

Beacon

Ethical & Legal Aspects of a Genomic Data Discovery Protocol

Michael Baudis | DSI Ethics | 2022-08-25



Global Alliance
for Genomics & Health

2017

30,000 patients will have their genome sequenced for rare-disease diagnosis

70,000 genomes (patients + relatives) will be sequenced to help rare disease diagnoses

23,000 cancer patients will have their genome sequenced

50,000 genomes will be sequenced for cancer diagnosis

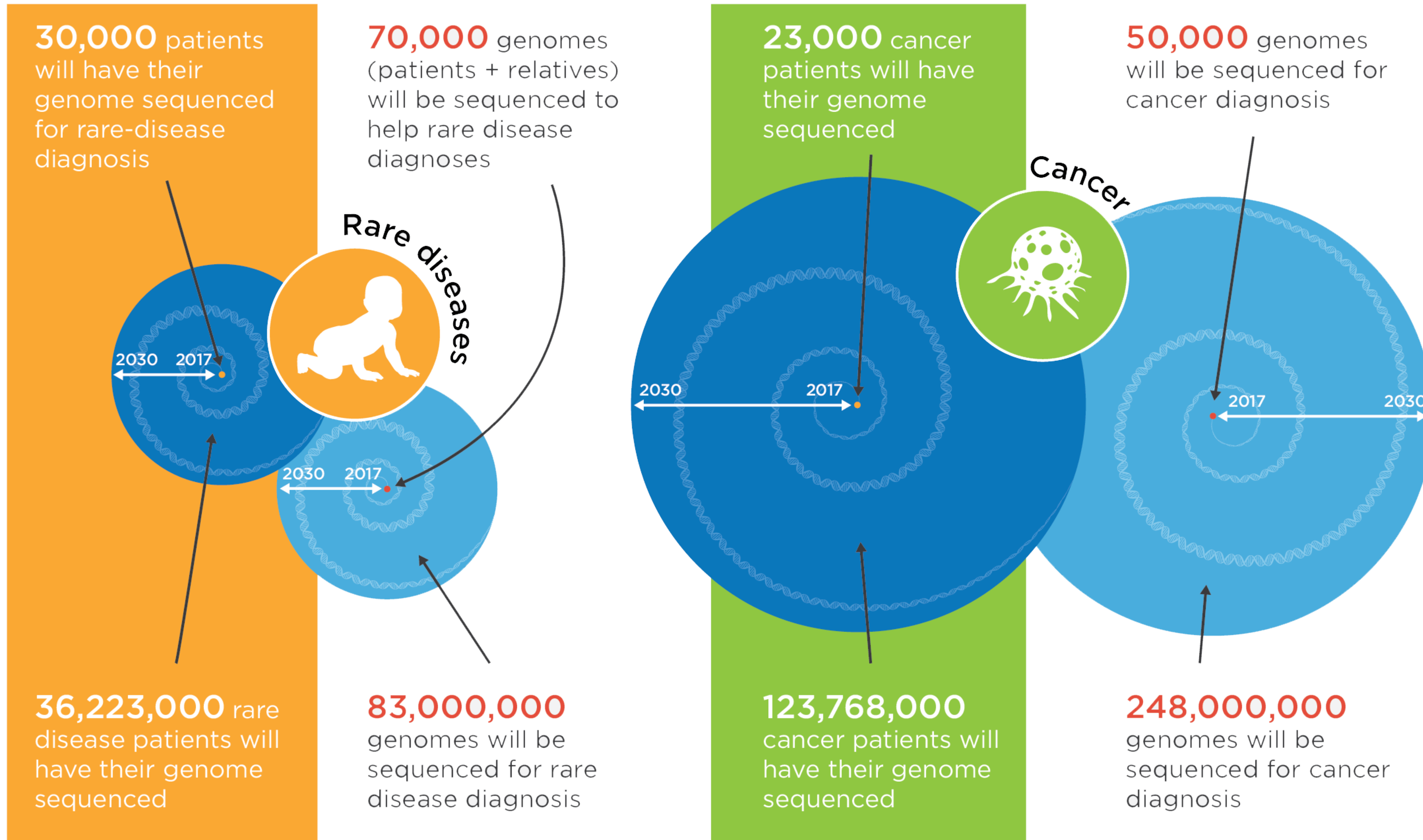
2030*

36,223,000 rare disease patients will have their genome sequenced

83,000,000 genomes will be sequenced for rare disease diagnosis

123,768,000 cancer patients will have their genome sequenced

248,000,000 genomes will be sequenced for cancer diagnosis



* Projected figures, based on current data and known status of genomics initiatives worldwide.

