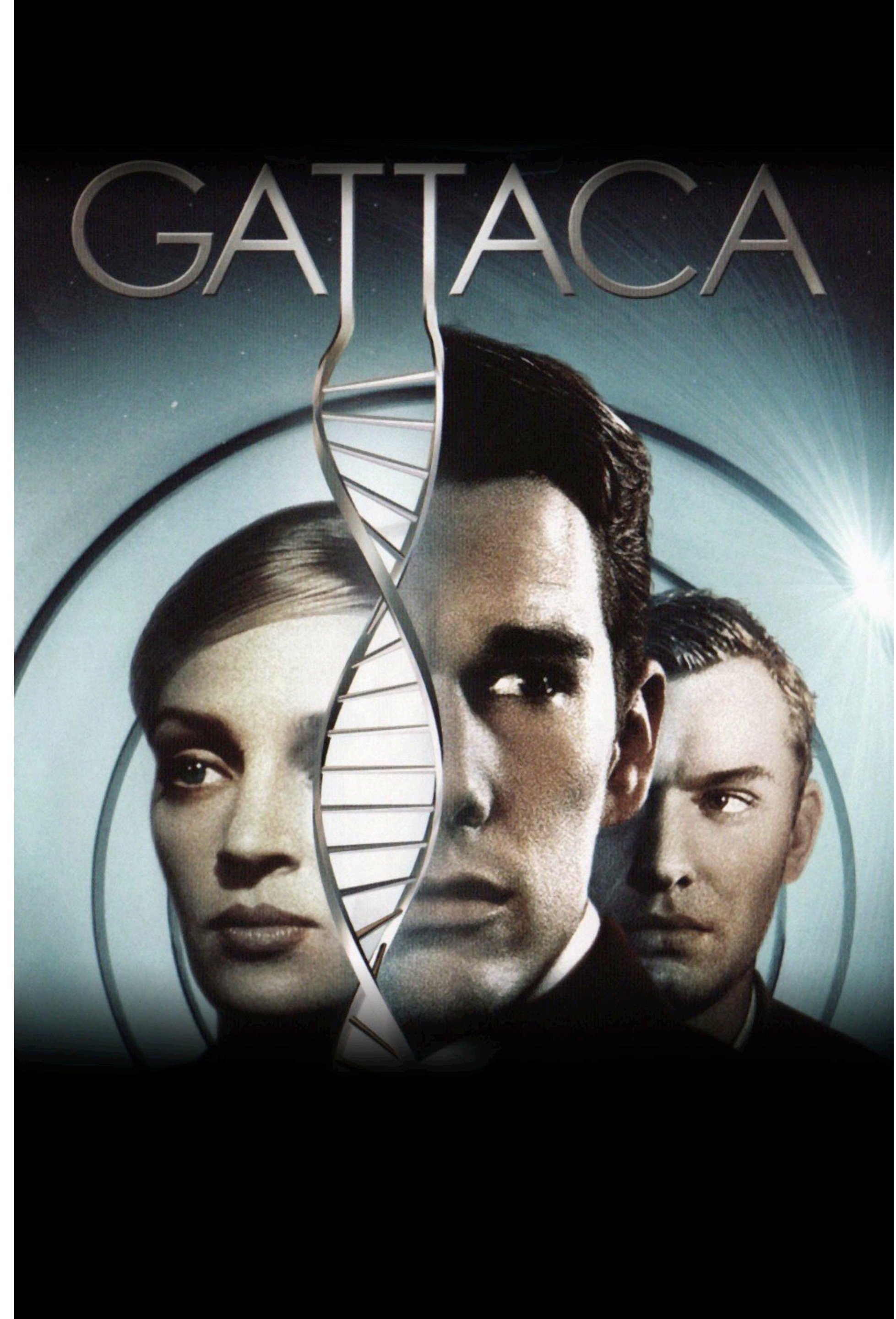


Genomes Privacy Laws Society

Technical, legal and ethics aspects of genomic data sharing

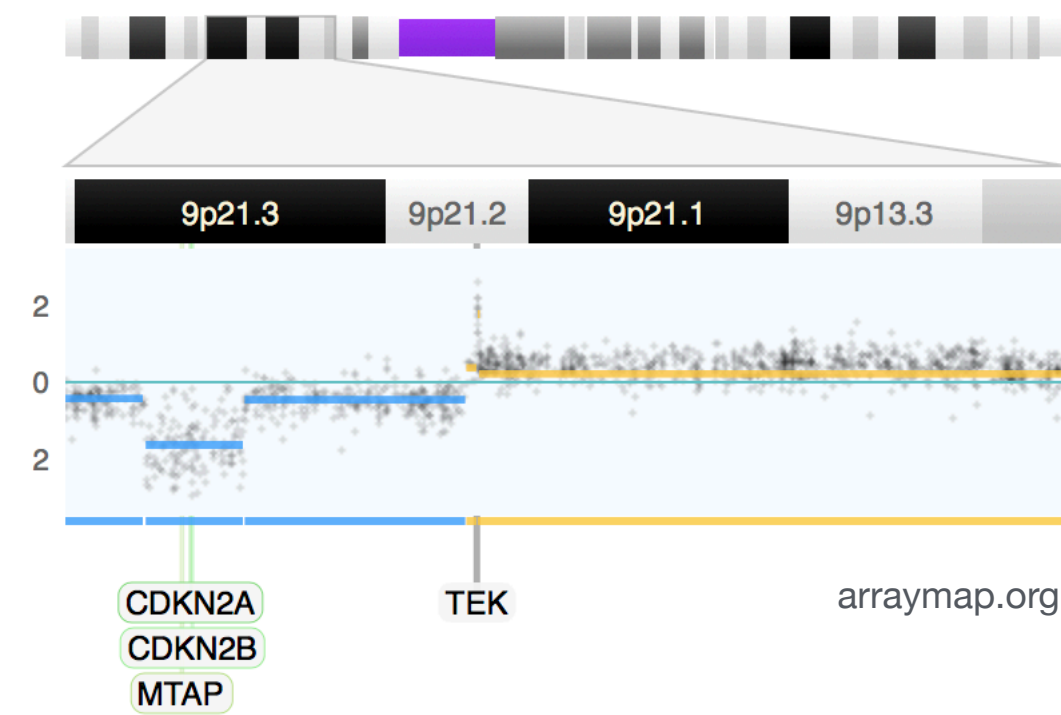
Michael Baudis | DSI Ethics | 2022-01-12



Genome screening at the core of “Personalised Health”

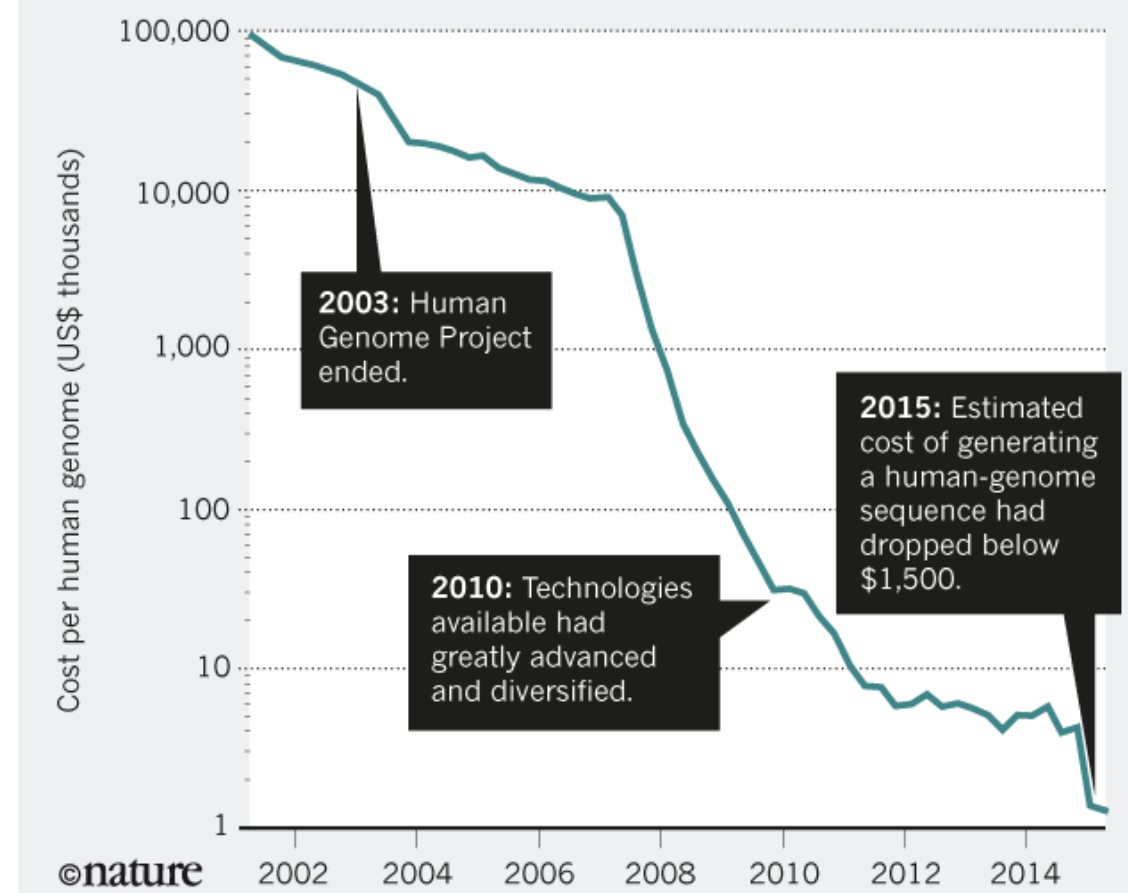
- ▶ **Genome analyses** (including transcriptome, metagenomics) are core technologies for Personalised Health™ applications
- ▶ The unexpectedly large amount of **sequence variants** in human genomes - germline and somatic/cancer - requires huge analysis efforts and creation of **reference repositories**
- ▶ **Standardized data formats** and **exchange protocols** are needed to connect these resources throughout the world, for reciprocal, international **data sharing** and **biocuration** efforts
- ▶ Our work @ UZH:

- ▶ **cancer** genome repositories
- ▶ **biocuration**
- ▶ **protocols & formats**

