Towards a federated network of nodes hosting human genetic and phenotype data

EMBL-EBI

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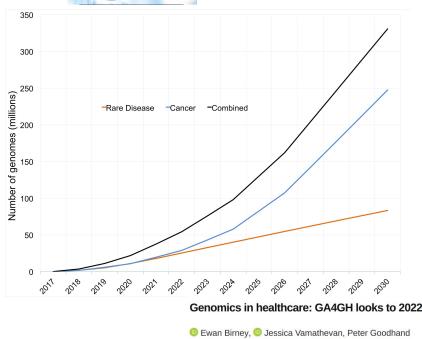
Global genetic data sharing

Historically via International Nucleotide Sequence

Database Collaboration (INSDC)

- Human genetic data sharing in research
 - dbGaP, JGA, and EGA
- Emergence of national scale cohorts
 - Jurisdictional restrictions
 - Enhanced data security
 - Political sensitivity around export

Tens of millions of genomes will be sequenced



doi: https://doi.org/10.1101/203554

Genomics meets healthcare

Percentage of whole genomes and exomes that are funded solely by healthcare systems





o Ewan Birney, o Jessica Vamathevan, Peter Goodhand

doi: https://doi.org/10.1101/203554

What are the challenges?

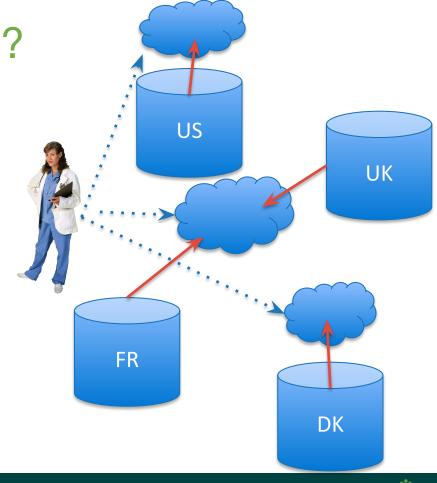
1) Data discoverability

Secure data sharing

3) Permissions automation

4) Interoperable researcher IDs

5) Portable pipelines



What are the challenges

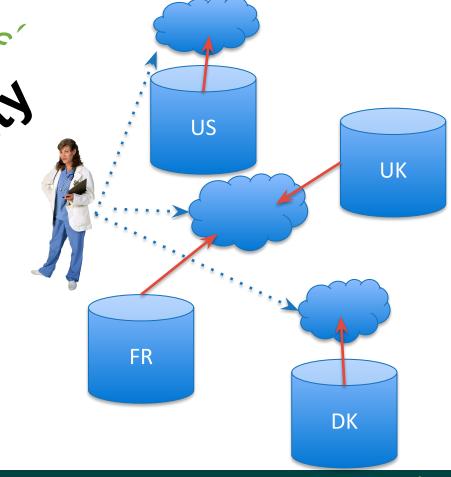
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Global Alliance for Genomics & Health

Collaborate. Innovate. Accelerate.



Global Alliance members include:

- 1. Universities and research institutes (32%)
- 2. Academic medical centers and health systems (10%)
- 3. Disease advocacy organizations and patient groups (5%)
- 4. Consortia and professional societies (5%)
- 5. Funders and agencies (5%)
- 6. Life science and information technology companies (43%)

GA4GH Connect



Discovery Large-Scale **Technical Work Streams Genomics** Data Use & **Researcher IDs** Cloud Genomic Knowledge **Standards Clinical & Phenotypic Data Capture Work Streams** Foundational **Regulatory & Ethics Data Security**

GA4GH Connect



Real-World Driver Projects

Technical Work Streams	Discovery
	Large-Scale Genomics
	Data Use & Researcher IDs
	Cloud
	Genomic Knowledge Standards
	Clinical & Phenotypic Data Capture
Foundational Work Streams	Regulatory & Ethics
	Data Security

GA4GH Connect



Collaborate. Innovate. Accelerate.

