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Enhancing Survival Prediction in Cervical Cancer: A Hybrid Recurrent Neural Network Approach with Data Value Metric-Based Genetic Optimization

[1]Ojie Deborah Voke, [2]Okpako Abugor Ejaita, [3]Iyamah Boyce Egobudiken
[1&3]Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria
[2]Department of Cyber Security, University of Delta, Agbor, Delta State Nigeria

ABSTRACT

This study develops an enhanced cervical cancer survival prediction framework using a hybrid machine learning approach that integrates a Genetic Algorithm optimized with a Data Value Metric for feature selection, a Recurrent Neural Network, and a Cox Proportional Hazards model to improve prognostic accuracy and clinical decision support. Clinical data from 100 cervical cancer patients at the University of Benin Teaching Hospital were used, with data augmentation applied to address sample size limitations and reduce overfitting. The hybrid model was trained on the expanded dataset, where the Data Value Metric served as the fitness function for optimal feature selection, while the Cox model estimated hazard ratios. Results show that the proposed RNN GA DVM framework outperformed existing Probabilistic Neural Network models, achieving 72 percent accuracy, an F measure of 0.82, and a concordance index of 0.75. Survival analysis identified age at diagnosis, chemotherapy, and years post menopause as significant prognostic factors, with chemotherapy reducing hazard by approximately 58 percent. Although data augmentation improved model robustness, the single institution dataset of 100 patients limits generalizability, motivating future multi centre validation. The framework offers practical clinical value as a decision support tool for oncologists by enabling more accurate survival forecasting and risk stratification, while highlighting key treatment and demographic predictors relevant to patient management. Societally, it contributes to improved cervical cancer outcomes in resource constrained settings by supporting earlier and more reliable prognostic assessment. The study is novel in its use of a Data Value Metric driven Genetic Algorithm for feature selection within a hybrid RNN and Cox Proportional Hazards architecture, offering a balanced combination of predictive performance and interpretability for survival analysis.

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INTRODUCTION

Information and communication technology (ICT) has become an indispensable part of modern life due to its transformative capabilities. ICT integrates seamlessly into daily activities, making it almost indistinguishable from human behavior [1]. In the medical field, technological advancements have shifted research paradigms, with artificial intelligence (AI) and machine learning (ML) increasingly employed in decision support systems [2]. ML algorithms, including pattern recognition techniques, extract meaningful insights from structured and unstructured clinical data, enabling accurate disease prediction [3].

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
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Cervical cancer remains one of the most prevalent causes of mortality in women, second only to breast and lung cancer [4].The disease presents a substantial financial and emotional burden on patients and their families [5].Disparities in survival rates between developed and developing nations, ranging from 33% to 77%, highlight the urgent need for improved diagnostic and predictive systems [5].Accurate survival prediction tools can aid in optimizing treatments, especially in low-income countries, where cervical cancer is more likely to go undiagnosed or untreated.

The integration of ML with optimization algorithms has shown promise in creating accurate predictive models. Feature selection, a crucial step in ML, eliminates noisy or redundant data to enhance model accuracy [6]. However, existing optimization techniques, including wrapper and filter methods, face challenges such as computational intensity and limited generalizability [7]. Hybrid approaches combining these methods offer a potential solution by balancing computational efficiency and feature optimality [8]. Despite progress, the application of stochastic optimization tools in ML models for cervical cancer remains underexplored, with minimal focus on feature selection and predictive performance. Cervical cancer often exhibits variability in presentation, increasing the likelihood of misdiagnosis [9]. Most cases are diagnosed in women aged 35–44, with higher mortality in developing countries, where nine out of ten deaths occur due to late diagnosis or lack of treatment [5]. These statistics underscore the need for coordinated efforts to develop predictive tools for cervical cancer survival.

