

Habitat Imaging Combined with Multiscale Peritumoral Radiomics and Pathological STAS Status for Predicting Early Postoperative Recurrence in Stage T1 Non-Small Cell Lung Cancer

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Research Article

Keywords: stage T1 non-small cell lung cancer, tumor habitat, peritumoral radiomics, spread through air spaces, machine learning, recurrence prediction

Posted Date: September 29th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10954685/v1>

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Additional Declarations: No competing interests reported.

Abstract

Background

Patients with stage T1 non-small cell lung cancer (NSCLC) still face a non-negligible risk of early recurrence after curative surgery. Spread through air spaces (STAS) is a valuable prognostic indicator but can only be confirmed postoperatively. Conventional radiomics often ignores intratumoral spatial heterogeneity and the peritumoral microenvironment, limiting predictive accuracy. This study aimed to develop a multimodal machine-learning model that integrates habitat imaging, multiscale peritumoral radiomics, and STAS status to improve recurrence prediction.

Methods

We retrospectively enrolled 216 stage T1 NSCLC patients (training : validation = 7 : 3). Intratumoral habitats were generated by K-means clustering optimized with the Calinski-Harabasz criterion. Radiomic features were extracted from the whole tumor, five habitat subregions, and 1-mm, 3-mm, 5-mm peritumoral zones. Three classifiers (Random Forest, Extra Trees, XGBoost) were built. Feature selection used t-tests, Pearson correlation, mRMR, and LASSO with 10-fold cross-validation. Independent risk factors were identified by multivariate logistic regression. Model performance was evaluated by ROC curves, DeLong tests, calibration curves, and decision curve analysis.

Results

Vacuole sign, gender, STAS status, pleural traction, and maximum diameter were independent predictors. The combined model (clinical + habitat + 3-mm peritumoral features) achieved the highest AUCs: 0.910 (95% CI: 0.8484–0.9711) in training and 0.865 (95% CI: 0.7772–0.9532) in validation. It showed good calibration and superior net clinical benefit over single-modality models. DeLong tests confirmed significant improvements over peritumoral-only models in validation ($P < 0.05$).

Conclusions

The proposed noninvasive multimodal model accurately predicts early postoperative recurrence in stage T1 NSCLC and may assist in individualized risk stratification and adjuvant therapy decisions, offering a practical imaging-informatics tool for early-stage lung cancer management.

1. Introduction

Lung cancer remains the leading cause of cancer-related mortality worldwide, with non-small cell lung cancer (NSCLC) accounting for approximately 85% of all cases. Surgical resection is the standard curative treatment for patients with early-stage disease, particularly those with stage T1 NSCLC. Nevertheless, postoperative recurrence rates remain substantial even in this early-stage population(1), highlighting an urgent need for precise prognostic tools to guide adjuvant therapy and personalized follow-up strategies.

In 2015, the World Health Organization (WHO) formally recognized spread through air spaces (STAS) as a distinct invasive pattern of lung cancer, characterized by the presence of tumor cells (in the form of micropapillary clusters, solid nests, or single cells) within air spaces beyond the main tumor boundary(2, 3). Accumulating evidence has since established STAS as a significant independent predictor of adverse prognosis, associated with increased recurrence rates and reduced survival(4), especially after sublobar resection(5).

Despite its well-documented prognostic value, STAS can currently only be identified via postoperative histopathological examination, which limits its utility in preoperative clinical decision-making. This gap has driven growing interest in developing noninvasive predictive biomarkers for STAS status and recurrence risk. Radiomics, a technique for high-throughput extraction of quantitative features from medical images, has emerged as a powerful tool for characterizing tumor heterogeneity and phenotypic traits(6). However, conventional radiomics methods typically analyze the tumor as a single homogeneous region, neglecting the complex spatial heterogeneity inherent to malignant growth.

To address this limitation, "habitat imaging" has been proposed as an advanced analytical framework. This method partitions tumors into distinct subregions or "habitats" through unsupervised clustering of radiomic features, enabling more granular characterization of intratumoral heterogeneity. Additionally, the peritumoral region—the tissue immediately surrounding the tumor—has gained recognition for its role in tumor invasion and progression, and may provide complementary prognostic information beyond the tumor core(1, 7).

The present study aimed to integrate these emerging concepts to build an accurate prediction model for postoperative recurrence in stage T1 NSCLC. We hypothesized that a multimodal model combining STAS status with intratumoral habitat signatures and peritumoral radiomic features would outperform models based solely on clinical variables, conventional whole-tumor radiomics, or peritumoral features alone. Through rigorous evaluation and comparison of multiple machine learning algorithms, this study sought to validate the enhanced predictive capacity of habitat imaging in capturing intratumoral heterogeneity for recurrence risk stratification.

2. Materials and Methods

2.1 Study Population and Ethical Approval

This retrospective study was conducted at Shanxi Bethune Hospital, with clinicopathological data collected from consecutive patients diagnosed with NSCLC between January 2019 and July 2022. The study protocol was approved by the hospital ethics committee (approval number: YXLL-2025-129), and the requirement for informed consent was waived due to its retrospective nature.

