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Research Article

Improving Prostate Cancer Risk Diagnosis Using a Modified Fuzzy Medical Expert System Based on Mamdani Logic

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Abstract:

Timely identification of prostate cancer significantly enhances the likelihood of successful treatment; however, diagnostic uncertainty remains a common challenge. This study introduces a Fuzzy Medical Expert System (F-MES) based on Mamdani inference, aiming to improve the accuracy of risk estimation for prostate cancer. The system incorporates four clinically validated input parameters: patient age, prostate-specific antigen (PSA), prostate volume (PV), and the percentage of free PSA (%FPSA) to produce a quantitative output representing Prostate Cancer Risk (PCR) in percentage. Designed for use in clinical environments such as hospitals and urology clinics, the F-MES provides risk interpretation and biopsy recommendations aligned with medical guidelines. A total of 500 fuzzy rules, adapted from standard clinical criteria, were implemented on this system within the Mamdani framework. We have implemented the FMES by using MATLAB and had several intensive numerical experiments, based on an evaluation of 90 benchmark patient records. We also compared the results to those of the previous research. It is shown that the FMES has a better performance that the other previous approach. It gives an accuracy of 81.11%, surpassing previous fuzzy models, which ranged from 60% to 77.5%. Performance metrics indicate a precision of 76.47%, recall of 88.64%, specificity of 73.91%, and an F1-score of 82.11%.

1. Introduction

Prostate cancer continues to represent a major global health burden, ranking among the leading causes of cancer-related morbidity and mortality in men, particularly those over the age of 50. Achieving early and precise diagnosis is critical for improving treatment success rates. Key risk factors include advanced age, genetic predisposition, obesity, and lifestyle influences [1]. In 2022 alone, prostate cancer ranked as the second most common cancer in men, accounting for more than 1.4 million new diagnoses and over 375,000 fatalities worldwide [2]. Despite the availability of conventional diagnostic tools such as prostate-specific antigen (PSA) testing, magnetic resonance imaging (MRI), and prostate biopsy, these approaches often suffer from limited specificity and interpretability. This diagnostic uncertainty requires decision support tools that can process ambiguous input data while maintaining clinical transparency.

In response to these diagnostic challenges, several researchers have explored the application of artificial intelligence (AI) and machine learning (ML) techniques for predicting prostate cancer risk. Approaches including Support Vector Machines (SVM), Random Forests, and deep learning have demonstrated strong predictive capabilities [3], [4]. However, their adoption in clinical practice is often hindered by their "black-box" nature, which limits

the transparency needed by clinicians to make well-informed and accountable decisions. In the field of oncology, explainability is vital, particularly when diagnostic outcomes influence invasive interventions or life-changing treatment decisions. While deep learning models like Convolutional Neural Networks (CNNs) excel in tasks such as image analysis, their complex structures and lack of interpretability present barriers to widespread clinical implementation [5].

One of the AI approaches that is popular for diagnosing medical problems is Mamdani fuzzy inference systems. The methods have been implemented for various medical applications, including various cancer risk prediction. However, several studies reported that the methods have the accuracies ranging from 60% to just under 80%, while promising, fall short of the clinical threshold generally considered acceptable for high-stakes screening tools. For instance, Mahanta and Panda [6] achieved 68.07% accuracy with 240 rules in their model. Similarly, Rawat et al. [7] observed a marginal improvement with an accuracy of 77.05% using 255 rules. These systems offer transparency, their limited rule sets and domain granularity, which constrain to capture of the complexity of real-world clinical data. Consequently, they often struggle to balance sensitivity and specificity, which are both critical in avoiding overdiagnosis and underdiagnosis. As a result, these systems often struggle to balance sensitivity and specificity adequately, which is crucial for avoiding both overdiagnosis and underdiagnosis in prostate cancer screening. Therefore, there is a clear need to enhance the diagnostic robustness of fuzzy systems by expanding rule coverage, aligning with validated clinical guidelines, and integrating real-world patient data.

In this research, we develop a new Fuzzy Medical Expert System (F-MES) for diagnosing prostate cancer risks. We utilize four clinically validated parameters: patient age, total prostate-specific antigen (PSA), prostate volume (PV), and the percentage of free PSA (%fPSA) as core inputs for assessing prostate cancer risk and supporting clinical decision-making. These factors are extensively documented in urological oncology literature for their predictive value in distinguishing between benign prostatic conditions and malignancies, thereby enhancing diagnostic precision and stratifying patients by risk level. Our novel innovation of the F-MES lies in its extensive knowledge base, comprising 500 IF–THEN fuzzy rules constructed through expert clinical consultation and grounded in internationally recognized standards, such as those recommended by the European Prostate Cancer Risk Calculator (EPCRC) and the World Health Organization (WHO). The rules are distributed across 24 linguistic domains, allowing the system to deliver granular, context-aware interpretations of input data. This design improves the system's generalizability to diverse patient populations and enhances its robustness in real-world diagnostic environments.

This system employs the Mamdani inference method in conjunction with centroid defuzzification, a widely recognized technique that determines the center of gravity of the resulting fuzzy set to produce continuous Prostate Cancer Risk (PCR) scores expressed as percentages. This defuzzification strategy enables more clinically interpretable and flexible risk stratification compared to conventional binary or categorical classification schemes. Such flexibility is particularly valuable in oncology, where diagnostic ambiguity and overlapping symptoms are common challenges [12].

