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Prediction of surgical outcomes in ovarian cancer based on CT imaging

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Abstract. This study aims to investigate the commonly used prediction models for the outcomes of ovarian cancer surgery. The study will select 71 cases from the TCGA-OV dataset and divide them into a training set (n=51) and a validation set (n=20) at a ratio of 7:3. The project is based on PyRadiomics Python3.0.1 and extracts 107 basic image features from the image group data, including first-order statistics, shape, gray-level co-occurrence matrix, gray-level size zone matrix, GLRLM, etc. On this basis, the LASSO algorithm is used for feature dimensionality reduction. In building the model, a fuzzy matrix is used to analyze multiple evaluation indicators, including the area under the receiver operating characteristic (ROC) curve (AUC). This study hopes to provide more precise diagnostic and treatment plans for patients, with the goal of achieving better treatment outcomes.

Keywords: Image-based genomics, ovarian cancer, convolutional neural networks, support vector machines.

1. Introduction

Ovarian cancer is a malignant tumor occurring in the ovaries, with 90%-95% being primary ovarian cancer and 5%-10% originating from other organs. Ovarian cancer in stages I and II often presents with subtle clinical symptoms and has limited screening value. By the time of diagnosis, patients are usually in intermediate to advanced stages (III-IV), and treatment outcomes are often suboptimal. Even with rigorous drug therapy, 25% of patients with early, middle, and late-stage ovarian cancer may experience recurrence, with a 5-year survival rate of only 29%. Thus, although the incidence of ovarian cancer is lower than that of cervical cancer and endometrial cancer among gynecological diseases, it has the highest mortality rate among them. Breast cancer, with the highest incidence among female malignancies, poses a significant threat to women's health. The standard treatment for ovarian cancer involves tumor debulking surgery combined with postoperative chemotherapy to thoroughly remove visible lesions. If a single surgery does not achieve an ideal debulking rate, the patient's prognosis is poorer. Abdominal CT is the primary method for preoperative diagnosis, offering broad scanning coverage, speed, and cost-effectiveness. Currently, CT-based tumor diagnostic models have become the main tool for preoperative assessment of ovarian cancer. Traditionally, radiologists rely on visual inspection and their intuition and experience to assess the condition, leading to variability based on individual experience. However, images contain rich objective information. By employing radiomics core steps to extract high-throughput features and analyze the intrinsic properties of the region of interest,

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diagnosis based on these intrinsic properties can achieve higher consistency [4]. This article discusses the selection of radiomics methods and models in the process of predicting the surgical outcomes of ovarian cancer, mainly adopting the research method of literature review.

2. Literature Review

2.1. Overview of Radiomics

Radiomics was introduced by Dutch scholars, such as Lambin, in 2012 [1]. Radiomics involves the quantitative analysis of vast amounts of medical imaging data using automated or semi-automated software to extract quantifiable information based on imaging features. These imaging features can include histograms, textures, models, transformations, and shapes. While radiologists can classify images based on imaging features, some early microscopic changes are difficult to detect with the human eye. The rise of AI has advanced the development of radiomics. Machine learning (ML), a crucial branch of AI, includes techniques such as logistic regression, artificial neural networks (ANNs), support vector machines (SVMs), deep learning (DL), and convolutional neural networks (CNNs). The radiomics process involves six steps: (1) Planning, which includes identifying clinical problems and research design; (2) Image acquisition; (3) Image preprocessing and segmentation; (4) Extraction of imaging features; (5) Construction of radiomics models; (6) Evaluation and validation of radiomics model performance [2].

Radiogenomics is a research approach that connects radiomics imaging data with genomics. In recent years, other biological parameters have also been more broadly integrated into radiogenomics research. Radiogenomics was initially and primarily applied in the field of malignant tumors. Genetic mutations are not only causative factors in cancer but also play roles in chemotherapy effectiveness and recurrence. Major differences in protein expression within tumors can be correlated with radiomics features. Thus, radiomics, through non-invasive methods, can predict changes in tumor genomics, potentially benefiting cancer patients in risk prediction, treatment planning, prognosis assessment, and survival prediction.

