

Global Initiatives in Genomics and Health



Peter Goodhand
CEO • GA4GH

1 Why do we need standards?

2 GA4GH

Outline

3 Global Collaborations

Japanese Example

5 Getting Involved

Since data is distributed globally, we need interoperable standards to answer research questions



Standards are essential



Interoperability is key to data sharing and enabling the necessary ecosystem



What makes a good standard?





Clear and specific specification



Meets the needs of everyone in the system



Easy to adopt



Works as part of a broader ecosystem

For standards to help...

...they need to be deployed.

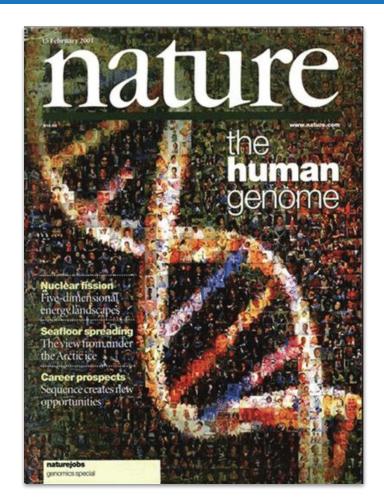
To be deployed...

...they need to built with adoption in mind.

To be adopted...

...we need to check what people need (everywhere).

How do we advance genomics globally?



The 1000 Genomes Project ecosystem





Common consent across all 26 populations and 5 continents



Common resources: Cell lines, arrays, exomes and genomic sequences



File formats (SAM and VCF) and data sharing methods



Software: samtools, FreeBayes, GATK, VCFtools, tabix, etc.

Interoperable

Together, able to address research questions and lay foundation for future projects



- → To fully realize the benefits of genomics in health, it is necessary to work globally
- → Collaboration is the only way to build standards and achieve global data sharing

GA4GH is a global forum





THE GA4GH MISSION...

The Global Alliance for Genomics and Health aims to accelerate progress in genomic science and human health by developing standards and framing policy for responsible genomic and health-related data sharing.

The GA4GH Ecosystem





GA4GH aims to...



Enable international data sharing



Promote sharing across the translational continuum



Encourage technology-enabled **federated approaches**



Promote interoperability

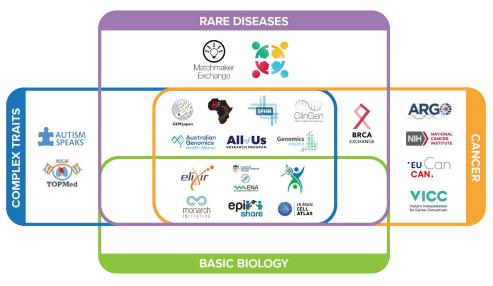
GA4GH achieves this by...

- ✓ Convening stakeholders
- Catalyzing sharing of data
- Creating harmonized approaches
- ✓ Acting as a clearinghouse
- **Fostering** innovation
- Commiting to responsible data sharing

Use cases: what are we trying to do?



