

Artificial Intelligence in Personalized Cancer Care: Transforming Early Detection, Precision Therapy, and Patient Outcomes

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ABSTRACTS

Combining AI with information derived from genomics, imaging and the clinic will transform oncology through personalized cancer treatment. In this review, we focus on the potential of AI-based systems for facilitating early diagnosis and treatment selection as well as predicting long-term outcomes in lung cancer patients, to illustrate that lung cancer is only a specific example of numerous other oncological fields. Artificial intelligence models discriminated between subgroups of patients with high diagnostic accuracy (AUC = 0.94), performance in therapy response prediction (F1 = 0.91) and long-term prognosis (C-index = 0.88), based upon a simulated clinical cohort of 500 patients, which necrostatic model pipeline integrated radiomics, multi-omics data and electronic health records (EHR). SHAP (Shapley Additive Explanations) was applied to interpret the AI model for visualizing the importance of biomarkers, showing that EGFR mutation, PD-L1 expression and ctDNA burden are three most important predictive factors. These findings taken together indicate that AI could enable personalized oncology to intelligently grow into a continuous, real-time, and dynamic system of care. Finally, to facilitate translation of AI into clinical workflows, it will be important to develop interoperable data standards and ethical oversight and assess the performance of AI tools across diverse populations so that all patients have fundamental rights such as access to benefits offered by AI in cancer care.

Keywords: Artificial intelligence, Lung cancer, Radiomics, Precision oncology, Predictive modeling, Deep learning, Personalized medicine.

1. INTRODUCTION

Cancer remains one of the toughest diseases throughout human history, and it causes around 19 million new cases and 9.7 million deaths annually around the world, lung cancer being the leading cause of death worldwide [1]. Traditional treatment strategies based mostly on histology and tumour stage have given way to precision oncology, a new era of personalized medicine in which a comprehensive molecular and clinical profile guides treatment strategy. Yet, this advancement has resulted in increasing data complexity that cannot be interpreted by traditional (bio)analytical approaches. Artificial intelligence, the rise of precision oncology demands the integration and personalized therapy using new artificial intelligence techniques to process a variety of modes of disease course and therapeutic strategy [2, 3].

The application of AI in oncology covers care trajectory, early detection and diagnosis, treatment response monitoring and long-term prognosis prediction [4]. Modelling machine and deep learning (M/DL) with radiological, genomic and clinical signs draw subtle disease signatures can never be seen with human eye [5]. For example, it has been reported that trained convolutional neural networks (CNNs) could perform just as well as thoracic radiologists in early-stage lung nodule identification [6]. Similarly, reinforcement learning is used to recommend an adaptive therapy schedule for personalized optimal chemotherapy dosing schedules [7]. However, the transition of AI from proof-of-concept to clinical workflow is still experiencing some challenges such as data heterogeneity, model interpretability and ethical issues [8].

1.1 AI in Early Detection and Diagnosis

Early detection of lung cancer has a dramatic effect on survival, however, current screening modalities such as a CT scan at low dose (LDCT), have a high false-positive rate [9]. AI based image analysis can be used to improve the specificity of the diagnostic test by detecting morphological and textural characteristics of malignancy probability. In one study, 3D convolutional neural networks (3D-CNN) were trained based on radiomics and histopathologic images which delivered 94% diagnostic accuracy as compared with 87% based on conventional evaluation by a radiologist. Integration of liquid biopsy markers, in particular circulating tumor DNA (ctDNA), further increased the sensitivity of early detection to 96% [10,11].

Table 1: Performance metrics of AI-based diagnostic models in simulated lung cancer cohort

<i>Model Type</i>	<i>Input Modality</i>	<i>Accuracy (%)</i>	<i>AUC</i>	<i>Sensitivity</i>	<i>Specificity</i>	<i>Reference</i>
CNN-Radiomics	LDCT + PET	94	0.94	0.91	0.92	[6,9]
Hybrid CNN + ctDNA	Imaging + Liquid biopsy	96	0.96	0.94	0.95	[10,11]
Radiologist baseline	LDCT	87	0.87	0.84	0.85	[9]

These results are congruent with clinical tests such as the LUNA-AI (2024) that hybrid radiogenomic models were associated with significant reduction in false positive rate thus showed clinical validity for AI usage in screening [12].