2.2. Research Progress on Radiomics in Ovarian Cancer

Ovarian cancer is a gynecological tumor with high disability and mortality rates, making early diagnosis and treatment a significant clinical challenge. Radiomics, a novel medical imaging technology developed in recent years, has significant applications in early diagnosis, pathological classification, prognosis assessment, and treatment monitoring. The following is a review of relevant research on radiomics in ovarian cancer:

Recently, scholars both domestically and internationally have conducted imaging analyses and in-depth studies [1]. This project aims to extract clinically significant samples from clinical data and perform quantitative analysis on these images using computer and machine learning methods to obtain quantifiable expressions of microstructure, grayscale distribution, texture, and other parameters. This provides a more comprehensive basis for developing clinical diagnosis and treatment plans.

Radiomics technology enables automated identification and localization through the study of morphological and texture features, laying the groundwork for its application in disease diagnosis and treatment. Additionally, radiomics can integrate with serum biomarkers and genetic information to achieve multimodal data fusion analysis, further improving the diagnostic accuracy and predictive performance of ovarian cancer.

Furthermore, radiomics technology can be applied to clinical pathological grading, prognosis evaluation, and treatment monitoring. Based on this, combining clinical pathological parameters and prognosis assessments can propose more accurate and complete diagnostic methods. Imaging technology allows for real-time monitoring of treatment efficacy in ovarian cancer cells, guiding clinical planning. Although there has been some progress in imaging research on ovarian cancer, issues such as insufficient data, stability and reproducibility of image features, and optimization of model algorithms remain. Future efforts should focus on integrating large sample multi-center image analysis methods to establish precise radiomics analysis for ovarian cancer.

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2.3. Common Radiomics Technologies and Models

The integration of imaging technology with computer technology effectively uncovers numerous biological characteristics, providing a foundation for early diagnosis, prognosis evaluation, and treatment monitoring. Common feature extraction techniques in radiomics research include first-order statistical features, shape features, texture features, and deep neural networks. Various feature selection algorithms, such as LASSO and random forests, are used to improve image classification and recognition accuracy. For image classification, methods such as SVM, random forests, and deep neural networks are primarily used for rapid and accurate classification and diagnosis. Performance evaluation of these algorithms is based on metrics such as accuracy, recall, precision, and F1 score.

In recent years, imaging technology has seen increasingly widespread applications in healthcare. Research content should include early screening, precision medicine, prognosis evaluation, and treatment monitoring, focusing on intelligent diagnosis and intervention based on multimodal information and fusion of multimodal data. Radiomics can extract cancer features from multiple levels, including morphology, structure, and texture, to achieve early detection and diagnosis of cancer, providing a foundation for precise cancer treatment, efficacy evaluation, and prognosis assessment. This project will also study multimodal information fusion methods to offer more precise and personalized support for clinical diagnosis and treatment planning. In summary, based on specific research needs, different imaging technologies and models should be adopted to achieve precise diagnosis and treatment of ovarian cancer.

3. Research Steps

3.1. Data Loading and Preprocessing

Data will be collected from the ovarian cancer module of the TCGA public database. This project will focus on the TCGA-OV database, which includes genomic and clinical data from 147 ovarian cancer patients. 71 cases will be selected, with data such as patient age and survival time extracted using 3D Slicer version 5.0.3. Tumor segmentation will also be performed using this software. A 7:3 sample ratio will be used to establish a three-year survival prediction model.

Inclusion and exclusion criteria will be based on the research objectives. Data sourced from the TCGA database ensures that CT images and survival times of patients are available. Images that cannot distinguish between tumor and normal tissue will be excluded due to clarity issues.

Initially, data from Excel will be stored as two data frame objects (data_1 and data_2) and then merged into a single data frame object (data). The data will be randomly shuffled and standardized.

3.2. Feature Selection within the process of Model Building

3.2.1. Lasso Algorithm

Lasso is a type of linear regression model based on L1 regularization. It selects features from the data and adjusts model parameters. Lasso uses L1 regularization to drive some feature coefficients to zero, thus filtering and retaining the most valuable features. The method involves minimizing a loss function based on residual sum of squares (RSS) and a regularization term, which is the sum of the absolute values of the coefficients multiplied by a parameter alpha. This regularization term penalizes some parameters, promoting sparsity. The coordinate descent optimization method is then used to minimize the loss function, gradually reducing the weight of non-essential features to zero. Building on this, a new neural network-based autoregressive method will be proposed to effectively reduce overfitting and enhance generalization.