Compared to machine learning models like SVMs and deep neural networks, the F-MES offers a transparent, rule-based decision-making framework specifically tailored for prostate cancer risk prediction. Interpretability remains a fundamental requirement in clinical settings, where healthcare providers must understand the rationale behind system-generated recommendations to ensure safe and accountable patient care [13]. Mamdani-type fuzzy inference systems have shown considerable promise in various medical domains, such as diabetes management, cardiovascular risk assessment, and cancer screening. Their ability to capture expert knowledge in a manner that is both linguistically interpretable and mathematically rigorous makes them highly appropriate for clinical decision support applications [14].

To evaluate the performance of our FMES approach, we have done intensive experiments by using a standard test problem of 90 patient records. We compared the results to those of the previous research. It is shown that the FMES has a better performance than the other previous approaches. The system was validated using biopsy-confirmed patient records, where key performance indicators, accuracy, precision, recall, specificity, and F1-score were computed to evaluate predictive performance. The FMES gives an accuracy of 81.11%, surpassing previous fuzzy models, which ranged from 60% to 77.5%. Performance metrics indicate a precision of 76.47%, a recall of 88.64%, a specificity of 73.91%, and an F1-score of 82.11%. This evaluation framework enables a rigorous assessment of the system's clinical reliability and utility. The overarching goal is to deliver an interpretable and reliable tool for early prostate cancer detection that

reduces the likelihood of unnecessary biopsies and enhances the efficiency of diagnostic pathways in urological oncology.

The structure of this paper is organized as follows: Section 2 outlines the research methodology, including the system architecture, input variables, fuzzy rule base formulation, and the Mamdani inference mechanism used in the proposed Fuzzy Medical Expert System (F-MES). Section 3 presents the experimental design, dataset characteristics, performance evaluation metrics, and results obtained from clinical validation. Section 4 discusses the findings, compares the system's performance with existing models, and highlights its strengths and limitations. Finally, Section 5 concludes the study by summarizing key contributions and suggesting future research directions to further enhance the model's clinical applicability and scalability.

2. Research Method

This section describes the development process and structure of the proposed Fuzzy Medical Expert System (F-MES) designed to improve prostate cancer risk assessment. The methodology combines fuzzification of clinical variables, application of Mamdani inference, and defuzzification using the centroid method. The process follows a structured flow from data preparation to system evaluation.

2.1. Dataset and Preprocessing

The research workflow begins with the data collection phase, where clinical information is obtained from patient medical records, including biopsy-confirmed cases. The dataset was sourced from a previous clinical study consisting of 119 patient records [15]. The collected dataset then undergoes a data pre-processing stage, which involves data selection and labeling. During this process, key diagnostic parameters namely age, total prostate-specific antigen (PSA), prostate volume (PV), and percentage of free PSA (%fPSA) are selected based on established clinical guidelines. These variables are aligned with reference ranges recommended by the European Prostate Cancer Risk Calculator (EPCRC), which defines typical thresholds for prostate cancer risk assessment (e.g., age between 50–75 years, PSA levels of 0.4–50 ng/mL, PV of 10–110 mL, and %fPSA ranging from 0–100). After applying the selection criteria based on the European Prostate Cancer Risk Calculator (EPCRC) and data preprocessing steps, 90 valid patient cases were selected.

Following pre-processing, the dataset is input into the prediction model, which employs the Mamdani fuzzy inference mechanism to generate risk estimations. The output of this system is then evaluated through a comprehensive performance analysis, utilizing standard classification metrics including accuracy, precision, recall (sensitivity), and specificity. The final result of this workflow is a quantified estimate of prostate cancer risk, which is intended to support early diagnosis and guide clinical decision-making. The process steps are shown in Figure 1.

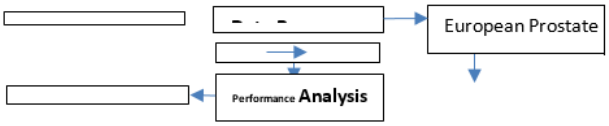

Figure 1. *The design of the research work*

2.2. System Design

The proposed Fuzzy Medical Expert System (F-MES) adopts a fuzzy logic approach to enhance interpretability and flexibility in handling imprecise clinical data, offering an alternative to traditional binary logic systems. Fuzzy logic is a computational framework that extends classical binary logic by allowing variables to take on continuous values between 0 and 1. This approach enables nuanced reasoning in situations involving uncertainty, imprecision, or overlapping data common characteristics in medical diagnostics. In this study, fuzzy logic is applied to map four clinical parameters (Age, PSA, PV, and %fPSA), into fuzzy linguistic terms through domain-informed membership.

The core inference mechanism uses a rule base consisting of 500 fuzzy IF–THEN rules, formulated after consultation with medical experts. The Mamdani inference method is frequently utilized in medical expert systems because of its rule-based structure, which closely mirrors how clinicians formulate diagnostic reasoning in linguistic terms. This model, first introduced by Ebrahim Mamdani in 1975. Within this framework, each rule is constructed in a standard IF–THEN format and evaluated by applying the minimum operator to determine the extent to which the input values satisfy the antecedent conditions, commonly referred to as the rule's firing strength. The outcomes of all activated rules are then combined using the maximum operator to generate an aggregated fuzzy output. This approach facilitates both transparency and interpretability, making it especially suitable for clinical decision support where explainability is essential.

