



Ben Elsworth

Lead Data Engineer

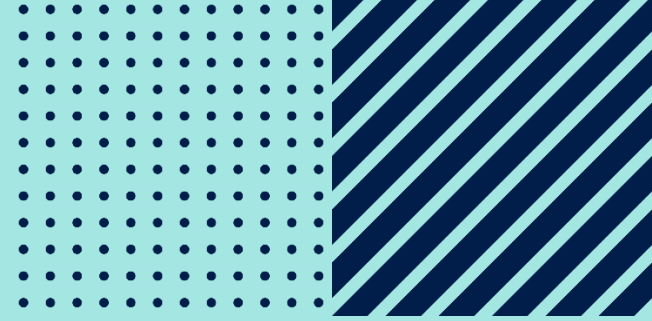
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Processing and releasing genetic data at Our Future Health





Forthcoming series of Charity Researcher Webinars



- We are pleased to announce a series of webinars for researchers organised in collaboration with our Charity Partners.
- For further details, please email partnerevents@ourfuturehealth.org.uk to register an interest
- Here are the dates for the upcoming webinars, which will feature several of our Early Adopters.

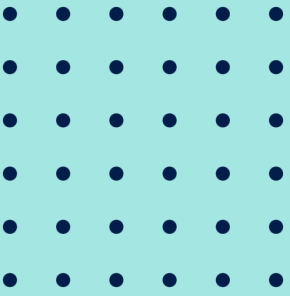
1. British Heart Foundation & Our Future Health – Wednesday, April 2, 9-11 am
2. Cancer Research UK & Our Future Health – Monday, May 12, 3-5 pm
3. Asthma and Lung UK & Our Future Health – Tuesday, June 10, 12-2 pm
4. Affiliate Charity & Our Future Health Webinars – Monday, June 16, 10-12 pm and Thursday, June 19, 2-4 pm

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Agenda

1. Programme Overview
2. Genetic Data
3. Where We Are
4. The Future





Our Future Health



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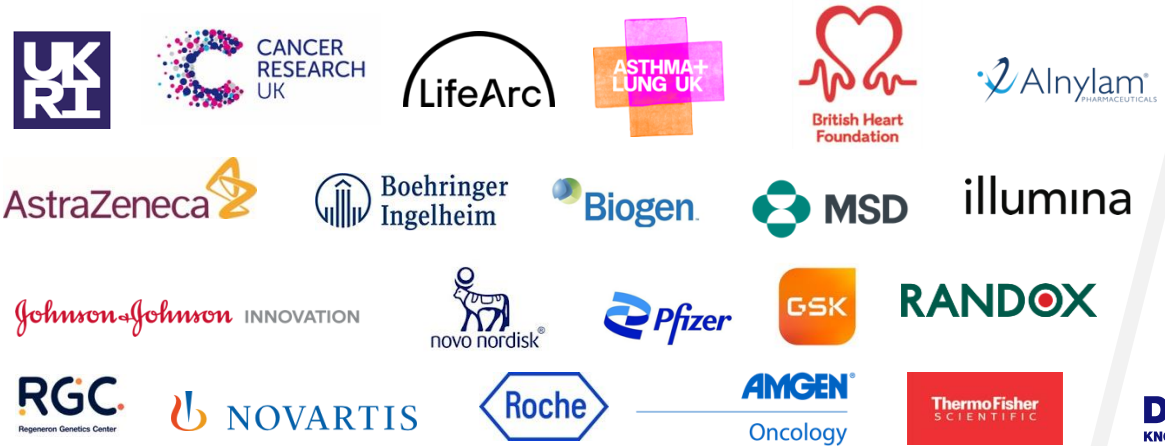


A strong collaboration across the life sciences sector and health system

- Our Future Health is designed to harness the power of collaboration so we can collectively help people live healthier lives for longer.
- We're a not-for-profit organisation combining support from industry, charities and government to build a world-leading health research programme



