



Universität  
Zürich<sup>UZH</sup>



Swiss Institute of  
Bioinformatics



Global Alliance  
for Genomics & Health  
Collaborate. Innovate. Accelerate.



# Data Discovery in Biomedical Genomics: Time for a New Paradigm

**Michael Baudis**

Professor of Bioinformatics

University of Zürich

Swiss Institute of Bioinformatics **SIB**

GA4GH Workstream Co-lead *DISCOVERY*

Co-lead ELIXIR Beacon API Development

Co-lead ELIXIR hCNV Community



Genomics  
has seen  
massive and  
ongoing  
changes in  
technology



# 200+ genomic data initiatives globally

Clinical/Genomic  
Medicine



Research



National

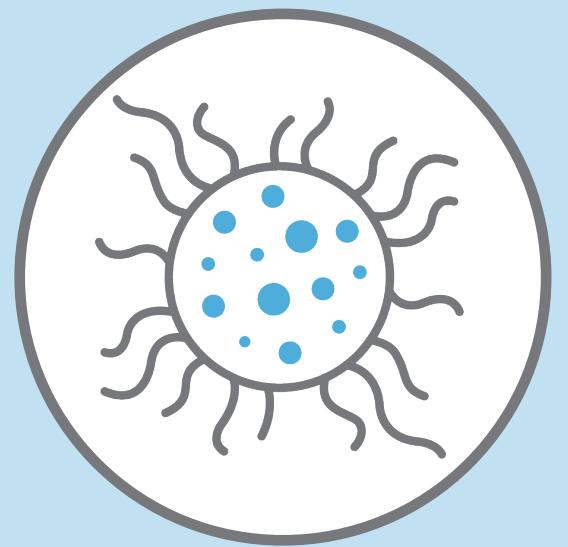


Cohorts

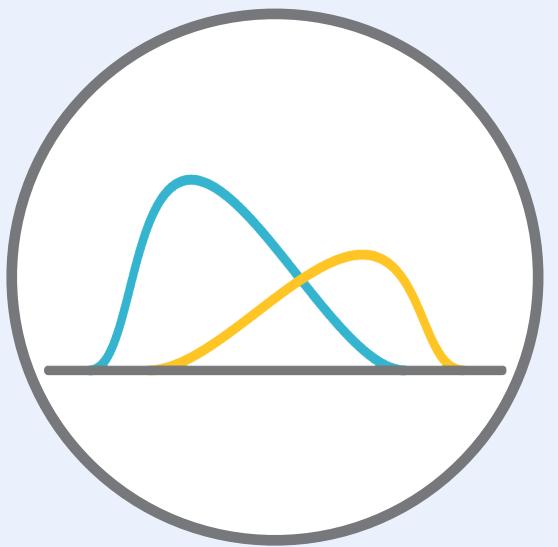




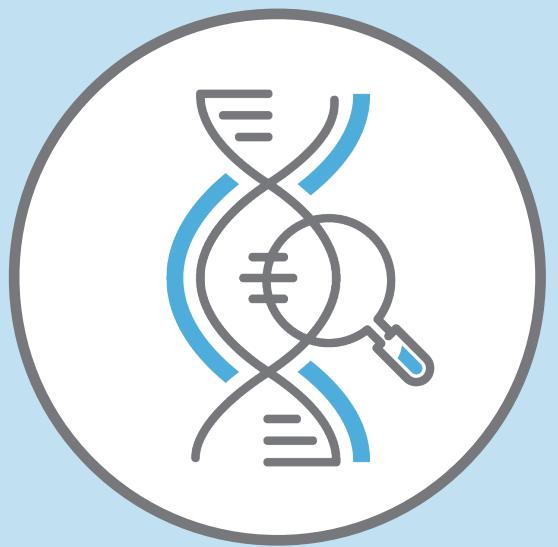
# Global Genomic Data Sharing Can...



