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WORKING PAPER

Identification of MR image biomarkers in brain tumour patients using machine learning and radiomics features

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Title: Identification of MR image biomarkers in brain tumour patients using machine learning and radiomics features

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Abstract (150 words, Font 12): Brain tumours are malignancies of brain tissues. It is crucial to characterise tumour tissues to determine whether the tumour is low-grade or high-grade, as both require different surgical planning. Our purpose is to identify MR image biomarkers in gliomas patients to characterise tumour as low-grade or high-grade non-invasively, compared to invasive brain biopsies. We used 285 gliomas patients (210 high-grade and 75 low-grade gliomas) data, including T1-weighted and gadolinium-enhanced T1-weighted MR images. We extracted 214 radiomics features from MR images using an open-source package, PyRadiomics. Further, we calculated the intraclass correlation coefficient among features to reduce the features with a correlation>0.95. After that, the remaining features are used to train a random forest classifier to distinguish between low-grade and high-grade gliomas patients. The classifier is tested using a validation set and test set prepared as per k-fold cross-validation. We repeated tests 1000 times and noted the top 25 features in each test. Further, the radiomics features, which are found top-performing in more than 95% of tests, are validated with genes expression data provided by The Cancer Genome Atlas and assembled using the TCGA-Assembler2 tool. We found that the top 25 features in each test can distinguish low-grade and high-grade gliomas with an accuracy of 0.82±0.06 (mean±stdev). We noted that three grey level size zone matrix features called large area emphasis, large area high grey level emphasis and zone variance, and one first-order statistics feature describing intensity range are found top-performing in more than 95% of tests. They are found correlated (P<0.001) with ASB11, WFDC10A, CARTPT and ENTPD7 genes the most compared to other genes. Such radiomics features can be potentially considered as MR image biomarkers to determine tumour grade non-invasively.

Purpose: To distinguish gliomas patient using radiomics and artificial intelligence in order to help patient-specific surgery planning non-invasively

Design/Methodology/ Approach: We extract radiomics features from brain tumour MRI and train machine learning model using such features to distinguish gliomas types. Moreover, we identify the stable radiomics features and employ them in a radio-genomics approach to understand their

correlation with genes.

Findings: We noted that among 214 radiomics features, grey-level size zone matrix features namely large area emphasis, zone variance and large area high grey-level emphasis, and a first order statistics feature called intensity range are promising to distinguish gliomas types. They reveal significant (P<0.001) correlation with genes ASB11, WFDC10A, CARTPT and ENTPD7.

Research Limitations/ implications: The research is based on global database of brain tumour patients using MRI and genomics data. However, a local dataset is warranted to validate its applicability. Moreover, a correlation study with histopatholgical findings will be quite useful to further understand radiomics features biological meaning.

Originality/ Value: The identification of the stable radiomics features and their relation with genes are original.

Keywords: Radiomics, Artificial intelligence, Brain tumour, MRI, Machine learning