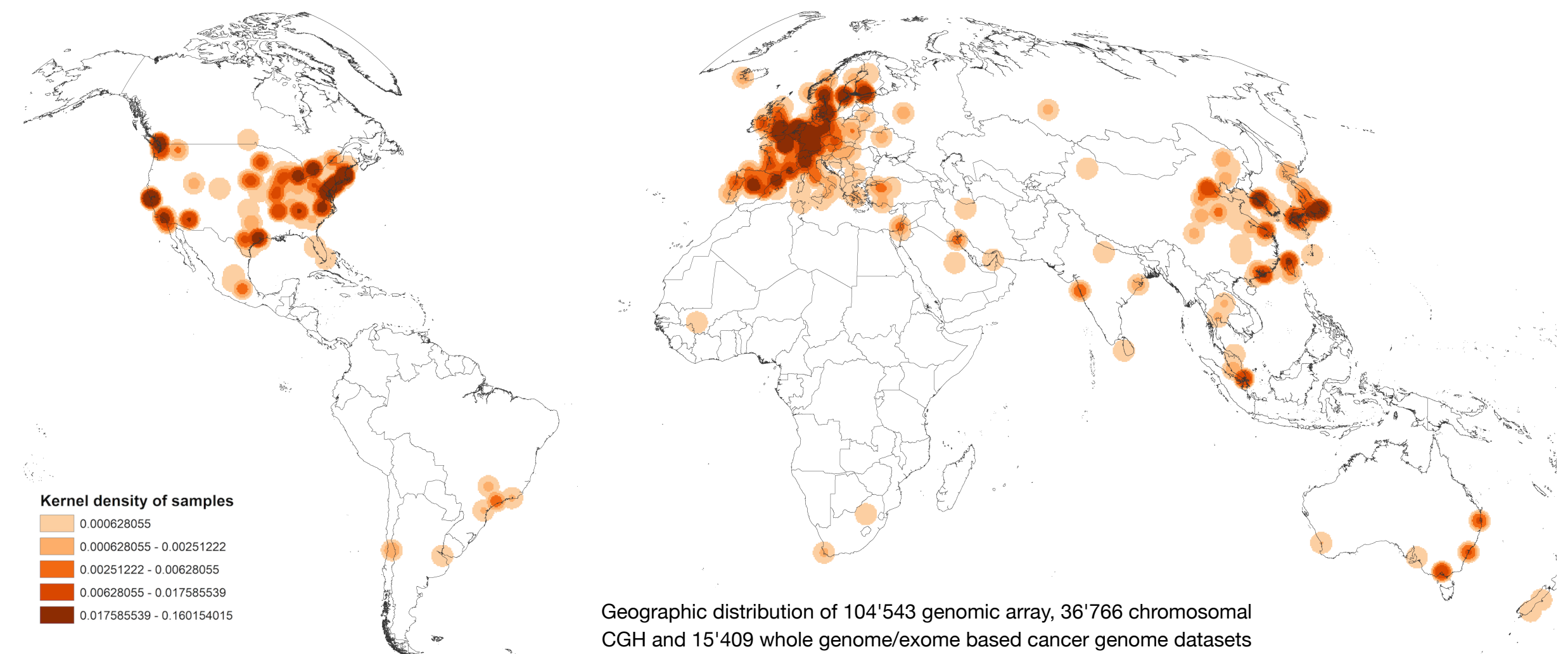


BETTER, CHEAPER, FASTER

The cost of DNA sequencing has dropped dramatically over the past decade, enabling many more applications.



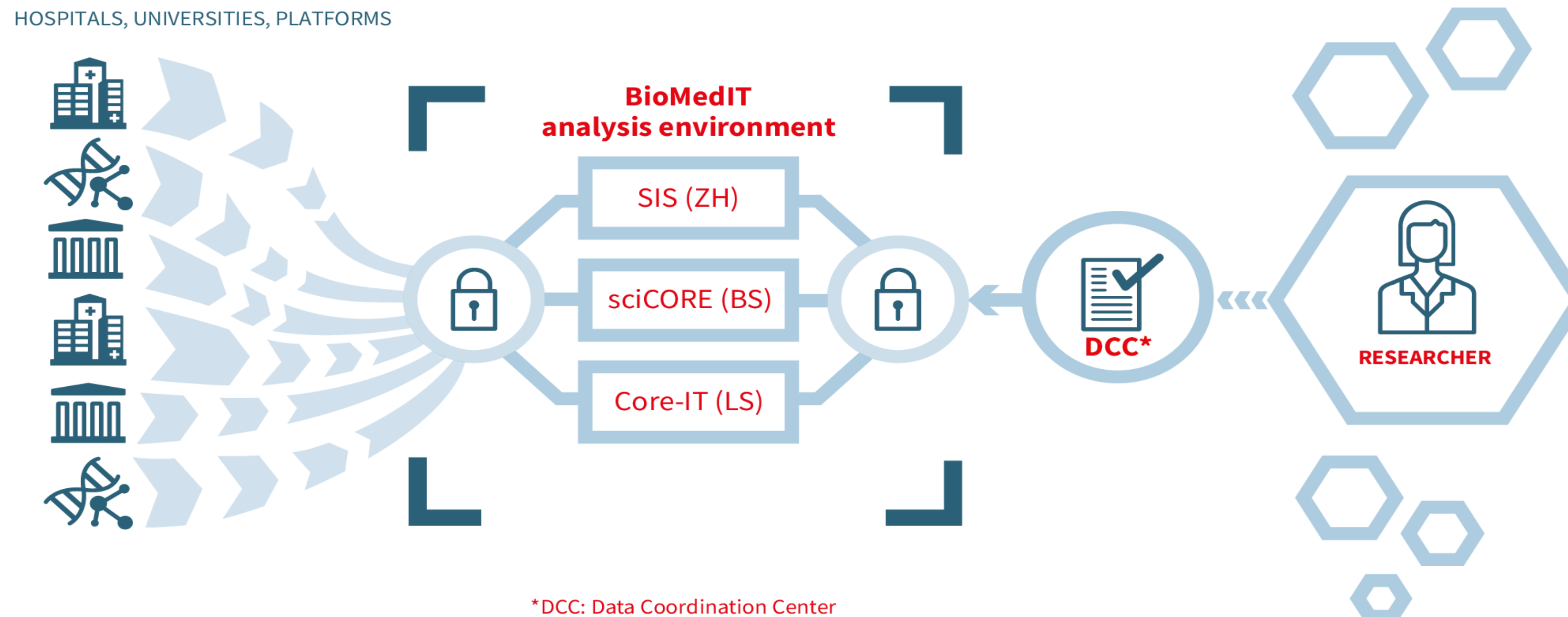
The future of DNA sequencing. Eric D. Green, Edward M. Rubin & Maynard V. Olson. Nature; 11 October 2017 (News & Views)



Geographic distribution of 104'543 genomic array, 36'766 chromosomal CGH and 15'409 whole genome/exome based cancer genome datasets

The BioMedIT network

BioMedIT provides researchers with access to a secure and protected computing environment for analysis of sensitive data without compromising data privacy



