Abstract: Cancer cells reprogram metabolic pathways to meet their needs for rapid proliferation and generation of biomass for tumor growth. To gain a comprehensive understanding of glucose metabolism in Hepatocellular carcinoma (HCC), we analyzed 179 genes involved in glucose related metabolic pathways with five independent datasets covering more than 1,000 HCC patient samples. We found that genes involved in the glucose metabolic pathway are consistently dysregulated with a predominant down-regulation in HCC tumors, while genes within glycolysis pathway is primarily upregulated as previous reported. The dysregulation of these genes were associated with patient prognosis. Unsupervised clustering analysis with the DEGs that were also associated with overall survival (OS) revealed a subgroup of patients with a worse prognosis including reduced OS, disease specific survival, and recurrence-free survival. This aggressive subtype had significantly increased expression of stemness-related genes and down-regulated metabolic genes, as well as increased immune infiltrates that contribute to a poor prognosis.

About the Speaker: Xiaoli Zhang is a Research Assistant Professor in the department of Biomedical Informatics and Center for Biostatistics. She graduated from Iowa State University in 2006 with a PhD in Molecular Biology and a MS in statistics. With her expertise in biostatistics and bioinformatics, she has collaborated extensively with medical center investigators with a focus on cancer research since she joined the Ohio State University in 2006. Her research interest is in understanding the mechanisms of cancer metastasis and drug resistance through studying cancer metabolic reprogramming, cancer immunology, tumor microenvironment, and cancer stem cells, and identifying prognostic and therapeutic targets for cancer treatment using publically available omics data.

Xiaoli Zhang, PhD
Friday, January 22\textsuperscript{nd}, 11:00am-12:00pm
Carmen Zoom