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Resumo	Pediatric brain tumors are the most common cause of death among all childhood cancers and surgical resection usually is the first step in disease management. During surgery, it is important to perform safe gross resection of tumors, retaining as much brain tissue as possible. Therefore, appropriate resection margin delineation is extremely relevant. Currently available methods for tissue analysis have limited precision, are time-consuming, and often require multiple invasive procedures. Our main goal is to test whether machine learning techniques are capable of classifying the pediatric brain tissue chemical profile generated by DESI-MSI, which is mainly lipidic, into normal or abnormal tissue and into low- and high-grade malignancy subareas within each sample. Our experiments show that deep learning methods outperform classical machine learning methods in the task of classifying brain tissue from DESI-MSI mass spectra, both in normal versus abnormal tissue, and, for malignant tissues, in low-grade versus high-grade malignancy. Our conclusion are based on the analysis of 34,870 annotated spectra, obtained from the neoplastic and non-neoplastic microanatomical stratification of individual samples from 116 pediatric patients who underwent brain tumor surgical resection at the Boldrini Children's Center between 2000 and 2020. Support Vector Machines, Random, Forests, and Least Absolute Shrinkage and Selection Operator (LASSO) were among the classical machine learning techniques evaluated.
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