Inclusion criteria were as follows: (1) preoperative unenhanced chest CT within 1 week before surgery, with slice thickness ≤ 1 mm; (2) solitary lesion with maximum diameter < 3 cm; (3) pathologically confirmed peripheral NSCLC.

Exclusion criteria were: (1) central lung cancer or multiple pulmonary lesions; (2) history of preoperative biopsy, radiotherapy, or chemotherapy; (3) concurrent pulmonary or thoracic diseases (e.g., interstitial fibrosis, pulmonary tuberculosis, pulmonary hamartoma, bronchiectasis); (4) severe respiratory motion artifacts on CT images; (5) prior pulmonary surgery within 5 years for other indications; (6) incomplete or lost follow-up data.

A total of 216 eligible patients were finally included and randomly allocated to a training cohort ($n = 151$) and a validation cohort ($n = 65$) at a 7:3 ratio. The patient recruitment workflow is illustrated in Figure 1, and the overall study design is presented in Figure 2.

2.2 Image Acquisition and Morphological Evaluation

All patients underwent chest CT scanning using a Siemens SOMATOM Definition Flash scanner in the supine position with breath-holding. The scanning range covered from the bilateral lung apices to the lung bases. Scanning parameters were as follows: tube voltage 120 kV, reference tube current 110–240 mAs, rotation speed 0.5 s per rotation, pitch factor 0.9.

Two radiologists with 15 years and 2 years of experience in thoracic imaging diagnosis, respectively, performed image analysis in a blinded manner (lung window setting: window width 1500 HU, window level -600 HU). The maximum tumor diameter, nodule type (solid, part-solid ground-glass, pure ground-glass), and morphological features (air bronchogram, bronchial truncation, vessel convergence, vacuole sign, lobulation, spiculation) were evaluated. Discrepancies were resolved by consultation with a senior radiologist.

2.3 Pathological Assessment of STAS

Two pathologists independently evaluated STAS status in a blinded manner. STAS was defined as the presence of micropapillary clusters, solid nests, or single tumor cells floating in air spaces at the lesion edge, without direct continuity with the main tumor body. To minimize false-positive results, a diagnosis of STAS positivity was made only when floating tumor cells were observed at least 3 alveolar layers away from the main tumor edge and detectable in more than 3 tissue sections. A total of 98 patients were classified as STAS-positive and 118 as STAS-negative. Representative pathological images are shown in Figure 3(8).

2.4 Follow-up

Prognostic information was obtained through electronic medical record review and telephone follow-up. The endpoint of this study was the presence or absence of tumor recurrence or metastasis. Recurrence was confirmed by imaging findings or pathological evidence from needle biopsy or bronchoscopy, including locoregional recurrence and distant metastasis. All patients were followed up for at least 3 years postoperatively.

2.5 Image Segmentation and Habitat Subregion Generation

Chest CT images were retrieved in DICOM format. A radiologist manually delineated the region of interest (ROI) of the primary tumor using ITK-SNAP (version 3.8.0), carefully avoiding extra-nodular blood vessels, bronchi, and pleural structures. The delineation results were verified by a second radiologist. All segmentation procedures were performed with blinding to follow-up outcomes.

For habitat imaging subregion segmentation, as illustrated in Figure 4a, 19 features were extracted from each voxel within the tumor ROI to characterize local imaging properties. K-means clustering was performed at the population level to ensure consistent cluster assignment across patients. Clustering was tested for 3 to 10 clusters, and the optimal number was selected based on the Calinski-Harabasz (CH) score, where a higher value indicates tighter intra-cluster similarity and greater inter-cluster difference. For more detailed information, please refer to Additional file 1 and the clustering results were used to generate five distinct habitat subregions per tumor (Figure 4c).

2.6 Peritumoral Region Delineation

Peritumoral ROIs were generated by expanding the tumor boundary outward by 1 mm, 3 mm, and 5 mm, respectively, to investigate the impact of different peritumoral ranges on model prediction performance. The expansion process of peritumoral regions is demonstrated in Figure 4b.

2.7 Radiomic Feature Extraction and Selection

In accordance with the Image Biomarker Standardization Initiative (IBSI) guidelines, radiomic features were extracted using Pyradiomics (version 3.0.1) from the whole tumor ROI, peritumoral zones (1 mm, 3 mm, 5 mm), and individual habitat subregions. The features fell into three categories: geometric, intensity-based, and texture features, including gray-level co-occurrence matrix (GLCM), gray-level dependence matrix (GLDM), gray-level run length matrix (GLRLM), gray-level size zone matrix (GLSZM), and neighborhood gray-tone difference matrix (NGTDM). Selected texture features extracted from the habitat subregions are presented in Figure 4d.

In cases where unsupervised clustering resulted in incomplete habitat subregions, the k-nearest neighbor (KNN) method was applied to impute missing features to ensure consistency across all habitats. Features from different subregions were integrated after Z-score normalization. Feature selection was

performed sequentially: Student's t-test was applied to retain features with a significance level of $P < 0.05$. Pearson correlation coefficients were calculated to assess feature redundancy; for feature pairs with a correlation coefficient > 0.9 , only one feature was retained.

