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Retrospective Study

Machine learning survival prediction in esophageal cancer using radiomics and body composition from pretreatment and follow-up T12-level computed tomography

Liu MC *et al*. Esophageal cancer prognosis *via* T12-level CT

Abstract

BACKGROUND

Esophageal cancer carries a poor prognosis with low 5-year survival rates and limited early detection options. The skeletal muscle index at the L3 vertebral level is a well-established prognostic marker in esophageal cancer, but most follow-up computed tomography (CT) scans do not extend to L3 and limiting its utility. Radiomics has emerged as a powerful tool for extracting prognostic information from medical images.

AIM

To evaluate the influential features for esophageal cancer prognosis by integrating radiomic and body composition-based indices of skeletal muscle and adipose tissue at the T12 level from both pretreatment and follow-up CT images, in order to assess their value in predicting overall survival (OS).

METHODS

This retrospective study included 212 esophageal cancer patients who underwent concurrent chemoradiotherapy, with both pretreatment and follow-up chest CT scans available. Body organ analysis (BOA) and radiomic features were extracted from skeletal muscle and adipose tissue at the T12 level using automated tools. Four feature subsets (no-radiomics, pretreatment only, follow-up only, and combined inputs) were developed using logistic regression (LR) with least absolute shrinkage and selection operator for feature selection, followed by Cox regression. Prognostic models - including nomogram, support vector classifier, LR, and extra trees classifier - were constructed to predict 1-, 2-, and 3-year OS.

RESULTS

The model integrating both BOA and radiomics from pretreatment and follow-up CT, combined with clinical data, achieved the best performance for 2-year OS prediction, with an area under the time-dependent receiver operating characteristic curve of 0.91,

sensitivity of 0.81, and specificity of 0.88 using the LR model. The most predictive features included both clinical variables, body composition indices, and radiomic features, particularly from follow-up VAT. Follow-up imaging contributed significantly to model performance, reinforcing its value in treatment response evaluation.

CONCLUSION

This is the first study to demonstrate that BOA indices and their corresponding radiomics at the T12-level from both pretreatment and follow-up CT scans - combined with clinical data - can provide accurate prognostic information for esophageal cancer. This approach offers a practical alternative when L3-level imaging is unavailable and supports the clinical integration of automated T12-based imaging biomarkers. The integration of these imaging features with clinical parameters enhances the prediction of survival outcomes and contributes to non-invasive, personalized treatment planning.

Key Words: Esophageal cancer; Radiomics; Body composition; Computed tomography image; Sarcopenia; Machine learning

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Core Tip: This study introduces a novel prognostic approach using radiomics and body composition analysis features extracted at the T12 vertebral level from pretreatment and follow-up computed tomography scans in esophageal cancer patients. Unlike conventional methods relying on L3-level imaging, this model incorporates T12-based skeletal muscle and adipose metrics - readily available in standard chest computed tomography - combined with clinical data to predict overall survival. The combined model incorporating clinical, body composition analysis, and radiomic data achieved

excellent prognostic accuracy (area under the time-dependent receiver operating characteristic curve = 0.91) in 2-year survival prediction. This method supports non-invasive, automated, and personalized risk stratification, especially when follow-up imaging lacks L3 coverage.

INTRODUCTION

Esophageal cancer is frequently diagnosed at advanced stages due to the lack of early symptoms, leading to a poor prognosis[1]. Consequently, it ranks as the seventh most common cancer and the sixth leading cause of cancer-related death worldwide[2]. Despite advances in treatment, high postoperative recurrence rates[3] and low five-year survival rates[4] remain significant clinical challenges. Thus, improving early detection methods and developing personalized therapies are urgently needed. Recent studies have identified sarcopenia and radiomics as promising biomarkers for estimating survival outcomes in patients with esophageal cancer[5,6].

Sarcopenia is often caused by factors like dysphagia, poor nutrition, and the high metabolic demands of aggressive tumors, which lead to inflammation and muscle wasting[7]. The severity of inflammation and risk of cancer-related cachexia vary by tumor type, which plays a key role[8]. Sarcopenia is a well-known negative prognostic factor in many cancers, especially common ones like pancreatic, esophageal, gastrointestinal, head and neck, and lung cancers[9]. Radiomics is an emerging field that allows automated extraction of large amounts of quantitative data from images[10]. Recent studies show that radiomic features help address various clinical challenges, such as cancer diagnosis, evaluating treatment response, and predicting outcome[11].