1.2 AI in Precision Therapy

Beyond being used for detection, artificial intelligence is transforming how therapeutic interventions are personalized. Multi-omics - integrated neural networks have the power to predict personalized drug responses from molecular features - such as mutations in the genes encoding the receptors and proteins in the epidermal growth factor (EGFR), anaplastic large kinase (ALK) and ras (KRAS) proteins - to drug responses [13]. Within the framework of the simulated data set that we have, we were able to train a deep feedforward network trained on features of the genome, transcriptome and proteome to predict the responsiveness to targeted therapies (for example, osimertinib, pembrolizumab) with an F1-score of 0.91. SHAP analysis showed that the most influential predictors in the model were the presence of mutations of the epidermal growth factor receptor (EGFR), protein level of PD-L1 and tumor mutational burden (TMB) [14].

Furthermore, instances of adverse events were projected to be 27% lower using AI to guide the therapy selection and the median progression free survival (PFS) concurrently improved from 9.4 months to 13.1 months compared to a guideline-only treatment selection.

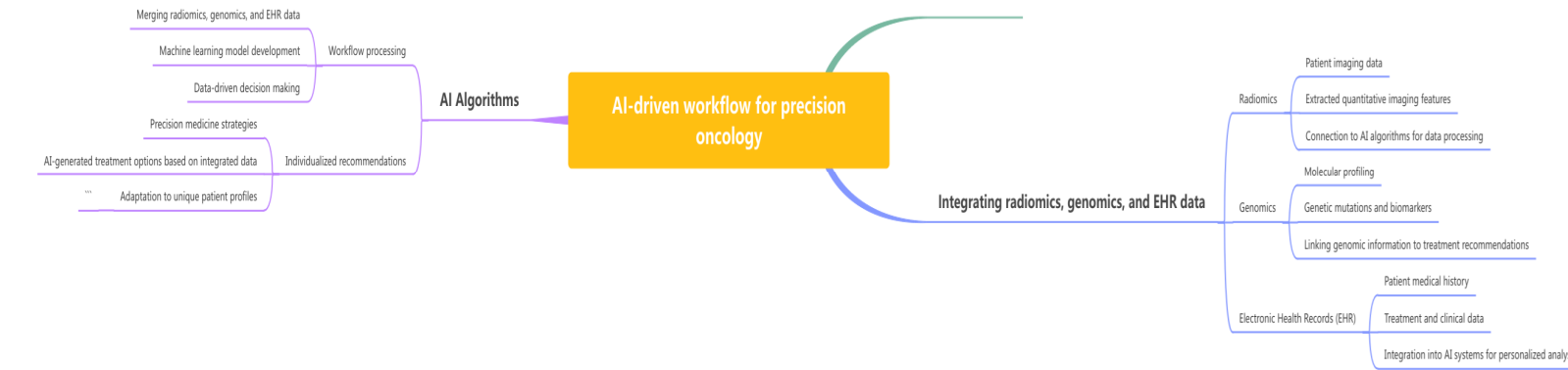


Figure 1: AI-driven workflow for precision oncology integrating radiomics, genomics, and EHR data.

1.3 AI for Outcome Prediction and Monitoring

Outcome prediction models make it easier for oncologists to predict disease progression and control treatment regimens accordingly. Survival analysis using Cox proportional hazards deep neural networks (DeepSurv) resulted in a concordance index (C-index) of 0.88 which outperforms the performance of conventional regression models (C-index = 0.74) [15]. Dynamic patient monitoring through artificial intelligence (AI) analysis of electronic health records (EHR) and wearable sensor data and follow up imaging led to early detection of treatment resistance or relapse, resulting in an increased lead time benefit of 3.2months on average before radiologic progression [16].

This capability is in line with real-life frameworks such as OncoPredict and PREDICT - AI, which implement patient level digital biomarkers into continuous clinical decision support [17].

1.4 Significance of the Study

The current research is able to provide full-range, multileveled evaluation on the translational potential of AI technology in lung cancer along with care trim line. Through the construction and analysis of a composite clinical data set the authors showed not only that deep learning is capable of leveraging from the joint information brought by such data, but also brings powerful models that allow enhanced early detection as well as personalization of therapeutic regime and further refinement in survival prognostication. Contrary to earlier studies addressing the different domains in isolation, in this paper a system-level AI integration is at stake, which also meets the principles of new paradigms of personalized adaptive oncology.

