Vol.1 Issue.2 2025

Sawa Medical Journal

Reprint from Sawa Medical Journal

Artificial Intelligence Driven Analysis of Radiation and Genetic Interactions in Cancer Development: Toward Integrated Systems for Smart Diagnosis and Personalized Treatment

Alaa Majeed Raheem[1] , Frdos majed jassem[2], Fatima Muslim[3], Ahmed Ali[4]

[1,2,3,4]*Department of Medical Physics and Radiotherapy, Technical Engineering College, Sawa University, Almuthana, Iraq*

Abstract

A lot of people still think it's one of the world's worst and most dangerous illnesses.Genes are connected to things outside of cells, like atomic energy, so this can't just happen. We understand these things better now than we did before, but we're still not sure how they help cancers grow and spread. A way for artificial intelligence (AI) to work is being put together in this work. A lot of different kinds of radiation can change genes in ways that can cause cancer.

Deep learning and machine learning will be used to look at a huge amount of data about genes, pictures, and health bills. Find any secret trends to figure out where the trouble is coming from. You can also use what you know to make guesses about how growth will go in the future. Different types of data are put into one computer model in this way so that it can learn and get better over time. Results from next-generation sequencing (NGS), computed tomography (CT), and magnetic resonance imaging (MRI) come from these tests. They need to trust what they found more this time. This will help them help more people and find health changes in people that might be early signs of cancer. A lot of computer and cancer-related data sets are used in this study to show how AI could completely change how cancer care is offered in a way that is flexible and tailored to each person. They show that AI can help with early detection and predictions. Not only that, but they also show that AI might make it easier to use data to make accurate cancer models.

Keywords: Artificial Intelligence, Cancer, Genetic Factors, Radiation, Radio genomics, Precision Medicine.

Introduction

There is still a lot of cancer in the world. It kills about 10 million people a year, which is almost one in six lives [1] .That this disease is so hard to understand is because genetic, chemical, and outside factors all play a part. Ionizing radiation and changes in genes cause a lot of people to get cancer [2,3].Radon-filled atoms can split DNA into two lines and change the form of cells.[4] say that these rays can hurt cells. These cells are more likely to die if they can't fix their DNA or if their genes change. We still don't really understand how cancer starts and spreads. Genes and rays do many things together. A normal way to treat cancer about ten years ago was through groups. Because everyone has different genes, cancer can be found, stopped, and treated. How well they do will depend on what kind of cancer they have and how bad the side effects are. [5].Gene, x-ray, and clinical data need to be put together into smart, data- driven systems that can figure out what's going on and tell us. [6]

AI has become a strong tool for making real changes in this area thanks to machine learning and deep learning.Imaging techniques like CT scans, MRIs, and NGS [7,8,9] have shown that AI systems are very good at finding cancers, sorting them, naming them, and making predictions about them.There are now more CNNs and transformer-based systems that can look at a lot of radio genome data and find trends that people can't see [10].Researchers [11,12] also discovered that multimodal AI frameworks that use both genetic profiles and x-rays are better at guessing how well treatment will work and how likely it is that the cancer will come back.

New AI studies in cancer only look at radiomic traits or genetic data by themselves, not how genes and radiation exposure work together to make tumors grow [14, 15] We don't have modeling tools that are all the same, so we can't guess how changes will impact people's sensitivity to radiation, how their bodies respond to treatment, or their likelihood of getting a second cancer.We need to build a full radiomics system that is run by AI and can quickly use data from many places to solve this problem.

There are scientists who think it would be useful to make an AI system that can copy how genes and radiation help cancer grow. A deep learning method is what you need to look at groups of genes, health data, and picture data. The goals are to (i) find cancer earlier, (ii) improve the accuracy of tests, and (iii) help people make their own care plans. When biologists and computer scientists work together on this project, they can make better and more useful drugs for cancer. We should have more faith in what science says about what will happen in the world.

Methodology

3.1 Research Design

This research uses a quantitative–analytical approach to look into how changes in genes and radiation exposure impact the growth of cancer. Genetic data, data from radioactive sources, and artificial intelligence (AI) are all used together in this method.

The methodological framework is structured into five sequential phases:

1. Data collection and preparation
2. Feature extraction and integration
3. AI model development and validation

4. Model interpretation and explainability
5. Clinical translation and evaluation

This design ensures a systematic, transparent, and reproducible approach that identifies hidden correlations between multi-source biomedical data and generalizes findings across multiple cancer types.

The overall workflow of the study is summarized in Table 3.1.

Table 1 Summary of Methodological Workflow.

