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A CUTTING-EDGE APPROACH TO PREDICTIVE PRECISION IN ONCOLOGY USING A GENETO-NEURO-FUZZY HYBRID MODEL

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ABSTRACT

Purpose: This study introduces a pioneering hybrid model that combines genetic algorithms, neuro-fuzzy logic, and mobile agent technology to enhance predictive precision for early-stage prostate cancer diagnosis.
Design/Methodology/Approach: One hundred and twenty records of prostate cancer patients were initially collected from the Delta State University Teaching Hospital, Oghara, Nigeria. Each patient's record included relevant data on prostate disease, such as age, PSA levels, clinical history, symptom severity, biopsy results, and other demographic and clinical factors. This data was extracted and stored as rules in a MySQL database, with the MySQL Fuzzy Extension enabling fuzzy data storage and processing.
Findings: Extensive simulations and clinical data analyses demonstrate the model's superior sensitivity and specificity in detecting early-stage prostate cancer compared to traditional diagnostic methods. Medical expert evaluations validate the model's effectiveness as a promising diagnostic alternative.
Research Limitation: While results are promising, the study is limited to simulations and a controlled clinical dataset.
Practical Implications: The system offers a practical, scalable early prostate cancer detection solution that could revolutionise current diagnostic practices.
Social Implications: Potential social benefits include improved patient outcomes, reduced healthcare costs, and better quality of life.
Originality/Value: This study presents an innovative integration of genetic algorithms, neuro-fuzzy systems, and mobile agent technology. This novel approach paves the way for advanced cancer diagnostics and precision medicine.
Keywords*: Diagnoses. fuzzy logic. genetic algorithm. neural network. prostate cancer*

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INTRODUCTION

In Nigeria, cancer represents a formidable public health challenge, with an estimated 72,000 cancer-related deaths and 102,000 new diagnoses each year (Fatiregun et al., 2020). Among men, prostate cancer ranks as one of the most prevalent forms, with rising incidence and mortality rates. Prostate cancer has significant health implications due to its often-silent progression and high morbidity. Globally, prostate cancer accounts for approximately 1.4 million new cases and 375,000 deaths annually, making it the second most common cancer and the fifth leading cause of cancer death among men (WHO, 2022). In West Africa, the age-standardized incidence rate of prostate cancer is 39.6 per 100,000 men, and the mortality rate is 27.9 per 100,000 (Ferlay et al., 2024).

The prostate gland, a crucial component of the male reproductive system, weighs approximately 18 grams but typically enlarges with age, potentially obstructing the urinary tract. This enlargement, often benign in early stages, can signal more serious conditions if it progresses to malignancy, presenting symptoms such as frequent urination, weak urine flow, and erectile dysfunction. Advanced prostate cancer can spread beyond the prostate to lymph nodes, bones, liver, and lungs, leading to life-threatening complications if not detected early.

The risk of prostate cancer escalates significantly with age, with the majority of cases occurring in men aged 65 and older, while cases in men under 40 are rare (American Cancer Society, 2022). Early-stage prostate cancer (stages I and II) is highly treatable and often managed effectively if localised. However, as prostate cancer progresses to stages III and IV, its spread to nearby tissues and distant organs renders it more difficult to control. This underlines the importance of early detection, which markedly improves the prognosis and the likelihood of a cure.

Current diagnostic methods for prostate cancer include the Prostate-Specific Antigen (PSA) blood test, Digital Rectal Examination (DRE), and biopsy. PSA testing measures the level of PSA protein in the blood, with levels below 10 ng/ml indicating low cancer risk, 10–20 ng/ml suggesting intermediate risk, and levels above 20 ng/ml signalling high risk. However, PSA tests are not without limitations: false positives are common, and only 25% of patients with elevated PSA levels have prostate cancer upon biopsy (Barry, 2001). DRE, which involves palpating the prostate through the rectum, has been shown to have a negative predictive value of 84.2% among 3,225 patients, making it somewhat effective but not definitive for early diagnosis (Jones et al., 2018). Although biopsy remains the most accurate method for confirming prostate cancer, it is invasive and resource-intensive, underscoring the need for non-invasive and accurate alternatives.

As healthcare advances toward integrating artificial intelligence and data science, soft computing techniques are emerging as promising tools for cancer diagnosis and prognosis. Information Technology (IT) applications in healthcare have improved diagnostic capabilities, enhancing patient outcomes by facilitating early detection and personalised treatment plans

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(Vasilis, 2020). This study aims to leverage these advancements by developing a Geneto-Neurofuzzy (GNF) inference model, combining genetic algorithms, neural networks, and fuzzy logic, to create a more accurate and sensitive tool for early prostate cancer diagnosis.

