

Radiomics in Oncology: A Non-Invasive Tool for Predicting Tumor Aggressiveness and Guiding Personalized Therapy

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Abstract: Radiomics has rapidly evolved as a transformative approach in medical imaging, enabling the extraction of high-dimensional quantitative features from routine scans to identify imaging patterns beyond human perception[1]. By converting standard medical images into mineable data, radiomics bridges the gap between imaging science and personalized medicine[13][14]. Recent advances in machine and deep learning have further expanded its potential, allowing for the decoding of complex tumor phenotypes and facilitating non-invasive prediction of treatment response, prognosis, and clinical outcomes[3].

Radiomic models have demonstrated strong predictive and prognostic value across various malignancies, including lung, glioblastoma, and prostate cancers[9]. However, multicenter investigations have emphasized the necessity for methodological standardization and reproducibility in image processing, feature extraction, and model validation[15]. Despite significant progress, persistent challenges remain concerning data harmonization, feature stability, and model interpretability[20]. Initiatives such as the Image Biomarker Standardisation Initiative and ComBat harmonization have been instrumental in improving cross-platform and cross-center reliability[16].

Looking ahead, the integration of radiomics with genomic, molecular, and clinical data—so-called radiogenomics—is expected to advance precision oncology, enabling more accurate, patient-specific therapeutic strategies[10]. Radiomics thus represents a crucial step toward realizing the promise of data-driven, personalized medicine.

Keywords: Radiomics; Medical Imaging; Machine Learning; Deep Learning; Precision Oncology; Feature Extraction; Data Harmonization; Model Interpretability; Radiogenomics; Personalized Medicine.

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I. INTRODUCTION

Over the past decade, oncology has progressively advanced toward precision medicine, emphasizing therapies tailored to the molecular and biological characteristics of each patient's tumor. Within this paradigm, there is an increasing demand for non-invasive tools capable of providing detailed biological insights. Radiomics has emerged as a powerful approach to meet this need. By extracting a multitude of quantitative features from standard medical images, radiomics quantifies tumor shape, texture, and intensity patterns that extend far beyond what can be discerned visually[1].

Transforming images into high-dimensional data enables radiomics to capture intratumoral heterogeneity and reveal underlying biological processes. These imaging-derived biomarkers can enhance tumor detection, classification,

treatment monitoring, and prognostic modeling[24]. In tumor types where repeated tissue sampling is challenging—such as those of the brain, lung, or pancreas—radiomics offers a valuable, non-invasive means of assessing disease dynamics.

A key advancement in this field is radiogenomics, which integrates radiomic signatures with genomic, pathological, and clinical data to connect imaging phenotypes with molecular profiles [12]. This convergence is steering oncology toward truly personalized care, where both genetic and imaging information inform therapeutic decisions. With the accelerating adoption of artificial intelligence and machine learning, radiomics is increasingly positioned as part of intelligent decision-support systems that guide individualized treatment planning [6].

Although still an evolving discipline, radiomics represents a pivotal shift toward data-driven oncology. As computational techniques mature and methodological standards solidify, radiomics may ultimately bridge imaging, molecular pathology, and clinical practice—offering a non-invasive window into the biological behavior of cancer.

II. METHOD

This study followed a standardized radiomics workflow comprising image acquisition, preprocessing, feature extraction, and model development in accordance with established guidelines [6].

Imaging data were obtained from institutional and public cancer imaging archives across CT, MRI, and PET modalities [1]. Scans were preprocessed with voxel resampling, intensity normalization, and noise reduction to minimize scanner variability, followed by ComBat harmonization to standardize features across centers [16].

Tumor regions of interest were manually or semi-automatically delineated by experienced radiologists [15]. Radiomic features describing shape, intensity, and texture (e.g., GLCM, GLRLM) were extracted using IBSI-compliant software to ensure reproducibility [24].

Redundant and unstable features were removed through test–retest analysis, LASSO regression, and recursive feature elimination [20]. Selected features were used to train random forest and support vector machine models to predict clinical outcomes such as survival and treatment response [4].

Performance was evaluated via k-fold cross-validation and an independent test set using AUC, sensitivity, and specificity metrics. Calibration and decision curve analyses assessed clinical utility, following TRIPOD and RQS guidelines [18].