Funders



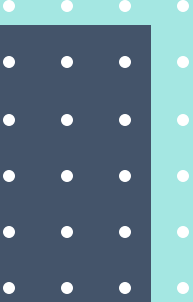
Affiliate charities



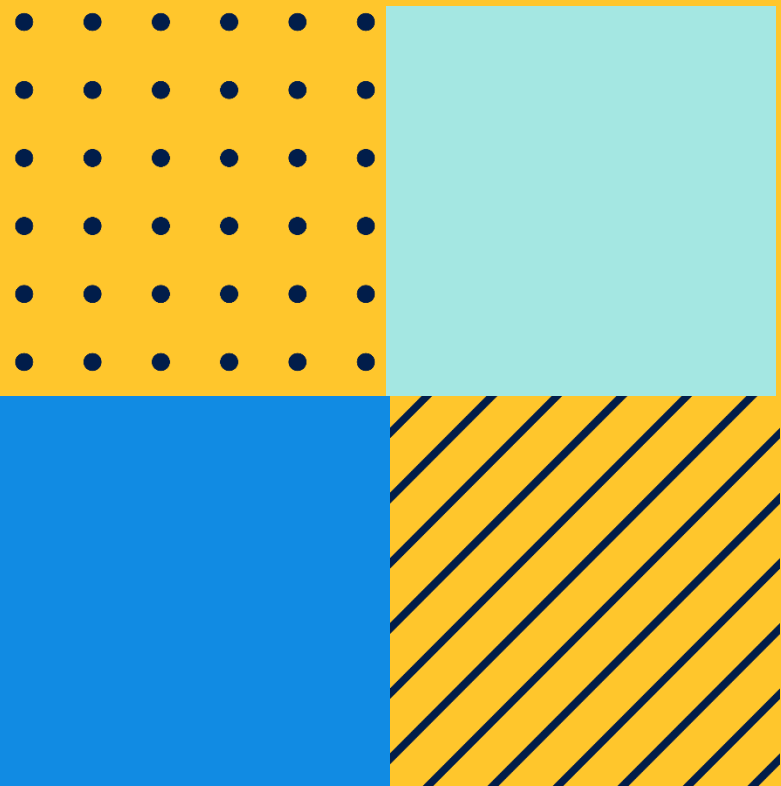


Central aims of the programme

- Build a new prospective cohort in the UK with the mission to help everyone live longer and healthier lives through the **discovery and testing of more effective approaches to prevention, earlier detection, and treatment of diseases.**
- Recruit 5 million volunteers from the UK adult population to create a unique resource which will **catalyse aetiological and translational research for both common and rare diseases.**
- **Facilitate translational research** by providing **access to data and stored biosamples**, and by **enabling recontact studies/trials with participants selectively invited** based on demographics, phenotypes, and disease risks.
- Provide **personal disease risk information for participants**, based on genetic and non-genetic information, and deliver **population health insights**, facilitating insights into the health of the whole population and the assessment of the **impact of interventions/policies at the individual level.**



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Recruitment



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Age
18+

UK
resident



Our Volunteers

- We're monitoring recruitment to ensure our participants are reflective of the UK population by **age, sex, ethnicity and deprivation**.
- Our Future Health will be the largest cohort of:
 - Multi-ethnicities in the UK
 - Non-European ancestry in the world
 - Young people and working age populations
 - Over 60s

+ What our participants donate to Our Future Health



Complete a baseline questionnaire (demographics & household, work & education, lifestyle, family history, personal health history)



Physical measurements taken at clinic appointment (height, weight, waist circumference, blood pressure, heart rate)



A blood sample for genotyping and for long-term storage of plasma, buffy coat, and DNA



DNA is genotyped using a custom array that captures 700k up-to-date variants of interest for optimal research insights