The specific objectives of this study are to design a computing model (GNF Inference Model) that integrates genetic algorithms, neural networks, and fuzzy logic to assess prostate cancer risk; and to evaluate the model's sensitivity, specificity, and diagnostic accuracy through clinical data analysis and simulations, aiming to deliver reliable and rapid diagnostic results that enhance early detection and improve treatment outcomes for prostate cancer patients.

Through this approach, this paper seeks to contribute to the growing body of evidence supporting the role of IT in healthcare, particularly in developing effective and scalable cancer diagnostic models to reduce the global burden of prostate cancer.

LITERATURE REVIEW

Information Technology-driven healthcare delivery and Computer-aided Diagnosis (CAD) is an active area of research and have shown immense results in medical diagnosis as well as in general healthcare (Adetunji et al., 2022; Nwankwo & Ukhurebor, 2021a; Victor-Ikoh et al., 2022; Umezurike et al., 2020; Umezurike et al., 2017a; Umezuruike et al., 2017b; Umezurike et al., 2019; Nwankwo & Umezurike, 2018; Nwankwo, 2017; Nwankwo, 2016). Ishioka et al. (2018) developed a CAD system using a convolutional neural network algorithm for detecting prostate cancer using a computationally expensive MRI.

Predictive Modeling in Oncology

Predictive modelling in oncology has become a cornerstone in advancing cancer diagnosis, treatment planning, and prognostication. By leveraging statistical methods, machine learning algorithms, and integrative data analysis, these models aim to enhance personalised medicine and improve patient outcomes. Historically, predictive models in oncology have relied on statistical techniques such as regression analysis and survival analysis. These methods utilise clinical and demographic data to estimate disease progression and patient survival rates.

However, their predictive accuracy is often limited due to cancer's complex and heterogeneous nature. The advent of machine learning (ML) and artificial intelligence (AI) has revolutionised predictive modelling in oncology. ML algorithms can process vast datasets, identifying patterns and correlations that may not be apparent through traditional methods. For instance, deep learning models have been employed to predict drug responses in cancer treatment, offering insights into personalised therapy options.

Moreover, AI has been instrumental in predictive biomarker discovery, particularly in immuno-oncology. Systematic reviews have highlighted the potential of AI algorithms to identify biomarkers that predict patient responses to immunotherapies, thereby guiding treatment decisions. Radiomics involves extracting quantitative features from medical images to develop

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predictive models. Studies have demonstrated that radiomic features, such as survival rates and treatment responses, can predict clinical outcomes in various cancers. For example, Aerts et al. (2014) conducted a large-scale radiomic study that identified features predictive of patient survival in lung and head-and-neck cancers. Integrating diverse data types, including genomic, proteomic, and imaging data, enhances the predictive power of models. Deep neural networks have facilitated multimodal data fusion, leading to more accurate predictions in oncology. Waqas et al. (2023) review discusses integrating multimodal data using deep learning techniques, emphasising their potential in cancer prediction.

Artificial Neural Network (ANN) is a biologically inspired method based on the structure of neurons in the brain (Sakshi et al., 2014). ANN is used explicitly for classification and prediction and could be an algorithm or a piece of hardware (Sharma et al., 2020). ANN models such as feed-backward, feed-forward, radial basis function network, single-layer, recurrent and self-organising maps (Usman & Adenubi,2013) find applications in various areas such as healthcare (Egba & Okonkwo, 2020; Dey et al., 2012), Finance and Banking (Acheme et al., 2023; Nwankwo et al., 2022; Nwankwo & Olayinka,2019), Industry(Nwankwo & Ukhurebor,2021b), Manufacturing, Agriculture (Olayinka et al., 2022; Osikemekha et al., 2022), Waste Management (Nwankwo et al., 2023d), Incidence resolution (Nwankwo et al., 2023c), Governance(Chinedu et al., 2021), Sharma et al. (2020) noted that the accuracy of ANN depends on the number of layers and types of activation functions deployed.

Genetic Algorithms in Oncology Prediction

Genetic algorithms (GAs), inspired by natural selection and genetics principles, have been increasingly applied in oncology to enhance predictive modelling, optimise treatment strategies, and identify potential biomarkers. Their ability to efficiently search large solution spaces makes them particularly valuable in addressing the complexities inherent in cancer research.