Demonstrate  
patterns in health  
& disease



Increase statistical  
significance of  
analyses



Lead to  
“stronger” variant  
interpretations



Increase  
accurate  
diagnosis



Advance  
precision  
medicine

# Different Approaches to Data Sharing



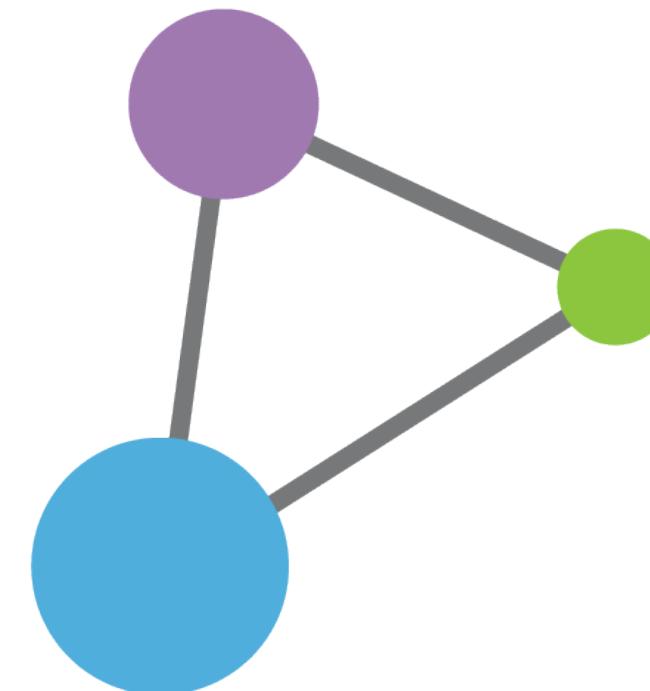
