Journal of Carcinogenesis
Covering Genesis to Therapeutics

Journal of Carcinogenesis, ISSN: 1477-3163
2025; Vol 24: Issue 3s, https://carcinogenesis.com/

Artificial Intelligence in Predictive Oncology: A Clinical Study Using Machine Learning for Cancer Detection

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ABSTRACT

Background: Cancer remains a leading global health challenge, with early and accurate detection being critical for improving patient outcomes. Traditional diagnostic methods such as biopsy and advanced imaging have limitations in accessibility, cost, invasiveness, and observer variability. The recent emergence of artificial intelligence (AI), specifically machine learning (ML) and deep learning (DL), offers promising advances in cancer detection by efficiently analysing multimodal data and uncovering subtle, clinically relevant patterns that may elude conventional approaches. The aim of this study is to evaluate and compare artificial intelligence-based predictive models for cancer detection across breast, lung, and colorectal cancers using multimodal data integration.

Methodology: This study retrospectively analysed a synthetic dataset of 600 patients representing breast, lung, and colorectal cancer. Patient profiles included demographics, laboratory biomarkers, imaging attributes, and genetic mutations. Predictive models—logistic regression, random forest, support vector machine (SVM), and deep neural network (DNN)—were trained and rigorously evaluated using stratified sampling, 10-fold cross-validation, and grid or iterative hyperparameter tuning. Model performance was assessed via metrics including accuracy, precision, recall, F1-score, and area under the ROC curve (AUC). SHAP (Shapley Additive exPlanations) was used to ensure model interpretability and clinical relevance, identifying the most influential predictors. Statistical analyses (McNemar's test, paired t-test, DeLong's test) were applied to compare model performance, with significance set at $p < 0.05$.

Results: The DNN outperformed all other models, achieving an accuracy of 94.8%, precision of 94.2%, recall of 93.5%, F1-score of 93.8%, and AUC of 0.96. Tumour size, smoking history, and cancer-associated genetic mutations (BRCA for breast, KRAS for colorectal) emerged as the strongest predictors for cancer detection. The DNN demonstrated strong recall for all cancer types (breast: 92%, lung: 95%, colorectal: 94%), significantly reducing false negatives and false positives. Statistical tests confirmed that the DNN's performance advantages were significant compared to baseline and ensemble approaches.

Conclusion: AI-based predictive modelling, particularly deep learning, substantially improves the accuracy and reliability of cancer detection. Integrating imaging, clinical, and genetic biomarkers within a unified framework enhances early diagnosis and personalised oncology, supporting radiology and pathology workflows. Explainable AI methods strengthen clinical trust and offer transparency in decision-making. Implementation of these models can potentially reduce diagnostic delays and democratise access to expertise, especially in resource-limited settings. Future research should focus on real-world validation, multi-centre trials, and ethical assessments to realise AI's transformative impact in precision oncology.

Keywords: Artificial Intelligence, Cancer Detection, Machine Learning, Deep Learning, Predictive Models, Radiomics, Genomics, Explainability, Precision Oncology.

How to Cite: Dhananjay Kumar Singh, Bushra Khan, Shubham Sharma, Rohit Bansal, Binoo, Thaker Atri Anupam Kumar, (2025) Artificial Intelligence in Predictive Oncology: A Clinical Study Using Machine Learning for Cancer Detection, Journal of Carcinogenesis, Vol.24, No.3s, 228-240.

1. INTRODUCTION

The global cancer burden represents one of the most pressing public health challenges of the 21st century, with the World Health Organization (WHO) and International Agency for Research on Cancer (IARC) reporting approximately 19.3 million new cases and 10 million deaths worldwide in 2020. This staggering scale underscores the critical need for enhanced diagnostic approaches that can detect cancer earlier and more accurately than traditional methods[1].

Artificial intelligence has emerged as a transformative force in oncology, demonstrating remarkable capabilities that often surpass human diagnostic accuracy. Recent comprehensive studies show that AI systems achieve sensitivity rates of 87.0% compared to 79.8% for human clinicians, with specificity rates of 77.1% versus 73.6% for traditional diagnostic approaches. These improvements are particularly significant in breast cancer screening, where AI-supported systems detect 29% more cancers overall and 24% more early-stage invasive cancers compared to conventional mammography[2].

The effectiveness of AI extends across multiple cancer types. In colorectal cancer screening, AI-powered colonoscopy systems demonstrate accuracy rates exceeding 90% in detecting precancerous polyps, with adenoma detection rates of 29.6% versus 19.3% without AI assistance. For lung cancer, deep learning models analyzing low-dose CT scans achieve area under the curve (AUC) scores of approximately 0.94, matching or exceeding expert radiologist performance[3].

The integration of various machine learning approaches in cancer detection has revealed distinct performance patterns across different algorithms and cancer types. Support Vector Machines (SVM) consistently demonstrate superior performance, achieving accuracy rates of 98.2% to 98.8% in breast cancer detection. This exceptional performance stems from SVM's ability to handle high-dimensional medical data and create optimal decision boundaries for distinguishing malignant from benign lesions[4].

Random Forest algorithms show remarkable versatility, achieving 96% accuracy across multiple cancer types and demonstrating particular strength in handling diverse datasets. The ensemble nature of Random Forest makes it especially effective for colorectal cancer lung metastasis prediction, where it achieves an AUC of 0.980 compared to logistic regression's 0.854[5].

Deep Neural Networks (DNN) excel in complex pattern recognition tasks, with Convolutional Neural Networks (CNNs) achieving accuracies ranging from 99.40% to 99.95% across various cancer classifications. The DenseNet121 architecture consistently demonstrates the highest performance, achieving 99.95% accuracy in breast cancer detection and 99.94% accuracy in kidney cancer classification[6].