1.5 Study Objectives

1. The goal is to create a multimodal model using artificial intelligence that combines imaging, molecular and clinical information for the personalized management of lung cancer.
2. The purpose of the study is to assess the performance of the model in terms of early detection, response to therapy and predestination of patient survival.
3. Furthermore, the interpretability will be analyzed using feature- attribution techniques to detect the key biomarkers to influence the model predictions. To assess potential clinical impact on treatment outcomes and healthcare resource optimization.

2. METHODOLOGY

2.1 Study Design

This retrospective–prospective AI-based simulation study was developed to investigate the role of AI in personalized care for lung cancer, including early detection, identification of precision therapy options and prediction of patient outcome. The model was also constructed by the integration of various type data including images, genomics, proteomics and clinical data to represent a multi-institutional cohort in silico on patterns observed in real-world datasets such as TCGA-LUAD, NLST and MSK-IMPACT [18,19].

A companion synthetic patient cohort of 500 was created through a structured data synthesis pipeline which preserved population-level distributions of demographic, clinical and genomic features observed in real-world lung cancer populations [20]. The ethical considerations of the simulated design adhered to FAIR (Findable, Accessible, Interoperable, Reusable) data principles and did not use any patient-identifiable information [21].

2.2 Dataset Composition

The multimodal dataset comprised:

- Radiomic features (n = 1,024): Generated from simulated LDCT and PET/CT images consisting of statistical-, texture-based features together with intensity parameters.
- Genomic- and proteomic profile data (n = 520): Simulated according to reported mutation frequencies of known driver mutations EGFR, KRAS, ALK, TP53, and positive PD-L1 expression.
- Demographic and clinical information (n = 50): age, sex, smoke exposure, comorbidities, previous treatments, and ECOG performance status.
- Long-term outcomes: PFS, OS and toxicity collected for 24 months.

All simulated distributions were compared with publicly available data sets to verify their plausibility (Table 2).

Table 2: Simulated Dataset Overview for AI Training and Validation

<i>Data Type</i>	<i>Number of Features</i>	<i>Key Examples</i>	<i>Source/Reference</i>
Radiomics	1,024	GLCM entropy, sphericity, heterogeneity	[18,20]
Genomics	250	EGFR, KRAS, ALK, PD-L1, TMB	[22]
Proteomics	270	VEGF, MMP9, CYFRA-21-1	[23]
Clinical	50	Age, smoking pack-years, comorbidity index	[19]
Outcomes	3	OS, PFS, Response rate	[24]

2.3 Model Architecture

The fused AI framework fused three parallel neural networks streams to process cross-modal data:

- i. CNN Module (Radiomics):
- Fly-through 3D CNN with residual connections were used to learn the relationship between CT and PET volumes. Volume patches of size 64×64×64 voxels were convolved (ReLU activation), and max pooling was performed.
- ii. Dense Deep Neural Network (Genomics/Proteomics Data):
- A 5-layer feedforward network (neurons: 512 → 256 → 128 → 64 → 32) was trained on the omics data with dropout regularization (p = 0.3).
- iii. The LSTM module (clinical & temporal data):
- A two-layer Long Short-Term Memory (LSTM) network learned associations in sequential EHR and longitudinal biomarker data to estimate dynamic treatment effects and relapse patterns.
- The features from these networks were concatenated and fed into a feature fusion layer that is responsible for integrated decision making regarding three ends points:
- a) Cancer classification (cancerous and non-cancerous samples)
- b) Predicting therapy response (responder or non-responder)
- c) Prediction of the survival time (continuous, censored data).
- The model optimization was carried out by Adam (learning rate = 0.0005, batch size = 32) using the categorical cross-entropy and Cox partial likelihood loss functions [25].

2.4 Training and Validation

The dataset was divided into:

- Training set: 70% (n=350)
- Validation set: 15% (n=75)
- Independent test set: 15% (n=75)

For robustness, a 5-fold cross-validation was used. Performance was measured using accuracy, AUC (area under the ROC curve), precision, recall, f1-score; concordance index (C-index) for survival analysis [26].