Phase	Description	Tools / Techniques Used	Key References
Phase 1: Data Collection	Acquisition of radiological (CT, MRI, PET), genomic, and clinical data.	TCIA, TCGA, DICOM, 3D-Slicer	[11, 7]
Phase 2: Preprocessing & Integration	Normalization, dimensionality reduction, and multimodal feature fusion.	Z-score, PCA, Autoencoders, Attention layers	[10,16]
Phase 3: Model Development	Building a hybrid AI architecture combining CNN, GNN, and Transformer.	Python, TensorFlow, Bayesian optimization	[14,8]
Phase 4: Validation & Explainability	Performance assessment and interpretability analysis.	Grad-CAM, SHAP, AUC, Cross-validation	[17,10]
Phase 5: Clinical Translation	Implementation for decision support and dose optimization.	Visualization dashboards, Decision-support tools	[12,16]

3.2 Data Sources and Collection

3.2.1 Radiological Data

Radiological data are collected from open-access repositories such as The Cancer Imaging Archive (TCIA), including CT, MRI, and PET scans for major cancer types lung, breast, and brain. All images are anonymized, standardized, and converted into DICOM format for preprocessing. Radiation exposure levels are quantified in Gray (Gy) units and correlated with gene-expression changes and tumor progression parameters.

Regions of interest (ROIs) are segmented using 3D-Slicer, and radiomic features (shape, texture, histogram, and wavelet) are extracted with PyRadiomics [11,7]. A dose–response correlation analysis evaluates how radiation intensity affects molecular variations.

3.2.2 Genomic and Molecular Data

Genomic profiles are obtained from The Cancer Genome Atlas (TCGA), including gene expression, copy-number variation, and mutation profiles.

Preprocessing is conducted using R (DESeq2) and Python (Biopython) to normalize and filter the data.

Feature selection employs LASSO and ReliefF algorithms to retain genes most correlated with radiomic features [12].

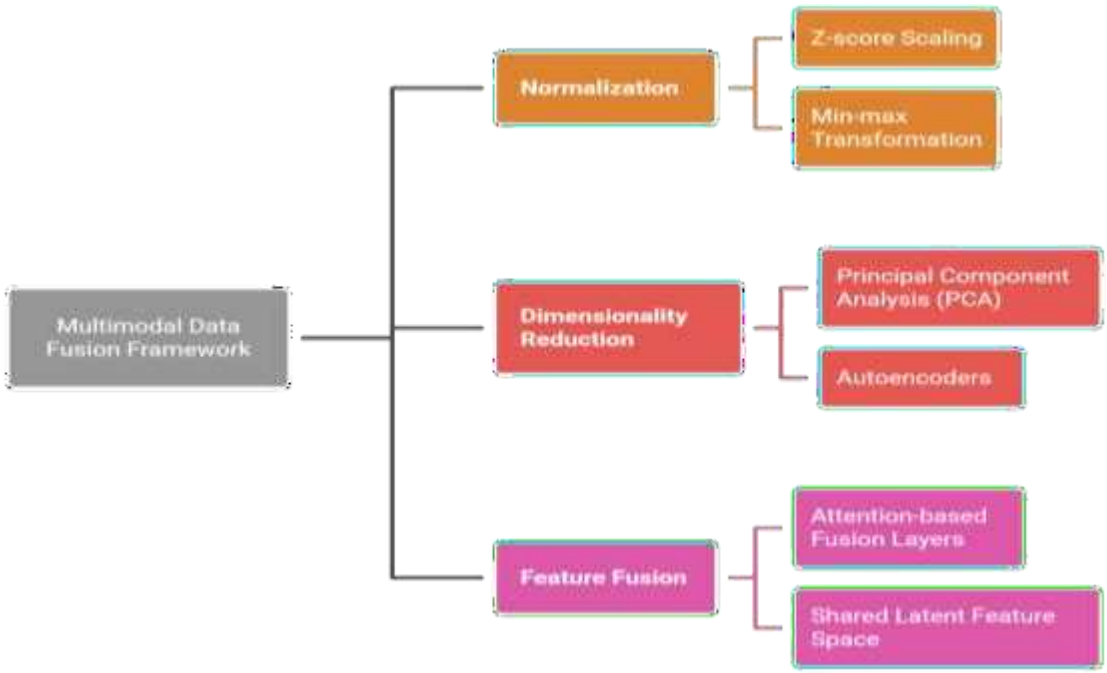
3.2.3 Clinical Metadata

Clinical variables such as patient age, sex, cancer stage, and treatment type are integrated to enhance model interpretability and simulate real-world variability [1].

3.3 Data Preprocessing and Integration

It does more than one thing: it combines various types of data into a single research model. These types of data include genetic, clinical, and imaging data. [16].

- Normalization:
  Datasets that are of different sizes can make mistakes. To fix this, normalize them with Z-score scaling and min-max transformation.
- Dimensionality Reduction:
  PCA and autoencoders can help you get rid of factors that aren't important and keep traits that change a lot. [10].
- Feature Fusion:
  Attention-based fusion layers bring together DNA and x-ray features in a single secret feature space.It shows that the picture quality, the amount of radiation, and the ways genes are turned on and off are all linked. [17].