The minimum redundancy maximum relevance (mRMR) algorithm was used to further filter redundant features and mitigate overfitting risk. Finally, the least absolute shrinkage and selection operator (LASSO) logistic regression with 10-fold cross-validation was applied to identify the most predictive features based on non-zero coefficients determined by the minimum criterion penalty parameter (λ).

2.8 Model Construction and Validation

Three mainstream machine learning classifiers were evaluated: Extra Trees, Random Forest, and eXtreme Gradient Boosting (XGBoost). Optimal hyperparameters were determined via 10-fold cross-validation on the training set, selecting the configuration with the best median performance. Multiple prediction models were constructed for different feature sets: Habitat model: built with radiomic features from tumor habitat subregions

Peritumoral models: built with features from 1 mm, 3 mm, and 5 mm peritumoral zones respectively (PERI-1mm, PERI-3mm, PERI-5mm)

Clinical model: built with clinical, imaging morphological features and STAS status, selected via univariate screening followed by multivariate logistic regression

Combined model: integrated clinical factors, habitat features, and optimal peritumoral features

Model predictive performance was evaluated using receiver operating characteristic (ROC) curves, with pairwise comparisons performed via the DeLong test. Calibration curves and the Hosmer-Lemeshow test were used to assess prediction accuracy and reliability. Decision curve analysis (DCA) was conducted to evaluate the clinical net benefit of each model.

2.9 Statistical Analysis

Normality and homogeneity of variance tests were performed for continuous variables. Normally distributed data were compared using independent samples t-test, while skewed data were compared using the nonparametric Mann-Whitney U test. Categorical variables were compared using the chi-square test. A P-value < 0.05 was considered statistically significant.

All statistical analyses and machine learning implementations were performed using Python (version 3.7.12), with Statsmodels (version 0.13.2) for statistical analysis and Scikit-learn (version 1.0) for machine learning algorithms.

Table 1. Clinicopathological and imaging characteristics of the training and validation cohorts

Characteristic	Training Set (n=151)	Validation Set (n=65)	P value
Age (years, mean $\pm$ SD)	59.9 $\pm$ 9.02	59.45 $\pm$ 8.82	0.796
Maximum diameter (cm, mean $\pm$ SD)	1.69 $\pm$ 0.64	1.64 $\pm$ 0.63	0.592
STAS status, n (%)			0.655
Yes	70 (46.36)	28 (43.08)	
No	81 (53.64)	37 (56.92)	
Gender, n (%)			0.009
Male	42 (27.81)	30 (46.15)	
Female	109 (72.19)	35 (53.85)	
Smoking history, n (%)			0.005
Yes	38 (25.17)	29 (44.62)	
No	113 (74.83)	36 (55.38)	
Surgical procedure, n (%)			0.484
Lobectomy	90 (59.60)	42 (64.62)	
Sublobar resection	61 (40.40)	23 (35.38)	
Nodule nature, n (%)			0.239
Ground-glass nodule	20 (13.25)	4 (6.15)	
Solid nodule	72 (47.68)	30 (46.15)	
Part-solid nodule	59 (39.07)	31 (47.69)	
Pulmonary emphysema, n (%)			0.128
Yes	18 (11.92)	13 (20.00)	
No	133 (88.08)	52 (80.00)	
Air bronchogram, n (%)			0.633
Yes	24 (15.89)	12 (18.46)	
No	127 (84.11)	53 (81.54)	
Bronchial truncation, n (%)			0.804
Yes	35 (23.18)	14 (21.54)	
No	116 (76.82)	51 (78.46)	
Lobulation, n (%)			0.721
Yes	69 (45.70)	28 (43.08)	
No	82 (54.30)	37 (56.92)	
Spiculation, n (%)			0.723
Yes	45 (29.80)	21 (32.31)	
No	106 (70.20)	44 (67.69)	
Vessel convergence, n (%)			0.081
Yes	88 (58.28)	46 (70.77)	
No	63 (41.72)	19 (29.23)	
Pleural traction, n (%)			0.858
Yes	77 (50.99)	34 (52.31)	
No	74 (49.01)	31 (47.69)	
Satellite lesions, n (%)			0.725
Yes	7 (4.64)	2 (3.08)	
No	144 (95.36)	63 (96.92)	
Peritumoral ground-glass band, n (%)			0.800

Characteristic	Training Set (n=151)	Validation Set (n=65)	P value
Yes	21 (13.91)	10 (15.38)	0.874
No	130 (86.09)	55 (84.62)	
Vacuole sign, n (%)			
Yes	54 (35.76)	24 (36.92)	
No	97 (64.24)	41 (63.08)	

3. Results

3.1 Patient Characteristics

The final cohort comprised 216 patients (72 males, 144 females), aged 33–79 years, with a mean age of 60.50 ± 10.23 years.

Table 1 summarizes the clinicopathological and imaging characteristics of the training and validation cohorts. Although the 7:3 random allocation resulted in balanced distributions for most variables, significant differences were observed for gender ($P = 0.009$) and smoking history ($P = 0.005$). To account for these imbalances, both variables were included as covariates in the multivariate logistic regression and machine learning models.