One of GAs' primary applications in oncology is feature selection, which involves identifying the most relevant genetic markers or clinical features for accurate cancer classification. For instance, Deng et al. (2021) proposed a hybrid gene selection approach combining Extreme Gradient Boosting (XGBoost) and a multi-objective genetic algorithm to improve cancer classification accuracy. Similarly, Seddik and Ahmed (2021) utilised GAs alongside dimensionality reduction techniques for ovarian cancer detection, achieving significant improvements in predictive performance.

GAs have been employed to optimise predictive models by selecting optimal parameter sets and enhancing model performance. Cattelani and Fortino (2023) introduced a dual-stage optimiser that adjusts for systematic overestimation in multi-objective genetic algorithms applied to biomarker selection in cancer prediction. In personalised medicine, GAs have been applied to predict tumour responses to various treatments. A study by researchers at the University of California, San Diego, developed an AI algorithm that utilises tumour genetics

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to forecast responses to chemotherapy drugs, aiding in selecting effective treatment plans. The combination of GAs with other computational methods has shown promise in oncology.

Park and Lee (2021) developed a molecular generative model that integrates GAs with tree search algorithms to generate anticancer molecules based on genetic profiles, facilitating drug discovery. Additionally, Wong et al. (2010) explored the use of GAs in protein folding and protein-ligand docking, contributing to understanding molecular interactions in cancer. While GAs offer significant advantages in oncology prediction, challenges such as computational complexity, convergence to local optima, and the need for large datasets remain. Future research is focused on developing more efficient algorithms, integrating GAs with machine learning techniques, and applying them to real-world clinical data to enhance their applicability in personalised cancer treatment.

Neuro-Fuzzy Systems in Predictive Analytics

On the other hand, fuzzy logic (FL) is a system of reasoning capable of drawing approximate or estimated deductions or inferences from imprecise rather than exact data (Acheme et al., 2020; Olayinka et al., 2018). In essence, it is a reasoning system that resembles human reasoning when a health practitioner decides to decide between 'very mild' and 'very severe' occurrence of prostate cancer, the decision options may be 'very mild', 'mild', 'moderate', 'severe' or 'very severe'**.** These linguistic variables may produce the following fuzzy value range as in Table 1.

Table 1: Linguistic variables and their fuzzy range

S/N	Linguistic variables	Fuzzy value
1	very mild	$0.0 \leq x < 0.2$
2	mild	$0.2 \leq x < 0.4$
3	moderate	$0.4 \leq x < 0.6$
4	severe	$0.6 \leq x < 0.8$
5	very severe	$0.8 \leq x \leq 1.0$

FL has been used in the automated diagnosis of several healthcare problems, such as typhoid fever (Akinrotimi & Oladele, 2018), tuberculosis (Morgan et al., 2018), Malaria (Khalid & Eltahir, 2016), Bacterial Meningitis (Oye & Thomas,2019), Ebola Hemorrhagic Fever(Emokhare & Igbape, 2015), and many more medical entities, as these entities are easily defined as Fuzzy sets.

Neuro-fuzzy systems combine the adaptive learning capabilities of neural networks with the interpretability of fuzzy logic systems, making them powerful tools for handling complex, uncertain, and nonlinear data. The Adaptive Neuro-Fuzzy Inference System (ANFIS) is one of the most widely recognised frameworks, leveraging neural networks for adaptive learning and fuzzy logic for reasoning (Jang, 1993). This hybrid approach allows the system to learn from data and generate interpretable rules, making it suitable for various predictive applications. Neuro-fuzzy systems have been widely used in medical diagnostics. For instance, a systematic

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review demonstrated their utility in predicting neurological disorders such as epilepsy and Parkinson's disease, highlighting their potential in clinical decision support (Bali & Garba, 2021). These systems effectively handle the inherent uncertainty in medical data, offering reliable predictions to assist healthcare professionals.

In manufacturing, neuro-fuzzy models predict system states and optimise processes. For example, an ANFIS model was successfully applied to predict buildings' heating and cooling loads, enhancing energy efficiency and management (Jang, 1993). In financial analytics, neuro-fuzzy systems forecast stock prices and market trends. Their ability to manage uncertainty and volatility has made them popular in this field.

