malaria	Category	Symptom code	Name of symptoms/findings	MB	MD
MTE1	Tertiana Malaria	Clinical	G1	Fever pattern with periodic every 48 hours (tertian)	0.7	0.1
	(P. vivax/ovale)	Clinical	G2	High fever, accompanied by shivering and sweating	0.6	0.15
		Clinical	G3	Shivering yes (phase beginning fever)	0.5	0.2
		Clinical	G4	Sweat lots after phase fever	0.4	0.25
		Clinical	G5	Headache general, moderate	0.3	0.3
		Clinical	G6	Muscle/joint pain yes, moderate	0.35	0.25
		Clinical	G7	Nausea/vomiting sometimes	0.25	0.35
		Clinical	G8	moderate anemia	0.4	0.2
		Clinical	G9	Frequent, mild diarrhea	0.2	0.4
		Clinical	G10	Decline very frequent appetite	0.25	0.3
		Lab	G11	Positive RDT P. vivax/ ovale	0.95	0
		Lab	G12	Microscopic Schizont/trophozoite typical, parasitic a little	0.85	0.05
		Lab	G13	Low parasitemia (<1%)	0.6	0.2
		Lab	G14	Normal/low hemoglobin down	0.1	0.3
		Lab	G15	Normal blood sugar	0.05	0.35
MTO2	Tropical malaria	Clinical	G16	Irregular fever pattern/every 24 hours	0.65	0.1
	(P. falciparum)	Clinical	G17	Continuous high fever, no regular	0.7	0.1
		Clinical	G18	Shivering yes, often more heavy	0.6	0.15
		Clinical	G19	Sweat may appear, often sweating cold	0.45	0.25
		Clinical	G20	Severe headache	0.4	0.25
		Clinical	G21	Muscle/joint pain yes, more great	0.45	0.2
		Clinical	G22	Frequent nausea/vomiting	0.35	0.25
		Clinical	G23	Severe anemia	0.65	0.1
		Clinical	G24	Diarrhea sometimes, light	0.2	0.35
		Clinical	G25	Decline frequent appetite	0.3	0.3
		Lab	G26	Positive RDT P. falciparum	0.98	0
		Lab	G27	Microscopic trophozoite ring multiple gametocytes sickle	0.9	0.03
		Lab	G28	High parasitemia (>5%, can be >20%)	0.99	0
		Lab	G29	Hemoglobin drops sharply (severe anemia)	0.7	0.1
		Lab	G30	Blood sugar can be low (hypoglycemia)	0.05	0.35

3.2. Model hybrid metode forward chaining and certainty factor

The use of forward chaining as a rule-based inference method that was successfully formulated with the IF-THEN format [26]. Forward chaining rules can be seen in Table 2. Furthermore, the CF method is applied to quantify the degree of certainty or confidence associated with each conclusion, as presented in Table 2.

Table 2. Forward chaining rules

No	Code	Rule
1	MTE1	IF [G01] AND [G02] AND [G03] AND [G04] AND [G05] AND [G06] AND [G07] AND [G08] AND [G09] AND [G10] AND [G11] AND [G12] AND [G13] AND [G14] AND [G15] THEN MTE1.
2	MTO2	IF [G16] AND [G17] AND [G18] AND [G19] AND [G20] AND [G21] AND [G22] AND [G23] AND [G24] AND [G25] AND [G26] AND [G27] AND [G28] AND [G29] AND [G30] THEN MT02.

3.3. Basic data on selected symptoms

The following is a sample of respondents who selected clinical symptoms, and the lab results from the medical staff can be seen in Table 3. Calculate the CF value using the basic formula [27] as follows:

$$CF[H, E] = MB[H, E] - MD[H, E] \quad (3)$$

Table 3. Selected symptom data

Category	Symptom code	Name of symptoms/findings	MB	MD	CF=MB-MD
Clinical	G1	Fever pattern with periodic every 48 hours (tertian)	0.7	0.1	0.7–0.1=0.60
Clinical	G2	High fever, accompanied by shivering and sweating	0.6	0.15	0.6–0.15=0.45
Lab	G11	Positive RDT P. vivax / ovale	0.95	0	0.95–0=0.95
Lab	G12	Microscopic schizont / trophozoite typical, parasitic a little	0.85	0.05	0.85–0.05=0.80
Clinical	G20	Severe headache	0.4	0.25	0.4–0.25=0.15

3.4. Calculation of CF malaria tertiana

After that calculates the combined CF value for the calculation of tertiana malaria CF, with the formula [28].

