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INTEGRATING QUANTITATIVE AND CONVOLUTIONAL FEATURES TO ENHANCE THE EFFICIENCY OF PATHOLOGY CLASSIFICATION IN CT IMAGING

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Abstract. The paper proposes an approach that combines radiomic features and deep learning to enhance the accuracy of image classification obtained from lung computed tomography (CT) scans. The deep convolutional neural network ResNet18 was used to extract convolutional features from CT images. Radiomic features describing texture, shape, and intensity were combined with these convolutional features to improve the feature description of the lung CT image dataset. Using Principal Component Analysis (PCA) and feature selection methods, the most informative set of 250 features was obtained. Machine learning models, including Random Forest and Support Vector Machines (SVM), were used for classification. The SVM classifier showed the best results, achieving a classification accuracy of 0.97. The addition of genetic data allowed an improvement in classification accuracy. The study underscores the importance of combining advanced computational methods and data processing methodologies to solve image classification tasks.

Keywords: radiomics; deep learning, machine learning, genetic data, computed tomography scans

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ИНТЕГРАЦИЯ КОЛИЧЕСТВЕННЫХ И СВЕРТОЧНЫХ ПРИЗНАКОВ ДЛЯ ПОВЫШЕНИЯ ЭФФЕКТИВНОСТИ КЛАССИФИКАЦИИ ПАТОЛОГИЙ НА ИЗОБРАЖЕНИЯХ КОМПЬЮТЕРНОЙ ТОМОГРАФИИ

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Аннотация. В работе предложен подход, сочетающий в себе признаки радиомики и глубокого обучения для повышения точности классификации изображений, полученных с помощью компьютерной томографии (КТ) легких. Для извлечения свёрточных признаков из КТ-изображений была использована глубокая свёрточная нейронная сеть ResNet18. Радиомические признаки, описывающие текстуру, форму и интенсивность, были объединены с этими свёрточными признаками для улучшения признакового описания набора данных КТ изображений лёгких. С помощью метода главных компонент (МГК) и методов отбора признаков был получен наиболее информативный набор, состоящий из 250 признаков. Для классификации применялись модели машинного обучения, включая Случайный лес и Метод опорных векторов (МОВ). Классификатор МОВ показал лучшие результаты, достигнув точности классификации 0,97. Добавление генетических данных позволило улучшить точность классификации. Исследование подчёркивает важность объединения передовых вычислительных методик и методологий обработки данных для решения задач классификации изображений.

Ключевые слова: радиомика; глубокое обучение; машинное обучение; генетические данные; компьютерная томография

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Introduction

Algorithms play a central role in many classification tasks, covering a variety of areas. Machine learning methods for non-binary classification are of paramount importance, requiring adaptations to the specific features of each area. In particular, the combination of image processing methods, such as extracting deep convolutional and textural features, allows for analyzing textures in medical images and identifying and classifying pathologies.

Deep convolutional features, formed by convolutional neural networks, are an important component in image processing. Deep learning architectures like ResNet18, ResNet101, and ResNet152 have shown

high performance in feature extraction tasks. These networks are trained to recognize complex image textures, automatically extracting high-level representations, making them invaluable for understanding complex structures in medical images.

Textural features complement deep convolutional features by providing information about variations in pixel intensity and their spatial distribution. These features encompass statistical measures, capturing textural characteristics within images. Methods such as the Gray-Level Co-occurrence Matrix (GLCM), Gabor filters, Local Binary Patterns (LBP), and others study the structure of textures present in images. They enable the identification of areas with significant intensity variations, oriented textures, fine-grained textural differences, and even specific morphological aspects within images.

Existing methods for processing CT images have several notable limitations that require careful consideration [1]. Many modern CT image processing methods primarily rely on image features. These features often lack sufficient depth and informativeness, which can lead to reduced diagnostic accuracy, especially in cases where complex textures in images have diagnostic significance. On the other hand, in some cases, existing methods may not effectively utilize the capabilities of deep learning methods. Deep learning architectures, such as ResNet18, allow for the extraction of convolutional features that can significantly improve diagnostic accuracy [2].