The systems' fuzzy rules make their predictions more interpretable, aiding financial decision-making (Park & Lee, 2021). These systems adaptively learn from data, making them suitable for dynamic environments (Jang, 1993). Fuzzy logic components handle imprecision and uncertainty effectively, which is crucial for applications like medical diagnostics (Bali & Garba, 2021). Fuzzy rules make these systems transparent and interpretable, addressing one of the typical limitations of black-box models (Park & Lee, 2021). While neuro-fuzzy systems have shown promise, challenges such as computational complexity and the requirement for extensive training datasets remain. To address these, researchers are exploring integrating neuro-fuzzy systems with other advanced machine learning techniques and their application to big data and IoT. These advancements enhance scalability, efficiency, and accuracy in predictive analytics (Bali & Garba, 2021; Jang, 1993).

MATERIALS AND METHODS

Proposed Architecture

The proposed architecture of the system is shown in Figure 1. The model has five major components: user interface, knowledge base, model aggregator (fuzzy logic, ANN, and GA), inference engine, and a decision-support component. The vital signs, symptoms, and laboratory outcomes related to prostate cancer constitute the input for the user interface. The knowledge base (KB) supports manipulating the input to produce an intermediate result. This intermediate result will be fed into the Genetic-Neuro-Fuzzy Hybrid Inferential Engine. The output from this engine is automatically processed further by the decision support module (DSM) to generate the diagnostic results.

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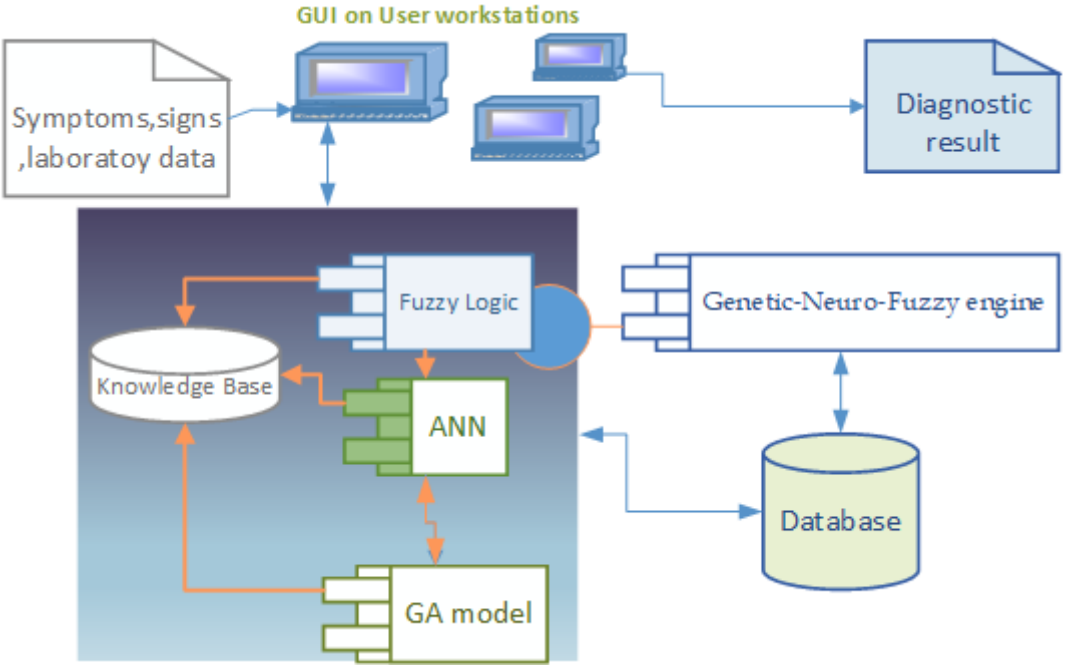

Figure 1: Proposed architecture for the detection of Prostate Cancer

Data Collection and Augmentation

One hundred and twenty records of prostate cancer patients were initially collected from the Delta State University Teaching Hospital, Oghara, Nigeria. Each patient's record included relevant data on prostate disease, such as age, PSA levels, clinical history, symptom severity, biopsy results, and other demographic and clinical factors. This data was extracted and stored as rules in a MySQL database, with the MySQL Fuzzy Extension enabling fuzzy data storage and processing. This extension provided additional operators and functions for handling fuzzy sets and logic operations, making it suitable for managing medical data's inherently uncertain and variable nature.

Data augmentation techniques were applied to artificially increase the dataset size and variability to enhance the dataset and improve the reliability of the model. Two main augmentation methods were utilised:

Synthetic Data Generation: Using Gaussian noise addition, we perturbed continuous variables like PSA levels and age within medically acceptable limits, generating new data points that retained the statistical properties of the original data. For instance, slight variations in PSA levels were created while ensuring the new values remained within clinically meaningful ranges. This approach allowed for an expanded dataset that captures more subtle variances in patient data.