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

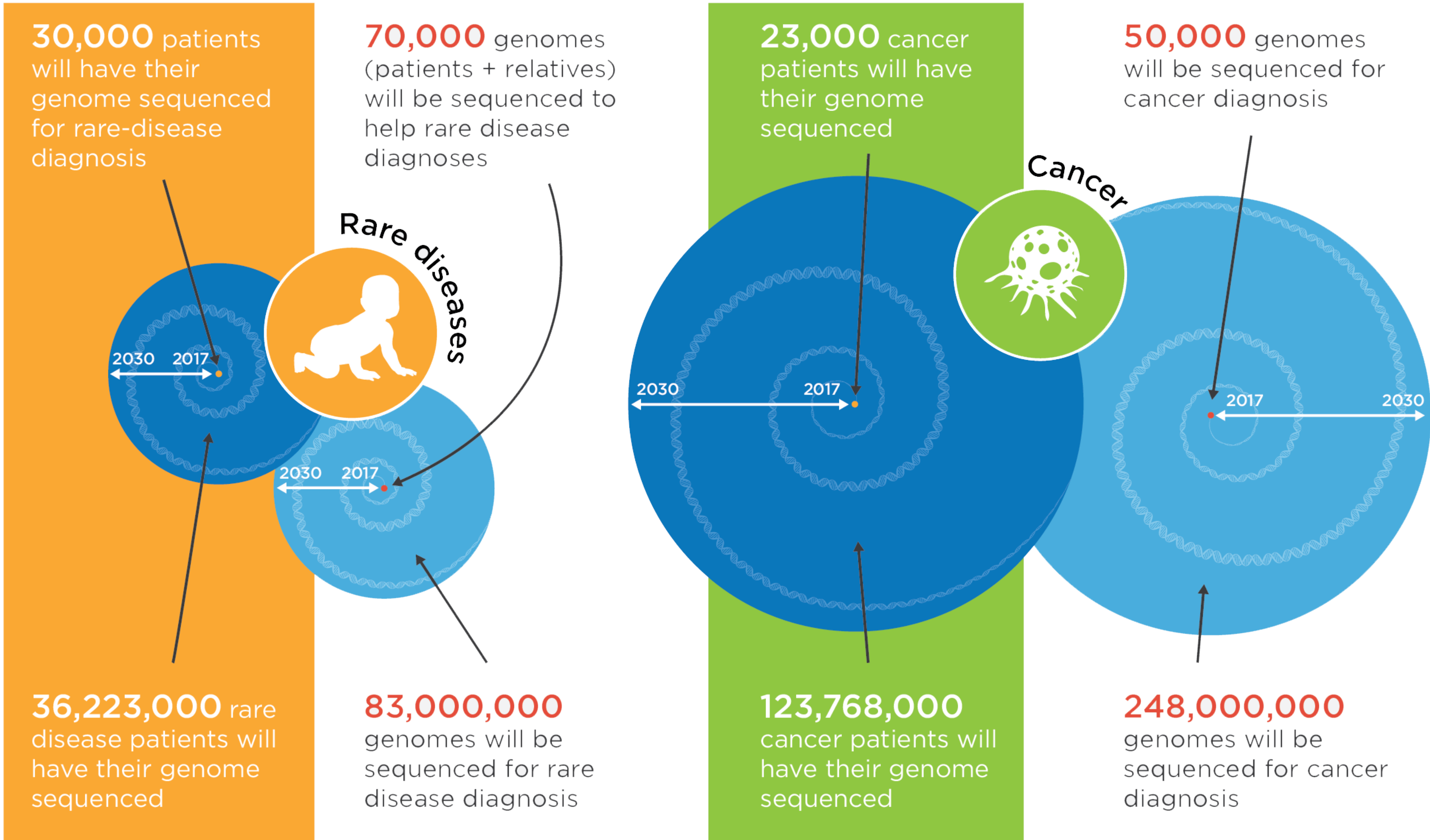
2030*

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

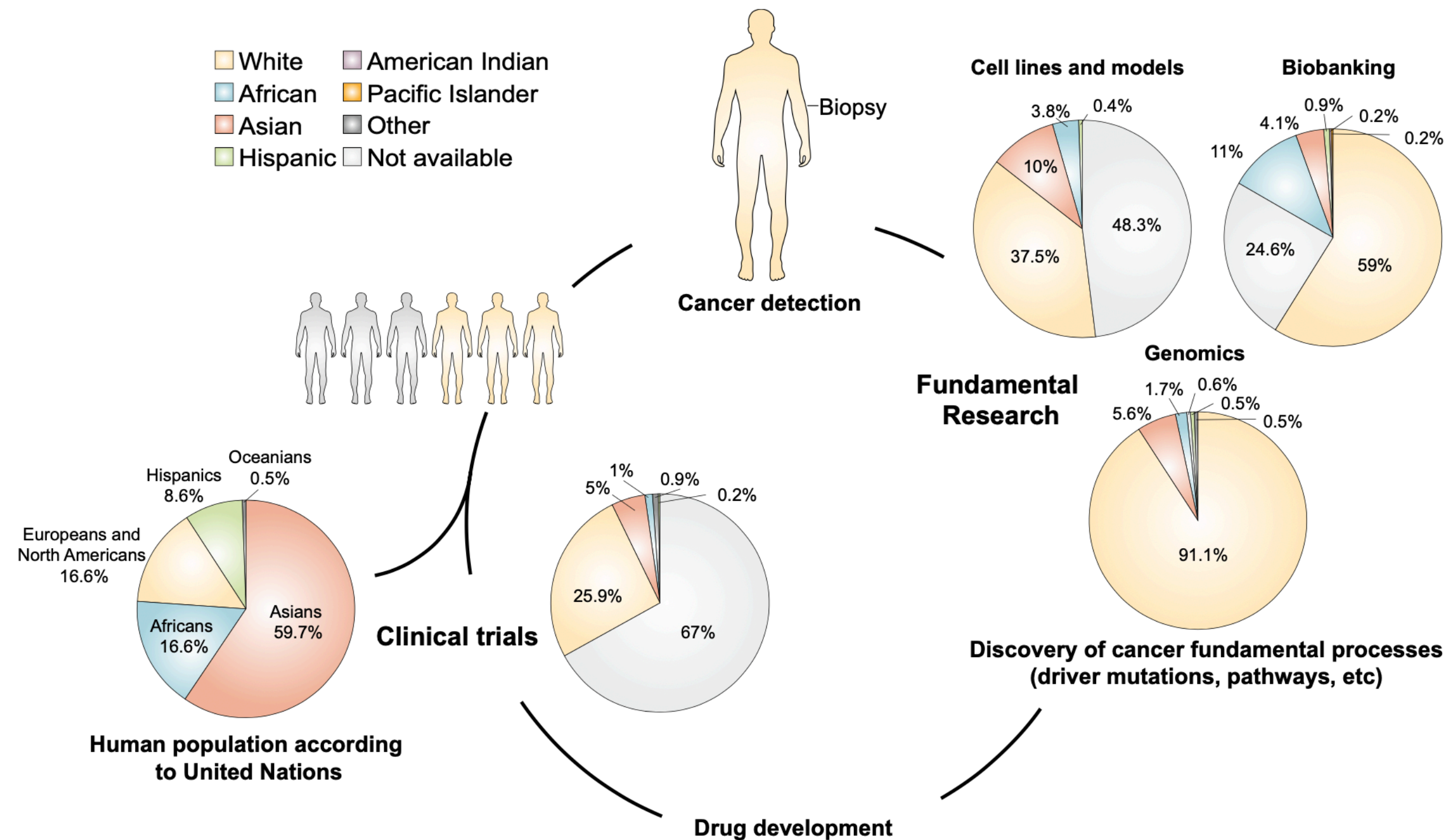


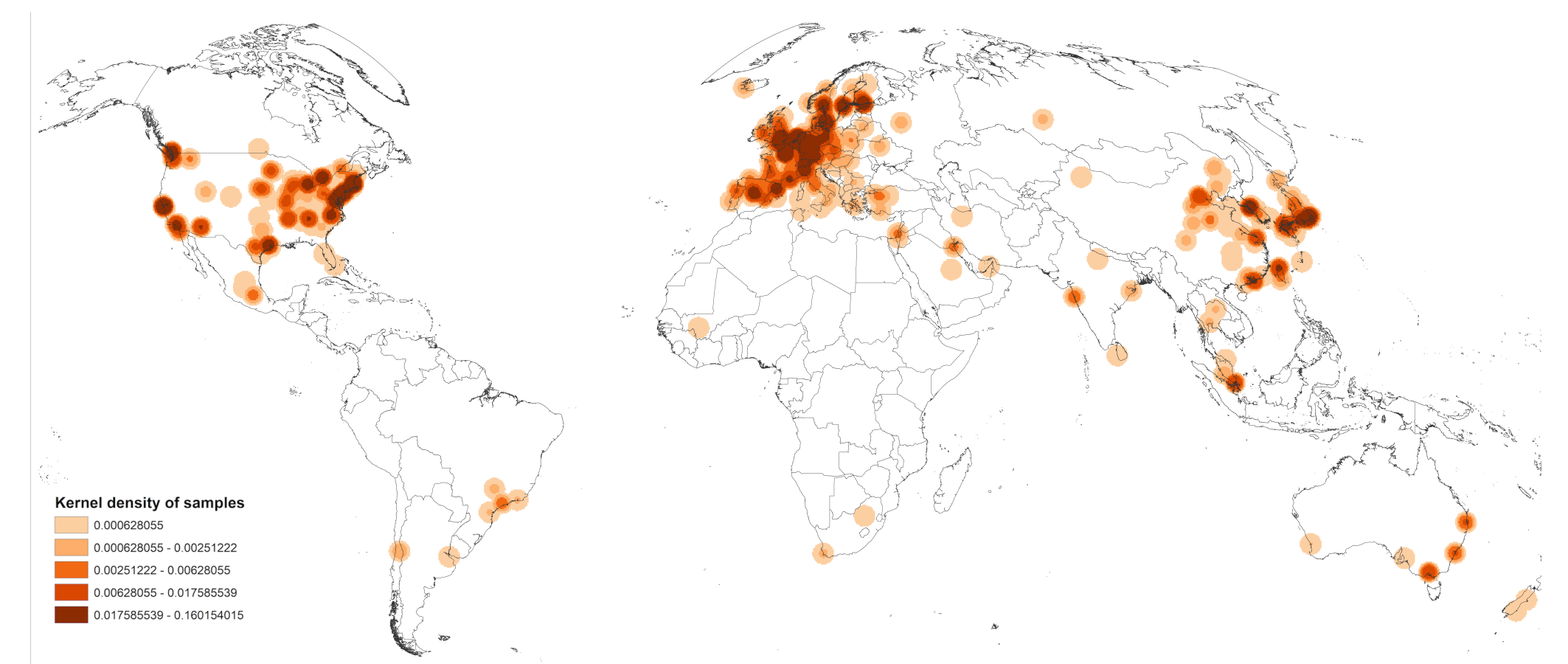
Figure 1. Racial/Ethnic disparities in cancer research. Racial/ethnic inclusion was studied in several aspects of oncological research, from cell lines and patient-derived xenografts to biobanking, genomics and clinical trials.

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





Enabling genomic data sharing for the benefit of human health

The Global Alliance for Genomics and Health (GA4GH) is a policy-framing and technical standards-setting organization, seeking to enable responsible genomic data sharing within a **human rights framework**

 **Genomic Data Toolkit** →

 **Regulatory & Ethics Toolkit** →

 **Data Security Toolkit** →

[VIEW OUR LEADERSHIP](#)

[MORE ABOUT US](#)

[BECOME A MEMBER](#)

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 ...