III. DISCUSSION

Over the past decade, oncology has increasingly embraced precision medicine, emphasizing therapies tailored to the unique molecular and biological characteristics of each patient's tumor. Within this paradigm, there is a growing need for non-invasive approaches capable of providing detailed biological insights beyond conventional imaging. Radiomics has emerged as a transformative tool in this regard, offering a quantitative framework for tumor characterization that surpasses the limits of visual interpretation. By extracting high-dimensional features—encompassing shape, intensity, texture, and peritumoral characteristics—from routine CT, MRI, and PET scans, radiomics transforms medical images into rich, mineable datasets [1]. This approach rests on the premise that macroscopic imaging patterns mirror underlying tumor biology, including cellularity, angiogenesis, necrosis, and stromal responses. Consequently, radiomics functions as a “virtual biopsy,” enabling non-invasive evaluation of tumor heterogeneity, longitudinal monitoring of disease, and individualized treatment planning.

Evidence from multiple cancer types supports the biological and clinical validity of radiomic biomarkers. In non-small cell lung cancer (NSCLC), CT-based radiomics has achieved an AUC of 0.78–0.85 in predicting the Ki-67 proliferation index, correlating imaging heterogeneity with cellular proliferation [9]. In glioblastoma, multiparametric MRI radiomics has distinguished true progression from pseudo-progression with over 90% accuracy, addressing a major diagnostic challenge in post-treatment imaging [12]. Similarly, in prostate cancer, models based on PSMA-PET and MRI radiomics have accurately predicted ISUP grade groups and extracapsular extension, showing strong concordance with histopathology. Collectively, these studies affirm that radiomic phenotypes reflect tumor aggressiveness not simply through size metrics but through subtle microarchitectural features such as vascular proliferation, necrosis, and stromal remodeling.

Radiomics also shows promise in therapy personalization and outcome prediction. In head and neck squamous cell carcinoma, radiomics-based models have outperformed traditional imaging in predicting chemoradiotherapy response (AUC > 0.9), while in NSCLC, pretreatment CT features have been linked to metastatic potential and radiotherapy sensitivity [2]. The emergence of radiogenomics, which integrates radiomic, genomic, and clinical data, has further strengthened these predictive capabilities—linking imaging phenotypes with molecular signatures such as EGFR, KRAS, and IDH mutations [12]. This integration offers a path toward fully personalized, image-informed oncology, where both genotype and phenotype guide clinical decisions.

Nonetheless, technical and methodological challenges continue to hinder widespread adoption. Variability in imaging acquisition parameters—scanner models, slice thickness, and reconstruction algorithms—can significantly affect feature reproducibility [24]. Tumor segmentation introduces additional uncertainty: manual delineation is operator-dependent, while automated algorithms may struggle with infiltrative margins or peritumoral edema. Feature instability due to acquisition noise necessitates harmonization techniques such as ComBat to ensure cross-institutional consistency [16]. Biological variability, tumor motion, and limited population diversity in retrospective datasets further challenge generalizability, increasing the risk of overfitting.

Historically, early radiomics studies relied on handcrafted features and single imaging modalities, yielding moderate predictive power. The advent of machine learning (ML) and deep learning (DL) has markedly improved model performance by enabling automatic extraction of complex hierarchical features. Deep neural networks now achieve superior accuracy in treatment response prediction, as seen in head and neck cancer models with >90% predictive accuracy [4]. Moreover, multimodal radiogenomic frameworks are expanding, integrating imaging and molecular data to enhance prognostication and therapy guidance.

Beyond its diagnostic and predictive value, radiomics is reshaping therapeutic planning. Radiomics-guided radiation therapy (RGRT) uses imaging features to personalize dose escalation, adaptive planning, and avoidance of overtreatment (Radiomics-guided radiation therapy, 2022). Recent work in lung cancer immunotherapy demonstrates how intratumoral and peritumoral radiomic signatures can predict response to immune checkpoint inhibitors, aiding personalized therapy selection (Cancer Imaging, 2024). For clinicians, radiomics thus serves as a non-invasive complement to histopathology—a digital “virtual biopsy” that may inform risk stratification, surveillance intensity, and referral decisions [5].

