Application number/Title: 44606 - Identifying long runs of homozygosity in the UK Biobank

Applicant PI: Dr Sohini Ramachandran

Application Institution: Brown University (USA)

Keywords provided by the Applicant PI to describe the research project:
Consanguinity, genomic, homozygosity, recombination, uniparental disomy

Application Lay Summary:

It is thought that, in order for embryos to develop properly, each human must have genetic variability within their own genome (i.e., many genomic sites where they inherit different DNA from their biological parents) and must inherit half of their genome from their biological mother and half of their genome from their biological father. The goal of this project is to characterize normal variability in "homozygosity", or the inheritance of the same DNA letter from both parents at a genetic site, at the scale of the UK Biobank. To date, population-genetic studies of homozygosity have shown that population histories can lead to long stretches of genomes without variability (for example, in cultures where marriage between relatives occurs); little is known about the normal rate of observing these long stretches of identical DNA within a genome, or the health consequences of such "runs of homozygosity". It is thought that long runs of homozygosity may result in disease, but this has not been tested with medical data. Our goal is to show that long runs of homozygosity are less deleterious than originally thought. The UK Biobank is the first publicly available dataset in which these rates can be characterized at large scale within genomes as well as a large scale across the UK Biobank. The methods we will use for this work are published and so we anticipate a very quick turnaround in this study of eight months.