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Synthetic Minority Over-sampling Technique (SMOTE): SMOTE was used to synthetically create additional patient records by generating new instances through interpolation following the mathematical model expressed as follows:

Let:

- Xi be a sample feature vector from the dataset.
- Xj be the nearest neighbour to Xi in the feature space.
- λ be a random variable drawn from a uniform distribution in the range [0,1], which controls the degree of interpolation between Xi and Xj.

A synthetic sample Xnew can be generated as:

$$Xnew = Xi + \lambda(Xj - Xi) \qquad (1a)$$

The interpolation was particularly useful for cases underrepresented in the original dataset, ensuring a more balanced and comprehensive dataset. SMOTE created synthetic instances by selecting pairs of similar records and generating new data points along the line between them, resulting in a dataset better suited for training an adaptive diagnostic model.

The augmented dataset, containing the original and synthetic records, was subsequently validated by a medical expert to ensure clinical relevance and reliability. With the expanded dataset, the proposed Geneto-Neuro-fuzzy inference model is better equipped to capture the diverse characteristics of prostate cancer, potentially improving its diagnostic sensitivity and specificity.

Fuzzification and Defuzzification

In this phase, we transformed the crisp laboratory and symptomatic markers of prostate cancer into fuzzy linguistic variables using a function (see equation 1b) and with the triangular Membership function in equation (2).

$$A = \{(X_i, \mu_{A\,(X_i)}) | X_i \in \nu, \mu_A\,(X_i) \in [0, \quad 1]\} \qquad (1b)$$

$$\mu_A\,(X_i) = \begin{cases} 1 & if\ xi < a \\ \dfrac{x_i - a}{b - a} & if\ a \le x_i < b \\ \dfrac{c - x_i}{c - b} & if\ xi \le x_i < c \\ 0 & if\ c < x_i \end{cases} \qquad (2)$$

Where

$\mu_A(x_i)$: MF of X_i in A

μ_A : membership degree of Xi in A.

a, b and c: parameters that govern the MF.

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Each rule consists of 24 input variables and an output variable. The results from fuzzifying the prostate marker variables were systematically fed into the Artificial Neural Network (ANN) for comprehensive analysis. The ANN utilised a three-layered feedforward architecture comprising an input, hidden, and output layer. This structure ensures a robust and efficient processing flow, capturing the intricate relationships between input variables and diagnostic outcomes.

A back-propagation algorithm with a sigmoid activation function optimised the ANN's performance. This algorithm is renowned for its effectiveness in training neural networks, as it iteratively adjusts the weights of the connections between neurons to minimise the error in predictions. The sigmoid function, applied to the hidden and output layer neurons, introduces non-linearity into the model, enabling it to capture complex patterns in the data. The trained ANN model consists of 24 nodes in the input layer, each representing a unique prostate cancer variable. These variables encompass a range of diagnostic markers, providing a comprehensive dataset for the neural network to analyse. By integrating these diverse inputs, the ANN can make nuanced predictions about prostate cancer presence and severity, significantly enhancing the diagnostic process.

This detailed architecture and training methodology ensures that the ANN is finely tuned to detect subtle variations in prostate marker variables, leading to more accurate and reliable diagnostic outcomes. Advanced algorithms and a structured feedforward approach underscore the system's capability to transform raw data into actionable medical insights, ultimately contributing to improved patient care and clinical decision-making.

In the d*efuzzification phase***,** the fuzzy set is transformed into a precise quantity (crisp set) using the max membership principle, centroid method, weighted average method, mean max membership, center of sums, or 'Centre of largest Area' (CoA). We used the CoA for its computational simplicity, as computed in equation (3).

$$\text{CoA}=\sum_{l=1}^{n} \mu Y(xi)xi / \sum_{l=1}^{n} \mu Y(xi)xi \quad (3)$$

where $\mu Y(x_i)$ is the degree of input i in MF with x_i as the center value

Genetic-Neuro-Fuzzy Modeling

A hybrid system tagged GENFIS was proposed by (Omisore et al., 2017). The system combines genetic algorithms, neural networks, and fuzzy logic components. The essence is to provide a system that can easily be tailored to meet intelligent modelling needs, especially in disease diagnosis. In this study, we attempt to utilise the model for prostate cancer diagnosis. This predictive system utilises a feed-forward propagation method with six neural layers, as in Figure 2. Computations are done at active nodes, the output layers, and the input layers passive.