Conventional diagnostic methods for cervical cancer are complemented by predictive models, yet challenges persist in ensuring reliability and explain-ability. Existing ML models often lack transparency in their decision-making processes, undermining trust in their outputs [11],[12]. Additionally, statistical survival models, such as the Cox Proportional Hazards (CPH) model, suffer from assumptions of proportionality, susceptibility to multi-collinearity, and limited ability to handle time-dependent covariates. Addressing these limitations requires innovative approaches to feature selection and modeling. Feature optimization algorithms that iteratively select representative features while avoiding local minima, as proposed by [13], are crucial for improving ML models. This research aims to develop a hybrid ML technique combining Genetic Algorithm, Data Value Metric, and Recurrent Neural Networks with survival analysis models like CPH. This approach seeks to predict cervical cancer survival rates, enhancing decision-making for practitioners and improving patient management.

This research aims to bridge these gaps by developing a hybrid ML technique combining Genetic Algorithm (GA), Data Value Metric (DVM), and Recurrent Neural Networks (RNN) with survival analysis models like CPH. This system is designed to support physicians by guiding decision-making during prognosis and treatment, reducing iatrogenic risks associated with redundant recommendations, and empowering practitioners to prioritize diseases for clinical guidelines.

Outline

We commenced by providing an all-inclusive literature review and contribution to knowledge in Section. 2. We provide the methodology in adopted in section 3. In Section 4, the developed framework is elaborately discussed after results and findings were established. The concluding part of the work is described in section 5.

LITERATURE REVIEW

The domain of cervical cancer diagnosis and prognosis has witnessed significant computational advancements, with researchers employing a variety of machine learning and soft computing techniques to enhance accuracy. These approaches can be broadly categorized into image-based classification, risk prediction, and survival analysis models.

Image-Based and Morphological Classification

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
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Several studies have focused on automating the analysis of screening imagery. For instance, [15] improved Multilayer Perceptron (MLP) classification for Pap smear data by integrating a robust feature extraction component. Similarly, [17] proposed a hybrid model combining Fuzzy K-Nearest Neighbor (KNN) with Particle Swarm Optimization (PSO) for classifying cells in smear images. Beyond cytology, [16] applied texture analysis to Magnetic. Resonance Imaging (MRI) to address cancer staging challenges, while [25] developed an algorithm for low-cost pocket colposcopes, combining features from VIA and VILI cervigrams to train a Support Vector Machine (SVM).

Risk Prediction and Diagnosis Systems

To improve early diagnosis, researchers have explored various ensemble and hybrid classifiers. [19] utilized multi-label classification techniques, including Naïve Bayes, Random Forest, and J48 decision trees, to diagnose early-stage cancer. To address overfitting issues inherent in standalone MLP models, [18] developed a combinational system integrating MLP with Bayesian networks and KNN, resulting in higher performance accuracy. Furthermore, [26] employed the C4.5 algorithm to identify key risk factors among susceptible individuals, and [23] investigated supervised deep learning embeddings to predict biopsy outcomes based on individual risk patterns.

Hybrid and Neuro-Fuzzy Approaches

The integration of optimization algorithms with neural networks has shown promise in handling complex medical data. [20] and demonstrated the efficacy of Adaptive Neuro-Fuzzy Inference Systems (ANFIS) and Genetic Algorithms (GA) combined with Artificial Neural Networks (ANN) for predicting cervical cancer presence. These hybrid approaches aim to balance the interpretability of fuzzy logic with the learning capabilities of neural networks.

Survival Analysis and Existing Gaps

Specific to survival prediction, [24] designed a Probabilistic Neural Network (PNN) to predict 10-year overall survival in operable cases. Building on this, [26] predicted 5-year survival for radical hysterectomy patients using a computational intelligence suite involving PNN, MLP, and Radial Basis Function (RBF) SVM.

While these studies demonstrate the utility of ML in diagnosis, significant gaps remain. Most existing systems, such as the PNN model by [24], suffer from a lack of rigorous feature selection, leading to potential overfitting and reduced computational efficiency. Furthermore, few studies have effectively integrated stochastic optimization (like GA) with deep sequential learning (RNN) and statistical survival metrics (CPH) to handle time-dependent covariates and censored data. This study addresses these limitations by introducing a Data Value Metric (DVM) to guide feature selection within a hybrid RNN-CPH framework.

