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Fuzzy medical expert system for prediction of prostate cancer

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ABSTRACT

We developed the fuzzy medical expert system (F-MES) based on fuzzy inference system (FIS) Mamdani using a different approach to prostate cancer risk (PCR) prediction. The difference in our research is that we modify the membership function on the input variable according to medical standards. We used the same input variables as the previous study, namely age, prostate-specific antigen (PSA), prostate volume (PV), and percentage (%) free PSA (%FPSA). The data on the input variable is used as input into F-MES and displays the output in the form of a percentage (%) of PCR. If the PCR is >50%, then the patient is advised to undergo a biopsy test. We conducted an analysis with the doctor to create a simple domain and rule base of 24 rules. Our number of rules is lower than previous studies of 80 and 240, but our prediction results are better the F-MES evaluation used the same 56 patients, that the F-MES we developed had an accuracy of 857%. This score is better than previous studies of 75% and 76%. Our F-MES is simple but effective and can be used as a supporting tool in decision-making in medical diagnosis.

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1. INTRODUCTION

The prostate is a gland in the male reproductive system that encircles the urethra, producing seminal fluid and aiding urine flow from the bladder [1]. Prostate cancer (PC) involves abnormal cell growth in the prostate, commonly affecting older men, though it can also occur in younger individuals. While the exact cause is unknown, genetic mutations in prostate cells contribute to this malignancy [2], [3]. Risk factors include age over 50, family history, obesity, unhealthy lifestyles (such as smoking and excessive alcohol consumption), vasectomy, exposure to carcinogens, and sexually transmitted infections (STIs) [4]. Early detection of PC is challenging due to a lack of clear symptoms, necessitating medical diagnosis [5]. Common diagnostic methods include the prostate-specific antigen (PSA) blood test, prostate ultrasound, magnetic resonance imaging (MRI), and biopsy [6].

Medical diagnosis requires analyzing complex data, which can be enhanced by artificial intelligence (AI). Expert systems utilize advanced algorithms to assist in computer-aided diagnosis, with fuzzy logic being a prominent method [7]–[9]. Fuzzy logic mimics human reasoning and handles more than just binary outcomes, making it a suitable choice for expert systems in medical diagnosis.

Uncertainty and inaccuracy are prevalent in daily life, particularly in medical diagnosis, where ambiguity is common [10]. Identifying a disease can be difficult since similar symptoms may indicate different conditions, and diseases can manifest differently in individuals. Misdiagnosis can negatively impact treatment

quality, costs, and survival rates [5], [11]. Fuzzy logic-based expert systems have been applied in various fields, including medicine, to aid in decision-making, especially for PC [5], [12]. Researchers have utilized fuzzy systems to assess PC risk (PCR) based on variables such as age, prostate-specific antigen (PSA), prostate volume (PV), and free PSA percentage (%FPSA).

The research of Paquin *et al*. [6] grouped the variables for PC diagnosis into sets: age (very young, young, middle age, old), PSA (very low, low, middle, high, very high), and PV (small, middle, big, very big), resulting in 77 rules with 75% accuracy from 56 patient data. Mahanta and Panda [5] used similar groupings but increased PSA sets, leading to 240 rules and 76% accuracy. Kaur *et al*. [13] simplified the variables, using three sets for age, PSA, PV, and FPSA, resulting in 188 rules. Previous studies lacked medical standards for variable domains, resulting in suboptimal accuracy and excessive rules. In contrast, our research employs WHO-standard input variables verified by experts, simplifying the sets for improved accuracy. We categorized age into three sets (young: 0-55, middle: 55-65, old: 65-100) and simplified PSA, PV, and %FPSA into "Normal" and "Abnormal" sets. This study aims to develop a fuzzy Mamdani-based medical expert system using simpler, clinically validated variables to improve PCR prediction accuracy.

2. METHOD

2.1. Prostate cancer

The prostate is a small gland at the base of the bladder, part of the reproductive system, and produces semen. PC occurs in this gland and is often associated with urinary problems, mainly affecting men over fifty [14]. In most cases, PC affects men over the age of 50. According to WHO, PC is one of the most common cancers in men, affecting about 1.3 million globally [7]. In Indonesia, PC ranks 5th as the most common type of cancer suffered by men. Figure 1 shows an illustration of PC.

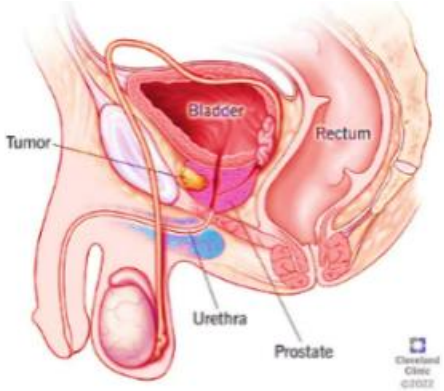


Figure 1. Cancer in the prostate or PC

2.2. Stage of fuzzy medical expert system

Fuzzy logic has been widely used to assist in diagnosing various diseases by handling uncertainty and complex decision-making [5], [15], [16]. We developed a fuzzy medical expert system (F-MES) that uses membership functions and rulebases based on expert doctors' knowledge. Input variables like age, PSA, PV, and FPSA are processed using the Mamdani fuzzy inference system (FIS) to predict PCR levels. The system applies IF-THEN fuzzy rules, with the output defuzzified using the centroid method to generate a final prediction [17]. The structure of the F-MES is shown in Figure 2.

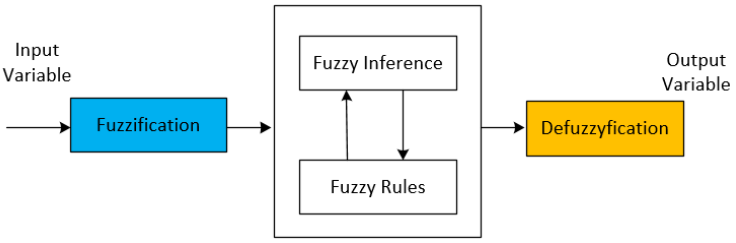


Figure 2. Stage for architecture of a F-MES

2.3. Input variables

Our study used four input variables similar to previous research: Age, PSA, PV, and FPSA [5], [13], [18]. These crisp inputs are processed using the Mamdani FIS, producing a defuzzified output representing the PCR percentage. Figure 3 illustrates the input and output variables.