The system then performs defuzzification using the centroid method to transform the aggregate fuzzy set into a clear numeric value that represents the

predicted Prostate Cancer Risk (PCR) in percentage form. All phases of development, including fuzzification, inference, and defuzzification, were implemented using MATLAB software [16]. The system architecture is structured into three main components: (1) input fuzzification, (2) fuzzy inference using the Mamdani method, and (3) defuzzification via the centroid technique. This architecture is illustrated in Figure 2, which maps clinical input to final PCR output.

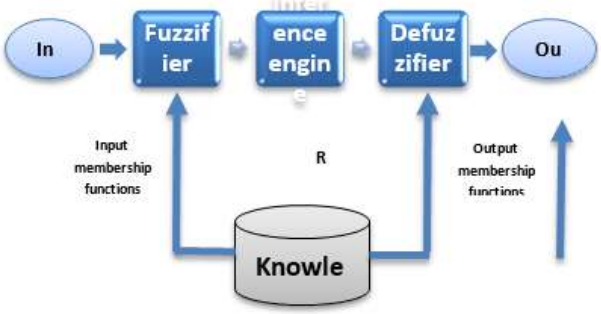

Figure 2. *The F-MES system architecture*

2.3. Fuzzification of Input and Output Variables

The fuzzification process converts clear clinical measurements into linguistic terms using domain-specific membership functions, which allows the system to manage the uncertainty inherent in medical data [17] [18].

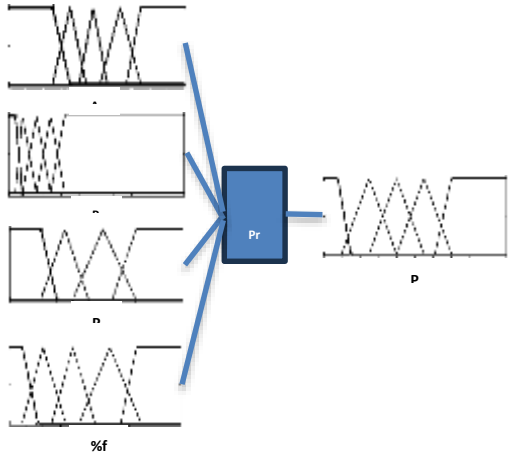

Figure 3. *Input and output variables of the F-MES*

2.3.1. Input Variables

The FMES system uses four clinical input parameters: Age, PSA, PV, and %fPSA. Each input is classified into a fuzzy set according to established clinical standards and expert recommendations.

a) Age

Age is categorized into five fuzzy sets based on WHO aging criteria [19]: Very Young, Young, Middle, Old, and Very Old. The corresponding fuzzification scheme is shown in Table 1, and the membership functions are presented in Figure 4.

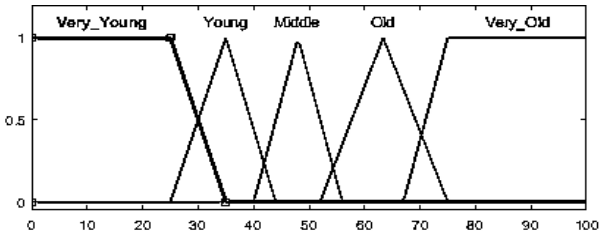

Figure 4. *Membership functions for "AGE"*

Table 1. *Fuzzification of "Age" input variable*

Input Variable	Crisp Set	Fuzzy Set
Age (year)	0-35	Very Young
	25-44	Young
	40-56	Middle
	52-75	Old
	67-100	Very Old

b) Prostate-Specific Antigen (PSA)

PSA is a protein biomarker whose levels tend to increase with age [20]. Based on the clinically validated range of 0.4–50 ng/ml from the European Prostate Cancer Risk Calculator, PSA was divided into five fuzzy categories: Very Low, Low, Normal, High, and Very High. The fuzzification mapping is shown in Table 2, and the membership functions in Figure 5.

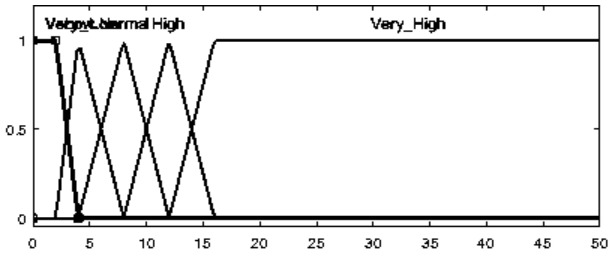

Figure 5. *Membership functions for "PSA"*

Table 2. *Fuzzification of "PSA" input variable*

Input Variable	**Crisp Set**	**Fuzzy Set**
PSA (ng/ml)	0-4	Very Low
	2-8	Low
	4-12	Normal
	8-16	High
	12-50	Very High

c) Prostate Volume (PV)

The prostate, a gland located just below the bladder, produces seminal fluid. Its volume (PV) was calculated using the prolate ellipsoid formula (TPV = $\pi/6$ * Width * Length * Height), which relies on

measuring the organ's dimensions [21], [22]. Enlargement is common after age 60 due to hormonal changes [23]. PV was classified into four fuzzy categories: Small, Medium, Large, and Very Large. Table 3 highlights the fuzzification details, and Figure 6 displays the corresponding membership functions.