**Centralized Genomic Knowledge Bases**



**Data Commons**  
Trusted, controlled repository of multiple datasets

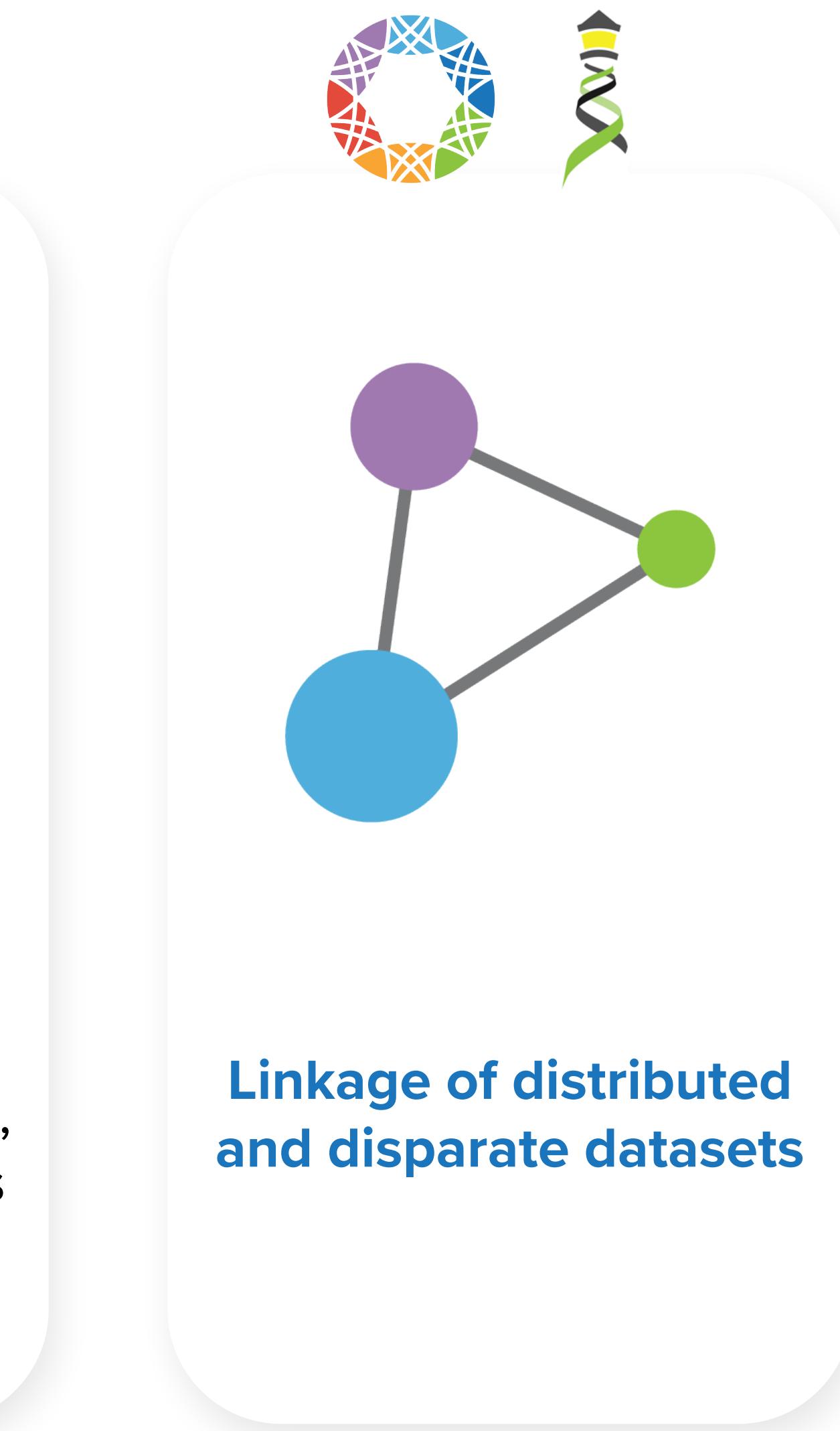
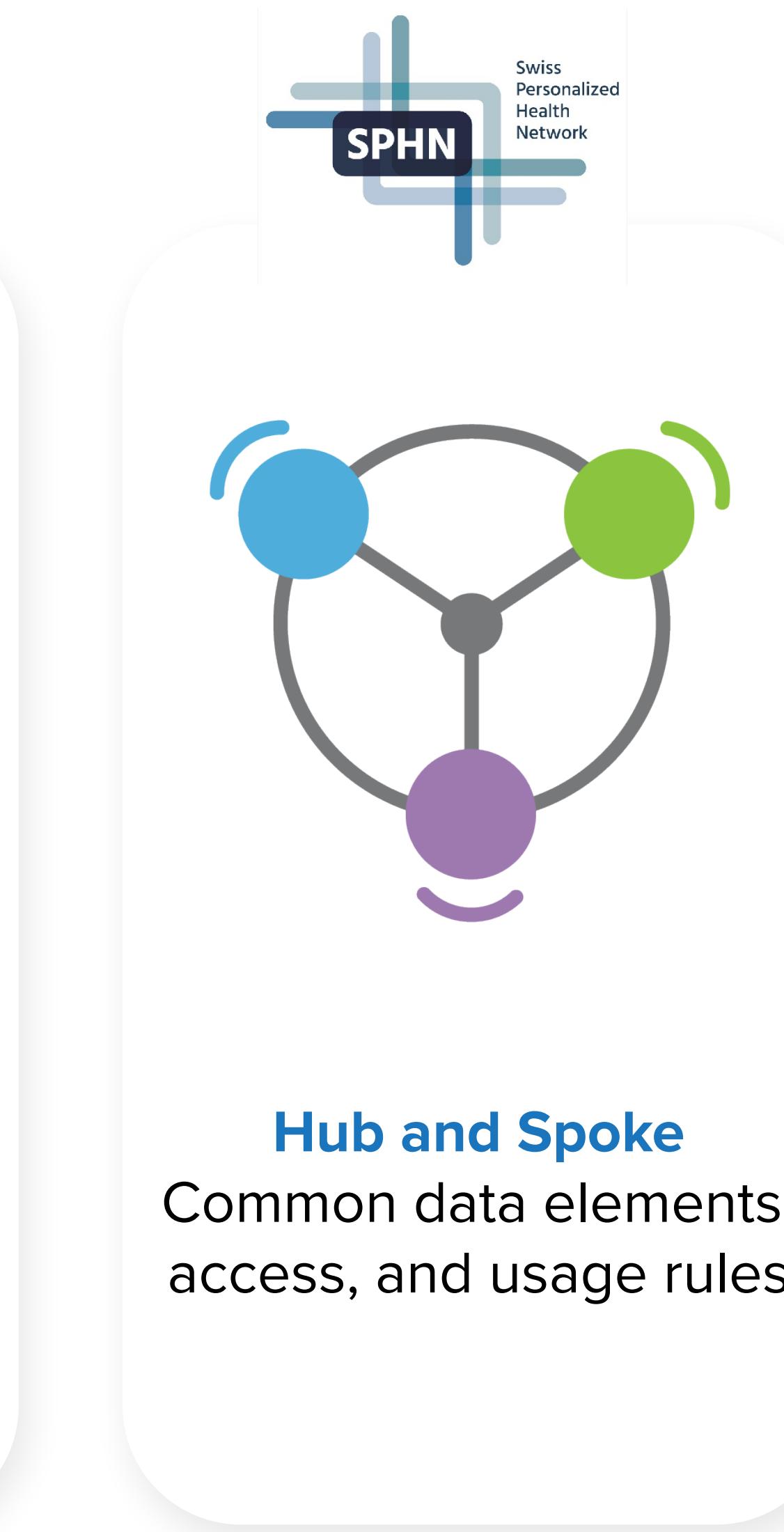
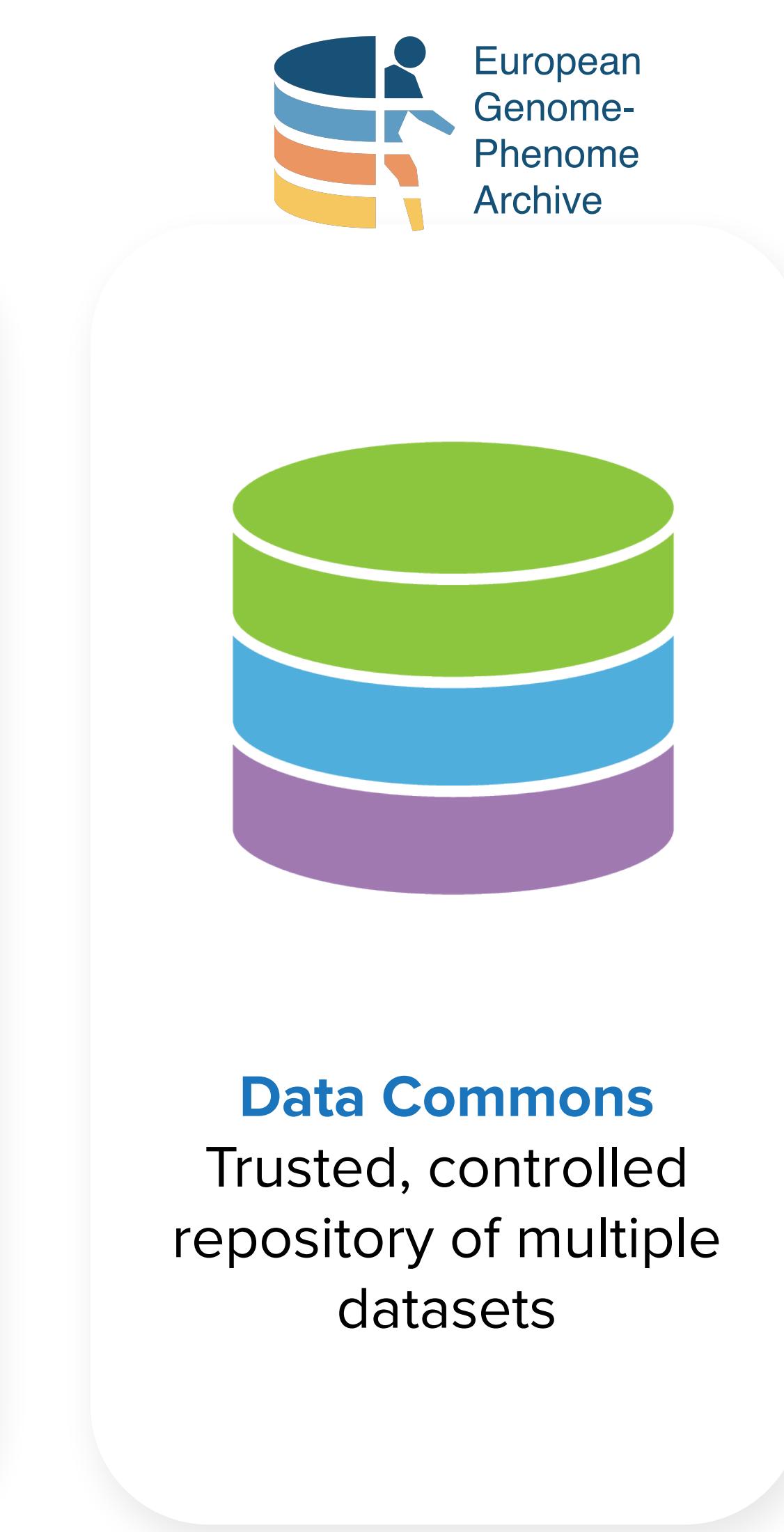
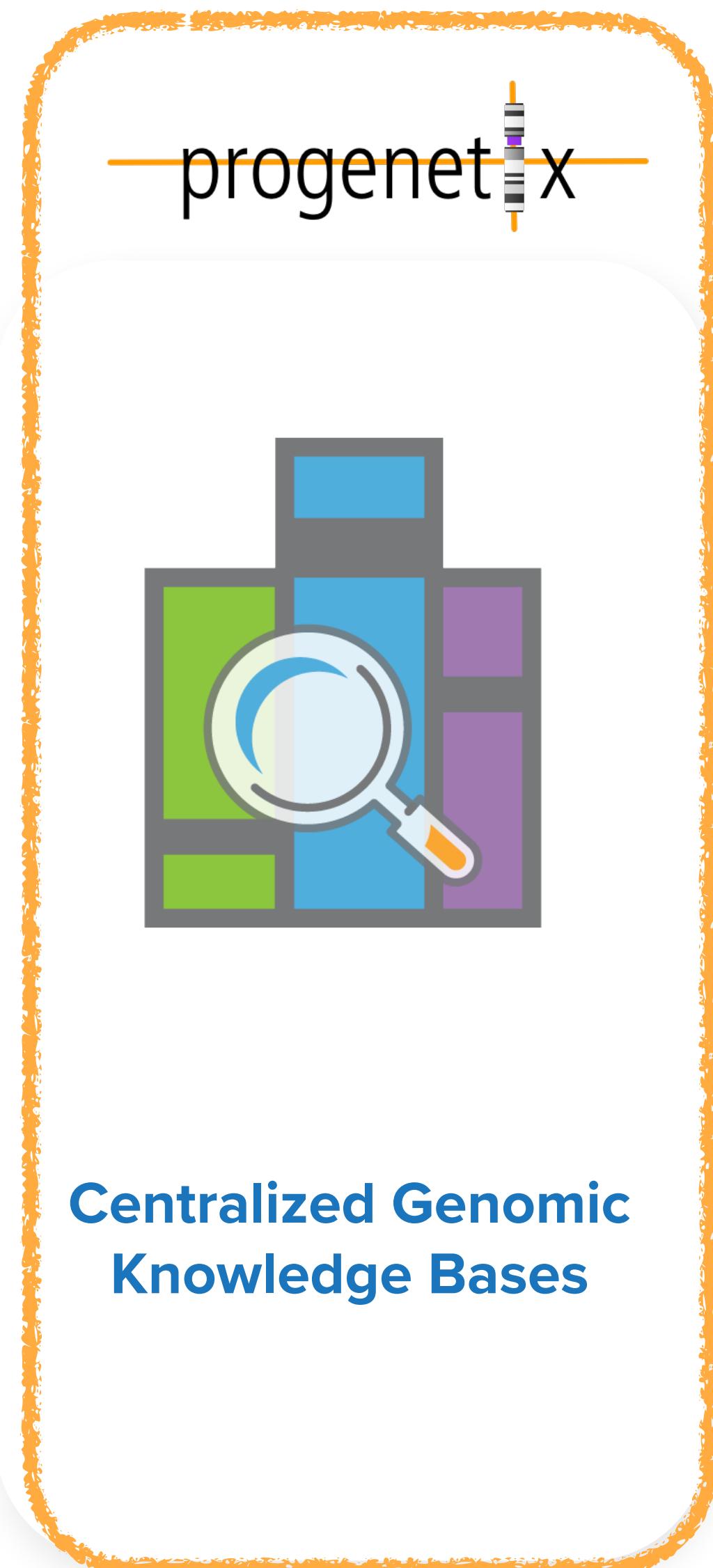