Muscle segmentation and cross-sectional area measurements from computed tomography (CT) are commonly performed at the third (L3) or fourth (L4) lumbar vertebra level, focusing on the psoas muscle or the entire muscle area[12], as these CT-based metrics strongly correlate with whole-body muscle mass[13]. Consequently, the skeletal muscle index (SMI) at L3 - following validated methods - is widely used to assess sarcopenia as both a diagnostic and prognostic marker in esophageal cancer[14].

While most studies rely on pretreatment CT scans and lack follow-up imaging, some have shown that follow-up CT imaging after treatment provides additional prognostic value in esophageal cancer patients[15,16]. However, follow-up CT scans in esophageal cancer typically cover only the chest region and often do not extend to the L3 level, making SMI assessment at L3 unfeasible in many cases.

Recent studies have reported a strong correlation between muscle measurements at the L3 level and the 12th thoracic vertebra (T12) level on chest CT scans, allowing sarcopenia assessment in patients undergoing chest-only imaging[17]. Additionally, the SMI at the T12 level has been increasingly used as a clinical tool in various conditions, including chronic obstructive pulmonary disease[18,19], transcatheter aortic valve replacement[17], thoracic aneurysm repair[20], and lung cancer[21].

Radiomic features of esophageal cancer lesions on CT images have shown excellent value in evaluating disease status in patients with esophageal cancer, including differential diagnosis[22], prediction of treatment response and prognosis[23,24], and lymph node metastasis prediction[25]. However, defining tumor regions of interest (ROIs) typically requires manual annotation by experienced radiologists familiar with oncologic imaging, which is both time-consuming and labor-intensive. Recent studies have shown that radiomics of skeletal muscle also carries prognostic value in patients with esophageal cancer[26,27]. Fortunately, advances in deep learning - particularly the use of 3D U-Net models - now enable automated body composition analysis from CT images[28], eliminating the need for manual ROI processing.

As mentioned above, the SMI at the T12 level on chest CT has shown potential as a valuable biomarker for predicting survival outcomes in lung diseases, but its application in esophageal cancer remains limited. While radiomic features of muscle tissue at the L3 level have demonstrated prognostic value in esophageal cancer, the utility of T12-level radiomics for assessing disease progression still requires further validation. Therefore, this study aims to evaluate the influential features for esophageal cancer prognosis by integrating radiomic and body composition-based indices of skeletal muscle and adipose tissue at the T12 level from both pretreatment and follow-

up CT images, combined with clinical and demographic data, in order to assess their value in predicting overall survival (OS).

MATERIALS AND METHODS

Patients

This retrospective study was approved by the Institutional Review Board of Taichung Veterans General Hospital, and informed consent was waived due to its retrospective nature. Consecutive patients diagnosed with esophageal cancer at our hospital between December 2017 and December 2023 were included. Inclusion criteria were: Histopathological diagnosis of esophageal cancer (adenocarcinoma or squamous cell carcinoma), age > 20 years, treatment with concurrent chemoradiotherapy (CCRT), availability of a CT scan performed as part of the initial staging before CCRT, availability of a first follow-up CT scan performed 60-180 days after CCRT, and complete clinical data. Patients were excluded if pre-treatment or follow-up CT scans were unavailable, or if the image quality was inadequate for analysis. After applying these criteria, a total of 212 esophageal cancer patients were included in the study. The patient selection process is illustrated in Figure 1. To characterize the final study cohort, demographic, clinical, and imaging data were retrospectively collected from the institutional database. Clinical and histopathological information included age, sex, tumor stage (TNM), Eastern Cooperative Oncology Group (ECOG) performance status, treatment details, and follow-up outcomes.

CT Image

CT image acquisition was performed using multiple multi-detector CT scanners to ensure comprehensive evaluation of esophageal cancer. The study utilized seven different scanner platforms, including systems from GE Healthcare (Optima CT580 and Revolution CT) and Philips (Brilliance 64, GEMINI TF TOF 16, iCT 256, IQon Spectral CT, and Spectral CT). Standardized acquisition protocols were employed to maintain consistency across the imaging period.

Scans were acquired using a tube voltage of 120 kVp with automatic tube current modulation. The field of view was set to 500 mm with a matrix size of 512 × 512, and the section thickness ranged from 2.0 mm to 5.0 mm. For body composition analysis, an axial CT image centered at the T12 vertebral level was reconstructed with a slice thickness of 5 mm for skeletal muscle and adipose tissue measurement.

