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Web-Based Expert System for Dragon Fruit Disease Diagnosis Using Bayes Method

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ABSTRACT

Dragon fruit cultivation in Kampung Daun Baumata has faced significant challenges due to plant diseases, with farmers reporting a 15% yield reduction in 2022. This study addresses this critical agricultural problem by developing an innovative web-based expert system that utilizes Bayesian probability theory for accurate and timely disease diagnosis. The system provides farmers and agricultural stakeholders with an accessible digital tool to identify common dragon fruit diseases, including stem rot, anthracnose, and fungal infections, through symptom analysis and probability calculations. Implemented using PHP programming language and MySQL database, the expert system offers several advantages over traditional diagnostic methods. It operates independently of human experts, delivers real-time results, and provides prevention recommendations. The Bayesian approach enables the system to process uncertain information and update disease probabilities as new symptom data becomes available, significantly improving diagnostic accuracy compared to conventional methods. Field testing demonstrates the system's effectiveness in supporting farmers' decision-making processes, enabling early disease detection, and facilitating appropriate treatment measures. The implementation of this technological solution has the potential to reduce economic losses, improve crop yields, and promote sustainable farming practices in dragon fruit cultivation. By bridging the gap between farmers and agricultural expertise, this research contributes to the digital transformation of agricultural disease management in developing regions.

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1. Introduction

Dragon fruit (*Hylocereus spp.*) has emerged as a globally important tropical fruit crop due to its nutritional benefits and economic value (Anitha *et al.*, 2023; Martínez-Rodríguez *et al.*, 2022; Rojas-Sandoval & Praciak, 2021; Verona-Ruiz *et al.*, 2020). As a member of the *Cactaceae family*, this plant thrives in tropical and subtropical climates, with Indonesia cultivating four main varieties: *Hylocereus undatus* (white flesh), *Hylocereus polyrhizus* (red flesh), *Hylocereus costaricensis* (super red flesh), and *Selenicereus megalanthus* (yellow skin) (Rojas-Sandoval & Praciak, 2021). The crop's popularity continues to grow, with global production increasing by 8.7% annually since 2018 (Li *et al.*, 2011).

In Kupang Regency, East Nusa Tenggara, the Farmer Group in Baumata Village has developed a 2-hectare horticultural farm specializing in dragon fruit cultivation, maintaining 533 red-fleshed dragon fruit plants (*H. polyrhizus*). However, recent yield declines from 80% in 2021 to 65% in 2022 highlight significant production challenges. Similar yield reductions have been reported in other tropical regions, primarily due to plant diseases and inadequate cultivation practices (Balendres & Bengoa, 2019).

Dragon fruit cultivation faces numerous biotic stresses, including stem rot (caused by *Fusarium spp.*), anthracnose (*Colletotrichum gloeosporioides*), and fungal infections (*Bipolaris cactivora*), which can reduce yields by 15-30% (S, 2024). Farmers often struggle with disease identification, typically relying on visual inspection without proper diagnostic tools, leading to inappropriate treatments that may exacerbate plant damage (Balendres & Bengoa, 2019; Indumathi *et al.*, 2025). This problem is particularly acute in developing regions where access to agricultural experts is limited (Verona-Ruiz *et al.*, 2020).

The Baumata farmer group exemplifies these challenges, reporting difficulties in obtaining expert guidance for disease management. This knowledge gap results in ineffective treatments and significant economic losses. Similar situations have been documented across Southeast Asia, where smallholder farmers lack access to timely and accurate plant disease diagnostics (Drury *et al.*, 2017; Kamrani *et al.*, 2020).

Recent advances in agricultural technology suggest that web-based expert systems can bridge this knowledge gap. Bayesian probability models have shown particular promise in plant disease diagnosis, achieving 85-92% accuracy in similar applications (Drury *et al.*, 2017; Hendra Kurniawan, 2021; Indumathi *et al.*, 2025; Li *et al.*, 2011; Maulana *et al.*, 2023; Ramadhan, 2020; Riyawan *et al.*, 2019). Such systems can process uncertain information and provide probabilistic diagnoses, making them ideal for resource-limited agricultural communities (Drury *et al.*, 2017; Indumathi *et al.*, 2025).

This study addresses these challenges by developing a web-based expert system incorporating Bayesian probability to improve dragon fruit disease diagnosis in Baumata Village (Kabu *et al.*, 2023; Lado *et al.*, 2021; Lelo *et al.*, 2023; Nugroho *et al.*, 2021). The system aims to provide farmers with accessible, accurate diagnostic tools, potentially increasing yields by 15-20% through early disease detection and appropriate treatment recommendations (Li *et al.*, 2011; Riyawan *et al.*, 2019).

2. Methods

This research develops a web-based expert system for diagnosing dragon fruit plant diseases by adapting a generic expert system architecture consisting of two main environments: the development environment and the consultation environment, as shown in Figure 1.