**Hub and Spoke**  
Common data elements, access, and usage rules



**Linkage of distributed and disparate datasets**

# Different Approaches to Data Sharing

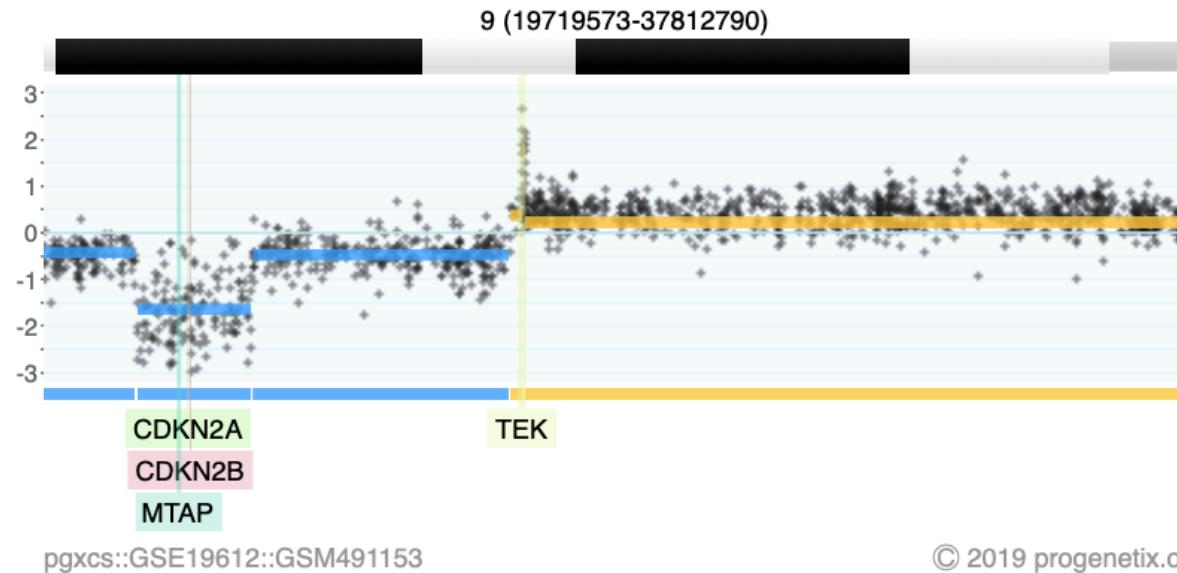


# Theoretical Cytogenetics and Oncogenomics

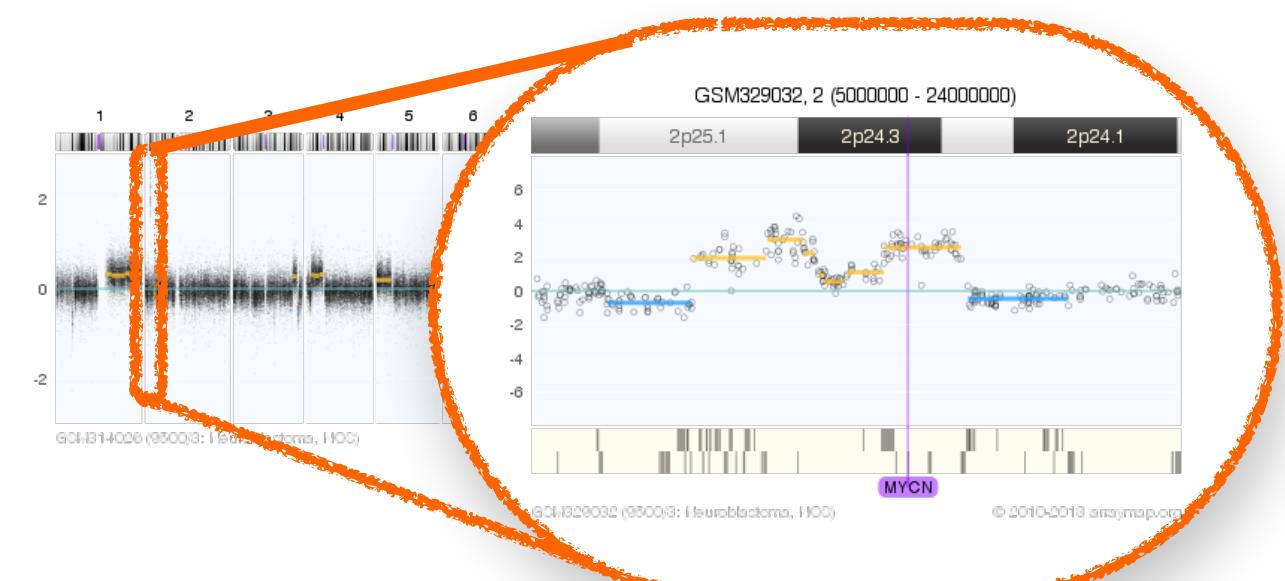
## Research | Methods | Standards

### Genomic Imbalances in Cancer - Copy Number Variations (CNV)

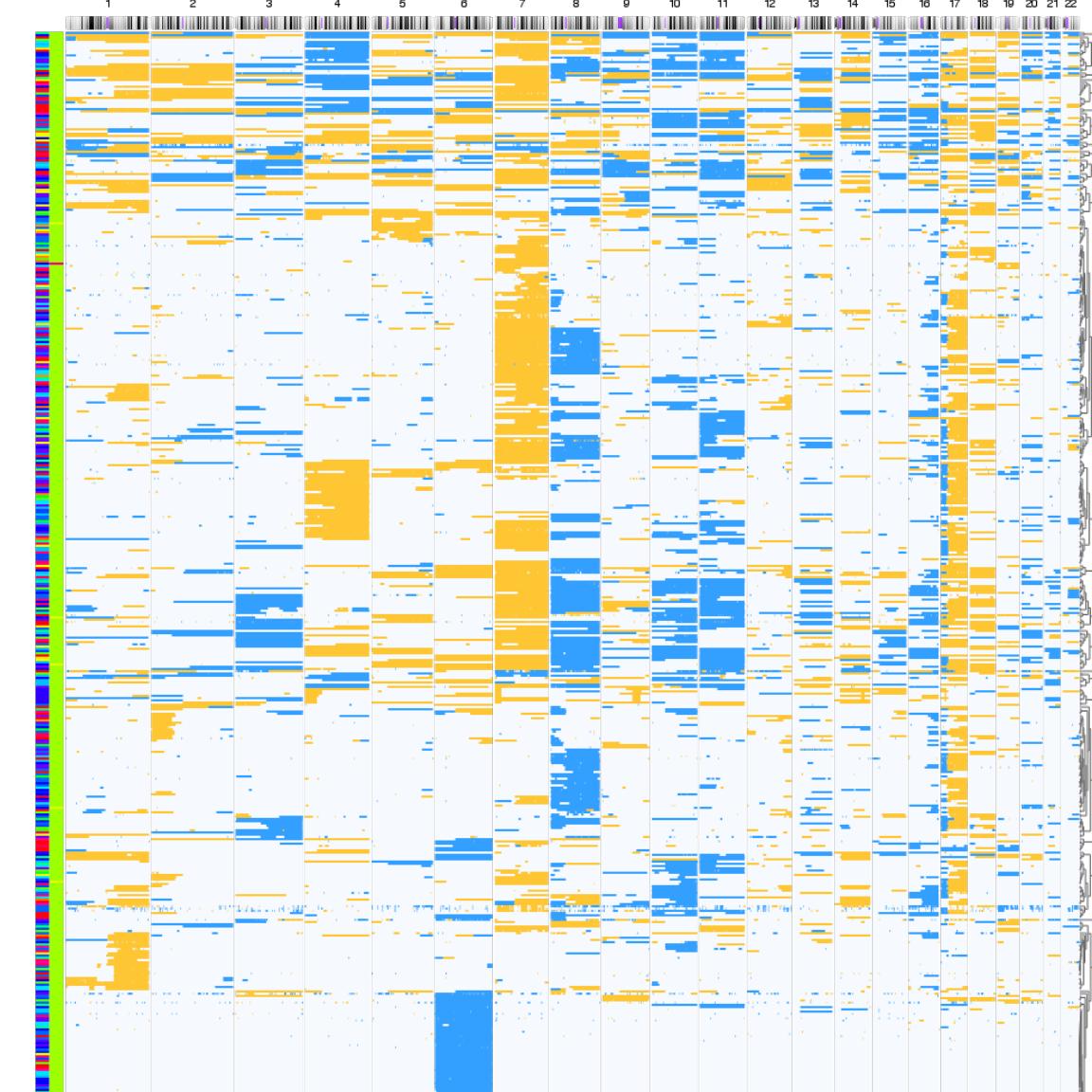
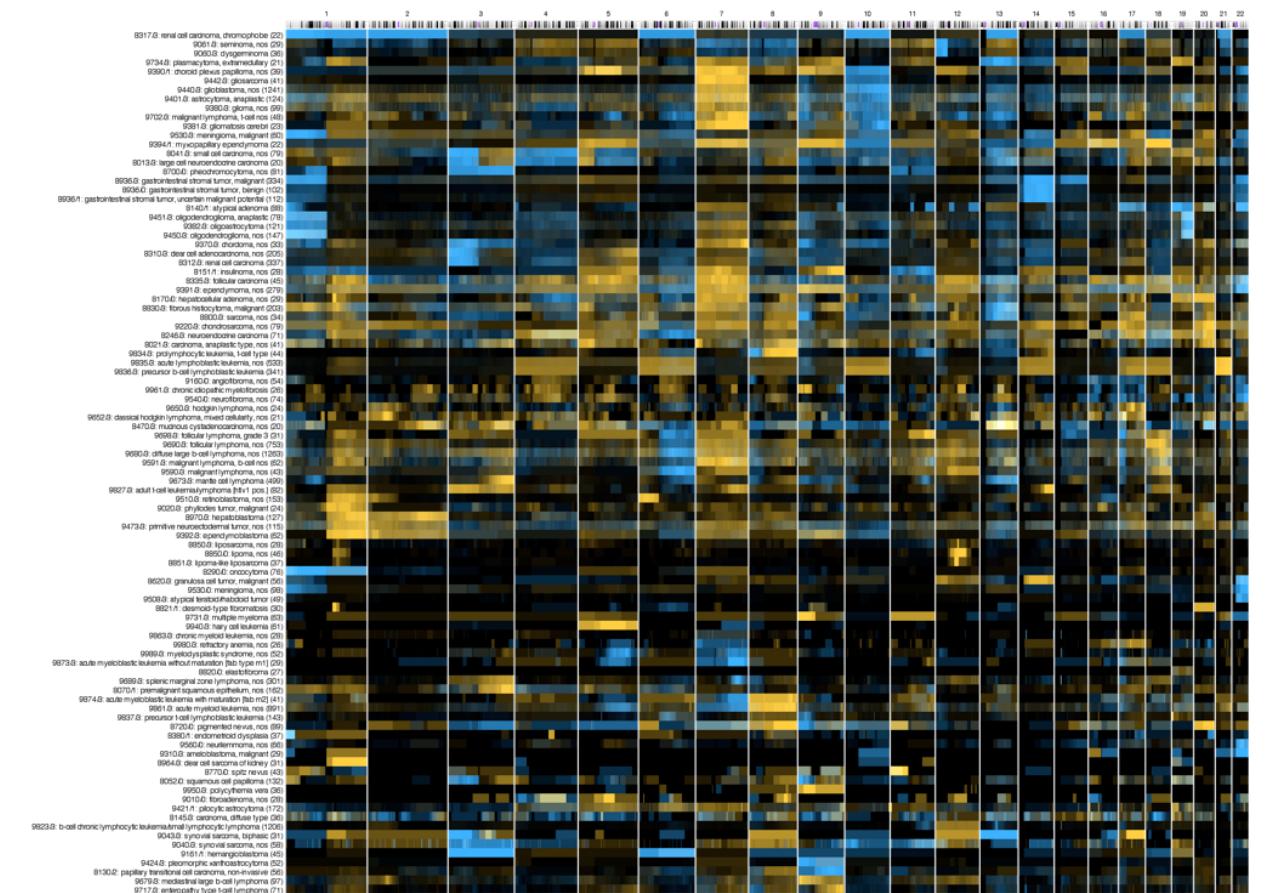
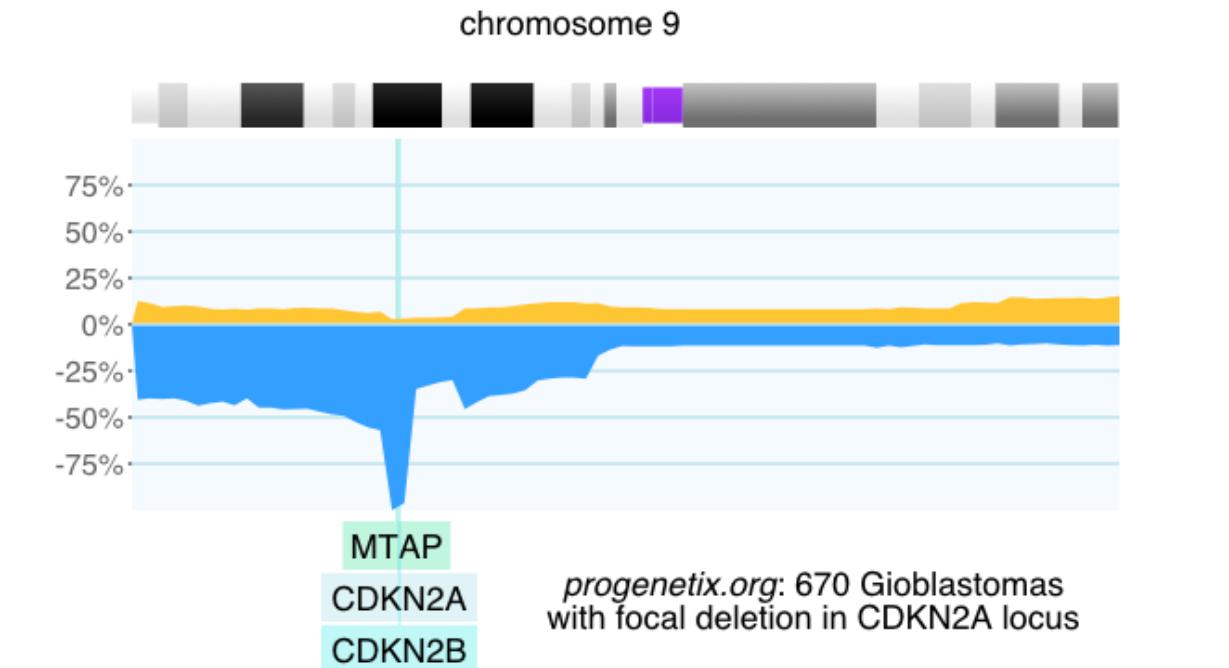
- Point mutations (insertions, deletions, substitutions)
- Chromosomal rearrangements
- **Regional Copy Number Alterations** (losses, gains)
- Epigenetic changes (e.g. DNA methylation abnormalities)