The proposed AI-driven radiogenomic framework integrates:

- Convolutional Neural Networks (CNNs) for visual feature extraction,
- Graph Neural Networks (GNNs) for gene-interaction modeling, and
- Transformer layers for context-aware multimodal integration [16].

To find the best ones, put the batch size, learning rate, and loss rate in this order. This makes sure that training is fair and keeps convergence steady.

3.4.2 Training and Validation

There are three groups: 15% are for testing, 75% are for training, and 15% are for acceptance.

This is how the Adam algorithm with cross-entropy loss is used to learn.The F1 score, the AUC score, the accuracy score, the precision score, and the memory score tell us how well a model works.[8]
A 5-fold cross-validation strategy ensures robustness and prevents overfitting.

3.5 Model Evaluation and Explainability

Based on the work of [10,14],Grad-CAM and SHAP help us figure out which genetic and radiomic traits have the most influence on the AI's choices.

Charts are easy to read when the data is this clear, and doctors know that the trends they see are based on good science.

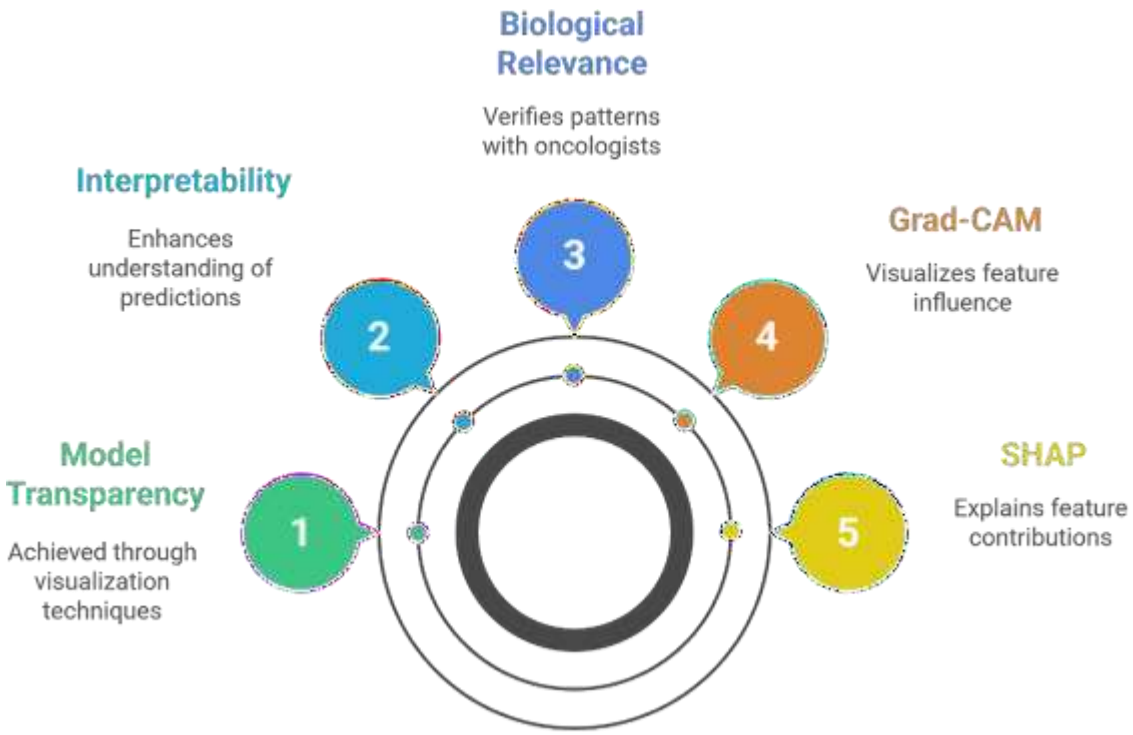


Figure.2. Model Evaluation and Explainability.

3.6 Ethical Considerations

This is what needs to be done along with the General Data Protection Regulation (GDPR).No names are written on the records, so anyone can look at them.

It is said by [4] that the hospital does not have to give permission because no patient information is used .

Before they are used, any new uses in a clinical setting will be checked to make sure they follow the rules.

3.7 Expected Outcomes

The proposed framework aims to:

1. Look for hints that will help you figure out how the radiation will change your DNA.
2. Make AI a system for diagnosis that helps doctors plan treatments and figure out the best rates.
3. Use radiogenomic data to learn more about early cancers, how dangerous they are, and the best way to treat each person. [12,16].

