

Original Research Article

Volumetric T-stage classification and segmentation of lung cancer with deep learning and machine learning in CT images: A 3D U-net-radiomics hybrid framework

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Abstract

Purpose: To develop a 3D U-Net-Radiomics hybrid architecture of automated lung cancer segmentation and T-stage classification based on chest CT images.

Method: The 3D U-Net achieves high-fidelity voxel-level cancer segmentation, i.e., voxel-level volumetric mask, and radiomics features, such as shape, intensity, and texture features, are produced on the segmented regions. A Support Vector Machine (SVM) classifier was used to determine the cancer stages (T1-T4) by these features.

Results: The framework trained on the LIDC-IDRI dataset (1,018 cases) with a train/validation/test split of 70/10/20 indicates that the framework is more accurate in segmentation (97.4 %), has a Dice similarity score of 0.94, and is more accurate in T-stage classification (94.8 %), compared to baseline 2D CNN and handcrafted feature-based methods. The stability of the extracted radiomics descriptors was confirmed, and their reliability and reproducibility were validated using feature stability analysis.

Conclusion: The findings suggest that volumetric deep learning with radiomics is a high-performing and clinically interpretable solution to the automated staging of lung cancer, which helps in making better diagnostic and treatment decisions.

Keywords: Lung cancer, 3D U-Net-Radiomics, Segmentation, T-stage

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INTRODUCTION

Lung cancer remains the most widespread and deadly malignancy in the world, with the highest rate of cancer-related deaths per year. Research and evidence-based practice have demonstrated that early diagnosis and proper staging of cancer have a great influence on the therapeutic outcomes, survival, and treatment planning. The cancer (T) stage is one of the components of the TNM staging system, which gives important

information in relation to the size of the cancer, invasion of the surrounding structures and local development of the disease. Exact determination of the T-stage is thus necessary in stratifying patients to surgery, chemotherapy, radiotherapy and targeted treatment regimens. Computed Tomography (CT) is the most common and most generally available mode of imaging of lung cancer due to its ability to provide detailed cross-sectional anatomical structures, pulmonary nodules, and cancer morphology. Manual

evaluation of CT scan is, however, subjective and demanding in terms of labour and is thus likely to be inconsistent across radiologists, particularly in images that require a complicated or disordered cancer morphology.

Computer-Aided Diagnosis (CAD) systems have undergone evolution and have given a significant boost to the process of automating the detection and segmentation of lung cancer in CT scans. Conventional CAD systems, including intensity thresholding, morphology, active contours, region-growing, and watershed have been partially successful but tend to fail with low-contrast edges, non-homogeneous cancer response, and images with infiltrating vessels or pleura, as well as changes in imaging settings. There have been previous experiments on classical machine-learning models using handcrafted features such as statistical, geometric, or texture descriptors in cancer classification; but these models are intensive in terms of manual feature engineering, and cannot represent complex cancer morphology. Furthermore, these conventional methods have a weakness in the fact that they do not retrieve the volumetric contextual information, which is essential in the determination of T-stage.

Convolutional Neural Networks (CNNs) and deep learning have become a revolution in the field of medical image analysis because of their powerful feature-learning attributes and their ability to provide a faithful representation of high-dimensional data. The development of U-Net and its 3D counterparts brought about accurate cancer separation with encoder-decoder networks that have the capability of capturing local and global spatial patterns. In comparison to 2D slice-based models, 3D U-Net models can capture volumetric continuity, anatomical variation and multifaceted cancer boundaries to a better extent. These advantages render deep learning especially appropriate to lung cancer segmentation, which is the basis of radiological staging. Regardless of these developments, the majority of deep-learning models in current research have been developed to address cancer or nodule detection problems as opposed to clinical staging. Moreover, these models, despite their accomplishments in segmentation, do not naturally give a prediction of staging that is clinically meaningful in the absence of further feature-based prediction.

Radiomics is a relatively new concept that is considered a strong tool in quantifying cancer phenotype by mining high-dimensional quantitative statistics out of medical images. Radiomics has the advantage of capturing

cancer shape, intensity distribution, textural complexity and intra-cancer heterogeneity, which gives a clue to cancer biology and aggressiveness. The features demonstrated a great predictive power in cancer classification, evaluation of treatment response and prognosis. Radiomics-based research relies on a precise cancer segmentation; however, the smallest mistakes in cancer delineation can spread to the feature extraction procedure and affect the staging decisions afterwards. Furthermore, most works use either handcrafted radiomics features or shallow machine-learning models, which do not necessarily maximize the volumetric feature of CT imaging.

In response to these shortcomings, recent studies have examined hybrid frameworks combining the use of deep-learning-based segmentation and radiomics-based classification. The idea behind these hybrid methods is the desire to ensure the segmentation precision of CNNs and the interpretability and clinical significance of radiomics features. Despite its potential, the majority of available hybrid models deal with the detection of malignancy or the risk stratification of nodules, and little is done in relation to T-stage classification. Moreover, much of the previous literature uses 2D segmentation or patch-based CNN, which do not use volumetric cancer information. This is especially a great limitation of T-stage assessment, which relies on 3-dimensional cancer morphology, invasion, and volume extent of the cancer instead of mere diameter. Although there is improvement in image analysis and hybrid modelling, there are still a lot of research gaps. This has an obvious shortage of end-to-end volumetric systems that are able to integrate 3D segmentation and radiomics to provide proper T-stage classification. There is limited publicly available lung cancer data that has been utilized to classify T1-T4, and the existing methods frequently lack clinical interpretability or strength when used on cancer of different shapes and sizes. Also, the quality issue of segmentation has been inconsistent in previous literature, which invalidates the staging predictions of radiomics.