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*

SCIENCE 10 JUNE 2016 • VOL 352 ISSUE 6291

GA4GH API promotes sharing

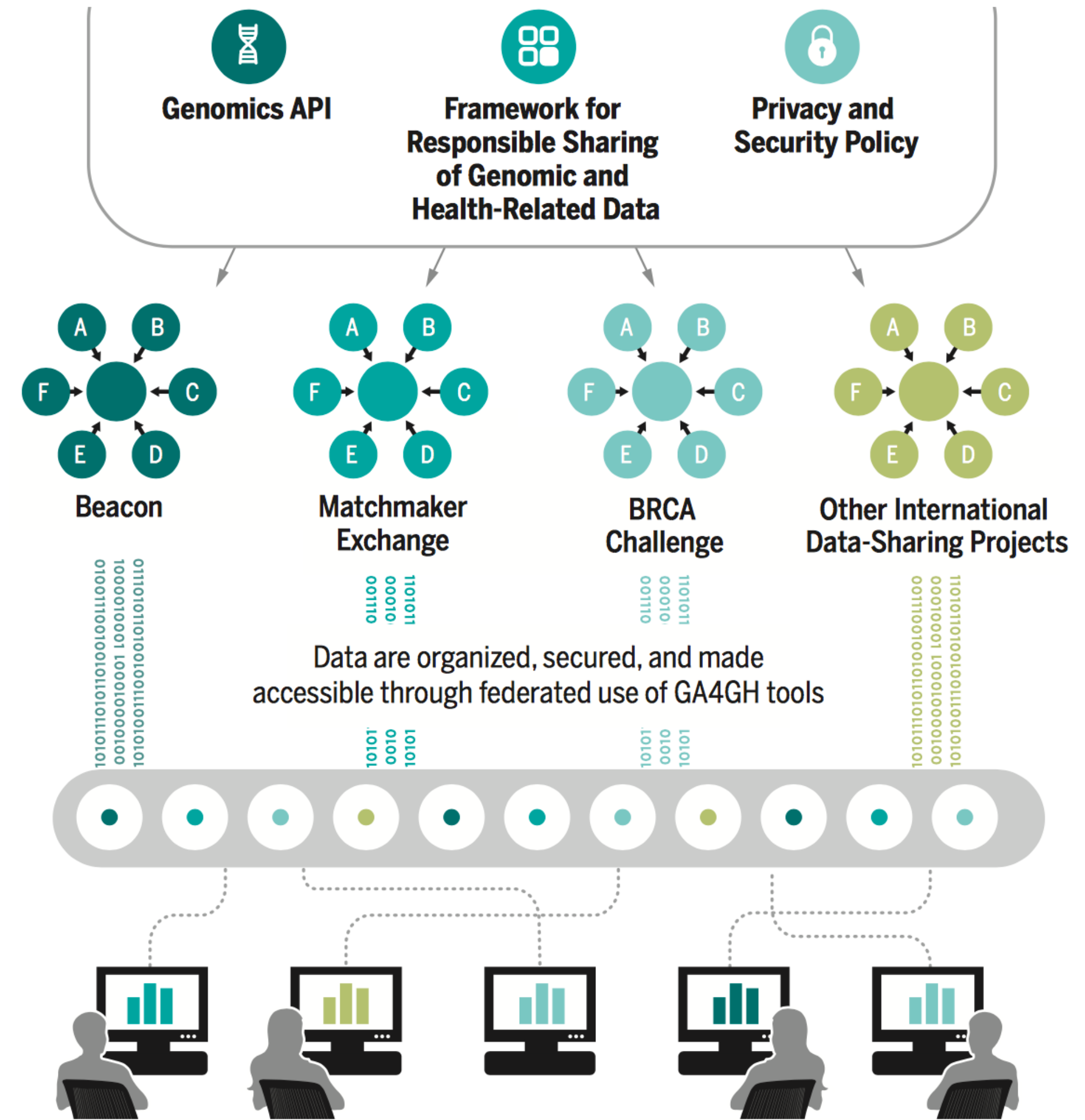


GENOMICS

A federated ecosystem for sharing genomic, clinical data

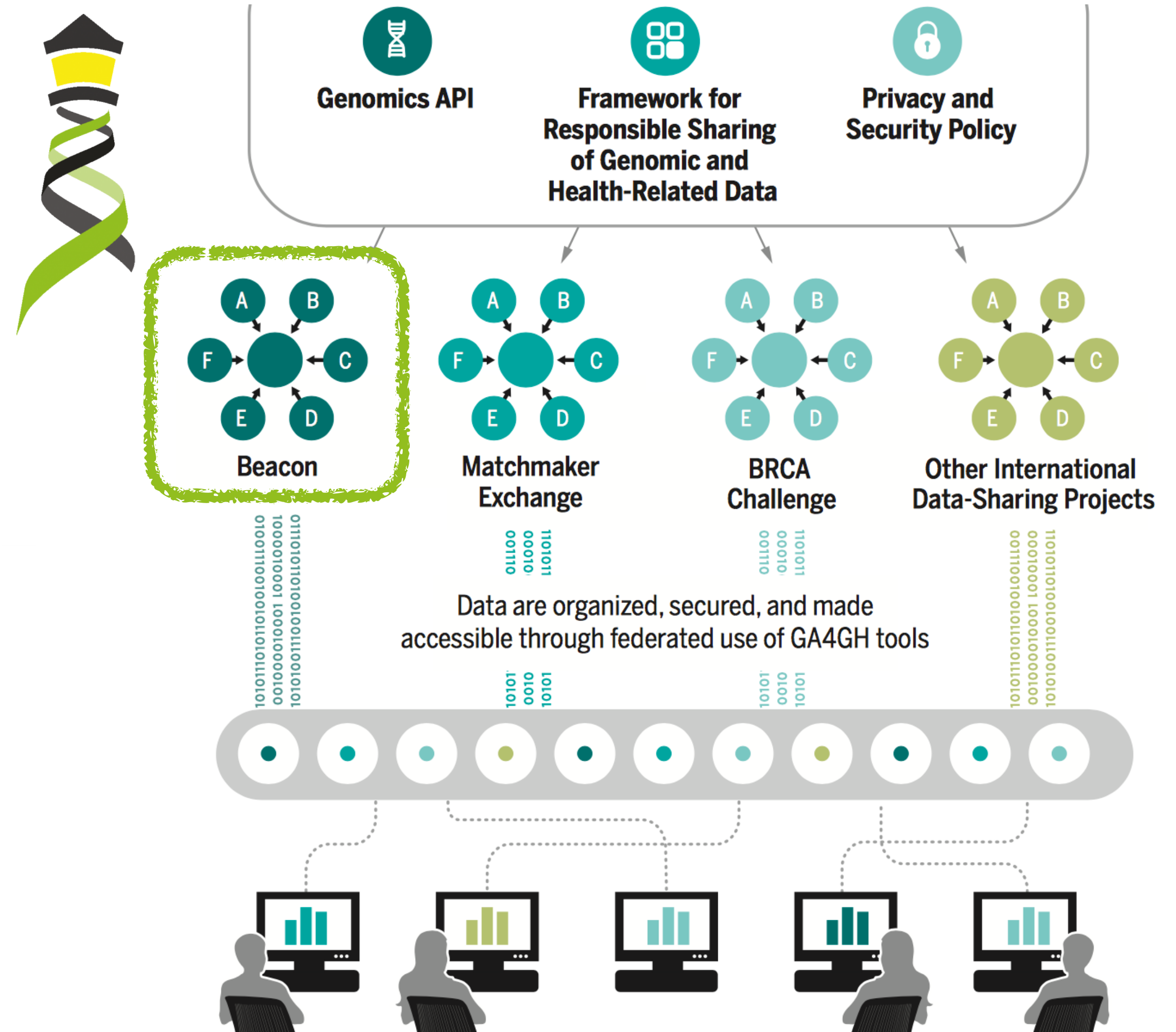
Silos of genome data collection are being transformed into seamlessly connected, independent systems

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





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





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.

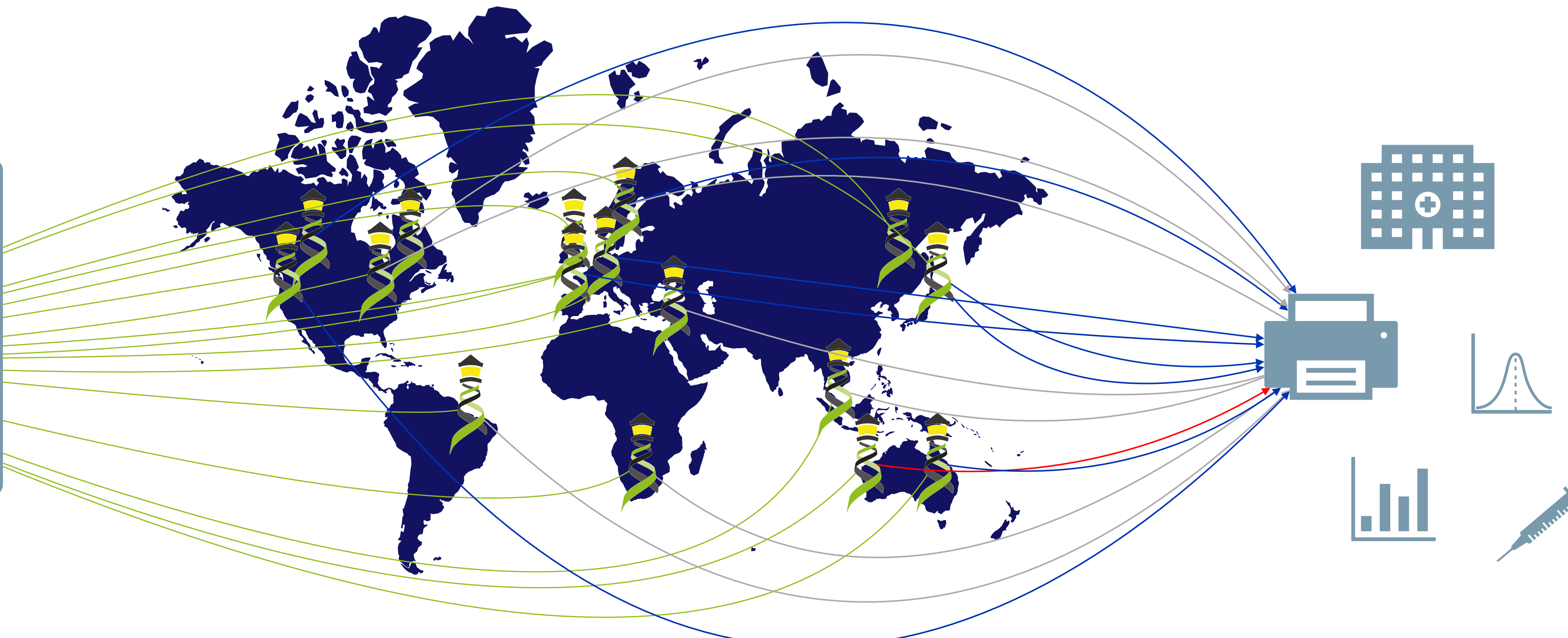
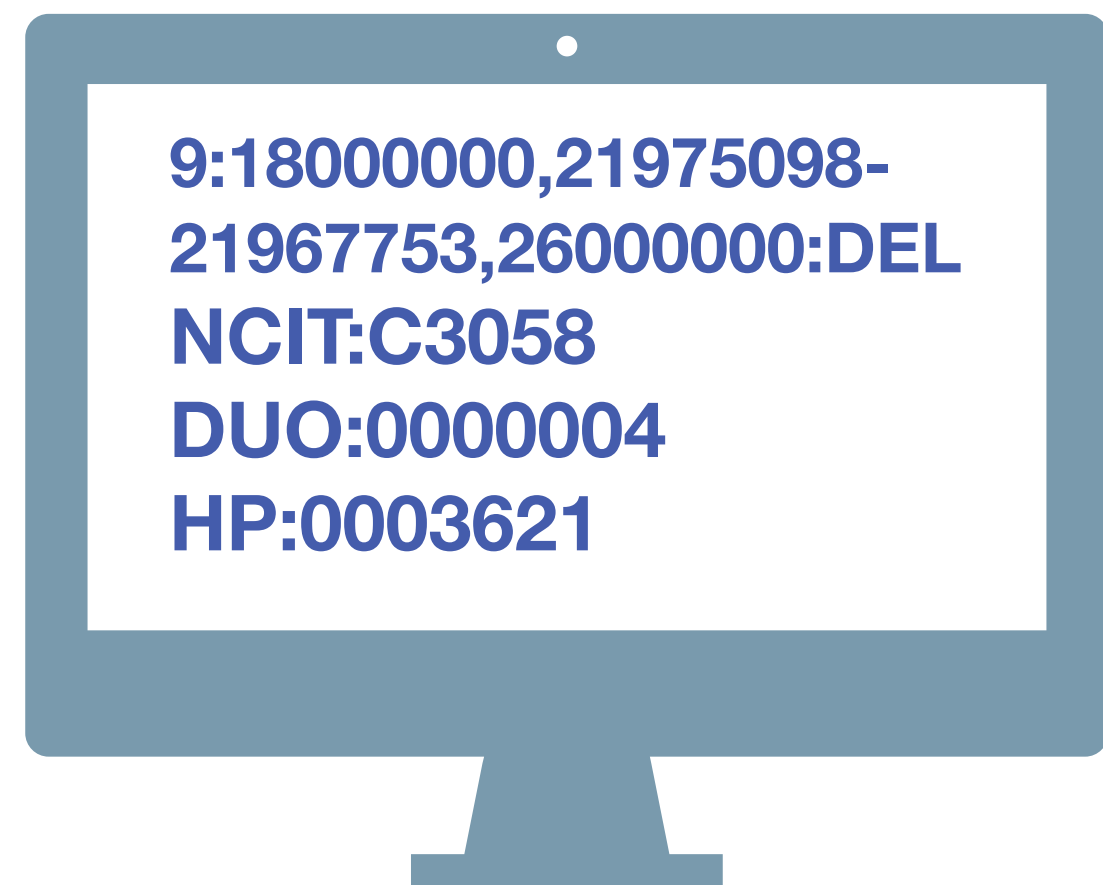
A Beacon network federates
genome variant queries
across databases that
support the **Beacon API**

