Resistance of high-grade tumors to treatment involves cancer stem cell features, deregulated cell division, acceleration of genomic errors, and the emergence of cellular variants that rely upon diverse signaling pathways. This heterogeneous tumor landscape limits the utility of the focal sampling provided by invasive biopsy when designing strategies for targeted therapies. In this roadmap review paper, we propose and develop methods for enabling the mapping of cellular and molecular features in vivo to inform and optimize cancer treatment strategies in the brain. This approach leverages 1) the spatial and temporal advantages of in vivo imaging compared with surgical biopsy, 2) the rapid expansion of meaningful anatomical and functional MR signals, 3) widespread access to cellular and molecular information enabled by next-generation sequencing, and 4) the enhanced accuracy and computational efficiency of deep learning techniques. As multiple cellular variants may be present within volumes below the resolution of imaging, we describe a mapping process to decode micro- and even nano-scale properties from the macro-scale data by simultaneously utilizing complimentary multiparametric image signals acquired in routine clinical practice. We outline design protocols for future research efforts that marry revolutionary bio-information technologies, growing access to increased computational capability, and powerful statistical classification techniques to guide rational treatment selection [1)]

1)

Parker JG, Servati M, Diller EE, Cao S, Ho C, Lober R, Cohen-Gadol A. Targeting intra-tumoral heterogeneity of human brain tumors with in vivo imaging: A roadmap for imaging genomics from multiparametric MR signals. Med Phys. 2022 Nov 13. doi: 10.1002/mp.16059. Epub ahead of print. PMID: 36371678.