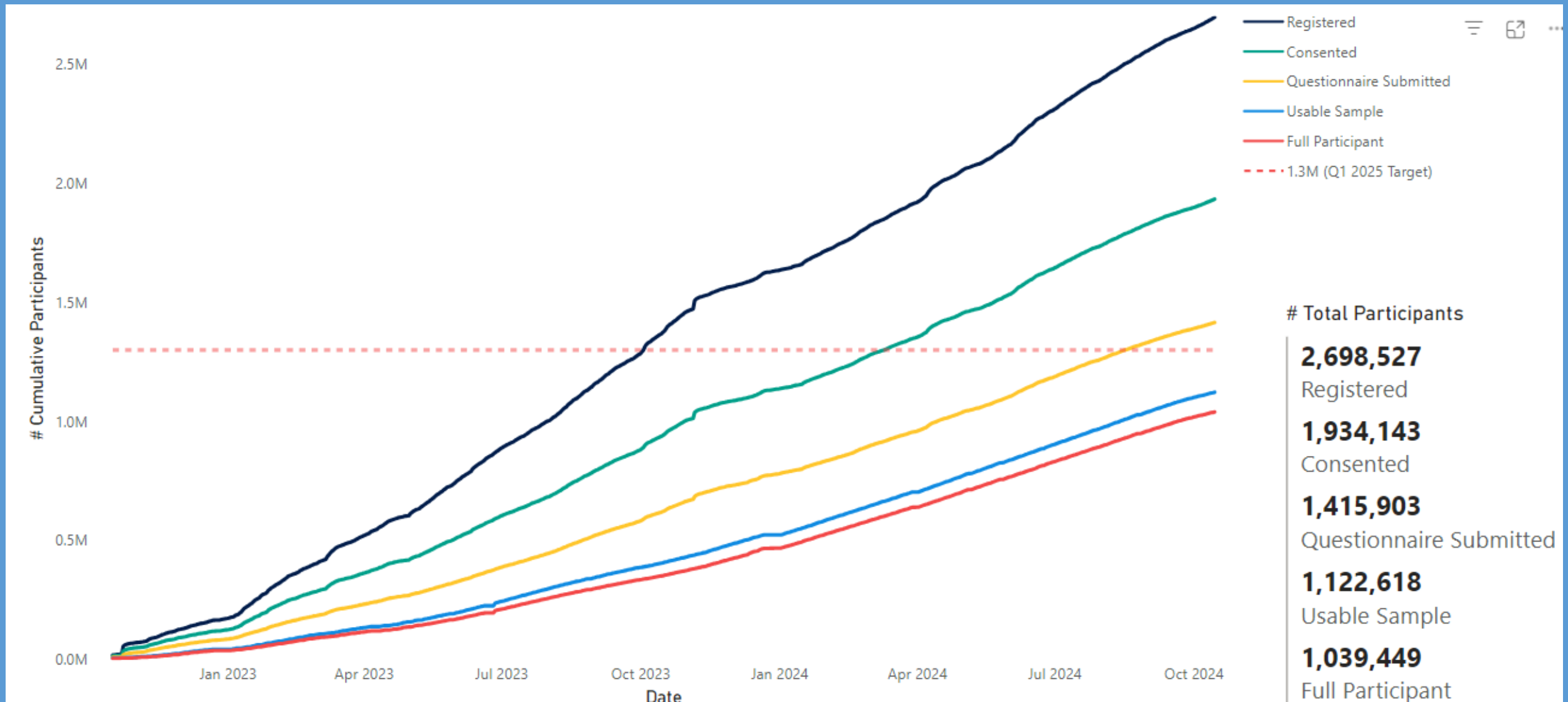


Provide permission for data linkage to health-related datasets (e.g., primary care, secondary care, cancer, death)



Provide permission to be recontacted for further surveys/ biospecimens/assessments and to be invited to additional studies/trials

+ Recruitment to date



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13 participants
May 2021

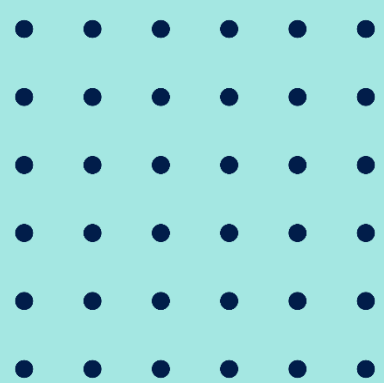
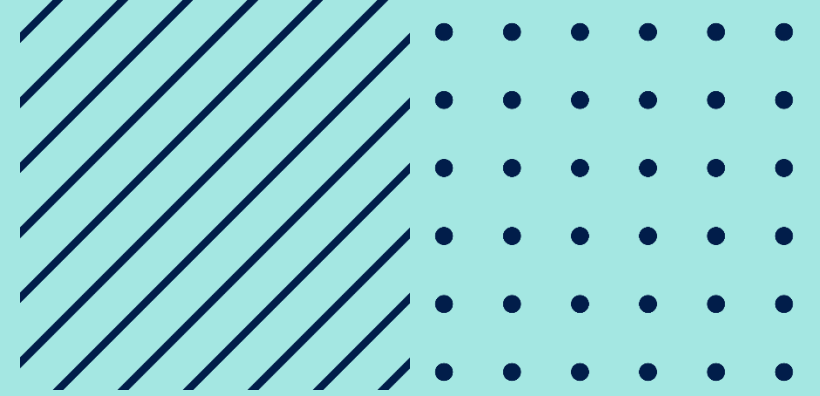


The Our Future Health custom genotype array types 700,000 variants for aetiologic and translational research

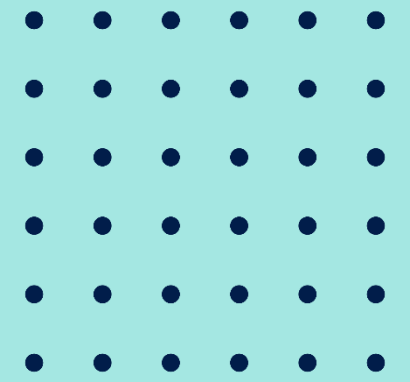
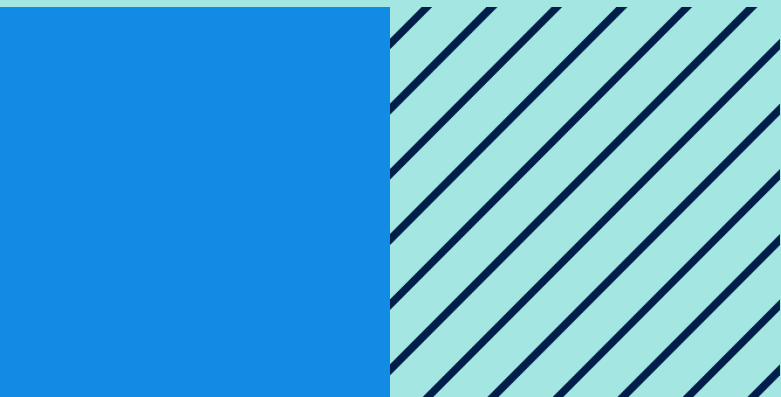
- GWAS backbone is **optimised for multi-ethnic imputation capability**
- Design incorporates **up to date sets of disease- and phenotype-associated genetic variants** from the Genotype Assay Working Group including polygenic risk score (PRS), GWAS catalog, ACMG, and ClinVar sets
- The array is also designed to **predict blood types and assess pharmacogenetic variants** to further enhance healthcare insights.
- We have built an integrated genotyping workflow and have contracted with Genomics to provide imputed data, polygenic and integrated risk scores.
- Further **concordance analyses** will enable any additional array optimisation and a final assessment of accuracy relative to a gold standards (WGS, blood type serology)