		Real-World Driver Projects										
Technical Work Streams	Discovery	✓		✓		✓		✓				
	Large-Scale Genomics		✓		✓		~		~			
	Data Use & Researcher IDs	✓		/		✓	~			✓	nent	
	Cloud		/	/					/	4	ngager	
	Genomic Knowledge Standards		/				/	/	/		Partner Engagement	
	Clinical & Phenotypic Data Capture	/			/	/	/			/	Pa	
Foundational Work Streams	Regulatory & Ethics											
	Data Security											

2017 Driver Projects



Global Alliance for Genomics & Health

Collaborate, Innovate, Accelerate,



All of Us Research Program
United States



Australian Genomics

Australia



BRCA Challenge International



CanDIG Canada



ClinGen United States



ELIXIR Beacon Europe



ENA / EVA / EGA Europe



Genomics England United Kingdom



Human Cell Atlas



ICGC-ARGO International



Matchmaker Exchange International



Monarch Initiative



National Cancer Institute Genomic Data Commons United States



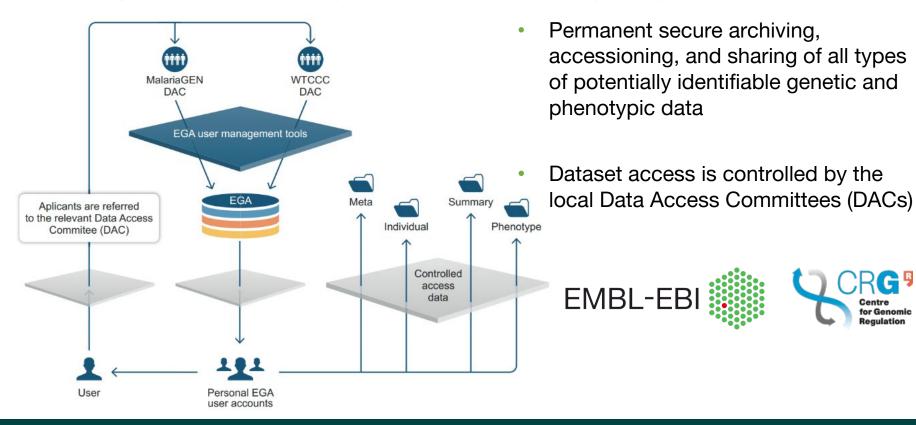
TOPMed United States



Variant Interpretation for Cancer Consortium

International

European Genome-phenome archive (EGA)



for Genomic Regulation

European Genome-phenome archive (EGA)



European Genome-phenome archive (EGA)

By the numbers

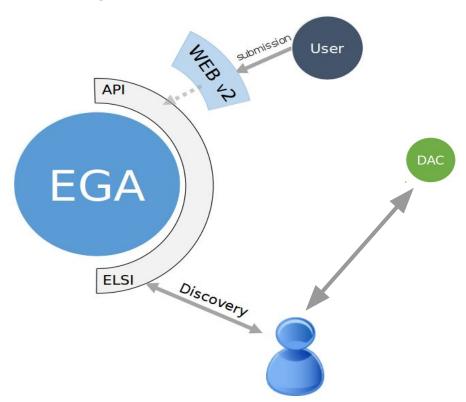
- 1,698 studies
- 3,591 datasets
- 777 data providers
- >10,000 requestors

By volume

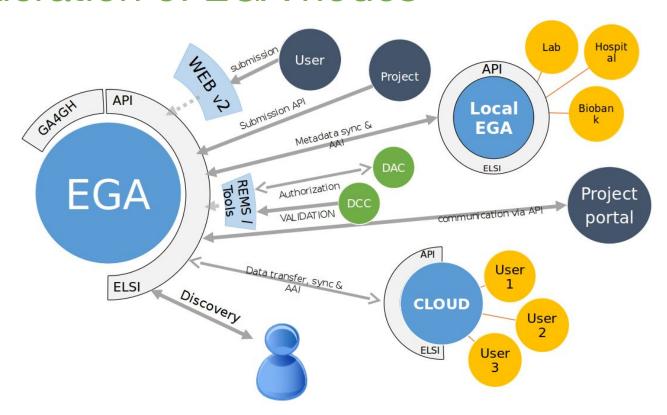
3.5 Petabytes



EGA (circa 2015)