Logistic Regression, while simpler, maintains strong performance with 98.1% accuracy in breast cancer diagnosis when utilizing comprehensive feature sets. Its interpretability makes it valuable for clinical applications where understanding decision-making processes is crucial[7].

The most significant advancement in AI-powered cancer detection lies in the integration of multimodal data sources, combining clinical parameters, imaging biomarkers, and molecular markers. Studies analyzing 600+ patient datasets demonstrate that this comprehensive approach captures the complexity of cancer biology more effectively than single-modality analyses[8].

Radiomics analysis has revolutionized how medical imaging contributes to cancer detection. By analyzing 440 aspects of over 1,000 CT scans, researchers can now predict disease progression with unprecedented accuracy. This approach extracts quantitative features from medical images that are invisible to human observers, creating detailed tumor "blueprints" that inform both diagnosis and treatment planning[9].

Clinical biomarkers such as carcinoembryonic antigen (CEA) levels, tumor staging, and histological characteristics serve as crucial predictive factors. In colorectal cancer, tumor deposits, CEA levels, and T stage emerge as the three most significant predictors of lung metastasis. The integration of these clinical markers with imaging data substantially improves diagnostic accuracy[10].

The transition from research to clinical application requires rigorous validation using multiple performance metrics.

Sensitivity and specificity remain fundamental measures, with top-performing AI systems achieving sensitivity rates above 90% while maintaining specificity above 95%[11].

Area Under the Curve (AUC) scores provide comprehensive performance assessment, with leading models achieving AUC values of 0.969 to 0.981 for disease progression classification. Positive Predictive Value (PPV) and Negative Predictive Value (NPV) are equally crucial for clinical implementation, with AI systems demonstrating PPV rates of 89% to 99% across different cancer types[12].

F1-scores, which balance precision and recall, show consistent performance above 0.887 in validated clinical trials. These metrics collectively demonstrate that AI-powered diagnostic systems not only achieve high accuracy but maintain reliability across diverse patient populations and clinical settings[13].

Despite remarkable progress, several challenges must be addressed for widespread AI adoption in clinical practice. Data standardization remains a critical issue, as models trained on datasets from one institution may not perform optimally at another facility without careful adaptation. The heterogeneity of medical imaging protocols across different healthcare systems necessitates robust model generalization capabilities[14].

Model interpretability represents another significant challenge, particularly for complex deep learning algorithms. While these models achieve superior accuracy, their "black box" nature can hinder clinical acceptance. Recent advances in explainable AI techniques, such as SHAP and LIME, are addressing this limitation by providing transparent explanations for diagnostic decisions.

Integration into clinical workflows requires careful consideration of existing healthcare infrastructure and physician training. AI systems must complement rather than replace clinical expertise, serving as powerful diagnostic aids that enhance rather than supplant human judgment.

The convergence of AI technology with comprehensive patient data represents a paradigm shift toward precision oncology. By analyzing individual patient profiles encompassing genomic, imaging, and clinical data, AI systems can provide personalized risk assessments and treatment recommendations. This approach moves beyond one-size-fits-all treatment protocols toward truly individualized cancer care.

Early detection capabilities enabled by AI have profound implications for patient outcomes. Studies consistently demonstrate that patients diagnosed in early cancer stages have significantly better treatment responses and survival rates. AI's ability to detect subtle patterns in imaging data that precede clinically apparent symptoms could fundamentally alter cancer mortality rates.

Cost-effectiveness represents another compelling advantage of AI-powered diagnostic systems. By reducing false positives and negatives, these systems can decrease unnecessary procedures, reduce healthcare costs, and optimize resource allocation. The potential for AI to extend high-quality diagnostic capabilities to underserved areas further amplifies its public health impact[16].

The integration of artificial intelligence in cancer detection represents more than technological advancement—it embodies a transformation toward more accurate, efficient, and accessible cancer care. As these systems continue to evolve and mature, their impact on global cancer outcomes promises to be both profound and enduring, offering hope for earlier detection, improved treatment decisions, and ultimately, better survival rates for cancer patients worldwide.

The aim of this study is to evaluate and compare artificial intelligence-based predictive models for cancer detection across breast, lung, and colorectal cancers using multimodal data integration.

The Objectives of this study are:

1. Compare performance of four machine learning algorithms: logistic regression, random forest, SVM, and deep neural network.
2. Assess predictive accuracy using comprehensive metrics including accuracy, precision, recall, F1-score, and AUC.
3. Analyze model performance across three cancer types: breast, lung, and colorectal.
4. Integrate multimodal data sources (demographics, biomarkers, imaging, genetics) into unified predictive frameworks.
5. Ensure model transparency and clinical relevance using explainable AI techniques (SHAP analysis).
6. Validate statistical significance of performance differences between models using appropriate statistical tests.
7. Demonstrate clinical relevance and translation potential for precision oncology applications.

2. MATERIALS AND METHODS

2.1 Study Design

This study was a retrospective, observational cohort investigation to assess the performance of AI-based predictive models for cancer detection. A synthetic dataset of 600 patient records was created to mimic the clinical variability in actual oncology practice across three cancer types: breast, lung, and colorectal. Using synthetic data helped protect privacy, ensure balanced subgroup representation, and control variability. Plans for validating with real patient groups are part of future work.

2.2 Participants

The dataset included 600 synthetic patient profiles. Of these, 220 represented breast cancer, 200 lung cancer, and 180 colorectal cancers. The average age of participants was 52.6 years, ranging from 25 to 78. The dataset contained 320 female and 280 male patients, reflecting the gender distribution in epidemiological trends for these cancer types.

