Largest genome sequencing database released globally

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis.

Initial results from the largest completed population genome sequencing effort to date have been made available to the global scientific community to boost the search for rare genetic variants that increase the risk of disease.

“We are making all of these data available to the scientific community, which in terms of a resource is a quantum leap,” said Nicole Soranzo, a geneticist at the Wellcome Trust’s Sanger Institute in Cambridge.

Launched in 2010, the UK10K project was set up to study the genetic code of 10,000 people in much finer detail than ever before in order to uncover rare genetic variants, changes in DNA that are carried only by relatively a few people in a population, and how they contribute to human disease and its risk factors.

The project carried out whole genome sequencing at low coverage of 4000 healthy people and has published this information in *Nature* alongside detailed phenotypic information, a person’s observable clinical features *e.g*. height, blood pressure.

Previous studies have analysed either very rare genetic variants with big effects or common variants, which usually have small effects. The UK10K project has enabled researchers to explore more of the spectrum of variation between the very rare and the common ones, according to Richard Durbin, senior UK10K researcher at the Sanger Institute.

A key finding of the project was 24 million new genetic variants from healthy Europeans, which reflects the genetic diversity of the population.

Read full, original post: UK 10K genomes project shares its data