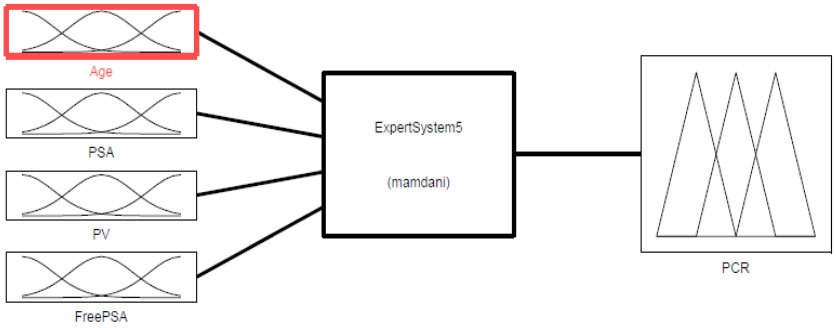


Figure 3. Input and output variables of F-MES

2.3.1. Age

Age is a parameter in assessing PC risk, with men over 50 being more susceptible, especially without a family history of PC [19]. Two-thirds of PC cases are diagnosed in men aged 65 or older [5]. Unlike previous studies, our research uses WHO-standard age sets, verified by expert doctors. Age is grouped into three fuzzy sets: "Young," "Middle," and "Old" [19]. The first and third sets use trapezoidal membership functions, while the "Middle" set uses a triangular membership function. The fuzzy set and the age variable membership function are shown in Table 1 and Figure 4. Next, based on Table 1, create membership function in the form of a curve input "Age" as Figure 4. For example, there is a condition that someone has age-44, based on the membership function degrees is obtained age=44, $\mu_{Young}(44) = 0.55$, and $\mu_{Middle}(44) = 0.6$, and $\mu_{Old}(44) = 0$.

Table 1. Fuzzification the input variable "age"

Input variable	Crisp set	Fuzzy set
Age (year)	0-55	Young
	35-65	Middle
	55-100	Old

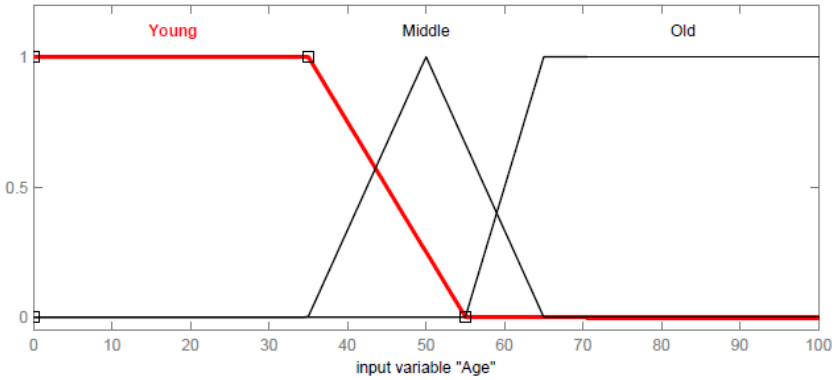


Figure 4. Membership functions for "age"

2.3.2. Prostate-specific antigen

PSA is a protein produced by prostate cells, essential for sperm movement. PSA levels naturally increase with age due to prostate tissue growth, which varies by age. Normal PSA levels are around 2.5 ng/ml for men aged 40, 4.5 ng/ml for men aged 60, and 6.5 ng/ml for men over 70 [20]. In this study, the

"PSA" variable has two sets: "Normal" (trapezoidal membership function) and "Abnormal" (ascending trapezoid). Table 2 shows the crisp sets, and Figure 3 illustrates the PSA membership function. Next, based on Table 2, create membership function in the form of a curve input "PSA" as Figure 5. If someone has a PSA=7.6 ng/ml, based on the membership function in Figure 5, then the value of the membership degree is Normal and Abnormal PSA=7.6, $\mu_{Normal}(44) = 1$, and $\mu_{Abnormal}\ (7.6) = 0$.

Table 2. Fuzzification of the input variable "PSA"

Input variable	Crisp set	Fuzzy set
PSA (ng/ml)	0-35	Normal
	25-35	Abnormal

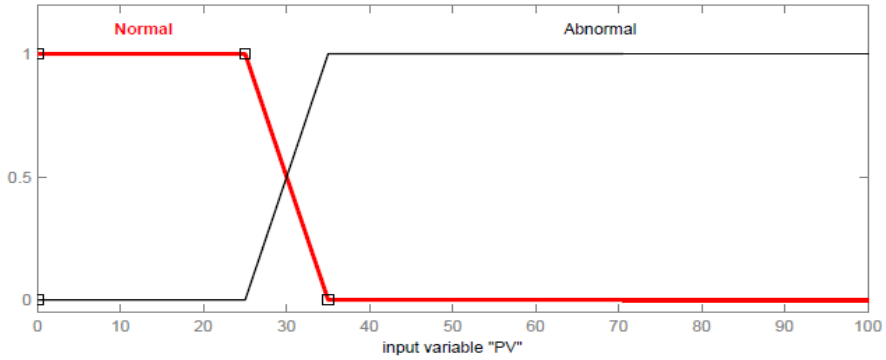


Figure 5. Membership functions for "PSA"

2.3.3. Prostate volume

The PV is a gland located under the bladder and around the urethra, producing fluid that carries semen during ejaculation. PV is measured using the prolate elliptical formula: TPV=π/6* W*L*H [19]. As men age, length changes significantly, especially around age 60, with a normal prostate size of 15-25 milliliters [21]. Based on medical standards, PV is categorized into two sets: "Normal" and "Abnormal," both using trapezoidal membership functions. Table 3 shows the fuzzy sets, and Figure 4 illustrates the PV membership function. Next, based on Table 3, create membership function in the form of a curve input "PV" as Figure 6. If someone has PV=38 ml, based on the membership function, the following membership degree values: PV=38, $\mu_{Normal}(38) = 0$, and $\mu_{Abnormal}\ (38) = 1$.