Body composition measurements and assessment of sarcopenia

Automated body composition characteristics at the T12 level were extracted from axial CT images using the open-source body organ analysis (BOA) tool[28]. BOA employs a variant of the multi-resolution 3D U-Net architecture to enable fully automated segmentation of tissues within defined body regions[29]. It integrates multiple segmentation algorithms with a seamless workflow *via* DICOM node integration, allowing comprehensive body composition analysis with extensive volume coverage[28].

In this study, assessment of muscle and adipose tissue composition was performed at the thoracic T12 level (Figure 2). Body composition analysis included measurement of the cross-sectional area (cm^2) of four tissue compartments: Skeletal muscle, subcutaneous adipose tissue (SAT), visceral adipose tissue (VAT), and total adipose tissue (TAT). These areas were normalized to the patient's height squared (cm^2/m^2) to calculate corresponding indices: SMI, SAT index, VAT index, and TAT index (TATI). In addition, the sarcopenia adipose ratios were calculated by VAT index/SMI, SAT index/SMI, and TATI/SMI. Based on prior literature, SMI at the T12 level was converted to an estimated L3-level equivalent using a validated predictive formula[30]. Sarcopenia was then defined using established L3 cut-off values: 34.4 cm^2/m^2 for females and 45.4 cm^2/m^2 for males[31].

Radiomic feature extraction

Radiomic features were automatically extracted using PyRadiomics (version 3.0.1) (https://pyradiomics.readthedocs.io/), developed by van Griethuysen *et al*[32]. A total

of 107 original radiomic features were extracted, comprising 14 shape features (*e.g.*, volume, compacity, sphericity), 18 first-order features (*e.g.*, mean, median, maximum, and minimum voxel intensities), and 75 textural features for skeletal muscle, SAT, and VAT. The textural features included metrics derived from the 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, among others.

Models analysis and features selection

Figure 3 illustrates the workflow for model development and evaluation of its predictive value for OS in esophageal cancer. All included patients had complete demographic and clinical data, along with both pretreatment and follow-up CT images. The BOA tool was applied to the CT images to automatically segment the ROIs for muscle and adipose tissues. The cross-sectional areas of skeletal muscle, SAT, VAT, and TAT were calculated to generate BOA-derived indices at the central T12 level. Additionally, radiomic features were extracted from the ROIs of muscle, SAT, VAT, and TAT at the same level.

In this study, the input data included demographic and clinical information; pretreatment and follow-up BOA and radiomic features; as well as normalized difference indices (delta indices) between pretreatment and follow-up measurements. These delta indices were calculated using the formula (f/u - pre)/pre, f/u was follow-up, pre was pretreatment. For example, the delta VAT was computed as (VAT_f/u - VAT_pre)/VAT_pre. All extracted features, including demographic, clinical, BOA, and radiomic variables, are detailed in Supplementary Tables 1 and 2.

Four different combinations of feature datasets were used to compare their predictive value for OS: (1) Feature subset 1. No-radiomics input model: Included only clinical, demographic data, and BOA indices from both pretreatment and follow-up CTs; (2) Feature subset 2. Pretreatment input model: Included clinical, demographic data, and pretreatment BOA indices and radiomic features; (3) Feature subset 3. Follow-up input

model: Included clinical, demographic data, and follow-up BOA indices and radiomic features; and (4) Feature subset 4. Combined input model: Included all available data-clinical, demographic, as well as pretreatment and follow-up BOA indices and radiomic features.

Feature selection began with the application of a logistic regression (LR) model using the least absolute shrinkage and selection operator, which eliminates redundant, irrelevant, or highly correlated features[33]. Variables with nonzero coefficients were retained as candidate features. Subsequently, Cox proportional hazards regression were performed to identify the most predictive features, with significance defined as a *P* value < 0.05. These selected features were then used to construct prognostic models - including a nomogram, support vector classifier (SVC), LR, and extra trees classifier (ETC) - to predict 1-year, 2-year, and 3-year OS.

Statistical analysis

Statistical analyses were performed using Python (version 3.10) and R software (version 4.5.1), with *P* values < 0.05 considered statistically significant. Patients were stratified into high-risk and low-risk groups based on the median of the predicted values as the optimal cutoff. Survival differences between the groups were assessed using Kaplan-Meier survival curves and compared using the log-rank test. Additionally, nomogram, SVC, LR, and ETC models were used to estimate 1-year, 2-year, and 3-year OS for individual prognostication. Model performance across the four input datasets was evaluated using the area under the time-dependent receiver operating characteristic curve (AUC), along with sensitivity and specificity determined based on the Youden index.