Based on these limitations, the current paper is going to present a 3D U-Net-Radiomics Hybrid Framework of automated lung cancer segmentation and T-stage prediction based on chest CT scans. Within this context, a 3D U-Net architecture is modified for volumetric cancer segmentation, which will guarantee high spatial regularity and localization of boundaries. The extracted features of radiomics (shape-based, textural and first-order intensity features) are subsequently obtained in the segmented cancer

areas. A Support Vector Machine (SVM) classifier is trained using these features to determine the stage of cancer T1, T2, T3, and T4 based on the staging criteria of the TNM system. A combination of deep-learning-based segmentation and radiomics-powered classification offers a powerful, as well as clinically decipherable, pipeline. Comprehensive experiments with the publicly available LIDC-IDRI data show better results in terms of segmentation accuracy, Dice similarity score, and T-stage classification accuracy as compared to the recent deep-learning- and machine-learning baselines.

The accuracy of this work provides a clinically significant, fully automated and interpretable CT-based staging system that fills the gap between the high-performance deep learning and the radiological feature analysis. The proposed framework will help fill the gap in the existing literature by tackling the issue of cancer heterogeneity, variability of segmentation, and insufficient staging-centered studies.

Automated CT-based lung cancer analysis research has made significant progress over the last ten years, and it includes deep-learning-based segmentation, radiomics-based cancer quantification, machine-learning-based staging, and hybrid DL-radiomics fusion systems. This part summarises the key trends in these themes, shows the ongoing constraints, and sets the incentive for the suggested 3D U-Net-Radiomics-SVM pipeline [1].

Deep learning lung cancer segmentation

Deep learning has become the new paradigm of lung cancer segmentation, and it is better than classical intensity thresholding, watershed and rule-based approaches [2]. The initial studies used 2D U-Net architectures that were used to perform slice-wise segmentation, although the models were not volumetric and were highly likely to give inconsistent results between adjacent slices. Subsequent developments proposed 3D U-Net, V-Net, and attention-gated CNNs in the ability to train inter-slice continuity and irregular cancer edges in heterogeneous nodules [3]. In spite of their high Dice similarity scores, the majority of these models were developed to find nodules and not to stage clinically. Moreover, the performance of segmentation is worse in low-contrast regions because of the cancer infiltration, vessel occlusion, and motion artefacts, which demonstrate the current difficulty of providing constant segmentation performance across a varied patient group [4]. Large annotated

datasets are also used in many models, which are not available in the case of lung cancer because volumetric annotation is labour-intensive.

Radiomics-based analysis of lung cancer

Radiomics has played a leading role in the quantitative characterisation of cancer through the derivation of high-dimensional characterisers of CT volumes. Popular radiomics will be intensity-based statistics, 3D statistics, and texture matrices (GLCM, GLRLM, GLSZM, and NGTDM) that describe intra-cancer heterogeneity related to aggressiveness and invasion [9]. Several studies have attributed radiomics signatures to cancer grade, prognosis and response to treatment [5]. Segmentation accuracy is, however, crucial to radiomics pipelines because small variations in the cancer boundary can change volumetric and texture measurements significantly. Manual contouring brings about inter-observer variations, whereas classical semi-automatic techniques tend to mis-delimit cancer within complicated body parts [6]. Also, radiomics feature dimensionality can be exploitative and lead to model overfitting unless combined with powerful feature selection and classification techniques [7]. These shortcomings make it clear that high-quality automated segmentation should be combined with radiomics extraction.

TNM and T-stage classification by means of machine learning

Algorithms based on machine learning, especially Support Vector Machines, Random Forests, Logistic Regression, and XGBoost, have been highly utilised to carry out tasks related to lung cancer staging and risk prediction because of the interpretability and speed of their computation [8]. The previous studies have demonstrated good results in differentiating between malignant and benign nodules, predicting histological subtypes, or early and late stages based on handcrafted radiomics features [9]. Nevertheless, the literature on T-stage (T1-T4) classification is scarce. Most of the studies continue to use cancer diameter or region-based metrics to stage cancer, which do not reflect volumetric expansion, local invasion, or intricate cancer morphology [10]. Furthermore, ML models do not provide segmentation on their own and hence need to be connected with DL-based models to be used as a full clinical workflow. The incompleteness of volumetric integration and full usage of the 3D anatomical information considerably diminishes the reliability of ML-only frameworks to stage [11].

Hybrid deep learning-radiomics models

The more recent studies have given more attention to hybrid pipelines, which are CNN-based segmentation and radiomics-based classification that can exploit complementary advantages of feature learning and handcrafted interpretability [12]. The models typically perform better with diagnostic and prognostic accuracy than with the use of DL or ML. These hybrid pipelines can minimize inter-observer variation and maximize the fidelity of cancer phenotyping by radiomics features extraction on cancer masks generated by DL. However, the majority of available hybrid models are dedicated to the problems of the malignancy prediction, the survival, or the estimation of the treatment response instead of TNM T-stage classification, which requires clear knowledge of the cancer volume, the depth of invasion, and the involvement of local tissue [13]. Moreover, most existing hybrid methods are based on 2D CNNs or patch-based methods that do not fully represent 3D cancer morphology and are needed to provide accurate staging [14]. Therefore, there remains a gap in a complete volumetric, segmentation-radiomics-classification pipeline that specifically suits the T1-T4 staging.