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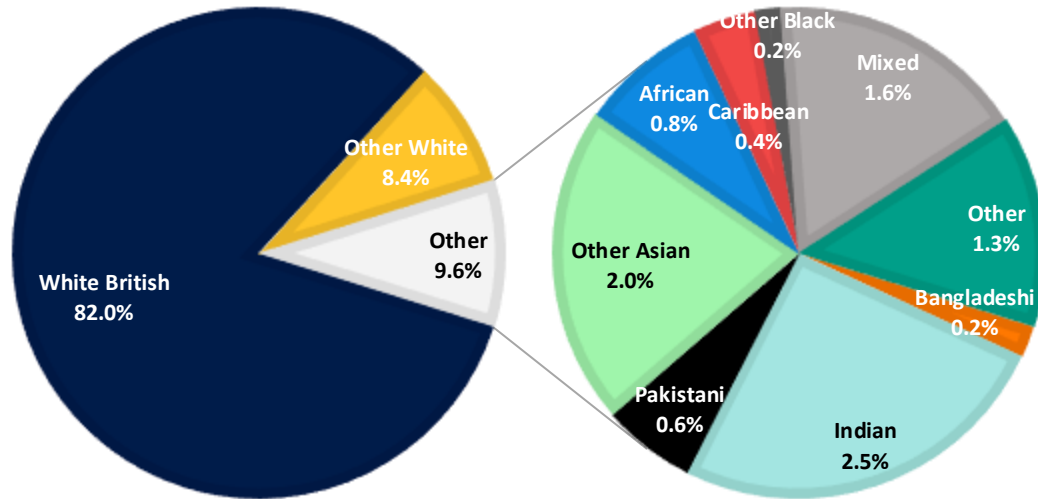
Progress to Date



Demographics - 1,035,446 full participants

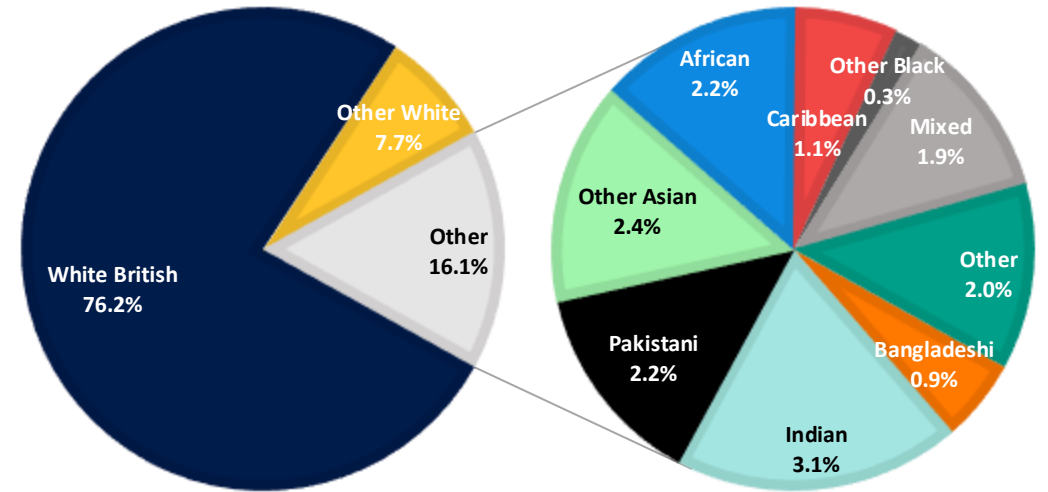
PERCENTAGE OF ETHNICITIES OF FULL PARTICIPANTS

- White British
- Other White
- Bangladeshi
- Indian
- Pakistani
- Other Asian
- African
- Caribbean
- Other Black
- Mixed
- Other



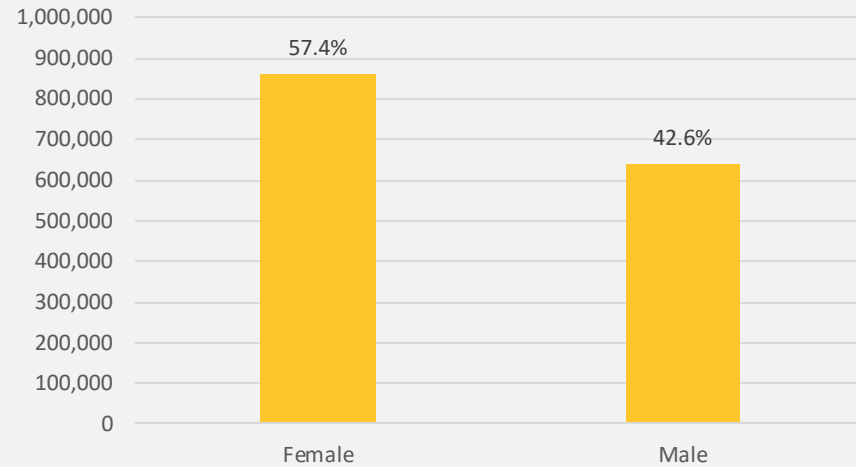
PERCENTAGE OF ETHNICITIES OF CENSUS 2021

- White British
- Other White
- Bangladeshi
- Indian
- Pakistani
- Other Asian
- African
- Caribbean
- Other Black
- Mixed
- Other