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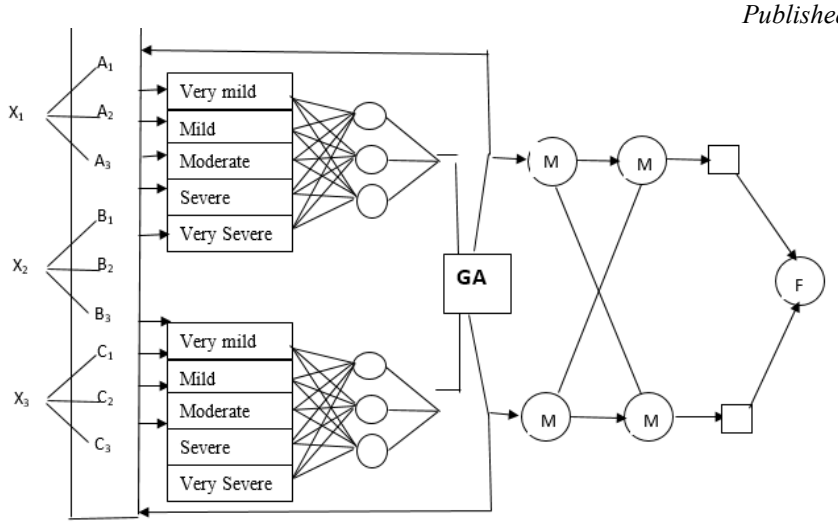

Figure 2: Genetic-Neuro-Fuzzy (GNF) model

The reasoning algorithm employs Mamdani's Inference Mechanism, chosen for its simplicity, intuitive rule base, and widespread acceptance in the field. This mechanism facilitates transparent and interpretable decision-making processes. The system's architecture consists of multiple layers, each with specific functions to process and analyse inputs. The first layer comprises active nodes that receive numeric input values. These values correspond to the severity of diagnostic marker variables, which are critical for evaluating the condition under diagnosis.

The outputs from this layer are linguistic labels that accurately represent the input severity levels, translating quantitative data into qualitative descriptors. The second layer takes the linguistic labels generated by the first layer as input. This layer's primary function is to determine the membership grade of each input, which quantifies the degree to which a particular input belongs to a defined category. The system can effectively evaluate and interpret the diagnostic marker variables by calculating these membership grades, facilitating accurate and reliable medical diagnoses. This detailed, multi-layered approach ensures that the reasoning algorithm processes data efficiently and provides easy outputs for medical professionals to interpret and act upon. Integrating Mamdani's Inference Mechanism enhances the overall robustness and reliability of the diagnostic system, making it a powerful tool for improving medical diagnostic accuracy and outcomes. See Equation 4:

$$L_2(x_i) = \mu_{Ai}(x_i) \qquad (4)$$

The fuzzy value is computed using triangular MF (see Equation 5)

$$\mu_{Ai}(x_i) = (x_i - b) / (a - b) \qquad (5)$$

where a and b are the triangular MF variables that determine its shape as $b \leq x_i \leq a$

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The third layer acts as multipliers, and the nodes compute the firing strengths of associated rules (Equation 6).

$$L_3(x_i) = \mu_{Ai}(x_i) * \mu_{Bi}(x_i) * \mu_{Ci}(x_i) \quad (6)$$

Nodes are fixed in the fourth layer, but it normalises the firing power of each rule. The k^{th} rule normalised strength is determined (see equation 7):

$$L_4(X_i) = wk / \sum_{j=1}^{3} \mu Y w j \quad \textbf{(7)}$$

The product of the normalised firing power of a rule and output value is the observed fifth layer that determines the variable's value addition to the diagnosis process (Equation 8).

$$L_5(x_i) = L_4(x_i) * L_3(x_i) \quad (8)$$

The sixth layer comprises a single fixed node labelled Z, representing the GNF's final output. It obtains the cumulative sum of all incoming signals (Equation 9)

$$Y = \sum_{i=1}^{n} L_5(x_i) \quad \textbf{(9)}$$

Finally, the crispy numeric value in Equation (9) is classified to present a readable result of the patient's diagnosis (Equation 10).

$$Output = \begin{cases} Very\ Mild & Y \leq 0.2 \\ Mild & 0.2 \leq Y < 0.4 \\ Moderate & 0.4 \leq Y < 0.6 \\ Severe & 0.6 \leq Y < 0.8 \\ Very\ Severe & 0.8 \leq Y < 1.0 \end{cases} \quad (10)$$