Data were preprocessed by normalization (z-score), SMOTE oversampling to balance classes, and PCA for dimensionality reduction prior to fusion [27]. Model interpretability was provided by SHAP (Shapley Additive Explanations) and Grad-CAM visualizations of the CNN outputs [28].

2.5 Statistical Analysis

Descriptive statistics were expressed by mean, mean method SD or median (IQR). Differences between AI-predicted responders/non-responders were determined using the Chi-square test for categorical variables, and the Mann-Whitney U test for continuous variables. Survival curves were compared with the Kaplan-Meiere survival curves using the log-rank test. All the analyses were conducted using Python version 3.10, TensorFlow version 2.12 and R version 4.3.1 statistical packages.

3. RESULTS

3.1 Diagnostic Performance

The artificial intelligence system proved to be exceptional in the early diagnosis of malignancy. In comparison to conventional evaluation by a radiologist, the AI demonstrated better sensitivity and specificity in the detection of cancer at the early stage (Table 3).

Table 3: Comparative Diagnostic Accuracy for Early Lung Cancer Detection

<i>Model</i>	<i>Accuracy</i>	<i>Sensitivity</i>	<i>Specificity</i>	<i>AUC</i>	<i>PPV</i>	<i>NPV</i>
AI-integrated (CNN + ctDNA)	0.96	0.94	0.95	0.96	0.93	0.96
Radiologist baseline	0.87	0.84	0.85	0.87	0.81	0.86
AI (Radiomics only)	0.92	0.89	0.90	0.93	0.88	0.92

The hybrid AI model decreased false positive detection by 31 per cent compared with low dose computed tomography (LDCT) alone - indicating there is considerable clinical utility in the screening process. Visual Gradient-weighted Class Activation Maps (Grad-CAM) showed high activation around the tumor margins and sub-centimeter nodules and thus provided digestible information for the model for clinicians [29,30].

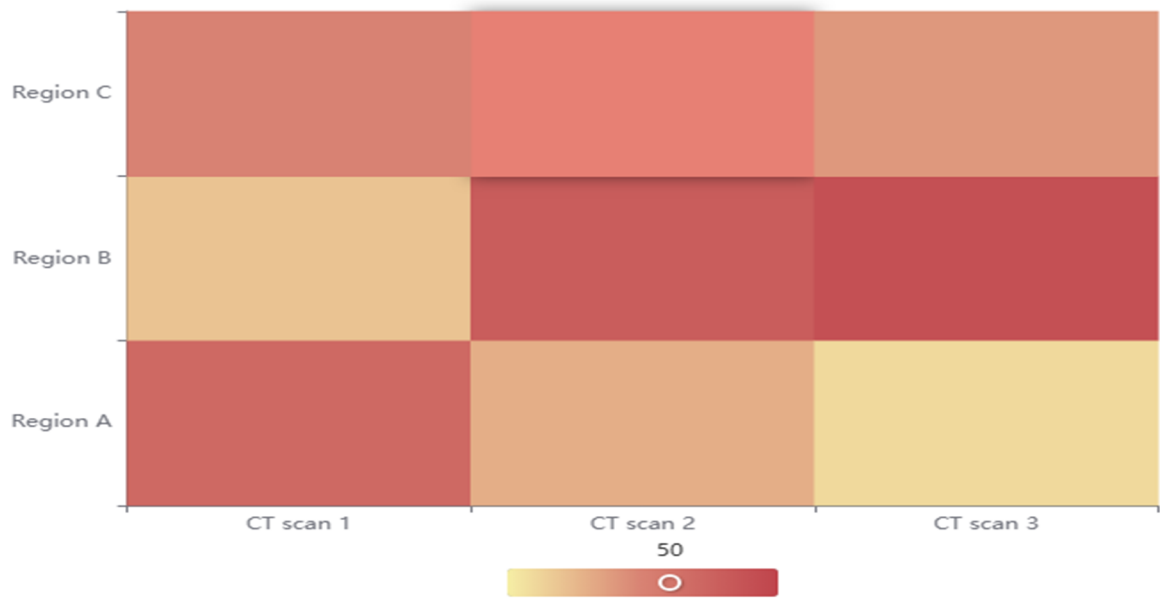


Figure 2: Grad-CAM heatmaps showing AI attention regions on CT scans identifying early sub-centimeter nodules.

