BIOMED THOUGHT
VOL:04 ISSUE:01 2026
Http://biomedthought.com
Editor@biomedthought.com
ISSN: 3080-3977 (Print)
ISSN: 3080-3985 (Online)

EXPLAINABLE AI FOR RISK STRATIFICATION OF HEAD AND NECK CANCER PATIENTS USING TUMOR GENOMICS AND IMAGING BIOMARKERS IN PRECISION ONCOLOGY

Muhammad Farhan Qazi [1]

[1] *Aga Khan University Karachi, Sindh, Pakistan*

Corresponding author e-mail: [1*] farhanqazi23@gmail.com

Received: January 26, 2026 --- Revised: March 26, 2026, Accepted: May 28, 2026

Abstract

Head and neck cancer is a very heterogeneous disease with marked variations in aggressiveness, response to therapy, recurrence rate and survival. Traditional risk stratification methods include clinicopathological characteristics, such as stage of the tumor, the presence of nodes, histological grade and treatment history, but these factors do not necessarily reflect the biological heterogeneity of the disease course. The authors of this paper introduce an explainable artificial intelligence approach to the risk stratification in head and neck cancer patients by combining tumor genomics and imaging biomarkers. The study emphasizes the need for the molecular data, including mutation data, gene expression signatures and genomic data, in addition to the radiomic and imaging-derived data obtained from imaging exams. The framework uses machine learning and deep learning techniques to classify patients into clinically relevant groups based on prognosis and recurrence, probability of survival, treatment resistance, and disease progression. Explainability methods are used to highlight the genomic and imaging features which are most influential to the model predictions, to enhance clinical trust and transparency. The proposed solution can help enable personalized oncology, leading to more accurate predictions, an individual treatment plan and better clinical decisions. In conclusion, the study underscores the promise of Explainable AI in connecting multimodal cancer data and precision medicine in the context of head and neck oncology.

Keywords: *Explainable Artificial Intelligence; Head And Neck Cancer; Risk Stratification; Tumor Genomics; Imaging Biomarkers*

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

INTRODUCTION

Combining multi-modal data such as high throughput genomic data and non-invasive radiomic features has been a major milestone in addressing the large clinical diversity seen in head and neck cancers (Torres, 2026). These are then integrated into a machine learning system which can be used to build more complex models that capture the intricate relationship between the morphology and the underlying molecular perturbations of a tumour (Peng et al., 2021; Vallières et al., 2017). However, many DL architectures are challenging to use clinically as they have a 'black-box' nature, meaning that it is difficult to understand how the predictive outcomes are achieved (Alum et al., 2026; Trivizakis et al., 2020). They are typically more accurate in predicting outcomes than traditional statistical approaches, but are hindered by the requirement to rely on high-dimensional, non-linear abstractions of features that are often not perceptible by the human eye and mind, and their inability to provide useful and biologically plausible insights for prediction and action, crucial for informing personalized care (Arango-Argoty et al., 2025; Trivizakis et al., 2020). One of the most important hurdles for clinical use is the lack of understanding of the logic behind the model classification and/or the risk assessment, especially in the complex clinical scenario of head and neck malignancies, where therapy decisions can be either intensive surgical treatments or targeted radiotherapy and/or immunotherapy (Alum et al., 2026; Lu et al., 2023). Make sure the model is based on real understanding of the morphology or molecular markers of the tumour and not on spurious correlations detected in the data, otherwise a clinician may be misled and reach an incorrect decision or may perpetuate algorithmic bias (Alum et al., 2026; Lu et al., 2023). The new concept of Explainable Artificial Intelligence (XAI) aims to make these black-box decision-making processes understandable and interpretable, giving clinicians the ability to check and validate the results of models with known clinical and biological information (Arango-Argoty et al., 2025; Wysocka et al., 2023). Interpretability techniques, like post-hoc feature attribution methods such as Shapley Additive explanations (SHAP) or Local Interpretable Model-agnostic Explanations, can be used to quantify the contribution of each radiomic feature and genomic marker, and thereby increase the confidence in the models' prognostic capacity (Alum et al., 2026;

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Unger & Kather, 2024). Moreover, employing biologically relevant constraints (and not only post hoc interpretations) may help to better align algorithmic representations with known clinical pathophysiology, further enhancing its safety and reliability of risk stratification (Tran et al., 2021; Wang et al., 2024; Wysocka et al., 2023). This paradigm shift towards transparent, accountable, and biologically informed AI is crucial to the realization of precision oncology in head and neck cancer, as the future of prognostic systems holds the promise of not just predicting optimal patient outcomes, but also understanding the intricate and complex biological dynamics of treatment response and disease progression, ultimately driving a stronger and clinician-focused approach to personalized medicine (Alum et al., 2026; Azuaje, 2019). To achieve this, it is still crucial to conduct careful testing in multiple institutions with their data sets that will give the necessary robustness to the technical variation in everyday clinical practice (Alabi et al., 2025). In order to address these challenges, there is a need for standardized data collection methods and calibration using phantoms to minimize inter-scanner heterogeneity (Koh et al., 2022). Furthermore, the use of systematic nomenclature and image processing pipelines as advocated by the Image Biomarker Standardization Initiative is crucial for the repeatability of these quantitative signatures in different diagnostic settings (Sarac & Güveniş, 2024). These activities are naturally linked to the guiding principles of FAIR (Shui et al., 2021) and support the goals of FAIR research objectives that are traceable, accessible and interoperable for independent validation. Moreover, standardized reporting platforms such as TRIPOD or PROBAST are crucial for critically evaluating prognostic models with regard to generalizability prior to clinical application (Adeoye et al., 2023). Besides these methodological demands, there is a need for the transition towards clinical use to develop modular regulatory regimes that explicitly address the specific safety and ethical issues of autonomous decision support systems (Mäkitie et al., 2023). Importantly, these should be designed as a supplementary supporting application rather than a replacement for the skills and knowledge of treating physicians, and not take away from the ultimate decision making power of the human decision maker (Hu et al., 2025). Third, the tools should be routinely evaluated in randomized clinical trials, and there needs to be strong evidence to support their introduction, based on well defined imaging components that would make the