Univariate and multivariate logistic regression analyses were performed to identify independent predictors of recurrence. Multivariate analysis revealed that vacuole sign, gender, STAS status, pleural traction, and maximum tumor diameter were independent risk factors for early recurrence in stage T1 lung cancer(5, 6). These features were numerically encoded for subsequent machine learning modeling. Additional file 2 compares the predictive performance of various clinical models; the AUC for the RandomForest model on the training set was 0.876 (95% CI: 0.8130–0.9400), and the AUC on the validation set was 0.819 (95% CI: 0.7043–0.9341).

3.2 Optimal Clustering Number for Habitat Imaging

Figure 5a illustrates the Calinski-Harabasz score across cluster numbers from 3 to 10, and Figure 5b shows the voxel distribution across the five habitat subregions. Based on the CH score, the optimal number of clusters for the K-means algorithm was determined to be 5. Accordingly, each tumor ROI was partitioned into 5 habitat subregions for subsequent feature extraction and model construction. The distribution of voxels across the five habitat subregions is presented in Figure 5b.

3.3 Feature Selection Results

Radiomics analysis generated a total of 9,170 features for each region, including 1,800 first-order features, 70 shape features, and various texture features. Additionally, we extracted features from five distinct subregions to analyze the habitat, resulting in a cumulative count of 45,850 features ($9,170 \times 4$). Additional file 3 outlines the distribution of these features across the dataset.

After the sequential feature selection pipeline, 10 features were retained for the habitat model. For the peritumoral zones, 31, 33, and 33 features were retained for the 1 mm, 3 mm, and 5 mm margins respectively. The LASSO feature selection process for habitat features is shown in Figure 6.

3.4 Performance of Habitat Models

Among the three classifiers tested for the habitat model, Random Forest achieved the highest AUC of 0.876 (95% CI: 0.8130–0.9400) in the training cohort, followed by Extra Trees (AUC = 0.848, 95% CI: 0.7815–0.9139) and XGBoost (AUC = 0.817, 95% CI: 0.7380–0.8950). In the validation cohort, Random Forest also demonstrated superior predictive performance with an AUC of 0.819 (95% CI: 0.7043–0.9341). Detailed performance metrics of different algorithms for the habitat model are listed in Table 2.

Table 2. Performance comparison of different machine learning algorithms for the habitat model

Model	Accuracy	AUC	95% CI	Sensitivity	Specificity	PPV	NPV
Random Forest-training	0.788	0.876	0.8130-0.9400	0.829	0.773	0.576	0.924
Random Forest-validation	0.815	0.819	0.7043-0.9341	0.706	0.854	0.632	0.891
Extra Trees-training	0.775	0.848	0.7815-0.9139	0.780	0.773	0.561	0.904
Extra Trees-validation	0.769	0.794	0.6691-0.9192	0.353	0.917	0.600	0.800
XGBoost-training	0.848	0.817	0.7380-0.8950	0.585	0.945	0.800	0.860
XGBoost-validation	0.769	0.748	0.6168-0.8795	0.471	0.875	0.571	0.824

3.5 Comparison of All Prediction Models

The predictive performance of all models is summarized in Table 3 and Figure 7a. Across all models, the combined model integrating habitat features, optimal peritumoral features, and clinical factors achieved the highest AUC values: 0.910 (95% CI: 0.8484–0.9711) in the training cohort and 0.865 (95% CI: 0.7772–0.9532) in the validation cohort.

In the training cohort, the combined model had the highest AUC but was only significantly superior to the PERI-5mm model ($Z = 3.11$, $P < 0.05$); no statistically significant differences were observed when compared with the clinical, habitat, PERI-1mm, and PERI-3mm models (all $P > 0.05$).

In the validation cohort, the combined model significantly outperformed all three single-modality peritumoral models (PERI-1mm, PERI-3mm, PERI-5mm; $Z = 2.46, 2.08$, and 4.40 respectively, all $P < 0.05$). Single-modality peritumoral models (especially the 5 mm model) exhibited poor generalization ability. The multimodal fusion strategy effectively compensated for the diagnostic limitations of pure imaging models, though the incremental gain over clinical-only or habitat-only models was modest (Additional file 4). Calibration curves (Additional file 5) and DCA curves (Figure 7b) demonstrated good goodness-of-fit for the combined model, which also provided higher clinical net benefit across a wide range of threshold probabilities.

Table 3. Performance comparison of all prediction models

Signature	Accuracy	AUC	95%CI	Sensitivity	Specificity	PPV	NPV
Clinic-Training	0.834	0.883	0.8220-0.9434	0.780	0.855	0.667	0.913
Habitat-Training	0.788	0.876	0.8130-0.9400	0.829	0.773	0.576	0.924
PERI1mm-Training	0.841	0.859	0.7840-0.9333	0.683	0.900	0.718	0.884
PERI3mm-Training	0.841	0.898	0.8393-0.9558	0.780	0.864	0.681	0.913
PERI5mm-Training	0.755	0.795	0.7152-0.8748	0.707	0.773	0.537	0.876
Combined-Training	0.874	0.910	0.8484-0.9711	0.780	0.909	0.762	0.917
Clinic-validation	0.754	0.858	0.7611-0.9545	0.882	0.708	0.517	0.944
Habitat-validation	0.815	0.819	0.7043-0.9341	0.706	0.854	0.632	0.891
PERI1mm-validation	0.708	0.721	0.5907-0.8505	0.588	0.750	0.455	0.837
PERI3mm-validation	0.723	0.746	0.6197-0.8729	0.824	0.687	0.483	0.917
PERI5mm-validation	0.631	0.588	0.4473-0.7292	0.118	0.812	0.182	0.722
Combined-validation	0.692	0.865	0.7772-0.9532	0.941	0.604	0.457	0.967