Table 3. Fuzzification of the input variable "PV "

Input variable	Crisp set	Fuzzy set
PV (ml)	0-35	Normal
	25-100	Abnormal

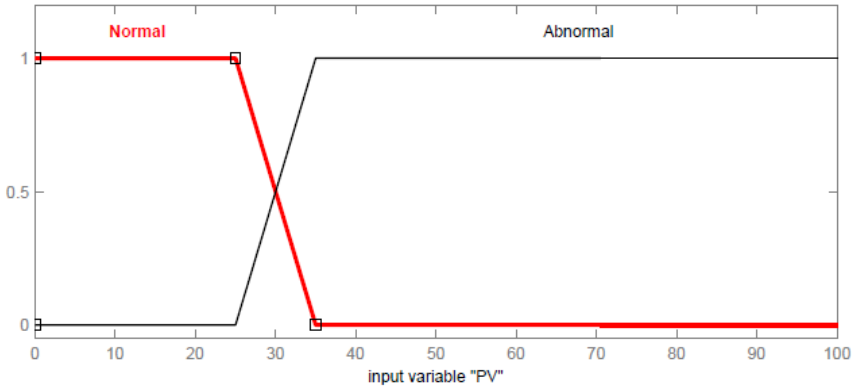


Figure 6. Membership functions for "PV"

2.3.4. Percentage of free PSA

PSA is a protein in the serum that circulates in both bound and unbound forms [22]. The %FPSA value is calculated using the equation %FPSA = $\frac{Free\ PSA}{Total\ PSA} * 100\%$. Normal %FPSA is ≤25%, with some doctors recommending ≤18% and suggesting a biopsy if it falls to ≤12% [4]. Early detection of PC is crucial for effective treatment, and %FPSA serves as a valuable indicator [6]. We categorize %FPSA into two fuzzy sets based on medical standards: "Normal" and "Abnormal," using trapezoidal membership functions. Table 4 and Figure 7 illustrate the fuzzy set and membership function for %FPSA. Next, based on Table 4, create membership function in the form of a curve input "%FPSA" as Figure 7. If someone has %FPSA=10.53 ng/ml, based on the membership function, the value of membership degrees is obtained: %PSA=10.53, $\mu_{Normal}(10.53) = 1$, and $\mu_{Abnormal}(10.53) = 0$.

Table 4. Fuzzification of the input variable "%FPSA"

Input variable	Crisp set	Fuzzy set
% FPSA	0-32	Normal
	18-92	Abnormal

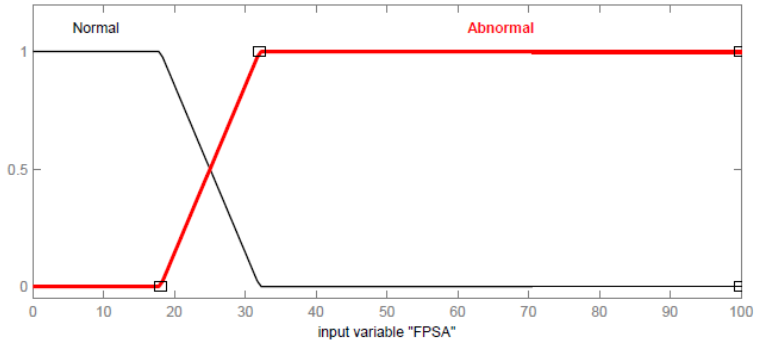


Figure 7. Membership functions for "%FPSA"

2.4. Output variable

The output of the F-MES is the PCR, which determines low or high-risk levels based on the input variables: Age, PSA, PV, and %FPSA. A PCR value of ≥50% indicates a high likelihood of PC, prompting a recommendation for a biopsy [5]. The PCR output is categorized into two sets: "Low" and "High," represented using a trapezoidal membership function. Table 5 and Figure 8 illustrate the output membership sets and functions. Next, based on Table 5, create membership function in the form of a curve output "PCR" as Figure 8.

Table 5. Fuzzification of the input variable "PCR"

Input variable	Crisp set	Fuzzy set
PCR (%)	0-60	Low
	40-100	High

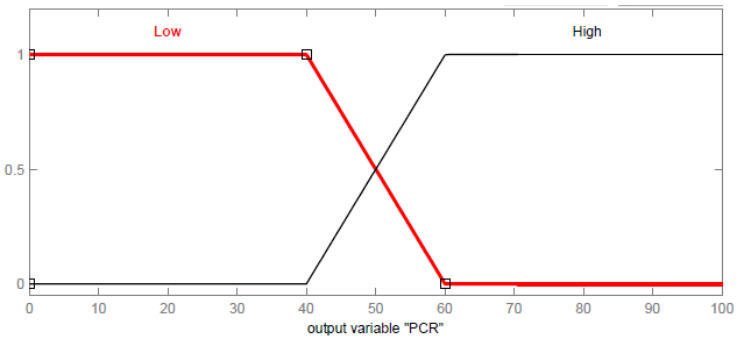


Figure 8. Membership functions for output "PCR"

2.5. Fuzzy rule base

The main part of a fuzzy logic system that contains a series of "IF-THEN" conditional statements that model human knowledge or experience about a problem [23]. In this F-MES, there are four input variables: Age (3 sets: "Young," "Middle," "Old"), PSA (2 sets: "Normal," "Abnormal"), PV (2 sets: "Normal," "Abnormal"), and %FPSA (2 sets: "Normal," "Abnormal"). This results in 24 rule bases for estimating PCR. The PCR output has two categories: "Low" and "High." An analysis of data from 56 patients determined the variable weights as follows: Age = 0.12, PSA = 0.4, PV = 0.34, and %FPSA = 0.13, so we define the rule base,

