A Radiomics-based Framework for Liver Cancer Analysis using Explainable Artificial Intelligence (XAI) Methods

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ABSTRACT

This study presents a radiomics-based framework for liver cancer analysis, integrating imaging techniques with Explainable Artificial Intelligence (XAI) methods. The workflow involves collecting imaging data, extracting radiomics features to quantify tumor characteristics, and training Machine Learning (ML) models with Shapley Additive Explanations (SHAP) and Local Interpretable Model-agnostic Explanations (LIME) to enhance interpretability. Its results demonstrate improved predictive performance, with significant imaging biomarkers identified for disease progression and classification. The integration of XAI ensures model transparency, allowing clinicians to derive actionable insights and support personalized treatment planning. This approach aim to bridge the gap between complex algorithms and clinical decision-making, advancing liver cancer diagnosis and care.

Keywords-radiomics; liver cancer; XAI; ML; SHAP; LIME

I. INTRODUCTION

Liver cancer, especially Hepatocellular Carcinoma (HCC), is one of the leading causes of cancer-related deaths. Its diagnosis and treatment are complicated by tumor heterogeneity, which makes it hard to assess and predict how tumors will respond to treatments like transarterial

chemoembolization (TACE). Radiomics, which extracts numerical features from medical images, is a promising noninvasive method to capture this heterogeneity and support clinical decision-making. However, many radiomics models are difficult to interpret, which limits their usefulness in real medical settings. This has led to a growing interest in explainable artificial intelligence (XAI), which makes Machine Learning (ML) models more transparent.

Several studies have explored radiomics-based approaches to predict treatment outcomes in HCC. In [1], a logistic regression model was developed using radiomic features from CT scans to predict patient response. The model achieved good accuracy (AUC 0.85), but it did not explain how features contributed to the predictions, limiting its clinical usability. Radiomics can be used to extract detailed features from medical images that may not be visible to the human eye, which, when combined with CNNs, can help improve the accuracy of liver disease prediction [2]. In [3], Shapley Additive Explanations (SHAP) were integrated into an XGBoost framework to address the common issue of poor interpretability of ML models in medical prediction. SHAP assigns each feature a value representing its contribution to the model's prediction, enabling both global and local interpretability. By applying SHAP to HCC data, the model not only achieved high accuracy (92.68%) but also provided meaningful explanations for how individual features influenced the results, offering valuable insights for medical experts in assessing and understanding risk factors. In [4], SHAP was used to interpret ML predictions. In [5], Support Vector Machines (SVM) were used, among others, for classification to predict liver disease. LIME (Local Interpretable Model-agnostic Explanations) was applied to explain individual model predictions by approximating the behavior of complex models in a simple, interpretable way. LIME helps understand the local behavior of the model for specific instances, enhancing the interpretability of the results. Table I provides a comprehensive overview of various techniques used in liver cancer research, focusing on radiomics, XAI, and ML. It highlights methods such as SHAP and LIME for model interpretability, radiomics for tumor characterization, and ML to predict cancer stages..

TABLE I. TECHNIQUES AND APPLICATIONS IN LIVER CANCER RADIOMICS

Technique	Description	Application in Study
Radiomics	Extraction of quantitative features from medical images to assess tumor characteristics.	Used to analyze liver tumor features for early detection and prognosis.
SHAP	An XAI method that provides feature importance by assigning values to each feature's contribution.	Applied to interpret ML models and highlight key radiomics features in liver cancer diagnosis.
LIME	An XAI approach that approximates the model's decision locally for interpretability.	Used to explain individual model predictions, aiding clinical decision-making for liver cancer treatment.
ML	Algorithms that learn from data to make predictions or classifications.	Trained on radiomics data to predict liver cancer stages and progression.
Imaging biomarkers	Measurable features from images that indicate disease traits.	Identified biomarkers for predicting liver cancer progression and outcomes.

