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Defining the Transcriptomic Architecture of Memory in the Hippocampus

The search for the memory engram has been a defining endeavor for the field of neuroscience. Major strides have been made in this search from identifying regionalization of memory function, specifying the cells encoding the individual bits of memory, and uncovering specific molecular programs that underlie memory storage. However, to date, the structure of the engram at the molecular level remains elusive. In this project we aim to identify the arrangement of molecular programs across the hippocampal network with the storage of a spatial memory. We will accomplish this with two aims. In the first aim, we will use bulk RNA sequencing to profile and compare the transcriptomes of functionally distinct hippocampal sub-regions and test for a specific diversity of gene programs changes across the hippocampal network necessary to support memory. In the second, we will use Spatial Transcriptomics to profile and compare the spatially arranged gene expression profile of hippocampal cells and test for a distinctive spatial distribution of molecular programs within the hippocampal network necessary to support memory. Accomplishment of these aims will yield a first look into the spatial organization of gene expression programs across the hippocampal network with memory.