A federation of EGA nodes



Authentication and Authorisation (AAI)

- Fundamental requirements
 - Who are you? What are your credentials?
 - What resources have you been granted access to?
 - Securely share user information managed at user's home organisation with remote services
- Two axes of human data sharing
 - Researcher Identity: Collection of researchers that may access the dataset at any given time, and the credentials they must supply.
 - Data Use: Informed consent form specifies appropriate restrictions on secondary data use.
- GA4GH security working group

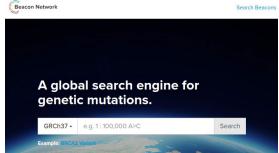


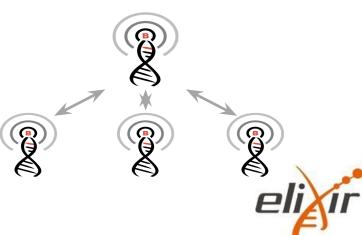
Data Discovery

- Discovery by genotype
 - Beacon Network
 - Do you have evidence for this allele in your database?
 - Open, registered, and controlled access
- Consent codes
 - Groups datasets together in terms of consent agreements
 - Researchers can search by access requirements
 - Data Use Ontology (DUO)
 - Automate dataset application / access











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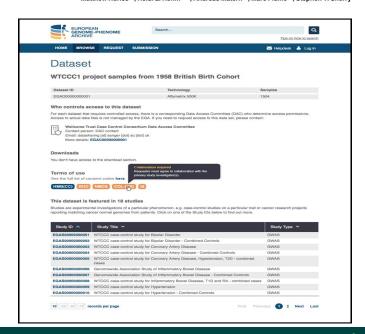




VIEWPOINTS

Consent Codes: Upholding Standard Data Use Conditions

Stephanie O. M. Dyke¹*, Anthony A. Philippakis², Jordi Rambla De Argila^{3,4}, Dina N. Paltoo⁵, Erin S. Luetkemeier⁵, Bartha M. Knoppers¹, Anthony J. Brookes⁵, J. Dylan Spalding⁷, Mark Thompson⁸, Marco Roos⁸, Kym M. Boycott⁸, Michael Brudno^{10,11}, Matthew Hurles¹², Heidi L. Rehm^{2,13}, Andreas Matern¹⁴, Marc Fiume¹⁵, Stephen T. Sherry¹⁶





Secure Data Transfer





- Secure access to sensitive human data
 - Sequencing read and variant data



- Real-time secure streaming to project portal
- Inspection of underlying read data in a read viewer (e.g. IGV)
- Bring the analysis pipelines to the data
 - Standardised API for accessing the genetic data
- Htsget protocol
 - v1.0 launched in October







Samtools BCFtools HTSlib

EUROPEAN

ARCHIVE

GENOME-PHENOME



Genomics

Viewer

Genome Maps



Key partnerships

- ELIXIR
 - EXCELERATE (2015-2019)
 - Implementation studies
 - TrAIT: EGA backend for TranSMART (2016), IMI Oncotrack (2016), Real-time RD-visualisation (2017), Beacon (2017)



Global Alliance for Genomics & Health

- GA4GH
 - Large Scale Genomics
 - Data Use and Researcher ID
 - Discovery
 - Clinical data and phenotype capture
 - Data Security
 - Regulatory and Ethics

Projects

- AMP-T2D
 - Federated browsing, searching, and analysis of human genetic information linked to type 2 diabetes and related traits
- RD-Connect
 - Platform connecting databases, registries, biobanks and clinical bioinformatics
- UK Biobank
 - Sharing genetic data from hundreds of thousands of individuals
- CORBEL





RBEL

EGA Team





