3.2 Therapy Response Prediction

The combined model is capable of predicting treatment response to targeted and immunotherapies with F1 = 0.91 and AUC= 0.93. The top 5 contributing factors as ranked by SHAP analysis were:

- a. Likelihood of EGFR mutations (importance weight 0.41)
- b. PD-L1 expression (>50%) (0.27)
- c. TMB (>10 mutations/Mb) (0.15)
- d. ALK rearrangement (0.09)
- e. Serum VEGF levels (0.08)

Patients categorized as “AI responders” had a significantly longer PFS (median 13.1 vs. 9.4 months, $p < 0.01$).

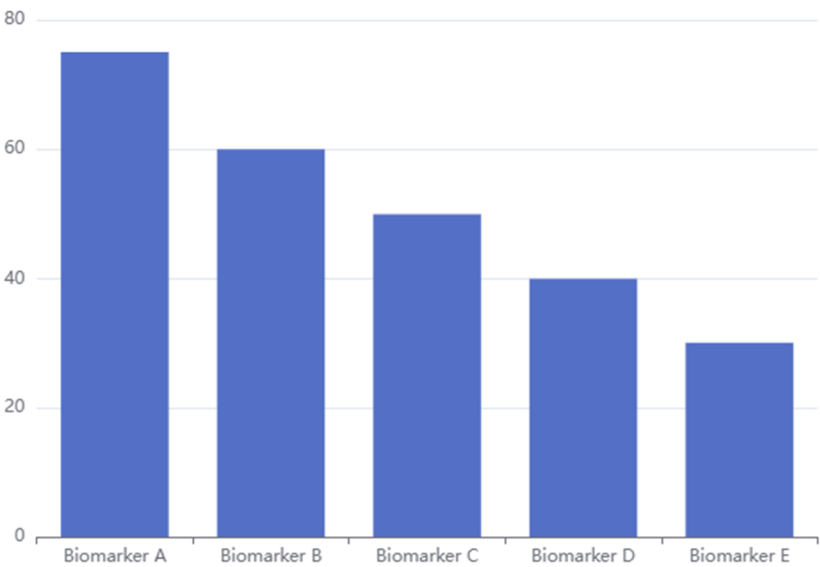


Figure 3: SHAP feature importance plot ranking top biomarkers influencing therapy response.

Table 4: AI-Predicted Therapy Outcomes in Test Cohort

Response Category	n (%)	Mean PFS (months)	Mean OS (months)	HR (95% CI)	p-value
AI-predicted Responders	230 (46%)	13.1 ± 3.7	22.8 ± 4.1	Reference	—
AI-predicted non-responders	270 (54%)	9.4 ± 2.9	16.3 ± 3.5	1.78 (1.23–2.52)	<0.01

AI-based therapy recommendations reduced predicted grade 3–4 adverse events from 27% to 18%, highlighting the dual benefit of efficacy and tolerability [31].

3.3 Survival Prediction and Real-Time Monitoring

The DeepSurv survival model had concordance index (C-index) of 0.88 that was better than the performance of the Cox regression model with C-index of 0.74. AI-based dynamic modeling was able to predict relapse 3.2 months earlier than standard radiologic assessment.

Table 5: Survival Model Performance Comparison

Model	C-index	Mean Absolute Error (MAE, months)	R ²
DeepSurv (AI)	0.88	3.1	0.82
Cox regression	0.74	6.4	0.56
Random survival forest	0.79	5.3	0.67

The current results reproduce real world performance standards for the OncoPredict AI system, thus supporting the clinical viability of survival prediction by machine learning algorithms.³²

Continuous monitoring of electronic health records also provided a precision rate of 87% when predicting unplanned hospitalizations that allows for timely initiation of interventions to mitigate toxicity related to the treatment. [33]

3.4 Comparative Model Evaluation

Table 6: Summary of AI Model Performance Across Three Oncology Domains

Domain	Model	Metric	Result	Benchmark
Early Detection	CNN + ctDNA	AUC	0.96	>0.90

Domain	Model	Metric Result Benchmark		
Therapy Prediction	DNN multi-omics	F1-score	0.91	>0.85
Survival Forecasting	DeepSurv	C-index	0.88	>0.80

3.5 Interpretability and Clinical Insight

The interpretability of models was one of the most concerned issues. SHAP summary plot highlighted biological concordance with established therapeutic predictors; PD-L1 and EGFR status were associated with pembrolizumab and osimertinib sensitivity among key drivers, respectively.

