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Article

Prognostic Prediction of Head and Neck Cancer through Radiomics: A Stacking Ensemble Approach with Machine Learning and Deep Learning Machine Learning Models

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Abstract: Background: Head and neck squamous cell carcinoma (HNSCC) poses a major challenge for global healthcare due to its high rates of mortality and morbidity. While radiotherapy remains a primary treatment option, its effectiveness can vary due to tumor heterogeneity. Advances in artificial intelligence (AI) have enabled the application of radiomics to enhance cancer prognosis predictions. **Method:** This study proposes a stacking ensemble learning approach combined with deep learning models to predict prognosis in HNSCC patients. We utilized a dataset comprising 215 CT images with contoured Gross Tumor Volume (GTV) and Planning Target Volume (PTV) from HNSCC patients. Radiomics features were extracted and analyzed using a stacking ensemble machine learning (SEML) model, while deep learning machine learning (DLML) models were used to optimize prediction performance. **Result:** Our results indicated that the SEML model outperformed the DLML model in predicting prognosis outcomes, achieving an accuracy of 93%, sensitivity of 100%, and specificity of 83%. No significant difference was found between PTV and GTV for prediction performance (chi-square test, $p > 0.05$). **Conclusion:** This study highlights the effectiveness of the SEML model in improving prognostic accuracy for HNSCC patients, with implications for enhancing clinical decision-making and personalizing treatment strategies.

Keywords: head and neck; radiomics; stacking ensemble; deep learning model

1. Introduction

Head and neck squamous cell carcinoma (HNSCC) represents a substantial challenge to healthcare systems globally, impacting over 16,000 individuals annually in Hong Kong alone [1]. The five-year survival rate for late-stage patients is below 50%, and radiotherapy is the predominant treatment modality [2]. Due to tumor heterogeneity, achieving effective locoregional control is challenging, often necessitating personalized treatment plans. Accurate prognosis prediction is essential for optimizing treatment strategies.

Traditionally, the tumor, node, and metastasis (TNM) staging system has been utilized for cancer prognosis, evaluating tumor size, lymph node involvement, and metastatic progression based on biopsy results. However, this process is often time-consuming and invasive. Recent advancements in medical imaging, particularly Computed Tomography (CT) and Magnetic Resonance Imaging (MRI), have produced high-quality images that facilitate more cost-effective tumor analysis. Moreover, breakthroughs in AI technology have accelerated the ability to obtain accurate cancer prognoses using radiomics.

Radiomics involves the quantitative extraction of image features, such as signal intensity and texture [3]. These features are analyzed with AI to provide objective prognostic insights. Various studies have demonstrated the efficacy of radiomics, with some achieving 100% accuracy in distinguishing oral squamous cell carcinoma using support vector machines (SVM) [4]. Machine learning algorithms, including generalized linear models, SVM, random forest (RF), decision trees (DT), and extreme boosting (EB), have shown promising results in cancer prognosis. For instance, Xiong et al. achieved an accuracy of 93.3% in esophageal cancer prognosis using an RF model [5].

Recent research emphasizes that combining multiple algorithms can enhance prediction accuracy, which can be achieved through ensemble learning algorithms. A notable approach is the voted ensemble machine learning algorithm (VEML), which integrates predictions from various classifiers, yielding an accuracy of 88.3% in HNSCC prognosis prediction [6].

While significant advancements in AI and ensemble learning have been made, the application of stacking ensemble learning methods in cancer prognosis, particularly in radiomics, remains underexplored. This study aims to fill this gap by employing a stacking ensemble approach to improve HNSCC prognosis prediction.

2. Methodology

2.1. Research Workflow

The research workflow included data retrieval, raw data filtering, image importation, and feature extraction. Two models were utilized: a two-layer stacking ensemble model and deep learning models. The performance of both models was subsequently compared (Figure 1).

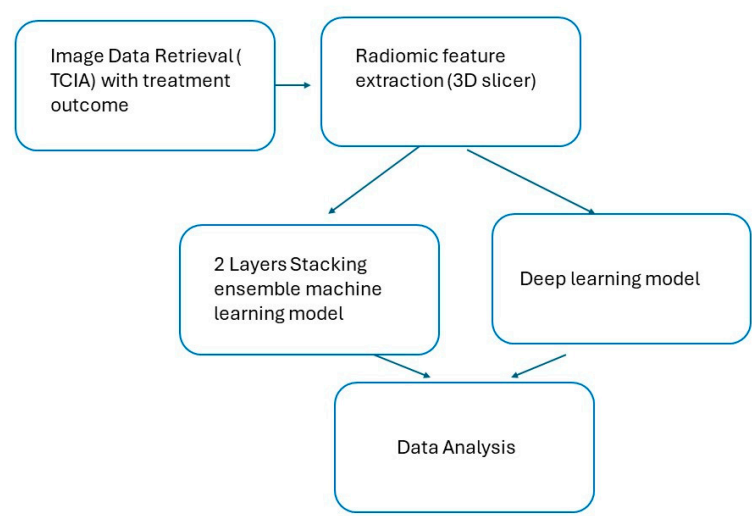


Figure 1. Research Workflow.

