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EDITORIAL

Radiomics in Oncology

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Tumour histology classification is based on biopsy, that is invasive, destructive (reducing the number of monitoring opportunities) and suffers from poor cost efficiency. Biopsy sampling of a random spatial subregion of a tumour at a single time point may not be able to reflect the complex tumour state accurately [1-4]. Furthermore, it is well known that a hallmark of tumours is their spatial and temporal heterogeneity. On the other hand, imaging provides an opportunity to extract valuable information regarding tumour characteristics in a non-invasive way. It's not subjected to bias selection, since the entire tumour can be assessed multiple times during the course of the disease (before, during and after treatment). However, currently imaging evaluation is based on the subjective opinion of radiologists, is time consuming, varies significantly protocol-wise and therefore suffers from low reproducibility.

Over the past decade the advances in computational image analysis methods have provided a unique opportunity to transform digital standard of care medical images to mineable high dimensional data (radiomics) that potentially reflect tumour biology and predict patient outcome in several tumour types [2, 5-15]. A relatively small number of studies have addressed the critical question of whether radiomic metrics correlate with histopathological and genomic changes in regions of interest [5, 15-18].

In this issue of the Hellenic Journal of Radiology, there are two very interesting articles on radiomics in oncology. Manikis and colleagues [19] investigate the role of T2- based MRI radiomic features for discriminating tumour grading in soft tissues sarcomas. Bisdas and colleagues [20] provide a comprehensive systematic review on the current evidence for the clinical value of radiogenomics in glioblastomas. Both papers highlight the potential important role that radiomics can play in oncology. However, existing radiomic approaches have not encoded the extent of variability between different regions within the tumour (habitats) [21, 22] and between multiple metastatic tumour sites within the patient [23]. Yet, genomic heterogeneity within the tumour and across metastatic tumour sites in the same patient is a major cause of treatment failure and development of resistance to targeted therapies [24-27] as well as specific patterns of malignant cell spread within the peritoneal cavity [28]. The lesion-specific properties, immunological components of the tumour microenvironment, may modulate malignant cell invasion and expansion, thereby shaping evolutionary selection [27,29]. However, quantification by repeated multiple tissue sampling in the same patient is challenging to implement in routine clinical practice.

Standard-of-care imaging offers a unique opportunity to non-invasively quantify and dynamically track spatial tumour heterogeneity. Nevertheless, most of the radiomics methods to date have been developed and applied to measure average intra-tumour heterogeneity based on a single disease site per patient in primary tumours [5, 15-18]. In the metastatic setting, the largest metastasis has been typically chosen for radiomics analysis and thought to be representative of the overall tumour burden heterogeneity [15, 18, 30]. In addition, most of the studies lack robust biological validation due to poor methodology for radiomics feature extraction, retrospective design and lack of adequate methods for accurate spatial co-registration of imaging with tissue sampling [11]. Most importantly, radiomics research is still working in the space of correlation rather than integration with other multi-omics data. The fact that tumours displays spatial heterogeneity at such disparate physical scales suggests that a combined approach to integrate the relevant data sources (genomics, transcriptomics, radiomics) is needed to unravel the complexity of the disease. R

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