[1]	If(Age="Young")AND(PSA="Normal")AND(PV="Normal")AND(%FPSA="Normal")THEN(PCR=Low")
[2]	If(Age="Young")AND(PSA="Normal")AND(PV="Normal")AND(%FPSA="Abnormal")THEN(PCR=Low")
[3]	If(Age="Young")AND(PSA="Normal")AND(PV="Abnormal")AND(%FPSA="Normal")THEN(PCR=Low")
[4]	If(Age="Young")AND(PSA="Normal")AND(PV="Abormal")AND(%FPSA="Abnrmal")THEN(PCR=Low")
[5]	If(Age="Young")AND(PSA="Abnormal")AND(PV="Normal")AND(%PSA="Normal")THEN(PCR="Low")
[6]	If(Age="Young")AND(PSA="Abnormal")AND(PV="Normal")AND(%PSA="Abnormal")THEN(PCR="Low")
[7]	If(Age="Young")AND(PSA="Abnormal")AND(PV="Abnormal")AND(%PSA="Normal")THEN(PCR="Low")
[8]	If(Age="Young")AND(PSA="Abnormal")AND(PV="Abormal")AND(%PSA="Abnormal")THEN(PCR="Low")
[9]	If(Age="Middle")AND(PSA="Normal")AND(PV="Normal")AND(%PSA="Normal")THEN(PCR="Low")
[10]	If(Age="Middle")AND(PSA="Normal")AND(PV="Normal")AND(%PSA="Abnormal")THEN(PCR="Low")
[11]	If(Age="Middle")AND(PSA="Normal")AND(PV="Abnormal")AND(%PSA="Normal")THEN(PCR="Low")
[12]	If(Age="Middle")AND(PSA="Normal")AND(PV="Abnormal")AND(%PSA="Abnormal")THEN(PCR="Low")
[13]	If(Age="Middle")AND(PSA="Abnormal")AND(PV="Normal")AND(%PSA="Normal")THEN(PCR="High")
[14]	If(Age="Middle")AND(PSA="Abnormal")AND(PV="Normal")AND(%PSA="Abnormal")THEN(PCR="Low")
[15]	If(Age="Middle")AND(PSA="Abnormal")AND(PV="Abnormal")AND(%PSA="Normal")THEN(PCR="Low")
[16]	If(Age="Middle")AND(PSA="Abnormal")AND(PV="Abnormal")AND(%PSA="Abnormal")THEN(PCR="Low")
[17]	If(Age="Old")AND(PSA="Normal")AND(PV="Normal")AND(%PSA="Normal")THEN(PCR="Low")
[18]	If(Age="Old")AND(PSA="Normal")AND(PV="Normal")AND(%PSA="Abnormal")THEN(PCR="Low")
[19]	If(Age="Old")AND(PSA="Normal")AND(PV="Abormal")AND(%PSA="Normal")THEN(PCR="Low")
[20]	If(Age="Old")AND(PSA="Normal")AND(PV="Abnormal")AND(%PSA="Abnormal")THEN(PCR="Low")
[21]	If(Age="Old")AND(PSA="Abnormal")AND(PV="Normal")AND(%PSA="Normal")THEN(PCR="High")
[22]	If(Age="Old")AND(PSA="Abnormal")AND(PV="Normal")AND(%PSA="Abnormal")THEN(PCR="Low")
[24]	If(Age="Old")AND(PSA="Abnormal")AND(PV="Abnormal")AND(%PSA="Normal")THEN(PCR="Low")
[25]	If(Age="Old")AND(PSA="Abnormal")AND(PV="Abnormal")AND(%PSA="Abnormal")THEN(PCR="Low")

Rule based is used to calculate the value (α-predicate) and z-value for each rule using the MIN function in the implication function application [17]. For example, with the input data age = 44, PSA = 7.6, PV = 38, and %FPSA = 10.53. The α-predicate and z-values are determined as shown in Table 6.

Table 6. Values MIN, α-predicate, and z

No	Age	PSA	PV	%PSA	α1-24 (MIN)	z1-24	No	Age	PSA	PV	%PSA	α1-24 (MIN)	z1-24
1	Young=0.55	Normal=1	Normal=0	Normal=1	0	0	13	Middle=0.6	Abnormal=0	Normal=0	Normal=1	0	0
2	Young=0.55	Normal=1	Normal=0	Abnormal=0	0	0	14	Middle=0.6	Abnormal=0	Normal=0	Abnormal=0	0	0
3	Young=0.55	Normal=1	Abnormal=1	Normal=1	0.55	11	15	Middle=0.6	Abnormal=0	Abnormal=1	Normal=1	0	0
4	Young=0.55	Normal=1	Abnormal=1	Abnormal=0	0	0	16	Middle=0.6	Abnormal=0	Abnormal=1	Abnormal=0	0	0
5	Young=0.55	Abnormal=0	Normal=0	Normal=1	0	0	17	Old=0	Normal=1	Normal=0	Normal=1	0	0
6	Young=0.55	Abnormal=0	Normal=0	Abnormal=0	0	0	18	Old=0	Normal=1	Normal=0	Abnormal=0	0	0
7	Young=0.55	Abnormal=0	Abnormal=1	Normal=1	0	0	19	Old=0	Normal=1	Abnormal=1	Normal=1	0	0
8	Young=0.55	Abnormal=0	Abnormal=1	Abnormal=0	0	0	20	Old=0	Normal=1	Abnormal=1	Abnormal=0	0	0
9	Middle=0.6	Normal=1	Normal=0	Normal=1	0	0	21	Old=0	Abnormal=0	Normal=0	Normal=1	0	0
10	Middle=0.6	Normal=1	Normal=0	Abnormal=0	0	0	22	Old=0	Abnormal=0	Normal=0	Abnormal=0	0	0
11	Middle=0.6	Normal=1	Abnormal=1	Normal=1	0.6	48	23	Old=0	Abnormal=0	Abnormal=1	Normal=1	0	0
12	Middle=0.6	Normal=1	Abnormal=1	Abnormal=0	0	0	24	Old=0	Abnormal=0	Abnormal=1	Abnormal=0	0	0

2.6. Defuzzification with FIS Mamdani

Defuzzification is the process of getting the right value of a fuzzy set. In FIS Mamdani, every consequence of the IF-Then rule must be represented by a fuzzy set with a monotonous membership function [17], [24]. Figure 9 shows defuzzification using FIS Mamdani.