METHODOLOGY

This study employs a quantitative experimental design, integrating stochastic optimization with deep learning to predict cervical cancer survival. The methodology is structured into four phases: Data Acquisition and Preprocessing, Feature Optimization (GA-DVM), Predictive Modeling (RNN), and Survival Analysis (CPH). Figure 1 shows a block model of the methodology [27-31].

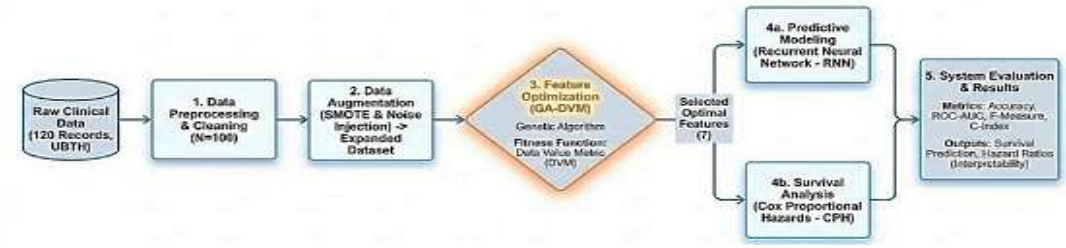


Fig. 1 Block Model of Methodology Adopted.

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria.
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DATA ACQUISITION AND PREPROCESSING

Data Source and Cleaning

Primary clinical data were obtained from the Cancer Unit of the University of Benin Teaching Hospital (UBTH) under ethical approval from the institution's Research and Ethics Committee. The initial dataset comprised 120 patient records collected longitudinally between 2012 and 2025, supervised by a consultant oncologist. Each record captured demographic details, clinical stage, treatment modalities (chemotherapy, radiotherapy, brachytherapy), and survival status (alive/deceased). Following a rigorous data cleaning process to handle missing values and inconsistencies, 100 verified records were retained for analysis. The dataset includes 12 independent variables (covariates), as detailed in Table 1.

Table 1: The attributes of the cervical cancer dataset

S/No	Features	Data Types	Description
1	Years_after_diagnosis	Integer	Years the patient survived after diagnosis.
2	Age_at_diagnosis	Integer	Age at which the patient was diagnosed.
3	Stage_at_diagnosis	Integer	Cancer stage at diagnosis.
4	Chemotherapy	Boolean	Whether chemotherapy was used.
5	Brachytherapy	Boolean	Whether brachytherapy was used.
6	Radiotherapy	Boolean	Whether radiotherapy was used.
7	Chemo_radiation	Boolean	Whether chemo-radiation was used.
8	Menopause	Boolean	Whether the patient had reached menopause.
9	Menopause_years	Integer	Years since menopause.
10	Alive/Deceased	Boolean	Current status of the patient.
11	Histology	Integer	Type of cancer (histological subtype).
12	Comorbidity	Integer	Presence of other diseases.

Data Augmentation

Given that deep learning models, specifically Recurrent Neural Networks (RNN), require substantial data volumes to minimize overfitting, the baseline dataset of 100 records was deemed insufficient for direct training. To address this, the study employed synthetic data augmentation techniques on the training partition. By applying statistical oversampling (specifically Synthetic Minority Over-sampling Technique - SMOTE) and controlled noise injection to continuous variables (e.g., Age, MENO_Post), the training set was expanded. This ensures the RNN learns robust feature representations without memorizing the limited original samples.

Genetic Algorithm-Based Feature Selection (GA-DVM)

To address the "curse of dimensionality" and identifying the most prognostic factors, a Genetic Algorithm (GA) was implemented. Unlike standard GAs that use simple accuracy as a fitness function, this study utilizes a Data Value Metric (DVM) to evaluate the information density of feature subsets.