$$CFcombine = CF[H, E]\ old + CF[H, E]\ gejala * (1 - CF[H, E]\ old) \quad (4)$$

The detailed calculation is shown in Table 4. CF final malaria tertiana: 0.998

Table 4. Calculation of CF malaria tertiana

Step	Symptom code	CF symptoms	Previous CF	CF combination	Detailed calculation
1	G1	0.60	0.00	0.6	0+0.6× (1-0) =0.6
2	G2	0.45	0.600	0.78	0.6+0.45× (1-0.6) =0.6+0.18=0.780
3	G11	0.95	0.780	0.989	0.780+0.95× (1-0.780) =0.780+0.209=0.989
4	G12	0.80	0.989	0.998	0.989+0.8× (1-0.989) =0.989+0.0088=0.9978

3.5. Calculation of tropical malaria CF

After that calculates the combined CF value for the calculation of tropical malaria CF, with the formula:

$$CFcombine = CF[H, E]old + CF[H, E]gejala * (1 - CF[H, E]old) \quad (5)$$

Detailed calculations are shown in the Table 5. CF final tropical malaria: 0.150

Table 5. Calculation of tropical malaria CF

Step	Symptom code	CF symptoms	Previous CF	CF combination	Detailed calculation
1	G20	0.15	0.00	0.15	0+0.15× (1-0) =0.15

3.6. CF interpretation scale

The CF scale indicates the degree of certainty of a malaria diagnosis: a CF >0.5 means very likely, 0.2–0.5 needs confirmation, and <0.2 indicates a weak indication. The following Table 6 details the interpretation of each CF range to aid medical decision-making.

Table 6. Interpretation scale

Range CF	Interpretation	Information
CF >0.5	Strong positive	Diagnosis is very likely
0.2≤ CF ≤0.5	Possible malaria (tertian and tropical)	Diagnosis need confirmation
CF <0.2	No strong indications	Diagnosis small the possibility

The results of the integration of the forward chaining and CF methods can be formulated in the form of an algorithm as follows:

1. Enter the patient's facts (symptoms + lab results).
2. Calculate the CF of each symptom: CF = MB - MD.
3. Initialize CF_total = 0 for each hypothesis.
4. For each symptom that matches the hypothetical rule:
5. CF_total = CF_total + CF_gejala * (1 - CF_total).
6. Compare Tertiana vs Tropical CF_total.
7. Choose the hypothesis with the largest CF.
8. Interpretasikan hasil: >0.5 Strong Positive, 0.2–0.5 Possible, <0.2 No Indication.

3.7. Final diagnosis

Based on the results of manual calculations, the diagnosis of tertiana malaria was obtained with a "strong positive" interpretation. The researcher implemented a hybrid method into the python programming language with the same results as manual calculations and can be seen in Figure 4 which displays the list of tertiana and tropical symptoms as well as the input of symptoms that get the diagnosis result.

```
patmawatihasan@MacBook-Air-patmawati / % /usr/bin/python3 /Users/patmawatihasan/sistem_pakar_malaria.py
=== Optimasi Model Hybrid Forward Chaining dan Certainty Factor untuk Diagnosis Malaria berbasis Data Klinis dan Laboratorium ===
Pilih gejala yang dialami pasien (masukkan kode seperti G1, G2, dst. Ketik 'selesai' untuk akhiri).

DAFTAR GEJALA MALARIA TERTIANA (G1–G15):
G1: Pola demam dengan Periodik tiap 48 jam (tertiana) (MB=0.7, MD=0.1)
G2: Demam Tinggi, disertai menggigil & keringat (MB=0.6, MD=0.15)
G3: Menggigil Ya (fase awal demam) (MB=0.5, MD=0.2)
G4: Keringat banyak Setelah fase demam (MB=0.4, MD=0.25)
G5: Sakit kepala Umum, sedang (MB=0.3, MD=0.3)
G6: Nyeri otot/sendi Ada, sedang (MB=0.35, MD=0.25)
G7: Mual/muntah Kadang (MB=0.25, MD=0.35)
G8: Anemia Ringan–sedang (MB=0.4, MD=0.2)
G9: Diare Sering, Ringan (MB=0.2, MD=0.4)
G10: Penurunan Nafsu Makan Sangat Sering (MB=0.25, MD=0.3)
G11: RDT Positif P. vivax/ovale (MB=0.95, MD=0)
G12: Mikroskopis Skizon/trofozoit khas, parasit sedikit (MB=0.85, MD=0.05)
G13: Parasitemia Rendah (<1%) (MB=0.6, MD=0.2)
G14: Hemoglobin Normal / sedikit turun (MB=0.1, MD=0.3)
G15: Gula darah Normal (MB=0.05, MD=0.35)

DAFTAR GEJALA MALARIA TROPIKA (G16–G30):
G16: Pola demam Tidak teratur / tiap 24 jam (MB=0.65, MD=0.1)
G17: Demam Tinggi terus–menerus, tidak beraturan (MB=0.7, MD=0.1)
G18: Menggigil Ya, sering lebih berat (MB=0.6, MD=0.15)
G19: Keringat Bisa muncul, sering berkeringat dingin (MB=0.45, MD=0.25)
G20: Sakit kepala Berat (MB=0.4, MD=0.25)
G21: Nyeri otot/sendi Ada, lebih hebat (MB=0.45, MD=0.2)
G22: Mual/muntah Sering (MB=0.35, MD=0.25)
G23: Anemia Berat (MB=0.65, MD=0.1)
G24: Diare Kadang, Ringan (MB=0.2, MD=0.35)
G25: Penurunan Nafsu Makan Sering (MB=0.3, MD=0.3)
G26: RDT Positif P. falciparum (MB=0.98, MD=0)
G27: Mikroskopis Trofozoit cincin multipel, gametosit sabit (MB=0.9, MD=0.03)
G28: Parasitemia Tinggi (>5%, bisa >20%) (MB=0.99, MD=0)
G29: Hemoglobin Turun tajam (anemia berat) (MB=0.7, MD=0.1)
G30: Gula darah Bisa rendah (hipoglikemia) (MB=0.05, MD=0.35)

--- Input Gejala ---
Masukkan kode gejala (contoh: G1) atau 'selesai': G1
Gejala G1 ditambahkan.
Masukkan kode gejala (contoh: G1) atau 'selesai': G2
Gejala G2 ditambahkan.
Masukkan kode gejala (contoh: G1) atau 'selesai': G11
Gejala G11 ditambahkan.
Masukkan kode gejala (contoh: G1) atau 'selesai': G12
Gejala G12 ditambahkan.
Masukkan kode gejala (contoh: G1) atau 'selesai': G20
Gejala G20 ditambahkan.
Masukkan kode gejala (contoh: G1) atau 'selesai': SELESAI

=== HASIL DIAGNOSIS ===
CF Malaria Tertiana: 0.998
CF Malaria Tropika: 0.150
DIAGNOSIS: Malaria Tertiana (P. vivax/ovale) – POSITIF KUAT

Catatan: Ini bukan pengganti diagnosis medis profesional. Selalu konsultasikan dokter.
```