2-event, homozygous deletion in a Glioblastoma



MYCN amplification in neuroblastoma  
(GSM314026, SJNB8\_N cell line)



## Cancer Genomics Reference Resource

- **open** resource for oncogenomic profiles
- over **116'000 cancer CNV profiles**
- more than **800 diagnostic types**
- inclusion of reference datasets (e.g. TCGA)
- standardized encodings (e.g. NCIt, ICD-O 3)
- identifier mapping for PMID, GEO, Cellosaurus, TCGA, cBioPortal where appropriate
- core clinical data (TNM, sex, survival ...)
- data mapping services
- recent addition of SNV data for some series



### Cancer CNV Profiles

ICD-O Morphologies  
ICD-O Organ Sites  
Cancer Cell Lines  
Clinical Categories

### Search Samples

arrayMap  
TCGA Samples  
1000 Genomes  
Reference Samples  
DIPG Samples  
cBioPortal Studies  
Gao & Baudis, 2021

### Publication DB

Genome Profiling  
Progenetix Use

### Services

NCIt Mappings  
UBERON Mappings

### Upload & Plot

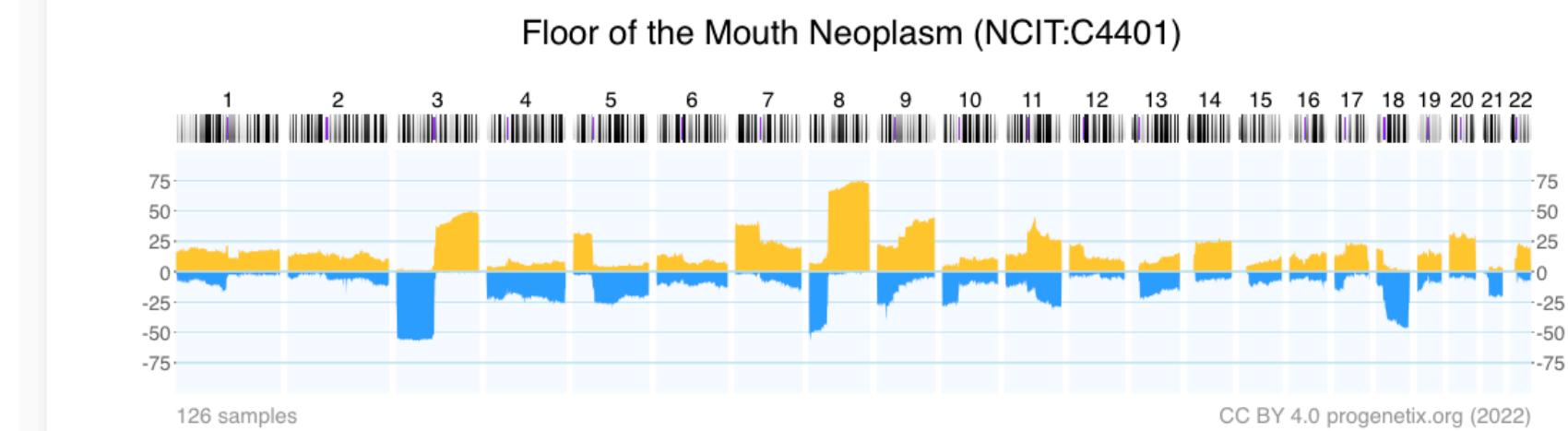
### Beacon<sup>+</sup>

Documentation  
News  
Downloads & Use  
Cases  
Sevices & API

### Baudisgroup @ UZH

## Cancer genome data @ progenetix.org

The Progenetix database provides an overview of mutation data in cancer, with a focus on copy number abnormalities (CNV / CNA), for all types of human malignancies. The data is based on *individual sample data* from currently **142063** samples.