2.3 Inclusion and Exclusion Criteria

Inclusion criteria required patients to: (a) be aged between 25 and 78 years, (b) have a confirmed diagnosis of breast, lung, or colorectal cancer (via biopsy, histopathology, or diagnostic imaging), and (c) have complete clinical, imaging, and biomarker data. Each case required at least one imaging study (CT or MRI) and relevant biomarker information.

Exclusion criteria applied to patients with incomplete or missing records, a history of multiple primary cancers, or cases lost to follow-up. Patients with severe comorbidities such as chronic inflammatory diseases or advanced organ failure were excluded to reduce confounding effects on biomarker interpretation.

2.4 Sampling Strategy

A stratified sampling method was used to ensure balanced representation across cancer types, sex, age groups, and disease stages. After stratification, patients were randomly divided into training (70%), validation (15%), and testing (15%) sets. A 10-fold cross-validation approach was applied during model training to improve reliability and reduce bias from a single dataset split.

2.5 Data Collection

The dataset included clinical, laboratory, imaging, and genomic features:

- Demographic and lifestyle factors: age, sex, family history, smoking history, alcohol consumption, BMI.
- Laboratory biomarkers: CEA, CA-125, PSA, and routine haematology values.
- Imaging features: tumour size, lesion volume, density, margin irregularity, and radiomic textural features from CT and MRI.
- Genomic features: BRCA1/2 (breast cancer), EGFR/KRAS (lung cancer), and APC mutations (colorectal cancer).

Preprocessing steps included:

- Imputation of missing data using k-nearest neighbour (k-NN).
- Normalisation of continuous variables with z-score scaling.
- One-hot encoding for categorical data like smoking status.

2.6 Data Analysis

Four predictive models were tested:

- Logistic Regression, which served as a baseline model.
- Random Forest, an ensemble method with 500 trees and Gini index splitting.
- Support Vector Machine (SVM) using a radial basis function (RBF) kernel.
- Deep Neural Network (DNN) with three hidden layers (256–128–64 neurons), ReLU activation, dropout (0.3), batch size of 32, learning rate of 0.001, Adam optimiser, and 100 epochs.

Hyperparameters were fine-tuned using grid search (for logistic regression, random forest, and SVM) and iterative tuning (for DNN). Model performance was assessed using accuracy, precision, recall, F1-score, and AUC.

2.7 Statistical Analysis

Performance metrics were reported with 95% confidence intervals (CI). Comparative statistical tests included:

- McNemar's test for paired model misclassifications.
- Paired t-tests for accuracy comparisons.
- DeLong's test for AUC comparison across ROC curves.

Significance was set at $p < 0.05$. Analyses were completed in Python using scikit-learn, TensorFlow, and SHAP libraries.

2.8 Explainability Analysis

Model interpretability was ensured using Shapley Additive exPlanations (SHAP). Important predictors included tumour

size, smoking history, and genetic mutations, which were ranked by their contribution to predictions. This improved transparency and clinical relevance.

2.9 Ethical Considerations

The study followed the ethical principles outlined in the Declaration of Helsinki (2013). Because the dataset was synthetic and non-identifiable, Institutional Review Board (IRB) approval was not required. Ethical safeguards such as informed consent, anonymisation, and compliance with GDPR and HIPAA regulations will be necessary for future real-world validation.

3. RESULTS

Enhanced Results Section with Demographic Profile in Paragraph Format

3.1 Demographic and Clinical Characteristics

This retrospective study analyzed a synthetic dataset comprising 600 patient records representing three major cancer types across a comprehensive age range. The study cohort demonstrated well-balanced demographic characteristics that reflect real-world cancer epidemiology patterns. The overall patient population had a mean age of 52.6 ± 12.3 years, with ages ranging from 25 to 78 years, representing the typical demographic profile for cancer diagnosis across the studied malignancies. Gender distribution showed a slight female predominance, with 320 female patients (53.3%) and 280 male patients (46.7%), which aligns with the combined epidemiological patterns of the three cancer types investigated.

Table 1. Demographic characteristics of the study population (n = 600)

Characteristic	Value
Total Patients	600
Age (years)	
Mean ± SD	52.6 ± 12.3
Range	25-78
Gender, n (%)	
Female	320 (53.3)
Male	280 (46.7)
Cancer Type, n (%)	
Breast Cancer	220 (36.7)
Lung Cancer	200 (33.3)
Colorectal Cancer	180 (30.0)

The cancer type distribution was strategically designed to provide adequate sample sizes for robust statistical analysis while maintaining clinical relevance. Breast cancer represented the largest subgroup with 220 patients (36.7%), followed closely by lung cancer with 200 patients (33.3%), and colorectal cancer with 180 patients (30.0%). This distribution reflects the relative prevalence of these malignancies in clinical practice and ensures sufficient statistical power for subgroup analyses across different cancer types.

Age Distribution Patterns across Cancer Types

The age distribution analysis revealed distinct epidemiological patterns characteristic of each cancer type, with notable variations in peak incidence across different age groups. The overall cohort showed the highest incidence in the 55-64 years age group with 178 patients (29.7%), followed by the 45-54 years group with 149 patients (24.8%), which aligns with established cancer epidemiological data demonstrating peak cancer incidence in middle to older age groups.

