Abstract title:

**AI-driven multimodal analysis integrating WSI, Methyl-Seq, and OncoKids Cancer Panel to improve diagnostic precision of pediatric tumors.**

Abstract (250 word max):

Previously, we added clinical and genomic data from more than 1,000 pediatric cancer patients from our racially and ethnically diverse patient population at Children’s Hospital Los Angeles (CHLA) to the CCDI(dbGaP Study Accession: phs002518). We are now augmenting this dataset with new types of data, and to develop tools for integrating the diverse datasets in CCDI to improve diagnosis and treatment of all children with cancer. To date, almost 700 CNS and non-CNS solid tumors in our cohort have been identified, screened, and key whole slide images (WSI) selected. We developed a computational pipeline to access and organize metadata for each WSI, and to quantitatively assess tumor morphology of WSI slides. In parallel, we have also generated whole-genome enzymatic methyl-seq data from 170 CNS tumors, and developed a methyl-seq bioinformatics pipeline with a CNS tumor classifier compatible with methyl-seq data. Tools to leverage these multimodal data to improve diagnosis and characterization of the tumors is an active area of investigation. We have trained a CNS tumor classifier applicable with Methylseq samples. Our pipeline is fully automated from raw bioinformatics processing to a classification report detailing predicted classification, classification score, UMAP clustering analysis, copy number profiling, and quality control metrics. Additionally, we have developed AI/ML tools to converge results from WSI analysis, methylation values, and OncoKids Cancer Panel results to enhance diagnostic decision-making. Our long-term goals are to incorporate additional data formats into our suite of multimodal analytic tools and to make these tools available to the CCDI community.

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