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In Surgical Oncology, Radiomics: Challenges and Applications

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Abstract

Many people who have cancerous tumors can get better with surgery. Since multimodality treatment has been linked to promising outcomes in some types of cancer, more attention has been paid to the combination of surgery and chemotherapy. Despite these findings, there is still clinical disagreement regarding the ideal patient selection and timing for neo-adjuvant or adjuvant strategies. By assisting in the prediction of tumor behavior and response to therapy, the emerging field of radiomics, which involves the extraction of advanced features from radiographic images, has the potential to revolutionize oncologic treatment and advance personalized therapy. Predicting prognosis, recurrence, survival, and therapeutic response for various cancer types using radiomics and machine learning in patients who have received neo-adjuvant and/or adjuvant chemotherapy is the focus of this review. Although neoadjuvant and adjuvant studies show above average accuracy in predicting progression free survival and overall survival, widespread application of this technology faces numerous obstacles. The inclusion and rapid adoption of radiomics in prospective clinical studies has been hampered by the absence of auto- segmentation, limited data sharing, and standardization of common procedures for analyzing radiomics.

Keywords: Tumors • Radiomics • Neoadjuvant

Introduction

We used both the tumor and ALN radiomic features to create the ALN tumor radiomic signature in light of the link between ALN and the primary tumor site. This resulted in a higher AUC than when we used ALN or tumor radiomic features alone. More importantly, the predictive power may be enhanced by combining ALN and tumor radiomic features with clinical, pathologic, and molecular subtype characteristics. In our model, independent validation cohorts were tested to ensure the competence of the constructed signatures. In addition, our findings revealed associations between MRI radiomic features and tumor microenvironment characteristics like immune cells, long non-coding RNAs, and types of methylated sites, as well as significant differences in MRI radiomics before and after neo-adjuvant chemotherapy [1].

Literature Review

Computer software extracts a large number of predefined high throughput features from radiomics to characterize lung lesions using Artificial Intelligence (AI). Statistical methods then filter the features that are most relevant to the results. Finally, a diagnostic and predictive model is developed using machine learning. At the moment, a lot of attention is being paid to how radiomics can be used to diagnose and evaluate pulmonary nodules. The significance of texture in the diagnosis of pGGNs was examined by Hwang, et al. However, due to the small number of cases (64), fewer features were extracted. A radiomics based model performed better in our previous studies for predicting sub-centimeter GGNs; however, this study also included pGGNs and part solid nodules [2]. The diagnosis of part solid nodules is straight forward due to the satisfactory correlation of the solid components on CT imaging with pathologically invasive components; however, the diagnosis of pGGNs is challenging and the invasiveness is frequently underestimated. In order to increase the diagnostic accuracy of pGGNs and provide a foundation for rational clinical decision making, the goal of this study was to develop a comprehensive model of pGGNs based on conventional CT features and radiomics.

The effectiveness of a treatment can be evaluated using criteria from pathology or radiology. A "hard" endpoint is the pathologic response; however, only 16% of NSCLC patients who undergo surgical resection can have it evaluated. Therefore, the primary component of evaluating NSCLC treatment response is radiologic response. Based on a one-dimensional evaluation of the tumor's size, the Response Evaluation Criteria in Solid Tumors (RECIST) provides a standardized, objective method for reporting therapy response [3].

Discussion

Oncology trial endpoints like response rate and progression-free survival are defined using RECIST criteria. The radiologic evaluation of treatment response in clinical practice largely relies on tumor size, with a qualitative assessment of other tumor characteristics like homogeneity and shape added in. In order to solve this problem, we created Pyradiomics, a comprehensive open-source platform that makes it possible to process and extract radiomic features from medical image data by employing a wide range of engineered, hard-coded feature algorithms. In addition to a back-end interface that enables automation of data processing, feature definition, and batch handling, pyradiomics provides a flexible analysis platform with a front end interface in 3D slicer, a free open-source platform for medical image computing. Pyradiomics can be installed on any system because it is implemented in python, a well-known open-source language for scientific computing. [4].

In epithelial cell lines, EGFR is a receptor tyrosine kinase that controls normal cell growth. About 40% of glioblastomas have EGFR mutations, but lower grade gliomas rarely have them. The splice variant III (EGFRvIII) is the most common extracellular EGFR mutation in glioblastoma, occurring in 31% of patients. There is a moderate relationship between EGFR amplification and tumor blood flow and volume in radiogenomic studies using perfusion

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imaging. Approaches based on support vector machines have demonstrated that EGFRvIII mutant gliomas have deep peritumoral infiltration, indicating a more aggressive or infiltrative phenotype. Neovascularization, cell density, and a preference for the frontal and parietal regions in EGFRvIII tumors have all been demonstrated by additional multivariate approaches employing a larger number of multi-parametric features [5].

Data mining, which is the process of finding patterns in large data sets, can be done with large, high-quality, and carefully curated data sets that are available. Artificial intelligence, machine learning, or statistical methods can be used in this process. On one end, there are supervised and unsupervised methods like neural networks, support vector machines, and Bayesian networks for machine learning. Even though these methods make use of a priori knowledge by training sets, they are agnostic in the sense that they do not make any assumptions about what each feature means. As a result, all features are given equal weight when learning starts. Hypothesis driven methods that group features according to predetermined information content are at the other end of the data mining spectrum [6]. The best models are those that are tailored to a specific medical context and, as a result, start with a well-defined endpoint. Both of these approaches have merit.

Conclusion

Radiomics have shown extraordinary commitment in customizing chemotherapy treatment and choices for patients. The studies examined in this paper have demonstrated the usefulness of radiomics and machine learning in determining which patients benefit from chemotherapy and which do not. To make radiomic analysis more widely used and effective in clinical settings, stronger auto-segmentation algorithms, increased data sharing, and standardization are required.

Acknowledgement

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Conflict of Interest

None.

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