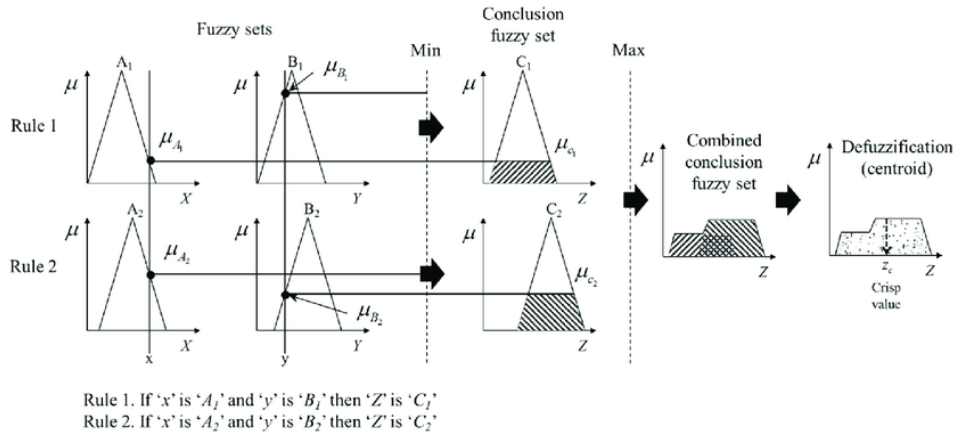


Figure 9. General FIS with Mamdani

The output of the inference results of each rule is given expressly (crisp) based on the predicate α (fire strength). The final result is in the form of PCR (%) which is obtained using the weighted average calculation in (1)

$$z = \frac{\int \mu C(z).zdz}{\int \mu C(z).dz} \quad (1)$$

2.7. Classification algorithm

The classification algorithm is a method in the KDD process that identifies and groups data based on attributes during the data mining stage. The algorithms used include K-nearest neighbor (KNN), Naïve Bayes, logistic regression, neural networks, support vector machine (SVM), and decision trees. These algorithms were tested using RapidMiner Studio with 119 training samples and 56 test samples. Figure 10 illustrates the classification algorithm test model. Training data is used as the basis for system maintenance in learning classes. The classification algorithm is used (Apply model) to learn data from training data and will be able to classify from testing data.

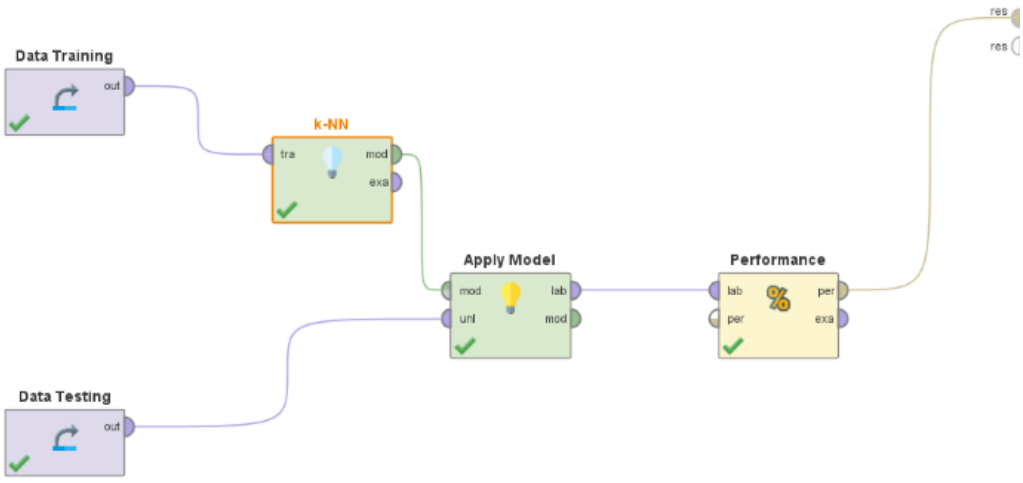


Figure 10. Classification algorithm test model in Rapid Miner Studio

3. RESULTS AND DISCUSSION

3.1. PCR prediction result

The test data included four input variables: Age, PSA, PV, and %FPSA, with the output variable being PCR. Data from 56 patients were analyzed using the MATLAB fuzzy logic toolbox and compared with biopsy results. A PCR value >50% indicates a "Positive" biopsy result, while values ≤50% are categorized as "Negative" [5]. The comparison results between the F-MES and biopsy outcomes are presented in Table 7. Based on Table 7, we model using machine learning to find patterns and correlations of each variable. We used the Rapid Miner studio and the Decision Tree algorithm shown in Figure 11.

