Project Title: Predictive immune signature analysis for clinical application	**Code: SOMS4**

Host School / Institute: School of Medical Sciences/ Charles Perkins Centre	**Address:** Charles Perkins Centre

Certificates & Clearances required: No

Primary Supervisor: Dr Helen McGuire

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Co-Supervisor/team: This project will take place within the laboratory of Prof Barbara Fazekas and in association with the Ramaciotti Facility for Human Systems Biology. Our team consists of biology researchers interested in the immune system, immunologists as well as bioinformatic and statistical support.

Project Type: Laboratory based; Data Analysis; Clinical

Project Category: Immunology & Infection; Cancer

Skills / Attributes of a successful student: We are looking for an enthusiastic, dedicated, hard working student who ask lots of questions. While practical experience in cytometry and subsequent analysis is welcome, this is not essential. The student will be trained in all aspects of laboratory and bioinformatic methods.

Project Keywords: Immune signature; Biomarker; Mass Cytometry; Lung Cancer; Checkpoint inhibitors

Project Description: Mass cytometry, or Cytometry by Time-Of-Flight (CyTOF), is a powerful platform for high-dimensional single-cell analysis of the immune system. It enables the simultaneous measurement of over 40 markers on individual cells through the use of monoclonal antibodies conjugated to rare-earth heavy metal isotopes. Our lab has a great amount of immunological knowledge of the various immune subsets found in blood samples and we can delve into and describe subtle populations using this technique, so mass cytometry presents an opportunity to investigate cumulative subtle changes across many specific immune subsets in a range of clinical cohorts.

We are really excited to develop an analysis pipelines with clinical utility, for example to provide predictive tests that could inform clinical management, particularly for cancer diagnosis. Based on our previous studies in several autoimmune diseases such as rheumatoid arthritis and psoriasis, which revealed remarkably stable changes in the size of multiple peripheral blood cell subsets, we are conducting studies into cohorts of melanoma and lung cancer patients before and after therapy with the checkpoint inhibitor, anti-PD-1.

We are using a data analysis approach originally developed to analyse gene expression signatures in highly multiparametric datasets to analyse the cell subset distribution within samples. So far we have identified an immune signature in baseline blood samples that robustly identified patients who would subsequently make clinical responses to anti-PD-1 therapy, a really exciting finding that this summer project will follow up on. We also recognise this project is well suited to machine learning, which will be used in future application of the predictive signature in clinical settings, so there is a great opportunity to take a strong computational focus in this project if this is where you interest lies.