All of Us Advisory Panel Meeting

April 27, 2022
Program Updates
Program Mission (small updates)

Our Mission

Accelerate health research and medical breakthroughs, enabling individualized prevention, treatment, and care for all of us.

Nurture partnership for decades with at least a million participants who reflect the diversity of the U.S.

Deliver one of the largest, richest biomedical datasets that is broadly available and secure.

Catalyze an ecosystem of communities, researchers, and funders who make All of Us an indispensable part of health research.

Made possible by a team that maintains a culture built around the program’s core values.
Five Year Goals (For 2026)

- Enrollment and retention
- Gathering and curating data and specimens via the core protocol
- Ancillary studies
- Researcher access and impact
- Participant return of value
Five Year Goals
By 2026, we will:

- Enroll 1 million participants who reflect the diversity of the US, cover the lifespan, and have shared all baseline elements. Of these participants, 500,000 are actively engaged in the program.

- Expand data available for 1 million participants, to include surveys, health data streams, a whole genome sequence, environmental data, and physical measures.

- Develop and launch a scalable ancillary studies program that expands the cohort and delivers additional phenotypic, lifestyle, environmental, and biologic data.

- Establish a diverse global community of 10,000 researchers productively using All of Us data.

- Incorporate participant return of value into data collections and assess its impact, including return of information to participants on genomics and EHR.
Status of the Program: Enrollment Number

Enrollment Update

- **487,000+** Participants
- **293,000+** Electronic Health Records
- **334,000+** Participants who have completed initial steps of the program
- **357,000+** Biosamples

Numbers current as of April 26, 2022
Since We Last Met: Controlled Tier + Genomics released into the Research Workbench

Researcher Workbench Controlled Tier
Launched on March 17, 2022

- **98,600+** Whole Genome Sequences
- **165,000+** Genotyping Arrays
- **593,000,000+** Unique Variants
  - Includes 100M+ variants with ≥3 occurrences not seen in gnomAD 3.0 (n = 71,702)

Gnomics Analysis Tools
- Hail and PLINK in addition to R, Python, and Jupyter Notebooks

ResearchAllofUs.org/Data-Tools/Workbench/
All of Us’ Inclusion of Underrepresented Groups Will Enhance Diversity of Genomic Studies

First genomic data set

~50% diverse by race/ethnicity,
80% underrepresented in biomedical research

All Global GWAS values from www.gwasdiversitymonitor.com. Values current as of February 17, 2022
Researcher Workbench Users

Our Researchers

1,940+ Registered Researchers across a range of institutional roles and career stages

330+ Institutions

Research currently underway

1,430+ Active projects

37+ Publications in peer-reviewed journals

Top conditions being studied

In the Researcher Workbench include:

- Cardiovascular disease
- Hypertension
- Mental Health
- Cancer
- Diabetes

*Includes 36 Historically Black Colleges and Universities and Hispanic-Serving Institutions.
The Controlled Tier Research Community

305
Controlled Tier Researchers
across a range of institutional roles and career stages

220+
Institutions have signed
Controlled Tier Rider

Researchers nationwide are using the
Researcher Workbench

163

27

40

Academic Institutions*
Non-Profit Organizations
Health Care Organizations

Controlled Tier Research Currently Underway

155
Active projects

Career Stages of researchers
Accessing the Controlled Tier Dataset include:
- Early Career
- Fellow
- Mid Career
- Trainee
- Undergraduate
- Project Personnel

Topics being studied:
In the Controlled Tier include:
- Genomics
- COVID
- Fitbit
- Mental Health
- Women’s Health
- SGM Health
- Kidney Disease
- Glaucoma

Figures accurate as of April 19, 2022
Researcher Workbench Usage Increased After the Launch of Controlled Tier

Number of Registered Researchers Over Time

1,942 researchers
across 330 institutions
(as of 4/25/2022)

Number of Workspaces Created Over Time

1,580 workspaces
(as of 4/25/2022)
## Genomic Data Is Paired With Rich Phenotypic Data

<table>
<thead>
<tr>
<th>Count</th>
<th>Data Types</th>
</tr>
</thead>
<tbody>
<tr>
<td>77,000+</td>
<td>Whole Genome Sequences, Electronic Health Records, Physical Measurements, Survey Responses</td>
</tr>
<tr>
<td>95,000+</td>
<td>Whole Genome Sequences, Physical Measurements, Survey Responses</td>
</tr>
<tr>
<td>78,200+</td>
<td>Whole Genome Sequences, Electronic Health Records</td>
</tr>
<tr>
<td>3,500+</td>
<td>Whole Genome Sequences, Fitbit Records</td>
</tr>
</tbody>
</table>

Representing >30% of all participant Fitbit records.
Nearly 100,000 participants responded to 1 or more of the 6 COPE surveys administered between May 2020 and March 2021.

Topics Covered:
- Social Distancing Experiences
- COVID-19 Related Symptoms
- COVID-19 Related Testing
- COVID-19 Related Treatment
- COVID-19 Related Impact
- General Well-Being
- Social Support
- Anxiety
- Mood
- Stress
- Physical Activity
- Loneliness
- Substance Use
- Resilience
- Discrimination
- Vaccine Perceptions

COVID Data on Researcher Workbench: COVID-19 Participant Experience (COPE) Survey
Returning Genomic Results to Participants and More to Come

Array data generated

Whole Genome Sequences generated

Non-Health Genetic Traits
- Traits
- Genetic Ancestry
Currently returning to participants
>76,770 participants have viewed traits or ancestry

Health-Related Genetic Traits
- Hereditary Disease Risk
- PGx
Launched in winter
Researchers Convention: Minority Student Research Symposium and Science Day

- 930 total registered attendees
- Two-days of live virtual events (March 31st and April 1st):
  - 2 keynotes (Power of Mentorship & Fireside Chat with researchers)
  - 3 plenary sessions
- Minority Student Research Symposium (MSRS):
  - 27 student presentations
- Science Day:
  - 12 abstract presentations from 48 submissions

Example Projects

- Actionable PGx variants
- Biological Age as an independent predictor of stroke risk

>96% of participants carry an actionable PGx variant similar across all ancestries

\[ \text{AoU: time-to-event curves by Phenotype tertile} \]

Strata: --- Young — Intermediate — Oldest

Cumulative event

0.00 0.05 0.10 0.15

0 2 4 6 8 10 12 14