Figure 4. Calculation results using Python

3.8. Accuracy testing

In the testing stage, using 100 samples from responses for clinical data and 100 respondents for clinical data + laboratory, the results of the diagnosis can be seen in Tables 7 and 8. Based on the clinical diagnosis of 100 respondents alone, the results were obtained that 81% were identified as having malaria. Of these, 34% strong positive suffered from tertiana malaria, while 47% strong positive suffered from tropical malaria. In addition, there were 11% who were categorized as likely to be malaria prone to tertiary, and 4 respondents who were likely to be malaria tending to be tropical. Only 4 respondents did not show strong indications of malaria. Meanwhile, based on the results of clinical and laboratory diagnosis of 100 respondents, it was found that 98 people were identified as having malaria. The details showed that 59 strong positive respondents had tertiana malaria, while 39 strong positive respondents had tropical malaria. Only 2 respondents showed no strong indications of malaria.

Table 7. Clinical data testing

Respond	Symptom code	CF results		Status	
		Malaria tertiana	Tropical malaria	Malaria tertiana	Tropical malaria
1	G1; G2; G5; G6; G17	0.802	0.600	Strong positive	
2	G5; G8; G9; G24	0.200	0.000	No strong indication of malaria	
3	G2; G6; G8; G10; G19	0.604	0.200	Strong positive	
4	G3; G7; G9; G10; G20	0.300	0.150	Possible malaria (tertiana inclined)	
…	……	……	…….	…….	…….
98	G1; G25; G21; G5; G18; G10	0.600	0.587	Strong positive	
99	G16; G23; G4; G22	0.150	0.818		Strong positive
100	G2; G7; G9; G20; G6	0.505	0.150	Strong positive	

Table 8. Clinical and laboratory data testing

Respondent	Symptom code	CF results		Status	
		Malaria tertiana	Tropical malaria	Malaria tertiana	Malaria tropika
1	G1; G2; G3; G4; G11	0.993	0	Strong positive	
2	G1; G7; G8; G9; G10; G11	0.984	0	Strong positive	
3	G2; G3; G9; G16; G11; G12	0.996	0.55	Strong positive	
….	……..	….	…..	……	……..
98	G18; G19; G20; G21; G25; G26; G29	0	0.998		Strong positive
99	G16; G20; G23; G24; G26	0	0.997		Strong positive
100	G4; G5; G7; G21; G24; G26; G29	0.15	0.994		Strong positive

Figure 5 is a comparison of the accuracy of malaria positive clinical data was obtained for 81% and clinical and laboratory data for 98% who stated an increase of 17% malaria positive accuracy, if using clinical and laboratory data stating that the optimization of the hybrid forward chaining model and CF for malaria diagnosis based on clinical and laboratory data was successfully diagnoses 98% of malaria positive. The need for validation by an expert or doctor to test the accuracy of clinical data and laboratory data by dr. Nurul Amirah Sudirman as shown in Table 9.