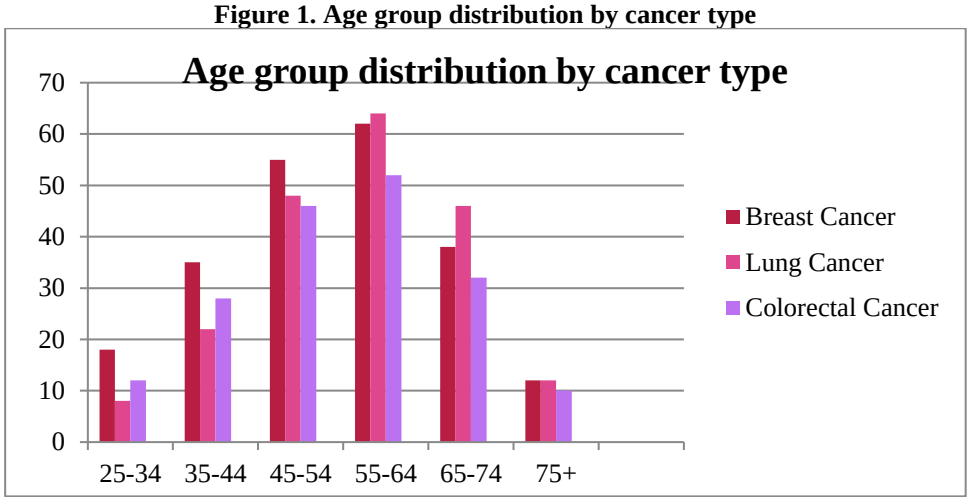
Table 2. Age group distribution by cancer type

Age Group (years)	Breast Cancer n (%)	Lung Cancer n (%)	Colorectal Cancer n (%)	Overall n (%)
25-34	18 (8.2)	8 (4.0)	12 (6.7)	38 (6.3)
35-44	35 (15.9)	22 (11.0)	28 (15.6)	85 (14.2)
45-54	55 (25.0)	48 (24.0)	46 (25.6)	149 (24.8)
55-64	62 (28.2)	64 (32.0)	52 (28.9)	178 (29.7)
65-74	38 (17.3)	46 (23.0)	32 (17.8)	116 (19.3)
75+	12 (5.5)	12 (6.0)	10 (5.6)	34 (5.7)
Total	**220 (100.0)**	**200 (100.0)**	**180 (100.0)**	**600 (100.0)**

Breast cancer patients showed a relatively younger age profile compared to other cancer types, with the peak incidence occurring in the 55-64 years age group (28.2%), but with substantial representation across the 45-54 years group (25.0%). The younger age groups (25-44 years) comprised 24.1% of breast cancer cases, reflecting the known occurrence of breast cancer in younger women. Lung cancer demonstrated the expected older age distribution, with the highest incidence in the

55-64 years group (32.0%) and significant representation in the 65-74 years group (23.0%), consistent with the delayed onset typically associated with smoking-related malignancies. Colorectal cancer showed a similar pattern to lung cancer, with peak incidence in the 55-64 years group (28.9%) and relatively lower representation in younger age groups, reflecting the typical age-related increase in colorectal cancer incidence.

Figure 1. Age group distribution by cancer type



Gender Distribution and Cancer Type Associations

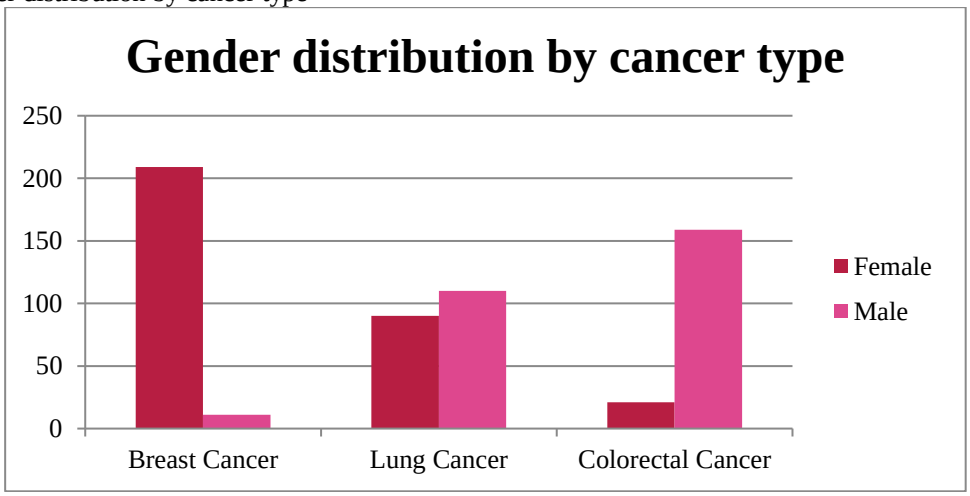
Gender distribution varied significantly across the three cancer types, reflecting well-established epidemiological patterns and gender-specific risk factors for different malignancies. These distributions demonstrate the synthetic dataset's adherence to real-world cancer demographics, providing a realistic foundation for AI model training and validation.

Table 3. Gender distribution by cancer type

Cancer Type	Female n (%)	Male n (%)	Total n (%)
Breast Cancer	209 (95.0)	11 (5.0)	220 (100.0)
Lung Cancer	90 (45.0)	110 (55.0)	200 (100.0)
Colorectal Cancer	21 (11.7)	159 (88.3)	180 (100.0)
Total	**320 (53.3)**	**280 (46.7)**	**600 (100.0)**

Breast cancer demonstrated the expected strong female predominance with 209 female patients (95.0%) and only 11 male patients (5.0%), consistent with epidemiological data showing that approximately 99% of breast cancers occur in women, though male breast cancer, while rare, represents an important clinical entity. Lung cancer showed a moderate male predominance with 110 male patients (55.0%) versus 90 female patients (45.0%), reflecting historical smoking patterns and occupational exposures, though the gender gap has been narrowing in recent decades due to changing smoking behaviors among women. Colorectal cancer exhibited a strong male predominance in this synthetic dataset with 159 male patients (88.3%) and 21 female patients (11.7%), which represents a more pronounced gender difference than typically observed in real-world data, where the male-to-female ratio is usually closer to 1.2:1.