2.2. Patient Data

Data for this study were sourced from The Cancer Imaging Archive (TCIA), a publicly accessible repository for cancer medical images maintained by the National Cancer Institute (NCI). The dataset, labeled "HNSCC," comprised planning CT images of patients who underwent radical radiotherapy for HNSCC between 2003 and 2013. It included radiotherapy structures such as GTV and PTV, alongside clinical data including age, sex, diagnosis, smoking status, staging, and three- and five-year survival outcomes.

A thorough quality check resulted in a final sample of 164 cases from the original 215 collected.

Radiomics features were extracted from the GTV and PTV structures using 3D Slicer (version 4.10.2) with the PyRadiomics extension. The features were categorized into various groups, including shape, first-order statistics, gray-level zone matrix (GLSZM), gray-level dependence matrix (GLDM), gray-level run-length matrix (GLRLM), gray-level co-occurrence matrix (GLCM), and neighborhood gray-tone difference matrix (GLTDM). A total of 107 radiomics features were extracted for analysis.

2.3. Machine Learning Models

Cancer prognosis is typically assessed based on specific time points, such as the five-year survival rate [13]. This allows for objective comparisons across different cancer studies, as patients who survive five years post-treatment are generally classified as "cancer survivors."

In this study, the five-year survival rate was selected as the treatment outcome to ensure comparability with other research. Of the 164 cases, 118 patients survived, while 46 did not. An overfitting test was performed by randomly selecting 46 cases from the 117 patients who survived to balance the sample outcomes.

2.4. Machine Learning Process

Two machine learning models were employed: The Two-layer Stacking Ensemble Machine Learning Model and Deep Learning Machine Learning Model

2.4.1. Two-layer Stacking Ensemble Machine Learning (SEML) Model

In this model, the radiomics data were divided into three sets: training (70%), validation (15%), and testing (15%). Four classifiers were utilized: decision trees (DT), random forests (RF), support vector machine (SVM), and generalized linear model (GLM). The training set was used to train the models, which were then validated with the validation set to generate predictions. Predicted outcomes were quantified numerically, with values of 0 representing survival beyond five years or death from other causes, and 1 indicating death within five years of diagnosis.

The stacking ensemble model consists of heterogeneous classifiers organized in a two-layer structure. The base classifiers were initially trained with the radiomics data. The meta-learner was trained using the prediction results from the base classifiers, with XGBoost selected as the meta-classifier. The selection of an appropriate meta-classifier is crucial for model performance. Previous studies have indicated that XGBoost is optimal for recurrent HNSCC prognosis [14–16]. The final prediction outcome was the training result of the XGboost. Details of protocol were illustrated in Figure 2.