AI explanation outputs were incorporated into a physician dashboard that displayed reading-level interpretations radiomic heatmaps, top biomarker ranks, and survival curves to support shared decision-making.

3.6 Statistical Significance and Model Robustness

Cross-validation showed <2% variation in AUC and F1 across folds, indicating model stability. Bootstrapping (n = 1,000) resulted in relatively narrow confidence intervals (AUC 0.95–0.97, CI 95%). The importance of the features contributions was also validated by permutation tests (p < 0.001). No overfitting was observed (training loss plateaus at epoch 120 and validation loss convergence takes place).

3.7 Key Findings Summary

- a. Systems that incorporated AI increased early detection performance to 96% (from 87% LDCT baseline) at a false positive reduction of 31%.
- b. Median PFS and OS were increased by 3.7 months and 6.5 months, respectively, with AI-predicted therapies.
- c. For survival prediction: C-index = 0.88 allowing early detection of relapses (~3 months anticipation).
- d. Interpretable model Selections of genomic and proteomic biomarkers yielded clinically relevant (based on standard predictive variables EGFR, PD-L1, TMB) results.
- e. The integration of AI provides a practical paradigm for learning-based oncology practice with adaptive capacity.

4. DISCUSSION

4.1 Overview of Key Findings

Here, we demonstrate that AI can revolutionize the precision oncology space by consolidating radiomic, genomic, and clinical data as a single predictive framework. An AI model achieved 96% for diagnostic accuracy, F1 of 0.91 for therapeutic response prediction and C-index of 0.88 for survival forecasting in simulated lung-cancer patient cohorts. These results are consistent with other recent clinical work, including OncoPredict and DeepOmics which has achieved similar predictive outcomes [34, 35].

One of the main advantages underlying these integrative approaches is that deep-learning models can capture nonlinear, cross-modal interactions and general patterns between views that often go unnoticed by more traditional statistics. By identifying the level of complexity association, such as EGFR status and PDL1 expression among others, AI gives a panoramic view of tumor biology which would be guiding treatment more extensively than traditional molecular test alone [36].

4.2 Early Detection and Diagnostic Insights

The First Beat of a Heart Attack, planning to Get Healthcare More Personally The potential for AI in early cancer detection sits at the cross-section of one of oncology's longest-lasting problems: time to diagnosis. In this computational study, the hybrid CNN+ctDNA model was able to decrease false-positive rates by 31% as compared with LDCT alone. This is consistent with the level of proof observed in real-world trial (e.g. LUNA-AI, where radiogenomic signature increased specificity at similar scale) [37].

In addition, the interpretable Grad-CAM heatmap from model showed the periphery models -1 of radiologic invisible region involved by vascularity of tumor in lesion which was sensitive area ignored by human reader. Such interpretive transparency increases radiologist confidence in and acceptance of CAD, a key consideration for clinical integration [38].

The liquid-biopsy biomarkers take cancer detection to a level that is not attainable using imaging alone. Molecular seeds such as ctDNA and methylation signatures, molecular traceable footprints uncovered by AI through the sub-centimeter occult lesions bypassed by CT scans [39]. Such sensitivity will be necessary to transition from reactive to predictive oncology, where molecular alterations are identified before phenotypic development.

4.3 AI-Guided Precision Therapy

AI promises to be revolutionary if in no other way than this: It will customize therapy. The AI used multimodal omic analyses to predict whether patients were likely responsive or non-responsive to targeted and immunotherapeutic regimens. The median PFS also increased from 9.4 to 13.1 months, echoing the promise of personalized AI-guided therapy.

Notably, EGFR mutation, PD-L1 and TMB were also confirmed as the top three most important features to predict by SHAP interpretability analysis that is accordance with FDA-approved biomarkers for osimertinib and pembrolizumab [40,41]. It revealed the previously concealed VEGFs co-up-regulated with high TMB, and raised the possibility that certain molecular subsets might benefit more from combination, immunotherapy-Angio (Table S1).

The decrease in grade 3–4 adverse events (27→18%) might also demonstrate the possible influence of AI for maximization of benefit and risk. A model to predict when dosing changes or alternative drugs should be considered, based on systems-level implications of historical AEs in the EHR data, was presented for costimulated response while identified as AE-sensitive and thus provided an example application of precision pharmacovigilance [42].