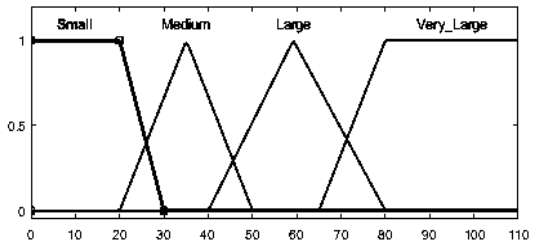

Figure 6. *Membership functions for "PV"*

Table 3. *Fuzzification of "PV" input variable*

Input Variable	Crisp Set	Fuzzy Set
PV (ml)	0-30	Small
	20-50	Medium
	40-80	Large
	65-110	Very Large

d) Percentage of Free PSA (%Fpsa)

Prostate-specific antigen (PSA) circulates in the bloodstream in both free and protein-bound forms [24], [25]. This biomarker is instrumental in differentiating between benign and malignant prostate conditions [26]. Based on medical standards, %fPSA was categorized into five fuzzy sets: Very Low, Low, Normal, High and Very High. Table 4 presents the fuzzification approach, and Figure 6 illustrates its membership functions

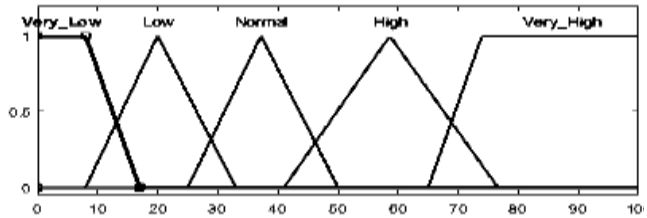

Figure 7. *Membership functions for "%FPSA"*

Table 4. *Fuzzification of "%fPSA" input variable*

Input Variable	Crisp Set	Fuzzy Set
%fPSA (ml)	0-17	Very Low
	8-33	Low
	25-50	Normal
	41-76	High
	65-100	Very High

2.3.2. Output Variable

The output variable, Prostate Cancer Risk (PCR), has a sharp percentage value between 0% and 100%, mapped into five fuzzy categories: Very Low, Low, Middle, High, and Very High. The fuzzification scheme is shown in Table 5, and the membership functions are illustrated in Figure 8. Patients with PCR > 50% are considered high risk and are recommended for further diagnostic evaluation, such as biopsy.

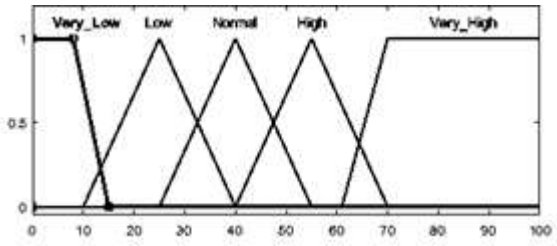

Figure 8. *Membership functions for output "PCR*

2.4. Fuzzy Rule Base

The fuzzy rule base integrates four clinically significant input variables Age, PSA, PV, and %fPSA, each divided into multiple fuzzy sets: Age (5), PSA (5), PV (4), and %fPSA (5). The combination of these sets yields a total of 500 fuzzy rules ($5 \times 5 \times 4 \times 5$), enabling the system to model a wide range of diagnostic scenarios. Each rule adheres to a standard IF–THEN structure. For instance:

IF Age is Old AND PSA is High AND PV is Medium AND %fPSA is Low THEN PCR is High

These rules were developed in consultation with medical experts and aligned with clinical guidelines provided by the World Health Organization (WHO) and the European Prostate Cancer Risk Calculator (EPRCC) [6]. The system categorizes the Prostate Cancer Risk (PCR) into five linguistic output levels: Very Low, Low, Middle, High, and Very High. To distinguish clinically significant cases, a threshold value of 50% was applied. Patients with PCR ≥ 50% are classified as high risk, warranting further diagnostic evaluations such as prostate biopsy. This threshold is consistent with EPCRC and WHO recommendations. Representative fuzzy rules are shown in Table 6 to illustrate the inference structure: This system utilizes the Mamdani inference method, which is preferred in medical decision-making due to its linguistic interpretability and transparency. Rule evaluation is conducted using the minimum (min) operator to determine firing strength, while maximum (max) aggregation combines outputs from all active rules [27], [28], [29]. Compared to alternatives like the Sugeno and Tsukamoto models, Mamdani offers superior readability for human experts and is better suited to handling complex nonlinear relationships often observed in clinical data [30], [31].

