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| Project Reference | T1/74 |
| Project Title | **Exploiting single-cell data for functional interrogation of genetic variation associated with fibrotic disease** |
| Theme(s) | Theme 1: Genomics for drug development & pharmacogenetics |
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| Department | Population Health Sciences |
| Project Summary | Identifying genetic differences between individuals who develop a specific disease and those who do not is a first step in bringing new disease insight. However, understanding why those differences (associations) are important, and how we can ultimately use that information to find new treatments, is a key challenge. In the last few years, there has been an explosion in technologies and methods to measure gene expression and regulation right down to the single-cell and even single-nucleus level. Furthermore, we can now directly track gene expression changes across diseased and unaffected areas of tissue from the same patient. Together, these new data provide detailed maps of gene activity in disease and we can combine this with our genetic associations to dig deeper into the molecular mechanisms that drive disease. Fibrosis (scarring) is a pathological process that is the consequence of an aberrant wound-healing response. Fibrosis can affect most organs, is a consequence of many common chronic diseases, and accounts for a significant proportion of global mortality. In this project, you will apply cutting-edge bioinformatic approaches to integrate single-cell gene expression and population-level genetic data to functionally interrogate genome-wide association data for fibrotic disease.  |