Limited Population Diversity in Cancer Studies

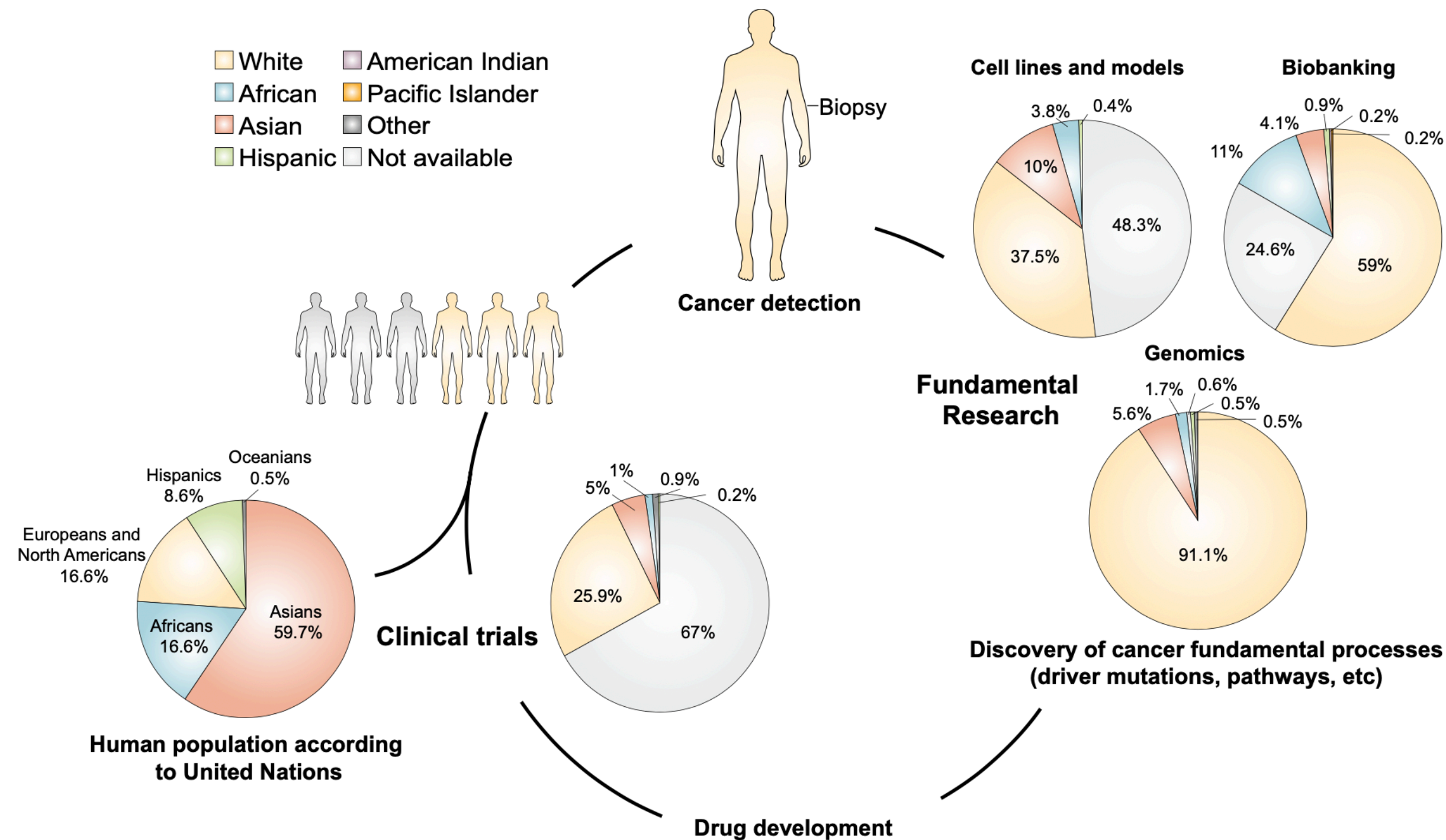


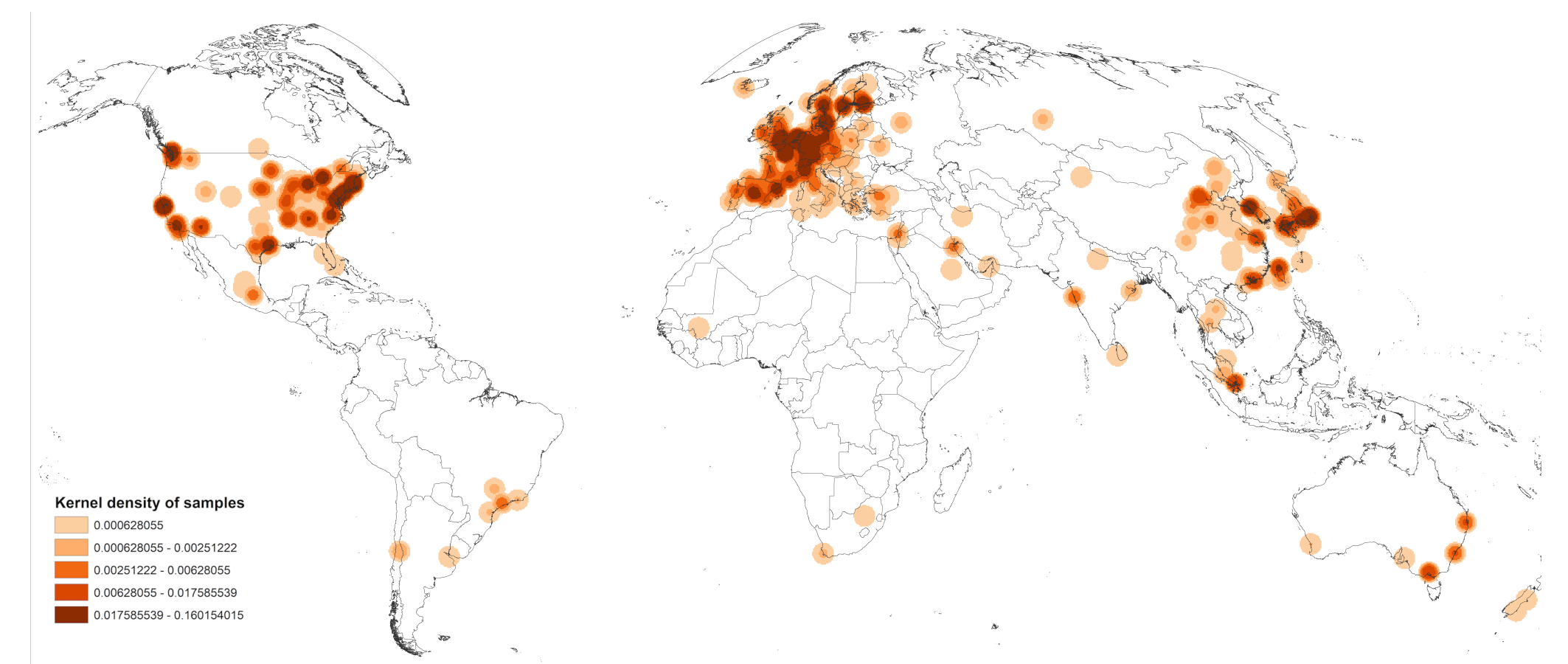
Figure 1. Racial/Ethnic disparities in cancer research. Racial/ethnic inclusion was studied in several aspects of oncological research, from cell lines and patient-derived xenografts to biobanking, genomics and clinical trials.