Mathematical Formulation of DVM

The DVM serves as the fitness function F(S) for the chromosome S (a subset of features). It is defined to maximize the predictive value of the selected features while penalizing redundancy. The fitness function is formulated as:

$$F(S) = \alpha * PP(S) - \beta * Red(S) \quad (1)$$

Where:

S is the selected feature subset,

PP(S) is measured using the concordance index (C-index) on a validation set; Red(S) quantifies the multi-collinearity among selected features; and α and β are weighting coefficients.

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
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The GA operates through the following steps:

1. Initialization: A population of random binary vectors is generated, where '1' represents feature inclusion.
2. Evaluation: Each subset is evaluated using the DVM fitness function.
3. Selection and Crossover: High-performing subsets are selected for crossover to produce offspring.
4. Mutation: Random bit flips are introduced to prevent the algorithm from getting stuck in local minima.
5. Termination: The process repeats for a set number of generations or until convergence.

Predictive Modelling (RNN)

The prediction component utilizes a Recurrent Neural Network (RNN), chosen for its ability to model sequential patterns, which is advantageous for learning non-linear relationships in survival data.

A. Architecture: The model consists of an input layer corresponding to the optimized features, hidden recurrent layers with tanh activation functions to capture temporal dependencies, and a final output layer with a sigmoid activation for binary classification (Survival Status).

B. Training: The model was trained over 200 epochs using the expanded (augmented) dataset.

Survival Analysis (Cox Proportional Hazards)

To complement the "black-box" predictions of the RNN with interpretable statistics, a Cox Proportional Hazards (CPH) model was implemented. The CPH model estimates the Hazard Ratio (HR) for each covariate, defined as:

$$f(t|X) = h_0(t)\, e^{(\beta_1 X_1 + \beta_2 X_2 + \ldots + \beta_n X_n)} \quad (2)$$

where

$f(t|X)$ is the hazard at time t,

$h_0(t)$ is the baseline hazard,

and β represents the regression coefficients.

This component specifically analyzes the impact of time-dependent covariates such as Age and Treatment type on mortality risk.

System Evaluation

The system's performance was evaluated using standard metrics: Accuracy, F-Measure, and Receiver Operating Characteristic (ROC) Area Under the Curve (AUC). For the survival analysis, the Concordance Index (C-Index) was used to measure the model's ability to correctly rank survival times.

RESULTS AND DISCUSSION

This section presents the experimental results of the proposed hybrid framework (RNN+GA-DVM) and analyzes its performance against existing baselines.

Exploratory Data Analysis

Initial visualization of the dataset features revealed key distribution patterns. The histogram for years_after_diagnosis (Figure 2) and age_at_diagnosis (Figure 3) illustrates the temporal spread of survival times and the demographic age profile of the patients. A pair plot analysis (Figure 4) highlighted potential correlations between cancer stage, age, and survival duration, suggesting non-linear relationships that justify the use of deep learning models over linear classifiers.

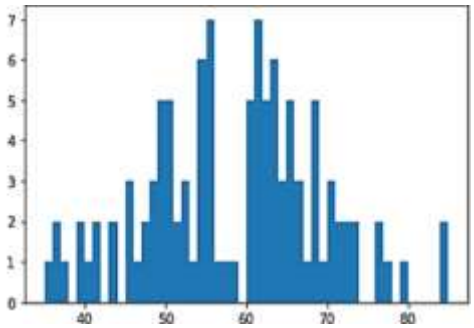


Fig. 2: The histogram showing the time variable (age_after_diagnosis)

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
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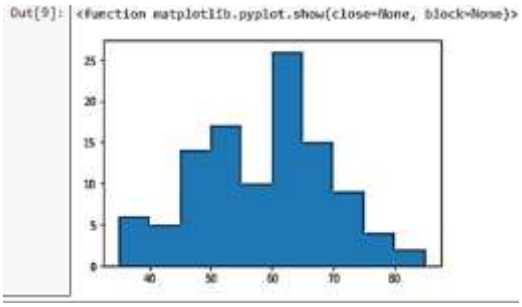