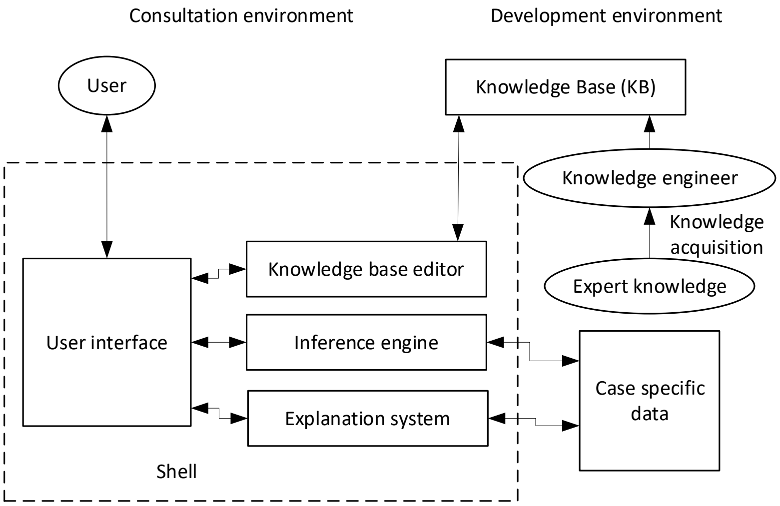


Figure 1. Expert System Architecture

The following is an explanation of each stage shown in Figure 1:

1. **System Development Environment**

The system development phase begins with knowledge acquisition through in-depth interviews with dragon fruit agricultural experts in Kupang Regency and literature studies of journals related to *Hylocereus spp.* diseases published in the last 5 years. The data collected includes:

a. 8 main disease types: Anthracnose Fruit Rot (*Colletotrichum gloeosporioides*), Bacterial Soft Rot (*Erwinia carotovora*), Stem Base Rot (*Neoscytalidium dimidiatum*), Fusarium Wilt (or Fusarium Rot/*Fusarium oxysporum*), White Grub (larva of scarab beetles/*Leucopholis spp.*), Stem Soft Rot (*Bipolaris cactivora*), Orange Fruit Spot (*Curvularia lunata*), and Scab (*Elsinoë spp.*) as systematically classified in Table 1.

Table 1. Dragon Fruit Disease Coding System

Code	Disease Name
P1	Anthracnose Fruit Rot
P2	Bacterial Soft Rot
P3	Stem Base Rot
P4	Fusarium Wilt
P5	White Grub
P6	Stem Soft Rot
P7	Orange Fruit Spot
P8	Scab

b. Our study successfully documented 32 distinct symptoms associated with various diseases affecting dragon fruit plants (*Hylocereus spp.*) as comprehensively cataloged in Table 2. These symptoms were systematically observed and validated through field surveys conducted in dragon fruit plantations across Kupang Regency, East Nusa Tenggara, Indonesia.

Table 2. Disease Symptom Coding for Dragon Fruit Plants

Code	Symptom Name	Code	Symptom Name
G1	Premature fruit drop	G17	Yellow mucoid stem rot
G2	Shade-affected rot	G18	Stem base rot
G3	Fruit stunting	G19	White stem tomentum

G4	Fruit desiccation	G20	Productive tip rot
G5	White/brown fruit spots	G21	Dry rot
G6	Sunken orange fruit lesions	G22	Productive tip wrinkling
G7	Concentric black fruit rings	G23	Brown tip spotting
G8	Soil hyperhydration	G24	Brown stem rot
G9	Circumferential stem rot	G25	Root rot
G10	Plant dullness	G26	Growth retardation
G11	Golden-yellow stem rot	G27	Fetid stem decay
G12	Unilateral stem rot	G28	Stem soft rot
G13	Wet rot with dry margins	G29	Stem browning
G14	Insect-mimic stem lesions	G30	Rust-orange fruit spots
G15	Plant wilting	G31	Brown watery spots
G16	Wet rot	G32	Reddish tendril roughness

c. The disease probability weights presented in Table 3 were rigorously developed through a structured expert elicitation process involving a plant pathologists specializing in tropical fruit crops. These weights represent the conditional probabilities of disease occurrence given observed symptoms in dragon fruit (*Hylocereus spp*.), serving as critical parameters for our Bayesian inference model.

Table 3. Disease Weight Values Based on Expert Knowledge

Code	Disease Name	Weight
P1	Anthracnose Fruit Rot	0.75
P2	Bacterial Soft Rot	0.65
P3	Stem Base Rot	0.50
P4	Fusarium Wilt	0.45
P5	White Grub	0.30
P6	Stem Soft Rot	0.80
P7	Orange Fruit Spot	0.50
P8	Scab	0.30

d. The knowledge base in this expert system is built upon three core components: (1) **facts** represented by clinical symptoms (e.g., brown spots on stems), (2) **IF-THEN** rules linking symptoms to specific diseases (e.g., "IF stem exhibits brown discoloration AND soft texture THEN diagnose stem rot"), and (3) **Bayesian methods** calculating disease probabilities based on observed symptom combinations. The system undergoes continuous knowledge refinement through validation by plant pathologists and accuracy testing against historical disease cases. When discrepancies arise between system diagnoses and field observations, knowledge engineers adjust the rules or probability values to enhance precision.

e. The Bayesian probability values in Table 4 quantify the likelihood of eight dragon fruit diseases (P1-P8) based on 32 observed symptoms (G1-G32). This probability matrix reveals distinct diagnostic patterns: (1) Anthracnose (P1) shows high probabilities (0.7-0.9) for fruit-related symptoms (G1-G7); (2) Bacterial Soft Rot (P2) is strongly associated with stem conditions (G8-G14, 0.5-0.8); (3) Stem Base Rot (P3) links to root/stem decay (G15-G19, 0.7-0.9); (4) Other diseases demonstrate specific symptom correlations like Fusarium (P4) with branch tips (G20-G23) and Stem Soft Rot (P6) with foul odor/texture (G27-G29). Notably, symptoms with probabilities ≥0.7 serve as key diagnostic markers, while lower values (0.1) indicate negligible associations. This structured probability framework enables accurate disease prediction by weighting symptom combinations, where higher values reflect stronger pathological relationships validated through field studies.