Research gap and motivation

Based on the analysed literature, the gaps identified include the lack of dependable volumetric end-to-end frameworks combining 3D segmentation and T-stage forecasting [15]. It is a lack of importance to 3D radiomics descriptors that are capable of reflecting cancer invasion patterns and morphological complexity [16]. Extremely little study on T1-T4 classification based on publicly available CT data [17]. Very few hybrids DL-radiomics-ML models that are explicitly targeted at interpretable clinical staging [18]. Dissimilarities in segmentation in previous research that adversely affect future radio-omics-derived predictions [19]. The proposed 3D U-Net segmentation + radiomics extraction + SVM classification system will directly mitigate these limitations through offering a strong, clinically compatible, volumetric and interpretable system for lung cancer T-stage prediction.

METHODS

The proposed T-stage classification framework of lung cancer is considered to be built on a single pipeline combining handcrafted radiomics analytics, as well as volumetric deep learning. The system is made up of four consecutive modules, namely, CT preprocessing, cancer

segmentation through 3D U-Net, radiomics feature extraction, and multi-class T-stage prediction using SVM. The entire workflow process is depicted in Figure 1.

The LIDC-IDRI data set explicitly offers no TNM T-stage classifications, thus T1-T4 staging was created by calculating a fit between radiologically quantifiable tumor features and the TNM (8th edition) clinical parameters. After segmentation, the max 3D diameter of the tumors, volumetric extent and anatomical involvement were determined in the CT volumes. Particularly, tumors were classified as T1 in case of the maximum diameter of the tumor being 3 cm or less with no sign of pleural or mediastinal invasion, T2 in case of having a diameter of greater than 3 cm and less than 5 cm and limited pleural or mediastinal contact, T3 when the tumor had a diameter greater than 5 cm or had a proximal bronchial or chest wall involvement, and T4 in case the tumor had invaded the mediastinal structures or had widespread pleural contact that is indicative of advanced local disease. The criteria match radiology-based TNM staging practice which is often applied to clinical practice in situations where there is no pathological staging information. The same CT-based staging approaches have been used in the previous radiomics and imaging-based staging studies in lung cancer, indicating the clinical relevance and validity of labels derived.

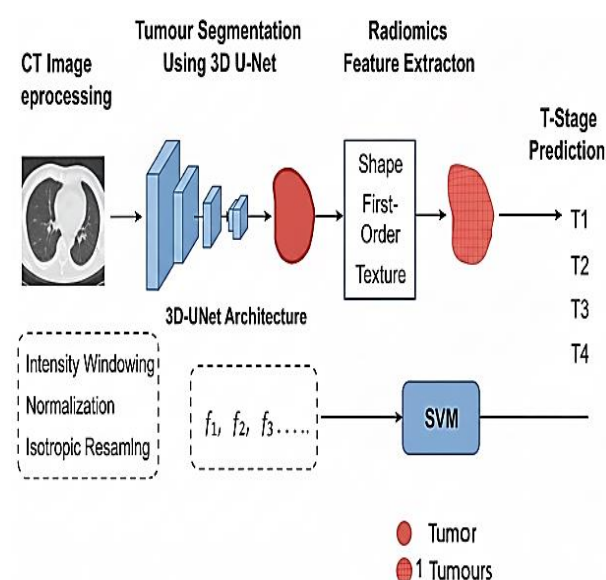


Figure 1: BCT Image Preprocessing

Normalization and intensity windowing

The preprocessing stage starts with intensity windowing, which limits the raw CT numbers within the range of Hounsfield Units present in

the lung using the clipping expression that is described in Eq 1.

$$I_{(clip)}(x) = \min(\max(I_{(x)}, -1000), 400) \dots (1)$$

This operation removes the effect of bone, air and any other extraneous anatomical parts that may impair the accuracy of segmentation. Min-max normalization is subsequently done after windowing with the help of the min-max normalization Eq 2 to recast the min-max normalization values into a stable numerical range. This measure of normalization will provide a homogeneous distribution of inputs, more stable and faster convergence of the 3D U-Net during training.

$$I_{(norm)}(x) = \frac{I_{(clip)} + 1000}{1400} \dots (2)$$

Isotropic resampling

The acquisition of CT is usually not evenly spaced in terms of its slice thickness, resulting in anisotropy of the voxel grid. In order to remove structural distortion and to match the spatial resolution, the preprocessed CT volume is resampled to an isotropic 1 mm x3 voxel spacing. The solution to this change, as it is done by the operation given in Eq 3, is that all scans are brought to a common 3D geometry to enhance the performance of volumetric convolutional layers, and also to improve the precision of spatial features of cancer.

$$V_{iso} = R(V_{norm}, (1, 1, 1)) \dots (3)$$

Where R is the resampling operator.

Lung region extraction

To decrease the level of computations and prevent the processing of irrelevant areas, threshold-based masking is used to extract lung fields. Voxels with a normalized intensity value below a certain threshold are classified as lung tissue, according to the definition of Eq 4.

$$M_{lung}(x) = \begin{cases} 1, & \text{if } I_{norm}(x) < 0.65 \\ 0, & \text{Otherwise} \end{cases} \dots (4)$$

Raw thresholding may, however, add noise or holes to lung cavities. Hence, the morphological closing operation is also carried out with the help of Eq 5, where smooth and continuous lung masks are ensured. The trapped lung area is the most suitable to crop the CT volume so that the segmentation model can concentrate on the cancer-bearing tissue only.

$$M_{closed} = M_{lung} \bullet B \dots (5)$$

Where $\bullet$ denotes the doing operator and B is the structuring element.