Guerrero S, López-Cortés A, Indacochea A, et al. Analysis of Racial/Ethnic Representation in Select Basic and Applied Cancer Research Studies. *Sci Rep.* 2018;8(1):13978.

Publication Landscape of Cancer CNV Profiling

Publication statistics for cancer genome screening studies. The graphic shows our assessment of publications reporting whole-genome screening of cancer samples, using molecular detection methods (chromosomal CGH, genomic array technologies, whole exome and genome sequencing).

For the years 1993-2018, we found 3'229 publications reporting 174'530 individual samples in single series from 1 to more than 1000 samples. Y-axis and size of the dots correspond to the sample number; the color codes indicate the technology used.

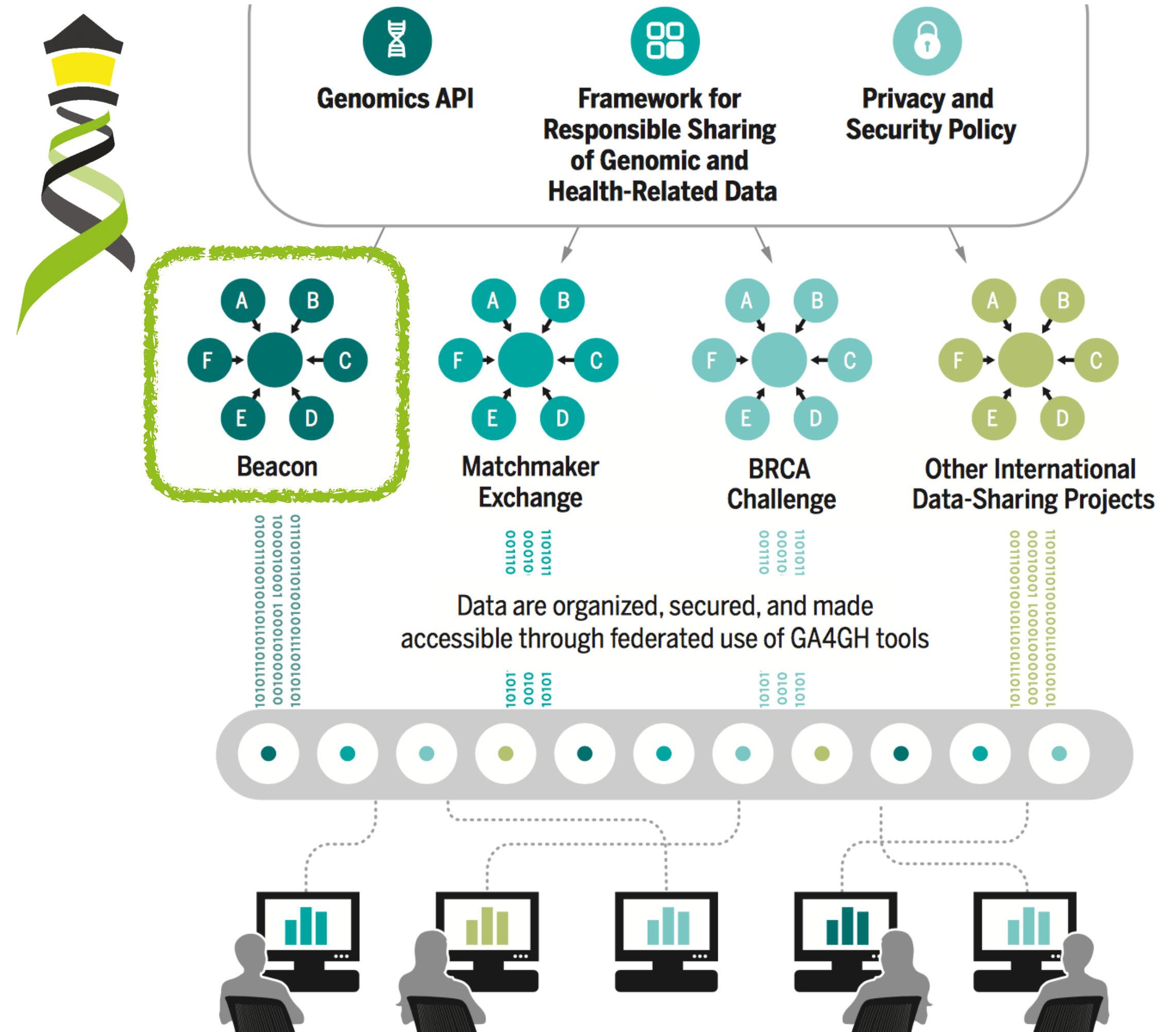


The vision: Federation of data





A federated data ecosystem. To share genomic data globally, this approach furthers medical research without requiring compatible data sets or compromising patient identity.



