Identifying Genetic Drivers of Disease and Drug Response through population-scale induced Pluripotent Stem Cell Models

Advisors: Professor Joseph Powell & Dr Drew Neavin

Student

Recruiting for: PhD Student

The successful applicant will have:

- Completed honours
- Interest in statistical genetics or computational biology
- Knowledge of programming in R or Python

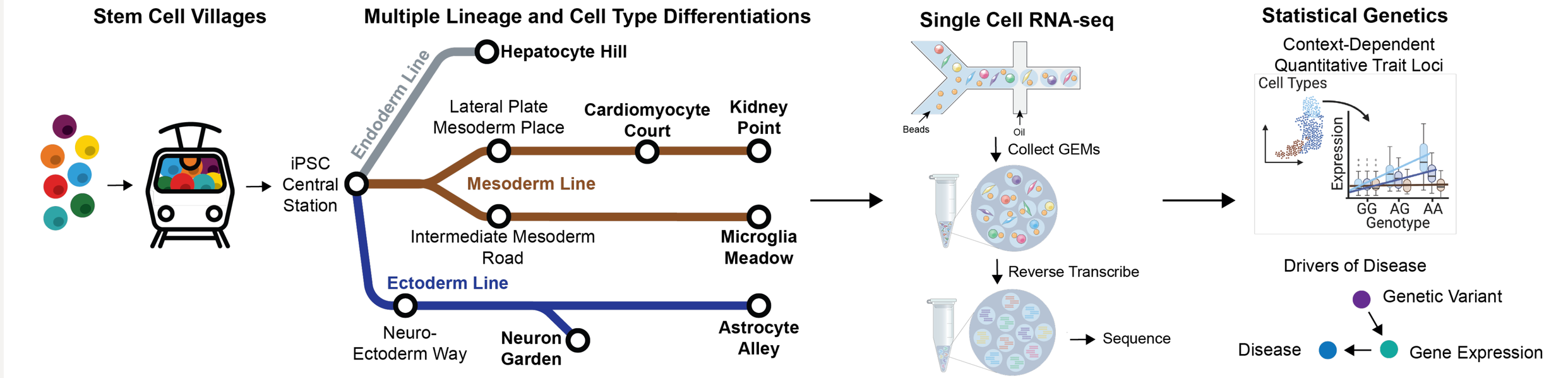
Goals of Project

1. Classify cell types and cell states across cellular developmental lineages
2. Map the relationship between genetic effects and genome regulation and characterise how these are specific to certain developmental timepoints
3. Identify genetic effects that regulate gene expression only during therapeutic drug exposure
4. Connect these cell-type/state-specific genetic effects to human diseases

Skills to be Gained

- Statistical genetics
- Single cell analysis
- Large-scale computational analyses
- Human genetics and disease

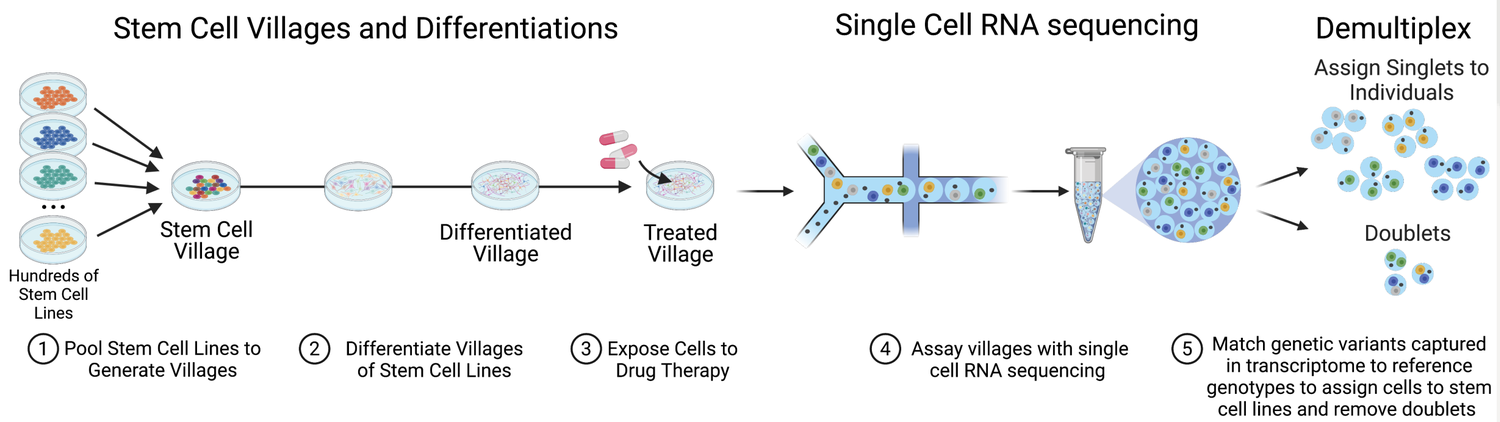
Long-term Program Interest



The long-term goals of this research program are to understand genetic regulation over cellular development to multiple different cell types. This project will focus on a specific lineage.

Key Concepts

Stem cell villages are pools of unrelated individuals that are cultured and differentiated together. Using village methods for statistical genetics only possible due to the rise of single cell RNA sequencing which assays the transcriptome of each cell separately and the genetic variants captured in the transcriptional profiles can be matched to the genetic profiles of each stem cell line to assign each cell to the correct donor.



Key Papers

Cuomo et al, *Nat Comms*, 2020.

Jerber et al, *Nat Gen*, 2021.

Mitchell et al, *bioRxiv*, 2020.

Neavin et al, *bioRxiv*, 2021.

Wells et al, *bioRxiv*, 2021.

Contact

- Joseph Powell
  @drjosephpowell
  j.Powell@Garvan.org.au
- Drew Neavin
  @drneavin
  d.neavin@garvan.org.au