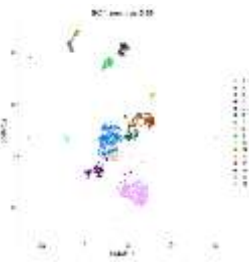


## MSc Project: Deep learning for Image Processing in Spatial Transcriptomic.

We are seeking a skilled **M2 student** to develop our new image-processing pipeline for spatial transcriptomic. The primary focus of this position involves image realignment, RNA spot detection, MERFISH decoding, cell segmentation. We are searching for an individual who can contribute their talent and expertise to improve our research efforts in these areas.

We aim to define the genetic program controlling the development and maintenance of muscle morphologies and the axon-muscle connectome architecture in *Drosophila* legs at the single-cell level. To achieve our goals, we employ single-cell RNA profiling and a novel 3D spatial transcriptomic approach combined with genetic techniques to visualize and selectively modify the genotype of individual cells in a developing or adult organism. We use a unique technology for MERFISH, which is an imaging method capable of simultaneously measuring the copy number and spatial distribution of hundreds to thousands of RNA species in single cells [1].

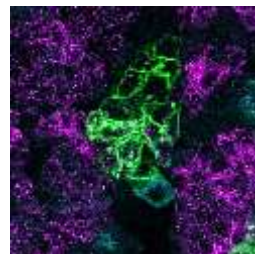
The goal of the MSc project is to process the sequences of raw images acquired by our new MERFISH set up to recover maps of single RNA in 3D. This involves image realignment, RNA spot detection, MERFISH decoding, cell segmentation. Our current pipeline has to be extended from 2D to 3D, which is challenging due to the amount of data to be handled. We will first consider traditional image-processing tools before data-driven approaches (e.g., [2]).



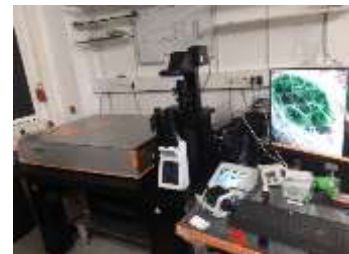
Single cell Seq



Flywalker



smFISH/spatial transcriptomic



STED microscopy

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### References:

- [1] [Spatially resolved, highly multiplexed RNA profiling in single cells](#), K.H. Chen, A.N. Boettiger, J.R. Moffitt, S. Wang, X. Zhuang, *Science* (348), aaa6090, 2015.
- [2] [SPACEL: deep learning-based characterization of spatial transcriptome architectures](#), H Xu et al., *Nature Communications* (14), 7603, 2023.