4. Discussion

In this study, we proposed a novel multimodal approach integrating STAS status, clinical-imaging features, intratumoral habitat analysis, and peritumoral radiomics to predict early postoperative recurrence in peripheral NSCLC. Our results demonstrated that the combined model incorporating STAS status, habitat subregion signatures, and 3 mm peritumoral radiomic features achieved superior predictive performance. This study provides a reproducible and reliable tool for prognostic evaluation of early-stage lung adenocarcinoma, which may facilitate treatment strategy adjustment and enable computer-aided personalized management in clinical practice.

Surgical strategies for early-stage lung adenocarcinoma increasingly favor sublobar resection to preserve pulmonary function and reduce complications(9, 10). However, multiple studies have indicated that STAS-positive patients with stage I lung adenocarcinoma have significantly higher recurrence rates after sublobar resection compared with those undergoing lobectomy(11). Accordingly, lobectomy is currently recommended for STAS-positive stage I lung adenocarcinoma. Accurate identification of patients at high risk of early recurrence is therefore critical for individualized patient management. Our findings suggest that the combination of habitat imaging radiomics and STAS status can more precisely identify patients at high recurrence risk, who may benefit from more aggressive postoperative therapeutic strategies(12, 13).

Radiomic features of the tumor core have been widely applied for prognosis prediction in lung adenocarcinoma(14). However, few studies have leveraged peritumoral imaging features to assist such prediction, and the optimal definition of the peritumoral region remains controversial. Wu et al. confirmed that peritumoral CT radiomic features are reliable for predicting NSCLC prognosis(15), and suggested that peritumoral zones extending 15 mm, 20 mm, or 30 mm from the tumor boundary may yield optimal performance. Chen et al. constructed models using radiomic features extracted from 3 mm, 6 mm, and 9 mm peritumoral zones, and reported that the 9 mm peritumoral signature achieved the highest AUC (0.82 in the training set, 0.67 in the validation set)(16). Another study by Lin et al. extracted features from 3 mm and 6 mm peritumoral zones and found that the 3 mm zone yielded higher prediction accuracy(17). Similarly, Chang et al. reported that features from the 3–6 mm peritumoral zone had the highest predictive accuracy for chemotherapy response among 3–6 mm, 6–9 mm, and 9–12 mm zones(18).

Building on this evidence, we selected 1 mm, 3 mm, and 5 mm peritumoral ranges for evaluation. Consistent with several prior studies, our results showed that radiomic features from the 3 mm peritumoral zone contributed the most to prognostic performance when integrated into the combined model. This

finding supports the notion that the immediate peritumoral microenvironment within a few millimeters of the tumor edge carries critical information about local invasiveness, which is closely associated with early recurrence.

STAS has received extensive attention since its formal recognition. Studies have consistently linked STAS to increased locoregional recurrence after sublobar resection(2, 13), supporting the recommendation for lobectomy in STAS-positive patients. However, STAS remains an independent prognostic factor even after radical resection. Preoperative assessment of STAS is currently not feasible, and whether intraoperative manipulation may contribute to STAS artifact remains debated, meaning STAS status is typically only determined postoperatively. Nevertheless, we maintain that further risk stratification based on postoperative STAS status is clinically relevant for subsequent patient management decisions. Our study confirmed STAS as an independent predictor of early recurrence in stage T1 lung cancer, underscoring its indispensable value in predictive modeling. It should be noted that despite standardized definitions, STAS assessment remains challenging in practice; factors such as poor section quality, improper tissue preservation, and intra-alveolar macrophage clusters may confound evaluation(19). Standardization and harmonization of STAS assessment methods remain an important direction for future research.

We reviewed published radiomics models for early-stage lung adenocarcinoma prognosis constructed using real-world data(20–24). Most existing models utilize either intratumoral radiomics alone or peritumoral radiomics alone, combined with basic clinical and morphological features, with sample sizes ranging from 119 to 295 patients. Zhang et al. developed a radiomics model for prognostic risk stratification in 217 postoperative lung adenocarcinoma patients, reporting a C-index of 0.71 for a multivariate Cox model combining radiomic risk score and clinical features(24). They also found that CNN-based deep learning models were inferior to handcrafted radiomics models for prognosis prediction. Kirienko et al. built a radiogenomics model combining [18F]FDG PET/CT radiomics and gene expression profiles, which achieved an AUC of 0.87; however, the study included only 74 samples and lacked external validation, and the addition of gene sequencing significantly reduced cost-effectiveness(22). Compared with these studies, our model integrates four dimensions of information—STAS status, clinical-imaging features, intratumoral habitat analysis, and multiscale peritumoral radiomics—achieving competitive predictive performance with a purely CT-based imaging informatics approach.

