Radiomics to predict 1p/19q chromosomal codeletion status of low-grade gliomas

Introduction

Non-invasive identification of molecular changes in brain tumors could aid therapeutic decision-making, ameliorate response to chemotherapy treatments and, consequently, increase overall survival. Radiomics is a valuable tool for extracting quantitative features from magnetic resonance images, providing non-visual information that can be used in data mining. In this work, we demonstrate the use of radiomics, combined with machine learning algorithms, for non-invasively predicting the status of 1p/19q chromosomal codeletion in low-grade gliomas [1].

Methods

For this study, we used the LGG-1p19qDeletion dataset from The Cancer Imaging Archive database. This dataset is composed of 159 cases of low-grade gliomas, with 1p/19q chromosomal codeletion confirmed by biopsy and fluorescence in situ hybridization, and segmented region-of-interest masks from Axial T2-weighted images. The PyRadiomics library was used to extract radiomic features. Data were pre-processed (normalization, dimensionality reduction, and synthetic augmentation) and subsequently classified by a parametrized multilayer perceptron neural network[3].

Results

The classification reached 85% precision, 88% sensibility, and 73,5% specificity. Support vector machine and random forest algorithms were used for comparison, with 77,5% and 75% precision, respectively. The area under the Receiver Operating Characteristic showed 82% result (true positive rate versus false positive rate).

Discussion

Our study showed that radiomics is capable of providing quantitative information that can be used for adequately to identify molecular and genetic markers in low-grade gliomas. During pre-processing , normalization kept the features in the same order of magnitude; dimensionality reduction projected the features from a high-dimensional space to a subspace of lower dimensionality, maintaining the similarity between the data; and a synthetic increase of the training set prevented the classification algorithm from behaving biased towards unbalanced data. The multilayer perceptron neural network showed better accuracy and sensitivity than the support vector machine and random forest algorithms, and better specificity than the support vector machine algorithm, in the classification of 1p/19q chromosomal codeletion. In conclusion, ourwork presented a non-invasive technique for effectively predicting 1p/19q chromosomal codeletion, through analysis of radiomics features extracted from T2-weighted images, based on multilayer perceptron neural network classification.

References

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