Brain cancer participates in a complex intertwined relationship with metabolism via genetic and tumor microenvironment influences. Regardless of the initiating factors, the presence of cancer results in metabolic aberrations that serve as important markers for disease detection and diagnosis. We aim to acquire diagnostic biochemical information, primarily via characteristic lipid profiles, directly from human brain tissue using desorption electrospray ionization – mass spectrometry (DESI-MS) for intraoperative diagnosis and tumor margin assessment. Lipid profiles are related to biochemical changes underlying the morphological changes used for histopathological diagnosis. Our previous work using lipid profiles in human brain tumors (e.g. glioma) allowed differentiation of tumor subtype, grade, and tumor cell concentration. In our current work, we have expanded the types of human brain tissue analyzed by DESI-MS to include normal tissue and pituitary tumors. Preliminary results suggest that the five principal classes analyzed, i.e. normal, meningioma, low-grade glioma, high-grade glioma, and pituitary tumors, have characteristic lipid profiles that allow for discrimination. While the lipid profile results are compelling, the simultaneous detection of additional metabolites, either endogenous or oncological, has the potential to enhance brain cancer discrimination. Small molecule metabolites with m/z <200, e.g. lactic acid, detected in the negative mode were found to differ between the five principal classes – an analogous metabolite profile. One promising metabolite, N-acetyl-aspartic acid (NAA), was detected in situ and appears to decrease in neoplastic areas. The detection of NAA was valuable in discriminating brain cancer and is hypothesized to aid in
determining tumor margins. Lipid and metabolite information acquired by DESI-MS related to diagnosis and tumor margin determination has significant potential to aid in the surgical resection of human brain tumors.