Pairing single cell -omic technologies

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Motivation

- We developed the first single cell technique to profile protein location on DNA.
- There has been huge advancement in assessing the transcriptome (via single cell RNA-seq)

Project Description

- We propose to integrate these techniques to address an important biological question during development

Context

- Heterogeneity across cell populations and tissues, as well as limitations in profiling technologies in rare populations limits our capacity to understand cellular biology

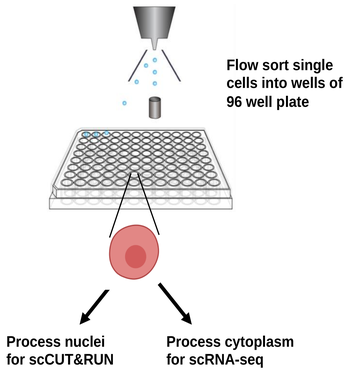

Figure 1. Paired single cell CUT&RUN and scRNA-seq

We will apply this technology during neural differentiation to assess the role of a conserved and essential protein complex called BAF.

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Determining gene expression during neural differentiation through coupled protein localization and RNA-seq in single cells

Project Deliverables

- We will initially optimize the pairing in high cell populations, titrating from 500,000 to 10 cells within ~4-6 months
- Next, we will optimize for single cells over the next ~4-6 months
- Application to ~5,000 single cells throughout neural differentiation will begin over the last ~4 months and continue into the following year

Potential Impact

- This will be the first pairing of factor profiling and scRNA-seq within one individual cell
- This will revolutionize our ability to interpret mechanistically how factors impact the transcriptome.

References and/or Acknowledgements

- I'd like to acknowledge members of the Hainer lab, including Dave Klein, Ben Patty, Santana Lardo, Emimy Brown, Braulio Bonilla, and Jasmine Dioguardi
- Reference for single cell CUT&RUN: Hainer et al 2019 *Cell* and Patty and Hainer 2021 *Nature Protocols*