Table 6. *Expert fuzzy system rules for prostate cancer risk*

Rule	IF Conditions				Then Outcome
	Age	PSA	PV	%FPSA	PCR
1	Very Young	Very Low	Medium	Normal	Low
2	Young	Normal	Small	High	Normal
3	Middle	Very High	Very Large	Very Low	High
4	Old	High	Medium	Very High	Normal
5	Very Old	Normal	Small	Very Low	Very High
...					
500					

2.5. Inference and Defuzzification Process

The proposed F-MES adopts the Mamdani fuzzy inference method, a widely recognized approach in medical expert systems due to its intuitive structure and ability to model nonlinear and uncertain clinical relationships [28]. This method facilitates interpretable reasoning that is aligned with clinical judgment, making it well-suited for healthcare diagnostics [29].

The inference process in the proposed system involves four main stages. First, the fuzzification stage maps each explicit input variable (Age, PSA, PV, and %fPSA) into a corresponding fuzzy set using a predefined triangular or trapezoidal membership function. Next, during rule evaluation, the minimum (min) operator is used to determine the firing strength, which indicates the extent to which the input values satisfy the antecedent conditions of each fuzzy rule. These activated rules are then aggregated using the maximum (max) operator, resulting in a composite fuzzy set that captures the combined effect of all applicable rules on Prostate Cancer Risk (PCR). To transform fuzzy outputs into precise and clinically interpretable risk scores, this study employs the centroid defuzzification technique, also known as the center of gravity (COG) or center of area (COA) method. This technique determines the equilibrium point of the aggregated fuzzy output by computing the weighted average across its domain, thus providing a single crisp value representative of the fuzzy inference result. The centroid method is widely used due to its intuitive interpretation and consistency in medical decision-making contexts [32]. As a result, it produces a single, crisp Prostate Cancer Risk (PCR) value that maintains the interpretability required in medical decision-making, while ensuring smooth transitions between risk categories based on the underlying fuzzy logic structure [33]. Centroid defuzzification is mathematically expressed in Equation (1):

$$Z = \frac{\int \mu_c(z) * z \, dz}{\int \mu_c(z) dz}$$

In the above Equation (1), $\mu_c(z)$ denotes the degree of membership at a given point z. These parameters determine the interval over which the weighted average is computed. By applying this method, the system generates a risk score that is not only obtained through a rigorous mathematical formulation but also aligns with clinical reasoning, offering a more flexible and interpretable alternative to the rigid binary thresholds commonly used in traditional diagnostics.

To illustrate the performance of the proposed Fuzzy Medical Expert System (F-MES), a simulation was conducted for a patient with the following clinical values: Age = 75 years, PSA = 10 ng/ml, Prostate Volume (PV) = 34 ml, and %fPSA = 7.6. Based on the predefined membership function, these crisp values were converted into fuzzy degrees as follows: each input value is converted into fuzzy membership degrees as follows:

- Age = 75, μOld = 0.62
- PSA = 10, $\mu Normal$ = 0.55, $\mu High$ = 0.50
- PV = 34, $\mu Medium$ = 0.93
- %fPSA = 7.6, $\mu Very\ Low$ = 1

Based on these fuzzy degrees, several rules were activated. The firing strength (α) for each rule was computed using the minimum operator. Sample evaluations are presented below:

- Rule 1: IF Age is Very Old AND PSA is Normal AND PV is Medium AND %fPSA is Very Low THEN PCR is High

α_1 = min (0.62, 0.50, 0.93, 1) = 0.50

- Rule 2: IF Age is Very Old AND PSA is High AND PV is Medium AND %fPSA is Very Low THEN PCR is Very High

α_2 = min (0.62, 0.50, 0.93, 1) = 0.50

The aggregated fuzzy output was obtained by applying the maximum (max) operator to all rule outputs.

$= max\ (\alpha_1, \alpha_2)$
$= max\ (0.50, 0.50)$
$= 0.50$

Each activated rule contributes to shaping the output membership function, resulting in a composite fuzzy region. The defuzzification process was carried out using the centroid method via the MATLAB Fuzzy Logic Toolbox, which produced a final Prostate Cancer Risk (PCR) score of 72.1%. Since this value is below the established clinical threshold of 50%, the system advised that a biopsy is not required for this patient. All stages of fuzzification, rule evaluation, aggregation, and defuzzification were implemented systematically within MATLAB.

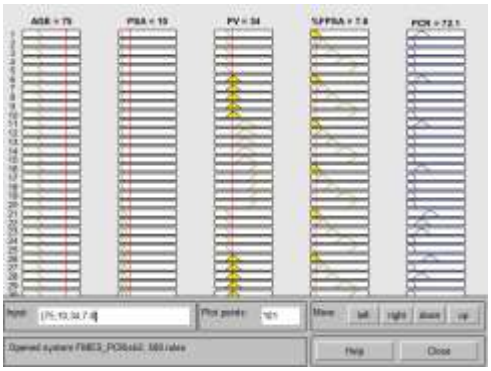

Figure 9. *Calculation of PCR for Age=75 years, PSA=10 ng/ml, PV=34 ml, and %fPSA=7.6*

2.6. Performance Evaluation

The performance of the proposed Fuzzy Medical Expert System (F-MES) was assessed using a dataset of 90 clinically validated cases. System-generated predictions were compared with actual biopsy outcomes and further verified through manual fuzzy logic inference. Evaluation metrics were derived from the confusion matrix, encompassing Accuracy, Precision, Recall (Sensitivity), Specificity, and F1-score, as defined in Equations (2) through (6).