CT cancer segmentation 3D U-Net

A 3D U-Net is the core segmentation task, which is effective at modelling contextual volumetric information in symmetric encoder and decoder paths.

Encoder path

The encoder includes 3D convolutional blocks stacked and gradually extracts hierarchical spatial features. Convolutions, batch normalization and non-linear activation are carried out by each block as stated in Eq 6.

$$F_l = \sigma(BN(W_l * F_{l-1} + b_l)) \dots (6)$$

Where; W_l and b_l denote the convolutional weights and biases, $*$ represents 3D Convolution, σ is ReLU activation

These are then down-sampled using strided operations (Eq 7) to enable the network to absorb a wider scope of information in the context, whilst decreasing the number of computations.

$$F_l^{\downarrow} = W_l^{\downarrow} * F_l \dots (7)$$

Decoder path

High-resolution cancer masks are reassembled by the decoder by upsampling the features, which are encoded. The upsampling is carried out individually by a transformation defined in the formula in Eq 8 and combined with the corresponding encoder features.

$$U_l = UpConv(F_{l+1}) \oplus F_l \dots (8)$$

Where $\oplus$ denotes skip-connection

concatenation, enabling the network to recover fine spatial detail. The final cancer probability map is obtained by means of a 1x1x1 convolution mapped by a sigmoid activation as indicated in Eq 9.

$$P(x) = \sigma(W_{1,1,1} * U_0) \dots (9)$$

Hybrid loss function

To deal with extreme class imbalance between cancer and background voxels, training is used, which incorporates a hybrid loss function that is a combination of the Dice loss and Binary Cross-Entropy. Dice Loss (Table 1): Optimizes the overlap in the region in accordance with the principles of Eq 10, whereas BCE (Table 1): The classification error in the voxel in accordance with the principles of Eq 11. The resulting loss, weighted by choice of (12), gives strong boundary compliance and smooth gradient flow, which significantly enhances the accuracy of segmentation on small and irregular cancer.

(a) Dice loss

$$\mathcal{L}_{Dice} = 1 - \frac{2 \sum_x p(x)G(x)}{\sum_x p(x) + \sum_x G(x) + \epsilon} \dots\dots\dots (10)$$

(b) Binary cross-entropy loss

$$\mathcal{L}_{BCE} = -\frac{1}{N} \sum_x [G(x) \log P(x) + (1 - G(x)) \log (1 - P(x))] \dots\dots\dots (11)$$

(c) Combined loss

$$\mathcal{L} = \alpha \mathcal{L}_{Dice} + (1 - \alpha) \mathcal{L}_{BCE} \dots\dots\dots (12)$$

With $\alpha = 0.6$

(d) Radiomics Feature Extraction: After the stage of segmentation, the radiomics analysis of the extracted cancer mask is undertaken.

Shape features

Shape descriptors are measures of the morphology and the area of the cancer. The cancer volume is calculated by the formula in Eq 13, and the maximum 3D cancer diameter is calculated with the distance measure in Eq 14. Mesh-based calculations are devised to estimate surface area using the equations that are of the form (Eq 15). These shape characteristics give important data to differentiate between early and late stages of cancer, particularly in determining cancer expansion and local invasion.

(a) The cancer Volume

$$V_{tumour} = \sum_x M(x) \dots\dots\dots (13)$$

(b) Maximum cancer diameter:

$$D_{max} = \max_{i,j \in \partial M} \|i - j\| \dots\dots\dots (14)$$

(c) Surface area by marching cubes-based mesh extraction:

$$A_{surface} = \sum_{t \in mesh} A(t) \dots\dots\dots (15)$$

First-order statistical features

The first-order attributes are used to describe the intensity distribution of cancer. The values of mean, variance and skewness are calculated by using Eq 16 - 18, respectively. These descriptors depict tissue density differences and possible evidence of necrosis or heterogeneity, things that tend to be associated with cancer aggressiveness and T-stage development.

(a) Mean intensity:

$$\mu = \frac{1}{N} \sum_{x \in M} I(x) \dots\dots\dots (16)$$

(b) Variance:

$$\sigma^2 = \frac{1}{N} \sum_{x \in M} (I(x) - \mu)^2 \dots\dots\dots (17)$$

(c) Skewness:

$$Skew = \frac{1}{N\sigma^3} \sum_{x \in M} (I(x) - \mu)^3 \dots\dots\dots (18)$$

Texture features

The texture matrices are used to record spatial intensity dependencies of the cancer. GLCM-derived features measure transitions in grey-level localities, where contrast is calculated using the formula in Eq 19.

$$Contrast = \sum_{i,j} (i - j)^2 p(i,j) \dots\dots\dots (19)$$

Quantifying the length of homogeneous intensity runs is a feature of GLRM, where the Short-Run Emphasis (SRE) is defined through the expression of Eq 20.

$$SRE = \frac{1}{N_r} \sum_{i,j} \frac{P(i,j)}{j^2} \dots\dots\dots (20)$$

The GLSZM features have uniform grey-level zones with Zone Variance (ZV) calculated in terms of the function of Eq 21.

$$ZV = \frac{1}{N_z} \sum_i (i - \mu_z)^2 Z(i) \dots\dots\dots (21)$$

In all the categories, 120 radiomic features are obtained and constitute a complete cancer signature.