The aim of this work is to combine radiomic and deep convolutional features to develop an algorithm for the detection and classification of cancer in lung CT images [3, 4].

Materials and Methods

Data acquisition

For this study, the NSCLC Radiogenomics dataset was used, which includes CT images of lung patients with various types and stages of lung cancer [6]. This dataset contains medical imaging, genomics, and clinical data. The NSCLC Radiogenomics dataset was prepared with the following objectives:

1. Understanding the genome-image relationships: it serves as a resource for exploring and uncovering the complex relationships between genomic data and characteristics of medical images.

2. Development of prognostic biomarkers: researchers can use this dataset to develop and evaluate prognostic biomarkers of medical images, potentially improving patient stratification and treatment planning. In this study, medical data from 80 patients were used.

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Feature Extraction

The paper developed a set of features by extracting two types of features: radiomic and convolutional [7]. Let's consider them in detail.

Radiomic features

For the study, 660 radiomic features were extracted for each computed tomography, including first-order features based on shape and texture. Table 1 shows the main texture and shape features extracted from CT images. For further work, 129 different textural features were selected, including Haralick [8], Gray Level Co-occurrence Matrix (GLCM) [9], gradient, Gabor [10], and Local Binary Patterns (LBP).

Haralick Features (based on GLCM): Haralick features were chosen for their ability to detect subtle textural differences in the image. They are particularly useful for identifying fine-grained textural patterns, which may indicate specific pathological features in lung nodules. These features are calculated based on GLCM. For example, one of the Haralick features, contrast, can be calculated as follows:

$$\text{Contrast} = \sum_{i,j} P(i,j) \cdot |i-j|^2,$$

where $P(i,j)$ is the normalized GLCM, i and j are the gray levels in the image.

Other Haralick features have their own equations, but they similarly involve calculations based on the GLCM:

Table 1

Description of the features along with their biological rationale and their association with the morphology of the region of interest (RoI)

Features	Biological rationale and their association with the morphology of the RoI
Gray-Level Co-occurrence Matrix (Texture)	Localizes regions with significant intensity variations within the nodule. It helps identify areas with different textures or patterns inside the RoI
Steerable Gabor (Texture)	Captures oriented textures through changes in direction and scale, which can be useful in describing the microarchitecture or structural patterns within the RoI
Haralick (Texture)	Uses second-order derivatives to capture subtle textural differences in the nodule. It helps in identifying fine-grained textural patterns that may be indicative of certain pathological features
Law (Texture)	Represents spots, ripples, and wave-like appearances in the nodule. These features can be relevant in characterizing specific morphological aspects of the RoI
Fourier (Shape)	This feature involves both low-frequency components, which describe the global shape of the nodule, and high-frequency components, which capture local details or irregularities in the nodule's morphology
Explicit Descriptor (Shape)	This feature includes measures related to contrast, edge sharpness, and the halo effect around the nodule. These aspects can provide insights into the distinctiveness and shape characteristics of the RoI

$$P(i,j)=\frac{N_{ij}}{N_T},$$

where N_{ij} is the number of times a pixel with intensity i is adjacent to a pixel with intensity j in the image, N_T is the total number of pixel pairs in the GLCM, which is equal to the sum of N_{ij} for all possible combinations of i and j.

In other words, $P(i,j)$ quantifies the probability that a pixel with intensity i is adjacent to a pixel with intensity j in the image, considering all possible pixel pairs. This probability is normalized by dividing by the total number of pixel pairs N_T to ensure that $P(i,j)$ represents a probability distribution across all pixel pairs.