$$Accuracy = \frac{Number\ of\ correct\ prediction}{Total\ number\ of\ case} * 100\% \quad (2)$$

$$Precision = \frac{TP}{TP\ +\ FP} \quad (3)$$

$$Recall = \frac{TP}{TP\ +\ FN} \quad (4)$$

$$Specificity = \frac{TN}{TN\ +\ FP} \quad (5)$$

$$F1 - score = 2 * \frac{Precision * Recall}{Precision\ +\ Recall} \quad (6)$$

3. Numerical Experiment and Results

3.1. Numerical Experiment

A total of 90 patient records were selected from an initial pool of 119 cases, following eligibility criteria outlined in the European Prostate Cancer Risk Calculator (EPRCC) [34]. The inclusion criteria ensured that all patients were male, aged above 50 years, and had prostate-specific antigen (PSA) values within the range of 0.4–50 ng/mL, volume prostate range of 10-50 ml, which aligns with international clinical screening thresholds. The system was developed using a Mamdani-based Fuzzy Medical Expert System (F-MES) architecture, incorporating four primary clinical input variables: age, PSA level, prostate volume (PV), and percentage of free PSA (%fPSA). These inputs were fuzzified into linguistic categories, processed through a knowledge base consisting of 500 fuzzy rules, and evaluated using Mamdani inference. The aggregated fuzzy output was defuzzied using the centroid method to generate a Prostate Cancer Risk (PCR) score, expressed as a percentage. A threshold of 50% PCR was used to differentiate between high-risk and low-risk patients in accordance with WHO and EPCRC recommendations. The outputs were validated against biopsy-confirmed diagnoses, serving as the ground truth for evaluating the model's diagnostic performance.

3.2. Results and Discussion

Based on our numerical experiments, it is noted that the F-MES achieved notable predictive accuracy in distinguishing between positive prostate cancer and negative cases. From the 90 patients evaluated, the system correctly identified 39 true positives and 32 true negatives, resulting in an overall accuracy of 81.11%. The confusion matrix (Table 8) shows that the model produced 12 false positives and 5 false negatives, suggesting a high recall (88.64%) and relatively strong specificity (73.91%). Precision reached 76.47%, and the F1-score stood at 82.11%, confirming a balanced performance between sensitivity and specificity.

Such performance metrics indicate the model's capability to reduce both underdiagnosis and overdiagnosis, two major challenges in prostate cancer screening. The inference mechanism, grounded in 500 medically informed fuzzy rules, enables nuanced interpretation of overlapping clinical values. This attribute is particularly

important in identifying borderline cases that traditional binary classification methods often fail to address effectively. Moreover, the consistent prediction outcomes of the F-MES with a low mean absolute error (MAE) of 11.16% reinforce its reliability for use in preliminary screening or as a clinical second opinion. The interpretability of the model, achieved through Mamdani inference and centroid defuzzification, allows clinicians to understand the reasoning behind each prediction, enhancing the trustworthiness of the system in real-world medical contexts.

Table 7. *Comparison of clinical-based and F-MES-based assessments*

Patient ID	Age (Year)	PSA (ng/ml)	PV (ml)	%fPSA	Biopsy Result	Mahanta et al. [6]		F-MES	
						PCR (%)	Biopsy Result	PCR (%)	Biopsy Result
1	51	6.76	15	4.14	Positive	57.78	Positive	55	Positive
2	51	44	83	31.82	Positive	30	Negative	43.6	Negative
3	53	4.5	39	18.89	Negative	19.96	Negative	43.1	Negative
4	53	5.83	25	6.86	Negative	53.32	Positive	55	Positive
5	53	8.34	25	7.43	Negative	73.83	Positive	61.7	Positive
6	54	5.62	28	14.95	Negative	21.96	Negative	47.1	Negative
7	54	17.3	90	27.46	Negative	30	Negative	48.3	Negative
8	54	17.3	45	8.9	Positive	73.91	Positive	71.2	Positive
9	55	10.51	54	22.45	Negative	23.57	Negative	47.5	Negative
10	56	8.9	26	34.16	Negative	18.8	Negative	47.5	Negative
11	56	9.05	39	8.51	Positive	74.07	Positive	55	Positive
12	57	12.56	52	65.84	Negative	30	Negative	43.4	Negative
13	58	4.48	67.5	16.07	Negative	16.09	Negative	42.5	Negative
14	58	4.62	48	11.04	Negative	17.62	Negative	43.8	Negative
15	58	5.2	58	23.46	Negative	12.8	Negative	40	Negative
16	58	16.39	27	92.07	Negative	30	Negative	45	Negative
17	59	8.36	55	7.54	Positive	74.31	Positive	55	Positive
18	59	18.2	77	17.75	Negative	73.76	Positive	55	Positive
19	59	19.48	79	25	Positive	30	Negative	55	Positive
20	59	22.51	42	7.02	Negative	74.22	Positive	81.6	Positive
21	59	22.65	66	10.82	Negative	73.88	Positive	76.7	Positive
22	60	6.58	65	14.74	Negative	24.82	Negative	44.9	Negative
23	60	10.6	30	16.79	Positive	61.27	Positive	55	Positive
24	60	11.45	46	19.48	Negative	53.47	Positive	50.9	Positive
25	60	14.79	38	6.9	Positive	74.39	Positive	76.4	Positive
26	60	15.51	35	21.02	Negative	30	Negative	43	Negative
27	61	4.6	37	10.87	Negative	25.02	Negative	30.7	Negative
28	61	10.33	62	25.36	Negative	23.78	Negative	48.5	Negative
29	61	10.36	35	19.79	Negative	47.88	Negative	48	Negative
30	61	10.59	56	17	Positive	60.72	Positive	59.3	Positive
31	61	18.3	62	6.99	Positive	74.46	Positive	82.1	Positive
32	62	6.12	52	24.18	Negative	12.86	Negative	40	Negative
33	62	6.2	25	4.35	Positive	56.05	Positive	55	Positive
34	62	8.37	43	11.23	Negative	40.23	Negative	48.7	Negative
35	62	8.79	45	10.92	Positive	48.39	Negative	50.8	Positive
36	62	20	53	5.2	Positive	74.55	Positive	82.1	Positive
37	63	8.8	31	22.5	Positive	19.22	Negative	55	Positive
38	64	5.7	36	29.82	Negative	12.71	Negative	45.7	Negative
39	64	6.96	45	9.2	Negative	60.28	Positive	36.7	Negative
40	64	8	40	7.5	Positive	74.39	Positive	55	Positive
41	64	11.08	26	10.11	Negative	59.05	Positive	47.1	Negative
42	64	16.28	21	6.94	Positive	74.7	Positive	82.3	Positive
43	65	4.39	30	21.64	Negative	13.42	Negative	42.1	Negative
44	65	5.15	47	15.73	Negative	19.46	Negative	44.9	Negative
45	65	7.61	23	5.78	Positive	70.95	Positive	55	Positive
46	65	7.82	75	22.76	Negative	13.04	Negative	40	Negative
47	65	8.33	32	14.53	Positive	38.08	Negative	55	Positive
48	66	4.38	33	23.52	Negative	12.78	Negative	42.1	Negative
49	66	6.72	61	13.84	Positive	25.38	Negative	46.4	Negative