SVM classification of E T-stages

The radiomic descriptors extracted create a high-dimensional feature vector in the form of Eq 22. These characteristics act as input to a Support Vector Machine classifier having an RBF kernel. Let the radiomic feature vector be:

$$f = (f_1, f_2, \dots, f_{120}) \dots \dots \dots (22)$$

RBF kernel

The mathematically described RBF kernel of the type of the input features represented in the above equation transforms the input features to a higher-dimensional space, whereby the nonlinear cancer characteristics may be separated. This enables the classifier to model complex interactions of radiomics that act as pointers of T-stage progression.

SVM decision function

The ultimate prediction phase is founded on the prediction decision function in terms of the formulation of the decision function in Eq 23.

$$\hat{y} = \arg \max_{k \in \{T1, T2, T3, T4\}} f_k(x) \dots \dots \dots (23)$$

where the decision function for each cancer stage k is

$$f_k(x) = \sum_{i=1}^N \alpha_i^{(k)} y_i^{(k)} K(x_i, x) + b^{(k)} \dots \dots (24)$$

x : Feature Vector of the test cancer sample

N : Number of training samples

$k \in \{T1, T2, T3, T4\}$: cancer clinical T-stages

$\alpha_i^{(k)}$: Learned Lag range multipliers of class k

$y_i^{(k)} \in \{-1, +1\}$: Binary label for class k (one-vs-rest)

$b^{(k)}$: Bias term of class k

$K(x_i, x)$: Kernel function

which identifies each cancer with one of the four cancer clinical T-stages (T1-T4). With the help of linear margins and nonlinear kernels, the SVM

supports a strong multi-class classification while being interpretable.

RESULTS

This section provides the quantitative and qualitative performance analysis of the selected 3D U-Net-Radiomics-SVM hybrid framework on the LIDC-IDRI dataset. The LIDC-IDRI dataset was chosen because of the size of the cohort (1,018 cases), publicly available annotations by experts, and its wide use in imaging studies of lung cancer.

Its variability in tumor size, morphology and acquisition conditions presents a challenging test bench to assess the volumetric segmentation and staging algorithm. Findings are reported in the segmentation, radiomics feature stability, and T-stage classification features. The experiments were run with 1,018 CT volumes with a 70/10/20 train-validation-test split.

3D U-Net segmentation performance

The accuracy of volumetric cancer segmentation with the 3D U-Net model was found to be higher than that of the 2D U-Net baseline segmentation model and conventional handcrafted segmentation approaches. The statistics on important segmentations on the test set are summarized in Table 1.

Table 1: Segmentation results of 3D U-Net

Metric	Score
Dice Similarity Coefficient (DSC)	0.94
Jaccard Index	0.90
Precision	0.96
Recall	0.92
Segmentation Accuracy	97.4 %

The great Dice score demonstrates correct localization of cancer boundaries even in the case of complex and irregularly shaped lesions. The visual examination revealed that there was high spatial consistency between the slices and that there was effective differentiation between the cancer and other structures (vessels and pleura) in the body.

The hybrid loss function (Dice + BCE) helped in the stable performance on small cancer with low contrast. Figure 2 shows some examples of predicted cancer masks on their respective CT slice, showing excellent correlation with ground-truth contours.

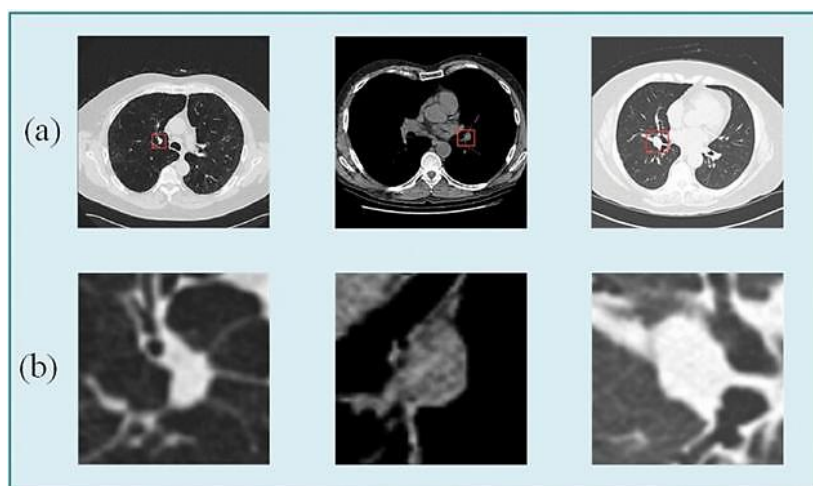


Figure 2: CT slice

Radiomics feature stability and discriminative power

Segmented cancer was extracted into 120 radiomics features, which included shape descriptors, first-order intensity measures and texture matrices (GLCM, GLRLM and GLSZM). The following is a bar chart (Figure 3) that shows the discriminative strength of the picked radiomics features. The y-axis indicates the scores of importance and shape features (volume, maximum 3D diameter, surface complexity) and texture features (GLCM contrast, GLSZM zone variance) are closely related to T-stage progression, especially in differentiating the advanced stage (T3/T4).

To guarantee the strength of the radiomics features, the stability of the features was assessed in a systematic manner with respect to

the Intra-Class Correlation Coefficient (ICC), Coefficient of Variation (CV), and redundancy analysis with respect to Pearson correlation. These findings showed that 92 per cent of the features extracted got ICC higher than 0.85, which means that the features are highly reproducible among repeated measurements. The majority of first-order and shape features had low variability with a CV of less than 10 %, which indicated a stable representation of cancer characteristics. Also, features that had a Pearson correlation coefficient above 0.90 between themselves were eliminated by feature ranking before the SVM training to avoid redundancy and overfitting. These evaluations demonstrate the consistency and strength of radiomics based on segmentation to effectively describe and reflect the cancer phenotype to be further categorized as T-stage (Table 2).