3.2.2. Traditional Radiomics Methods

This project will use the PyRadiomics library in Python to extract quantitative features from images. Radiomics is a technique for extracting features such as texture, shape, and grayscale from images. The process involves: acquiring medical imaging data (CT, MRI, etc.), segmenting images to separate

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regions of interest from the background, and marking tumors or other affected areas. The PyRadiomics-based image processing method will then be applied and analyzed. These features help analyze lesion morphology, structure, and tissue characteristics. After feature extraction, data will be filtered and selected to improve algorithm performance. Statistical methods and machine learning techniques will be used to address these issues. The obtained data will be applied to disease diagnosis, staging, and prognosis evaluation. Interaction testing will ensure that the new dataset has strong generalization capability. The project aims to provide new insights for cancer diagnosis, prognosis assessment, and treatment monitoring, supporting personalized and precise medical treatments. Advances in radiographic imaging technology provide physicians with more data, aiding in more accurate patient assessment and treatment planning.

3.2.3. t-Test

A statistical method known as the t-test (student's t-test) compares the means of two groups to ascertain whether there is a significant difference between them. The t-test's basic idea is to compare the means of two samples to determine whether they are from the same population. It assumes equal variance between the two groups (homogeneity of variance) and calculates the t-value based on sample means and variances to determine if there is a significant difference between the sample means.

The formula for calculating the t-value is:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} \tag{1}$$

where: $\bar{X}_1$ and $\bar{X}_2$ are the means of the two sample groups. s_1 and s_2 are the standard deviations of the two sample groups. n_1 and n_2 are the sample sizes of the two groups.

After calculating the t-value, the degrees of freedom (typically the sample size minus 1) are used to find the critical t-value from the t-distribution table. The significance of the t-value is determined based on this critical value and the chosen significance level (usually 0.05). If the absolute value of the t-value exceeds the critical t-value, the null hypothesis is rejected, indicating that there is a significant difference between the means of the two samples. If not, the null hypothesis is not rejected, suggesting that the means of the two sample groups are equal.

3.2.4. Homogeneity of Variance Test

The homogeneity of variance test is used to determine whether the variances between two or more samples are equal. In statistics, the assumption of homogeneity of variance is crucial for many statistical methods, such as the t-test and ANOVA, which assume that the variances of the samples are the same. Variances between samples can have an impact on statistical data processing.

Common methods for testing homogeneity of variance include Levene's test, Bartlett's test, and Fligner-Killeen test. Statistical analysis relies on computing test statistics and comparing them to threshold values to assess differences between statistics. If the p-value from Levene's test exceeds the significance level (commonly set at 0.05), the assumption of equal variances can be accepted, indicating that the variances of the two samples are similar.

3.3. Model Training within the process of Model Building

3.3.1. Support Vector Machine (SVM)

Support Vector Machine (SVM) is a machine learning method that utilizes pre-selected nonlinear mappings to transform data into high-dimensional feature spaces. SVM excels in establishing nonlinear decision boundaries and demonstrates robust performance. However, it faces challenges when dealing with large-scale datasets.

The theoretical foundation of SVM involves transforming linearly inseparable data into a high-dimensional feature space where linear separation becomes feasible. The critical step is to determine the

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optimal hyperplane for partitioning the samples. For binary classification problems, Figure 1 illustrates samples from two distinct categories represented by circles, with L denoting the category boundary (hyperplane). The margin is defined as the distance between this hyperplane and the nearest data points, represented by L1 and L2 in Figure 1. SVM's ultimate goal is to identify the specific hyperplane, L1 and L2, which maximizes these margins and is considered the optimal hyperplane.

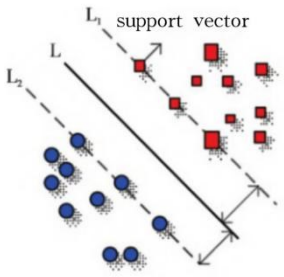

Figure 1. SVM optimal hyperplane

3.3.2. Random Forest

Random Forest is an ensemble learning-based machine learning method comprising multiple trees that learn independently and aggregate their predictions through voting or averaging. Key aspects of Random Forest include:

Decision Tree Integration combines multiple trees, each a weak learner, to achieve higher predictive accuracy and stability.

Random Feature Selection randomly selects a subset of features for each decision tree to reduce inter-attribute dependencies, mitigate overfitting, and enhance model generalization.

Bootstrapping constructs training sets for each decision tree using bootstrap sampling, ensuring diversity among the generated networks.

Voting or Averaging integrates predictions from individual trees using majority voting for classification or averaging for regression tasks.