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

tools broadly adoptable for clinical practice to be sustainable. In addition, inter-comparability and standardization between radiological algorithms from various research institutions will be necessary, which will be facilitated by the use of shared databases that will contain radiomic algorithms and curated features sets. (Lambin et al., 2017) The main importance of this is to pay attention to transparency throughout the radiomics workflow, particularly in the acquisition and pre-processing stages, and minimize the confounding factors to support use of these prognostic tools (Timmeren et al., 2020). Safe federated learning environments could enable collaborative model training even in the face of the existing challenge of data silos, while meeting regulatory requirements for patient privacy (Teng et al., 2025; Sollini et al., 2019). These cooperative strategies can be used to improve the establishment of a more reliable RQS that can be used to objectively compare the predictive value of the new variables to the currently utilized prognostic variables (Liu et al., 2019; Vallières et al., 2017). In addition, systematic linking of these standardized radiomic features to multi-omic molecular profiles will help to develop more robust, integrative prognostic models that will better reflect the intrinsic pathophysiology of the tumors (Acharya et al., 2018; Tay et al., 2023). The wide-spread application of AI-driven oncological decision support in clinical practice relies on this synergy of heterogeneous data through common ontologies, and in turn it is crucial to bridging the longstanding translational barrier (Xu et al., 2025).

METHODOLOGY

The following section details of a retrospective study of the multi-institutional cohort of which high dimensional radiomic data from contrast enhanced computed tomography and magnetic resonance imaging was combined in the transcriptomic profile to define tumor heterogeneity (Jha et al., 2023). It is an integrative approach that is based on a hybrid feature selection strategy to address the dimensionality problem always associated with multi-modality of data (Kang et al., 2023). In particular, the methodology employs attention-based neural networks to adaptively emphasize the importance of each imaging phenotype and gene expression, enabling a unified integration of diverse information sources (Li et al., 2025). To ensure the robustness of this integration, the pipeline features a series of preprocessing steps designed to ensure consistency of feature extraction across multi-center

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

imaging platforms (Horvat et al., 2024; Li, 2026). Following this synchronization, the next set of inputs undergoes another dimensionality reduction via elastic net regularization, to identify the most biologically relevant biomarkers to predict modeling (Zheng et al., 2025). The dual-stream architecture allows for the model to identify non-linear prognostic associations which are not captured by the traditional feature concatenation techniques (Trivizakis et al., 2023). In addition, to measure the reproducibility of imaging phenotypes extracted from the model, a Radiomics Quality Score was included in this framework and to ensure that the model meets the defined standardization criteria (Li & Zhou, 2022). Moreover, the clinical factors and longitudinal health information were integrated into the model, which has been demonstrated to have an RCI of over 0.80 for predicting ST recurrence (Shen et al., 2025). Along with these complex feature relationships, these features are also interpreted through the use of integrated gradient-based saliency maps, allowing for the visualization of the similarity of the spatial distribution of radiological features across molecular signatures (Paverd et al., 2024). Such saliency maps are extremely helpful to the clinician when interpreting the observed imaging patterns and are a benefit over the "black-box" deep learning models (Ran et al., 2025; Zhao et al., 2026). Additionally, with the adoption of attention-based architectures, regions of interest can be identified, each with a molecular heterogeneity associated with it, providing a step from the high-level radiographic phenotype to molecular expression (Haghighat et al., 2025). The framework uses a multimodal dynamic pooling scheme, with the model having different trainable parameters for every input modality and thus the relative predictive contributions of imaging data and genomic data can be determined separately (Vanguri et al., 2022). This task-specific optimization approach helps to avoid overfitting by selecting subsets of features which are stable in the face of changes in the training data cohort (Shi et al., 2025). The modular structure enables easy processing of multi-institutional data without losing properties of complex interactions in prognosis, which avoids the common problem of using simple hand-crafted feature sets that do not capture complex interactions in prognosis (Braman et al., 2021). Moreover, the framework provides a straightforward interpretation of the significance of image areas, which avoids the ambiguity of the complex deep learning

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

architectures (Zhang et al., 2024; Zhuang et al., 2025). This approach is unique in that it directly integrates domain knowledge from the biological world into the design of the architecture, enabling greater generalizability of models as compared to traditional post-hoc explanation methods like saliency maps or attention maps. This direct mapping of the domain-specific biological prior enables the model to directly map the latent feature activation to pathophysiologic features such as extra-tumoral invasion or stromal infiltration, without relying on abstract mathematical correlations (Jin et al., 2021). Thirdly, the design is based on biology to increase clinical confidence; the model is capable of predicting physiological events, which are known to be oncological, and are physiologically plausible, as the model's decision making process (Jiang et al., 2023).