Table 7. Results of the comparison of F-MES accuracy comparison against biopsy results

No	Age (year)	PSA (ng/ml)	PV (ml)	%FPSA	Biopsy Result from Doctor	F-MES	No	Age (year)	PSA (ng/ml)	PV (ml)	%FPSA	Biopsy Result from Doctor	F-MES
1	44	7,6	38	10,53	Negative	Negatif	29	62	51,74	29	6,8	Positive	Positive
2	51	6,76	15	4,14	Positive	Negatif	30	63	8,8	31	22,5	Positive	Positive
3	51	44	83	31,82	Positive	Positive	31	64	5,7	36	29,82	Negative	Negatif
4	53	4,5	39	18,89	Negative	Negatif	32	64	6,96	45	9,2	Negative	Negatif
5	53	5,83	25	6,86	Negative	Negatif	33	64	11,08	26	10,11	Negative	Negative
6	53	8,34	25	7,43	Negative	Negatif	34	64	16,28	21	6,94	Positive	Positive
7	54	5,62	28	14,95	Negative	Negatif	35	65	4,39	30	21,64	Negative	Negative
8	54	17,3	90	27,46	Negative	Positive	36	65	5,15	47	15,73	Negative	Negative
9	54	17,3	45	8,9	Positive	Positive	37	69	15,31	74	30,57	Positive	Positive
10	55	10,51	54	22,45	Negative	Positive	38	69	61	46	9,93	Negative	Positive
11	56	8,9	26	34,16	Negative	Positive	39	73	7,25	19	5,52	Negative	Negative
12	56	9,05	39	8,51	Positive	Positive	40	73	47,4	87	15,89	Positive	Positive
13	56	16	146	8,44	Negative	Positive	41	74	12,52	27	11,82	Negative	Negative
14	57	12,56	52	65,84	Negative	Positive	42	74	150	54	16,67	Positive	Positive
15	58	4,48	67,5	16,07	Negative	Negatif	43	76	13,61	61	19,91	Positive	Positive
16	58	4,62	48	11,04	Negative	Negatif	44	76	13,83	54	19,96	Positive	Positive
17	58	5,2	58	23,46	Negative	Negatif	45	76	21	86	5,43	Positive	Positive
18	58	16,39	27	92,07	Negative	Positive	46	77	10	60	6	Positive	Positive
19	59	0,28	168	42,86	Negative	Negatif	47	77	12,05	28	27,05	Positive	Positive
20	59	8,36	55	7,54	Positive	Positive	48	77	56	51	7,34	Positive	Positive
21	59	19,48	79	25	Positive	Positive	49	78	4,5	180	20,44	Negative	Negative
22	60	6,58	65	14,74	Negative	Negative	50	65	8,33	32	14,53	Positive	Positive
23	60	10,6	30	16,79	Positive	Positive	51	66	4,38	33	23,52	Negative	Negative
24	61	10,59	56	17	Positive	Positive	52	66	7,65	89	23,66	Negative	Negative
25	61	18,3	62	6,99	Positive	Positive	53	66	9	74	18,89	Positive	Positive
26	62	6,12	52	24,18	Negative	Negative	54	66	9,86	49	23,83	Negative	Negative
27	62	8,79	45	10,92	Positive	Positive	55	67	4,39	28	0,91	Negative	Negative
28	62	20	53	5,2	Positive	Positive	56	80	69,51	28	28,77	Positive	Positive

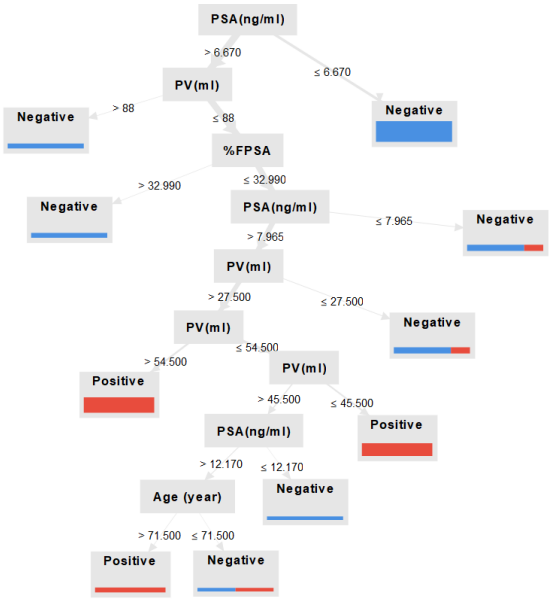


Figure 11. PCR prediction patterns with decision trees

Figure 11 shows that if PSA ≤ 6.67, the PCR prediction is "Negative." For PSA < 6.67, the PV value must be considered. If PV > 88, the PCR is "Negative"; if PV ≤ 88, the %FPSA is evaluated. If %FPSA > 32.99, the PCR is "Negative," but if %FPSA < 32.99, the PSA is considered. If PSA > 7.9 and PV > 27.5, the PCR is "Positive." Among 56 patients, 26 had "Positive" biopsies and the rest "Negative". The accuracy of the predicted results is calculated using the following equation,

$$Accuracy = \frac{Jumlah\ prediksi\ benar}{Total\ data} x100\% = \frac{48}{56} = 85{,}7\% \quad (2)$$

Table 8 highlights the differences between our research and previous studies. While we use the same four input variables-age, PSA, PV, and FPSA-our research employs simpler domains for easier development of the F-MES. Additionally, the accuracy of our PCR risk prediction surpasses that of prior research. Figure 12 illustrates some of these differences.

Table 8. Differences in our research from other studies

No	Authors and years	Variable number	Domain number	Rulebase number	Method	Accuracy (%)
1	Paquin *et al*., 2015 [6]	4	17	80	Fuzzy Mamdani	75
2	Mahanta and Panda, 2020 [5]	4	16	240	Fuzzy Mamdani	76
3	This research, 2024	4	9	24	Fuzzy Mamdani	85,7