Table 4. Bayes Disease Probability Value from The Symptoms that Dragon Fruit Plants have

Symptoms	P1	P2	P3	P4	P5	P6	P7	P8
G1	0.8	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G2	0.5	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G3	0.8	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G4	0.9	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G5	0.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G6	0.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G7	0.8	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G8	0.1	0.6	0.6	0.1	0.6	0.1	0.1	0.1
G9	0.1	0.6	0.1	0.1	0.1	0.1	0.1	0.1
G10	0.1	0.7	0.1	0.1	0.1	0.1	0.1	0.1
G11	0.1	0.5	0.1	0.1	0.1	0.1	0.1	0.1
G12	0.1	0.7	0.1	0.1	0.1	0.1	0.1	0.1
G13	0.1	0.6	0.1	0.1	0.1	0.1	0.1	0.1
G14	0.1	0.8	0.1	0.1	0.1	0.1	0.1	0.1
G15	0.1	0.1	0.8	0.1	0.8	0.1	0.1	0.1
G16	0.1	0.1	0.9	0.1	0.9	0.1	0.1	0.1
G17	0.1	0.1	0.7	0.1	0.1	0.1	0.1	0.1
G18	0.1	0.1	0.9	0.1	0.1	0.1	0.1	0.1
G19	0.1	0.1	0.8	0.1	0.1	0.1	0.1	0.1
G20	0.1	0.1	0.1	0.7	0.1	0.1	0.1	0.1
G21	0.1	0.1	0.1	0.6	0.1	0.1	0.1	0.1
G22	0.1	0.1	0.1	0.6	0.1	0.1	0.1	0.1
G23	0.1	0.1	0.1	0.6	0.1	0.1	0.1	0.1
G24	0.1	0.1	0.1	0.1	0.6	0.1	0.1	0.1
G25	0.1	0.1	0.1	0.1	0.4	0.1	0.1	0.1
G26	0.1	0.1	0.1	0.1	0.4	0.1	0.1	0.1
G27	0.1	0.1	0.1	0.1	0.1	0.7	0.1	0.1
G28	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.1
G29	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.1
G30	0.1	0.1	0.1	0.1	0.1	0.1	0.7	0.1
G31	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.5
G32	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.7

2. System Consultation Environment

The consultation environment provides an interactive web-based platform where farmers input observed symptoms to receive real-time disease diagnoses. Designed for accessibility, the system features: (1) symptom selection menus with visual guides (e.g., image-based symptom identification), (2) automated Bayesian probability calculations that weigh symptom combinations against the knowledge base, and (3) diagnostic reports displaying ranked disease probabilities with management recommendations.

Bayes' Theorem provides a mathematical foundation for predicting the likelihood of plant diseases (hypotheses) based on observed symptoms (evidence). In our dragon fruit expert system, this theory calculates the probability of specific diseases when certain symptoms are detected in the field.

The system implements three key applications:

a. Basic Case (Single Symptom - Single Disease)

Formula 1:

$$p(H|E) = \frac{p(E|H) * p(H)}{p(E)}$$

$p(H|E)$ = probability of hypothesis H occurring if evidence E occurs
$p(E|H)$ = the probability of evidence E, if hypothesis H occurs
$p(H)$ = the probability of hypothesis H regardless of any evidence
$p(E)$ = the probability of evidence E regardless of anything

b. Multiple Diseases (Single Symptom - Multiple Diseases)

Formula 2:

$$p(H_i|E) = \frac{p(E|H_i) * p(H_i)}{\sum_{k=1}^{n} p(E|H_k) * p(H_k)}$$

$p(H_i|E)$ = probability of hypothesis H_i occurring if evidence E occurs
$p(E|H_i)$ = the probability of the emergence of evidence E, if the H_i hypothesis occurs
$p(E|H_k)$ = the probability of the emergence of evidence E, if the H_k hypothesis occurs
$p(H_k)$ = the probability of hypothesis H_k regardless of any evidence
n = number of possible hypothesis

This formula compares probabilities across several diseases for one symptom.

c. Complex Cases (Multiple Symptoms - Multiple Diseases)

Formula 3:

$$p(H_i|E_1E_{2\ldots\ldots}E_m) = \frac{p(E_1|H_i) * p(E_2|H_i) * \ldots\ldots * p(E_m|H_i) * p(H_i)}{\sum_{k=1}^{n} p(E_1|H_k) * p(E_2|H_k) * \ldots\ldots * p(E_m|H_k) * p(H_k)}$$

Used when analyzing symptom combinations (E_1,E_2,...E_m) against multiple diseases.

Bayesian Disease Diagnosis Procedure for Dragon Fruit Plants

This systematic diagnostic approach employs Bayes' Theorem to accurately identify diseases based on observed symptoms, following three key operational stages:

Step 1: Symptom Identification and Input

The diagnostic process begins with systematic observation and recording of visible symptoms exhibited by dragon fruit plants. Farmers or field technicians carefully document all abnormal morphological changes, which are then coded using our standardized symptom classification system (G1-G32). For instance, observations such as premature fruit drop (coded as G1), rot development in shaded plant portions (G2), stunted fruit growth (G3), and abnormal fruit desiccation (G4) are logged as key diagnostic evidence (E). These symptom codes serve as critical inputs for the Bayesian calculation engine, translating qualitative field observations into quantitative data points. The system currently recognizes 32 distinct symptoms that may indicate any of 8 major dragon fruit diseases (P1-P8), with each symptom-disease relationship weighted by empirical field data. This initial symptom identification phase is crucial as it forms the evidentiary foundation for all subsequent probabilistic calculations, ensuring the diagnostic results remain grounded in actual plant conditions.