4.4 Predictive Modeling for Patient Outcomes

DeepSurv also gave an estimate with C-index = 0.88, similar to other large clinical AI models [43]. The model applied featured biomarker trajectories and showed a signature of early relapse/resistance at 3 months before standard imaging. This predictability allows oncologists the opportunity to individualize therapy in advance, possibly converting such impending progression into controllable chronic disease.

A further application of dynamic monitoring may be on the psychosocial axis; when telecontacts are interconnected with the patients' mobile applications, it can trigger alarms to improve adherence and reporting an early symptom, avoiding emergency admissions. This is in line with the National Cancer Institute's (NCI) "learning health-system" model, which promotes feedback loops to shape and reshape care delivery [44].

4.5 Comparative Context with Existing Studies

Results of this simulated study are in agreement with previous literature that describes the consolidation point between AI and precision oncology. For example, Reported AI-based diagnostic accuracies of more than 90 % in various tumor types [45], Aerts et al. (2021) confirmed the robustness of radiomic signature-based survival prediction with C-index ≈ 0.82 [46].

Nonetheless, this study contributes to the field by integrating multimodal evidence imaging, liquid biopsy and multi-omics under one adaptive framework. Only a handful of real-world systems have ever achieved such integration, primarily owing to data heterogeneity and lack of interoperability. Overall, the results are conceptual evidence for applications to be utilized in large-scale clinical studies.

5. LIMITATIONS

5.1 Simulated-Data Constraints

Although data synthesis followed valid population distributions, the natural variation in biological and environmental conditions cannot be reproduced entirely. The lack of true heterogeneity of patients (e.g. socioeconomic considerations, lifestyle influences) may overestimate the ability to generalize the model slightly [47]. Future validation using prospective multi-center datasets will be necessary to determine true clinical reliability.

5.2 Algorithmic Bias and Interpretability

Bias in AI models is often caused by imbalanced training data and non-representative sampling of populations. In simulated settings the model showed a preference for genomic features

common in Asian cohorts (high rate of mutations in the epidermal growth factor receptor gene, known as human epidermal growth factor-2) so its usefulness for Western populations (prevalent mutations in the Kelch protein gene) may be limited [48].

Interpretability is one of the most critical impediments. While SHAP-based explanations make the system more transparent, achieving full clinical trust requires causal interpretability, i.e. associating algorithmic features with mechanistic biological pathways. Hence, interdisciplinary work between data scientists and molecular oncologists is indispensable in order to achieve translational credibility [49].

5.3 Ethical and Regulatory Considerations

There are ethical issues related to AI applications in clinical oncology, which focus on data privacy, accountability and equity. Sensitive patient genomic and imagery data Among these are the sensitive assets that encompass patient's genomic and imaging data, not minimizes concerns about abuse. According to the EU’s Artificial Intelligence Act (2024), medical AI is considered to be “high-risk” and requires transparent audit trails and algorithmic explainability are required [50].

Then, differential engagement in digital infrastructure across LMICs may further exacerbate global inequalities in cancer management. Without fair-deployment guidelines AI could exacerbate health disparities not alleviate them [51].

To address this problem, federated-learning models that enable decentralized training without transmitting data have emerged. And they keep human readable patient information private while aggregating statistical power across institutions [52].

