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Summary of research

Key words: Cancer, pleiotropy, prediction, genetic susceptibility, environmental

Most diseases have a strong genetic component. To date scientists have identified a few of the genes that increase risk of disease (e.g. cancer), but many remain elusive. One reason for that is that scientists study one disease at a time. This is quite unsatisfactory because we know that some people tend to have multiple diseases either simultaneously or at different times, and that having one disease increases the risk of having another. For example, being overweight increases one's risk of developing cancer. We believe that using statistical modelling of two or more diseases simultaneously could help in identifying more susceptibility genes and help constructing better models of risk prediction.

Our aims are to investigate to which degree different cancers are determined by the same genes; and to which degree cancer biomarkers and risk factors are determined by the same set of genes as cancer. For instance, we know that

being overweight increases the risk of developing colorectal cancer, but we don't know for sure if that link is at the genetic level (same genes make one overweight and more prone to cancer) or at the environment level (e.g. an unhealthy lifestyle makes one, both, overweight and prone to cancer). We request data on any cancer diagnosis, genetic information and biomarker and risk factor information on the whole UK Biobank cohort (no samples are required). Our primary cancer sites of interest are: Breast, lung, colorectal, prostate, melanoma, non-Hodgkin Lymphoma.

Our project will help to understand cancer aetiology and this will translate into better prevention policies and more effective cancer screening programs. It also has the potential of discovering new therapeutic targets aimed at combating cancer and offers the possibility of drug repositioning (using an available drug to treat a different condition).