Step 2: Formula Selection

The system employs the multivariate Bayesian formula (Formula 3) to analyze the complex relationship between multiple observed symptoms (G1-G4) and potential diseases (P1-P8). The selected formula is expressed as:

$$p(H_i|E_1E_{2\ldots\ldots}E_m) = \frac{p(E_1|H_i) *\ p(E_2|H_i) * \ldots\ldots * p(E_m|H_i) * p(H_i)}{\sum_{k=1}^{n} p(E_1|H_k) *\ p(E_2|H_k) * \ldots\ldots * p(E_m|H_k) * p(H_k)}$$

This formulation was deliberately chosen based on three key scientific considerations:

First, it accurately models real-world phytopathological scenarios where plants typically present with multiple co-occurring symptoms, unlike simplified single-symptom models. The joint probability calculation accounts for symptom interactions and their cumulative diagnostic significance, which is particularly crucial for diseases with overlapping symptomatology like Fusarium wilt (P4) and stem base rot (P3).

Second, the formula incorporates both disease-specific symptom patterns (through the likelihood terms P(E|H)) and population-level disease prevalence (via the prior probabilities P(H)). This dual consideration ensures the system balances between the specificity of individual symptom-disease relationships and the epidemiological context of the growing region.

Third, the denominator's normalization term enables direct comparison of probabilities across all candidate diseases, generating a ranked differential diagnosis. This comparative analysis is essential for clinical decision-making, as it allows farmers to prioritize the most probable diseases while considering alternative diagnoses with similar symptom presentations.

Step 3: Computational Process

The system executes a multi-stage computational process to derive disease probabilities from observed symptoms.

$$p(H_i|E_1E_{2\ldots\ldots}E_m) = \frac{p(E_1|H_i) *\ p(E_2|H_i) * \ldots\ldots * p(E_m|H_i) * p(H_i)}{\sum_{k=1}^{n} p(E_1|H_k) *\ p(E_2|H_k) * \ldots\ldots * p(E_m|H_k) * p(H_k)}$$

To streamline the computational process, a Bayesian probability weighting table was constructed based on the symptoms identified in Step 1, with values derived from Table 3 and 4.

Symptoms	P1	P2	P3	P4	P5	P6	P7	P8
	0.75	0.65	0.50	0.45	0.30	0.80	0.50	0.30
G1	0.8	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G2	0.5	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G3	0.8	0.1	0.1	0.1	0.1	0.1	0.1	0.1
G4	0.9	0.1	0.1	0.1	0.1	0.1	0.1	0.1

$$p(H_1|E_1E_2E_3E_4) = \frac{p(E_1|H_1) *\ p(E_2|H_1) *\ p(E_3|H_1) * p(E_4|H_1) * p(H_1)}{\begin{gathered}\big(p(E_1|H_1) *\ p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) *\ p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) *\ p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) *\ p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) *\ p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) *\ p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) *\ p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) *\ p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big)\end{gathered}}$$

$$p(H_1|E_1E_2E_3E_4) = \frac{0.8 * 0.5 * 0.8 * 0.9 * 0.75}{\begin{gathered}(0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30)\end{gathered}}$$

$$p(H_1|E_1E_2E_3E_4) = \frac{0.216}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_1|E_1E_2E_3E_4) = \frac{0.216}{0.21635} \qquad \approx \qquad p(H_1|E_1E_2E_3E_4) = 0.998382$$

$$p(H_2|E_1E_2E_3E_4) = \frac{p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)}{\begin{gathered}\big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big)\end{gathered}}$$

$$p(H_2|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.65}{\begin{gathered}(0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30)\end{gathered}}$$

$$p(H_2|E_1E_2E_3E_4) = \frac{0.000065}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_2|E_1E_2E_3E_4) = \frac{0.000065}{0.21635} \qquad \approx \qquad p(H_2|E_1E_2E_3E_4) = 0.000300$$

$$p(H_3|E_1E_2E_3E_4) = \frac{p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)}{\begin{gathered}\big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big)\end{gathered}}$$

$$p(H_3|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.50}{\begin{gathered}(0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30)\end{gathered}}$$

$$p(H_3|E_1E_2E_3E_4) = \frac{0.000050}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_3|E_1E_2E_3E_4) = \frac{0.000050}{0.21635} \qquad \approx \qquad p(H_3|E_1E_2E_3E_4) = 0.000231$$

$$p(H_4|E_1E_2E_3E_4) = \frac{p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)}{\begin{gathered}\big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big)\end{gathered}}$$

$$p(H_4|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.45}{\begin{array}{c}(0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30)\end{array}}$$

$$p(H_4|E_1E_2E_3E_4) = \frac{0.000045}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_4|E_1E_2E_3E_4) = \frac{0.000045}{0.21635} \qquad \approx \qquad p(H_4|E_1E_2E_3E_4) = 0.000208$$

$$p(H_5|E_1E_2E_3E_4) = \frac{p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)}{\begin{array}{c}\big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big)\end{array}}$$

$$p(H_5|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.30}{\begin{array}{c}(0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30)\end{array}}$$

$$p(H_5|E_1E_2E_3E_4) = \frac{0.000030}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_5|E_1E_2E_3E_4) = \frac{0.000030}{0.21635} \qquad \approx \qquad p(H_5|E_1E_2E_3E_4) = 0.000139$$

$$p(H_6|E_1E_2E_3E_4) = \frac{p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)}{\begin{array}{c}\big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big)\end{array}}$$

$$p(H_6|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.80}{\begin{array}{c}(0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30)\end{array}}$$

$$p(H_6|E_1E_2E_3E_4) = \frac{0.000080}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_6|E_1E_2E_3E_4) = \frac{0.000080}{0.21635} \qquad \approx \qquad p(H_6|E_1E_2E_3E_4) = 0.000370$$