5. Limitations

This study has several limitations that should be acknowledged. First, as a retrospective single-center study, potential selection bias may exist. Second, the sample size is moderate, which may limit the generalizability of the model; larger multicenter cohorts are needed for further validation. Third, the study population is ethnically homogeneous, and future validation in multi-ethnic populations is warranted. Finally, manual segmentation of tumor ROIs is time-consuming and labor-intensive, though advances in automated medical image segmentation technology are expected to address this issue in clinical translation.

6. Conclusion

In summary, this retrospective cohort study established a prediction model for early postoperative recurrence in stage T1 NSCLC by integrating preoperative CT-based radiomics (habitat imaging and multiscale peritumoral features) with pathologically confirmed STAS status. The combined model demonstrated favorable predictive performance in the validation cohort, and may assist clinicians in formulating postoperative surveillance and adjuvant treatment strategies for patients with early-stage lung cancer.

Declarations

Ethics approval and consent to participate

This study was approved by the Ethics Committee of Shanxi Bethune Hospital (approval number: YXLL-2025-129). Owing to the retrospective nature of the study, the requirement for informed consent was waived by the ethics committee.

Consent for publication

This study used anonymized CT imaging data that do not contain any personally identifiable information. Therefore, consent for publication is not applicable.

Availability of data and materials

The datasets generated and/or analyzed during the current study are not publicly available owing to patient privacy concerns and institutional ethical restrictions, but are available from the corresponding author upon reasonable request.

Competing interests

All authors declare that they have no competing interests.

Funding

This work was supported by the Shanxi Provincial Basic Research Program (Free Exploration Category) through two Youth Science Research Projects: (1) Grant No. 202403021222392, titled "Unsupervised clustering-based radiomics study of multi-phase CT for depicting intratumoral heterogeneity in NSCLC," hosted by Ronghua Wang at Shanxi Bethune Hospital (January 2025 – December 2027); and (2) Grant No. 202203021212110, titled "Deep learning combined with whole-mount pathological sections for imaging biomarkers of angiogenesis in lung cancer," hosted by Juan Guo at Shanxi Bethune Hospital (January 2023 – December 2025). The funders played no role in the study design, data collection, analysis, interpretation, or manuscript writing.

Authors' contributions

Conceptualization: Bihua Zheng. Data curation: Bihua Zheng and Ronghua Wang. Formal analysis: Bihua Zheng and Shan Wu. Writing – original draft: Bihua Zheng. Writing – review & editing: Ronghua Wang, Juan Guo, and Shan Wu. Supervision: Shan Wu. All authors made substantial contributions to the conception or design of the work, or the acquisition, analysis, or interpretation of data; drafted or substantively revised the manuscript; approved the submitted version; and agree to be personally accountable for their own contributions and to ensure that questions related to the accuracy or integrity of any part of the work are appropriately investigated, resolved, and documented in the literature. The corresponding author (Shan Wu) confirms that all listed authors have approved the manuscript prior to submission, including the author list and order, and takes full responsibility for the integrity of the data, the accuracy of the analysis, and the transparency of the research process, including ensuring that all data, materials, and code are preserved and available for reanalysis in accordance with field standards.

Acknowledgements

The authors thank the Department of Radiology and Department of Pathology at Shanxi Bethune Hospital for their support in data collection and image evaluation. We also gratefully acknowledge the Shanxi Provincial Basic Research Program (Grant Nos. 202403021222392 and 202203021212110) for funding this study.

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Figures

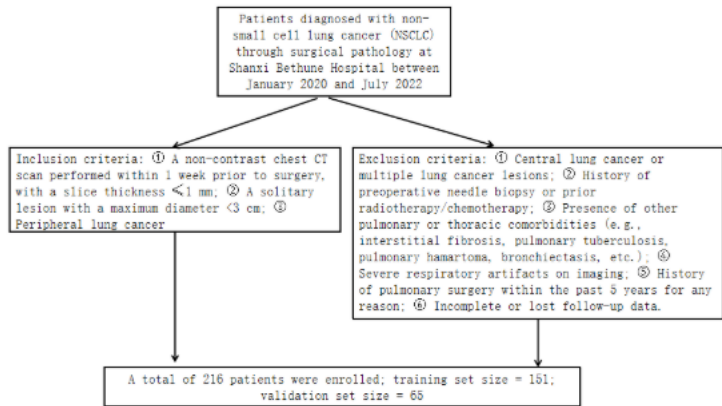


Figure 1

Patient recruitment flowchart showing inclusion and exclusion criteria and final cohort allocation.

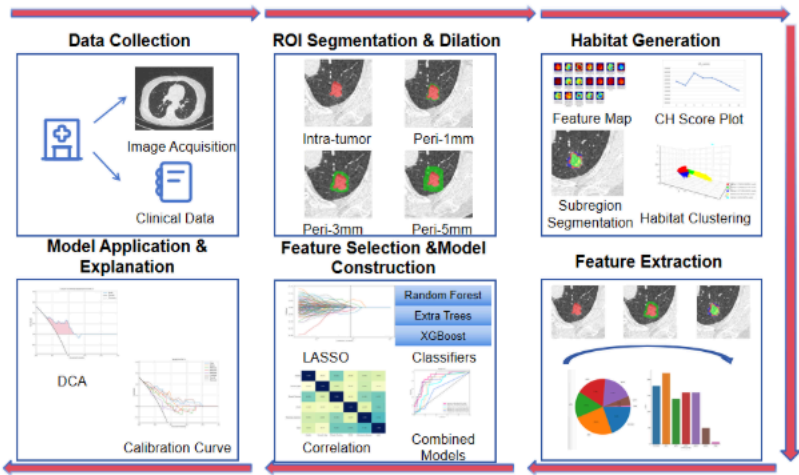


Figure 2

Schematic diagram of the study design and overall workflow, from image acquisition to model construction and validation.