2. Gray-Level Co-occurrence Matrix (GLCM) features: GLCM statistics, including Energy, Correlation, and Entropy, are chosen to provide insights into the spatial relationships of pixel intensities within the nodule. These statistics help quantify aspects like uniformity, correlation, and randomness in texture patterns. Common GLCM statistics include:

– Energy:

$$\text{Energy}=\sqrt{\sum_{i,j}P(i,j)^2},$$

– Correlation:

$$\text{Correlation}=\frac{\sum_{i,j}(i-\mu)(j-\mu)P(i,j)}{\sigma_i\sigma_j},$$

– Entropy:

$$\text{Entropy} = -\sum_{i,j} P(i,j) \cdot \log\left(P(i,j)\right),$$

where μ represents the mean or average gray level of the image. It is calculated as follows:

$$\mu = \sum_{i,j} i \cdot P(i,j),$$

3. Gradient: Gradient-based features do not have a single equation but often involve calculating gradients (first-order derivatives) of the image to measure variations in pixel intensities. For example, the magnitude of the gradient can be computed as:

$$\text{Magnitude} = \sqrt{\left(\frac{\partial I}{\partial x}\right)^2 + \left(\frac{\partial I}{\partial y}\right)^2},$$

where (I) is the image, and $\left(\frac{\partial I}{\partial x}\right)$ and $\left(\frac{\partial I}{\partial y}\right)$ are the partial derivatives in the horizontal and vertical directions, respectively.

4. Gabor Features: Gabor filters are defined by a sinusoidal wave modulated by a Gaussian function, and they can be used to extract texture features. The equation for a 2D Gabor filter is:

$$G(x, y; \lambda, \theta, \psi, \sigma, \gamma) = \exp\left(\frac{x'^2 + \gamma^2 y'^2}{2\sigma^2}\right)\cos\left(2\pi\frac{x'}{\lambda} + \psi\right),$$

where (λ) is the wavelength (distance between the peaks of the sinusoidal wave in the Gabor filter), (θ) is the orientation (specifies the orientation angle of the sinusoidal wave in the Gabor filter), (ψ) is the phase offset (introduces a phase shift in the sinusoidal wave), (σ) is the standard deviation of the Gaussian envelope (determines the spread or width of the Gaussian envelope around the sinusoidal wave), (γ) is the aspect ratio (controls the elliptical shape of the filter's Gaussian envelope), and (x') and (y') are rotated coordinates (coordinates represent the spatial location in the image after a rotation by the angle θ). By varying these parameters, Gabor filters can capture different types of texture information.

5. Local Binary Patterns (LBP): LBP is a texture descriptor that encodes the local spatial pattern of pixel intensities. It works by comparing the intensity of a central pixel with its neighbors, classifying each neighbor as either brighter or darker than the central pixel. LBP features can capture patterns such as textures with varying granularity.

Convolutional features

In the study, various deep neural networks were explored for feature extraction from CT images. Specifically, the characteristics of three widely used deep networks, Resnet18 [11], Resnet101 [13], and Resnet152 [14], were compared. The results showed that features extracted from Resnet18 outperformed those from other networks (Resnet101 and Resnet152) in the task of classifying CT images. For this reason, Resnet18 was chosen as the preferred network for feature extraction, which was then combined with radiomic features to create the final feature set. This feature set was used for training machine learning models and assessing their effectiveness in classifying lung CT images for the presence of nodules and their T stage.

Transfer learning was used to fine-tune the pre-trained Resnet18 model on the CT dataset. A 1x512 dimensional vector from the last convolutional layer was extracted as features for each CT image [12].

Feature selection

Statistical analysis and machine learning-based classification were conducted to identify key features with a strong correlation to genetic data. Specifically, a combination of Principal Component Analysis