Patient ID	Age (Year)	PSA (ng/ml)	PV (ml)	%fPSA	Biopsy Result	Mahanta et al. [6]		F-MES	
						PCR (%)	Biopsy Result	PCR (%)	Biopsy Result
50	66	7.65	89	23.66	Negative	12.9	Negative	40	Negative
51	66	9	74	18.89	Positive	53.84	Positive	44.7	Negative
52	66	9.86	49	23.83	Negative	21.69	Negative	47.1	Negative
53	67	4.39	28	0.91	Negative	23.99	Negative	35	Negative
54	67	5.65	24	10.27	Positive	46.65	Negative	51.1	Positive
55	67	6.24	65	21.96	Negative	13.31	Negative	40	Negative
56	67	8.2	36	20.37	Positive	31.78	Negative	55	Positive
57	67	9.68	41	7.44	Positive	74.18	Positive	55	Positive
58	67	15.93	69	6.09	Positive	74.82	Positive	74.9	Positive
59	67	28	47	15	Positive	74.15	Positive	67.4	Positive
60	68	5.09	47	2.36	Negative	42.96	Negative	46	Negative
61	68	5.51	45	11.25	Negative	21.28	Negative	48	Negative
62	68	7.2	33	3.61	Positive	67.21	Positive	55	Positive
63	68	9.25	91	3.57	Positive	74.03	Positive	45.7	Negative
64	68	12.1	61	16.12	Negative	74.25	Positive	56.8	Positive
65	68	23.7	109	10.04	Positive	73.55	Positive	60	Positive
66	69	8.8	34	8.98	Positive	74.4	Positive	64.3	Positive
67	69	11.06	38	29.84	Negative	26.64	Negative	49.5	Negative
68	69	15.31	74	30.57	Positive	30	Negative	60	Positive
69	70	5.39	42	12.8	Negative	19.91	Negative	47.5	Negative
70	70	13	40	15.46	Negative	74.39	Positive	68	Positive
71	70	19.2	44	10.1	Positive	73.49	Positive	75.6	Positive
72	70	21.94	29	7.11	Positive	75.17	Positive	81.2	Positive
73	70	27.7	63	8.99	Negative	74.4	Positive	78.2	Positive
74	71	6.08	48	21.38	Positive	13.52	Negative	47.5	Negative
75	71	12.64	50	7.99	Positive	74.39	Positive	66.7	Positive
76	71	22	57	12	Positive	74.59	Positive	71.4	Positive
77	72	6.64	32	27.41	Negative	12.43	Negative	49.4	Negative
78	72	13.31	33	3.83	Positive	74.4	Positive	74.3	Positive
79	72	13.31	33	3.76	Positive	74.4	Positive	74.3	Positive
80	72	20	48	7.9	Positive	74.22	Positive	81.2	Positive
81	72	46	36	10.7	Positive	73.81	Positive	74.4	Positive
82	73	4.65	41	41.94	Negative	12.52	Negative	15.2	Negative
83	73	7.25	19	5.52	Negative	67.73	Positive	76.2	Positive
84	73	7.6	74	31.32	Positive	12.09	Negative	54.5	Positive
85	73	19	90	6.84	Positive	73.98	Positive	76.9	Positive
86	73	29.52	91	9.82	Negative	73.73	Positive	76.9	Positive
87	73	47.4	87	15.89	Positive	74.11	Positive	63	Positive
88	74	12.52	27	11.82	Negative	74.47	Positive	73.9	Positive
89	75	4.61	16	17.57	Positive	18.39	Negative	55	Positive
90	75	10	34	7.6	Positive	73.98	Positive	72.1	Positive