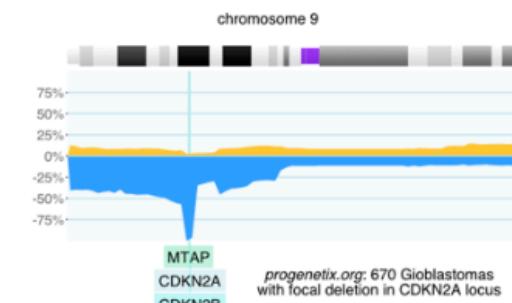
[Download SVG](#) | [Go to NCIT:C4401](#) | [Download CNV Frequencies](#)

Example for aggregated CNV data in 126 samples in Floor of the Mouth Neoplasm.  
Here the frequency of regional **copy number gains** and **losses** are displayed for all 22 autosomes.

### Progenetix Use Cases

#### Local CNV Frequencies

A typical use case on Progenetix is the search for local copy number aberrations - e.g. involving a gene - and the exploration of cancer types with these CNVs. The [\[ Search Page \]](#) provides example use cases for designing queries. Results contain basic statistics as well as visualization and download options.



#### Cancer CNV Profiles

The progenetix resource contains data of **834** different cancer types (NCIt neoplasm classification), mapped to a variety of biological and technical categories. Frequency profiles of regional genomic gains and losses for all categories (diagnostic entity, publication, cohort ...) can be accessed through the [\[ Cancer Types \]](#) page with direct visualization and options for sample retrieval and plotting options.

#### Cancer Genomics Publications

Through the [\[ Publications \]](#) page Progenetix provides **4164** annotated references to research articles from cancer genome screening experiments (WGS, WES, aCGH, cCGH). The numbers of analyzed samples and possible availability in the Progenetix sample collection are indicated.

## Cancer Genomics Reference Resource

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progenetix



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Bioinformatics

### Cancer Types by National Cancer Institute NCI Code

The cancer samples in Progenetix are mapped to several classification systems. For each of the classes, aggregated data is available by clicking the code. Additionally, a selection of the corresponding samples can be initiated by clicking the sample number or selecting one or more classes through the checkboxes.

Sample selection follows a hierarchical system in which samples matching the child terms of a selected class are included in the response.

Filter subsets e.g. by prefix   Hierarchy Depth: 4 levels

No S

#### Head and Neck Squamous Cell Carcinoma (NCIT:C34447)

Subset Type

- NCI Thesaurus OBO Edition NCIT:C34447 ↗

Sample Counts

- 2061 samples
- 57 direct NCIT:C34447 code matches
- 200 CNV analyses
  - Download CNV frequencies ↗

Search Samples

Select NCIT:C34447 samples in the [Search Form](#)

Raw Data (click to show/hide)

Download SVG | Go to NCIT:C34447 | Download CNV Frequencies

- NCIT:C6958: Astrocytic Tumor (5882 samples, 5896 CNV profiles)
- NCIT:C6960: Oligodendroglial Tumor (703 samples, 703 CNV profiles)
- NCIT:C8501: Brain Stem Glioma (2 samples, 2 CNV profiles)
- NCIT:C3716: Primitive Neuroectodermal T... (2213 samples, 2214 CNV profiles)
- NCIT:C4747: Glioneuronal and Neuronal Tumors (89 samples, 89 CNV profiles)
- NCIT:C6965: Pineal Parenchymal Cell Neoplasm (51 samples, 51 CNV profiles)

## Cancer Genomics Reference Resource

- **open** resource for oncogenomic profiles
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—progenetix—



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Edit Query

Assembly: GRCh38 chro: refseq:NC\_000009.12 Start: 21500001-21975098

End: 21967753-22500000 Type: EFO:0030067 Filters: NCIT:C3058

progenetix

Matched Samples: 657

Retrieved Samples:

Variants: 276

Calls: 659

UCSC region ↗

Variants in UCSC ↗

Dataset Responses (JSON) ↗

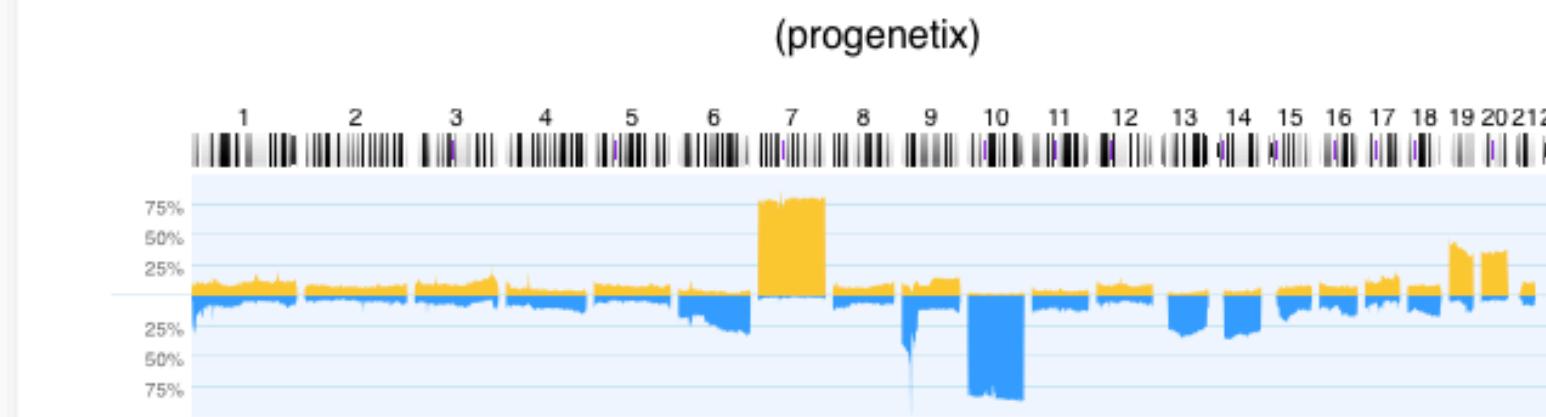
Visualization options

Results

Biosamples

Biosamples Map

Variants



Reload histogram in new window ↗

Matched Subset Codes	Subset Samples	Matched Samples	Subset Match Frequencies
pgx:icdot-C71.4	4	1	0.250
pgx:icdom-94403	4286	653	0.152
NCIT:C3058	4370	653	0.149
pgx:icdot-C71.1	14	2	0.143
pgx:icdot-C71.9	7204	640	0.089
NCIT:C3796	84	4	0.048
pgx:icdom-94423	84	4	0.048
pgx:icdot-C71.0	1714	14	0.008