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

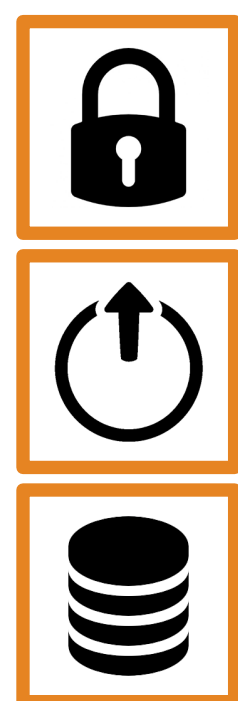


Making Beacons Biomedical - Beacon v2

- Scoping queries through "biodata" parameters
- Extending the queries towards clinically ubiquitous variant formats
 - ▶ cytogenetic annotations, named variants, variant effects
- Beacon queries as entry for **data delivery**
 - ▶ Beacon v2 permissive to respond with variety of data types
 - Phenopackets, biosample data, cohort information ...
 - ▶ handover to stream and download using htsget, VCF, EHRs
- Interacting with EHR standards
 - ▶ FHIR translations for queries and handover ...
- Beacons as part of local, secure environments
- Authentication to enable non-aggregate, patient derived datasets
 - ▶ ELIXIR AAI with compatibility to other providers (OAuth...)



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"**.



Making Beacons Biomedical - Beacon v2

- Scoping queries through "biodata" parameters
- Extending the queries towards clinically ubiquitous variant formats

- ▶ cytogenetic annotations, named variants, variant effects

- Beacon queries as entry for **data delivery**

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- Authentication to enable non-aggregate, patient derived datasets

- ▶ ELIXIR AAI with compatibility to other providers (OAuth...)

Definitely breaks the
"Relative Security
by Design"
Concept!

Mitigation by
tailored
implementation and
security practices

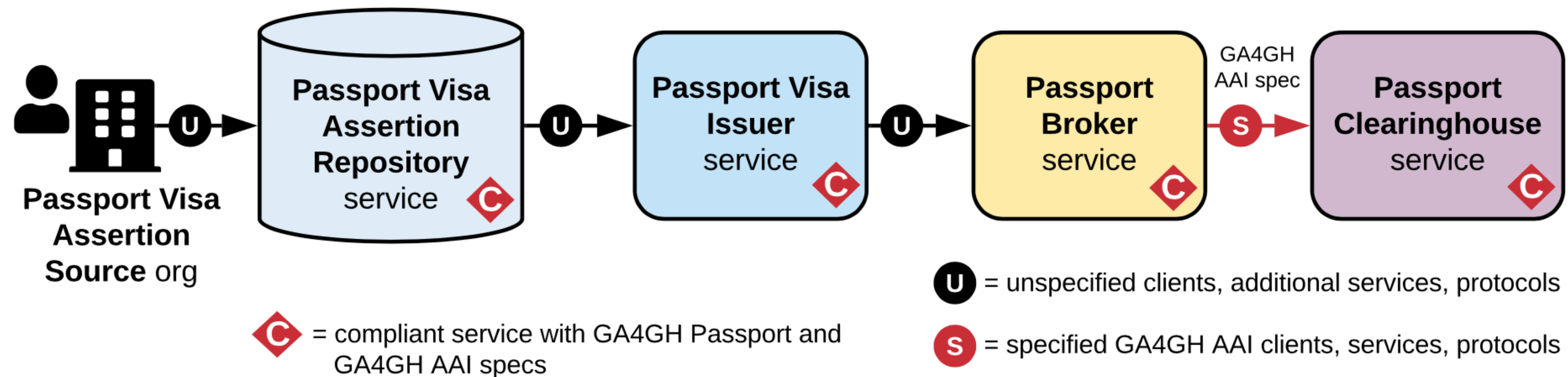
GA4GH Passports



Global Alliance
for Genomics & Health



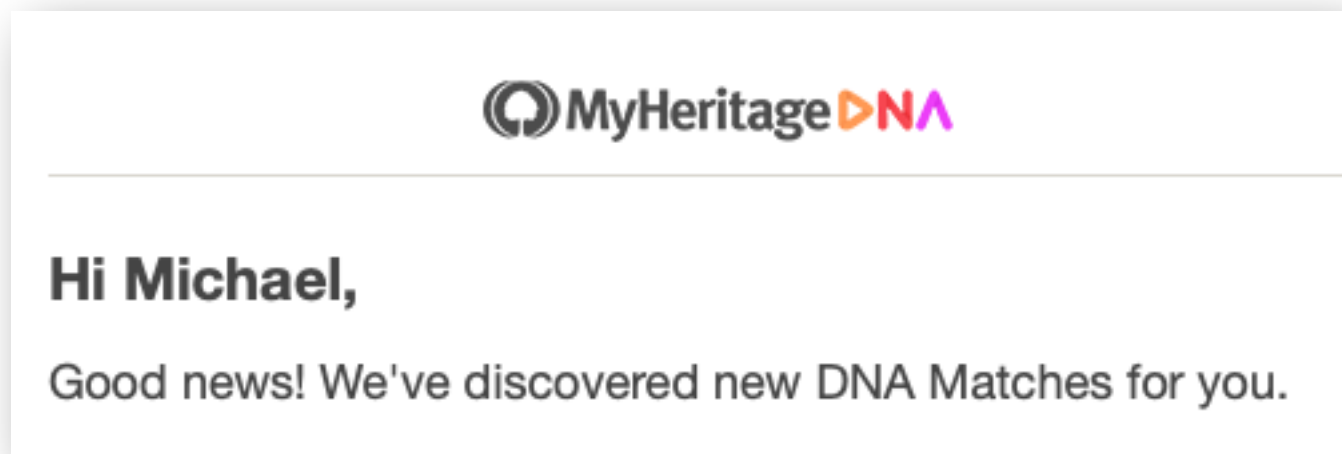
Communicating a user's data access authorizations