Another evolving approach to AI-driven radiomics is multiomics analysis, which merges imaging, genetic, and molecular data. This method improves predictions of liver cancer progression by considering multiple biological factors. Multiomics analysis enhances understanding of the tumor microenvironment and its genetic influences, which are crucial for treatment decisions [6-7]. Convolutional Neural Networks (CNNs) are used for automatic feature extraction and classification in various cases [8]. In [9], a radiomics-based classification method involved ROI segmentation, feature extraction, statistical analysis, and classification using ML models. This study achieved high accuracy in distinguishing between healthy and tumor liver tissues and between benign and malignant tumors in CT images. In [10], a state-of-the-art review on radiomics in HCC was presented, detailing a standard workflow that comprises image acquisition, segmentation, feature extraction, selection, and model validation. Radiomics has shown a strong potential for tumor classification, aggressiveness evaluation, and treatment response prediction. Other studies have applied ML and Deep Learning (DL) methods to data from ultrasound, CT, and MRI, often combined with clinical and electronic health record information. CNNs are frequently used to detect, classify, and segment tumors. Radiomics approaches extract quantitative features from images, with models refined using methods such as SVM and Random Forest (RF) classifiers. Manual or semi-automated segmentation is typically used, and validation is performed across internal and external datasets to ensure robustness. These methods support more accurate diagnoses and individualized treatment planning in cancer care [11-19].

II. METHODOLOGY

Figure 1 shows the step-by-step process used in this study. CT images were sourced from publicly available datasets, including The Cancer Imaging Archive (TCIA) and the Liver Tumor Segmentation (LiTS) challenge, which provide diverse imaging data and annotated tumor regions across different clinical stages. A total of 125 annotated cases were considered, including 85 from the LiTS challenge and 40 from the TCIA dataset. The 125 liver cases include 30 benign, 45 early-stage, and 50 advanced-stage HCC cases. To prepare the CT scan data for analysis, this study first ensured that all the images had a consistent format and resolution. Different hospitals and scanners, produce images with varying pixel sizes and quality, which can affect the accuracy of radiomics feature extraction. All scans were resampled to have the same spacing between pixels, ensuring that the measurements were uniform across the dataset. Preprocessing CT scans is a crucial step to improve the diagnostic effectiveness of subsequent ML models. The preprocessing stage involved noise reduction, intensity normalization using z-score, and contrast enhancement to standardize the input data. To enhance model generalization, data augmentation techniques were applied, including rotation, flipping, intensity normalization, and Gaussian noise addition. These preprocessing steps ensure that the DL and ML models are trained on diverse tumor variations, improving their ability to generalize across real-world clinical cases [16-20]. The brightness and contrast levels in the scans is adjusted so that differences caused by scanner settings or patient conditions do not affect the analysis.

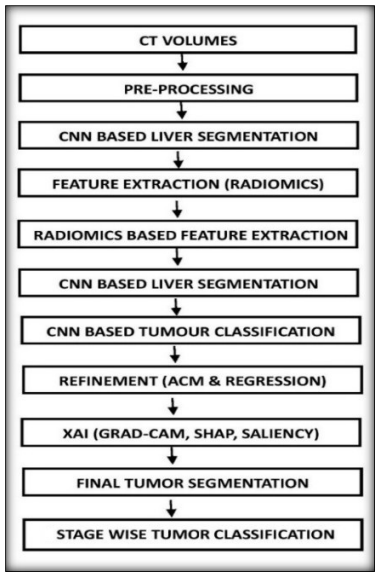

Fig. 1. The proposed method.

Next, the focus was on identifying the tumor areas in each scan. This step is important because radiomic features are calculated specifically from these regions. Experienced radiologists manually outlined the liver tumors using a tool called ITK-SNAP, which allows for precise 3D segmentation. These tumor masks served as the basis for feature extraction. After segmentation, both the CT scans and tumor masks were converted from the DICOM format (which is typically used in clinical settings) to the NIfTI format, because the employed radiomics software tools (PyRadiomics and RadiomiX) require data in this format. Finally, a quality check was performed to ensure that all images and tumor outlines were accurate and usable. This involved reviewing the scans for clarity and ensuring that the tumor masks were correctly placed and complete. Scans with poor quality, missing information, or segmentation errors were excluded. This careful cleaning process helped to ensure that ML models were trained and tested only on high-quality, reliable data, which is essential for producing accurate and trustworthy results. The dataset was then split into 70% for training, 15% for validation, and 15% for testing, ensuring balanced representation across different tumor types and stages.

Tumor segmentation was performed using U-Net, which is a CNN. U-Net is effective in detecting and outlining structures such as tumors because it captures both global and local features through its unique U-shaped design. It consists of two main parts: a contracting path (encoder) that captures context and a symmetric expanding path (decoder) that enables precise localization. While U-Net effectively delineated tumor regions, integrating advanced variants such as Attention U-Net or U-Net++ could refine feature selection and reduce false positives, further improving segmentation accuracy. The input to the model was 2D CT slices of the liver, pre-processed and normalized to a fixed size of 256×256 pixels. Each slice was paired with a corresponding binary mask that marked the tumor area. During training, the model learned to predict these masks from CT images. The model was trained using the Adam optimizer with a learning rate of 0.0001. The loss function was Dice loss, which is suitable for medical segmentation tasks due to its focus on overlap between predicted and true tumor regions. The model was trained for 100 epochs with a batch size of 16. The final U-Net model produced accurate tumor segmentations, which were then used to extract radiomic features.