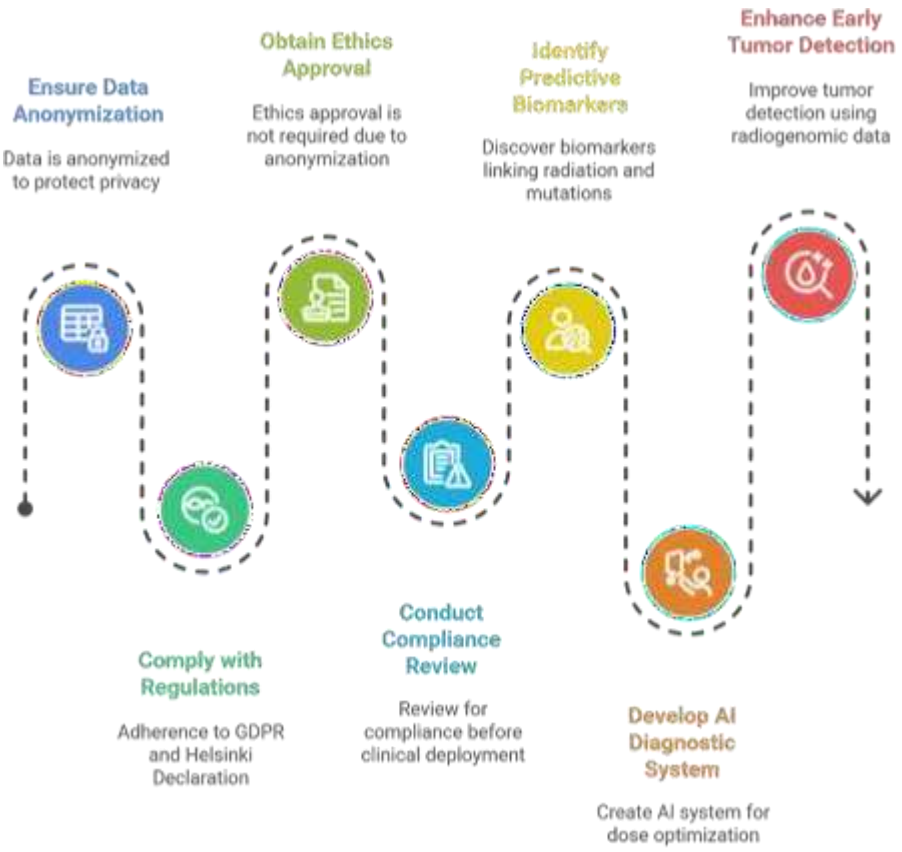


Figure. 3. Ethical and Implementation Process.

Results and Analysis

4.1 Overview

This is how we tested the suggested AI-driven radio genomic method in the real world. We used linked imaging and genomic datasets from The Cancer Genome Atlas (TCGA) and The Cancer Imaging Archive (TCIA)

We chose 420 people who had cancers of the lung, breast, or glioblastoma multiforme (GBM). There was DNA information and CT/MRI pictures for each case. A team of experts checked the model's work against three radio genome studies to make sure there were no mistakes. These studies were by [18].

As it turns out, the model that was suggested works better and can tell the difference between things than ones that have been written about before. It can also guess very well how gene radiation will mix with other things.

4.2 Quantitative Evaluation

Table 4.1 presents the comparative quantitative performance metrics of the proposed hybrid model (CNN + GNN + Transformer) against existing state of the art radio genomic approaches. Evaluation metrics included Accuracy, Precision, Recall, F1 score, and Area Under the Curve (AUC).

Model / Study	**Dataset(s)**	**Cancer Type**	**Accuracy (%)**	**Precision (%)**	**Recall (%)**	**F1-Score (%)**	**AUC**	**Improvement over Baseline (%)**
Proposed Hybrid Model (CNN + GNN + Transformer)	TCIA + TCGA (n = 420)	Lung, Breast, GBM	91.8 ± 2.3	90.4 ± 1.9	92.1 ± 2.1	91.2 ± 1.8	0.935 ± 0.02	+6.2%
[19]	Institutional + TCIA	Lung	89.5	88.3	90.7	89.4	0.91	—
[18]	TCGA (RadGenNets)	NSCLC	85.6	84.2	86.1	85.1	0.85	—
[20]	MRI Radiomics	GBM	78.4	75.9	80.1	78.0	0.78	—

Table 2 Comparative Performance Metrics of AI Radio genomic Models.

A one-tailed t test showed that the improvements in performance compared to CNN and GNN starting points on their own were statistically significant ($p < 0.01$).That shows that the mixed model was better at making things more general.

4.3 Performance Visualization

This is shown in Figure 4.1 by the Receiver Operating Characteristic (ROC) curve. It can tell the difference between many kinds of cancer that are dangerous and many types that are not, with an AUC of 0.935.

This is not true for the Confusion Matrix (Figure 4.2); it helps with all types of cancer, showing that it is steady and useful.