www.ga4gh.org/ga4gh-passports/

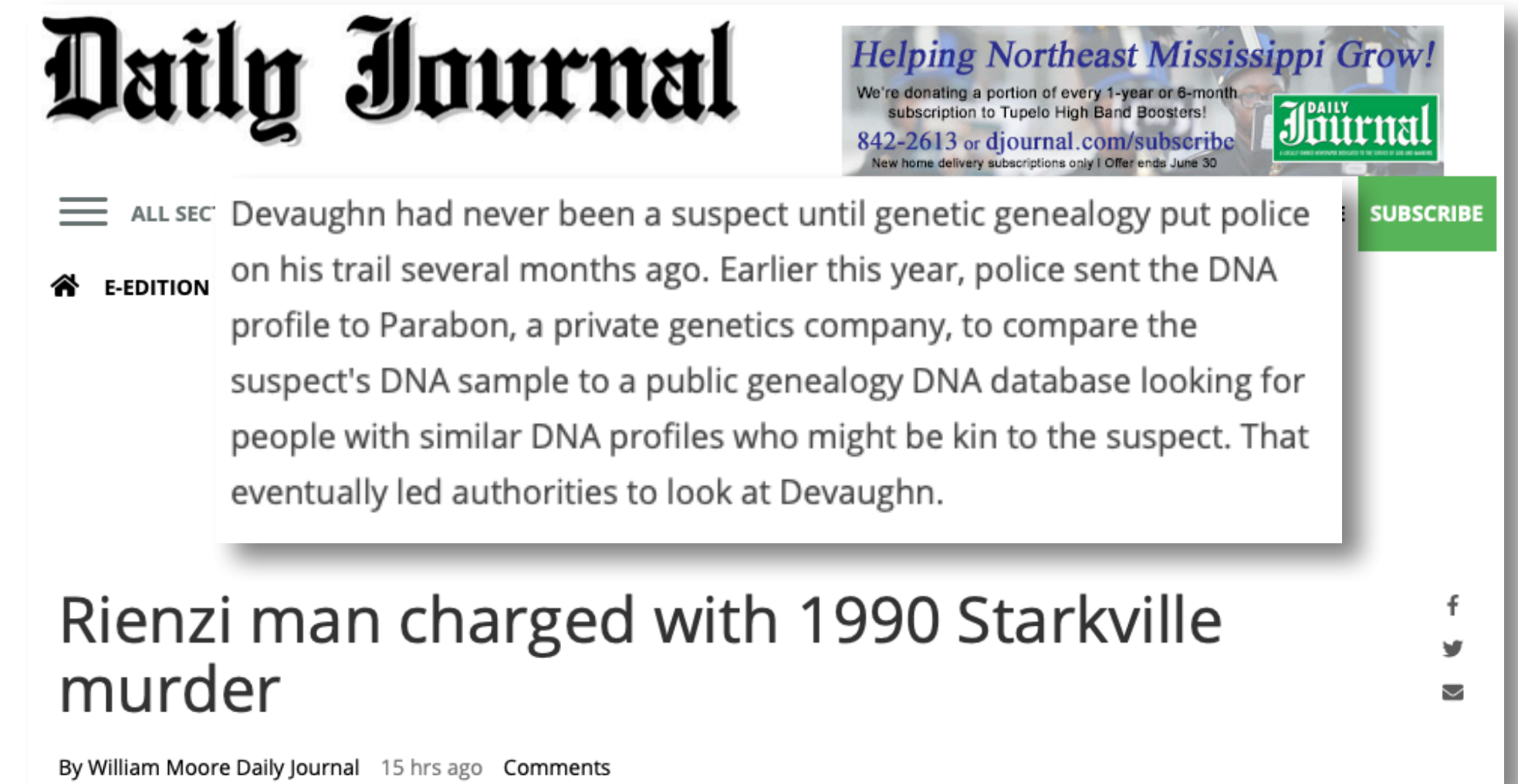
- format to communicate a user's data access authorizations based on either their role (e.g. researcher), affiliation, or access status
- works together with the GA4GH Authentication and Authorization Infrastructure (AAI) OpenID Connect Profile to streamline researchers' data access over federated data access protocols
- both standards approved in Dec 2019 with early implementation by Google Cloud services and ELIXIR





Long-Range Familial Searches

- Commercial, "Direct to Customer" DNA analyses are provided through independent sites and such affiliated to genealogy services (MyHeritage, Ancestry.com, 23andMe...)
- Genealogy sites identify individuals with matching haplotype blocks & provide a prediction about degree of genetic relation
- Law enforcement agencies (and who else?!) can send individual SNP profiles (e.g. recovered from evidence many years after a crime) using a *Jane Doe* identity, to identify relatives of the suspect - **long range familial search**



© Copyright 2018 Daily Journal, 1242 S Green St Tupelo, MS

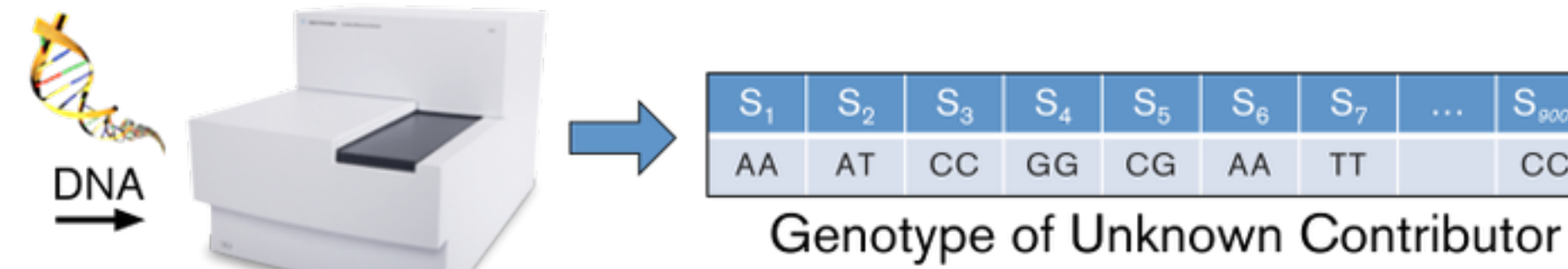


Phenotyping from DNA

From DNA to "Wanted" Posters?

- association of genomic variants with phenotypic data collection
- while hair, eye color are easy targets not useful for relevant phenotypic features especially if large environmental component
- huge biases based on input/collection data
- Belgium and Germany do not allow forensic DNA phenotyping
- Switzerland: Bundesrat decision on 2020-12-04 to allow phenotyping for law enforcement purposes

Paragon Nanolabs Inc.
The Snapshot DNA Phenotyping Service



Snapshot Prediction Results Composite Profile

Snapshot Prediction Results Genomic Ancestry

Region	Pct
Africa	63.3%
Europe	13.6%
Asia	8.8%
Africa	8.5%
North	5.9%

Model #1: Skin Color
 $(2.4) \cdot S_2 + (-1.7) \cdot S_5 + (0.6) \cdot S_{12}$

Model #2: Eye Color
 $(5.3) \cdot S_{16} + (3.6) \cdot S_{21} + (-7.1) \cdot S_{35}$

Model #3: Hair Color
 $(7.4) \cdot S_{12} + (4.3) \cdot S_5 + (1.4) \cdot S_{16}$

Snapshot Models

PARABON NANO LABS Blind Testing and Evaluation of a Comprehensive DNA Phenotyping System

Rachel Wiley¹, Xiangpei Zeng¹, Bobby Larue¹, Ellen M. Greytak², Steven Armentrout², Bruce Budowie^{1,3}

1) Institute of Applied Genetics, Department of Molecular and Medical Genetics, University of North Texas Health Science Center (UNTHSC), Fort Worth, TX; 2) Paragon NanoLabs, Inc., Reston, VA; 3) Center of Excellence in Genomic Medicine Research (CEGMR), King Abdulaziz University, Jeddah, Saudi Arabia

Introduction

DNA phenotyping refers to the prediction of ancestry and/or physical appearance from DNA. In forensics, these predictions have the potential to generate new investigative leads in cases where DNA does not match a known suspect or a database, and to discover more information about unidentified remains. In this study, the Paragon® Snapshot® DNA Phenotyping System, which predicts detailed biogeographic ancestry, pigmentation (eye color, hair color, skin color, and freckling), and face morphology, was evaluated in a blind experiment. This study represents the first public blind evaluation of a comprehensive DNA phenotyping system, including side-by-side comparisons of the composite images and the actual photographs of each subject.

Methods

- 24 subjects recruited for phenotypic and ancestral diversity by the University of North Texas Health Science Center (UNTHSC)
- 25 anonymous DNA samples sent to Paragon, including one two-person mixture (not made known to Paragon, but Paragon readily detected the mixture and identified the contributors)
- Each sample genotyped on the Illumina CytosNP-B50K chip (851,274 SNPs) and run through the Snapshot algorithms
- Phenotype predictions compiled into a detailed report for each subject, including a predicted composite in which differences from the average face for the same sex and ancestry were emphasized
- Age and body mass index (BMI) values then delivered to Paragon, and subjects with large differences from default age (25) and BMI (22) age-progressed by a forensic artist
- Photographs and self-reported ancestry and phenotypes collected by UNTHSC, and predictions for each Level 1 phenotype (sex, pigmentation, ancestry) compared to actual phenotypes
- Next phase will incorporate 3D scanning and craniofacial measurements to assess accuracy of predicted face morphology

Study funded in part by the National Geographic Society

Predictions Vs. Actual Appearance

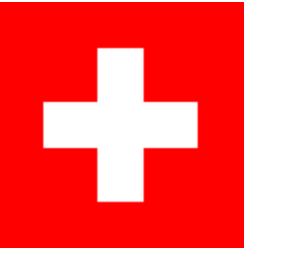
Prediction Results

Conclusions

This study demonstrated the predictive performance of the Paragon Snapshot DNA Phenotyping system. Overall, the predicted features were consistent with the actual phenotypes: skin color, eye color, hair color, freckling, and ancestry. This phase of the study serves as a preliminary assessment of Level 1 detail so that strengths and limitations could be identified to set up a more in-depth analysis of face morphology in phase 2.

"When the New York Times ran an informal test of the Paragon system with one of its reporters, it failed badly." (ACLU.org)

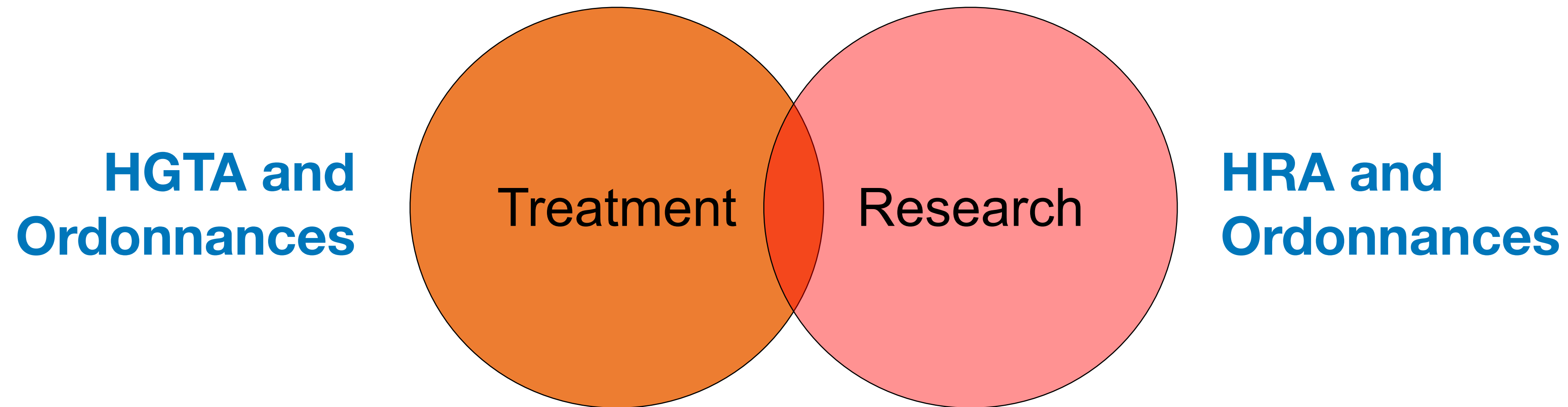
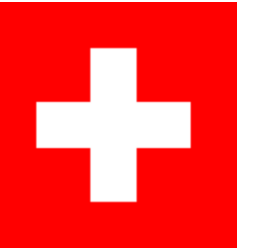
Federal Act on the Use of DNA Profiles in Criminal Proceedings and for Identifying Unidentified or Missing Person, DNA Profiles Act



An Area in Transition...