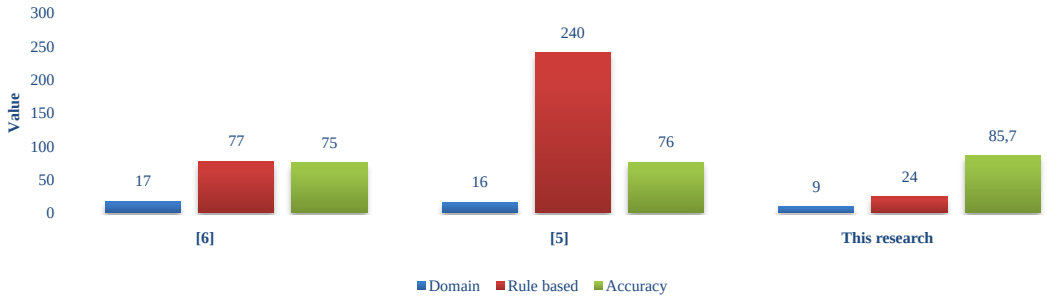
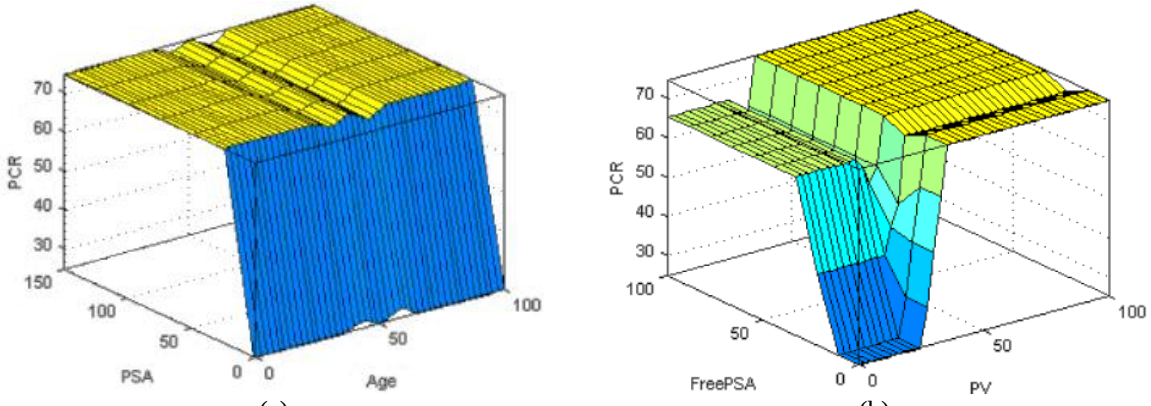


Figure 12. Graph comparing domain, rulebased, and accuracy with other research

To see the surface of the relationship between the two input and output variables, you can use the surface viewer MATLAB as shown in Figure 13. Surface viewer is a fuzzy logic designer application interface that supports the fuzzy Mamdani inference system [25]. The Surface viewer for the age and PSA input variables is shown in Figure 13(a) and the Surface viewer for the PV and FPSA input variables is shown in Figure 13(b).



(a) (b)

Figure 13. The surface viewer uses two variables as input and PCR as output, (a) surface age and PSA with input age=44, and PSA=7 and (b) uses the PV variable against the FPSA variable as input with the value of PV=38, and FPSAA=10%

We compared the F-MES with various classification algorithms, including KNN, naïve Bayes, logistic regression, neural networks, SVM, and decision trees, to evaluate its reliability. The classification was performed using RapidMiner Studio. As shown in Figure 14, the F-MES achieved an accuracy of 85.7%, outperforming all other algorithms. The naïve Bayes algorithm had the lowest accuracy at 60.07%, followed by logistic regression at 67.86%, neural networks and SVM at 71.43%, decision trees at 73.21%, and KNN with the highest accuracy of 80.36%.

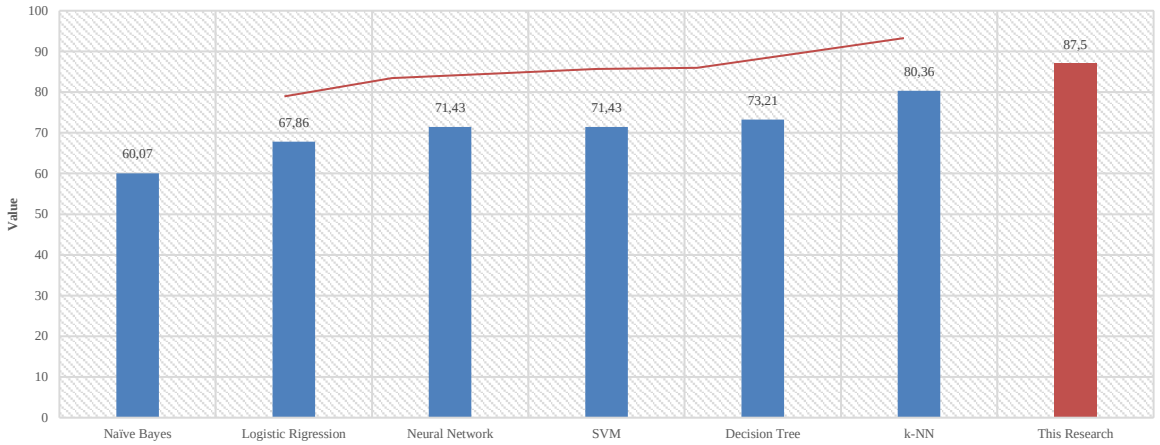


Figure 14. Comparison graph of F-MES accuracy with classification algorithm

3.2. Discussion

Based on the results presented, our research has limitations, primarily due to the use of limited data. To improve, we recommend adding variables such as race, family history, lifestyle, and eating habits. Additionally, the output should expand beyond diagnosis to include treatment recommendations. Combining the FES with other AI techniques and incorporating expert opinions may lead to more optimal results.

4. CONCLUSION

The study presents a fuzzy rule-based medical expert system (F-MES) designed to predict PCR using variables such as age, PSA, PV, and %FPSA. A decision tree analysis found that PSA had the highest influence on PCR. The system predicts PCR outcomes based on specific PSA, PV, and %FPSA values. In a test of 56 patients, the F-MES achieved an accuracy of 85.7%, outperforming previous studies and other classification algorithms like KNN and naïve Bayes. While the system is intended to assist doctors in biopsy decisions, its limitations include a small dataset, and further improvements could be made by integrating additional variables and AI techniques.

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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.

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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

DATA AVAILABILITY

Data availability is not applicable to this paper as no new data were created or analyzed in this study.