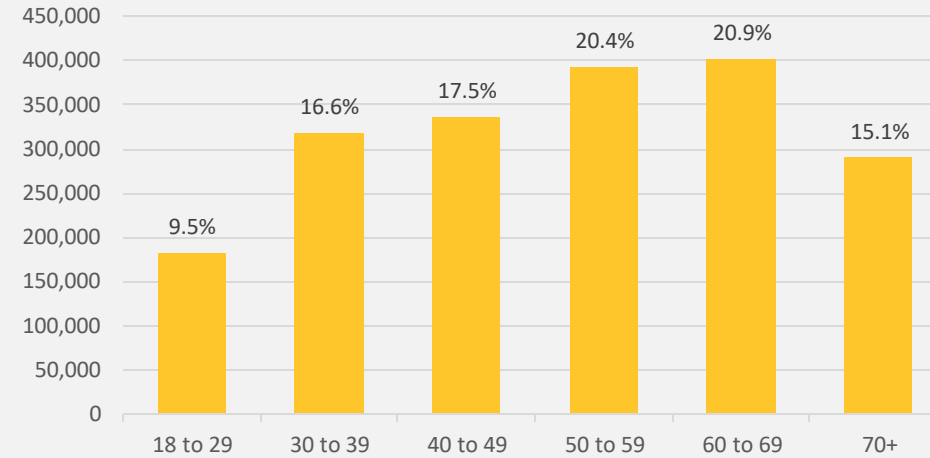


Demographics – 1,925,136 consented participants

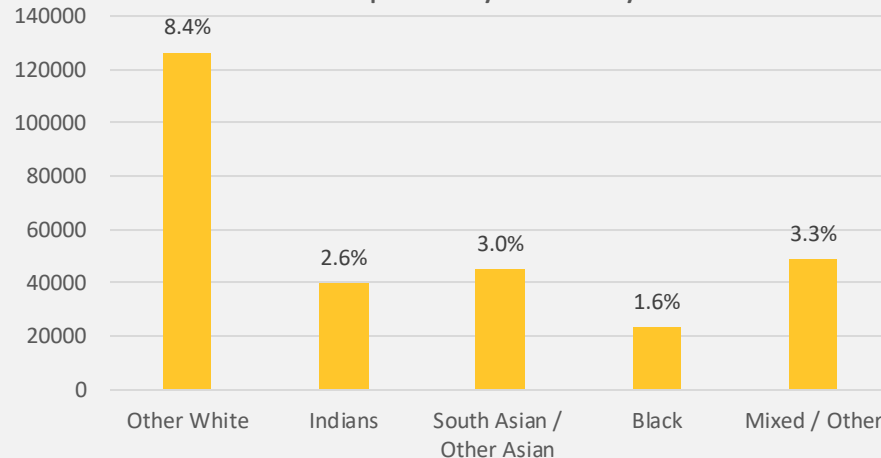
Number of male and female participants



Number of participants by age group

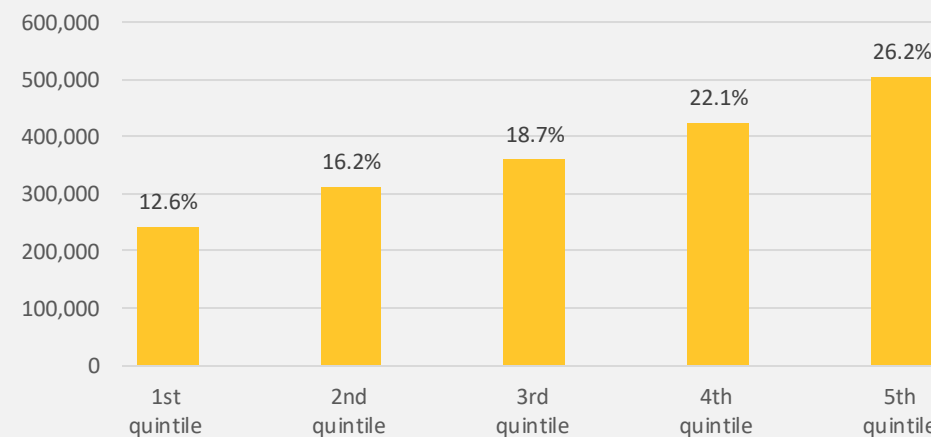


Participants by ethnicity



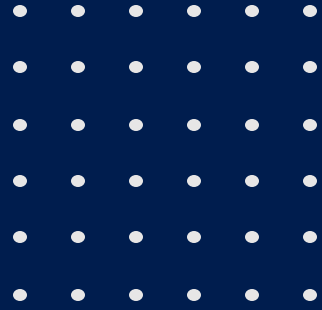
*1,219,122 (81.1%) White British participants

Distribution of participants across IMD* quintiles



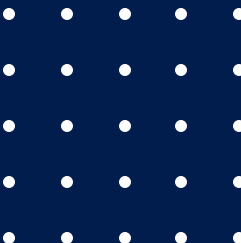
*Index of Multiple Deprivation - 1st quintile is most deprived; 5th is least deprived

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A platform for research

What data *do* we have and what data *will*
we have on our volunteers





Secure, de-identified data available to approved researchers in our Trusted Research Environment

1,414,260

participants with baseline health questionnaires

651,050

participants with genotype array data

1,151,453

participants with NHS-E secondary care data

1,025,498

participants with clinic measurements data

5,128

participants with imputed data *(for testing purposes only)*



Genetic Data / Software



Genetic data is...