- Currently: «Genetic Fingerprint»
- Future: Will it be allowed to take a deeper look and how far can genetic data be used to determine the characteristics of an unknown perpetrator (colour of hair and eyes, height, ethnicity, etc.)
- Switzerland: Bundesrat decision on 2020-12-04 to allow phenotyping for law enforcement purposes

Law's View on Modern Medicine



- How do we handle the growing overlap area?
 - ➔ unclear; current legislative movement:
HRA will relate more to HGTA in the future

HGTA : Federal
Act on Human
Genetic Testing

HRA: Human
Research Act

HGTA : Federal Act on Human Genetic Testing

HGTA new (probably 2021)	medical field	outside the medical field	
Investigated characteristics	medical relevant	especially protective values characteristics	other characteristics
General Requirements	Non-discrimination, information and consent, right to information, right not to know, avoidance of surplus information, protection of samples and genetic data, Circulation concerning public advertising, state of science and technology, penal provisions		
Initiation	Physician	Health professional (controlled taking of samples)	Consumer (DTC)
Persons concerned	Persons with and without capacity of judgement, pregnant woman (PND)	ONLY persons with Capacity of judgement	ONLY persons with Capacity of judgement
Communication of surplus information	as a rule according to decision of the person concerned	Not allowed	Not allowed
Laboratory	subject to authorization (cyto and molecular genetic studies)	subject to authorization (cyto and molecular genetic studies)	not subject to authorisation
Employers and Insurance institutions	Studies and Recovery of Results / Data only in regulated exceptional cases	Prohibition to carry out investigations and the Recovery of Results / Data	Prohibition to carry out investigations and the Recovery of Results / Data

Is Genomic Data Special?

Health Related Data & Privacy

Considerations when evaluating risks of data sharing

- Is the genetic condition outwardly visible?
- How severe is it? (serious disease, penetrance, age of onset)
- Is it associated with what could be considered to be stigmatizing health information (e.g., associated with mental health, reproductive care, disability)?
- Is it familial (i.e., potential carrier status/reproductive implications for family/relatives)?
- Does it provide information about the likely geographical location of individuals?
- Does it provide information about ethnicity that may be considered potentially stigmatizing information?

Sharing health-related data: a privacy test?

Stephanie OM Dyke¹, Edward S Dove² and Bartha M Knoppers¹

Greater sharing of potentially sensitive data raises important ethical, legal and social issues (ELSI), which risk hindering and even preventing useful data sharing if not properly addressed. One such important issue is respecting the privacy-related interests of individuals whose data are used in genomic research and clinical care. As part of the Global Alliance for Genomics and Health (GA4GH), we examined the ELSI status of health-related data that are typically considered 'sensitive' in international policy and data protection laws. We propose that 'tiered protection' of such data could be implemented in contexts such as that of the GA4GH Beacon Project to facilitate responsible data sharing. To this end, we discuss a Data Sharing Privacy Test developed to distinguish degrees of sensitivity within categories of data recognised as 'sensitive'. Based on this, we propose guidance for determining the level of protection when sharing genomic and health-related data for the Beacon Project and in other international data sharing initiatives.

npj Genomic Medicine (2016) 1, 16024; doi:10.1038/npjgenmed.2016.24; published online 17 August 2016

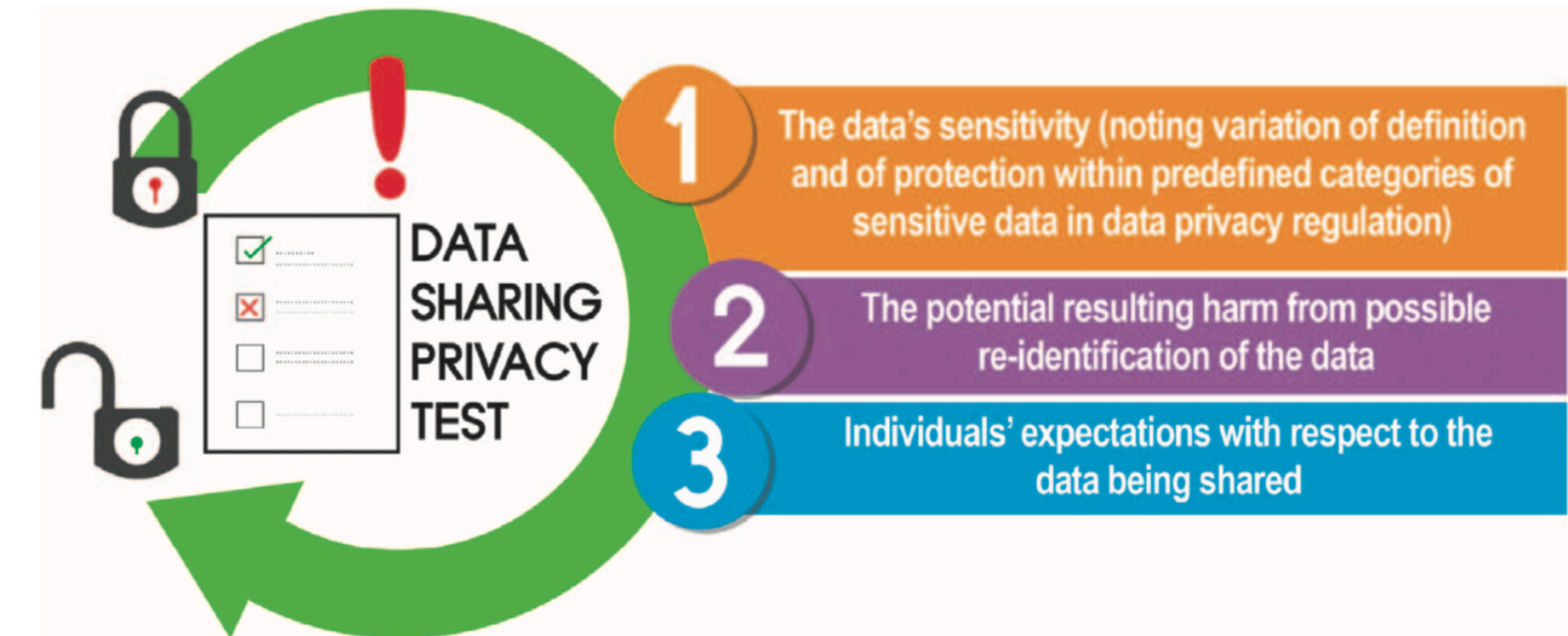
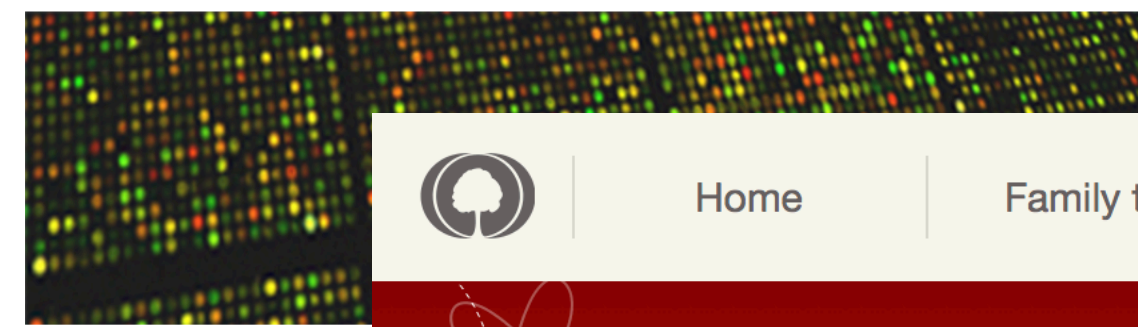


Figure 1. The three steps of a Data Sharing Privacy Test to distinguish degrees of data sensitivity within categories of data recognised as 'sensitive'.

John Yuyi, NYT 2018-02-09



Welcome to openSNP



openSNP lets customers of direct-to-customer genetic tests publish their test results, find others with similar genetic

- Home
- Family tree
- Discoveries
- DNA**
- Research

For Genotyping Users

Upload Your Genotyping File

Upload your raw genotyping

MyHeritage DNA

Valentine's Day **DNA SALE**

Only **59€** per kit ~~89€~~
When ordering 2+ kits

[Order now](#)

Shipping not included
Ends February 14th



Find out what your DNA says about you and your family.