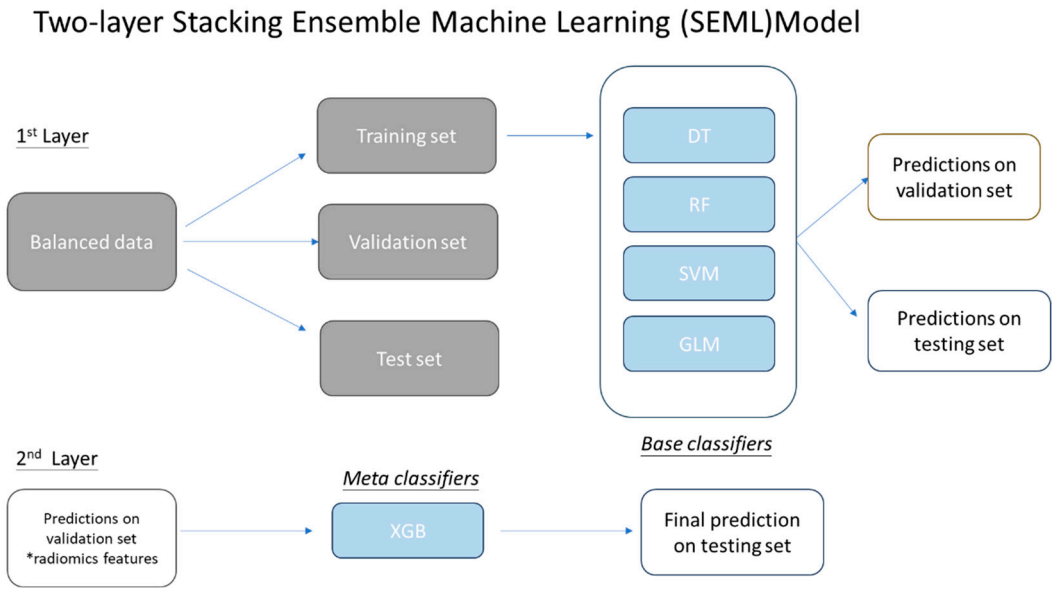


Figure 2. Workflow for adoption of stacking ensemble machine learning model.

2.4.2. Overfitting Test

As the dataset exhibited an unbalanced distribution of outcomes, an overfitting test was conducted using a balanced sample with an equal number of cases for each treatment outcome.

2.4.3. Deep Learning Machine Learning Models (DLML)

To compare the SEML model with deep learning methods, a deep learning machine learning model comprising three fully connected layers was trained. Each layer, except the last, utilized a Rectified Linear Unit (ReLU) activation function, while the final layer employed a sigmoid activation function to produce outputs in the range [0, 1]. A 70/30 split for training and testing was utilized.

2.5. Data Analysis

The predicted outcomes from the two-layer stacking model were compared with those from the base classifiers. Model performance was evaluated using the Receiver Operating Characteristic (ROC) curve, with metrics including the area under the ROC curve (AUC), accuracy, specificity, and sensitivity calculated using ROckit from the University of Chicago (1995).

3. Results

3.1. Demographic Cohort

The dataset comprised 215 patients, of which 51 were excluded due to missing data, resulting in 164 cases for analysis. Both PTV and GTV CT datasets were collected. Demographic details are summarized in Table 1.

Table 1. Patient demographics, staging and clinical data.

Patient and Tumour Characteristics (All n = 164)	Data
Age range (years)	24–91
Sex	
Female	25
Male	139
Staging	
Stage I	3
Stage II	3
Stage III	23
Stage IV	135
Diagnosis	
Ca Base of Tongue	60
Ca Tonsil	58
Ca others	46
Smoking status	

Smoker	54
Non-smoker	110

3.2. Prediction Performance of SEML and DLML Models

The SEML model demonstrated exceptional performance, with AUC ranging from 0.82 to 0.982 across all target volumes. For PTV radiomic features, the AUC reached 0.982. The model exhibited sensitivity of 100%, specificity of 83%, and accuracy of 93%. In contrast, the AUC for GTV features was slightly lower at 0.820, with sensitivity, specificity, and accuracy at 62.5%, 85.7%, and 73.3%, respectively. In comparison, the DLML model showed an AUC ranging from 0.605 to 0.774, with accuracy between 0.655 and 0.724, indicating superior performance of the SEML model (Table 2).

3.3. ROC Analysis

Despite the PTV radiomics features yielding better predictions, ROC analysis indicated no significant difference between PTV and GTV features (chi-square test, $p > 0.05$). (Figure 3)

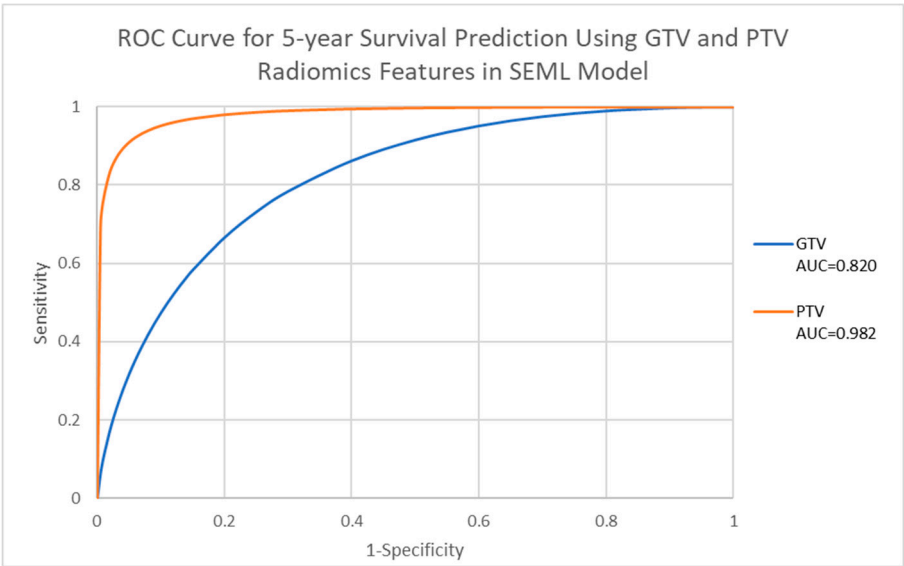


Figure 3. ROC curve of 5-year survival using GTV and PTV radiomics features in SEML model.