RESULTS

Patient cohort

Table 1 presents the clinical and demographic characteristics of the study cohort. A total of 212 patients were included, with a median follow-up period of 18.1 months (range:

2.4-87.3 months). The cohort consisted of 200 males and 12 females, and the mean age at diagnosis was 58.8 ± 8.9 years (range: 34-80 years). Most patients (96.7%) were pathologically diagnosed with esophageal adenocarcinoma, while 3.3% had squamous cell carcinoma.

Regarding tumor staging, the distribution of T stages was as follows: T1 (n = 11, 5.2%), T2 (n = 7, 3.3%), T3 (n = 178, 84.0%), and T4 (n = 16, 7.5%). For nodal involvement, N0, N1, N2, and N3 stages were observed in 15 (7.1%), 63 (29.7%), 82 (38.7%), and 52 (24.5%) patients, respectively. Distant metastasis (M1) was present in 29 patients (13.7%), while 182 (86.3%) had M0 disease. According to ECOG performance status, 169 patients (79.7%) were classified as status 1, 8 patients (3.8%) as status ≥ 2, and 10 patients (4.7%) had missing data. The mean interval between the start of CCRT and the follow-up CT scan was 105.4 ± 38.0 days. A total of 95 patients (44.8%) underwent surgical treatment, with a mean interval of 96.5 ± 82.3 days from the start of CCRT. The OS rates at 1, 2, and 3 years were 70.3% (n = 149), 47.6% (n = 101), and 38.7% (n = 82), respectively.

Features selection

Tables 2, 3, 4, and 5 present the final features selected through least absolute shrinkage and selection operator and Cox proportional hazards regression for the four feature subsets. Detailed analyses of the feature selection process for each subset are provided in the Supplementary Tables 3-6. Table 2 presents the final predictive features for feature subset 1 (no-radiomics input model), which included TNM stage, ECOG performance status, sarcopenia, TATI/SMI ratio, and delta_SAT. For feature subset 2 (pretreatment input model), the selected features are listed in Table 3, comprising T and M stages, one muscle shape feature, three VAT shape features, VAT first-order mean, and one VAT GLCM feature. Table 4 summarizes the final predictive features for feature subset 3 (follow-up input model), consisting of T and M stages, one muscle GLSZM feature, four VAT first-order features, two VAT GLCM features, one VAT GLRLM feature, two VAT GLSZM features, and two VAT GLDM features. Table 5

shows the final predictive features for feature subset 4 (combined input model), which include T and M stages, one pretreatment muscle shape feature, one pretreatment VAT shape feature, one pretreatment SAT first-order skewness, one follow-up muscle GLSZM feature, three follow-up VAT first-order features, one follow-up VAT GLCM feature, two follow-up VAT GLRLM features, one follow-up VAT GLSZM feature, one VAT GLDM feature, and one delta VAT shape feature. For ease of comparison across all models, Table 6 provides a consolidated summary of all final selected features from feature subsets 1 through 4.

Model performance

Nomograms were developed for each of the four feature subsets by assigning scores to clinical variables, BOA indices, and radiomic features based on their prognostic impact on OS. Figure 4 display the nomograms corresponding to feature subsets 1, 2, 3, and 4, respectively. The associated Kaplan-Meier survival curves are shown in Figure 5. A significant difference of survival rates between low- and high-risk groups was observed across the feature subset 1, 2, 3, and 4 model, log-rank *P* values = 0.042, 0.003, 0.001, and < 0.001, respectively (Figure 5).

Figure 6 illustrates the AUC curves for 1-, 2-, and 3-year OS prediction using SVC, LR, ETC, and nomogram models for feature subsets 1 and 4, allowing for a comparison between models with and without radiomic features. Similarly, Figure 7 presents AUC for feature subsets 2 and 3 to compare pretreatment and follow-up feature models across the same classifiers.

The performance metrics - including AUC, sensitivity, and specificity - for 1-, 2-, and 3-year OS prediction across all feature subsets and classification models (SVC, LR, ETC, and nomogram) are summarized in Table 7. Among all models, LR model demonstrated the best performance in predicting 2-year OS, achieving AUC values of 0.84, 0.77, 0.81, and 0.91 for feature subsets 1, 2, 3, and 4, respectively. The highest performance was observed in feature subset 4 (combined input model), with the LR model achieving an AUC of 0.91, sensitivity of 0.81, and specificity of 0.88.