3.3. Comparative Performance Analysis

To assess the efficacy of the proposed F-MES, a comparative analysis was performed against a previously developed fuzzy-based diagnostic model by Mahanta et al. [4]. As summarized in Table 9 and illustrated in Figure 10, the F-MES achieved substantial performance gains across all evaluated metrics. Specifically, the system recorded an accuracy of 81.11%, compared to 68.07% in the earlier model. Similarly, recall (88.64%), precision (76.47%), specificity (73.91%), and F1-score (82.11%) also improved significantly over Mahanta's corresponding values of 66.07%, 73.33%, 69.81%, and 69.84%, respectively. These improvements are attributable to two primary factors: the expanded fuzzy rule base 500 rules across 24 domains and the use of refined, clinically aligned membership functions during fuzzification. This configuration enables the F-MES to model more granular clinical relationships and adapt to patient variability more effectively than systems with fewer linguistic terms and limited rule sets. The system's high recall value highlights its effectiveness in identifying patients with elevated prostate cancer risk, a crucial requirement in clinical diagnostics to prevent missed or delayed treatment. Although the specificity (73.91%) is moderately

Table 8. *Comparison of clinical-based and F-MES-based assessments*

Performance metric		F-MES		Total
		Positive	Negative	
Doctor	Positive	39 (TP)	12 (FP)	51
	Negative	5 (FN)	34 (TN)	39
Total		44	46	90

Table 9. *Comparative performance of fuzzy-based diagnostic models including F-MES Evaluation*

Authors and Year	Domains	Fuzzy Rules	Accuracy (%)	Precision (%)	Recall (%)	Specificity (%)	F1-Score
Mahanta et al., 2020 [6]	16	240	68.07	73.33	66.67	69.81	69.84
This Study (2025)	**24**	**500**	**81.11**	**76.47**	**88.64**	**73.91**	**82.11**

improved compared to the previous model (69.81%), it still reflects meaningful progress in minimizing unnecessary biopsy recommendations, thus reducing the burden on patients and healthcare resources. Additionally, the F1-score of 82.11%, which harmonizes precision and recall, indicates the system's ability to maintain balanced performance in scenarios involving diagnostic uncertainty. This reliability is particularly important for diseases like prostate cancer, where overlapping biomarker values are common.

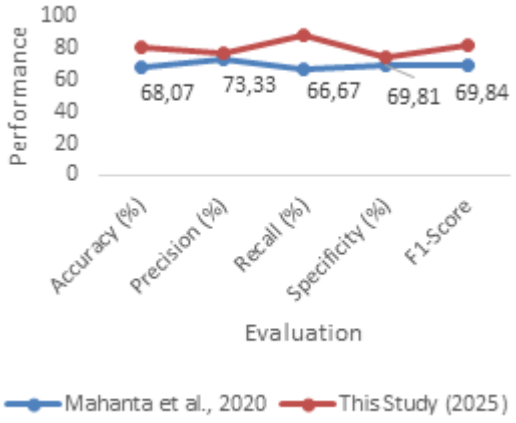

Figure 10. *Performance Comparison between the Proposed F-MES and Mahanta et al.'s (2020)[6]*

In contrast to black-box approaches such as Support Vector Machines (SVM) and deep neural networks, which often suffer from limited interpretability, the F-MES operates on transparent, rule-based reasoning. The adoption of the Mamdani inference method ensures that predictions are not only accurate but also explainable, an essential feature for integration into clinical workflows where decisions must be justifiable and aligned with professional judgment. F-MES not only demonstrates superior diagnostic accuracy but also meets the practical requirements of clinical interpretability and transparency. These qualities position it as a reliable tool for supporting prostate cancer screening, particularly as a second-opinion system or a component of intelligent clinical decision support platforms.

4. Conclusion

This research proposes and assesses a Fuzzy Medical Expert System (F-MES) based on Mamdani inference, aimed at improving early-stage prostate cancer risk prediction. The system utilizes clinically validated input parameters, including age, PSA levels, prostate volume (PV), and the percentage of free PSA (%fPSA). The FMES adopts a comprehensive rule base consisting of 500 fuzzy rules, derived from established clinical guidelines, that forms the foundation of the system's reasoning process. We have done intensive experiments by using 90 standard datasets from the literature. The experimental results show that the FMES outperforms the results in the previous research. The model achieved a diagnostic accuracy of 81.11%, surpassing existing fuzzy-based approaches. Further performance evaluation showed robust predictive capability, with a precision of 76.47%, a recall of 88.64%, a specificity of 73.91%, and an F1-score of 82.11%. Future enhancements will involve incorporating genetic and lifestyle-related factors and deploying the system on a cloud-based platform to increase its scalability and availability across diverse healthcare settings.

Author Statements:

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