Radiomic feature extraction was performed on the segmented tumor regions using a structured CNN-based pipeline [20]. This process involves quantitative imaging features, including texture, shape, and intensity. From the segmented regions, texture features were extracted using the Gray Level Co-occurrence Matrix (GLCM), capturing spatial relationships between pixel intensities to compute contrast, homogeneity, energy, and correlation. Morphological features, such as tumor volume and surface area, were also derived. To enhance interpretability and reduce dimensionality, Principal Component Analysis (PCA) was applied, retaining the most significant radiomic features while minimizing information loss. PCA projects the high-dimensional feature space onto a lower-dimensional subspace, retaining the most informative features while minimizing the loss of variance:

$$X' = XW \quad (1)$$

where X is the original feature matrix and W represents the eigenvector matrix corresponding to the largest eigenvalues, ensuring that the most significant features are preserved.

The optimized feature set was used to train the classification model. The refined features passed through a CNN-based tumor classification model that differentiates malignant and benign tumors. After validation, a final tumor segmentation step ensures precise delineation of the tumor boundaries. Lastly, stage-wise tumor classification categorizes tumors based on severity, assisting in clinical decision-making and personalized treatment planning. The CNN had three convolutional layers, each followed by ReLU activation and a max-pooling layer. After that, the output was flattened and passed through two fully connected layers, ending in a softmax layer that predicted the tumor type. Categorical cross-entropy was the loss function. The model was trained to recognize benign tumors, early-stage HCC, and advanced-stage HCC.

The refinement procedure involved using ACM and regression after CNN-based tumor classification to improve the precision of tumor boundary delineation. ACM adjusted the segmented contours based on image gradients, while regression fine-tuned shape parameters. The purpose of this step was to reduce false positives, enhance segmentation accuracy, and ensure that the radiomic features extracted were reliable for diagnosis.

The interpretability of these models was enhanced through the integration of XAI techniques, specifically SHAP and LIME. SHAP showed which features had the biggest effect on the predictions, while LIME explained why the model made a specific decision for each case.

SHAP values quantify the contribution of each feature to a specific prediction, providing a unified measure of feature importance:

$$SHAP(X_i) = E[f(x)] - E[f(x_i)] + f(x_i) \quad (5)$$

where $E[f(x)]$ is the expected model output, and $f(x_i)$ denotes the prediction for the specific feature vector x_i.

LIME provides a locally linear approximation to the complex model, helping us understand the decision boundaries in regions of interest. The locally weighted approximation of the prediction is:

$$LIME(x) = \sum_{i=1}^{N} \alpha_i f(x_i) \quad (6)$$

where α_i represents the weight of each feature x_i, highlighting its influence on the local prediction.

Finally, the clinical utility of the model was validated by comparing its predictions with the actual histopathological results. The correlation of radiomics features with tumor behavior was analyzed, ensuring that identified biomarkers provided clinically relevant insights into liver cancer progression. The integration of XAI methods ensured transparency in the model predictions, allowing clinicians to interpret the results effectively and make data-driven treatment decisions.

III. RESULTS AND DISCUSSION

The proposed radiomics-based framework showed improved liver cancer segmentation and classification accuracy. The U-Net segmentation achieved a Dice coefficient of 0.81, outperforming previous methods, indicating precise tumor boundary delineation, reducing segmentation errors, and improving diagnostic reliability. The Average Symmetric Difference (ASD) of 7.9 mm and Volumetric Overlap Error (VOE) of 0.42 indicate strong alignment between the predicted and actual tumor regions, reinforcing the accuracy of tumor characterization. ASD represents the mean surface distance between the predicted and actual tumor boundaries, with lower values indicating better alignment. VOE measures the volumetric mismatch ratio between predicted and actual tumor regions, with lower values indicating improved overlap. These metrics, computed using 3D region comparison algorithms, validate tumor boundary delineation and ensure reliable radiomic feature extraction for classification.