FINDINGS AND DISCUSSION

The result obtained from the modelling was validated using the data obtained from twelve (12) patients at Delta State University Teaching Hospital, Oghara, Nigeria, using MATLAB, as in Table 2. The result indicates that the GA component of the proposed model can extract a maximum of 13 out of 24 parameters as the best combination. In Table 2, selected parameters show that the model is sensitive to radiographic variables. The variables were selected for all cases with diagnostic results below 0.5 (50%), indicating early prostate cancer of stage I corresponding to 'very mild' with a value ≤ 0.2 and stage II corresponding to 'mild' within a range of '$0.2 \leq and < 0.4$'

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Table 2: GNF Inference Model Results

PiD	A_1	A_2	A_3	A_4	A_5	A_6	B_1	B_2	B_3	B_4	B_5	B_6	RESULTS
P01	1	1	1	0	0	0	0	0	0	0	0	0	0.3125
P02	1	0	1	0	0	0	0	0	0	0	0	0	0.2083
P03	1	1	0	1	1	0	0	0	0	0	0	0	0.4167
P04	0	1	1	1	0	0	0	0	0	0	0	0	0.3125
P05	0	1	1	1	1	0	0	0	0	0	0	0	0.4167
P06	0	1	1	1	0	0	0	0	0	0	0	0	0.3125
P07	1	1	0	0	0	0	0	0	0	0	0	0	0.2083
P08	0	1	1	1	0	1	0	0	0	0	0	0	0.4067
P09	1	0	1	1	1	0	0	1	0	0	0	0	0.5208
P10	0	1	1	0	1	0	0	0	0	0	0	0	0.3100

The results in Table 2 are also shown in Figure 3.

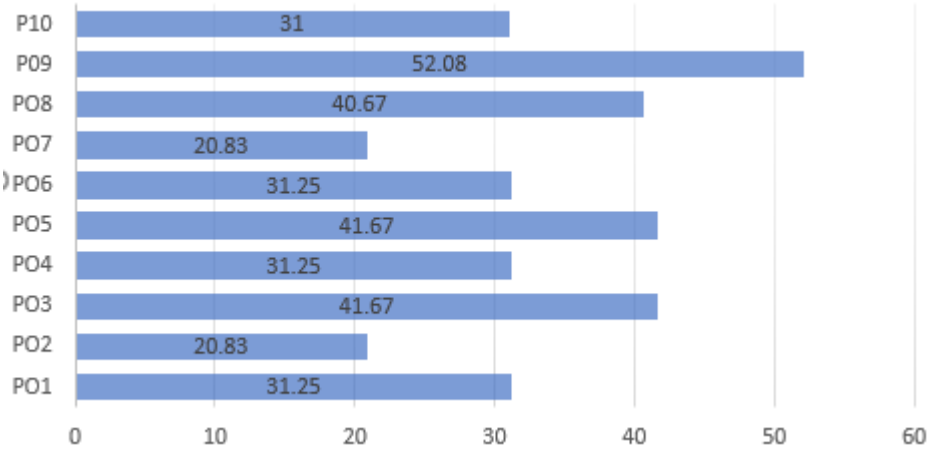

Figure 3: Prostate Cancer Diagnoses

In some previous studies, human experts and metrics validated the results. Responses in Table 3 show that an expert either accepts the model's result by assigning "√" or rejects it by indicating "x."

Table 3: Validation of the GNF Inference Model

Patient ID	P01	P02	P03	P04	P05	P06	P07	P08	P09	P10
Result (%)	31.3%	20.8%	42.0%	31.3%	42.0%	31.3%	20..5 %	42..0 %	52.1.0 %	31.3%
GENENFU	✓	✓	✓	✓	✓	✓	✓	✓	x	✓
Human Expert	✓	✓	✓	x	✓	✓	✓	✓	✓	x

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The GNF Interference Model and Medical Experts agreed that seven patients have prostate cancer, out of which two patients have stage I and five have stage II prostate cancer. Both the model and the expert disagreed on the outcome of the result of the other three patients. The sensitivity and accuracy of the model were also computed. Given a True Positive (TP) value for patients that have prostate cancer as those that were agreed on by the GNF Inference Model and human expert and a True Negative (TN) value indicating patients where consensus was not reached by the GNF Inference Model and human expert, and TNR as a total number of records. Therefore, the sensitivity and accuracy of the GNF Inference Model are:

$$\text{Accuracy} = (((TP + TN) / TRN) * 100\ \%) \quad (11)$$
$$\text{Sensitivity} = ((TP/TNR) * 100\%) \quad (12)$$

Hence, the proposed GNF Model exhibited a sensitivity of 70% and an accuracy of 80%.
The study's use of a Genetic-Neuro-Fuzzy (GNF) hybrid model with Mamdani's inference mechanism reflects agreement with Jang (1993), who emphasised the robustness of ANFIS in combining neural learning with fuzzy logic for handling uncertainty and non-linear data in medical applications.