GENOMICS

A federated ecosystem for sharing genomic, clinical data

Silos of genome data collection are being transformed into seamlessly connected, independent systems



The Global Alliance for Genomics and Health

Making genomic data accessible for research and health

- January 2013 - 50 participants from eight countries
- June 2013 - White Paper, over next year signed by 70 “founding” member institutions (e.g. SIB, UZH)
- March 2014 - Working group meeting in Hinxton & 1st plenary in London
- October 2014 - Plenary meeting, San Diego; interaction with ASHG meeting
- June 2015 - 3rd Plenary meeting, Leiden
- September 2015 - GA4GH at ASHG, Baltimore
- October 2015 - DWG / New York Genome Centre
- April 2016 - Global Workshop @ ICHG 2016, Kyoto
- October 2016 - 4th Plenary Meeting, Vancouver
- May 2017 - Strategy retreat, Hinxton
- October 2017 - 5th plenary, Orlando
- May 2018 - Vancouver
- October 2018 - 6th plenary, Basel
- May 2019 - GA4GH Connect, Hinxton
- October 2019 - 7th Plenary, Boston
- October 2020 - Virtual Plenary, June 2021 - Virtual Connect ...
- October 2021 - Virtual Plenary ...
- September 2022 - 10th Plenary, Barcelona

GENOMICS

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The Global Alliance for Genomics and Health*

SCIENCE 10 JUNE 2016 • VOL 352 ISSUE 6291



22 SEPTEMBER 2022 | BARCELONA, SPAIN

GA4GH 10th Plenary



Global Alliance
for Genomics & Health



Beacon



A **Beacon** answers a query for a specific genome variant against individual or aggregate genome collections

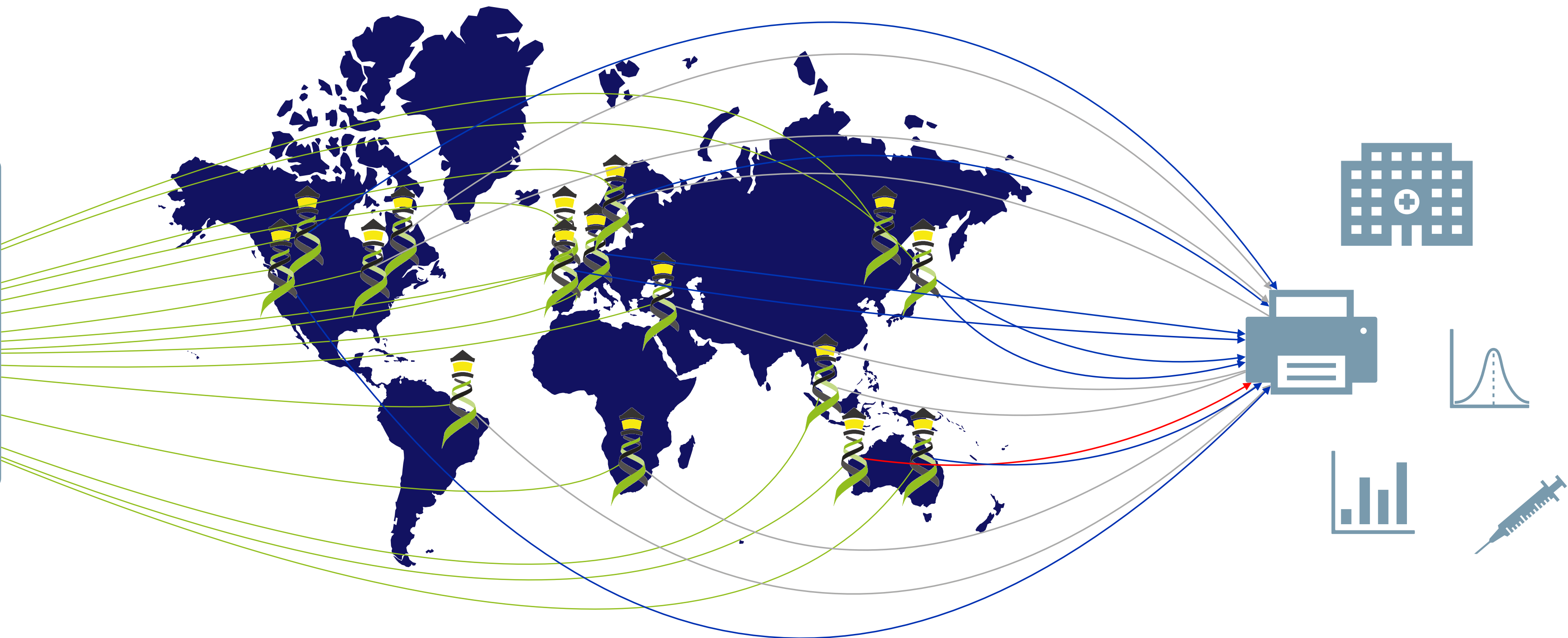
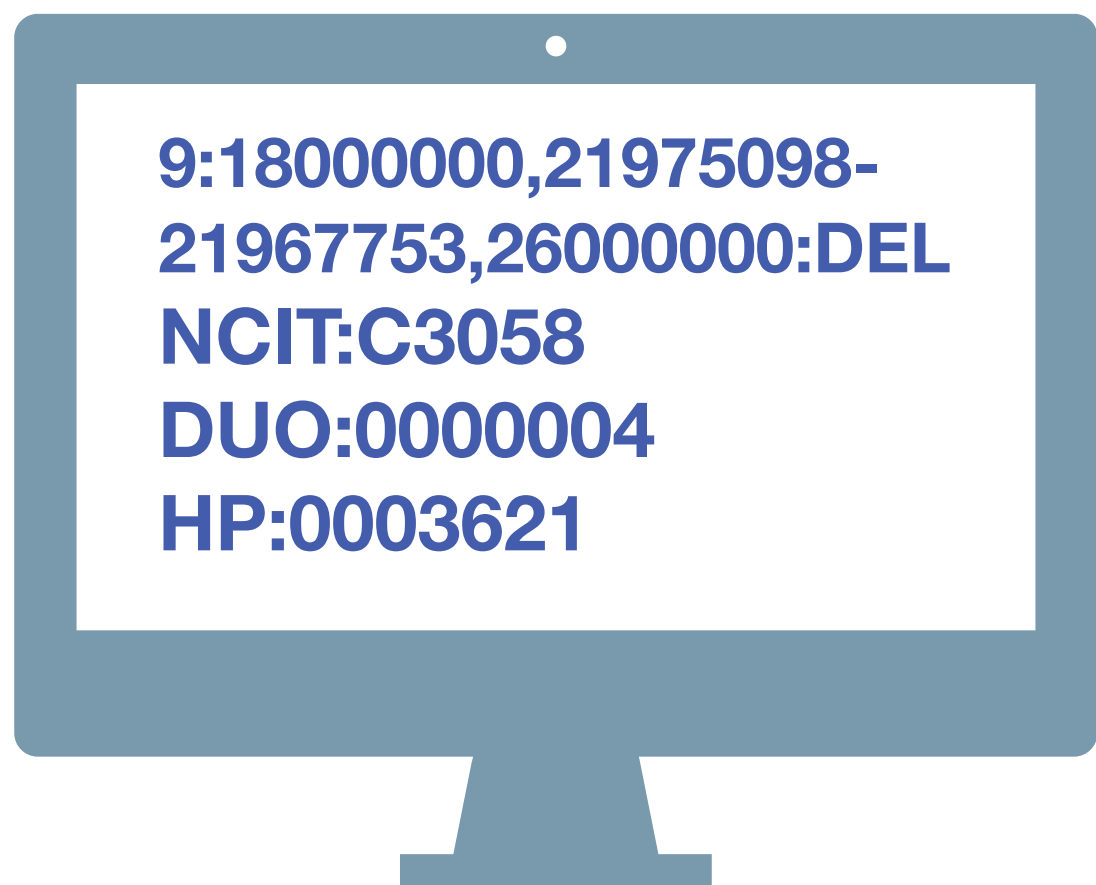
YES | **NO** | \0