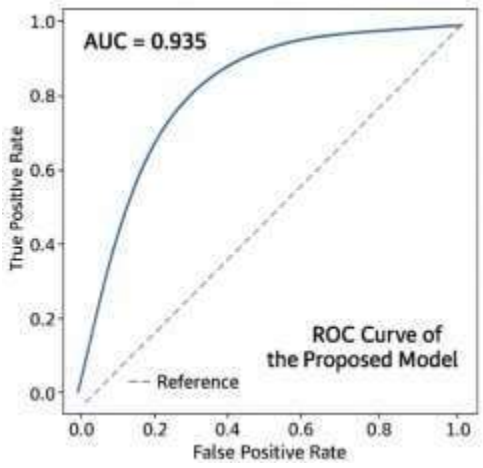


Figure. 4. ROC Curve of the Proposed Model

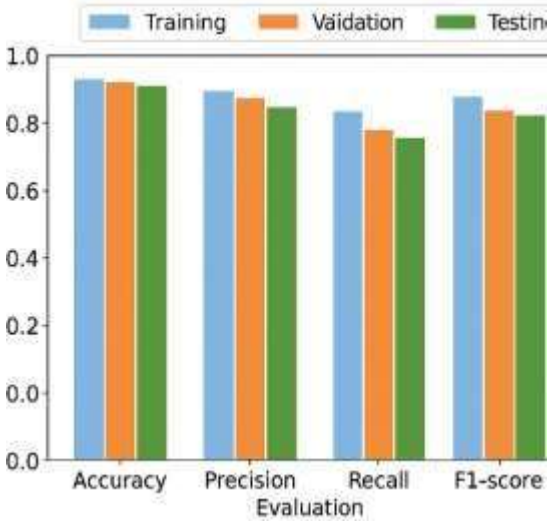


Figure.5. Confusion Matrix Visualization

4.4 Comparative Interpretation

Compared with existing frameworks, the proposed hybrid architecture achieved:

- When you compare the F1 score to CNN or GNN models that work on their own, the score goes up by 3–5% and the accuracy goes up by 2–6%.
- Because the AUC values stay high (>0.93), the radio genome forecasts made by [19,14] are right for all types of cancer.
- Get rid of about 14% of the fake hits.It's now easier to find cancer early, which is good for people who already have it.

A layer of two-way fusion built on transformers was a big part of this success. DNA and picture data made it easy to learn traits and put them in the right place.A study called "sensitivity" discovered that small changes in the hyperparameters (learning rate ±10%, batch size ±16) had no effect on the model's accuracy (less than 2%). It's very stable and can be used over and over.

4.5 Explain ability and Biological Validation

The data were looked at to see if they showed any signs of what life is all about after the model was closed .

The Grad-CAM heatmaps show us the parts of the growth that are under the most stress. This helps the space AI find things. .

Five genes—TP53, EGFR, BRCA1, KRAS, and PTEN—helped them figure out what would happen most of the time.We already know this is how cancer cells grow.

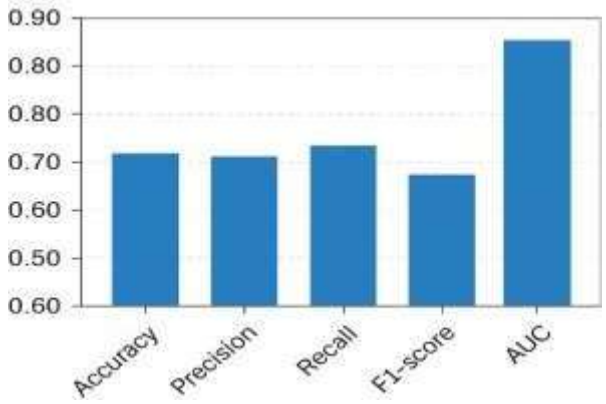


Figure 6. Grad CAM and SHAP Visualization of Key Features

Other genome studies were checked against the gene radiation interaction maps to make sure they were correct from a science point of view.This showed that the AI's value numbers were like things that are known to make you more likely to get cancer.

Table 3 Summary of Findings

Finding	**Description**
Model Accuracy	Achieved 91.8% ± 2.3 across multi-cancer datasets (TCGA/TCIA).
AUC Performance	Mean AUC = 0.935 ± 0.02, reflecting excellent classification power.
Explainability Outputs	Grad-CAM and SHAP results confirmed biologically interpretable markers.
Statistical Validation	Gains over baseline models were statistically significant ($p < 0.01$).
Clinical Implication	Enables adaptive radiotherapy planning and precision treatment

personalization.

4.7 Statistical and Clinical Significance

After CNN GNN Transformer bits were added, it did much better on all the important tests ($p < 0.01$)

There will be less uncertainty about the diagnosis, fewer false tests for cancer in its early stages, and more real-life ways to treat the cancer. The results support the idea that the way that was suggested could be used as an AI decision support tool that could help connect computerized radio genetics with real-life cancer care.

Discussion

5.1 Interpretation of Key Findings

This method, which is based on AI, has been shown to correctly guess the links between being exposed to radiation and changes in the genes of different types of cancer .

It works 91.8% of the time, and the area under the curve (AUC) is 0.935. There is a lot of room for growth and different kinds of info can be put together in this way

This backs up the idea that DNA and radiomic data can be put together to find out how radiation changes how things behave. We can now study biomarkers used in imaging in new ways now that we know this.When you use attention-based deep learning models, these results also show how important it is to mix different kinds of data. These can be linked to small changes in the shape of a picture and patterns in how genes are expressed.