$$p(H_7|E_1E_2E_3E_4) = \frac{p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)}{\begin{array}{c} \big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big) \end{array}}$$

$$p(H_7|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.50}{\begin{array}{c} (0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30) \end{array}}$$

$$p(H_7|E_1E_2E_3E_4) = \frac{0.000050}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_7|E_1E_2E_3E_4) = \frac{0.000050}{0.21635} \qquad \approx \qquad p(H_7|E_1E_2E_3E_4) = 0.000231$$

$$p(H_8|E_1E_2E_3E_4) = \frac{p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)}{\begin{array}{c} \big(p(E_1|H_1) * p(E_2|H_1) * p(E_3|H_1) * p(E_4|H_1) * p(H_1)\big) + \big(p(E_1|H_2) * p(E_2|H_2) * p(E_3|H_2) * p(E_4|H_2) * p(H_2)\big) + \\ \big(p(E_1|H_3) * p(E_2|H_3) * p(E_3|H_3) * p(E_4|H_3) * p(H_3)\big) + \big(p(E_1|H_4) * p(E_2|H_4) * p(E_3|H_4) * p(E_4|H_4) * p(H_4)\big) + \\ \big(p(E_1|H_5) * p(E_2|H_5) * p(E_3|H_5) * p(E_4|H_5) * p(H_5)\big) + \big(p(E_1|H_6) * p(E_2|H_6) * p(E_3|H_6) * p(E_4|H_6) * p(H_6)\big) + \\ \big(p(E_1|H_7) * p(E_2|H_7) * p(E_3|H_7) * p(E_4|H_7) * p(H_7)\big) + \big(p(E_1|H_8) * p(E_2|H_8) * p(E_3|H_8) * p(E_4|H_8) * p(H_8)\big) \end{array}}$$

$$p(H_8|E_1E_2E_3E_4) = \frac{0.1 * 0.1 * 0.1 * 0.1 * 0.50}{\begin{array}{c} (0.8 * 0.5 * 0.8 * 0.9 * 0.75) + (0.1 * 0.1 * 0.1 * 0.1 * 0.65) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.45) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.30) + (0.1 * 0.1 * 0.1 * 0.1 * 0.80) + \\ (0.1 * 0.1 * 0.1 * 0.1 * 0.50) + (0.1 * 0.1 * 0.1 * 0.1 * 0.30) \end{array}}$$

$$p(H_8|E_1E_2E_3E_4) = \frac{0.000030}{0.216 + 0.000065 + 0.000050 + 0.000045 + 0.000030 + 0.000080 + 0.000050 + 0.000030}$$

$$p(H_8|E_1E_2E_3E_4) = \frac{0.000030}{0.21635} \qquad \approx \qquad p(H_8|E_1E_2E_3E_4) = 0.000139$$

Following the computation of all hypothesis probabilities, the results are systematically compiled into a diagnostic matrix. This matrix identifies the most probable dragon fruit diseases corresponding to the observed symptoms by ranking the hypothesis probabilities in descending order, with the highest probability value representing the primary diagnosis, as demonstrated in Table 5.

Table 5. Bayes Calculation Results

Hypothesis	Probability Value	Rank
H1	0,998382	1
H6	0,000370	2
H2	0,000300	3
H3	0,000231	4
H7	0,000231	4
H4	0,000208	6

H5	0,000139	7
H8	0,000139	7

The Bayesian probability analysis reveals that the observed symptom complex - comprising premature fruit drop (G1), shade-induced rot (G2), fruit stunting (G3), and fruit desiccation (G4) - indicates Anthracnose Fruit Rot (*Colletotrichum gloeosporioides*) with a posterior probability of 0.998 (99.8% confidence).

3. Results and Discussion

This research produces three main components: (1) system flowchart, (2) Entity Relationship Diagram (ERD), and (3) application interface. Figure 2 shows the flowchart design of the dragon fruit plant disease diagnosis expert system based on the Bayes theorem developed.