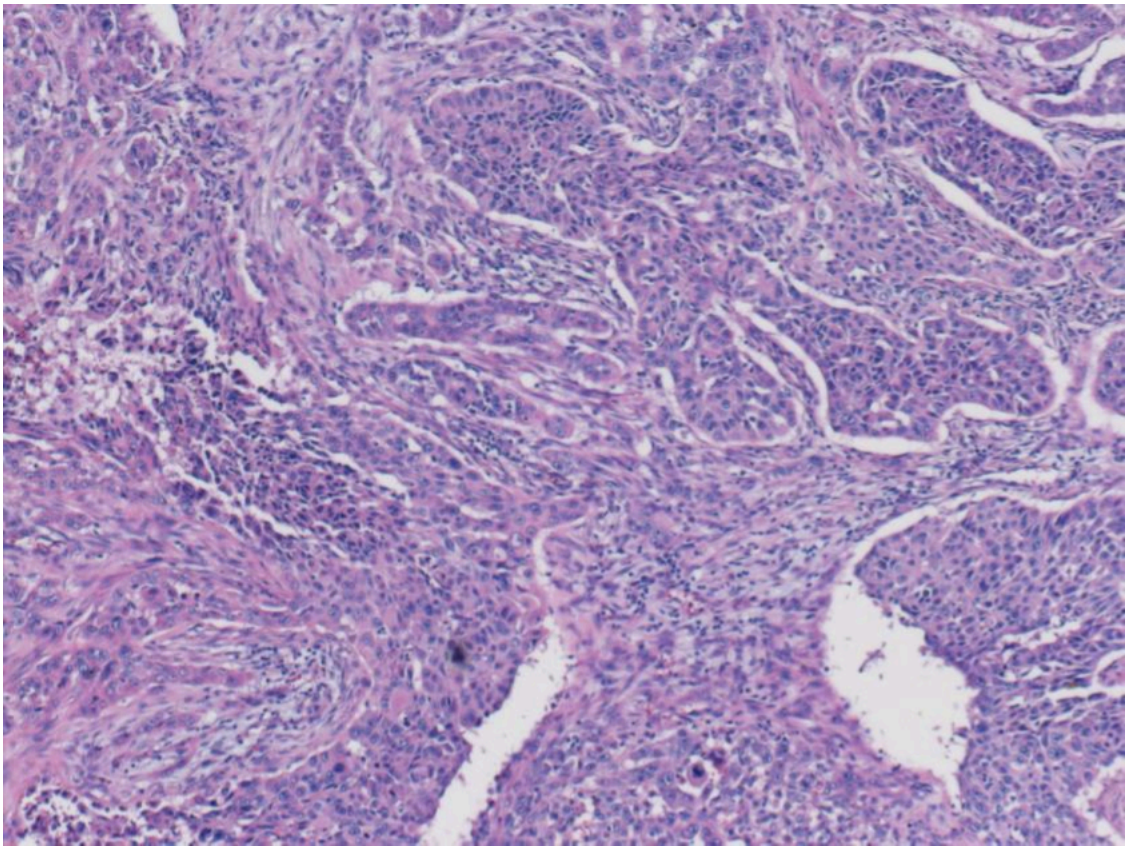


Figure 3
Representative pathological images of STAS-positive lung adenocarcinoma specimens

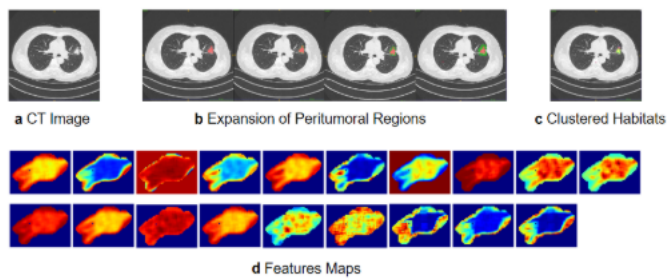


Figure 4
Illustration of image processing pipeline: (a) original CT image; (b) expansion of peritumoral regions at 1 mm, 3 mm, and 5 mm margins; (c) clustered habitat subregions; (d) original_firstorder_Entropy,original_firstorder_MeanAbsoluteDeviation,original_firstorder_Median,original_glcM_DifferenceAverage,original_glcM_DifferenceEn