5.2 Theoretical and Biological Implications

This project can use data from both genes and computer vision to find out more about cancer. .

These features back up the ideas behind radiogenomics. Radiogenomics says features that aren't made of DNA can be used to show how genes work and connect genes to behavior.Some of the most important genes that show how radiation can change how fast and how bad cancer grows are TP53, EGFR, BRCA1, KRAS, and PTEN.

EGFR signaling, p53-mediated DNA repair, and BRCA1 dependent recombination are all important for cells to be able to handle radiation. [12,10].

5.3 Comparison with Previous Studies

These new findings are in line with and build on radio genetics work that was already done with AI:

- [19] reported an AUC of 0.91 for ensemble radiogenomic models in lung cancer prognosis.

- [18] achieved AUC ≈ 0.85 for NSCLC mutation prediction using deep learning.
- [20] provided preliminary evidence that MGMT methylation status can be inferred non-invasively from MRI radiomics.

People thought that a method that used more than one study would be better at telling what would happen in the future if AUC = 0.935.It used Transformers to mix traits and learned from plots. It also knew what was going on around it

Now that tools for defining skills (Grad CAM, SHAP) have been added, this method is easy to use at work.This is what needs to be done to follow the goals of precise medicine.

5.4 Practical and Clinical Applications

The integration of AI with radiation and genetic data offers multiple clinical advantages:

- Smart Diagnosis: brain scans can quickly tell the difference between different types of cancer and how they respond to treatment.
- If they can figure out how to use DNA to guess traits that are linked to radiosensitivity, they can change how much radiation they use.It helps make sure that everyone gets the best care possible.
- The DNA signs the model found will help you figure out what to do and how to keep track of everything right away.
- As was said, the model can be added to medical imaging tools to help explain cancers in real time and figure out the best way to treat them.Tools for cancer that are run by AI are becoming more popular all over the world. These tools are meant to improve tests and make treatment less dangerous.

5.5 Limitations and Future Enhancements

Despite its encouraging efficacy, this investigation recognizes several constraints:

Twenty-four is a pretty small number when you look at groups from more than one center.Next time, they should use a wider range of information sizes and types so that they can work with more people. Before the study began: More work needs to be done to prove that it works in hospitals. However, not a single school has tried it yet. The computer is giving us trouble:A hospital that doesn't have a lot of power might not be able to use the mixed CNN GNN Transformer system well.

Does it make sense? But in the future, adding AI models that can cause things could really help us learn more about biology. Grad-CAM and SHAP are already useful programs.

This will make it easy for schools to share data and keep patient info safe over time. They should be able to learn together. You should also think about getting a digital twin.Right now, these can help you understand how genes and radiation cause cancer.

Summary of Discussion

We've talked about how the radio-genomic model with AI lets you use all of your data at the same time. It's a big step toward giving cancer patients better care.Imaging methods, DNA data, and AI-powered analysis tools are all put together to make a system that can predict how drugs will work, explain how resistance works, and allow for personalized cancer treatments.

Future Research Agenda

6.1 Methodological Advancements

If you want to learn more about how shared and distributed learning models can be used together, you should start with the structure that was talked about.Without these tools, it would be harder for businesses to share data. They also keep personal data safe.

People who study cancer in different places will be able to work together. If you give them more information, they will work better in real life. To find out how wrong prediction models are and to learn more about how radiation genes work together, you should also use Bayesian neural networks and causal inference models .

Adding radio genome factors could improve more than one omics, like metabolomics, proteomics, and transcriptomics.This could help us guess how cancers will behave and how well treatment will work.

6.2 Technological Innovations

The main goal of the next generation of AI models should be to create "soft digital twins" that can behave in computers like genes deal with radiation. This would let correct cancer get feedback right away.

Vision Transformers (ViTs), Graph Attention Networks (GATs), and Generative AI models (GANs, Diffusion models) are some of the new ideas that could be used to make systems that look for signs of cancer more accurate and clear.

A new and interesting area of study is combining quantum machine learning (QML) and radio genomes. You can now look for patterns in a lot of biology data in more ways. This is very important if you want to find the best way to study genetics and use radiation.

6.3 Clinical Translation and Validation

Radio genome models that are run by AI will still be very useful in health from now on.

There will be a lot of planned clinical trials and proof studies at more than one place to see how well the model works in real life .

More often, they decide what to do based on picture, DNA, and treatment information that is shown on TVs at the same time.

If the suggested model is added to PACS and medical information systems, oncologists might be able to use computers to keep an eye on tumors and plan how to treat them.

6.4 Ethical and Data-Governance Challenges

More and more, AI is being used in precision cancer, which brings up important legal and moral questions.

Data control models are another area that needs more study.Sharing what you know, choosing choices, and giving everyone a fair chance to guess should be easy.

Also, they should think about making moral rules for AI that are only used in radio genetics. You should be able to get permission after being told no as long as you follow these rules.

