

ICM Research Seminar

Wednesday 15th November

Rebecca Hanna

(Prof. M. Birch-Machin, Dr S. Amarnath)

Optimised detection of mitochondrial DNA strand breaks

Intrinsic and extrinsic factors that induce cellular oxidative stress will damage tissue integrity and promote ageing. At a sub-cellular level, this results in accumulative strand breaks to the mitochondrial DNA (mtDNA) genome. Limited repair mechanisms and close proximity of the genome to the site of superoxide generation, make mtDNA a prominent biomarker of oxidative damage. Using human DNA extracted by conventional methods, we describe a methodology that sensitively detects mtDNA strand breaks relative to a suite of short mitochondrial and nuclear DNA housekeeping amplicons which control for any variation in copy number. Some applications of this methodology will be discussed.

James Fletcher

(Prof. M. Haniffa, Prof. N. Reynolds)

Defining the landscape of human tissue mononuclear phagocytes using single cell RNA sequencing and mass cytometry

The mononuclear phagocyte system is a highly heterogeneous compartment of the immune system comprising many subsets of monocytes, macrophages and dendritic cells. As single cell analysis techniques increase in measurable parameters, this heterogeneity can be analysed in greater detail. Using human skin as a model organ for tissue immune cells, this project aims to utilise single cell RNA sequencing to dissect the human tissue mononuclear phagocyte compartment, and validate these findings using flow and mass cytometry.

Dr Edith Serrano Blesa

(Prof. J. Isaacs)

Use of Design of Experiments to optimize a SWATH-MS acquisition method for the discovery of protein biomarkers in serum

SWATH-MS is a recently described mass spectrometry technique that allows high coverage protein identification and accurate quantification. The parameters that impact detection by SWATH-MS are specially complex and so, optimization is sample and machine dependant. Design of experiments (DoE) uses statistical methodology for identifying the significant parameters and then optimising a response by fine-tuning them, thus improving the results in the analysis of complex protein samples.

Chair: Dr David Swan

Dental Lecture Theatre F, Medical School

1pm - 2pm