Kerrie Marie - Establishing a robust methodology to map lineage and model cell-state-switching in the metastatic cell

My research uses developmental biology as a lens through which to deconvolve cell states and their transitions. My future lab will define the cellular and molecular cues that drive specification and establishment of matrix-remodelling embryonic melanocytes as a model to understand an analogous phenotypic switch in the cancer of the melanocyte, melanoma. This phenotype is important as it is exploited by melanoma in metastatic outgrowth and resistance to therapies. To treat metastasis, we must understand how metastatic cells adapt to new environments/ challenges over time, which can be problematic to deconvolve in a complex cancer system, but are orchestrated in a developmental system. Sox10 is a Transcription Factor (TF), crucial to melanocyte development in the embryo, Zeb1 is an Epithelial-to-Mesenchymal TF that marks matrix-remodelling melanocytic cells, my work has also shown Collagen 6 (ColVI) is a key matrix-remodelling gene associated with this switch. To robustly model cell state switching I must develop a toolkit of: (1) endogenously tagged reporter cell lines to label the cell-state switch from $Sox10^{Hi}$ to $Zeb1^{Hi}$/$ColVI^{Hi}$; (2) a data analysis pipeline to integrate multimodal single-cell transcriptomic, chromatin accessibility and barcoding data.

Rosa Parisi - Epidemiology of clusters of multiple long-term conditions in England and the implications of social interventions

Patients experiencing multiple long-term conditions (multimorbidity) are frequently encountered by health services. This places a significant burden on patients and health services. Certain conditions are more likely to co-exist than others (multimorbidity disease clusters). Recent studies have identified the main clusters of multimorbidity. However, what is not known, and is the over-arching aim of this study, is an understanding of how patterns of multimorbidity clusters vary across the English population according to age, gender, ethnicity and social deprivation; and, what the effects of potential social interventions (eg changes in income) might be on clusters of multimorbidity.

John R Davis - Dissecting the interplay between metabolism and tissue mechanics

My research aim is to understand how tissue mechanics alters metabolism and vice-versa, and the role the cytoskeleton plays in this interaction. As both the metabolome and cytoskeleton are highly dynamic, to quantitatively dissect their relationship it is essential to control the spatial and temporal dynamics of tissue architecture and morphogenesis. Building upon my expertise in

mechanobiology, quantitative image analysis and bio-fabrication, the Dean's prize will allow me to develop spatially and temporally controlled 2D and 3D tissue culture systems to probe the link between biomechanics and metabolism. Additionally, founded on my expertise in Drosophila development, the Dean's prize will support work spatiotemporally characterising energy metabolism during embryogenesis.

Lamiece Hassan - Using AI-informed activity profiling based on passively collected sensing data for informing personalised lifestyle medicine targets in people with SMI

My research aims to use a combination of Artificial Intelligence (AI) and passively collected sensing ('wearables') data to objectively assess the physical health of people with Severe Mental Illness (SMI). The aim is to use this to guide physical health promotion efforts in this vulnerable population with severe health inequalities. Leveraging existing large accelerometery datasets, unsupervised machine learning based methods will be used to delineate clusters or 'activity profiles' of individuals with common patterns of activity. These will be developed, tested and refined with SMI-specific samples. Stakeholders will be engaged to determine acceptability and feasibility of integrating wearable-supported strategies for physical health promotion into NHS care.

Ruth Williams - Deciphering lineage decisions from the neural plate border to the neural crest

The overarching aim of my research is to understand the precise mechanisms that control the onset of NC lineage specification during early embryogenesis. To this end, I will combine next-generation multi-omics approaches with innovative developmental biology techniques to resolve the combinatorial action of transcription factors, their cognate regulatory elements and the inherent dynamic gene regulatory networks that direct naïve progenitors towards specific lineages. This will enhance understanding of the molecular nature of cell fate decisions, while also informing on the underlying causes of aberrant NC ontogeny and putative pleiotropic mechanisms employed during development and in NC-derived cancers.