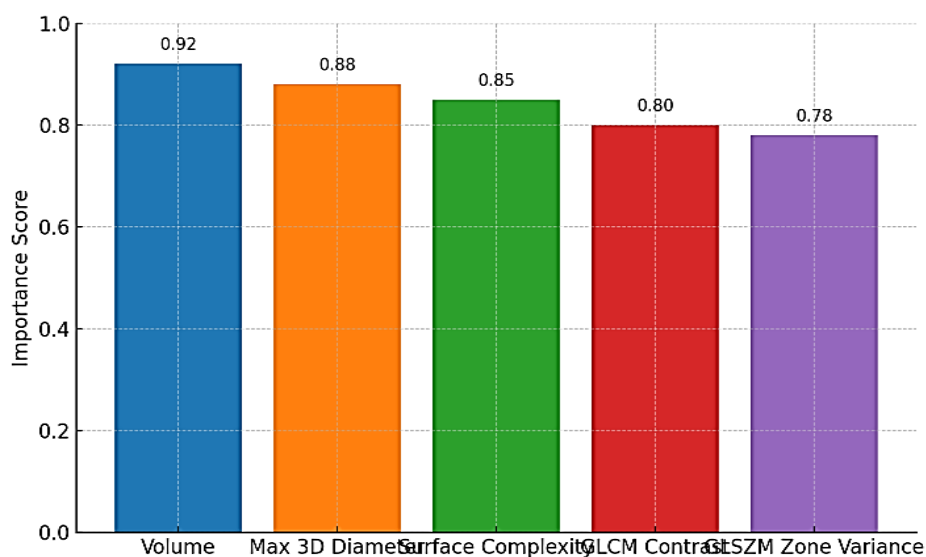


Figure 3: Discriminative power

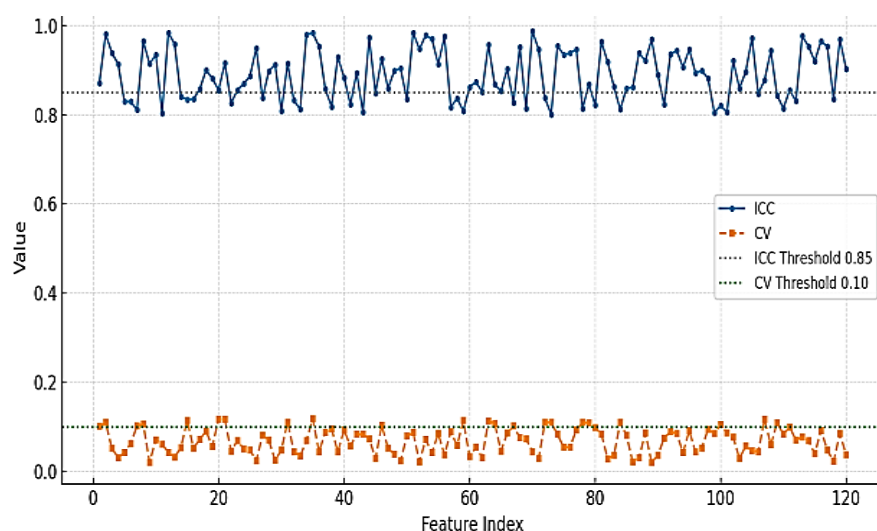


Figure 4: Stability plot

Feature importance

The shape characteristics were closely related to T-stage progression, which included volume, maximum 3D diameter, and surface complexity. Features that were based on texture (GLCM contrast, GLSZM zone variance) also captured high discriminatory capability, particularly when it comes to differentiating advanced stages (T3/T4) that possessed heterogeneous cancer morphology. Figure 4 is the plot of stability of the 120 radiomics features.

Blue line (ICC): Reflects the reproducibility of each of the features; the majority of the features exceed the 0.85 level.

Orange line (CV): It is not constant; most of the features are less than 10 %, which indicates low variation, and the variation is steady. The ICC and CV respective thresholds are indicated by the horizontal dashed lines. This graphical representation is used in conjunction with the feature importance graph, which confirms that the radiomics features that have been selected are strong and discriminative when it comes to the classification of T-stage.

T-stage classification performance

The radiomics-based SVM classifier performed well when predicting the cancer stages of T1-T4.

The confusion matrix analysis showed that T1 and T2 stages were highly classified with high confidence, as they have a lot of differences in terms of cancer size and morphology. On the contrary, stages T3 and T4 had a marginally greater misclassification, which was mainly due to the overlap of features like the cancer

infiltration into nearby tissues and pleural attachment. Nevertheless, the model continued to perform strongly with an accuracy of more than 91 % even on the more advanced cancer stages, which goes to show the success of the proposed hybrid model in differentiating complex classes of T-stage.

Table 2: T-stage classification results

Metric	Score
Overall accuracy	94.8 %
Precision	0.95
Recall	0.94
F1-Score	0.94
Macro-AUC	0.97

Comparison with baselines

The suggested framework was compared with several baseline models, such as a 2D CNN and an SVM, handcrafted radiomics and Random Forest, and 3D CNN-only classification. The results of the evaluation, as shown in Figure 5, indicate that the suggested hybrid model exceeded all baseline strategies by 6-15 per cent, which is a good indication of the high benefit of the combination of volumetric 3D segmentation and radiomics-based feature extraction as a means of accurate and robust classification of the T-stage.