- See how your DNA breaks out across 31 populations worldwide
- Discover DNA relatives from around the



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THE AVERAGE BRITISH PERSON'S DNA IS ONLY 36% BRITISH

GROW YOUR TREE

Find your ancestors in

ancestryDNA

Discover

“We’re an information economy. They teach you that in school. What they don’t tell you is that it’s impossible to move, to live, to operate at any level without leaving traces, bits, seemingly meaningless fragments of personal information. Fragments that can be retrieved, amplified”

–William Gibson in "Johnny Mnemonic" (1986)

Improving Data Privacy but Empowering Beneficial Use

Intersecting Areas of Development

- Make genomic (and functional) data "obfuscated" for malicious use
 - ▶ e.g. spiking / randomization of variants in "not-disease" loci
- access protection with defined user access using standardized protocols for users' roles and permissions, in contrast to individual per user, per dataset access requests over data access committees (DACs)
 - ▶ digital "differential" consent using e.g. data use ontologies
- intentional and unintentional (!) data providers have to be protected from abuse by legal regulations - though thin line regarding "overzealous" use by law enforcement
- alternative solution for active consent
 - ▶ encrypted wide-area networking solutions with managed access control (e.g. SPHN's BiomedIT) and limited access to anonymized data (e.g. using the Beacon protocol with "handover" scenarios)
 - ▶ (genomic) data ownership by the individual "data donors, together with strong privacy protection by law

Modernizing Patient Consent

forward looking, transparent and technically feasible regulations for enabling access to research material and data while empowering *patients*

Generalkonsent: Eine einheitliche Vorlage soll schweizweite Forschung erleichtern

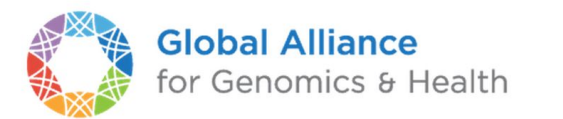
Art des Forschungsmaterials	Biologisches Material und genetische Daten	Nicht-genetische Daten
Personenbezug		
Unverschlüsselt (identifizierend)	Information + Einwilligung in jedes einzelne Forschungsprojekt	Information über Weiterverwendung für zukünftige noch unbestimmte Forschungsprojekte + Generalkonsent für Forschungszwecke
Verschlüsselt	Information über Weiterverwendung für zukünftige noch unbestimmte Forschungsprojekte + Generalkonsent für Forschungszwecke	Information über Weiterverwendung für zukünftige noch unbestimmte Forschungsprojekte + über Möglichkeit Weiterverwendung abzulehnen > Widerspruchsrecht
Anonymisiert	Genetische Daten: Information über Weiterverwendung für zukünftige noch unbestimmte Forschungszwecke + über Möglichkeit Weiterverwendung abzulehnen > Widerspruchsrecht Proben: Information zur Anonymisierung > Widerspruchsrecht	Ausserhalb des Geltungsbereichs des HFG



Switzerland: Definition of a unified "Generalkonsent", to provide a single framework to manage permissions for access to patient derived material and related data

Consent Codes: Upholding Standard Data Use Conditions

Stephanie O. M. Dyke^{1*}, 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. Boycott⁹, Michael Brudno^{10,11}, Matthew Hurles¹², Heidi L. Rehm^{2,13}, Andreas Matern¹⁴, Marc Fiume¹⁵, Stephen T. Sherry¹⁶

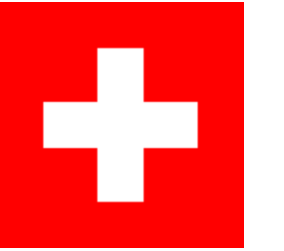


Consent Codes		
Name	Abbreviation	Description
Primary Categories (I^{ty})		
no restrictions	NRES	No restrictions on data use.
general research use and clinical care	GRU(CC)	For health/medical/biomedical purposes and other biological research, including the study of population origins or ancestry.
health/medical/biomedical research and clinical care	HMB(CC)	Use of the data is limited to health/medical/biomedical purposes, does not include the study of population origins or ancestry.
disease-specific research and clinical care	DS-[XX](CC)	Use of the data must be related to [disease].
population origins/ancestry research	POA	Use of the data is limited to the study of population origins or ancestry.
Secondary Categories (II^{ty}) (can be one or more extra conditions, in addition to I^{ty} category)		
other research-specific restrictions	RS-[XX]	Use of the data is limited to studies of [research type] (e.g., pediatric research).
research use only	RUO	Use of data is limited to research purposes (e.g., does not include its use in clinical care).
no "general methods" research	NMDS	Use of the data includes methods development research (e.g., development of software or algorithms) ONLY within the bounds of other data use limitations.
genetic studies only	GSO	Use of the data is limited to genetic studies only (i.e., no research using only the phenotype data).
Requirements		
not-for-profit use only	NPU	Use of the data is limited to not-for-profit organizations.
publication required	PUB	Requestor agrees to make results of studies using the data available to the larger scientific community.
collaboration required	COL-[XX]	Requestor must agree to collaboration with the primary study investigator(s).
return data to database/resource	RTN	Requestor must return derived/enriched data to the database/resource.
ethics approval required	IRB	Requestor must provide documentation of local IRB/REC approval.
geographical restrictions	GS-[XX]	Use of the data is limited to within [geographic region].
publication moratorium/embargo	MOR-[XX]	Requestor agrees not to publish results of studies until [date].
time limits on use	TS-[XX]	Use of data is approved for [x months].
user-specific restrictions	US	Use of data is limited to use by approved users.
project-specific restrictions	PS	Use of data is limited to use within an approved project.
institution-specific restrictions	IS	Use of data is limited to use within an approved institution.

SOM Dyke, et al. Consent Codes: Upholding Standard Data Use Conditions. *PLoS Genetics* 12(1): e1005772. <http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005772>

Contact: Dr. Stephanie Dyke (stephanie.dyke@mcgill.ca)

Data Ownership



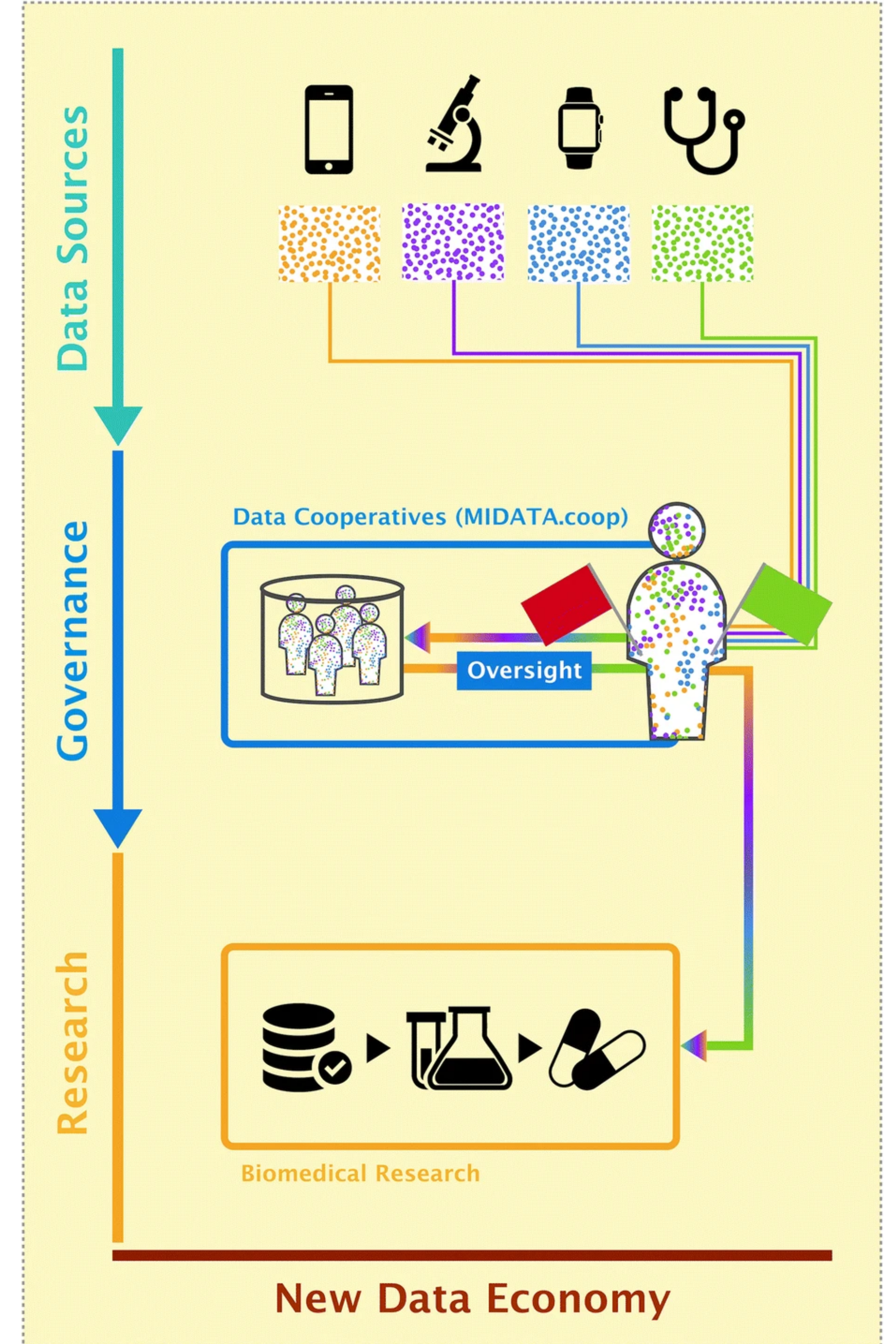
- Within Switzerland, there is no coherent approach on ownership of data as such (but academic discussion is ongoing, if that is needed).
- Restrictions of usage and disclosure of data other than personal data mainly stem from contractual relationships.
- In the field of research this leads mostly to a data ownership by the research institution.

Of course the restrictions of the different acts that are in the field need to be respected (procuring data lawfully, consent for further use, etc.)

Power to the People?!

Individuals as Owners & Managers of their Data

- (genomic) data ownership by the individual "data donors"
- supported by technological frameworks for data management and arbitration
- one vision here are "data cooperatives"
- need strong support from policy makers and financial sustainability support



Citizens aggregate data from different sources and make them available for research through data cooperatives. Cooperatives offer oversight mechanisms to filter data access requests and tools for the democratic governance of the data. Blasimme, A., Vayena, E. & Hafen, E. **Democratizing Health Research Through Data Cooperatives**. *Philos. Technol.* 31, 473–479 (2018). <https://doi.org/10.1007/s13347-018-0320-8>

Generalkonsent

BENEFIT

BLOCKCHAIN

HEALTH

PRIVACY

SECURITY

CONSENT

ACCESS

Right to Research

HACKERS

LAWS

Genetic
Information
Nondiscrimination
Act

Health
Insurance
Portability and
Accountability
Act

SAFETY

CRYPTOGRAPHY

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!**

Genomic Data & Privacy - Some Take-Home Messages

- Many clinical and research applications in genomics **need vast numbers of genomes** to evaluate e.g. genotype-phenotype relationships
- Such data cannot simply be provided by a few reference data curation resources - and those again rely on multitudes of original data resources > **federated data access** + **data curation**
- Genomic data is considered to potentially expose unwilling individuals through **re-identification**/de-anonymization but also through direct information (genotype -> phenotype/disease)
- Legislative bodies and law enforcement have varying and *curious* approaches to "genomic privacy", with a mix of de-legalizing genomic data generation (e.g. in Switzerland) or strictly limiting its use while also using "eminent domain" to co-opt such data for criminal persecution in a possibly extending set of use cases

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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