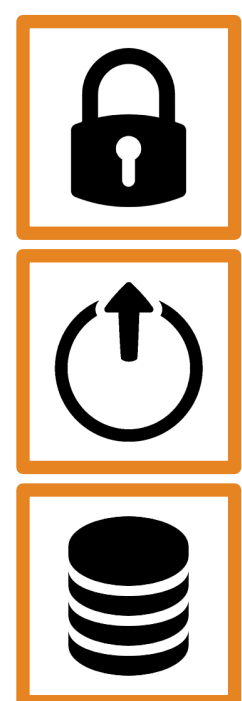
Have you seen this variant?
It came up in my patient
and we don't know if this is
a common SNP or worth
following up.

A Beacon network federates
genome variant queries
across databases that
support the **Beacon API**

Here: The variant has
been found in **few**
resources, and those
are from **disease**
specific **collections**.

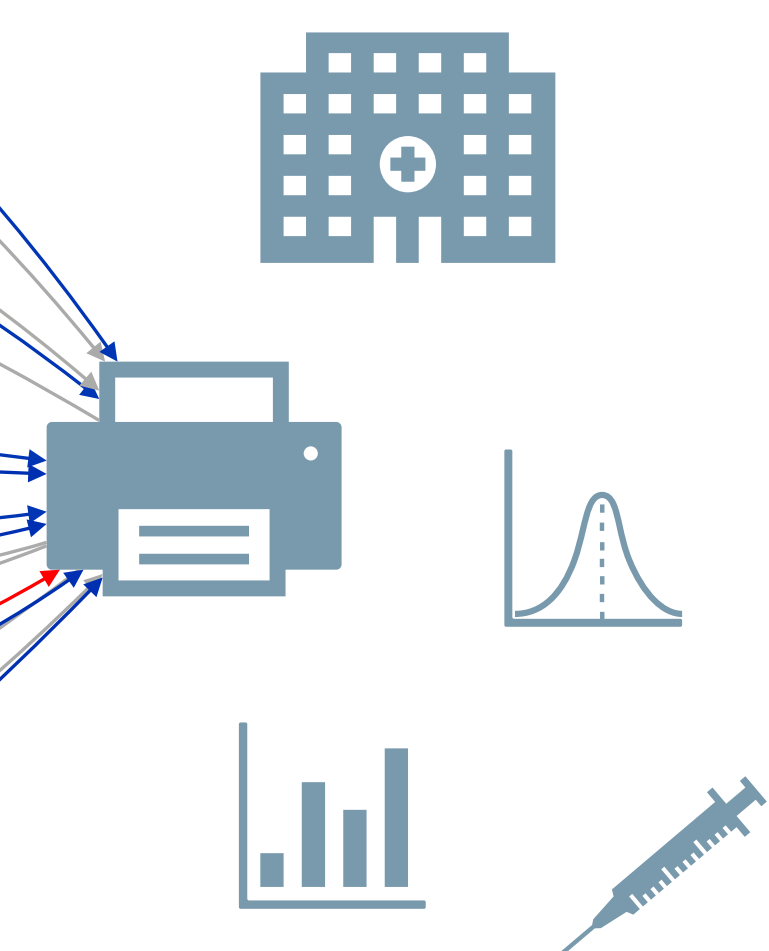
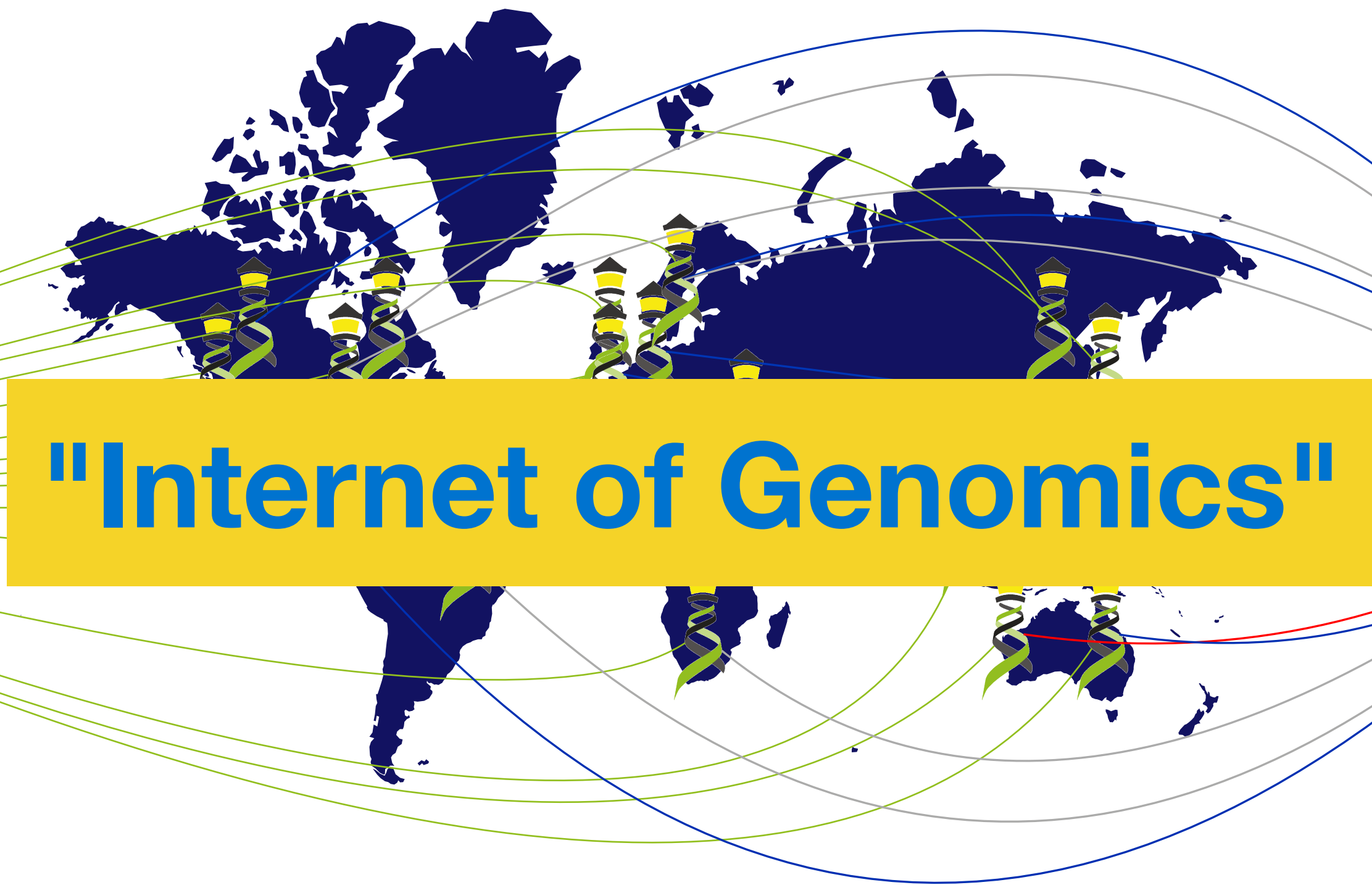
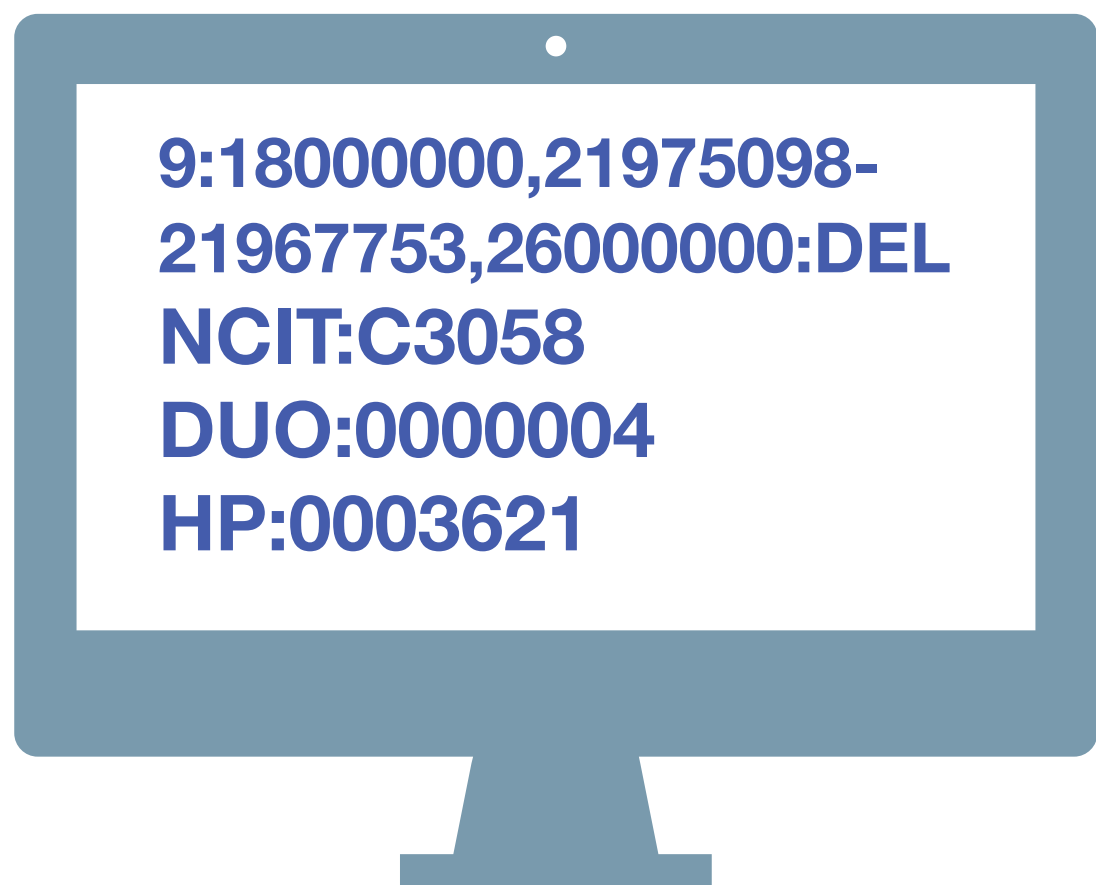


Have you seen deletions in this region on chromosome 9 in Glioblastomas from a juvenile patient, in a dataset with unrestricted access?