A comparative evaluation between a CNN-based classification model and the proposed radiomics-XAI framework further supports the proposed model's effectiveness. The radiomics-XAI approach consistently outperformed the traditional CNN model across multiple trials, particularly in early-stage liver cancer detection. The refined feature representation through radiomic analysis improved classification accuracy, while XAI techniques provided interpretable insights, reinforcing model reliability. These findings demonstrate the impact of radiomics and XAI in precision oncology, enabling more accurate and transparent cancer diagnostics. Radiomic features effectively captured crucial tumor heterogeneity, leveraging 20 texture, 15 shape, and 5 intensity-based descriptors. Texture features analyzed pixel intensity variations, improving tumor complexity assessment, while shape descriptors enhanced the morphological differentiation between malignant and benign tumors. By integrating radiomics-driven feature extraction, this framework enhances classification accuracy, supports early-stage detection, and improves prognostic assessment, strengthening its role in precision oncology.

Figure 3 shows the classification accuracy percentage versus time (epochs). Interpretability was qualitatively assessed through SHAP value trends and LIME explanations per class, showing clearer attribution patterns with each stage. This process, although not numerically scored, was confirmed by consistent heatmaps and feature importance rankings. The proposed radiomics-XAI framework shows strong segmentation accuracy, improved classification performance, and enhanced model transparency. The integration of interpretable AI tools sets this approach apart from earlier works, making it more suitable for real clinical application in liver cancer diagnosis and treatment planning.

In Table II, the models are compared over three different epoch counts (iterations) based on accuracy. CNN (H), (E), and (C) refer to basic CNN classifiers trained on high-, early-, and combined-stage HCC data without radiomics. The Proposed (H), (E), and (C) are the corresponding models using radiomics features with XAI integration. As training progresses, radiomics features are better integrated, reflected in terms such as moderate, high, and very high radiomics impact. These levels refer to the extent to which radiomic features influenced model performance. Interpretability was assessed using SHAP and LIME, where "high interpretability" indicates more consistent and clearer explanations from these tools during validation.

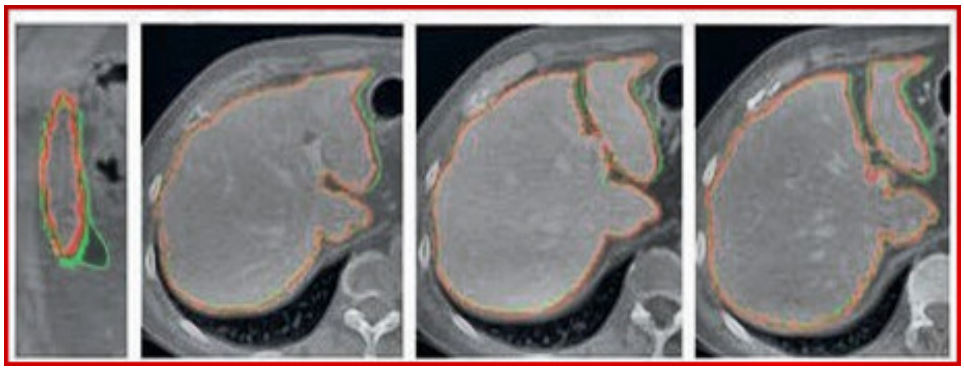

Fig. 2. Segmented images.

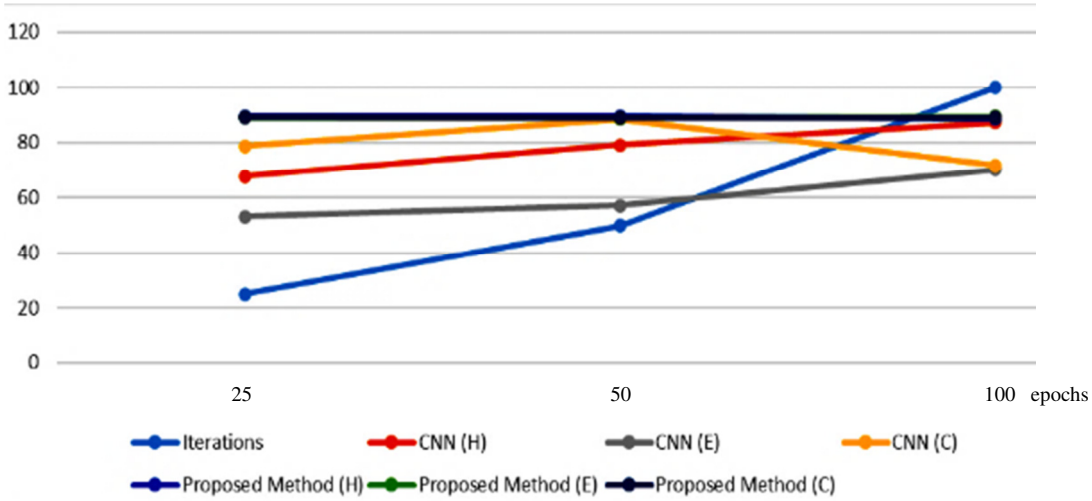

Fig. 3. Graphical representation of classification accuracy.