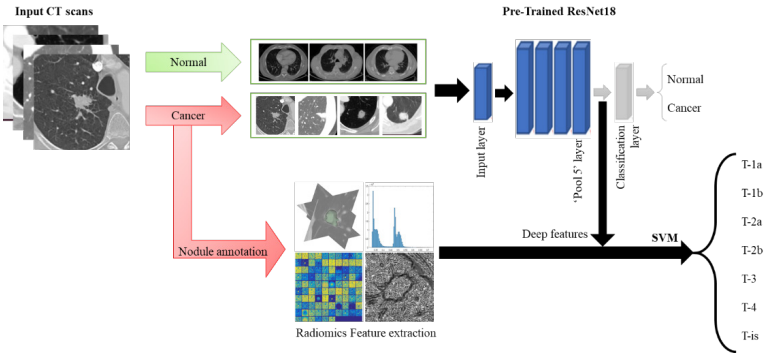

Fig. 1. Flowchart of the proposed method

(PCA) [15] and feature selection methods [16–18] was used to determine the most informative features from the categories of radiomic and convolutional features. Using a combination of PCA and feature selection methods, a set of 250 informative features, including both radiomic and deep features, was determined.

Classification

Subsequently, machine learning models, including Random Forest and Support Vector Machines (SVM) [19–21], were trained to classify lung CT images into seven categories based on the presence of nodules and their T stage. 5-fold cross-validation was used to evaluate the effectiveness of each model. Fig. 1 shows that after obtaining convolutional features, they are combined with radiomic features, which consist of shape, intensity, and texture features. The combined data is then subjected to a classification algorithm to classify them into 7 classes: T-1a, T-1b, T-2a, T-2b, T-3, T-4, T-is.

Experimental Results

The analysis of the lung CT image dataset showed that radiomic and convolutional features are highly informative in predicting the subtype of lung cancer and T stage. Radiomic features are quantitative features reflecting aspects of tumor visualization, including shape, texture, and intensity. On the other hand, convolutional features represent trainable image representations extracted by a pre-trained deep neural network.

The analysis identified a subset of radiomic features, including texture features, which strongly correlate with the genetic heterogeneity of lung cancer. Texture features are sensitive to variations in the spatial distribution of pixel intensities within the tumor and have been shown to be highly informative in predicting tumor heterogeneity and aggressiveness. Using a combination of PCA and feature selection methods, a set of 250 informative features, including both radiomic and deep features, was determined. These features were used to train machine learning models, including Random Forest and SVM classifiers with cubic kernel functions, to classify lung CT scans into seven categories based on the presence of nodules and their T stage.

The combination of convolutional and radiomic features achieved the highest classification accuracy, with an average F1-score of 0.95, Recall of 0.96, and Accuracy of 0.97 across the seven categories. The SVM classifier proved to be the most effective model, achieving an Accuracy of 0.97. These results demonstrate the potential of this approach in improving the accuracy of lung cancer diagnosis and treatment planning. Moreover, the convolutional features extracted using Resnet18 were particularly informative in predicting the presence and T stage of nodules in lung CT scans. This highlights the importance of using deep learning methods in combination with radiomic features for accurate and reliable lung cancer classification.

Overall, the results demonstrate the potential of CT tomography to improve the accuracy of lung cancer classification and provide more precise diagnosis and treatment planning for patients. By identifying

key CT scanning characteristics that have a high correlation, an automatic system was developed for classifying lung CT images into seven categories based on the presence of nodules and their T stage, which can improve patient treatment outcomes and reduce healthcare costs.

Discussion

The results of our study highlight the significant impact of incorporating radiomic features, including texture, shape, and intensity features, in the classification of CT images into seven distinct categories. To understand the relative performance of these features, we compared three different models: Deep Learning (No Radiomics, VGG-16), Deep Learning + Radiomics features, and Deep Learning + Radiomics features + gene data.

When we evaluate the performance of these models, it becomes evident that radiomic features play a vital role in improving the accuracy of CT image classification. The inclusion of radiomic features significantly enhances the F1-Score, Recall, and overall Accuracy of our classification models (Table 2).

