Commentary

World Journal of Medical Oncology

Hedgehog or ludum mutante in radiomics for precision oncology

Shi Hui Tay[1], Xin Zhang[1,2] and Melvin L. K. Chua[1,3,4]*

Corresponding Author

Melvin L. K. Chua , Department of Head and Neck and Thoracic Radiation Oncology, National Cancer Centre Singapore, 30 Hospital Boulevard, Singapore.

Email : *melvin.chua.l.k@singhealth.com.sg*

Received Date : *Dec 26 2023*
Accepted Date : *Dec 27 2023*
Published Date : *Jan 26 2024*

Keywords : Radiomics, Imaging, Precision oncology, Explainable AI, Nasopharyngeal cancer

INTRODUCTION

The use of precision oncology in the treatment of human tumors has become the next big thing in therapeutic approaches. The concept is straightforward yet compelling: to identify the genotypes and phenotypes of cancer in order to personalize treatment and risk assessment for each patient. In order to do this, techniques for next-generation sequencing (NGS) have been created to describe the genomes of tumors. Although this method has been successful in linking genotypes to appropriate medicines, testing is limited by the availability of tumor tissue. Therefore, considering that radiological scans, such as computed tomography and magnetic resonance imaging (MRI), are frequently conducted for cancer diagnosis, assessment of treatment response, and other purposes, research has looked into employing imaging as a data source for deeper phenotyping.surveillance for diseases. Thus, the field of study known as "radiomics" deals with the quantitative properties of pictures—such as forms, grayscale textures, and intensities—that are not visible to the human eye when extracted from designated regions of interest (ROI) on radiological images.

Tools from radioomics for clinical classification and cancer diagnosis

Numerous investigations have proven the potential of radiomics in diagnosis and clinical phenotypic stratification for treatment intensification or de-intensification over the years [1]. These published radiomics models claim to be able to forecast cancer patients' responses to particular drugs and/or predict their prognosis [2, 3]. However, due in part to low model reliability, radiomics deployment in the clinic is still difficult. In order to standardize the radiomics workflow, the Image Biomarker Standardization Initiative (IBSI) was established [4]. The radiomics quality score (RQS) was developed independently to help physicians assess the caliber of radiomics research [5].

We evaluate the work of Liu and colleagues [6] in light of this, as they created a radiomics signature to forecast post-radiation nasopharyngeal necrosis (PRNN) in patients suffering from locoregionally recurrent nasopharyngeal carcinoma (lrNPC). Pre-treatment MRI scans (T1-weighted with and without contrast enhancement, as well as T2-weighted sequences) of 761 patients—420 for training and 341 for validation—enrolled from four hospitals were used by the researchers to create the model. They created a 6-feature signature using a random forest model, which included 2 shape features, 3 texture features, and 1 first-order statistic that could distinguish between patients who were at low and high risk for PRNN. In the training dataset, the signature obtained AUCs of 0.722; for the internal and external validation cohorts, it obtained AUCs of 0.713 and 0.756, respectively. The affix exceeded the performance of established prognostic clinical factors, such as age, sex, disease-free interval, gross tumor volume, and re-irradiation dosage [7]. It was also generalized to other imaging parameters, centers, and patient subgroups (e.g., rT-categories, varying ages). The AUCs ranged from 0.888 to 0.671. The researchers compared the somatic transcriptome profiles of 29 patients with the radiomics features in order to give the model explanatory power. They linked the six radiomics traits to the signaling pathways for vascularity and fibrosis based on gene set enrichment studies.

Advantages and drawbacks

Overall, this study has a number of advantages. First, for lrNPC

patients whom reirradiation is anticipated, PRNN is a significant and clinically relevant consequence; soft tissue necrosis after reirradiation is a common and possibly crippling toxicity for these patients [8]. Therefore, from a clinical standpoint, it is beneficial to have a tool that can help with patient selection. Second, the study's investigators demonstrated the validity of their radiomics model through a series of thorough validation stages, including demonstrating the model's generalizability across various illness states and institutions.

Having said that, are we planning to use this radiomics instrument in the clinic starting tomorrow? There are a few noteworthy restrictions that should be mentioned. First, the AUCs for prediction are, at most, moderate at ~0.7. Secondly, it is unclear if the transcriptome profiling samples were spatially associated with the ROI where the radiometric features were taken out. When interpreting the robustness of the radio- transcriptionmic studies, this is an important factor to take into account. Third, there are significant obstacles to evaluating model reproducibility, including the absence of thorough documentation, the availability of open-source codes, and data accessibility.

Radiomics instrument translation from research to clinical practice What drastic measures are ultimately required to move radiomics tools from the laboratory to the clinical setting?

(1) Standardizing the radiomics workflow: An important first step is to harmonize the various processes, from image acquisition to model validation. The IBSI working group has developed a set of principles for benchmarking future radiomics studies in order to encourage adherence [4].

(2) ROI segmentation automation: This stage is crucial because radiomics feature extraction is delicately sensitive to minute changes in segmentation floods [9].

(3) Ensuring data quality: Given that tflese parameters can skew model performance, we propose the need for bencfl-marking criteria to assess the quality of datasets related to the accuracy of clinical annotation and the extent of data missingness for external validation of radiomics models.

(4) Transparency of study outcomes and validation: Independent groups conducting validation studies within a certain window time should be encouraged, rather than depending exclusively on the investigators. Regardless of the study's conclusions (positive or negative validation), the findings should be publicly disclosed, and journals should contribute to the publication of the results. Detailed reports, source codes, and anonymized data from the initial study must be made available in order to satisfy tflis.

(5) Explainability of the TFL radiomics model: We hypothesize that it would be optimal for radiomics models to incorporate the biological and clinical relationships that serve as the foundation for TFL development. By spatially connecting treatment response with target ROI or molecular profiles with treatment radiomics indices, this could be mitigated [10].

(6) Radiomics characteristics with spatial resolution: Differential treatment responses may be exhibited by distinct locations within a ROI. In light of this, exploring spatial-level radiomics may enhance its explanability when compared to bulk-level radiomics and is an intriguing avenue for the science to pursue.

CONCLUSION

Although research on radiomics' potential in precision oncology keeps coming out, the oncology community is still unclear about its relevance. In the future, the emphasis should shift from presenting yet another "hyped" radiomics model to demonstrating the scientific validity of the model for clinical application. In order to do this, it would be necessary to implement some of our suggested policies and ultimately test these models in prospective clinical trials guided by radiomics. Then and only then will radiomics live up to its potential as a precision oncology "ludum mutante."

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