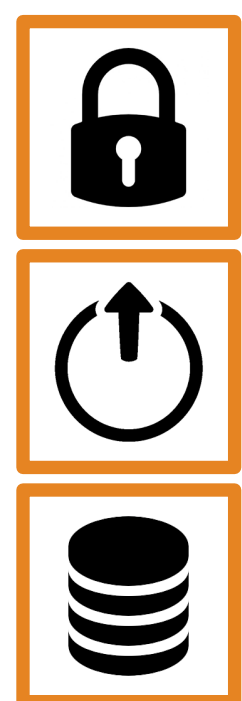


Beacon v2 API

The Beacon API v2 proposal opens the way for the design of a simple but powerful **"genomics API"**.



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The GA4GH Phenopackets v2 Standard

A Computable Representation of Clinical Data

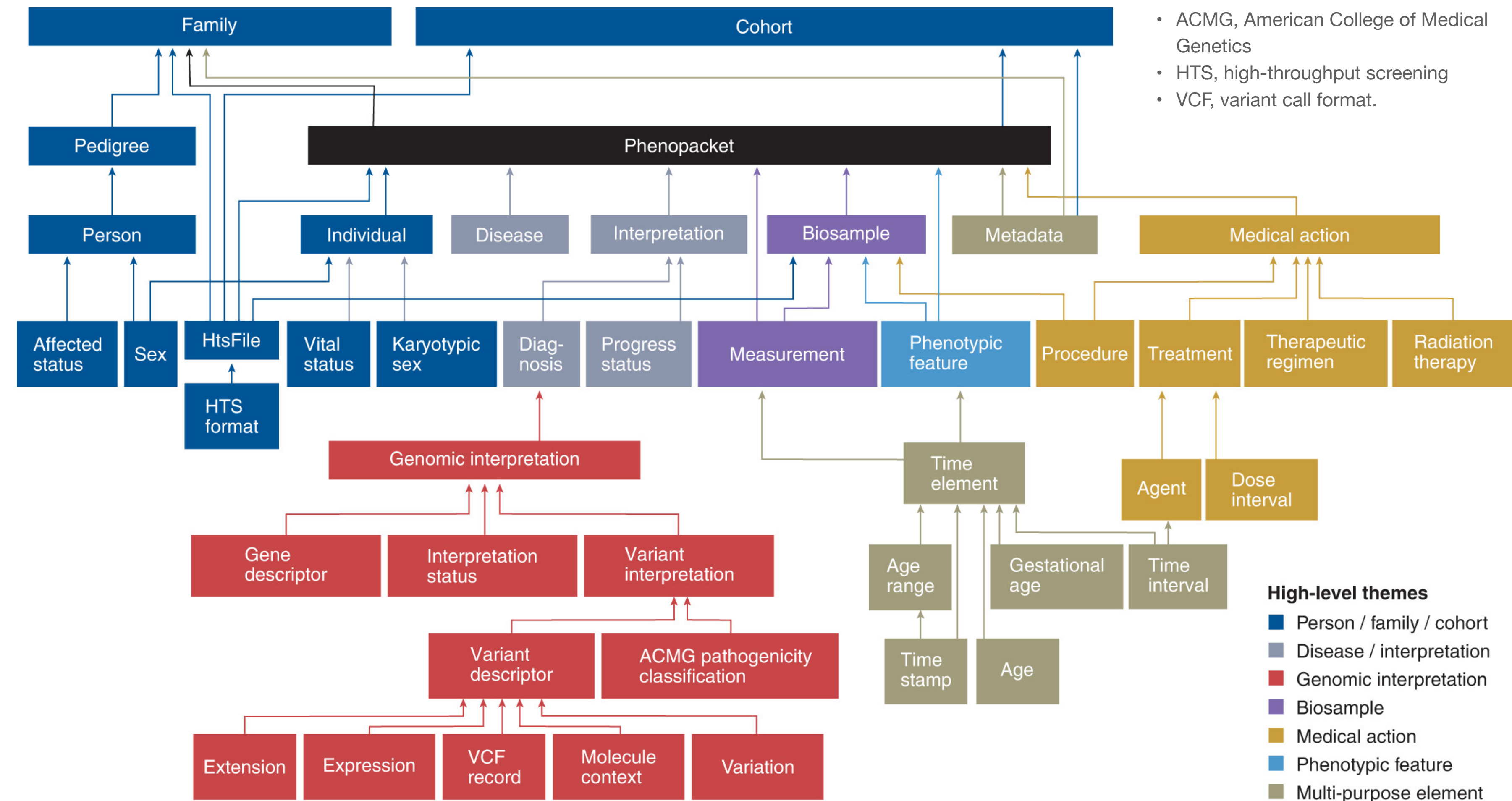


The GA4GH Phenopacket schema consists of several optional elements, each containing information about a certain topic, such as phenotype, variant or pedigree. An element can contain other elements, which allows a hierarchical representation of data.

For instance, Phenopacket contains elements of type *Individual*, *PhenotypicFeature*, *Biosample* and so on. Individual elements can therefore be regarded as **building blocks** of larger structures.

Jacobsen JOB, Baudis M, Baynam GS, Beckmann JS, Beltran S, Buske OJ, Callahan TJ, *et al.* 2022.

The GA4GH Phenopacket Schema Defines a Computable Representation of Clinical Data.
Nature Biotechnology 40 (6): 817–20.