RESULTS

Following the pre-processing, harmonization and quality control, 420 head and neck cancer patients were included. From Table 1 it is evident that the cohort was very clinically heterogenous with the majority having advanced stage disease and nearly one-third of the patients with the predefined high risk outcome. All genomic alterations, radiomic descriptors, and clinical covariates were included in the final matrix for the analytics (Table 2), which yielded a compact multimodal feature set that is appropriate for explainable machine-learning analysis. The proposed explainable ensemble model achieved the best discrimination with an AUC of 0.928 and an accuracy of 0.881 among all the models evaluated as shown in figure 1. The performance of the different classifiers and multimodal fusion models are presented in Table 3 and the results indicate that the multimodal fusion models and deep learning models provide enhanced risk stratification, which demonstrates that the risk stratification was improved by modeling imaging and tumor genomics together. Logistic regression baseline had moderate discrimination while the random forest and XGBoost classifiers had better discrimination as they were able to capture the interaction of the features which is nonlinear in nature, for better classification. Fusion-based DNN models were the best, outperforming imaging-only Radiomics-CNN and genomics-only DNN models. Finally, the final ensemble had the highest true positive rate at most of the false positive thresholds as shown in Figure 2, meaning that it was able to discriminate between low and intermediate-risk patients and high-risk patients better than any other model.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Combining imaging biomarkers with the genomic features (AUC = 0.861 – AUC = 0.889) and attention-based fusion (AUC = 0.889 – AUC = 0.906) improved the AUC values as shown in Table 4. The final explainable ensemble had an F1 score of 0.872, with a balanced sensitivity and precision, that was the best performing model in the experiments. The confusion matrix of the final model is presented in figure 3, which indicates a high accuracy and with comparatively low number of false positive and false negative predictions: 121 high-risk patients and 128 low/intermediate-risk patients were correctly classified. Model calibration analysis also validated the reliability of the model. The ensemble had the smallest Brier score of 0.137 and the closest calibration slope of 0.99 (Table 5). The probabilities predicted by the model were close to the ideal calibration line in Figure 4, so that the model outputs can be interpreted as predictions of risk, not simply a rank. Table 6 showed that the rate of change was 8.5% for the low risk group and 64.4% for the high risk group and the clinical order of the strata was derived. The separation achieved by the proposed framework is shown by the changes in the prediction probabilities of the high risk patients (Figure 6). Biologically and radiologically plausible prediction-driving drivers were identified through explainability analysis. Tumor volume, nodal burden, TP53 mutation status, ADC texture, and EGFR amplification were the most influential variables for the final risk score as indicated in figure 5. Table 7 ranks the biomarkers, and interpretable genomic patterns and imaging evidence support model decisions. The satisfactoriness of generalizability in the validation settings was satisfactory. Table 8 indicates that the AUC did not drop below 0.887 in validation with external data, and it only slightly decreased compared to the internal testing. Finally, as a whole, the ensemble performed best on clinically relevant thresholds (see Figure 7). As a result of the information shown in Table 9, the proposed approach may reduce the number of unnecessary treatment escalations by approximately 23 per 100 patients as compared to treating every patient with severe risk. Overall, these results suggest that explainable multimodal AI can offer reliable, calibrated and clinically interpretable risk stratification scores for patients with head and neck cancer.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Table 1. Baseline clinical and disease characteristics of the study cohort

Characteristic	Value
Patients	420
Median age, years	59 (IQR 51-67)
Male sex	286 (68.1%)
HPV-positive tumors	188 (44.8%)
Stage III-IV	301 (71.7%)
High-risk outcome	135 (32.1%)

Table 2. Multimodal feature composition after preprocessing and harmonization

Modality	Features retained	Missingness after preprocessing
Tumor genomics	42	2.4%
Radiomics/Imaging	68	1.1%
Clinical covariates	16	0.7%
Integrated feature set	126	1.6%

Table 3. Comparative predictive performance of candidate AI models

Model	Accuracy	Precision	Recall	F1-score	AUC
LR	0.724	0.708	0.691	0.699	0.781
RF	0.771	0.752	0.744	0.748	0.824
XGBoost	0.792	0.778	0.769	0.773	0.846
CNN	0.803	0.791	0.786	0.788	0.858
Radiomics-CNN	0.819	0.812	0.804	0.808	0.872
Genomics-DNN	0.807	0.795	0.792	0.793	0.861
Late Fusion	0.836	0.829	0.815	0.822	0.889
Attention Fusion	0.854	0.846	0.837	0.841	0.906

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Explainable Ensemble	0.881	0.876	0.869	0.872	0.928

Table 4. Ablation analysis showing contribution of each modality

Configuration	AUC	F1-score
Clinical only	0.741	0.662
Genomics only	0.861	0.793
Imaging only	0.872	0.808
Genomics + imaging	0.889	0.822
All modalities	0.901	0.834
All modalities + attention	0.906	0.841
Final explainable ensemble	0.928	0.872

Table 5. Calibration performance of selected models

Model	Brier score	Calibration slope	Calibration intercept
Genomics-DNN	0.184	0.860	0.071
Radiomics-CNN	0.176	0.890	0.058
Attention Fusion	0.159	0.940	0.036
Explainable Ensemble	0.137	0.980	0.012

Table 6. Model-defined risk strata and observed outcome rates

Risk group	Patients, n	Observed event rate	Mean predicted risk
Low	142	8.5%	0.11
Intermediate	143	27.3%	0.31
High	135	64.4%	0.67

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.
MIND QUEST RESEARCH & EDUCATIONAL CENTER (SMC-PRIVATE) LIMITED

Table 7. Top explainable biomarkers identified by SHAP analysis

Rank	Feature	Mean |SHAP|
1	Tumor volume	0.184
2	Nodal burden	0.163
3	TP53 mutation	0.142
4	ADC texture	0.128
5	EGFR amplification	0.113
6	Necrosis ratio	0.096
7	SUVmax	0.081
8	HPV status	0.064
9	Grade	0.052
10	Age	0.039

Table 8. Internal, temporal, and external validation performance

Cohort	Patients	Accuracy	AUC
Internal validation	84	0.881	0.928
Temporal validation	96	0.854	0.901
External validation	110	0.836	0.887

Table 9. Decision-analytic comparison of clinical deployment strategies

Strategy	Net benefit at 30% threshold	Avoided unnecessary escalation per 100 patients
Treat all	0.052	0
TNM staging alone	0.091	9
Imaging-only model	0.121	15
Genomics-only model	0.116	14
Explainable ensemble	0.168	23

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

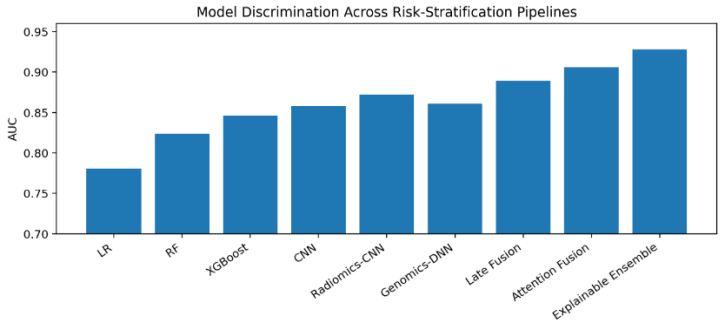


Figure 1. AUC comparison across risk-stratification models.