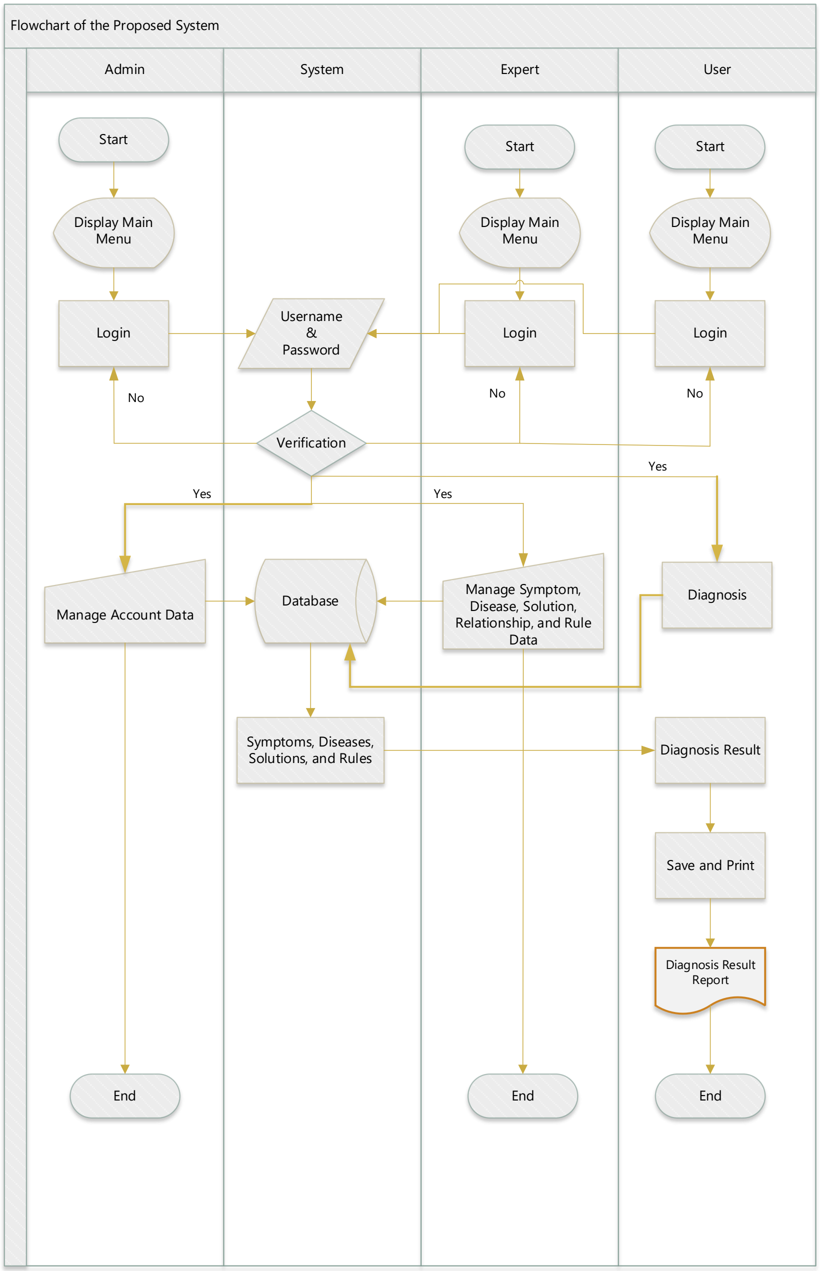


Figure 2. Flowchart of the Proposed System

The presented flowchart (Figure 1) illustrates the proposed system workflow, structured into four main components based on user roles: Administrator, System, Expert, and End User. The process initiates when each user type (Administrator, Expert, and User) accesses the system via the main menu interface and proceeds to the login stage. Upon entering their username and password credentials, the system performs a verification process. If authentication fails, the user is redirected to the login page. Conversely, upon successful verification, each user role is granted access to functionalities aligned with their specific responsibilities.

Once logged in, the Administrator is directed to input expert account data, which is subsequently stored in the system's central database. The Expert, upon successful login, is authorized to input domain-specific data, including symptoms, diseases, possible solutions, relational data, and rule sets. This data is also stored within the central database and constitutes the core foundation for decision-making processes within the system. The System component is responsible for managing, storing, and retrieving data related to symptoms, diseases, solutions, and inference rules, serving as the backbone for the expert system's operation.

Meanwhile, the End User, upon successful login, is granted access to the diagnosis functionality. The user can initiate a diagnosis process based on the pre-defined knowledge base populated by the expert. Once the system generates a diagnostic result, the user is provided with the option to view, save, and print the diagnostic report. Each activity sequence concludes with an "End" status, indicating the completion of the respective process flow.

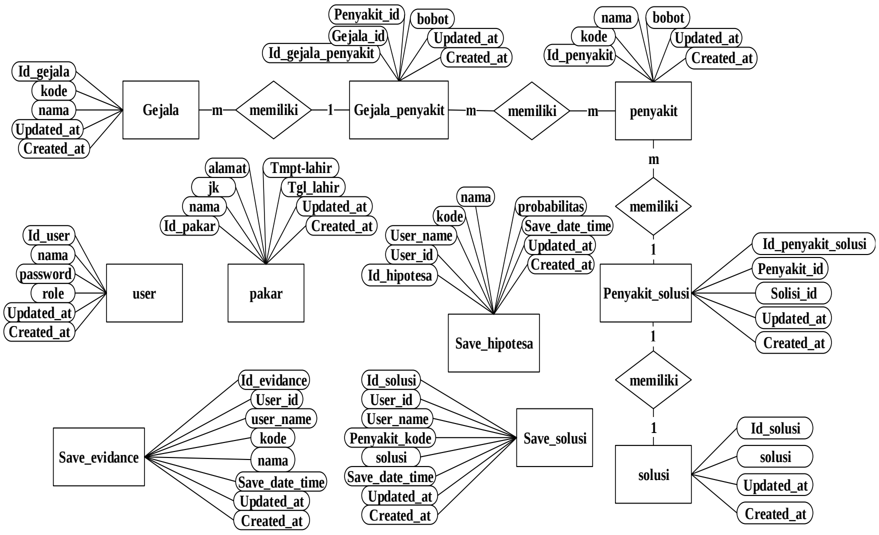


Figure 3. Entity Relationship Diagram (ERD)

Figure 3 shows the illustrated Entity Relationship Diagram (ERD) represents a comprehensive data model of an expert system designed to assist in diagnosing diseases based on symptom analysis and subsequently recommending appropriate solutions. This model integrates various entities, including users, domain experts, symptoms, diseases, and solutions, along with historical diagnostic data. The structured data relationships enable efficient knowledge management and inference processes, essential for an intelligent decision support system in the healthcare or medical consultation domain.

At the core of the system are the User and Pakar (Expert) entities. The User table stores individual credentials and role classifications, while the Pakar table stores expert-specific information, such as name, gender, address, and birth details. Experts are responsible for populating and maintaining the system's knowledge base by inputting validated data on symptoms, diseases, and treatment solutions.