Table 2

Comparative Performance of Classification Models

Model	F1-Score	Recall	Accuracy
S.K. Lakshmanaprabu et al. [21]	–	–	0.94
Deep Learning (No Radiomics)	0.75	0.68	0.78
Deep Learning + Radiomics features	0.91	0.88	0.93
Deep Learning + Radiomics features + gene data	0.95	0.96	0.97

Table 2 highlights a significant performance gap between using only deep learning and integrating radiomic features. Notably, the inclusion of genetic data further enhances performance, demonstrating the potential of multidimensional data integration. The invaluable role of radiomic features in improving diagnostic accuracy must be acknowledged. The limitations of the deep learning model without radiomic features can be attributed to its inherent constraints in capturing complex patterns in CT images. Radiomic features, in contrast, provide quantitative insights into tumor characteristics, making them sensitive to variations in pixel intensity and spatial distribution, crucial for predicting tumor heterogeneity and aggressiveness.

In our study, Principal Component Analysis (PCA) and feature selection methods allowed the extraction of a set of 250 informative features, including both radiomic and deep features. These features were essential for training machine learning models, including Random Forest and Support Vector Machines (SVM) with cubic kernel functions, for classifying lung CT scans. The SVM classifier, in particular, emerged as the most effective model, achieving an Accuracy of 0.97. The combination of convolutional and radiomic features achieved the highest classification accuracy, with an F1-score of 0.95, Recall of 0.96, and Accuracy of 0.97 across the seven categories.

Table 2 also shows another study that attempted to classify lung CT images. This approach employed an Optimal Deep Neural Network (ODNN) and Linear Discriminant Analysis (LDA) to analyze lung CT images. Deep features were extracted from these images and LDA was used for dimensionality reduction to classify lung nodules as either malignant or benign. The ODNN was then optimized using a Modified Gravitational Search Algorithm (MGSA) for lung cancer classification. This alternative approach reported an impressive sensitivity of 96.2%, specificity of 94.2%, and accuracy of 94.56%. Compared to this alternative study, our approach, enriched with radiomic features and genetic data, achieves an accuracy of 97%, representing a substantial 3% increase compared to models based on deep learning without radiomics. The addition of radiomic features significantly improved diagnostic accuracy, emphasizing the promise

of combining multi-modal data sources for redefining cancer classification and personalized treatment planning.

Furthermore, the comparison of different deep networks for feature extraction showed that Resnet18 outperforms other architectures, emphasizing its potential as the preferred choice for feature extraction in radiomic studies. Although our study focused on lung cancer classification, the developed approach can be applied to other types of cancer, demonstrating the potential of using multiple data sources, including genetic data and visualization data, to enhance the accuracy of cancer diagnosis and treatment planning. A limitation of our study is the relatively small sample size and manual segmentation. Future research using larger datasets and automated segmentation methods can provide further insights into the potential of our approach for lung cancer classification and personalized treatment planning.

Conclusions

The study aimed to explore the relationship between features based on computed tomography and genetic heterogeneity in lung cancer patients with the goal of improving the accuracy of cancer classification. It was shown that the integration of radiomics and deep learning methods can significantly improve the accuracy of lung cancer diagnosis and treatment planning, while the use of genetic data in combination with visualization data can help identify key features associated with lung cancer.

Adding radiomic features to deep features increased the classification accuracy by 13%, from 78% to 91%. Furthermore, the inclusion of genetic data further improved accuracy by 4%, reaching an impressive 95%. This demonstrates the substantial impact of multidimensional data integration on the performance of our classification models.

Our approach showed high accuracy in predicting the presence and T stage of nodules in lung CT scans, as well as the ability to differentiate between malignant and benign nodules. It was also found that convolutional features extracted using Resnet18 were particularly informative in predicting the presence and T stage of nodules, highlighting the potential of deep learning methods for feature extraction in radiomic studies.

The ability to accurately predict the presence and T stage of nodules in lung CT scans can have significant implications for individualized treatment planning and identifying patients at high risk of developing lung cancer. The study indicates the potential of using multiple data sources to develop automated cancer classification systems and personalized treatment planning to improve patient outcomes and reduce the burden of lung cancer. The obtained results underscore the importance of continuing to develop and refine innovative approaches to cancer diagnosis and treatment planning, with the ultimate goal of improving patient outcomes and reducing the impact of lung cancer on individuals and society.

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