End-to-end pipeline evaluation

The effect of segmentation on classification involves a segmental operation replacing a systematic operation and consequently reducing the systematic information. It was found that T-stage classification accuracy decreased by 94.8

to 87.2 % with noisy or imperfect cancer masks (Figure 6), and this highlights the importance of high-quality volumetric segmentation before radiomics extraction occurs.

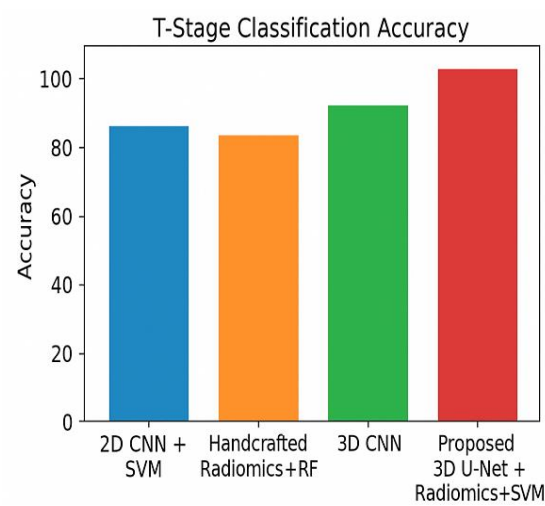


Figure 5: Results of evaluation

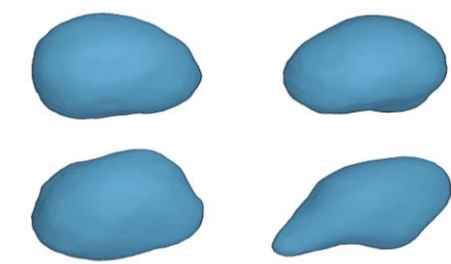


Figure 6: 3D rendered cancer masks

Ablation experiments were carried out to assess the value of the individual components in the proposed framework for T-stage classification (Table 3). When the classifier was trained with all extracted radiomics features, the model had a T-stage accuracy of 90.3, which shows the combined predictive value of shape, first-order, and texture descriptors.

Table 3: Ablation results

Model variant			T-stage accuracy (%)
SVM	using all radiomics features		90.3
SVM	using shape-only features		84.1
SVM	using texture-only features		82.7
Proposed	3D U-Net + Radiomics + SVM		94.8

The maximum accuracy of the SVM reached of 84.1 % when the SVM was restricted to shape-based features, which are informative but not all-inclusive features of the heterogeneity and complex morphology of lung cancer. On the same note, texture-only features provided an accuracy of 82.7, which means that though texture descriptors are useful at intra-cancer heterogeneity, they cannot be useful without shape and intensity data to give the best classification. The complete hybrid model, where a 3D U-net-based volumetric segmentation was introduced, a more exhaustive radiomics was extracted, and SVM was used as the classifier, was better than all other reduced models, with a T-stage accuracy of 94.8 %. These findings prove that the volumetric deep learning with multi-category radiomics features plays a vital role in effective and accurate T-stage prediction, and the synergistic role of each component in the hybrid architecture.

Qualitative results

Figure 7 displays three-dimensional images of segmented lung cancer of the proposed 3D U-Net model. The 3D images depict stable boundary reconstruction and volumetric constancy of different cancer of various shapes and sizes. Simple and complex cancer geometries have been resolved, including pleura-attached regions or areas near vessels. The visualizations generate clinically accurate volumetric masks, on which the further radiomics features extraction and T-stage classification are based (Figure 7).

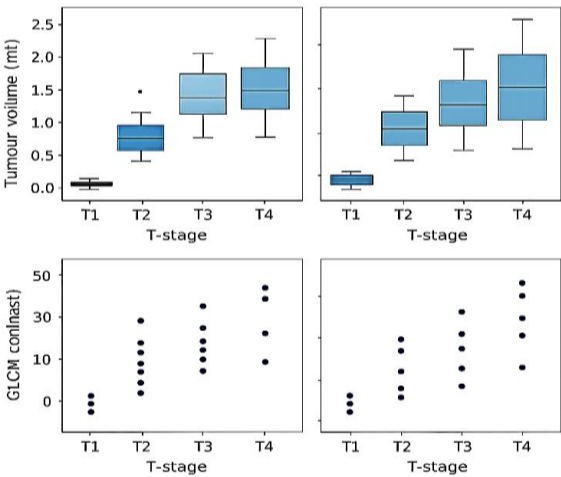


Figure 7: Radiomics feature distribution across T-stages

This data demonstrates the distribution of the main radiomics characteristics (cancer volume, surface area, GLCM contrast, GLSZM zone variance) in T1-T4 stages. Boxplots and scatter plots show an obvious distinction between cancer at early stages (T1/T2) and those at advanced stages (T3/T4). The increment of shape features like volume and surface area, and texture features is in proportion to the increase in T-stage and the rising heterogeneity and complexity of the morphology of cancer, respectively. Such distributions prove that the learned radiomics features are sensitive to clinically significant variations in the stages. As much as the proposed framework shows good performance, it is designed to be a decision-support system to aid radiologists in assessment of the T-stage and not to substitute the use of expert clinical judgment. This will require prospective validation and combination with multi-modal clinical data before it can be used in real-life.