The Symptom (Gejala) entity holds information on observable health indicators, uniquely identified by codes. Each symptom is linked to one or more Diseases (Penyakit) through a many-to-many relationship defined by the associative entity Gejala_penyakit. This relation includes a bobot (weight) attribute that quantifies the strength of association between a symptom and a disease. Similarly, each disease is associated with one or more Solutions (Solusi) through the Penyakit_solusi entity, which facilitates multiple treatment recommendations for a single disease.

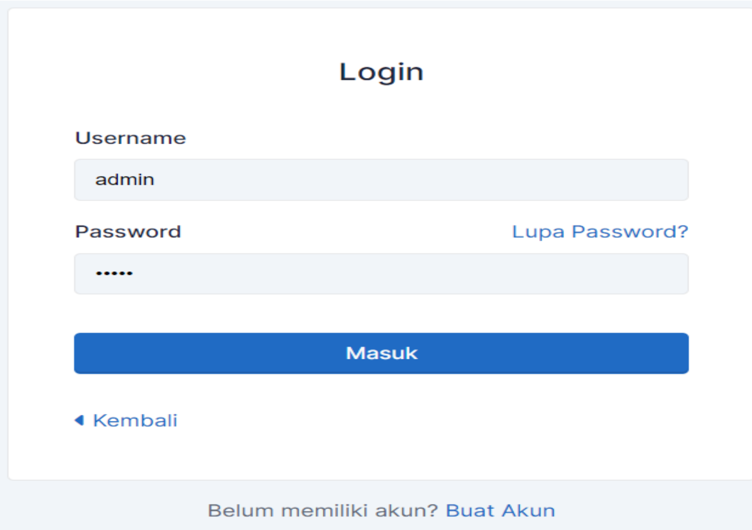
The system incorporates dynamic diagnostic features through the Save_evidence, Save_hipotesa, and Save_solusi entities. These serve as transactional records to log each user's diagnostic interaction. Save_evidence captures selected symptoms by a user during a diagnostic session. Save_hipotesa stores the inferred disease(s) and associated probabilities calculated based on the entered symptoms. Finally, Save_solusi contains the system's recommendations or treatment suggestions provided to the user, tailored to the diagnosed condition.

This ERD reflects a well-structured, normalized database schema that promotes data consistency, traceability, and scalability. It ensures the system can support complex inferences, facilitate personalized medical advice, and offer traceable records for both users and experts. The use of timestamps such as Created_at, Updated_at, and Save_date_time across all entities underscores the importance of temporal data tracking for system auditability and continuous improvement.

Figure 4. The Main Interface of the Web-Based

Figure 4 displays the main interface of the web-based expert system "SISPAK | BAYES", designed for diagnosing dragon fruit (*Hylocereus spp*.) diseases. The interface features six core navigation menus, each optimized for functionality and user experience:

a. **Home**: Serves as the primary dashboard, providing direct access to the diagnostic module.
b. **Dragon Fruit Info**: Contains botanical and agronomic details about Hylocereus species, including growth conditions and common cultivars.
c. **Gallery**: A visual repository of disease symptoms (e.g., anthracnose lesions, stem rot) with annotated case studies.
d. **Expert Consultation**: Facilitates real-time communication with plant pathologists for complex cases.
e. **Contact**: A dedicated channel for user feedback and technical support.
f. **Login**: A secure authentication portal for system administrators and domain experts to update the knowledge base.



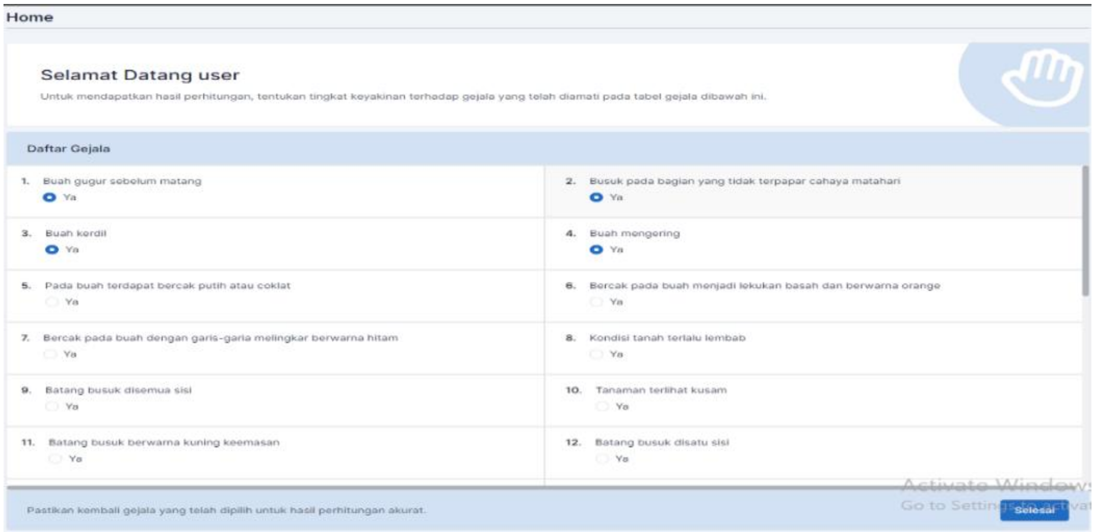
Login

Username: admin

Password: •••••

Figure 5. System Login Interface

Figure 5 displays a system login interface featuring two input fields (username with a sample "admin" entry and password displayed as dots for security), accompanied by a "Login" button for authentication and a "Back" button for navigation. The interface also includes two support links - "Forgot Password?" for account recovery and "Create Account" for new users. This minimalist design prioritizes functionality and basic security measures like password masking, though additional input validation enhancements could further strengthen system security. The layout effectively serves its purpose of regulating access to authorized users while maintaining user-friendly navigation.



