Radiomics

Radiomics is a field of medical study that aims to extract large amount of quantitative features from medical images using data-characterisation algorithms.

These features, termed radiomic features, have the potential to uncover disease characteristics that fail to be appreciated by the naked eye. The hypothesis of radiomics is that the distinctive imaging features between disease forms may be useful for predicting prognosis and therapeutic response for various conditions, thus providing valuable information for personalised therapy.

Radiomics is a new area of research in the field of imaging with tremendous potential to unravel the hidden information in digital images. The scope of radiology has grown exponentially over the last two decades; since the advent of radiomics, many quantitative imaging features can now be extracted from medical images through high-throughput computing, and these can be converted into mineable data that can help in linking imaging phenotypes with clinical data, genomics, proteomics, and other “omics” information. In cancer, radiomic imaging analysis aims at extracting imaging features embedded in the imaging data, which can act as a guide in the disease or cancer diagnosis, staging and planning interventions for treating patients, monitor patients on therapy, predict treatment response, and determine patient outcomes [1)].

PFS can be predicted non-invasively in patients with low-grade gliomas by a group of radiomics features that could reflect the biological processes of these tumors.

New techniques including diffusion kurtosis and radiomics will offer a higher level of quantification but will require validation in clinical trial settings [2)].

The role of radiomics in the diagnosis, monitoring, and therapy planning of brain tumors is becoming increasingly clear. Incorporation of quantitative approaches in radiology, in combination with increased computer power, offers unique insights into macroscopic tumor characteristics and their direct association with the underlying pathophysiology [3)].

Multiple radiogenomic studies provide a bridge between imaging features and tumor microenvironment. An overlap that can be integrated within the genophenotypical classification of CNS tumors for a better understanding of different clinically relevant entities [4)].

Lee et al. analyzed the spatial diversity of tumor habitats, regions with distinctly different intensity characteristics of a tumor, using various measurements of habitat diversity within tumor regions. These features were then used for investigating the association with a 12-month survival status in glioblastoma (GBM) patients and for the identification of epidermal growth factor receptor (EGFR)-driven tumors. T1 postcontrast and T2 fluid attenuated inversion recovery images from 65 GBM patients were analyzed in this study. A total of 36 spatial diversity features were obtained based on pixel abundances within regions of interest. Performance in both the classification tasks was assessed

using receiver operating characteristic (ROC) analysis. For association with 12-month overall survival, area under the ROC curve was 0.74 with confidence intervals [0.630 to 0.858]. The sensitivity and specificity at the optimal operating point ([Formula: see text]) on the ROC were 0.59 and 0.75, respectively. For the identification of EGFR-driven tumors, the area under the ROC curve (AUC) was 0.85 with confidence intervals [0.750 to 0.945]. The sensitivity and specificity at the optimal operating point ([Formula: see text]) on the ROC were 0.76 and 0.83, respectively. Our findings suggest that these spatial habitat diversity features are associated with these clinical characteristics and could be a useful prognostic tool for magnetic resonance imaging studies of patients with GBM [5)].

A radiomic signature allowing for the prediction of the EGFR expression level in patients with lower grade glioma was identified, suggesting that using tumour-derived radiological features for predicting genomic information is feasible [6)].

Results illustrate a causal relationship between imaging features and genomic tumor composition. Zinn et al. present a directly clinically applicable analytical imaging method termed Radiome Sequencing to allow for automated image analysis, prediction of key genomic events, and survival. This method is scalable and applicable to any type of medical imaging. Further, it allows for human-mouse matched coclinical trials, in-depth end point analysis, and upfront noninvasive high-resolution radiomics-based diagnostic, prognostic, and predictive biomarker development [7)].

Experimental results proved that the quantitative tumor location measurement could be a very important group of imaging features in biomarker estimation based on radiomics analysis of glioma [8)].

Radiomics is a potentially useful approach for estimating IDH1 mutation status noninvasively using conventional T2-FLAIR MRI images. The estimation accuracy could potentially be improved by using multiple imaging modalities [9)].

Advances in whole genome sequencing have led to identification of genes involved in a variety of diseases. Moreover, biomarkers indicating severity of disease or susceptibility to treatment are increasingly being characterized. The continued identification of new genes and biomarkers specific to disease subtypes and individual patients is essential and inevitable for translation into personalized medicine, in estimating both, disease risk and response to therapy. Taking into consideration the mostly unsolved necessity of tailored therapy in oncology the innovative project MOBIT (molecular biomarkers for individualized therapy) was designed. The aims of the project are: (i) establishing integrative management of precise tumor diagnosis and therapy including systematic biobanking, novel imaging techniques, and advanced molecular analysis by collecting comprehensive tumor tissues, liquid biopsies (whole blood, serum, plasma), and urine specimens (supernatant; sediment) as well as (ii) developing personalized lung cancer diagnostics based on tumor heterogeneity and integrated genomics, transcriptomics, metabolomics, and radiomics PET/MRI analysis. It will consist of 5 work packages. In this paper the rationale of the Polish MOBIT project as well as its design is presented. (iii) The project is to draw interest in and to invite national and international, private and public, preclinical and clinical initiatives to establish individualized and precise procedures for integrating novel targeted therapies and advanced imaging techniques [10)].

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