PATH-04. OPTIMIZING CELL-FREE DNA ASSAYS FOR LOW INPUT

ABSTRACT

PATIENTS AND METHODS: We aggregated an integrative dataset that consists of digitized whole-slide images, NGS sequencing panels, methylation arrays, and magnetic resonance imaging (MRI) data. The purpose is to develop a classification scheme that aids in the diagnostic process of central nervous system tumors (CPTs). Traditional grading of CPTs relies on histologic assessment, but morphologic criteria are not sufficient for proper tumor subtype classification. Here, we investigated the multi-modal associations of CPT subtypes and evaluated the potential of machine learning for improved diagnostic accuracy.

RESULTS: The classification into the 13 diagnostic categories was feasible, with an overall accuracy of 75% on the test set and a tumor-specific F1 score of 89%. Most misclassifications occurred between morphologically similar cell types, mainly lymphocytes and activated lymphocytes, monocytes and activated monocytes, as well as tumor cells and atypical cells with borderline cytology.

CONCLUSIONS: Machine learning enables an accurate and robust tumor classification based on cell morphology, opening the door for personalized therapy for CPTs.