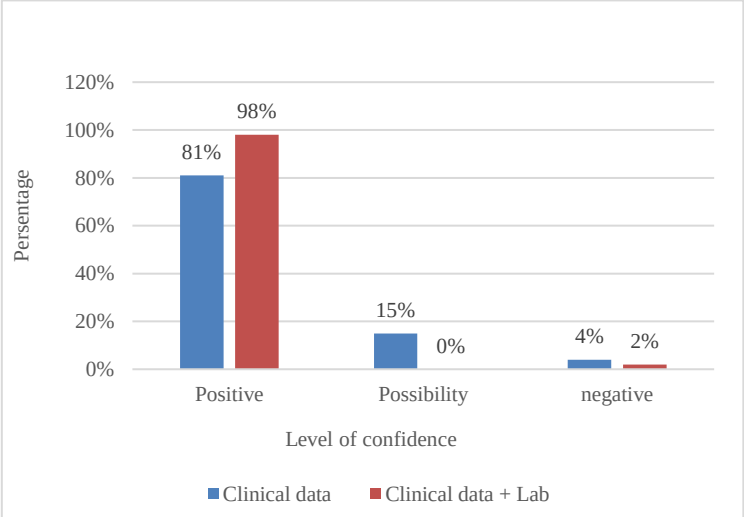

Figure 5. Accuracy comparison results

Table 9. Expert validation results

Respondent	Symptom code	CF results		Expert validation results		Accuracy
		Malaria tertiana	Tropical malaria	Malaria tertiana	Tropical malaria	
1	G1; G2; G3; G4; G11	0.993	0	✓	-	Appropriate
2	G1; G7; G8; G9; G10; G11	0.984	0	✓	-	Appropriate
3	G2; G3; G9; G16; G11; G12	0.996	0.55	✓	-	Appropriate
….	……..	….	…..	……	……..	
98	G18; G19; G20; G21; G25; G26; G29	0	0.998	-	✓	Appropriate
99	G16; G20; G23; G24; G26	0	0.997	-	✓	Appropriate
100	G4; G5; G7; G21; G24; G26; G29	0.15	0.994	-	✓	Appropriate

Testing the accuracy of the system is carried out by utilizing clinical data and laboratory results as the main source in the diagnosis process. The data is processed using the inference mechanism in the expert system to produce decisions. Furthermore, the results of the system output are compared with the results of the diagnosis given by medical experts as a reference for the truth. Validation from these experts is important to ensure the reliability of the system, so that the level of accuracy obtained can reflect the extent to which the system is able to mimic the thinking and decisions of an expert in diagnosing diseases using the formula described by C. Sammut and G. I. Webb in the encyclopedia of machine learning and data mining:

$$Accuracy = \left(\frac{Correcly\ classsified\ objects}{totsl\ number\ of\ objects}\right) \times 100\%$$

$$Accuracy = \left(\frac{98}{100}\right) \times 100\% = 98\% \quad (6)$$

4. CONCLUSION

This study developed a hybrid forward chaining and CF model for malaria diagnosis by integrating clinical symptoms with laboratory data, achieving a significant improvement in accuracy from 81% using clinical data alone to 98% when combined with laboratory results. The integration of subjective and objective information reduced diagnostic uncertainty, accelerated decision-making, and aligned strongly with expert validation, underscoring the system's potential to support primary healthcare in malaria-endemic regions such as Papua. Despite these promising outcomes, several limitations remain: the model was restricted to two malaria types (tertian and tropical), tested on a relatively small dataset of 200 respondents from a single health facility, and validated only by local experts, limiting generalizability. Usability aspects such as user experience and adoption were not assessed, and the system, while implemented in Python, has not yet been deployed as a real-time clinical application. Future research should expand the scope to include additional malaria variants and mixed infections, increase sample size and diversity across multiple endemic regions, and involve multi-institutional expert validation.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Patmawati Hasan	✓	✓	✓	✓	✓		✓	✓	✓	✓			✓	
Rahmat H Kiswanto		✓		✓		✓		✓	✓	✓	✓	✓		
Susi Lestari				✓		✓				✓				

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The author states that there is no conflict of interest in the conduct of the research.

DATA AVAILABILITY

The datasets used and analyzed in this study are not publicly available for reasons of medical confidentiality and ethical considerations. However, data may be obtained from the authors of correspondence upon reasonable request. All clinical and laboratory data were collected from the Elly Uyo Health Center, Jayapura City, Papua Province, with permission from relevant institutions and in accordance with applicable ethical guidelines.

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