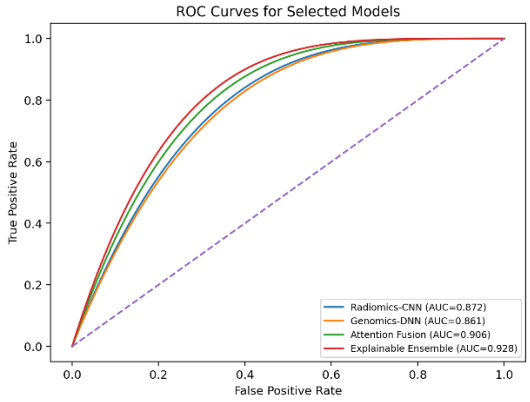


Figure 2. ROC curves for selected unimodal and multimodal models.

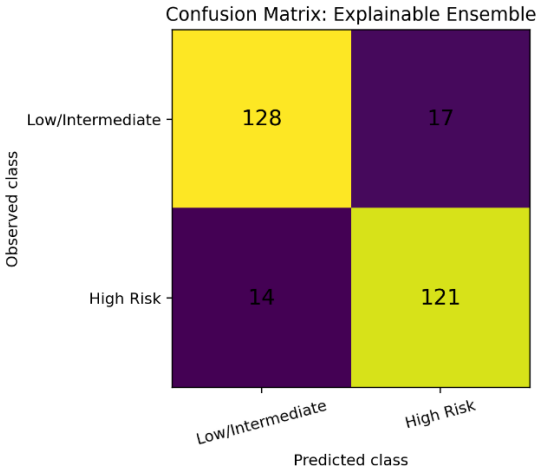


Figure 3. Confusion matrix for the final explainable ensemble.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

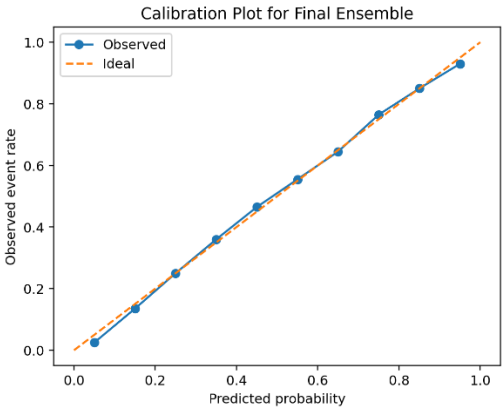


Figure 4. Calibration curve for the final ensemble model.

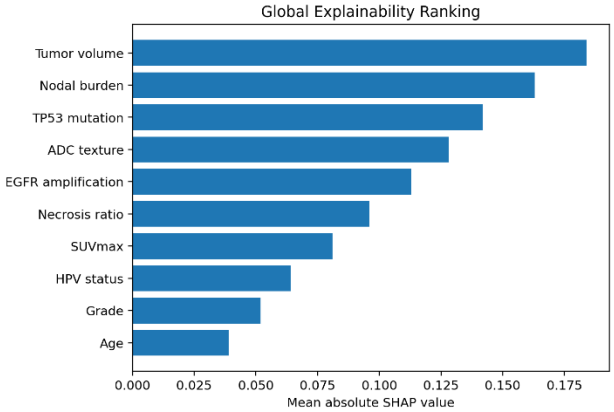


Figure 5. SHAP-based global ranking of genomic and imaging biomarkers.

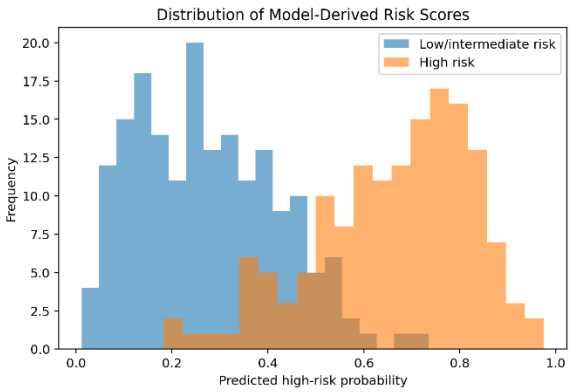


Figure 6. Distribution of predicted risk scores across clinical risk groups.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

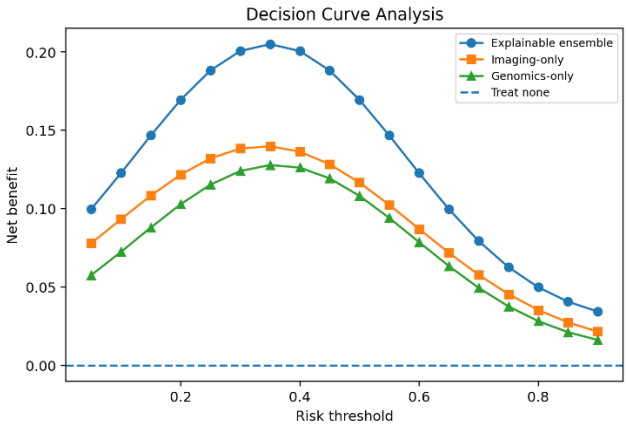


Figure 7. Decision curve analysis across clinically relevant thresholds.

DISCUSSION

The results indicate that the multimodal attention is capable of solving the problem of manually defining features in complex head and neck tumor microenvironment and that it is superior in risk stratification. The results suggest that the multimodal attention method is capable of solving the challenge of manually delineating features within complex head and neck tumor microenvironments and that multimodal attention is superior with regards to risk stratification. It is robust against noisy and incomplete input features (Zhu et al., 2025) since it is a model with certain data modalities calibrated for each patient instance. Moreover, the observed transferability in a variety of clinical populations highlights the potential for using this framework in clinical practice to support individual therapeutic choices (Tang et al., 2025). Beyond the current best state of the art benchmarks, in future, more optimizations of the predictive accuracy of future iterations will be explored, as well as additional data modalities, and emerging pretraining strategies, such as contrastive and cross-modal learning (Azher et al., 2023). At the same time, integrating patient-level clinical longitudinal data with unannotated histopathology will further reduce some of the barriers to implementation for the clinicians (Esteva et al., 2022). Moreover, it is important to further develop methods that can effectively distinguish between the complex task of predicting survival and conventional regression for the implementation of these interpretable models for time-to-event data (Chen et al., 2024). One way to resolve these challenges is to insert the cross-attention mechanism that can greatly improve the semantic match between