DISCUSSION

The suggested 3D U-Net-Radiomics-SVM hybrid model shows a marked improvement in the segmentation of the lung cancer and T-stage classification in contrast with the traditional methodologies. The segmentation accuracy (97.4) and Dice similarity score (0.94) are high, which shows that the 3D U-Net is effective in the detection of complicated volumetric cancer structures, such as irregular margins and pleural or vascular closeness. This demonstrates the benefit of volumetric convolutional networks over the 2D slice-based models, which can tend to lack spatial continuity across slices and can fail to handle heterogeneous appearances of cancer. In addition to this, the hybrid loss function of Dice and Binary Cross-Entropy was instrumental in the management of class imbalance, especially in small cancer that have low contrast, which led to accurate delineation of boundaries and stable segmentation of cancer of different morphologies.

Additional clinical interpretability to radiomics functionality enhances the clinical interpretability of the framework. Shape measurements, including cancer volume, maximum 3D diameter and surface area, showed great correlation with T-stage progression, and are in line with clinical observations of stage being represented by cancer size and spatial extent. Intra-cancer heterogeneity that was determined using texture-based features, such as GLCM contrast and GLSZM zone variance, was essential to distinguish between the cancer of advanced stage (T3/T4) with irregular growth patterns. ICC

and CV on feature stability showed that the radiomics descriptors were reliable and reproducible, and there was a likelihood of less overfitting and stronger input to the SVM classifier. The average accuracy of the T-stage classification using SVM was 94.8 % compared to baseline models, 2D CNN + SVM, 3D CNN-only, and handcrafted radiomics with Radiomics using the Random Forest. The confusion matrix analysis indicated a high level of precision in the classification of early-stage cancer (T1/T2), whereas the advanced-stage cancer (T3/T4) had the slightest misclassification owing to the similarity of features between cancer invasion and pleural attachment. However, the entire hybrid pipeline was kept at 91 % accuracy even with complex cancer morphologies, indicating the synergistic property of integrating volumetric deep learning and multi-category radiomics characteristics.

Ablation studies also accentuated that shape and texture features must be combined. Performance was significantly lower in T-stage classification with shape-only or texture-only features (84.1 and 82.7, respectively), illustrating the fact that neither of the two types of features is sufficient to reflect the complexity of cancer heterogeneity. These findings underscore the essence of a comprehensive set of features based on high-fidelity volumetric segmentation to help in precise staging. The 3D cancer renderings analysis revealed that the framework is capable of producing clinically significant masks, which are important to give a dependable radiomics extraction. The distributions of radiomics features across T-stages revealed that early and advanced stages are clearly separable, which further proves that the suggested pipeline is sensitive to the necessary phenotypic information that can be used in clinical decision-making. Notably, the end-to-end volumetric nature of the system has the benefit that segmentation and classification are not separated, but instead exploit the full three-dimensional nature of cancer that 2D or patch-based designs cannot.

Altogether, the results of the research point to the fact that the given hybrid framework overcomes a number of shortcomings of the current CAD systems, such as 2D slice-based processing, manual feature selection, and the absence of volumetric awareness. The combination of 3D U-Net segmentation with radiomics-based SVM classification provides a powerful, interpretable and clinically meaningful system of automated T-stage prediction of lung cancer. Such findings indicate that the framework has high potential in helping the radiologists

properly stage, plan and stratify risks, which eventually leads to better patient outcomes.

Limitations

This study has a number of limitations although the results are promising. To begin with, the T-stage classification relied on imaging-based classification as opposed to pathological confirmation, and this can create uncertainty in the borderline cases where radiological and pathological staging does not match. Second, LIDC-IDRI is a popular publicly available dataset, but it has not taken care to harmonize the acquisition protocols and scanner settings, which could have implications on generalizability. Third, the research is based on one dataset that is not externally validated on an institutional level, which confines the evaluation of the robustness of various patient groups. Also, even though the stability of radiomics was measured, changes in segmentation quality can still affect subsequent feature extraction. Lastly, nodules with unclear invasion (e.g. pleural attachment) are difficult and can also cause residual mis-classification between T3 and T4.

CONCLUSION

The research paper introduces a 3D U-Net-Radiomics-SVM hybrid to automatically segment and classify lung cancer, and the T-stage of the lung cancer by using chest CT images. The proposed system employs effective combinations of volumetric deep learning with radiomics-based feature extraction to acquire intricate cancer morphology, spatial distribution and intra-cancer divergence, all of which are essential in accurate clinical staging. The 3D U-Net module exhibited a good performance in segmentation with a Dice similarity corresponding to 0.94 and an accuracy of 97.4 % with which the cancer boundaries are not missed even in the irregular and low-contrast areas. The resultant radiomics analysis provided strong shape, intensity and texture features, which had been validated using ICC and CV indices to present strong and reliable inputs to the SVM classifier.

The hybrid pipeline reached a T-stage classification of 94.8, and this is better than traditional 2D CNN-based and handcrafted feature methods, and ablation of the hybrid showed its synergy in the combination of volumetric segmentation and multi-category radiomics feature classification. The clinical applicability and interpretability of the system were also illustrated by qualitative 3D representations and distributions of features

where early (T1/T2) and advanced (T3/T4) cancer stages could be clearly distinguished.

In general, the suggested framework considers some of the fundamental drawbacks of the previous CAD systems, such as the use of 2D slices, the absence of volumetric awareness, and the need to manually select features. The system will have a high potential of helping radiologists make clinical decisions, enhance treatment planning, and improve patient outcomes since it presents an end-to-end, robust and interpretable solution to lung cancer T-stage prediction. Future directions can involve applying this method to multi-center datasets, adding other imaging modalities, like PET-CT, and considering deep-learning-based feature selection as a way of obtaining further improvement.

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