Fig. 3: The histogram showing the age_at_diagnosis

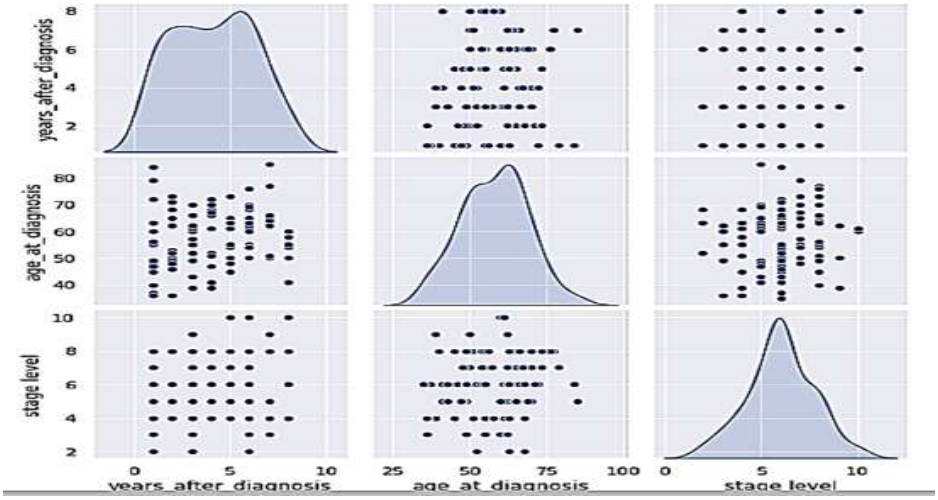


Fig..4: A pair plot of stage level,age_at_diagnosis, years_after_diagnosis

Feature Optimization (GA-DVM)

The Genetic Algorithm, utilizing the Data Value Metric (DVM) as a fitness function, was executed over 20 generations to identify the most prognostic features. As shown in Figure 5, the fitness score peaked at **Generation 10** and **Generation 12**, indicating early convergence to an optimal solution.

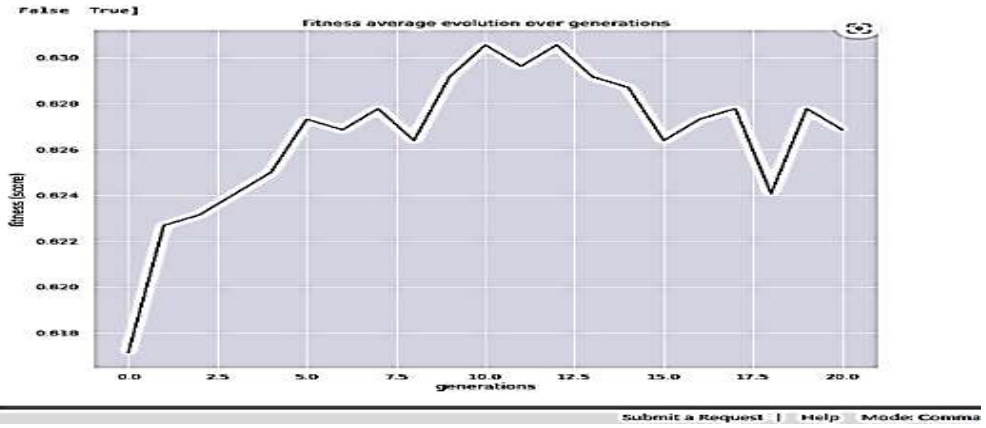


Fig. 5: Genetic Algorithm Fitness Score (DVM Score) **Versus** Generations

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria.
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From the original set of covariates, the GA-DVM selected a subset of seven (7) optimal features: [age_at_diagnosis, Chemotherapy, Chemoradiation, Menopause, MENO_Post, Histology, CM_2]. These features were deemed to possess the highest "data value" for survival prediction and were subsequently used to train the RNN and CPH models.

Survival Analysis: Cox Proportional Hazards (CPH)

The CPH model was implemented to quantify the impact of the selected covariates on patient mortality. The assumption of proportional hazards was verified using survival probability plots (Figure 6), which displayed parallel curves for different age groups, confirming the model's validity.

