



<b>Project Title: Extracting meaningful information about disease from state-of-the-art single-cell assays.</b>		<b>Code: WIMR3</b>
<b>Host School / Institute:</b> <a href="#">Westmead Institute for Medical Research</a>		<b>Address:</b> 176 Hawkesbury Rd, Westmead NSW 2145
<b>Certificates &amp; Clearances required:</b> No		
<b>Primary Supervisor:</b> <a href="#">Dr Ellis Patrick</a>		
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<b>Co-Supervisor/team:</b> Our lab works on projects spanning multiple diseases including melanoma, ovarian cancer, acute myeloid leukemia, Alzheimer's disease, multiple sclerosis and HIV. We also work with various high-throughput technologies included bulk and single-cell RNA-Seq, SWATH-MS, flow cytometry, CyTOF, cyclic IF imaging and imaging mass cytometry.		
<b>Project Type:</b> Data Analysis		
<b>Project Category:</b> Bioinformatics; Imaging		
<b>Skills / Attributes of a successful student:</b> A successful student will have a passion to learn more about how state-of-the-art biotechnologies are being used to understand disease pathogenesis and/or learn about high-dimensional analytical methods.		
<b>Project Keywords:</b> Single-cell RNA-Seq; High-parameter imaging; Bioinformatics; Machine learning		
<b>Project Description:</b> Cells do not act alone. There are an estimated 37 trillion cells in the human body with a large diversity of form and function. Understanding the interplay between different types of cells and their immediate environment is critical for understanding the mechanisms of cells themselves and their function in the context of human diseases. Recent advances in high-parameter single-cell technologies have fundamentally revolutionized our ability to phenotype cells and observe complex cellular relationships in tissue.  This has created an urgent and exciting need to develop the analytical methods that are required to harness these new technologies to provide novel insights into complex biological systems and diseases. The increase in size and high-dimensional nature of the data produced by technologies such as single-cell RNA sequencing, high-parameter flow and imaging mass cytometry necessitates analytical tools that are more complex, computationally efficient and require an increased need for interpretability than those currently used for standard cytometry assays.  In this project we will apply or develop analytical techniques to understand a disease using technologies such as single-cell RNA-Seq, high-parameter flow-cytometry, CyTOF and hyperion imaging. A driven student will have the opportunity to study a disease that they are passionate about.		