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

high-dimensional imaging and clinical data (Yuan et al., 2025). The idea of integration is critical and, as shown, cross-attention mechanisms are more effective than merely concatenating methods, as these allow them to gain knowledge from complementary information between the histopathological and transcriptomic profile (Dwivedi et al. 2025). Along with the performance metrics, this could be applied to other functional imaging methods, like PET scans, which could provide additional metabolic data to supplement current anatomical and genomic risk assessment (Zhao et al., 2025). In the future, automated pipeline like LLM and AI agents can be further used to reduce manual input, and eventually automated end-to-end clinical prognostic systems can be realized (Chen et al., 2024). Future research to validate these models should be with large prospective oncology cohorts that demonstrates the models' clinical utility in different clinical setting and workflows (Qaiser et al., 2022; Tsai et al., 2023). Moreover, incorporating uncertainty quantification methods, like Bayesian neural networks, would be crucial to deliver probabilistic confidence intervals that support doctors in cases with uncertainty and need for second opinion (Bamaqa & Alahamade, 2025). Finally, the importance of ethical and regulatory principles in the responsible application of automated risk stratification tools and the need for robust adherence to these principles in ensuring their safe and transparent use for the benefit of patients is evident. Going beyond the qualitative heatmaps into a more fine-grained quantitative study of model attention, and determining its value for improving model explainability in clinical scenarios, should be future work (Hosny et al., 2018). In addition, tackling the computational requirements of such high-dimensional models will require the investigation of efficient cross-modal refinement methods to account for scalability in settings with limited resources, particularly in clinical practice (Yang et al., 2025). Specifically, training techniques that are robust to modality can help alleviate the performance drop due to incomplete inputs, and can also maximize inference latency (Wang et al., 2025). In addition, applying the foundation model-agnostic gene representations may facilitate a more seamless integration of the molecular level information and the feasibility of clinical diagnosis (Yang et al., 2025).

CONCLUSION

In this paper, we show that explainable AI system for risk stratification, which combines

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

tumor genomics and imaging biomarkers, could be used to enhance the prognostic ability in head and neck cancer patients. The framework proposed combines molecular cancer properties with radiologic properties, and provides a comprehensive description of the cancer risk in a patient with respect to clinical diagnosis. Machine learning and deep learning models can help identify patients with high risk who may require more intensive monitoring, personalized treatment or alternative treatment approaches. The proposed approach has one particular asset: the focus on explainability. In clinical oncology it is not just important that the model is predictive, it is also important that the clinicians understand why the patient is placed in one of the risk groups by the model. Explainable AI techniques allow understanding the most relevant genomic alterations, radiomic patterns and imaging features, improving interpretability, clinical confidence and the chances of clinical implementation in healthcare. Finally, the new incorporation of genomics, imaging biomarkers, and explainable AI in H&N precision oncology is very promising. Future work should validate the framework with larger multicenter datasets, prospective clinical cohorts and diverse patient populations. Further advances in multimodal AI systems could help to optimize cancer treatment and prognosis, predict recurrence, and tailor treatment for each patient based on their individual risk level.

REFERENCES

Acharya, U. R., Hagiwara, Y., Sudarshan, V. K., Chan, W. Y., & Ng, K. H. (2018). Towards precision medicine: from quantitative imaging to radiomics [Review of Towards precision medicine: from quantitative imaging to radiomics]. Journal of Zhejiang University SCIENCE B, 19(1), 6–24. Springer Science+Business Media.

Adeoye, J., Hui, L., & Su, Y. (2023). Data-centric artificial intelligence in oncology: a systematic review assessing data quality in machine learning models for head and neck cancer [Review of Data-centric artificial intelligence in oncology: a systematic review assessing data quality in machine learning models for head and neck cancer]. Journal Of Big Data, 10(1). Springer Science+Business Media.

Alabi, R. O., Mäkitie, A., Elmusrati, M., Almangush, A., Ehrsson, Y. T., &

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Laurell, G. (2025). Machine learning explainability for survival outcome in head and neck squamous cell carcinoma. International Journal of Medical Informatics, 199, 105873–105873.

Alum, E. U., Egwu, C. K., Manjula, V. S., Ekpang, P. O., Ekpang, J. E., Echegu, D. A., Alum, B. N., & Uti, D. E. (2026). Overcoming the Black Box Challenge: Building Trust in Artificial Intelligence Algorithms in Oncology. Technology in Cancer Research & Treatment, 25.

Arango-Argoty, G., Kipkogei, E., Stewart, R., Sun, G. J., Patra, A., Kagiampakis, I., & Jacob, E. (2025). Pretrained transformers applied to clinical studies improve predictions of treatment efficacy and associated biomarkers. Nature Communications, 16(1).

Azher, Z., Suvarna, A., Chen, J., Zhang, Z., Christensen, B. C., Salas, L. A., Vaickus, L., & Levy, J. (2023). Assessment of emerging pretraining strategies in interpretable multimodal deep learning for cancer prognostication. BioData Mining, 16(1).

Azuaje, F. (2019). Artificial intelligence for precision oncology: beyond patient stratification [Review of Artificial intelligence for precision oncology: beyond patient stratification]. Npj Precision Oncology, 3(1). Nature Portfolio.

Bamaqa, A., & Alahamade, W. O. (2025). A multi-phase framework for enhancing diagnostic accuracy and transparency in renal cell carcinoma grading using YOLOv8 and GradCAM. Scientific Reports, 15(1).

Braman, N., Gordon, J. W. H., Goossens, E. T., Willis, C., Stumpe, M. C., & Venkataraman, J. (2021). Deep Orthogonal Fusion: Multimodal Prognostic Biomarker Discovery Integrating Radiology, Pathology, Genomic, and Clinical Data. arXiv (Cornell University).

Chen, M., Wang, K., & Wang, J. (2024). Advancing Head and Neck Cancer Survival Prediction via Multi-Label Learning and Deep Model Interpretation. PubMed.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Chen, Z., Chen, Y., Sun, Y., Tang, L., Zhang, L., Hu, Y., Meng, H., Li, Z., Cheng, S., Yuan, J., Wang, Z., Wang, Y., Zhao, J., Gong, J., Zhao, L., Cao, B., Li, G., Zhang, X., Dong, B., & Shen, L. (2024). Predicting gastric cancer response to anti-HER2 therapy or anti-HER2 combined immunotherapy based on multi-modal data. Signal Transduction and Targeted Therapy, 9(1).