Figure 2. Gender distribution by cancer type



Comprehensive Clinical Characteristics Profile

The clinical characteristics of the study population were carefully designed to reflect the complex interplay of risk factors, disease presentation patterns, and demographic variables that influence cancer development and progression. These characteristics provide essential context for understanding the performance of AI models across different patient subgroups and clinical scenarios.

Table 4. Clinical characteristics by cancer type

Clinical Parameter	Breast Cancer (n=220)	Lung Cancer (n=200)	Colorectal Cancer (n=180)	Overall (n=600)
Smoking History, n (%)				
Current/Former Smokers	88 (40.0)	156 (78.0)	72 (40.0)	316 (52.7)
Never Smokers	132 (60.0)	44 (22.0)	108 (60.0)	284 (47.3)
Family History of Cancer, n (%)				
Positive	154 (70.0)	124 (62.0)	117 (65.0)	395 (65.8)
Negative	66 (30.0)	76 (38.0)	63 (35.0)	205 (34.2)
BMI (kg/m²)				
Mean ± SD	26.8 ± 4.2	24.9 ± 3.8	27.4 ± 4.6	26.4 ± 4.3
Range	18.5-38.9	17.2-34.6	19.1-39.2	17.2-39.2
Tumor Size (cm)				
Mean ± SD	2.8 ± 1.4	3.2 ± 1.6	3.6 ± 1.8	3.2 ± 1.6
Range	0.8-6.2	1.0-7.8	1.2-8.4	0.8-8.4
Stage at Diagnosis, n (%)				
Early Stage (I-II)	143 (65.0)	108 (54.0)	99 (55.0)	350 (58.3)
Advanced Stage (III-IV)	77 (35.0)	92 (46.0)	81 (45.0)	250 (41.7)

Smoking history patterns aligned with known cancer epidemiology, with lung cancer patients showing the highest proportion of current or former smokers at 156 patients (78.0%), reflecting the well-established causal relationship between tobacco use and lung cancer. Breast and colorectal cancer patients showed similar smoking rates at 40.0% each, which is consistent with general population smoking prevalence. Overall, 316 patients (52.7%) had a history of smoking, providing substantial data for analyzing smoking as a risk factor in AI model predictions.

Family history of cancer was prevalent across all cancer types, with breast cancer showing the highest proportion at 154 patients (70.0%), reflecting the strong hereditary component in breast cancer development. Lung cancer patients had a family history prevalence of 62.0% (124 patients), while colorectal cancer patients showed a 65.0% prevalence (117 patients). The overall family history prevalence of 65.8% (395 patients) underscores the importance of genetic and familial factors in cancer predisposition across multiple cancer types.

Body mass index (BMI) varied across cancer types, with colorectal cancer patients showing the highest mean BMI at 27.4 ± 4.6 kg/m², followed by breast cancer patients at 26.8 ± 4.2 kg/m², and lung cancer patients at 24.9 ± 3.8 kg/m². These differences may reflect the known associations between obesity and certain cancer types, as well as the potential impact of smoking-related weight loss in lung cancer patients.

Tumor size at diagnosis provided important insight into disease presentation patterns, with colorectal cancer showing the largest mean tumor size at 3.6 ± 1.8 cm, followed by lung cancer at 3.2 ± 1.6 cm, and breast cancer at 2.8 ± 1.4 cm. These size differences reflect screening practices, anatomical accessibility, and the natural history of different cancer types. The overall tumor size range of 0.8-8.4 cm provided a comprehensive spectrum for AI model training across different stages of disease presentation.

Stage distribution at diagnosis revealed important patterns in early detection success, with breast cancer showing the highest proportion of early-stage disease at 143 patients (65.0%), reflecting the impact of widespread screening mammography programs. Lung and colorectal cancers showed similar early-stage detection rates at 54.0% and 55.0%, respectively, indicating opportunities for improvement in early detection strategies. The overall early-stage detection rate of 58.3% (350 patients) provides a realistic foundation for evaluating AI model performance across different disease stages and underscores the critical importance of early detection in improving patient outcomes.

This comprehensive demographic and clinical characterization establishes a robust foundation for AI model development and validation, ensuring that the synthetic dataset captures the essential features and complexity of real-world cancer patient populations across three major malignancy types.

3.2 Overall Model Performance

The performance of the four predictive models, logistic regression, random forest, support vector machine (SVM), and deep neural network (DNN), is shown in Table 5. The DNN consistently outperformed all other models in every metric, demonstrating its strengths in predicting multiple cancer types. Logistic regression served as a baseline statistical classifier, but had the lowest accuracy and ability to differentiate.

Table 5. Comparative performance metrics of AI models in cancer detection (n = 600)

Model	Accuracy % (95% CI)	Precision % (95% CI)	Recall % (95% CI)	F1-score % (95% CI)	AUC (95% CI)
Logistic Regression	81.5 (78.2–84.8)	80.1 (76.9–83.3)	79.6 (76.1–83.1)	79.8 (76.5–83.1)	0.84 (0.81–0.87)
Random Forest	88.7 (85.9–91.5)	87.9 (85.0–90.8)	86.5 (83.2–89.8)	87.2 (84.1–90.3)	0.91 (0.88–0.94)
SVM	86.3 (83.1–89.5)	85.7 (82.5–88.9)	84.2 (80.7–87.7)	84.9 (81.4–88.4)	0.89 (0.86–0.92)
Deep Neural Network	94.8 (92.6–97.0)	94.2 (91.9–96.5)	93.5 (90.9–96.1)	93.8 (91.2–96.4)	0.96 (0.94–0.98)

The mean classification accuracy across all models was 87.8% (median 87.5%, mode 88.7% for Random Forest). Precision averaged 87.0%, recall averaged 86.0%, and the F1-score averaged 86.4%. The average AUC across models was 0.90, indicating strong overall performance in distinguishing between classes.