We have many sources of real world scientific and health use cases

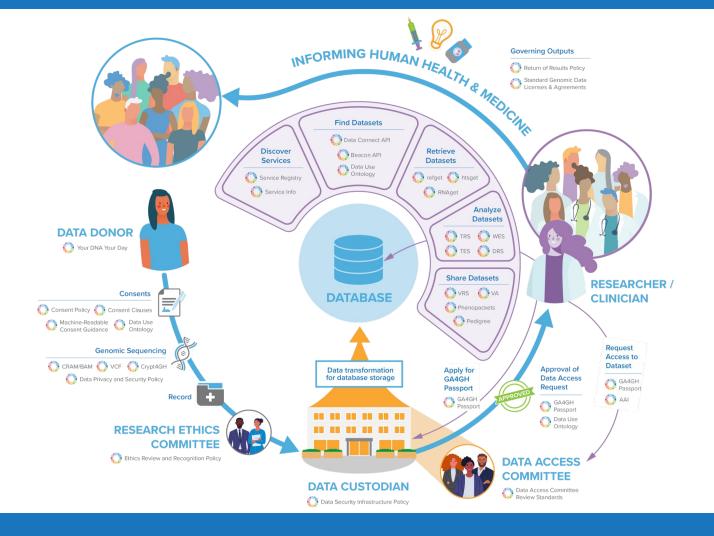


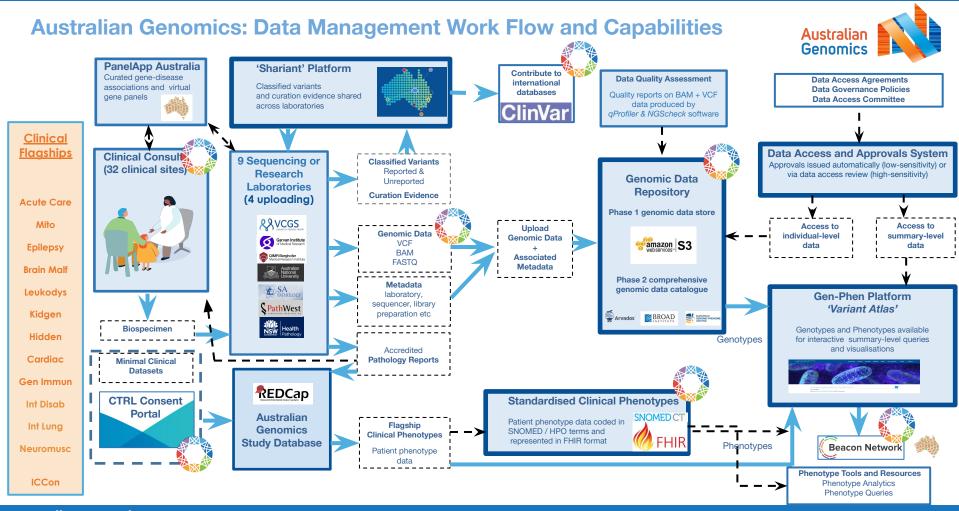
GENOMICS IN HEALTH
IMPLEMENTATION FORUM

Cancer Community

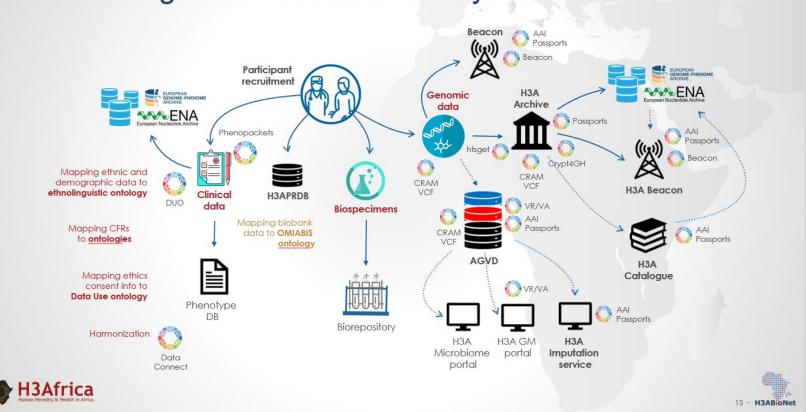
...and many more

Driver Projects





H3Africa genomic research ecosystem



Current GHIF Members

Foundation members:











Nordic Alliance for Clinical Genomics











000 عضوفي مؤسسة قطر Member of Qatar Foundation











Singapore













Collaborations









World Health

Organization





International 100K Cohort Consortium

Beyond One Million Genomes Project



THE MEDICAL GENOME INITIATIVE



Global Genomic Medicine Collaborative

















Global Collaborations





Science Council



International 100K Cohort Consortium







Human Genome Organisation

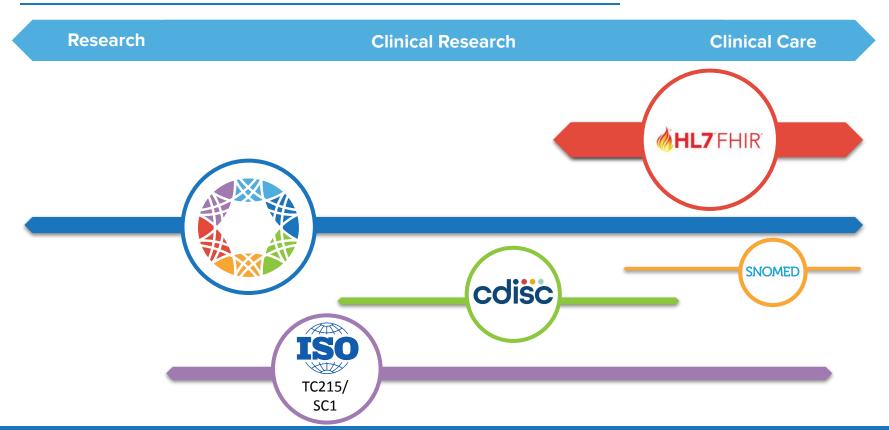






Alignment with Other Standards Organizations





Recent implementation updates















Watch these implementer talks from 9th Plenary: bit.ly/9thplenary-videos

ExampleMelissa Cline & Japan



CIHR COVID-19 Interoperability Initiative















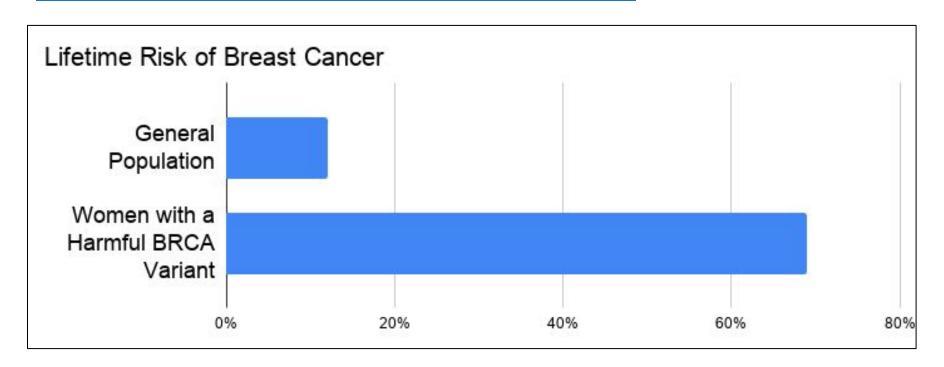




COVID-19 hg

BRCA Variation and Cancer Risk





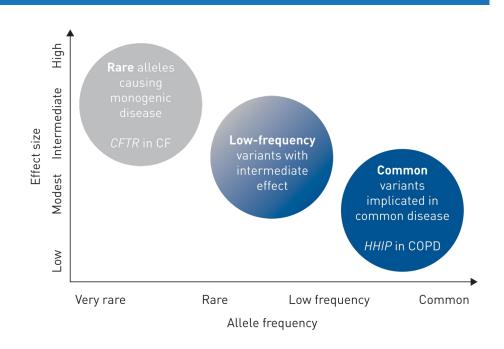
BRCA variation can also lead to ovarian, prostate, and pancreatic cancers

Allele Frequencies



Proof of Concept with BioBank Japan

- Rationale: Disease-causing cancer variants are rare by definition
- If a variant is frequent in some continental population, it can be classified as benign with no further evidence



Federated analysis of BioBank Japan Data



- RIKEN holds a large cohort of cancer patients and controls from BioBank Japan, which they cannot share directly.
- We shared a Docker container with them to analyze their patient cohort for variant co-occurrences and allele frequencies
- The container generated variant-level data, which we are now using together with the ENIGMA Consortium to interpret BRCA variants!







Yukihide Momozawa, RIKEN





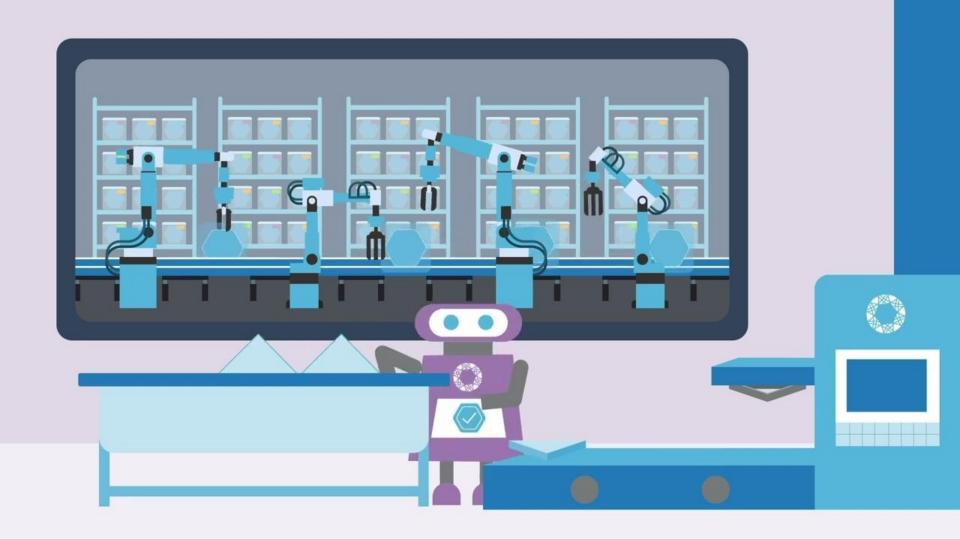
bioRxiv posts many COVID19-related papers. A reminder: they have not been formally peerreviewed and should not guide health-related behavior or be reported in the press as conclusive.

New Results

♣ Follow this preprint

Federated analysis of BRCA1 and BRCA2 variation in a Japanese cohort

Iames Casaletto, Michael Parsons, Yusuke Iwasaki, Yukihide Momozawa, Amanda B. Spurdle, Melissa Cline doi: https://doi.org/10.1101/2021.06.04.447169



Acknowledgements



GA4GH Host Institutions



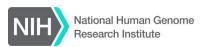






GA4GH Core Funders













GA4GH Supporting Funders





GA4GH Staff and Contributors

Contact us



Join a Work Stream!

Contact secretariat@ga4gh.org





