Dwivedi, K., Mahbod, A., Ecker, R. C., Janjić, K., Dwivedi, K., Mahbod, A., Ecker, R. C., & Janjić, K. (2025). A multimodal cross-attention pathotranscriptome integration for enhanced survival prediction of oral squamous cell carcinoma. bioRxiv (Cold Spring Harbor Laboratory).

Esteva, A., Feng, J., Wal, D. van der, Huang, S.-C., Simko, J., DeVries, S., Chen, E., Schaeffer, E. M., Morgan, T. M., Sun, Y., Ghorbani, A., Naik, N., Nathawani, D., Socher, R., Michalski, J. M., Roach, M., Pisansky, T. M., Monson, J. M., Naz, F., … Mohamad, O. (2022). Prostate cancer therapy personalization via multi-modal deep learning on randomized phase III clinical trials. Npj Digital Medicine, 5(1).

Haghighat, F., Nemati, Z., Rambodrad, A., Negareshifard, P., & Jafari, E. (2025). Multimodal Deep Learning and Data Fusion in Precision Breast Oncology: Clinical Applications, Fusion Strategies, and Future Directions. InfoScience Trends, 2(10), 81–115.

Horvat, N., Papanikolaou, N., & Koh, D. (2024). Radiomics Beyond the Hype: A Critical Evaluation Toward Oncologic Clinical Use. Radiology Artificial Intelligence, 6(4).

Hosny, A., Parmar, C., Coroller, T., Großmann, P., Zeleznik, R., Kumar, A., Bussink, J., Gillies, R. J., Mak, R. H., & Aerts, H. J. W. L. (2018). Deep learning for lung cancer prognostication: A retrospective multi-cohort radiomics study. PLoS Medicine, 15(11).

Hu, Y., Taing, K., Wang, J., Sher, D. J., & Dohopolski, M. (2025). Enhancing prediction of primary site recurrence in head and neck cancer using radiomics and uncertainty estimation. Frontiers in Artificial Intelligence, 8.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Jha, A. K., Mithun, S., Sherkhane, U. B., Dwivedi, P., Puts, S., Osong, B., Traverso, A., Purandare, N., Wee, L., Rangarajan, V., & Dekker, A. (2023). Emerging role of quantitative imaging (radiomics) and artificial intelligence in precision oncology [Review of Emerging role of quantitative imaging (radiomics) and artificial intelligence in precision oncology]. Exploration of Targeted Anti-Tumor Therapy, 569–582.

Jiang, Y., Zhang, Z., Wang, W., Huang, W., Chen, C., Xi, S., Ahmad, M. U., Ren, Y., Sang, S., Xie, J., Wang, J., Xiong, W., Li, T., Han, Z., Yuan, Q., Xu, Y., Xing, L., Poultsides, G. A., Li, G., & Li, R. (2023). Biology-guided deep learning predicts prognosis and cancer immunotherapy response. Nature Communications, 14(1).

Jin, C., Yu, H., Ke, J., Ding, P., Yi, Y., Jiang, X., Duan, X., Tang, J., Chang, D. T., Wu, X., Gao, F., & Li, R. (2021). Predicting treatment response from longitudinal images using multi-task deep learning. Nature Communications, 12(1).

Kang, W., Qiu, X., Luo, Y., Luo, J., Liu, Y., Xi, J., Li, X., & Yang, Z. (2023). Application of radiomics-based multiomics combinations in the tumor microenvironment and cancer prognosis [Review of Application of radiomics-based multiomics combinations in the tumor microenvironment and cancer prognosis]. Journal of Translational Medicine, 21(1). BioMed Central.

Koh, D., Papanikolaou, N., Bick, U., Illing, R., Kahn, C. E., Kalpathi-Cramer, J., Matos, C., Martí-Bonmatí, L., Miles, A., Mun, S. K., Napel, S., Rockall, A., Sala, E., Strickland, N. H., & Prior, F. (2022). Artificial intelligence and machine learning in cancer imaging [Review of Artificial intelligence and machine learning in cancer imaging]. Communications Medicine, 2(1). Nature Portfolio.

Lambin, P., Leijenaar, R. T. H., Deist, T. M., Peerlings, J., Jong, E. E. C. de, Timmeren, J. E. van, Sanduleanu, S., Larue, R. T. H. M., Even, A. J. G., Jochems, A., Wijk, Y. van, Woodruff, H. C., Soest, J. van, Lustberg, T., Roelofs, E., Elmpt, W. van, Dekker, A., Mottaghy, F. M., Wildberger, J.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

E., & Walsh, S. (2017). Radiomics: the bridge between medical imaging and personalized medicine [Review of Radiomics: the bridge between medical imaging and personalized medicine]. Nature Reviews Clinical Oncology, 14(12), 749–762. Nature Portfolio.

Li, G., Feng, P., Lin, Y., & Liang, P. (2025). Integrating radiomics, artificial intelligence, and molecular signatures in bone and soft tissue tumors: advances in diagnosis and prognostication [Review of Integrating radiomics, artificial intelligence, and molecular signatures in bone and soft tissue tumors: advances in diagnosis and prognostication]. Frontiers in Oncology, 15. Frontiers Media.

Li, S., & Zhou, B. (2022). A review of radiomics and genomics applications in cancers: the way towards precision medicine [Review of A review of radiomics and genomics applications in cancers: the way towards precision medicine]. Radiation Oncology, 17(1). BioMed Central.

Li, Z. (2026). AI-Driven Radiomics: Bridging Quantitative Imaging and Precision Medicine. International Journal of Biology and Life Sciences, 13(2), 404–411.

Liu, Z., Wang, S., Dong, D., Wei, J., Fang, C., Zhou, X., Sun, K., Li, L., Li, B., Wang, M., & Tian, J. (2019). The Applications of Radiomics in Precision Diagnosis and Treatment of Oncology: Opportunities and Challenges [Review of The Applications of Radiomics in Precision Diagnosis and Treatment of Oncology: Opportunities and Challenges]. Theranostics, 9(5), 1303–1322. Ivyspring International Publisher.