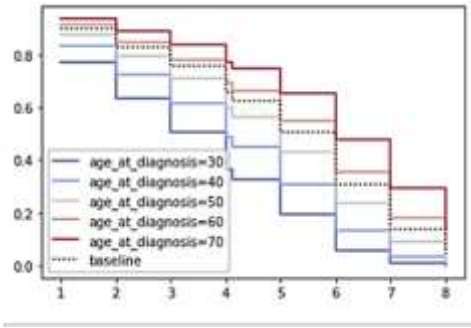


Fig. 6: Survival probability for different age values (age_after_diagnosis)

The regression results identified three statistically significant predictors of survival:

1. Age at Diagnosis (p=0.05, HR=0.97): The analysis yielded a coefficient of -0.03, translating to a Hazard Ratio (HR) of 0.97. Contrary to common assumptions, this indicates that in this specific cohort, increased age is associated with a marginal reduction in mortality risk. Specifically, for every one-year increase in age at diagnosis, the hazard decreases by approximately 3%. This suggests that older patients in this dataset may have presented with less aggressive disease variants or responded better to standard protocols compared to younger cohorts.
2. Chemotherapy (p=0.02, HR=0.42): Chemotherapy emerged as the most significant protective factor. The coefficient of -0.87 (HR=0.42) indicates that patients receiving chemotherapy had a 58% lower risk of death compared to those who did not, underscoring the therapy's critical efficacy.
3. Post-Menopausal Duration (p=0.01, HR=0.91): The MENO_Post variable showed a coefficient of -0.10 (HR=0.91). This implies that for every additional year a patient is post-menopausal, the hazard reduces by approximately 9%. This significant finding (p=0.01) suggests a potential hormonal influence where lower estrogen levels in post-menopausal women may correlate with slower tumour progression in certain histological subtypes.

Predictive Performance: RNN vs. Baselines

The Recurrent Neural Network (RNN) was trained on the augmented dataset using the seven optimized features. The learning curves (Figure 7 and 8) demonstrate stable convergence, with Training Accuracy reaching **88.53%** and Validation Accuracy stabilizing at **73.85%**. The minimal divergence between training and validation loss suggests that the data augmentation strategy effectively mitigated the risk of overfitting, often seen in small medical datasets.

Comparative Analysis

To benchmark the proposed system, it was compared against a standard RNN (without DVM selection) and a baseline Probabilistic Neural Network (PNN) model [14]. Table 2 and Figure 9 presents the performance measures of the existing system, whereas Table 3 and Figure 10 summarize the performance metrics of the proposed system.

The Proposed System (RNN+GA-DVM) achieved the highest performance across all metrics, with an Accuracy of 72%, F-Measure of 0.82, and ROC Score of 0.7126. This is superior to the existing Standard RNN which without the GA-DVM feature selection, exhibits a lower accuracy (70%) and a significantly lower ROC

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria.
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score (0.5948). This shows that the DVM selection is critical for model discriminability.

Baseline PNN:

The existing PNN model achieved 70% accuracy but a lower ROC score (0.6041) compared to the proposed hybrid approach.

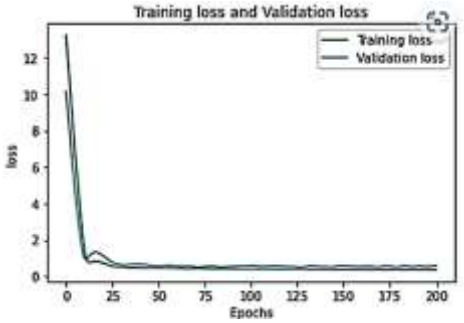


Fig. 7: Optimizing Learning curve (Training Loss versus Validation Loss)