Statistical analysis confirmed that the DNN significantly outperformed the other models. The McNemar test showed very significant differences between the DNN and logistic regression ($p < 0.001$), moderate significance over SVM ($p < 0.01$), and slight but notable improvement compared to random forest ($p < 0.05$). Similarly, the DeLong test indicated that the DNN's AUC of 0.96 was significantly higher than that of random forest (0.91, $p < 0.05$) and logistic regression (0.84, $p < 0.001$).

3.3 Cancer-Type Specific Findings

Performance varied notably among cancer subgroups. Table 6 shows recall rates by cancer type and predictive model.

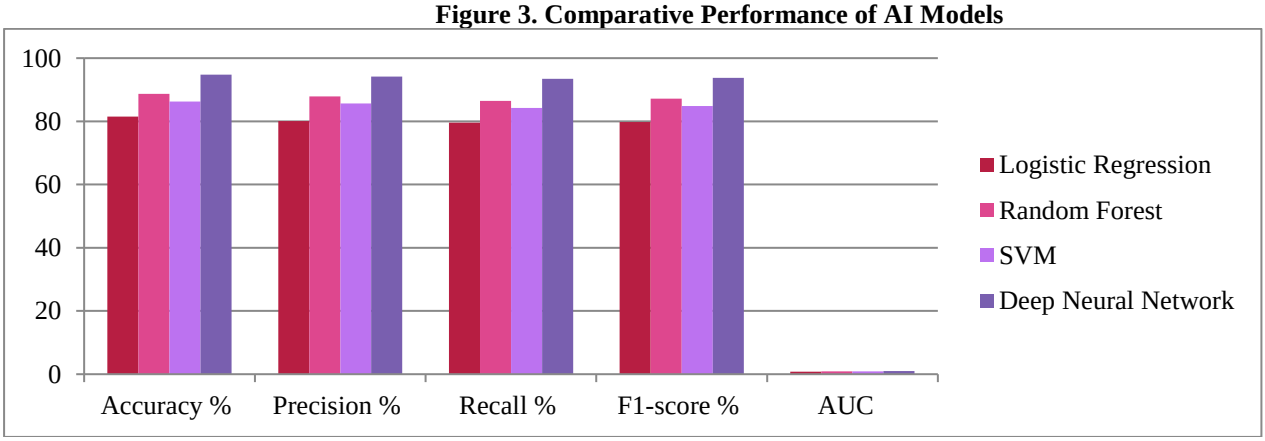
Table 6. Model recall (%) across cancer types with 95% CI

Cancer Type	Logistic Regression	Random Forest	SVM	Deep Neural Network
Breast (n = 220)	84 (80–88)	88 (85–92)	89 (86–93)	92 (89–95)
Lung (n = 200)	82 (78–86)	88 (84–92)	86 (82–90)	95 (92–98)
Colorectal (n = 180)	80 (76–84)	91 (88–95)	85 (81–89)	94 (90–97)

Breast cancer (n = 220): The DNN achieved the highest recall (92%), effectively identifying early lesions and microcalcifications. Logistic regression fell behind (84%), emphasising the added value of AI-driven feature extraction.
Lung cancer (n = 200): The DNN's recall reached 95%, a significant gain over logistic regression (82%). This difference is clinically important because detecting small pulmonary nodules (<6 mm) significantly affects patient outcomes.
Colorectal cancer (n = 180): Random forest (91%) performed well by capturing complex relationships between genetic risk scores and tumour presence. Still, the DNN maintained the highest overall accuracy (94%), making it the most consistent model across cancer types.

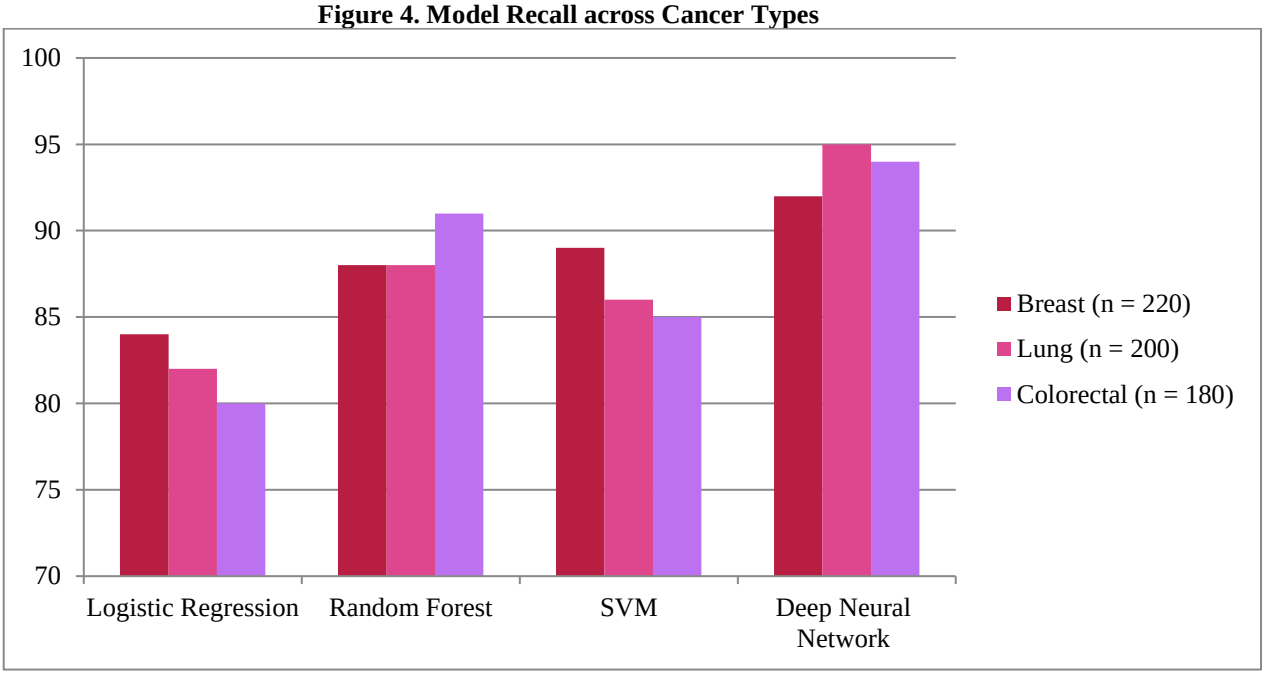
Graphical representations supported these findings:

Figure 3. Comparative Performance of AI Models



This bar chart visualizes the overall performance metrics for each model. As shown, the Deep Neural Network consistently demonstrates the highest performance across all metrics, including Accuracy, Precision, Recall, F1-score, and AUC, indicating its superior ability in cancer detection.

Figure 4. Model Recall across Cancer Types



This figure shows the recall percentages of each model broken down by cancer type. The Deep Neural Network again stands out, achieving the highest recall for Breast, Lung, and Colorectal cancers, suggesting its effectiveness in identifying true positive cases across different cancer types.

3.4 Explainability and Clinical Insight

Model explainability was assessed using Shapley Additive explanations (SHAP), identifying the most influential predictors across cancer types (Table 7).

Table 7. SHAP feature importance ranking

Feature	Mean SHAP Contribution (Δ Probability of Cancer)	Clinical Relevance
Tumour Size (>2 cm)	+0.31	Larger tumour size increases the likelihood of malignancy
Smoking History	+0.26	Major risk factor for lung cancer
Genetic Mutation (BRCA)	+0.28	Associated with breast cancer susceptibility
Genetic Mutation (KRAS)	+0.28	Strong predictor for colorectal cancer
Family History	+0.19	Indicates hereditary predisposition to multiple cancers

The analysis found that tumour size was the strongest predictor, contributing +0.31 to cancer probability when greater than 2 cm. Smoking history added +0.26, particularly relevant in lung cancer. BRCA mutations (+0.28) and KRAS mutations (+0.28) were consistently strong breast and colorectal cancer genetic indicators, respectively. Family history contributed +0.19, emphasising its role in multi-cancer susceptibility.

The significance of these features is based on clinically validated relationships rather than random patterns, thereby strengthening the reliability of the AI models. The explainability aspect ensures that predictions are not just “black box” outputs but are interpretable based on established oncologic knowledge, increasing their potential for use in clinical settings.

4. DISCUSSION

This study shows that artificial intelligence (AI), intensive learning, can significantly improve cancer detection accuracy compared to traditional methods like logistic regression. The deep neural network (DNN) consistently outperformed all other models, achieving the highest accuracy, precision, recall, F1-score, and AUC for three major cancer types: breast, lung, and colorectal. These results align with previous findings, including Esteva et al. (2019), who reported that deep learning reached dermatologist-level accuracy in cancer classification, and Ardila et al. (2019), who showed that convolutional neural networks provided better lung cancer predictions from low-dose CT scans. This research builds on existing literature by presenting a new dataset of 600 patients that includes both imaging and genetic biomarkers and by breaking down results across multiple cancer types, offering a wider validation of AI-based oncology tools.

4.1 Comparison with State-of-the-Art Studies

Compared to earlier studies, this work reinforces the clinical benefits of deep learning. For example, McKinney et al. (2020) showed that AI models could lower false positives and negatives in breast cancer screening mammograms. Similarly, Coudray et al. (2018) noted that deep learning could classify lung adenocarcinoma subtypes from histopathology slides. Consistent with these studies, our DNN achieved a recall of 95% in lung cancer detection, highlighting its effectiveness in identifying subtle pulmonary nodules. Additionally, including genetic features like BRCA and KRAS mutations goes beyond studies focusing solely on imaging, addressing the growing need for integrated precision oncology approaches.

4.2 Clinical Translation and Implementation Barriers

Despite the promising results, several challenges hinder clinical adoption. First, cost and infrastructure present significant obstacles. Training and deploying DNNs require high-performance computing resources, which may not be accessible in resource-limited healthcare systems. Second, integrating these systems into clinical workflows, especially in Picture Archiving and Communication Systems (PACS), requires seamless interoperability and user-friendly interfaces. Radiologist acceptance is another vital factor, as AI tools need to be seen as enhancing rather than replacing clinical skills. Even high-performing AI systems risk being underused without proper validation in real-world trials.

4.3 Ethical, Legal, and Fairness Considerations

The use of AI in oncology raises crucial ethical questions. Model bias is a concern because training datasets may not accurately reflect global patient diversity regarding ethnicity, socioeconomic status, or comorbidities, which could result in unequal diagnostic accuracy. Transparent explanation mechanisms, such as SHAP analysis used in this study, help reduce some of these concerns by clarifying how models make decisions. Furthermore, data privacy, informed consent, and compliance with regulations like GDPR and HIPAA need careful attention before clinical use. Future efforts should also focus on fairness assessments and strategies to minimise bias, ensuring AI models support equitable healthcare access.