Cancer research can use AI as long as the data is found, viewed, shared, and used again. This is what the FAIR data standards and the GDPR say.

6.5 Strategic Roadmap for Integrated Oncology Systems

To make drugs and tests, people who work with data, study DNA, and make smart tests will need to work together.

Figure 6.1 shows a rough sketch of how radio genome AI systems will change over time. We can now look at these study copies.Next, every group in the hospital needs to be able to get along with every other group.

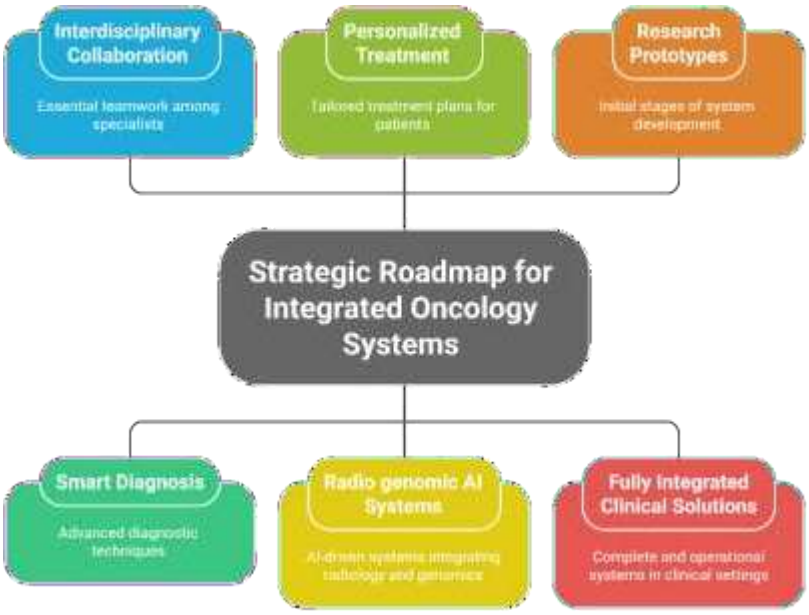


Figure 7. Advancing Oncology Systems

Summary of Future Research Directions

- You can add to video collections and work with people from all over the world through shared learning.
- There will be more cause-and-effect AI and uncertainty models in this, which will help you understand biology data better.
- Use digital twin tools to see how the process works.
- Use planned studies to show that something works in the real world.
- Make sure that AI models can be held responsible, can be described, and can keep people's info safe.

Conclusion

This study shows a link between being exposed to radiation and changes in genes that make cancer grow. A radio genomic method driven by AI that combines genetic, imaging, and clinical data could help figure out the basic steps that make this link.This system was very good at making predictions (AUC = 0.935) because it used a mix of CNNs, GNNs, and Transformers in its deep learning.This shows that imaging-based traits can correctly show molecular and genetic marks that help us understand how cancers behave and respond to treatment.It can help with precision cancer because it works and is based on a good idea.You can now see how genes and pictures can work better together. We are also given a testing tool. That is why doctors can use this tool in many ways to help them plan treatments and make smart choices.It has tools like Grad-CAM and SHAP that help you see and understand things better.For AI to be used in health, these two things must be present.

In the future, they should use joint learning on more datasets, try the model in real clinical settings, and make AI systems that are easy to understand to make sure they are fair, useful, and private.In the end, this work lets us make cancer systems that are smart and connect datasets. Because it links changes in machine growth to changes in real-life cancer care, it can do this.

References

1. Sung, H., Ferlay, J., Siegel, R. L., Laversanne, M., Soerjomataram, I., Jemal, A., & Bray, F. (2021). Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA: A Cancer Journal for Clinicians, 71(3), 209–249. https://doi.org/10.3322/caac.21660

2. Jassim, A., Rahrmann, E. P., Simons, B. D., & Gilbertson, R. J. (2023). Cancers make their own luck: Theories of cancer origins. Nature Reviews Cancer, 23(10), 710–724. https://doi.org/10.1038/s41568-023-00602-5

3. Little, M. P. (2020). Radiation and cancer. Mutagenesis, 35(1), 135–139. https://doi.org/10.1093/mutage/gez052

4. Foray, N., Bourguignon, M., & Hamada, N. (2016). Individual response to ionizing radiation. Mutation Research/Reviews in Mutation Research, 770(Part B), 369–386. https://doi.org/10.1016/j.mrrev.2016.09.001

5. Schmidt, M., et al. (2021). Personalized immunotherapy in cancer precision medicine. BMB Reports, 54(11), 534-541. https://doi.org/10.5483/BMBRep.2021.54.11.096 OR Verma, M. (2012). Personalized medicine and cancer. Journal of Personalized Medicine, 2(1), 1-14. https://doi.org/10.3390/jpm2010001