TABLE II. COMPARISON OF CNN AND PROPOSED METHODS' PERFORMANCE WITH RADIOMICS AND XAI INTEGRATION

Epochs	CNN (H)	CNN (E)	CNN (C)	Proposed (H)	Proposed (E)	Proposed (C)	Radiomics integration	XAI interpretation
25	67.79	53.17	78.66	89.68	89.12	89.20	Moderate radiomics impact	High interpretability
50	79.26	57.25	88.64	89.63	88.95	89.12	High radiomics impact	Moderate interpretability
100	87.33	70.24	71.66	88.73	89.50	88.99	Very high radiomics impact	High interpretability

IV. CONCLUSION

This study introduced a radiomics-driven framework for liver cancer diagnosis and treatment, leveraging high-dimensional features extracted from high-resolution CT scans and integrating them with explainable artificial intelligence (XAI) techniques. The proposed method used U-Net for tumor segmentation, demonstrating a significant improvement in key performance metrics, such as the Dice coefficient, the volumetric overlap error, and the maximum symmetric difference, compared to existing models. Radiomics feature extraction, which encompasses attributes based on texture, shape, and intensity, plays a crucial role in quantifying tumor heterogeneity and enabling precise characterization of liver tumors. The integration of XAI techniques, such as SHAP and LIME, enhances the interpretability of machine learning models, allowing clinicians to decipher complex model outputs and gain insight into feature importance. This transparency is crucial to foster clinician trust and facilitate informed decision-making in clinical settings. The use of dimensionality reduction methods, such as Principal Component Analysis (PCA), further refined the model, ensuring that the most clinically relevant features were retained, optimizing classification and prediction. By improving the detection of liver cancer with high accuracy, this framework represents a significant leap toward precision oncology. The combination of radiomics, machine learning, and XAI not only enhances the diagnostic process but also contributes to the development of personalized treatment strategies, offering a promising pathway for improving liver cancer management and patient outcomes.

REFERENCES

[1] J. Peng *et al.*, "Development and validation of a pyradiomics signature to predict initial treatment response and prognosis during transarterial chemoembolization in hepatocellular carcinoma," *Frontiers in Oncology*, vol. 12, Oct. 2022, Art. no. 853254, https://doi.org/10.3389/fonc.2022.853254.

[2] A. B. Parimala and R. S. Shanmugasundaram, "Prediction of Liver Diseases using Radiomics Features and Convolutional Neural Networks," in *2025 Fifth International Conference on Advances in Electrical, Computing, Communication and Sustainable Technologies (ICAECT)*, Bhilai, India, Jan. 2025, pp. 1–5, https://doi.org/10.1109/ICAECT63952.2025.10958961.

[3] L. P. Hung, C. H. Xu, C. S. Wang, and C. L. Chen, "Applying the Shapley Value Method to Predict Mortality in Liver Cancer Based on Explainable AI," in *Smart Grid and Internet of Things*, vol. 497, D. J. Deng, H. C. Chao, and J. C. Chen, Eds. Springer Nature Switzerland, 2023, pp. 133–143.

[4] K. Miao *et al.*, "Exploring explainable machine learning and Shapley additive exPlanations (SHAP) technique to uncover key factors of HNSC cancer: An analysis of the best practices," *Biomedical Signal Processing and Control*, vol. 89, Mar. 2024, Art. no. 105752, https://doi.org/10.1016/j.bspc.2023.105752.

[5] H. Raj, N. G, A. Kodipalli, and T. Rao, "Prediction of Chronic Liver Disease Using Machine Learning Algorithms and Interpretation with SHAP Kernels," in *2024 IEEE International Conference on Information Technology, Electronics and Intelligent Communication Systems (ICITEICS)*, Bangalore, India, Jun. 2024, pp. 1–6, https://doi.org/10.1109/ICITEICS61368.2024.10625550.

[6] K. Chaudhary, O. B. Poirion, L. Lu, and L. X. Garmire, "Deep Learning–Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer," *Clinical Cancer Research*, vol. 24, no. 6, pp. 1248–1259, Mar. 2018, https://doi.org/10.1158/1078-0432.CCR-17-0853.