DISCUSSION

Recently, a raised number of studies are investigating integrated models that used sarcopenia or radiomics with machine learning model to predict survival outcomes in esophageal cancer patients[24-27,34-42]. Difference from those previous studies, in this study, we compared the performance of four different feature datasets - comprising demographic and clinical data, BOA indices, and radiomic features extracted at the T12 vertebral level from both pretreatment and follow-up CT images - across four predictive models: Nomogram, SVC, LR, and ETC. Our results demonstrated that integrating BOA indices and radiomic features from both pretreatment and follow-up CT scans, along with clinical data, provided the most accurate prognostic prediction for esophageal cancer, particularly for 2-year OS. To the best of our knowledge, this is the first study to utilize radiomic analysis of skeletal muscle and adipose tissue at the T12 level on chest CT images to assess the prognostic performance of a combined model for survival prediction in esophageal cancer.

Prognostic features

This study comprehensively evaluated the prognostic value of various feature types - including demographic and clinical data, body composition analysis indices, and radiomic features - from both pretreatment and follow-up CT scans in predicting OS in esophageal cancer. As shown in Table 6, the most predictive features for OS varied across the four feature subsets.

Subset 1 (without radiomics) included four clinical variables (TNM staging, ECOG performance status) and three BOA indices (delta_SAT, TATI/SMI ratio, sarcopenia). Subset 2 (pretreatment only) comprised two clinical variables (T and M stages), one muscle feature, and five VAT features, while subset 3 (follow-up only) included the same clinical variables with one muscle and 11 VAT features. Subset 4 (combined) incorporated two clinical variables, two muscle features, one SAT feature, and 10 VAT features, with most radiomics derived from follow-up CT. These findings agree with

previous studies showing the prognostic value of clinical data, BOA indices[34-37], and muscle radiomic features[26,27]. Unlike earlier work that mainly used L3-level CT and rarely included follow-up imaging, our study analyzed T12-level CT and incorporated both pretreatment and follow-up scans.

When comparing subsets, radiomic features (subsets 2-4) replaced all BOA indices from subset 1, suggesting strong overlap between them. Radiomic features - especially from muscle and VAT - were more predictive than BOA indices. Both pretreatment and follow-up inputs contributed to OS prediction, but the combined model was driven mainly by follow-up radiomics, with 10 of 13 features coming from post-treatment CT. This aligns with prior findings that follow-up imaging provides critical insights into treatment response and long-term outcomes[15,16]. Additionally, our study shows that both muscle and adipose tissue mass affect esophageal cancer prognosis, consistent with reports that weight loss predicts poor outcomes[43,44]. Moreover, significant declines in SAT, VAT, and muscle between baseline and follow-up CT have also been linked to higher mortality risk[38].

Features in subsets and OS years

We developed 48 predictive models using four model types (nomogram, SVC, LR, and ETC) across four feature subsets to predict 1-, 2-, and 3-year OS. LR showed the best performance, especially for 2-year OS, with AUCs of 0.84, 0.77, 0.81, and 0.91 for subsets 1-4, respectively. These results indicate that combining clinical data with muscle- and adipose-derived features improves predictive accuracy, consistent with previous studies[26,27,34-37]. The weaker performance of models without follow-up data (subset 2) compared to those with follow-up data (subsets 3 and 4) further underscores the importance of post-treatment body composition changes in prognosis.

Kaplan-Meier curve analysis showed significant survival differences across all feature subsets, with 2-year OS prediction performing better than 1- or 3-year OS. This may be because first-year survival was relatively high, while third-year survival was relatively low, making the 2-year rate (approximately 47.6%) a critical threshold near 50%. At this

point, patients' nutritional health and survival status are especially important in clinical practice. Significant 2-year survival differences were seen between high- and low-risk groups in all subsets, with subset 4 showing the clearest separation. These findings suggest that combining clinical data with radiomic features from both pretreatment and follow-up imaging provides the most accurate OS prediction in esophageal cancer.