Varied and esoteric:

- Raw genotype data contains **7** different file types, **3** of which are specific to genetics
- Release data contains **25** different file types, **12** of which are specific to genetics

Relatively large:

- 710k genotyped / 160M imputed variants per person
- 4 different values for each genotype
- 1.8 trillion data points (P9 = 650k samples x 710k variants x 4 data points)

Often redundant:

- Raw genotype data for each participant contains the exact same data for 9 out of 10 columns
- 50 TB of raw data = 2 TB of release data

In demand:

- Researchers are very keen to get access ASAP.

Genetic software is often...

Frequently file based:

- Transformations from one file type into another

Not cloud native:

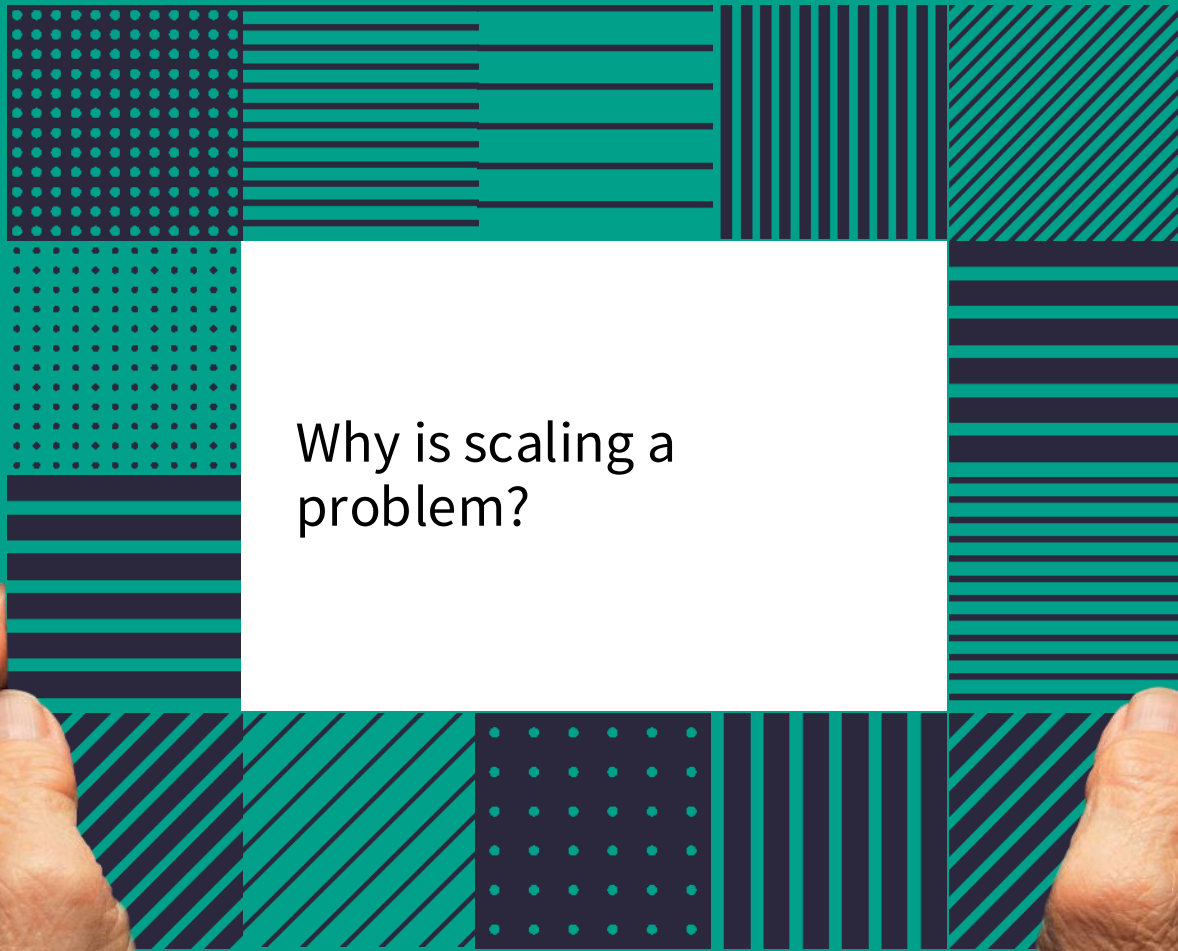
- Historically run using on premise compute

Domain specific:

- Little uptake outside the bioinformatics community

Not production ready / optimized:

- Single threaded
- Rigid format expectations



Why is scaling a
problem?



Why we can't use standard methods

Domain specific files and tooling don't lend themselves towards traditional methods.

- To add or remove a sample requires reading and writing all data every time
- This gets slower as the cohort grows
- Works for now, but alternative is required long term



Where are we up to?