Onboarding

Demonstrating Compliance

- Progenetix Beacon+ has served as implementation driver since 2016
- Beacon v2 as service with protocol-driven registries for federation
- GA4GH approved Beacon v2 in April 2022

Beacon v2 GA4GH Approval Registry

Beacons:    

 **European Genome-Phenome Archive (EGA)**

GA4GH Approval Beacon Test

This [Beacon](#) is based on the GA4GH Beacon [v2.0](#)

Visit us
Beacon API
Contact us

BeaconMap	Matches the Spec
Bioinformatics analysis	Matches the Spec
Biological Sample	Matches the Spec
Cohort	Matches the Spec
Configuration	Matches the Spec
Dataset	Matches the Spec
EntryTypes	Matches the Spec
Genomic Variants	Matches the Spec
Individual	Matches the Spec
Info	Matches the Spec
Sequencing run	Matches the Spec

 **Theoretical Cytogenetics and Oncogenomics group at UZH and SIB**

Progenetix Cancer Genomics Beacon+ Beacon+ provides a forward looking implementation of the Beacon v2 API, with focus on structural genome variants and metadata based on the...

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 **Centre Nacional Analisis Genomica (CNAG-CRG)**

Beacon @ RD-Connect

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BeaconMap	Matches the Spec
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 **University of Leicester**

Cafe Variome Beacon v2

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Matches the Spec Not Match the Spec Not Implemented



Genomic Data & Privacy - Key Areas

- **Re-identification**

- ▶ identification of an individual based on sets of genomic variants they (or close relatives) carry - so one needs some genome data first
- ▶ information to be gained is circumstantial (e.g. their genome is in a particular disease related dataset)
- ▶ currently only risk with some practical use (e.g. **long-range familial attacks**)

- **Genotype-to-Phenotype (G2P) attacks**

- ▶ determination of some disease risk or phenotypic features from a genome itself
- ▶ needs access to genome data which is illegal in many jurisdictions (but technically more & more feasible)
- ▶ real-world use cases are limited but abuse through wrong perception of utility

- **Genomic Determinism**

- ▶ assignment of individual abilities and personal development trajectories from genomic profiling
- ▶ topic of (some good, most bad) SciFi
- ▶ but: **Wehret den Anfängen!**

Technical, legal and ethics aspects of genomic data sharing

DSI Proposal Summary

- The area of "personalized" or "precision" health relies on the use of molecular characteristics - e.g. inherited genomic variations or mutations in a tumor genome - to tailor individual recommendations in such diverse areas as nutrition, pharmaceutical selection and dosing or use of preventive screening, up to the tailoring of antineoplastic therapies based on the molecular profiling of a patient's cancer cells. While it has been widely recognized that many of these applications can provide personal health benefits and have a positive impact on society at large, large questions remain regarding the secondary use of genomic data, the potential dangers arising from collection, storage and sharing of genomic information as well as the associated legal regulations.
- The need to have access to an ever increasing set of genomic data for biomedical research and treatment decisions is being addressed on an international level through such efforts as the Global Alliance for Genomics and Health **GA4GH** - of which **UZH is a founding member** - or European B1MG initiative. The Swiss Personalized Health Network **SPHN** provides the technical and logistic backbone for the exchange of genomic and clinically derived information for research applications and clinical re-use, while not directly generating data itself.
- Issues related to the generation, handling and application of personal genomic information span a large set of academic specialities, from **medicine, life science** research, **computational science** and **data security** to **ethics, law, psychology** as well as **communication** and **media sciences**. The topic of "**Technical, legal and ethics aspects of genomic data sharing**" is a natural fit for the Digital Society Initiative, offering participation and networking opportunities for a wide range of potential stakeholders from different faculties to develop projects in an area with **scientific relevance** and large **public interest**.

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Ethical & Legal Aspects of Genomics Data Sharing

... with special consideration of the Beacon protocol in the Swiss context

- Genomic / "-omics" data are integral part of biomedical research projects and clinical procedures (e.g. personalized cancer therapies, rare diseases...)
- Traditional "data access through research agreement" approaches do not accommodate **federated discovery** & analysis approaches needed in many genomics approaches (population variability, rare variants ...)
- The GA4GH Beacon v2 protocol allows genomic variant & biomedical data discovery on varying granularity (from "Boolean" to "document")
- Beacon is being implemented and considered in many international projects and resources, including Swiss ones (e.g. SPHN & UZH projects)
- What specific regulations & considerations for the different types of data & levels of granularity in the **Swiss** context?

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Getting the discourse

going

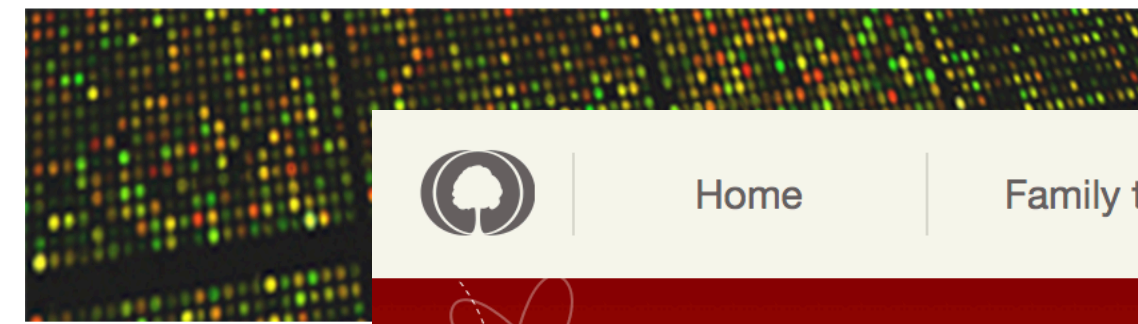
... and feed back to

stakeholders

John Yuyi, NYT 2018-02-09



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- DNA**
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