Efficiency and Scalability facilitates parallel learning of individual trees, enabling effective processing of large-scale datasets.

3.4. Model Optimization and Evaluation

GridSearchCV is employed to optimize SVM parameters, exploring various hyperparameter combinations through cross-validation. This method systematically evaluates different parameter sets to identify the optimal configuration, enhancing the model's generalization and predictive capabilities.

AUC represents the area beneath the Receiver Operating Characteristic (ROC) curve, which plots the True Positive Rate (TPR) against the False Positive Rate (FPR). AUC values range from 0 to 1, with higher values indicating superior classifier performance. An AUC of 0.5 suggests performance equivalent to random guessing.

Model evaluation commonly uses cross-validation to more accurately assess model performance by reducing the impact of data partitioning variability. K-fold cross-validation, in particular, is commonly employed to provide robust performance estimates.

The full name of ROC is "Receiver Operating Characteristic," which is used to evaluate classification and detection results. The ROC curve is a widely used and important statistical tool.

3.5. Confusion Matrix

In machine learning, the confusion matrix is also referred to as the error matrix. It is an intuitive tool specifically designed for supervised learning and is called the matching matrix in unsupervised learning. When evaluating the accuracy of imaging, the predicted class of the image is compared with the actual class, and the results are presented in a confusion matrix.

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A confusion matrix is typically described in the figure 2 below :

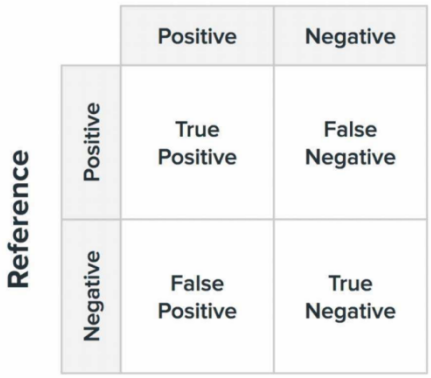

Figure 2. confusion matrix

Calculating True Positive Rate (TPR) and False Positive Rate (FPR) can be expressed as follows:

TPR = TP / (TP + FN), where TPR is the true positive rate.

FPR = FP / (FP + TN), where FP is the number of false positives, and TN is the number of true negatives.

A model's probability prediction is converted into a class label. Generally, if a sample's predicted probability exceeds the threshold, it is classified as a positive instance. If the predicted probability is below the threshold, it is treated as a negative instance.

To plot the ROC curve, FPR is placed on the horizontal axis, and TPR is placed on the vertical axis. The ROC curve is drawn based on different classification thresholds.

4. Discussion

While significant progress has been made in ovarian cancer imaging research, several limitations persist:

Contemporary research mostly concentrates on High-Grade Serous Ovarian Carcinoma (HGSOC), while overlooking other ovarian cancer variants. Notwithstanding its potential, radiomics has not been extensively implemented in clinical practice. Access to specialized equipment and skills necessary for radiomics analysis is not widely attainable. The absence of interdisciplinary collaboration impedes the progress of radiomics.

Future research should aim to expand the scope of studies, optimize techniques, encourage research in primary healthcare settings, and promote interdisciplinary collaboration. Integrating radiomics and artificial intelligence can enhance diagnostic accuracy and treatment planning, ultimately improving patient outcomes. Additionally, radiomics holds promise in drug evaluation, development, and immunotherapy research.

Despite current limitations, radiomics demonstrates significant potential in clinical efficacy evaluation. Continued research and technological advancements will lead to improved treatment prospects for ovarian cancer patients.

5. Conclusion

This study dedicates to investigating methods for predicting the prognosis of ovarian cancer post-surgery. Acknowledging that each patient carries significant hopes and expectations, the aim of this study is to offer more precise diagnoses and treatment plans through this research, ultimately leading to improved treatment outcomes. However, this paper encountered several challenges in pursuing this objective. During the investigation, only a portion of the ovarian cancer imaging data from a single hospital was utilized, with discussions held with a radiologist. However, the sample size collected for sorting and analysis was insufficient, which may limit the generalizability of the conclusions. Additionally, the exploration of commonly used imaging feature screening and data processing methods has not been as

thorough or comprehensive as desired. Moving forward, the author intends to conduct more extensive investigations in these areas. In future endeavors, the research will engage in deeper learning and practical applications related to various algorithms such as machine learning.

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