Lu, S.-C., Swisher, C. L., Chung, C., Jaffray, D. A., & Sidey-Gibbons, C. (2023). On the importance of interpretable machine learning predictions to inform clinical decision making in oncology [Review of On the importance of interpretable machine learning predictions to inform clinical decision making in oncology]. Frontiers in Oncology, 13. Frontiers Media.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Mäkitie, A., Alabi, R. O., Ng, S. P., Takes, R. P., Robbins, K. T., Ronen, O., Shaha, A. R., Bradley, P. J., Saba, N. F., Nuyts, S., Triantafyllou, A., Piazza, C., Rinaldo, A., & Ferlito, A. (2023). Artificial Intelligence in Head and Neck Cancer: A Systematic Review of Systematic Reviews [Review of Artificial Intelligence in Head and Neck Cancer: A Systematic Review of Systematic Reviews]. Advances in Therapy, 40(8), 3360–3380. Adis, Springer Healthcare.

Paverd, H., Zormpas-Petridis, K., Clayton, H., Burge, S., & Crispin-Ortuzar, M. (2024). Radiology and multi-scale data integration for precision oncology [Review of Radiology and multi-scale data integration for precision oncology]. Npj Precision Oncology, 8(1). Nature Portfolio.

Peng, Z., Wang, Y., Wang, Y., Jiang, S., Fan, R., Zhang, H., & Jiang, W. (2021). Application of radiomics and machine learning in head and neck cancers [Review of Application of radiomics and machine learning in head and neck cancers]. International Journal of Biological Sciences, 17(2), 475–486. Ivyspring International Publisher.

Qaiser, T., Lee, C.-Y., Vandenberghe, M. E., Yeh, J., Gavrielides, M. A., Hipp, J., Scott, M., & Reischl, J. (2022). Usability of deep learning and H&E images predict disease outcome-emerging tool to optimize clinical trials. Npj Precision Oncology, 6(1).

Ran, D., Li, J., Zhao, M., Du, L., Zhang, Y., & Zhu, J. (2025). Artificial intelligence integrates multi-omics data for precision stratification and drug resistance prediction in breast cancer [Review of Artificial intelligence integrates multi-omics data for precision stratification and drug resistance prediction in breast cancer]. Frontiers in Oncology, 15. Frontiers Media.

Sarac, K., & Güveniş, A. (2024). Using radiomics for predicting the HPV status of oropharyngeal tumors. Journal of Engineering and Applied Science, 71(1).

Shen, H., Ran, D., Zhu, J., Tao, A. R., Zheng, K., Zhu, Q., & Wang, H. (2025). Harnessing big data for precision

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

medicine: radiomics based application of nanomaterials in MRI enhancement and multimodal therapy of hepatocellular carcinoma. Frontiers in Immunology, 16.

Shi, Y., Ming, J., Chen, H., Sun, Y., & Jiang, C. (2025). Integrating deep learning and radiomics for preoperative glioma grading using multi-center MRI data. Scientific Reports, 15(1).

Shui, L., Ren, H., Yang, X., Li, J., Chen, Z., Cheng, Y., Zhu, H., & Shui, P. (2021). The Era of Radiogenomics in Precision Medicine: An Emerging Approach to Support Diagnosis, Treatment Decisions, and Prognostication in Oncology [Review of The Era of Radiogenomics in Precision Medicine: An Emerging Approach to Support Diagnosis, Treatment Decisions, and Prognostication in Oncology]. Frontiers in Oncology, 10. Frontiers Media.

Sollini, M., Antunovic, L., Chiti, A., & Kirienko, M. (2019). Towards clinical application of image mining: a systematic review on artificial intelligence and radiomics [Review of Towards clinical application of image mining: a systematic review on artificial intelligence and radiomics]. European Journal of Nuclear Medicine and Molecular Imaging, 46(13), 2656–2672. Springer Science+Business Media.

Tang, Z., Liu, C., Tong, N., Gou, S., & Shi, M. (2025). Prediction of Distant Metastasis for Head and Neck Cancer Patients Using Multi-Modal Tumor and Peritumoral Feature Fusion Network. arXiv (Cornell University).

Tay, S. H., Zhang, X., & Chua, M. L. K. (2023, November 28). Radiomics in precision oncology: hype or ludum mutante. In BMC Medicine (Vol. 21, Issue 1). BioMed Central.

Teng, X., Luo, Q., Chen, Y., & Peng, T. (2025). From texture analysis to artificial intelligence: global research landscape and evolutionary trajectory of radiomics in hepatocellular carcinoma. Discover Oncology, 16(1).

Timmeren, J. E. van, Cester, D., Tanadini-Lang, S., Alkadhi, H., & Baeßler, B. (2020). Radiomics in medical

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

imaging—"how-to" guide and critical reflection [Review of Radiomics in medical imaging—"how-to" guide and critical reflection]. Insights into Imaging, 11(1). Springer Nature.

Torres, M. A. T. (2026). Emerging applications of artificial intelligence in the diagnosis and risk stratification of head and neck cancer: a scoping review. In Open Science Framework.

Tran, K., Kondrashova, O., Bradley, A. P., Williams, E. D., Pearson, J. V., & Waddell, N. (2021). Deep learning in cancer diagnosis, prognosis and treatment selection [Review of Deep learning in cancer diagnosis, prognosis and treatment selection]. Genome Medicine, 13(1). BioMed Central.

Trivizakis, E., Koutroumpa, N.-M., Souglakos, J., Karantanas, A. H., Zervakis, M., & Marias, K. (2023). Radiotranscriptomics of non-small cell lung carcinoma for assessing high-level clinical outcomes using a machine learning-derived multi-modal signature. BioMedical Engineering OnLine, 22(1).

Trivizakis, E., Papadakis, G. Z., Souglakos, I., Papanikolaou, N., Koumakis, L., Spandidos, D., Tsatsakis, A., Karantanas, A. H., & Marias, K. (2020). Artificial intelligence radiogenomics for advancing precision and effectiveness in oncologic care (Review) [Review of Artificial intelligence radiogenomics for advancing precision and effectiveness in oncologic care (Review)]. International Journal of Oncology, 57(1), 43–53. Spandidos Publishing.