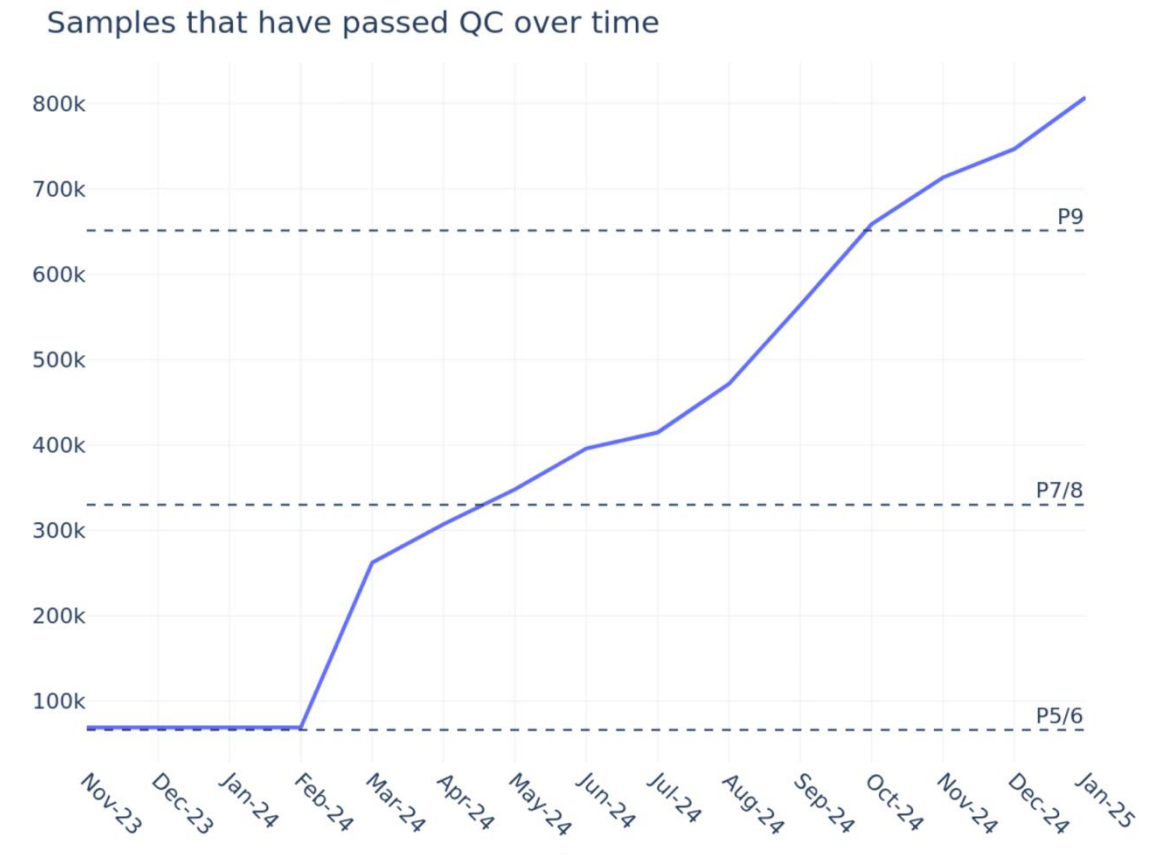


Overall

- To meet the quarterly release cycle, and withdrawal requirements, we have (probably) **built the most efficient and advanced genetic data processing and release pipelines in the world**, in record time.
- This requires **specific skills and expertise from across various domains**, e.g., engineering, bioinformatics, statistical genetics, product, delivery and management,
- **Compared to other similar initiatives, the squad is very small**. However, we are fortunate to have invaluable assistance from the wider organization.
- To date, we have **met all deliverables**, but this has not been without a cost, and we still deal with large amounts of technical and data debt.

Successes

1. Received, QC'd and tracked genotype data for over 1 million participants (2 million total).
2. Built robust and scalable pipeline that can produce genotype release data for millions of participants in under 24 hours
3. Within 12 months of receiving data we were able to create a genotype data release for 660k participants
4. Set up imputation data flow via Genomics Ltd and UK Biobank and released first data





