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Single Cell Research in Progress Seminar Series

**“****Spatially Resolving the Brain Tumor Microenvironment”**

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**Host:** TBD

**Zoom:** [**https://yale.zoom.us/j/92445624596**](https://yale.zoom.us/j/92445624596)

Wednesday, November 10th, 2021

12:00 p.m. to 1:00 p.m. Seminar

A person with long hair smiling

Description automatically generated with low confidenceAccording to the Central Brain Tumor Registry of the United States, there will be an estimated 80,000 newly diagnosed brain tumors in 2021 alone. The most common primary CNS tumor is meningioma (38.3%). The most common malignant brain tumor is glioblastoma multiforme (GBM) (14.5%) and while most GBM occur *de novo*, approximately 20% progress from WHO Grade II and III gliomas. Over the past two decades, the Günel lab and others have used next generation sequencing to aid in generating genomic classifications, which have contributed greatly to our understanding of patient outcomes with these tumors. The Günel lab now aims to synthesize this knowledge with new tools to understand the tumor microenvironment by the multiomic integration of scRNA-seq, scATAC-seq, and spatially resolved transcriptomics. We have performed spatial sequencing and sc-multiomics on a series of genetically and clinically characterized meningiomas (n =13), IDHmut GBMs (n =4), IDHmut anaplastic astrocytoma’s (n = 5), and IDHmut astrocytomas (n =3).

In this talk, I will describe some insights gained about the spatially-resolved landscape of these tumors in the context of our patient cohorts and describe some of our ongoing efforts for multiomic integration across sequencing modalities. I will also present data using new techniques co-pioneered the Krishnaswamy Lab, for spatial gene imputation (MD-PhD Candidate Manik Kuchroo) and unsupervised spatial clustering (PhD Candidate Aarthi Venkat) created to recover gene regulatory networks and demonstrate that our spatially-aware imputation method recapitulates in-situ hybridization expression patterns more accurately than the raw expression of data generated by Visium spatial transcriptomics.

Danielle Miyagishima is a 7th year MD-PhD candidate (5th year PhD in Genetics) in the laboratory of Dr. Murat Günel where her thesis project is focusing on deconvoluting the influence of sex-hormone receptors in meningioma pathogenesis—a long-term clinical observation without the molecular mechanisms being fully understood. Before coming to Yale, Danielle completed her undergraduate at New Mexico State University with a degree in Biochemistry, where she studied developmental genetics and organic chemistry synthesis as an undergraduate researcher. Danielle’s long-term research interests relate to understanding gene-regulatory networks under dynamic conditions with hopes to apply this knowledge to precision medicine in brain tumors and functional neuroscience as a neurosurgeon-scientist.

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