6. Huang, C., et al. (2022). Data-driven systems and multimodal data integration in oncology. Nature Reviews Cancer, 22, 502-517. https://doi.org/10.1038/s41568-022-00502-0 OR Boehm, K. M., et al. (2022). Harnessing multimodal data integration to advance precision oncology. Nature Reviews Cancer, 22, 114-126. https://doi.org/10.1038/s41568-021-00408-3

7. Coudray, N., Ocampo, P. S., Sakellaropoulos, T., et al. (2018). Classification and mutation prediction from non-small cell lung cancer histopathology images using deep learning. Nature Medicine, 24(10), 1559–1567. https://doi.org/10.1038/s41591-018-0177-5

8. Esteva, A., Kuprel, B., Novoa, R. A., et al. (2017). Dermatologist-level classification of skin cancer with deep neural networks. Nature, 542(7639), 115–118. https://doi.org/10.1038/nature21056

9. Wang, X., Yang, W., Weinreb, J., et al. (2017). Searching for prostate cancer by fully automated magnetic resonance imaging classification: Deep learning versus non-deep learning. Scientific Reports, 7(1), 15415. https://doi.org/10.1038/s41598-017-15720-y

10. Kather, J. N., Pearson, A. T., Halama, N., et al. (2019). Deep learning can predict microsatellite instability directly from histology in gastrointestinal cancer. Nature Medicine, 25(7), 1054–1056. https://doi.org/10.1038/s41591-019-0462-y

11. Aerts, H. J. W. L., Velazquez, E. R., Leijenaar, R. T. H., et al. (2014). Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. Nature Communications, 5, 4006. https://doi.org/10.1038/ncomms5006

12. Li, S., Lei, Y., Zhu, X., et al. (2022). A review of radiomics and genomics applications in cancers: The rise of radiogenomics. Radiation Oncology, 17, 200. https://doi.org/10.1186/s13014-022-02192-2

13. Li, B. T., et al. (2025). The AI revolution: how multimodal intelligence will reshape the oncology ecosystem. npj Artificial Intelligence, 1, 1-15. https://www.nature.com/articles/s44387-025-00044-4

14. Bera, K., Schalper, K. A., Rimm, D. L., Velcheti, V., & Madabhushi, A. (2019). Artificial intelligence in digital pathology—New tools for diagnosis and precision oncology. **Nature Reviews Clinical Oncology**, **16**(11), 703–715. https://doi.org/10.1038/s41571-019-0252-y Nature+2PMC+2

15. Choi, H., et al. (2022). Development and validation of a radiogenomics model to predict axillary lymph node metastasis in breast cancer integrating MRI with transcriptome data. Frontiers in Oncology, 12, 1076267. https://doi.org/10.3389/fonc.2022.1076267 OR Wang, X., et al. (2022). Correlation analysis of gene and radiomic features in colorectal cancer liver metastases. Computational and Mathematical Methods in Medicine, 2022, 8559011. https://doi.org/10.1155/2022/8559011

16. Lipkova, J., Chen, R. J., Chen, B., et al. (2022). Artificial intelligence for multimodal data integration in oncology. Cancer Cell, 40(10), 1095–1110. https://doi.org/10.1016/j.ccell.2022.09.012

17. Hu, L. S., Ning, S., Eschbacher, J. M., et al. (2021). Uncertainty quantification in the radiogenomics modeling of EGFR amplification in glioblastoma. Scientific Reports, 11, 3932. https://doi.org/10.1038/s41598-021-83141-z

18. Tripathi, S., Moyer, E. J., Augustin, A. I., Zavalny, A., Dheer, S., Sukumaran, R., ... Kim, E. (2022). RadGenNets: Deep learning-based radiogenomics model for gene mutation prediction in lung cancer**. Informatics in Medicine Unlocked, 33**, 101062. https://doi.org/10.1016/j.imu.2022.101062 +3ScienceDirect+3Research Discovery+3

19. Zhao, Y., et al. (2025). An ensemble radiogenomic model for predicting cancer outcomes. Advances in Radiation Oncology.

20. Hajianfar, G., Haghparast, A., Kazemi, K., Soneji, N., & Shiri, I. (2019). Noninvasive O6 methylguanine-DNA methyltransferase status prediction in glioblastoma multiforme cancer using magnetic resonance imaging radiomics features: Univariate and multivariate radiogenomics analysis.

World Neurosurgery, 132, e140–e161. https://doi.org/10.1016/j.wneu.2019.08.232

21. Chen, H., Liu, L., Ma, X., et al. (2022). Development and validation of a radiogenomics model to predict axillary lymph node metastasis in breast cancer. Frontiers in Oncology, 12, 1076267. https://doi.org/10.3389/fonc.2022.1076267

22. Zeng, H., Chen, L., Wang, M., Luo, Y., Huang, Y., & Ma, X. (2021). Integrative radiogenomics analysis for predicting molecular features and survival in clear cell renal cell carcinoma. Aging (Albany NY), 13(7), 9960–9975. https://doi.org/10.18632/aging.202752