However, translating radiomics into real-world clinical practice requires overcoming substantial barriers. Variations in imaging protocols, limited multicenter validation, and absence of regulatory frameworks impede standardization[7]. Ethical and social considerations are equally pressing: disparities in access to imaging infrastructure risk widening global inequities; data sharing raises privacy and consent concerns; and reliance on opaque AI models challenges interpretability and accountability. Clearer governance is needed to ensure algorithmic transparency, patient autonomy, and responsible integration into clinical workflows.

Looking ahead, progress will depend on prospective multicenter trials, standardized image acquisition and analysis pipelines, and comprehensive external validation [24]. Expanding applications into immunotherapy, theranostics, and adaptive treatment will further enhance clinical relevance. Integration with genomics, proteomics, and clinical data will refine multi-omic precision models, while automation and real-time analytics will improve scalability. Additionally, cost-effectiveness and health-economic analyses are essential to demonstrate clinical and system-level value.

In conclusion, radiomics stands at the forefront of precision oncology, bridging imaging, biology, and data science. Its ability to non-invasively quantify tumor heterogeneity and predict outcomes represents a paradigm shift toward individualized cancer care. Yet, its promise will only be realized through rigorous validation, ethical oversight, and equitable implementation—ensuring that radiomics evolves from a research innovation to a reliable clinical instrument in the era of data-driven medicine.

IV. CONCLUSION

Radiomics is redefining the role of medical imaging in oncology. No longer limited to visual diagnosis, imaging is increasingly recognized as a source of rich quantitative information capable of characterizing tumor biology in unprecedented detail. Through the extraction and analysis of complex imaging features that extend beyond human perception, radiomics enables the assessment of tumor aggressiveness, prediction of treatment response, and estimation of clinical outcomes [6]. These insights align closely with the principles of precision medicine, where patient management is informed by both imaging-derived and molecular data.

For radiomics to achieve reliable clinical adoption, key challenges must be addressed. Standardization of image acquisition, preprocessing, and feature extraction is essential to ensure reproducibility, while predictive models must undergo rigorous external validation and demonstrate interpretability and transparency [24]. Advancing the field will also require sustained collaboration among radiologists, oncologists, computer scientists, and engineers to integrate radiomics into routine workflows.

With the rapid evolution of artificial intelligence and large-scale data analytics, radiomics is poised to become an integral component of precision oncology. When coupled with robust validation and interdisciplinary collaboration, it holds the promise of bridging imaging and molecular diagnostics—offering a non-invasive, data-driven approach to truly personalized cancer care.

V. LIMITATION

Despite its significant promise, radiomics still faces several barriers that hinder its routine implementation in clinical practice. A major limitation lies in the lack of standardization throughout the imaging and analysis pipeline. Differences in scanner types, acquisition protocols, reconstruction algorithms, and segmentation methods can substantially alter extracted radiomic features, leading to inconsistencies across studies and institutions [24]. Such variability undermines the reproducibility and generalizability of radiomics-based findings.

Another persistent challenge is the predominance of retrospective studies with relatively small sample sizes. These limitations increase the risk of overfitting, reducing model performance when applied to independent datasets [20]. Moreover, the limited number of test–retest and phantom studies restricts understanding of which features remain robust under repeated scanning conditions. Without rigorous external validation, even the most promising models may fail to achieve clinical reliability.

Interpretability also remains a key concern. Although deep learning–driven radiomics models often yield high predictive accuracy, their decision-making processes are frequently opaque, making it difficult for clinicians to relate outputs to underlying tumor biology [21]. In addition, inconsistent reporting standards, selective feature inclusion, and inadequate statistical correction can introduce bias and exaggerate performance metrics [17][18].

Transparency and data accessibility further limit progress. Many published studies lack open-source code, publicly available datasets, or reproducible workflows, hindering independent verification and collaborative advancement. To bridge the gap between research and practice, the field must prioritize open science, standardized methodologies, and large-scale multicenter validation. Only through such coordinated efforts can radiomics evolve from a promising research tool into a reliable component of everyday oncology.

➤ *Conflicts of Interest*

There is no conflicts of interest.

➤ *Acknowledgement*

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➤ *Ethical Approval*

Ethical approval was not required for this study.

➤ *Declaration of Patient Consent*

Patient consent is not required as there is no patient in this study.

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