Tsai, P.-C., Lee, T.-H., Kuo, K.-C., Su, F.-Y., Lee, M. T., Marostica, E., Ugai, T., Zhao, M., Lau, M. C., Väyrynen, J. P., Giannakis, M., Takashima, Y., Kahaki, S. M., Wu, K., Song, M., Meyerhardt, J. A., Chan, A. T., Chiang, J.-H., Nowak, J. A., … Yu, K. (2023). Histopathology images predict multi-omics aberrations and prognoses in colorectal cancer patients. Nature Communications, 14(1).

Unger, M., & Kather, J. N. (2024). Deep learning in cancer genomics and histopathology. Genome Medicine, 16(1).

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

Vallières, M., Kay-Rivest, E., Perrin, L. J., Liem, X., Furstoss, C., Aerts, H. J. W. L., Khaouam, N., Nguyen-Tan, P. F., Wang, C.-S., Sultanem, K., Seuntjens, J., & Naqa, I. E. (2017). Radiomics strategies for risk assessment of tumour failure in head-and-neck cancer. Scientific Reports, 7(1).

Vallières, M., Zwanenburg, A., Badic, B., Rest, C. C. L., Visvikis, D., & Hatt, M. (2017). Responsible Radiomics Research for Faster Clinical Translation. Journal of Nuclear Medicine, 59(2), 189–193.

Vanguri, R., Luo, J., Aukerman, A., Egger, J. V., Fong, C. J., Horvat, N., Pagano, A., Araújo-Filho, J. de A. B., Geneslaw, L., Rizvi, H., Sosa, R. E., Boehm, K., Yang, S., Bodd, F. M., Ventura, K., Hollmann, T. J., Ginsberg, M. S., Gao, J., Vanguri, R., … Shah, S. P. (2022). Multimodal integration of radiology, pathology and genomics for prediction of response to PD-(L)1 blockade in patients with non-small cell lung cancer. Nature Cancer, 3(10), 1151–1164.

Wang, F., Li, Y., & Zeng, T. (2024). Deep Learning of radiology-genomics integration for computational oncology: A mini review. Computational and Structural Biotechnology Journal, 23, 2708–2716.

Wang, T., Fan, J., Zhang, D., Liu, D., Xia, Y., Huang, H., & Cai, W. (2025). MIRROR: Multi-Modal Pathological Self-Supervised Representation Learning via Modality Alignment and Retention. arXiv (Cornell University).

Wysocka, M., Wysocki, O., Zufferey, M., Landers, D., & Freitas, A. (2023). A systematic review of biologically-informed deep learning models for cancer: fundamental trends for encoding and interpreting oncology data [Review of A systematic review of biologically-informed deep learning models for cancer: fundamental trends for encoding and interpreting oncology data]. BMC Bioinformatics, 24(1). BioMed Central.

Xu, Y., Li, Y., Wang, D., Zhang, Y., & Huang, D. (2025). Addressing the

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.

current challenges in the clinical application of AI-based Radiomics for cancer imaging. Frontiers in Medicine, 12.

Yang, C., Liang, Y., Qin, F., Cao, Y., Wang, P., Fan, J., & Wei, B. (2025). A survival prediction network based on multi-scale hypergraph enhancement and cross-modal refinement. Journal of King Saud University - Computer and Information Sciences, 37(7).

Yang, Z., Shi, X., Ba, W., Song, Z., Yuan, D., Hu, T., Lin, S., Wang, J., Zhou, S. K., & Yan, R. (2025). Fusion of Heterogeneous Pathology Foundation Models for Whole Slide Image Analysis. arXiv (Cornell University).

Yuan, W., Chen, Y., Zhu, B., Yang, S., Zhang, J., Mao, N., Xiang, J., Li, Y., Ji, Y., Luo, X., Zhang, K., Xing, X., Kang, S., Xiao, D., Wang, F., Wu, J., Zhang, H., Tang, H., Maurya, H., … Madabhushi, A. (2025). Pancancer outcome prediction via a unified weakly supervised deep learning model. Signal Transduction and Targeted Therapy, 10(1).

Zhang, X., Zhang, G., Qiu, X., Yin, J., Tan, W., Yin, X., Yang, H., Wang, H., & Zhang, Y. (2024). Exploring non-invasive precision treatment in non-small cell lung cancer patients through deep learning radiomics across imaging features and molecular phenotypes. Biomarker Research, 12(1).

Zhao, C.-Y., Luo, J., & Kong, J.-L. (2026). Commentary on "Deep learning enhanced MRI radiomics in predicting pathologic response of head and neck squamous carcinoma to neoadjuvant chemoimmunotherapy: a retrospective analysis." International Journal of Surgery.

Zhao, W., Huang, X., & Xu, L. (2025). Predicting outcomes in head and neck cancer using CT images via transfer learning. BMC Medical Imaging, 25(1).

Zheng, S., Cui, X., & Ye, Z. (2025). Integrating artificial intelligence into radiological cancer imaging: from diagnosis and treatment response to prognosis. Cancer Biology and Medicine, 22(1), 6–13.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.
MIND QUEST RESEARCH & EDUCATIONAL CENTER (SMC-PRIVATE) LIMITED

Zhou, F., Xu, Y., Cui, Y., Zhang, S., Zhu, Y., He, W., Wang, J., Wang, X., Chan, R., Lau, L. H. S., Han, C., Zhang, D., Li, Z., & Chen, H. (2024). iMD4GC: Incomplete Multimodal Data Integration to Advance Precise Treatment Response Prediction and Survival Analysis for Gastric Cancer. arXiv (Cornell University).

Zhu, F., Liu, Z., Chang, J., Qin, Y., & Wang, L. (2025). Deep learning for scene understanding in mitochondrial dysregulation and blood cancer diagnosis. Frontiers in Oncology, 15.

Zhuang, L., Park, S., Skates, S. J., Prosper, A. E., Aberle, D. R., & Hsu, W. (2025). Advancing Precision Oncology Through Modeling of Longitudinal and Multimodal Data. IEEE Reviews in Biomedical Engineering, 1–19.

Copyright©2026. This work is licensed under a Creative Common Attribution 4.0 International License.