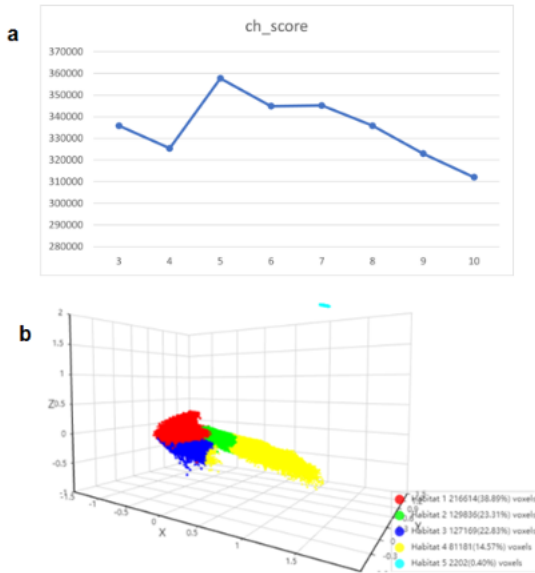


Figure 5

Determination of optimal cluster number for habitat imaging. (a) Calinski-Harabasz score across cluster numbers from 3 to 10, with the peak at $k=5$; (b) voxel distribution and proportion of the five habitat subregions.

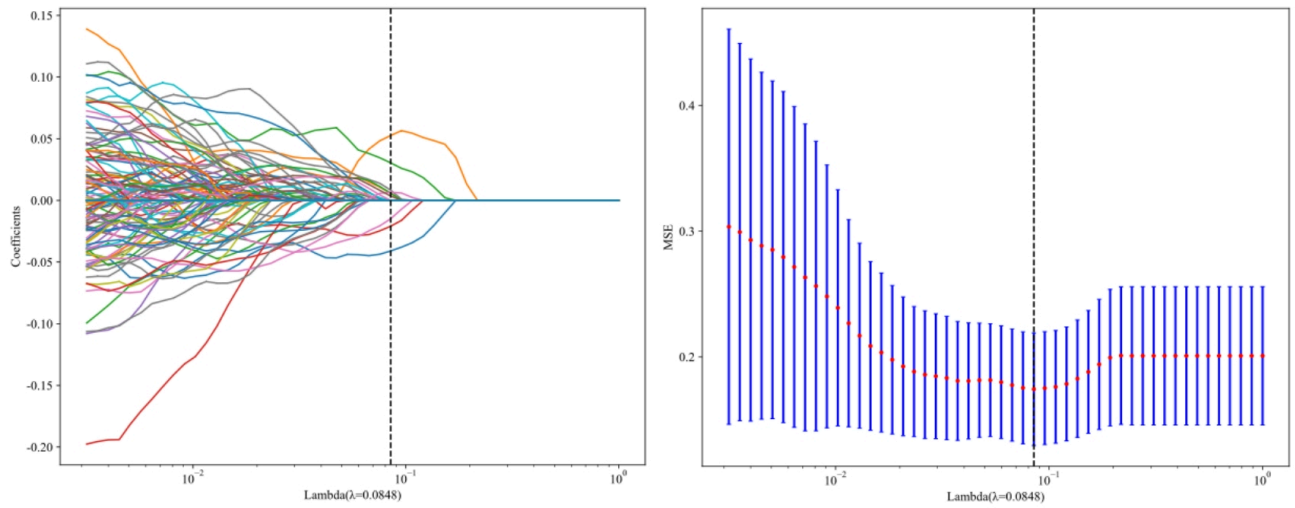


Figure 6

LASSO feature selection for habitat radiomics via 10-fold cross-validation. The optimal λ value was determined as 0.0848.

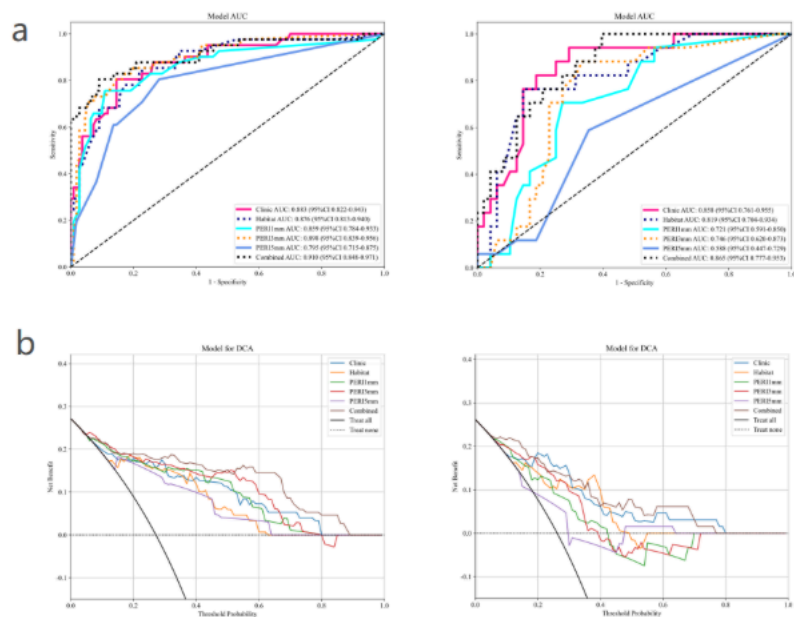


Figure 7

Model performance comparison. (a) ROC curves of all prediction models in the training cohort; (b) Decision curve analysis comparing clinical net benefit across models.

Supplementary Files

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