The study's validation of its predictions by medical experts corroborates practices in the literature where expert validation ensures predictive models' clinical relevance and usability (Bali & Garba, 2021).

While the sensitivity and accuracy metrics reported in this study indicate reasonable performance, studies such as Wong and Park (2010) argue that achieving sensitivity and accuracy above 90% in high-stakes domains like oncology is crucial to minimise false negatives in early cancer detection. Consequent to these findings, the authors believe there are potential areas for improvement relative to the broader body of research in predictive oncology using hybrid models.

The World Health Organization (WHO, 2021) highlights that cost-effective and accessible diagnostic tools are critical to reducing cancer mortality, particularly in low- and middle-income countries. It promotes a reduction in diagnostic errors. By achieving an accuracy of 80% and leveraging human expert validation, the proposed model reduces the likelihood of false positives and negatives. This minimises patients' psychological and financial burdens, contributing to better mental well-being and optimised healthcare resource allocation. This agrees with the position of Singh et al. (2017) that reducing diagnostic errors improves patient outcomes and trust in healthcare systems.

The model's ability to detect early stages of prostate cancer (stage I and II) fosters a shift toward preventative care rather than reactive treatment. Early detection improves survival rates and reduces treatment costs, encouraging individuals to seek timely medical advice. This also agrees with Albright et al. (2020) that early cancer detection has immense socio-economic benefits in improving treatment success rates and reducing healthcare expenditure. The model

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simplifies complex data interpretation, providing healthcare professionals with actionable insights. This enhances decision-making efficiency and confidence in diagnosing prostate cancer, ultimately improving the quality of care delivered (Bali & Garba,2021).

CONCLUSION

Integrating artificial intelligence (AI) into medical diagnostics has significantly enhanced diagnostic accuracy. This study illustrates the practical application of a hybrid machine-learning model for prostate cancer detection. This innovative approach incorporates cognitive and emotional filters to address contextual factors that can influence medical experts during diagnosis. The findings indicate that combining various soft computing techniques may yield a more effective diagnostic system with improved accuracy.

Specifically, the performance of our model demonstrates a notable improvement, underscoring the uniqueness and effectiveness of hybridisation in this context. This study utilised a triangular membership function to define linguistic labels, while a neural network was introduced for self-tuning capabilities. Additionally, a genetic algorithm was employed to select optimal parameters effectively.

The study's Genetic-Neuro-Fuzzy (GNF) hybrid model has profound social implications, particularly in improving early detection and treatment outcomes. First, the study demonstrates integrating advanced computational methods with available clinical and demographic data, potentially enabling cost-effective diagnostic solutions. This can bridge healthcare disparities, especially in resource-constrained settings with limited access to sophisticated medical diagnostics.

The study's novelty lies in its innovative integration of genetic algorithms, fuzzy logic, and neural networks to create a hybrid diagnostic model tailored for prostate cancer. Unlike traditional methods that rely on single techniques, this study introduces a Genetic-Neuro-Fuzzy System (GNF) that combines the optimisation capabilities of genetic algorithms, the adaptability of neural networks, and the interpretability of fuzzy logic. This triad enhances predictive precision and robustness. This study also employed the Gaussian noise addition and Synthetic Minority Over-sampling Technique (SMOTE) to overcome the challenge of imbalanced datasets in medical diagnostics. This ensures better representation of minority classes, such as early-stage cancer cases, making the model more reliable. Mamdani's inference mechanism ensures the system outputs are linguistically interpretable, bridging the gap between complex algorithms and healthcare practitioners. This contrasts with black-box models, which often lack transparency.

Although the proposed model was validated with a limited prostate cancer records dataset due to the rule base's initial formulation, the results were promising. Future work will further validate the proposed model using a larger dataset of real-life prostate cancer records from

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various hospitals across Nigeria. This expanded validation will help confirm the model's robustness and applicability in diverse clinical settings.

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