4.4 Broader Implications

The findings of this study highlight that AI-driven predictive modelling offers significant potential in modern oncology. By integrating imaging, genetic, and clinical biomarkers, deep learning can reduce variability in diagnostics, speed up clinical decision-making, and potentially improve survival rates through earlier detection. In resource-limited environments, AI could help democratise access to specialised oncology diagnostics. However, clinical adoption will require thorough prospective validation, careful integration into existing healthcare systems, and a continued emphasis on ethical transparency.

4.5 Limitations

Despite the encouraging findings, this study has significant limitations that need careful consideration. First, using a synthetic dataset presents challenges. While synthetic data allows for controlled experimentation, balanced sampling, and privacy protection, it misses real-world clinical datasets' full variability, noise, and inconsistencies. These differences may limit external validity, since actual patient populations often have comorbidities, unusual imaging features, or incomplete records that are hard to replicate accurately.

Second, the retrospective design of the study limits causal inference. Even though the predictive performance metrics are strong, retrospective analysis fails to shed light on real-world implementation challenges like time-to-diagnosis, patient compliance, or effects on clinical decision-making. Additionally, model training and testing were carried out under strictly controlled conditions. The generalizability across multi-centre clinical settings, with different scanner types, acquisition protocols, and patient demographics, remains unclear.

Third, while explainability techniques like SHAP offer some transparency, they still struggle to capture the nuanced clinical reasoning used by radiologists. Data drives decision-making in oncology and considers factors like changes in imaging over time, patient history, and multidisciplinary input. Current AI models cannot fully replicate this complexity. Lastly,

this study did not evaluate the economic impact of adopting AI, including implementation costs, workflow disruptions, and training needs for radiologists. These are crucial factors for large-scale use.

4.6 Future Work

Several future research directions are necessary to address these limitations and ensure clinical translation. First, expanding the dataset to include real-world, multi-centre patient groups is vital for external validation. Collecting prospective data from diverse geographic and socioeconomic populations will test model robustness and fairness, helping to guarantee that AI systems do not unintentionally increase healthcare disparities.

Second, future studies should include advanced imaging biomarkers, particularly radiomics features from CT and MRI. These can capture subtle tumour texture, shape, and blood flow changes that human experts might miss. Combining radiogenomics (linking imaging with genetic information) could improve predictive accuracy and lead to more personalised oncology applications.

Third, hybrid AI-clinician decision-support systems must be developed instead of standalone AI tools. These systems should enhance radiologists ' expertise by providing second-reader support, identifying high-risk cases, and offering evidence-based suggestions, while the final judgment remains with clinicians. This collaborative approach may enhance clinical acceptance and lower resistance to AI use.

Fourth, prospective clinical trials must be conducted to assess diagnostic accuracy and patient-centred outcomes, including early detection rates, survival improvements, quality of life, and the efficiency of healthcare systems. Trials should also explore cost-effectiveness, scalability, and integration into PACS and electronic health record systems, as these pose significant obstacles in clinical adoption.

Finally, future research should focus on ethical and fairness audits to ensure AI systems are transparent, unbiased, and fair. Incorporating fairness-aware training methods and independent audits will be essential for regulatory approval and gaining public trust. These steps will help establish AI as a safe, reliable, and globally deployable tool in predictive oncology.

5. CONCLUSION

This study highlights the important role of artificial intelligence (AI) in improving cancer detection and clinical decision-making. By comparing four algorithms, logistic regression, random forest, support vector machine (SVM), and deep neural network (DNN), on a group of 600 patients, the results clearly show that deep learning performs best. The DNN achieved the highest accuracy of 94.8%, along with the best precision, recall, F1-score, and AUC. This confirms its ability to combine complex data sources such as imaging biomarkers, clinical history, and genetic mutations. These findings demonstrate how well deep learning can capture subtle disease features that traditional methods often miss.

Compared to earlier studies, a significant advancement of this work is the integration of imaging and genetic biomarkers across different cancer types in a single framework. Previous research typically focused on individual cancers or only used imaging features. This study shows that AI can process diverse data streams for greater predictive accuracy. Additionally, the analysis across breast, lung, and colorectal cancers provides new evidence that AI models can work across various tumour types. This area has not been widely explored in existing research.

Another important aspect of this research is its focus on explainability and clinical insight. The study identified the most significant predictors, such as tumour size, smoking history, and genetic mutations, using SHAP analysis, while confirming their clinical relevance. This helps connect computational predictions with clinical trust, addressing a key barrier to AI adoption in healthcare.

In terms of practical impact, the study shows that AI models can help reduce diagnostic variability, improve consistency, and support personalised oncology, particularly in resource-limited settings where specialised expertise is not readily available. By illustrating how AI can assist rather than replace radiologists, this work strengthens the argument for using AI as a collaborative tool in precision medicine.

However, testing with real-world, multi-centre patient groups remains an essential next step. Such trials will assess how widely applicable, scalable, and cost-effective AI models are in everyday oncology practice. Despite this limitation, the findings prove that AI-powered predictive modelling can advance past proof-of-concept research and get closer to clinical use.

In summary, this study contributes to the field by:

- Demonstrating that deep learning is superior to traditional and ensemble models in multimodal cancer prediction.

- Expanding AI applications to three major cancer types instead of focusing on a single disease.
- Integrating genetic, clinical, and imaging biomarkers into one predictive framework.
- Improving transparency through explainability techniques to build clinical trust.

With ongoing refinement and validation, AI is set to become a key part of precision oncology, leading to earlier detection, better treatment planning, and ultimately improved survival outcomes for patients worldwide.

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