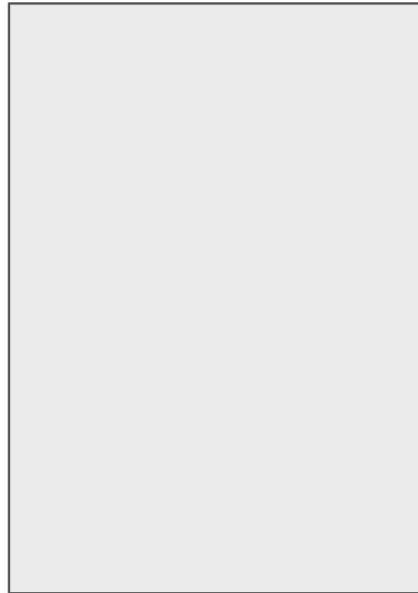
The future



VCF vs Zarr

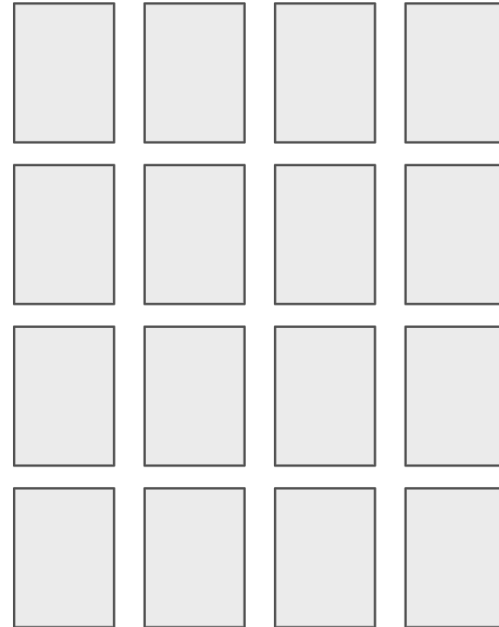
VCF

samples



variants

VCF Zarr



10,000 variants x 1,000 samples

VCFs are monolithic two dimensional objects that can only be searched efficiently by row

Zarr chunks the data by sample and more:

- Natively supports cloud object stores
- Single thread analytic performance is better than traditional methods
- Parallelisable

(GIGA)ⁿ SCIENCE

PAPER

Analysis-ready VCF at Biobank scale using Zarr

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¹Open Athena AI Foundation and ²Related Sciences and ³The New Zealand Institute for Plant & Food Research Ltd, Lincoln, New Zealand and ⁴Department of Biochemistry, School of Biomedical Sciences, University of Otago, Dunedin, New Zealand and ⁵Independent researcher and ⁶Tom White Consulting Ltd. and ⁷Our Future Health, Manchester, UK. and ⁸Program in Medical and Population Genetics, Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA and ⁹Analytic and Translational Genetics Unit, Massachusetts General Hospital, Boston, Massachusetts 02114, USA and ¹⁰NVIDIA Ltd, Reading, UK and ¹¹Big Data Institute, Li Ka Shing Centre for Health Information and Discovery, University of Oxford, UK and ¹²Novo Nordisk Foundation Center for Genomic Mechanisms of Disease, Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA and ¹³Wellcome Sanger Institute and ¹⁴Genomics England and ¹⁵Department of Cell and Molecular Biology, National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Uppsala University, Uppsala, Sweden and ¹⁶School of Computer Science, McGill University, Montreal, QC, Canada

*Joint first author.

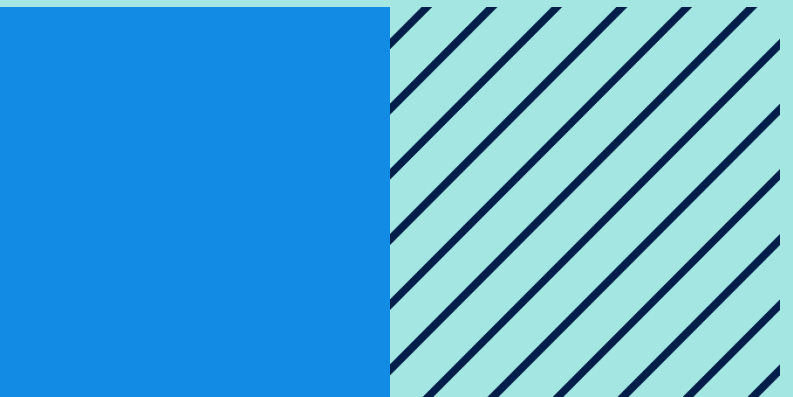
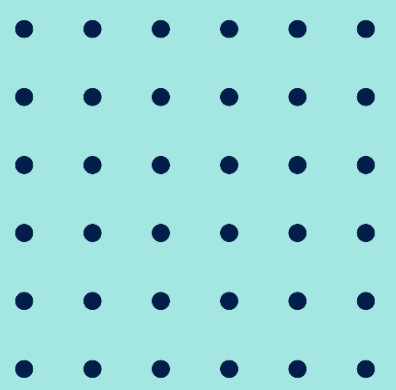
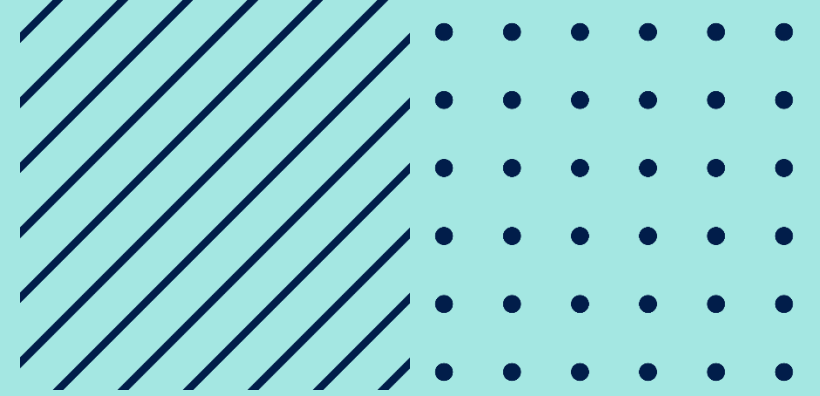
†Joint senior author.

‡jerome.kelleher@bdi.ox.ac.uk

Collab with groups around the world:

- Genomics England
- Broad / MIT
- Big Data Institute
- Novo Nordisk
- NVIDIA

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Thanks.
Any questions?