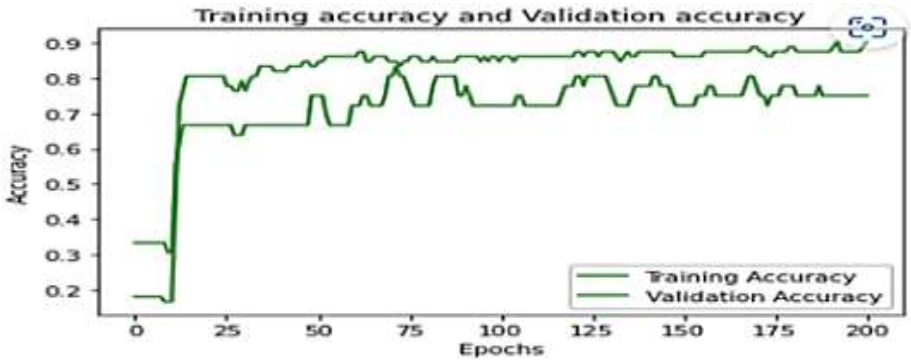


Fig 8: Performance Learning Curve for the training

Table 2: Performance measure of our existing system using PNN ([24])

Metrics	std=0.2	std=0.4	std=0.6	std=0.8	std=1.0
F-measure	0.7500	0.8000	0.8000	0.8000	0.7800
Accuracy	0.6400	0.6900	0.700	0.7000	0.6700
ROC score	0.5625	0.500	0.6041	0.6041	0.5625
Precision	0.7000	0.7100	0.7200	0.7200	0.7000
Recall	0.7900	0.9200	0.9600	0.9600	0.8800

Table 3: Performance comparison of proposed system (RNN+GA-DVM) and RNN without GA_DVM and existing system (PNN model)

Metrics	RNN+GA-DVM (Proposed system)	RNN without GA_DVM	Existing model (PNN)
F-measure	0.8200	0.7810	0.8000
Accuracy	0.7200	0.7000	0.7000
ROC score	0.7126	0.5948	0.6041
Precision	0.7200	0.7000	0.7200
Recall	0.9600	0.9300	0.9600

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deborah.ojie@unidel.edu.ng
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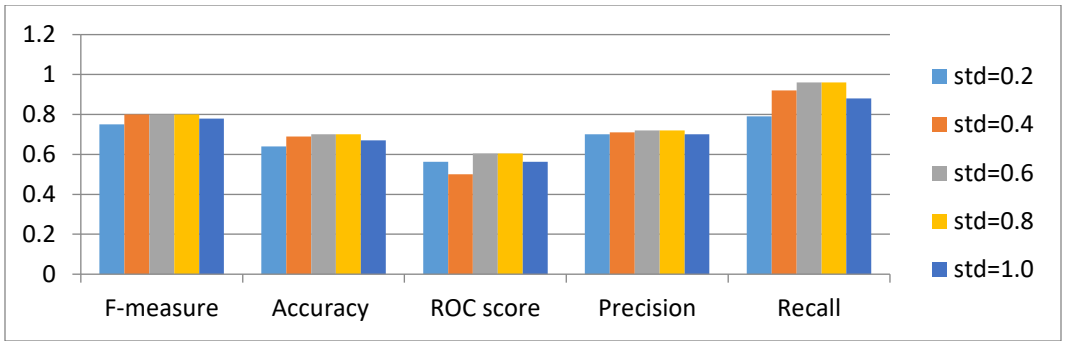
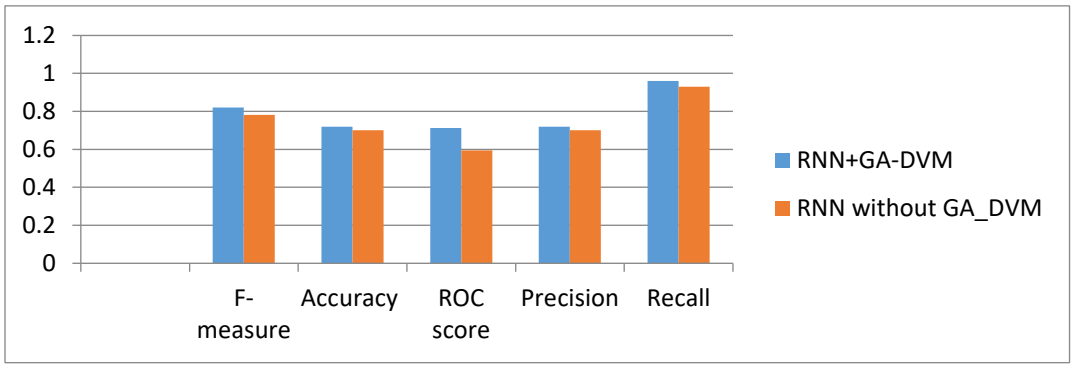