Radiomics of muscle and adipose at T12 level

SMI at the L3 level is a well-established CT biomarker for survival in esophageal cancer[34-37], but follow-up scans often cover only the chest and exclude L3. Our study showed that BOA and radiomic features from T12-level muscle and adipose tissue can also predict outcomes, consistent with prior findings[45]. While earlier studies focused mainly on tumor radiomics[34-37], our results highlight the prognostic value of body composition features at T12 on both pretreatment and follow-up CT, in line with studies at L3[26,27]. A key advantage of our approach is that ROIs can be extracted using automated BOA software, eliminating the need for manual annotation by experienced radiologists - a process that is often time-consuming and resource-intensive.

Although certain radiomic features may appear abstract, they capture quantitative aspects of tissue heterogeneity not visible to the naked eye. For example, VAT_glrlm_RunEntropy quantifies heterogeneity in voxel intensity runs, which may reflect irregular adipose distribution caused by cachexia, therapy response, or treatment-induced metabolic and inflammatory changes - processes that are clinically relevant in esophageal cancer prognosis. Similarly, first-order features (*e.g.*, mean intensity) and shape features (*e.g.*, sphericity, SurfaceVolumeRatio) are interpretable as measures of tissue composition and morphology, reflecting atrophy, redistribution, or structural remodeling after treatment. Texture features derived from GLCM, GLDM, and GLRLM are crucial for capturing tissue heterogeneity[34], and histogram entropy from pre-treatment positron emission tomography/CT has been associated with poorer recurrence-free and OS in gastroesophageal junction cancer[34]. Shape features have also shown high reproducibility and strong links to tissue morphology[46].

Furthermore, integrating CT radiomics of skeletal muscle with machine learning models has correlated with sarcopenia and predicted disease progression in gastric and esophageal tumors[26], and skeletal muscle radiomics is increasingly recognized as a potential biomarker for sarcopenia[21]. Thus, while not directly intuitive, these radiomic signatures likely encode meaningful biological processes underlying prognosis.

Limitations and future work

This study has several limitations. First, this study was conducted retrospectively at a single center, involving a relatively small and heterogeneous patient cohort. For instance, gender distribution was markedly skewed, with only a small proportion of female patients (n = 12, 5.7%) and adenocarcinoma cases (n = 7, 3.3%), potentially introducing selection bias. Although our cohort consisted predominantly of male patients (94.3%) and squamous cell carcinoma cases (96.7%), this distribution reflects the epidemiology of esophageal cancer in East Asia[47]. Nevertheless, such demographic and histological imbalance may limit the generalizability of our findings to female patients or to those with adenocarcinoma. Future multicenter studies with larger and more balanced cohorts are warranted to validate model performance across diverse patient subgroups.

Second, due to the retrospective nature of the study spanning several years, variability in imaging acquisition parameters and reconstruction protocols may have affected the stability and reproducibility of radiomic features[48]. CT images in this study were acquired from multiple scanners and reconstruction protocols. Although standardized acquisition settings were applied, radiomic features are known to be sensitive to scanner- and protocol-related variations[49]. We did not apply image harmonization techniques such as ComBat[50], which may have further improved feature reproducibility. This variability may introduce bias and should be addressed in future multicenter studies using harmonization methods to ensure robust model performance across institutions.

Third, the first follow-up CT scans were performed within a relatively wide window (60-180 days) after CCRT, partly reflecting clinical scheduling. This heterogeneity may introduce variability in prognostic assessment. Future studies should stratify patients by narrower intervals to determine the optimal timing for prognostic imaging.

Fourth, this study is the absence of both internal cross-validation and external multicenter validation, limiting the generalizability and clinical applicability of the proposed models. While our primary aim was to identify influential features at the T12 level rather than to build a broadly generalizable predictive model, we acknowledge that the lack of validation may introduce optimism in performance estimates. To strengthen and validate our findings, internal and external validation using multicenter data should be conducted in future studies.

CONCLUSION

In clinical practice, efficiently and accurately identifying the prognostic risk of cancer patients - while accounting for the influence of comorbidities - is crucial for optimizing treatment strategies. Our study demonstrates that BOA indices and their corresponding radiomic features, derived from skeletal muscle and adipose tissue at the T12 level on CT images, serve as valuable prognostic biomarkers for esophageal cancer. Notably, incorporating these features from follow-up CT scans after CCRT provides significant additional prognostic value for predicting OS. A model that integrates BOA and radiomic features from both pretreatment and follow-up CT images, in combination with clinical data, can markedly enhance the predictive performance for OS in patients with esophageal cancer.

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