x

3.4. Comparison of SEML and DLML Models

The SEML model consistently outperformed the DLML model in HNSCC prognosis prediction regarding sensitivity, specificity, accuracy, and AUC. ROC analysis further confirmed this finding, showing no significant difference between the SEML and SVM models (chi-square test, $p > 0.05$) (Figure 4).

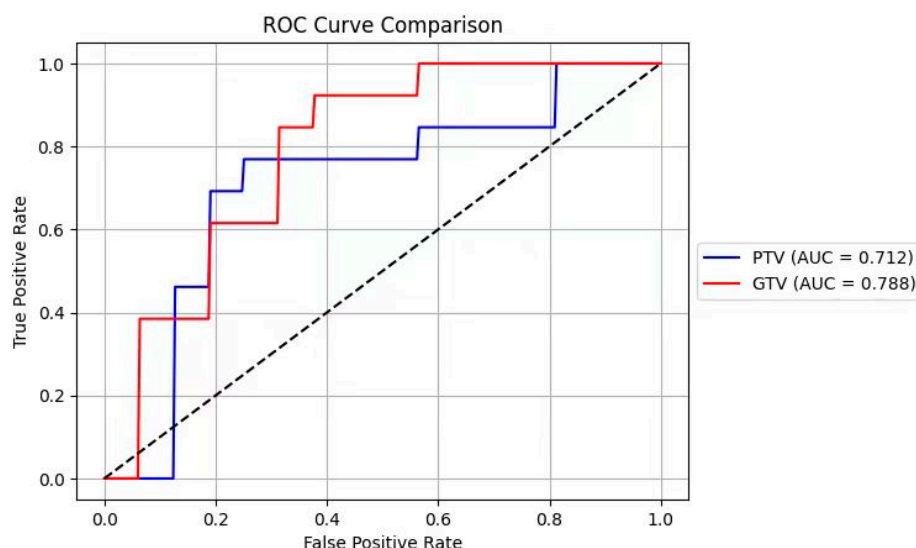


Figure 4. The ROC curve of GTV and PTV using Deep learning model.

4. Discussion

This study evaluates the performance of the SEML and deep learning models in predicting five-year survival in HNSCC patients using radiomics features. While no significant difference was observed between the models, the SEML demonstrated a notable improvement in prognostic prediction.

The SEML model employed in this research is the first to quantitatively explore a stacking ensemble approach for enhancing cancer prognosis predictions based on CT radiomics. Prior studies have highlighted the utility of machine learning in cancer prognosis, with notable successes such as an AUC of 0.61 for head and neck cancer using RF models [18] and a C-index of 0.782 for laryngeal squamous cell carcinoma prognosis [19].

The SEML model's superior performance compared to the DLML model underscores its potential in integrating various algorithms for enhanced prognostic accuracy. This approach leverages the strengths of individual classifiers, leading to significant improvements in predictive performance.

The findings align with previous research on stacking ensemble learning, which has demonstrated improved accuracy and higher AUC compared to single machine learning models [9–12]. The limitations of current applications in cancer prognosis highlight the need for further exploration of the stacking ensemble approach.

Incorporating clinical and genomic data alongside radiomics features could enhance predictive capabilities. Recent studies have indicated that radiomics-clinical (RC) models yield higher accuracy compared to radiomics-only models [21–23]. Similarly, radiomics-genomics (RG) models have shown promise in improving survival predictions [24,25]. This opens avenues for developing integrated models that utilize multi-modal data sources, enhancing the overall predictive power.

5. Conclusions

This study is the first to employ a stacking ensemble learning approach in a predictive model for forecasting cancer prognosis in HNSCC patients. The SEML model demonstrated high accuracy (98%), sensitivity (100%), and specificity (83%) in predicting five-year survival. The results affirm the effectiveness of the stacking ensemble approach in enhancing prognostic accuracy, laying a foundation for its clinical application and potential to facilitate personalized treatment for cancer patients.

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Data Availability Statement: The image data is available from: <https://www.cancerimagingarchive.net/collection/hnsc/>

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