Project title:	**"Single cell multi-omics to interrogate tumour cell responses of epigenetic targeting therapies"**
Main Supervisor:	**Vsevolod Makeev**
Research Group:	**Bioinformatics & Biostatistics Team, National Biomarker Centre**

Chromium Single Cell Multiome ATAC + Gene Expression (scMultiome) is an emerging and potentially groundbreaking technology that simultaneously produces profiles of transcriptional activity and chromatin accessibility genome-wide in a single cell. The potential of this technology to elucidate mechanisms of action of, and resistance to therapeutic agents has not been clearly demonstrated.

The goal of this project is to develop and implement computational methods to process and analyse scMultiome data, so that this technology could be used to discover mechanisms of transcriptional alteration by drugs targeting epigenetic regulation. Specifically, this PhD project will make use of an scMultiome experiment to study the effects of the EZH2 inhibitor Tazemetostat (TMZ) on small cell lung cancer (SCLC) cells and will take advantage of a previously acquired data set that examined how SCLC cells (bulk analysis) respond to TMZ.

Epigenetic targeting drugs are already in clinical use and entering clinical trials in haematological cancers and solid cancers including SCLC, but biomarkers to optimise their use are lacking. If the technology proves to be robust, it could be potentially used to discover predictive or therapy monitoring biomarkers or to better understand mechanisms of resistance.

scMultiome produces a large volume of sparse data and this studentship provides an exceptional opportunity for an individual with a strong foundation in computational analysis to apply their skills to complex, high-impact biological problems. We welcome candidates either with a formal bioinformatics or computational biology background or with a statistical data analysis background with a strong interest in molecular biology.

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