Home

Selamat Datang user

Untuk mendapatkan hasil perhitungan, tentukan tingkat keyakinan terhadap gejala yang telah diamati pada tabel gejala dibawah ini.

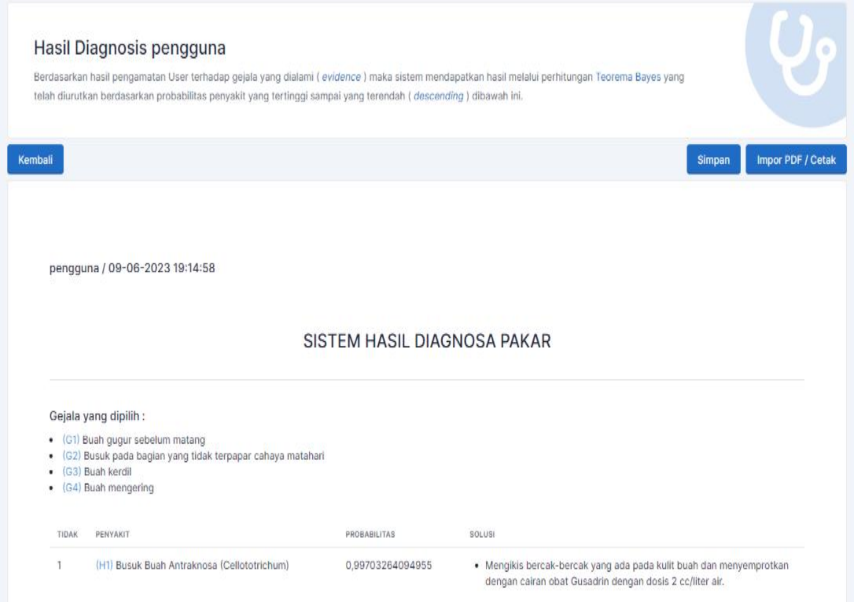
Daftar Gejala

1. Buah gugur sebelum matang ● Ya
2. Busuk pada bagian yang tidak terpapar cahaya matahari ● Ya
3. Buah kerdil ● Ya
4. Buah mengering ● Ya
5. Pada buah terdapat bercak putih atau coklat ○ Ya
6. Bercak pada buah menjadi lekukan basah dan berwarna orange ○ Ya
7. Bercak pada buah dengan garis-garia melingkar berwarna hitam ○ Ya
8. Kondisi tanah terlalu lembab ○ Ya
9. Batang busuk disemua sisi ○ Ya
10. Tanaman terlihat kusam ○ Ya
11. Batang busuk berwarna kuning keemasan ○ Ya
12. Batang busuk disatu sisi ○ Ya

Pastikan kembali gejala yang telah dipilih untuk hasil perhitungan akurat.

Figure 6. Symptom Selection Interface

Figure 6 shows a symptom selection interface from a dragon fruit disease diagnostic system, where users can indicate observed symptoms by selecting "Yes" next to each listed symptom (e.g., premature fruit drop, stem rot, or white/brown spots). The header ("Home") and welcome message ("Selamat Datang user") introduce the page, which guides users to select symptoms from a checklist to enable Bayesian probability calculations for disease diagnosis. The interface aims to simplify data input for farmers but requires refinement in language accuracy and symptom presentation clarity.



Hasil Diagnosis pengguna

Berdasarkan hasil pengamatan User terhadap gejala yang dialami (*evidence*) maka sistem mendapatkan hasil melalui perhitungan Teorema Bayes yang telah diurutkan berdasarkan probabilitas penyakit yang tertinggi sampai yang terendah (*descending*) dibawah ini.

pengguna / 09-06-2023 19:14:58

SISTEM HASIL DIAGNOSA PAKAR

Gejala yang dipilih :

- (G1) Buah gugur sebelum matang
- (G2) Busuk pada bagian yang tidak terpapar cahaya matahari
- (G3) Buah kerdil
- (G4) Buah mengering

TIDAK	PENYAKIT	PROBABILITAS	SOLUSI
1	(H1) Busuk Buah Antraknosa (Cellototrichum)	0,99703264094955	• Mengikis bercak-bercak yang ada pada kulit buah dan menyemprotkan dengan cairan obat Gusadrin dengan dosis 2 cc/liter air.

Figure 7. Diagnosis Results Interface

The design of the diagnosis results page, as shown in Figure 7, is intended to provide clear and structured information to users after they complete the diagnosis process by answering a series of questions prepared by the system. Following this process, the system automatically directs users to the diagnosis page, which presents the results of the disease diagnosis, including probability values and appropriate solution recommendations. This aims to ensure that users gain a comprehensive understanding of the health condition of dragon fruit plants and the steps that can be taken for further management.

4. Conclusions

Based on the analysis and testing that have been conducted, it can be concluded that the expert system application for diagnosing diseases in dragon fruit plants using the Bayes method has several significant advantages. First, the Bayes method is effective in determining the type of disease affecting dragon fruit plants, providing results in the form of accurate probabilities based on the calculations performed. Second, this system is highly beneficial for farmers in the Kampung Daun Baumata Farmers Group, Taebenu District, in diagnosing the diseases occurring in their plants. With the assistance of this expert system, farmers can more easily address the disease problems they face, thereby improving plant health and yield. Additionally, this system is capable of displaying comprehensive information regarding disease data, the symptoms presented, and appropriate treatment methods for diseases in dragon fruit plants. Thus, this application not only serves as a diagnostic tool but also as a valuable source of information that helps farmers manage their crops more effectively.

5. References

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