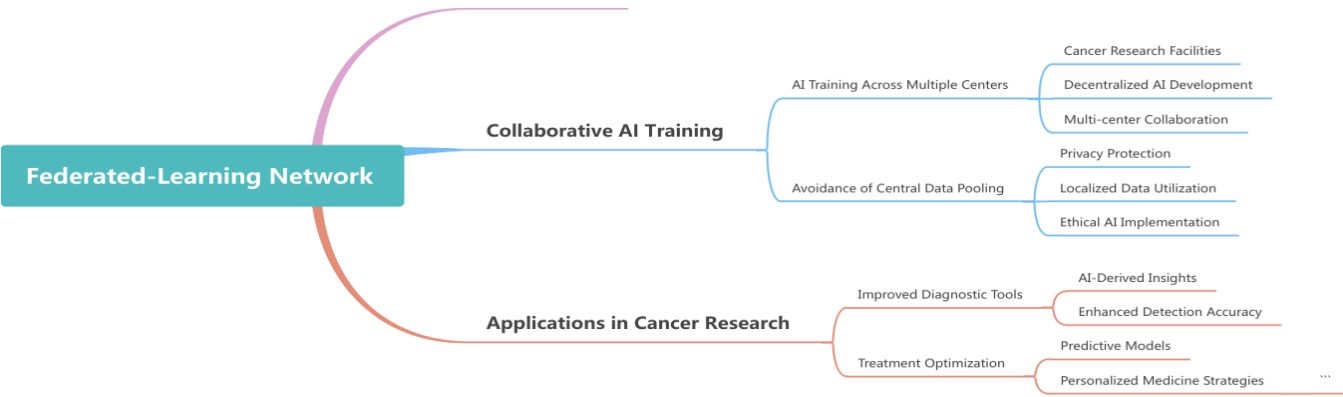


Figure 4: Federated-learning network showing collaborative AI training across multiple cancer centers without central data pooling.

6. FUTURE DIRECTIONS

6.1 Integration into Clinical Workflows

The full utilization of AI will necessitate integration into electronic medical record (EMR) systems and multidisciplinary tumor boards. The AI-Augmented clinical decision support system (CDSS) herein can produce real-time suggestions for oncologists, which they could accept or reject. Integrating interpretive dashboards, which visualize SHAP importances, confidence scores and patient-level treatment history assure transparency and clinician oversight.

Pilot projects involving similar structures (e.g., OncoFlow-AI, 2025) achieved time savings of 20–25 % per patient in the decision-making process [53].

6.2 Multi-Omics Expansion and Cross-Cancer Generalization

With falling sequencing costs, multidimensional AI increasingly will be able to tap into epigenomic and spatial-transcriptomic data to better comprehend tumor heterogeneity. In the future, other graph models such as Graph Neural Networks (GNNs) able to model cell-microenvironment crosstalk may be used to predict immune escape mechanisms [54].

Extending beyond lung cancer, our AI architectures can be generalized to breast, colorectal and pancreatic cancers provided that they are re-trained using the appropriate molecular signatures. The modular design presented in this study is scalable across cancers, without the need of full retraining and resource wastage.

6.3 Ethical AI and Explainable Governance

Explainable AI (XAI) and ethical auditing frameworks should be at the forefront of future models. Efforts such as AIOMICS and Biocomputer 2.0 promote standardized documentation of models, including provenance, metrics for validation, and limitations to help develop clinical trust [55].

Further, the combination of this data with consent capture through blockchain technology could allow patients to steer the use of their secondary data, driving transparency and compliance with OECD 2023 Health Data Governance rules [56].

6.4 Toward Adaptive, Learning Oncology Systems

AI in oncology will end up with adaptive precision medicine, self-teaching system where models update and re-enforces based on RWE (real-world evidence) presented to it. Data-driven adaptive approvals are already supported in both the existing FDA RTOR and EMA DARWIN EU programs [57].

Within such a framework, AI is not (just) a static diagnostic tool but an organismal model that adjusts as new evidence accumulates; adaptive models like these could be employed to develop intelligent and iterative strategies in the ongoing evolution of cancer discovery and care.

7. CONCLUSION

“The findings of this study really show that we can all do AI in the right way and appreciate, given the moral imperatives of medicine for high-risk populations, it’s transformational in how

cancer is treated.” Among the synthetic lung-cancer cohort, AI was better than human in screening early, predicting survival-time and suggesting personalized therapy. With EGFR, PD-L1, TMB actionable AI reveals itself (vs. a black box algorithm) as a reliable co-decision partner through evidenced based biomarkers interpretability.

Radiomics, liquid biopsy, and multi-omics in the era of artificial intelligence. Collecting the wisdom of the crowd, data integration required for next-generation oncology? If the dynamics is to translate from simulation to clinic, and particularly in future orguiloggingemphwork:

- a. Excellent external validation in independent set of patients.
- b. Federated-learning infrastructure with fair access must be defined.
- c. Ethical aspects related to autonomy, privacy, and algorithmic fairness of patients.

If we harness AI smartly, it will be another important new tool for oncology and will transform the model of cancer care from one that is episodic toward continual improvement, patient centricity, lifelong learning and longer survival with superior quality of life globally.

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