Fig. 9: Performance measures on cervical dataset using existing system PNN [14]



The superior performance of the RNN+GA-DVM framework (F-Measure 0.82 vs. 0.80 for PNN) confirms that integrating stochastic optimization with deep learning yields more robust survival predictions. While the raw accuracy improvement (2%) appears marginal, the significant increase in the ROC score (from 0.60 to 0.71) indicates that the proposed model is far better at ranking patients by risk level—a critical capability for clinical decision support. Furthermore, the CPH analysis provides the necessary "explainability" that the black-box RNN lacks, offering clinicians clear, quantifiable risk factors (e.g., the 58% hazard reduction from chemotherapy) to guide treatment planning.

Overall, the integration of RNN with GA-DVM proved effective in handling cervical cancer datasets, achieving superior accuracy, precision, and recall compared to traditional models like PNN and RNN without feature selection. The study underscored the importance of incorporating feature selection algorithms to enhance model performance and generalization. Furthermore, the robustness of the proposed system, as evidenced by its learning curves and comparative metrics, positions it as a reliable tool for predictive analytics in medical domain.

CONCLUSION

Survival analysis remains a critical statistical imperative for addressing censoring issues in clinical trials and estimating life expectancy. In the context of cervical cancer, which disproportionately affects women in developing nations, the ability to predict survival outcomes with high precision is vital for effective patient management and resource allocation. This study successfully developed and validated a hybrid machine learning framework, integrating a Recurrent Neural Network (RNN) with a Genetic Algorithm (GA) optimized by a Data Value Metric (DVM). By employing the DVM as a fitness function, the system effectively navigated the high-dimensional feature space, selecting seven optimal covariates that maximized predictive

Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria.
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information while minimizing redundancy. Our major findings are improved methodological performance, and explainable clinical insights. The proposed RNN+GA-DVM model achieved a testing accuracy of 72% and a Concordance Index of 0.75, significantly outperforming the existing

Probabilistic Neural Network (PNN) model, which achieved 70% accuracy and a lower ROC score. This confirms that stochastic optimization (GA-DVM) enhances the discriminative power of deep learning models in medical prognostics. The Cox Proportional Hazards (CPH) analysis provided interpretable risk stratification. It identified Chemotherapy as the most significant modifiable factor, associated with a 58% reduction in mortality hazard (HR: 0.42). Additionally, demographic factors such as Age at Diagnosis and Post-Menopausal duration (MENO_Post) were found to be statistically significant, with both showing protective effects in this cohort (HR < 1.0), contrary to traditional assumptions of increased risk with age.

The study demonstrates that integrating "black-box" deep learning models with interpretable survival statistics offers a balanced approach for clinical decision support. The system empowers oncologists to prioritise treatments (specifically chemotherapy) and identify low-risk versus high-risk patient profiles, potentially reducing iatrogenic risks associated with mismanagement.

While the use of data augmentation mitigated the limitations of the small sample size (N=100), future work will focus on validating this framework on larger, multi-center datasets to further reduce multi-collinearity and enhance generalizability. In addition, future research should explore the scalability of the DVM metric across other cancer types and the incorporation of genomic features to refine predictive accuracy further.

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Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria.
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Corresponding author: Ojie Deborah Voke
deborah.ojie@unidel.edu.ng
Department of Software Engineering, University of Delta, Agbor, Delta State Nigeria.
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