iCASE Project / AY 2025 -2026

Deciphering the role of tissue-resident immune cells in inflammatory disease

Project Reference: ICS-SCI-ST

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Industrial Partner: Ensocell

BBSRC DTP main strategic theme: Transformative technologies

BBSRC DTP secondary strategic theme: Bioscience for an integrated understanding of health

Project outline:

Over the last decade single cell sequencing has gone from being a labour intensive, highly specialised research project to a widely applied robust technology that is now scalable to millions of cells at reasonable cost. The international Human Cell Atlas (HCA) consortium has used single cell sequencing to generate a comprehensive reference map of all common cell types of all the major organs of the human body. In addition, the rapid development of novel spatial transcriptomics technologies has allowed us to better understand the relationship between cell types, deciphering cell-cell communication and signalling circuits that establish functional tissue niches.

Over the last few years experimental workflows have become more robust, the cost per sample has reduced and the throughput has increased, meaning the time is now right to apply this technology to human disease, and in particular examine the role of the immune system in inflammatory conditions of the liver, lung and gut.

The Teichmann laboratory has been at the forefront of developing single cell and spatial transcriptomics and is an international recognised leader in the field, with Sarah Teichmann being a founder and co-chair of the HCA consortium. The laboratory has pioneered both experimental and computational approaches to give new insights into the biology of multiple different organ systems, including the gastro-intestinal and respiratory systems (Oliver et al, Nature in press, Madissoon, Oliver et al., Nature Genetics 2023, Elmentaite et al Nature 2021). Our laboratory also has a long-standing track record of studying the immune system in specific organs and across the whole body.

The proposed project will focus on the computational analysis of existing published or in house data sets for inflammatory conditions across organs. The project offers flexibility to accommodate the student's interests, allowing for a greater emphasis on either computational analysis or wet lab experimentation, based on their preferences and career goals.

The Aims of the project will be:

1. Identify differentially expressed genes between health and disease for inflammatory gastrointestinal, respiratory diseases, or fibrotic diseases using highly granular cell type annotations that are becoming available as part of the generation of integrated organ atlases from the HCA biological networks.
2. Contribute to the generation of high-throughput spatial transcriptomics data from healthy and disease affected tissues.

3. Examine differences between healthy and diseased spatial transcriptomics data with a view to identifying disease specific niches and signalling pathways that maintain the abnormal function of the tissue. Studies on healthy intestinal tissue (Elmentaite et al, Nature 2021) have demonstrated the utility of this approach, which is being increasingly applied to comprehensively map tissues affected by inflammatory diseases.
4. Develop computational pipelines to integrate and analyse single cell and spatial transcriptomics methods tailored for identification of disease relevant cell types and pathways.