REFERENCES

[1] C. H. Pernar, E. M. Ebot, K. M. Wilson, and L. A. Mucci, "The epidemiology of prostate cancer," *Cold Spring Harbor Perspectives in Medicine*, vol. 8, no. 12, 2018, doi: 10.1101/CSHPERSPECT.A030361.

[2] M. S. Litwin and H. J. Tan, "The diagnosis and treatment of prostate cancer: A review," *JAMA - Journal of the American Medical Association*, vol. 317, no. 24, pp. 2532–2542, 2017, doi: 10.1001/jama.2017.7248.

[3] M. W. Farha and S. S. Salami, "Biomarkers for prostate cancer detection and risk stratification," *Therapeutic Advances in Urology*, vol. 14, no. 6, pp. 259–261, Jan. 2022, doi: 10.1177/17562872221103988.

[4] W. J. Catalona, "Prostate cancer detection in men with serum PSA concentrations of 2.6 to 4.0 ng/mL and benign prostate examination," *Jama*, vol. 277, no. 18, p. 1452, 1997, doi: 10.1001/jama.1997.03540420048028.

[5] J. Mahanta and S. Panda, "Fuzzy expert system for prediction of prostate cancer," *New Mathematics and Natural Computation*, vol. 16, no. 1, pp. 163–176, 2020, doi: 10.1142/S1793005720500106.

[6] F. Paquin, J. Rivnay, A. Salleo, N. Stingelin, and C. Silva, "Multi-phase semicrystalline microstructures drive exciton dissociation in neat plastic semiconductors," *arXiv preprint arXiv:1310.8002*, Aug. 2015.

[7] D. J. Van Booven *et al.*, "A systematic review of artificial intelligence in prostate cancer," *Research and Reports in Urology*, vol. 13, pp. 31–39, 2021, doi: 10.2147/RRU.S268596.

[8] N. Jindal *et al.*, "Fuzzy logic systems for diagnosis of renal cancer," *Applied Sciences (Switzerland)*, vol. 10, no. 10, 2020, doi: 10.3390/app10103464.

[9] J. M. Merigó, "Fuzzy decision making with immediate probabilities," *Computers and Industrial Engineering*, vol. 58, no. 4, pp. 651–657, 2010, doi: 10.1016/j.cie.2010.01.007.

[10] Y. Kumar and Y. Jain, "Research aspects of expert system," *International Journal of Computing & Business Research*, no. 6, p. 11, 2012.

[11] P. Baranyi, T. D. Gedeon, and L. T. Koczy, "General interpolation technique in fuzzy rule bases with arbitrary membership functions," *Proceedings of the IEEE International Conference on Systems, Man and Cybernetics*, vol. 1, pp. 510–515, 1996, doi: 10.1109/icsmc.1996.569844.

[12] R. Boadh *et al.*, "Study and prediction of prostate cancer using fuzzy inference system," *Materials Today: Proceedings*, vol. 56, pp. 157–164, 2022, doi: 10.1016/j.matpr.2022.01.040.

[13] K. Kaur *et al.*, "Implementation of an adaptive artificial neural network with fuzzy expert system for diagnoses the breast and prostate cancer: a hybrid technique," *Journal of Pharmaceutical Negative Results*, vol. 13, no. 8, pp. 3806–3812, 2022.

[14] L. A. Torre, F. Bray, R. L. Siegel, J. Ferlay, J. Lortet-Tieulent, and A. Jemal, "Global cancer statistics, 2012," *CA: A Cancer Journal for Clinicians*, vol. 65, no. 2, pp. 87–108, 2015, doi: 10.3322/caac.21262.

[15] B. A. Sproule, C. A. Naranjo, and I. B. Türksen, "Fuzzy pharmacology: Theory and applications," *Trends in Pharmacological Sciences*, vol. 23, no. 9, pp. 412–417, 2002, doi: 10.1016/S0165-6147(02)02055-2.

[16] H. E. Shiraz and N. Alias, "Using fuzzy logic to enhance the classification and diagnosing of hypertension," *Journal of Theoretical and Applied Information Technology*, vol. 97, no. 20, pp. 2430–2440, 2019.

[17] S. Kusumadewi and H. Purnomo, *Fuzzy logic applications for decision support (Aplikasi logika fuzzy untuk pendukung keputusan)*. Yogyakarta: Graha Ilmu, 2010.

[18] M. Rawat, P. Pathak, and P. Vats, "An approach to diagnosis of prostate cancer using fuzzy logic," *International Journal of Reconfigurable and Embedded Systems*, vol. 13, no. 1, pp. 192–200, 2024, doi: 10.11591/ijres.v13.i1.pp192-200.

[19] A. Dyussenbayev, "Age periods of human life," *Advances in Social Sciences Research Journal*, vol. 4, no. 6, 2017, doi: 10.14738/assrj.46.2924.

[20] M. K. David and S. W. Leslie, "Prostate specific antigen," *Australian Family Physician*, vol. 40, no. 10, p. 755, 2022.

[21] S. Aprikian *et al.*, "Improving ultrasound-based prostate volume estimation," *BMC urology*, vol. 19, no. 1, p. 68, 2019, doi: 10.1186/s12894-019-0492-2.

[22] P. C. Southwick, "The role of free PSA in the detection of prostate cancer," *Laboratory Medicine*, vol. 32, no. 5, pp. 259–263, 2001, doi: 10.1309/06E3-4LG5-KYEG-FGAC.

[23] A. 'Azzam and S. Indrawati, "Development of decision support system for employee selection using Adaptive Neuro Fuzzy Inference System," *MATEC Web of Conferences*, vol. 154, p. 01077, Feb. 2018, doi: 10.1051/matecconf/201815401077.

[24] A. M. Alqudah, "Fuzzy expert system for coronary heart disease diagnosis in Jordan," *Health and Technology*, vol. 7, no. 2–3, pp. 215–222, 2017, doi: 10.1007/s12553-017-0178-2.

[25] J. R. Jang, *Fuzzy logic toolbox*, 2nd ed. US: The MathWorks, Inc, 2010.

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