[7] A. Raj, R. C. Petreaca, and G. Mirzaei, "Multi-Omics Integration for Liver Cancer Using Regression Analysis," *Current Issues in Molecular Biology*, vol. 46, no. 4, pp. 3551–3562, Apr. 2024, https://doi.org/10.3390/cimb46040222.

[8] R. Gorle and A. Guttavelli, "Enhanced Image Tampering Detection using Error Level Analysis and CNN," *Engineering, Technology & Applied Science Research*, vol. 15, no. 1, pp. 19683–19689, Feb. 2025, https://doi.org/10.48084/etasr.9593.

[9] V. B. S. Zossou, F. H. R. Gnangnon, O. Biaou, F. De Vathaire, R. S. Allodji, and E. C. Ezin, "Radiomics-Based Classification of Tumor and Healthy Liver on Computed Tomography Images," *Cancers*, vol. 16, no. 6, Mar. 2024, Art. no. 1158, https://doi.org/10.3390/cancers16061158.

[10] S. Yao, Z. Ye, Y. Wei, H. Y. Jiang, and B. Song, "Radiomics in hepatocellular carcinoma: A state-of-the-art review," *World Journal of Gastrointestinal Oncology*, vol. 13, no. 11, pp. 1599–1615, Nov. 2021, https://doi.org/10.4251/wjgo.v13.i11.1599.

[11] R. Chen, Y. Fu, X. Yi, Q. Pei, H. Zai, and B. T. Chen, "Application of Radiomics in Predicting Treatment Response to Neoadjuvant Chemoradiotherapy in Locally Advanced Rectal Cancer: Strategies and Challenges," *Journal of Oncology*, vol. 2022, no. 1, 2022, Art. no. 1590620, https://doi.org/10.1155/2022/1590620.

[12] A. Pellat, M. Barat, R. Coriat, P. Soyer, and A. Dohan, "Artificial intelligence: A review of current applications in hepatocellular carcinoma imaging," *Diagnostic and Interventional Imaging*, vol. 104, no. 1, pp. 24–36, Jan. 2023, https://doi.org/10.1016/j.diii.2022.10.001.

[13] L. Wang, M. Fatemi, and A. Alizad, "Artificial intelligence techniques in liver cancer," *Frontiers in Oncology*, vol. 14, Sep. 2024, Art. no. 1415859, https://doi.org/10.3389/fonc.2024.1415859.

[14] Y. S. Sung, B. Park, H. J. Park, and S. S. Lee, "Radiomics and deep learning in liver diseases," *Journal of Gastroenterology and Hepatology*, vol. 36, no. 3, pp. 561–568, Mar. 2021, https://doi.org/10.1111/jgh.15414.

[15] M. Haghshomar, D. Rodrigues, A. Kalyan, Y. Velichko, and A. Borhani, "Leveraging radiomics and AI for precision diagnosis and prognostication of liver malignancies," *Frontiers in Oncology*, vol. 14, May 2024, https://doi.org/10.3389/fonc.2024.1362737.

[16] A. Castaldo *et al.*, "State of the Art in Artificial Intelligence and Radiomics in Hepatocellular Carcinoma," *Diagnostics*, vol. 11, no. 7, Jul. 2021, Art. no. 1194, https://doi.org/10.3390/diagnostics11071194.

[17] J. Miranda *et al.*, "Current status and future perspectives of radiomics in hepatocellular carcinoma," *World Journal of Gastroenterology*, vol. 29, no. 1, pp. 43–60, Jan. 2023, https://doi.org/10.3748/wjg.v29.i1.43.

[18] M. Zhang *et al.*, "Enhancing prognostic prediction in hepatocellular carcinoma post-TACE: a machine learning approach integrating radiomics and clinical features," *Frontiers in Medicine*, vol. 11, Jul. 2024, https://doi.org/10.3389/fmed.2024.1419058.

[19] K. Bera, N. Braman, A. Gupta, V. Velcheti, and A. Madabhushi, "Predicting cancer outcomes with radiomics and artificial intelligence in radiology," *Nature Reviews Clinical Oncology*, vol. 19, no. 2, pp. 132–146, Feb. 2022, https://doi.org/10.1038/s41571-021-00560-7.

[20] P. F. Christ *et al.*, "Automatic Liver and Tumor Segmentation of CT and MRI Volumes using Cascaded Fully Convolutional Neural Networks." arXiv, Feb. 23, 2017, https://doi.org/10.48550/arXiv.1702.05970.