Download Sample Data (TSV)

1-657 ↗

Download Sample Data (JSON)

1-657 ↗

# Cancer Cell Lines

## Cancer Genomics Reference Resource

- starting from >5000 cell line CNV profiles
  - 5754 samples | 2163 cell lines
  - 256 different NCIT codes
- genomic mapping of annotated variants and additional data from several resources (ClinVar, CCLE, Cellosaurus...)
  - 16178 cell lines
  - 400 different NCIT codes
- query and data delivery through Beacon v2 API

→ integration in data federation approaches

cancercelllines.org

Lead: Rahel Paloots



Cold  
Spring  
Harbor  
Laboratory

**bioRxiv**  
THE PREPRINT SERVER FOR BIOLOGY

New Results

**cancercelllines.org - a Novel Resource for Genomic Variants in Cancer Cell Lines**

Rahel Paloots, Michael Baudis

doi: <https://doi.org/10.1101/2023.12.12.571281>

This article is a preprint and has not been certified by peer review [what does this mean?].



Cancer Cell Lines

Search Cell Lines

Cell Line Listing

CNV Profiles by  
Cancer Type

Documentation

News

Progenetix

Progenetix Data

Progenetix  
Documentation

Publication DB

## Cancer Cell Lines by Cellosaurus ID

The cancer cell lines in [cancercelllines.org](http://cancercelllines.org) are labeled by their parentage hierarchically: Daughter cell lines are displayed below the primary cell line. For example, HeLa is listed as a daughter cell line of **HeLa (CVCL\_0030)** and so forth.

Sample selection follows a hierarchical system in which samples are retrieved based on the selected cell line. For example, selecting "HOS" for HeLa will also return the daughter lines by default - but can also be used to retrieve the primary cell line only.

### Cell Lines (with parental/derived hierarchies)

Filter subsets e.g. by prefix

Hierarchy Depth

No Selection

- > cellosaurus:CVCL\_0312: HOS (204 samples)
- > cellosaurus:CVCL\_1575: NCI-H650 (6 samples)
- > cellosaurus:CVCL\_1783: UM-UC-3 (9 samples)
- > cellosaurus:CVCL\_0004: K-562 (28 samples)
- cellosaurus:CVCL\_3827: K562/Ad (1 sample)
- > cellosaurus:CVCL\_0589: Kasumi-1 (9 samples)

### Cell Line Details

#### HOS (cellosaurus:CVCL\_0312)

##### Subset Type

- Cellosaurus - a knowledge resource on cell lines [cellosaurus:CVCL\\_0312](#)

##### Sample Counts

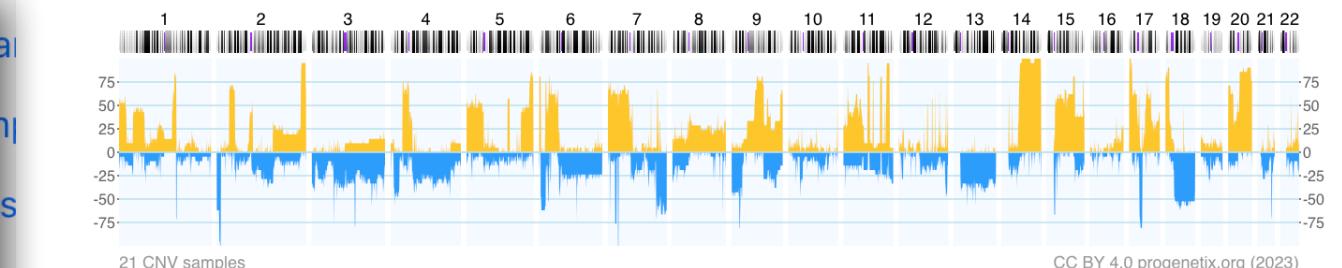
- 204 samples
- 57 direct cellosaurus:CVCL\_0312 code matches
- 21 CNV analyses

##### Search Samples

Select cellosaurus:CVCL\_0312 samples in the [Search Form](#)

##### Raw Data (click to show/hide)

HOS (cellosaurus:CVCL\_0312)



[Download SVG](#) | [Go to cellosaurus:CVCL\\_0312](#) | [Download CNV Frequencies](#)

**DATABASE**  
The Journal of Biological Databases and Curation

Follow this preprint

	Gene Matches	Cytoband Matches	Variants	
ALK	. ABC-14 cells harbored no ALK mutations and were sensitive to ... crizotinib while also exhibiting MNNG HOS transforming gene ( MET )	Rapid Acquisition of Alectinib Resistance in ALK-Positive Lung Cancer With High Tumor Mutation Burden (31374369)	ABSTRACT	
AREG	crizotinib while also exhibiting MNNG HOS	Rapid Acquisition of Alectinib Resistance	ABSTRACT	

Matched Samples: 1058  
Retrieved Samples: 1000  
Variants: 127  
Calls: 1444

UCSC region  
Variants in UCSC  
Dataset Responses (JSON)

Visualization options

Results Biosamples Variants Annotated Variants

Digest	Gene	Pathogenicity	Variant type	Variant Instances
7:140834768-140834769:G>A	BRAF		Missense variant	V: pgxvar-63ce6abca24c83054b B: pgxbs-3DfBeeAC
7:140734714-140734715:G>A	BRAF		Missense variant	V: pgxvar-63ce6acda24c83054b B: pgxbs-3fB2a14B
7:140753334-140753339:T>TGTA	BRAF	Pathogenic	V: pgxvar-	72d 0 54b E 54b

72d  
0  
54b  
E  
54b

# Different Approaches to Data Sharing



**Centralized Genomic Knowledge Bases**



**Hub and Spoke**  
Common data elements, access, and usage rules



**Linkage of distributed and disparate datasets**

# The EGA



Long term secure archive for human biomedical research sensitive data, with focus on reuse of the data for further research (or “*broad and responsible use of genomic data*”)



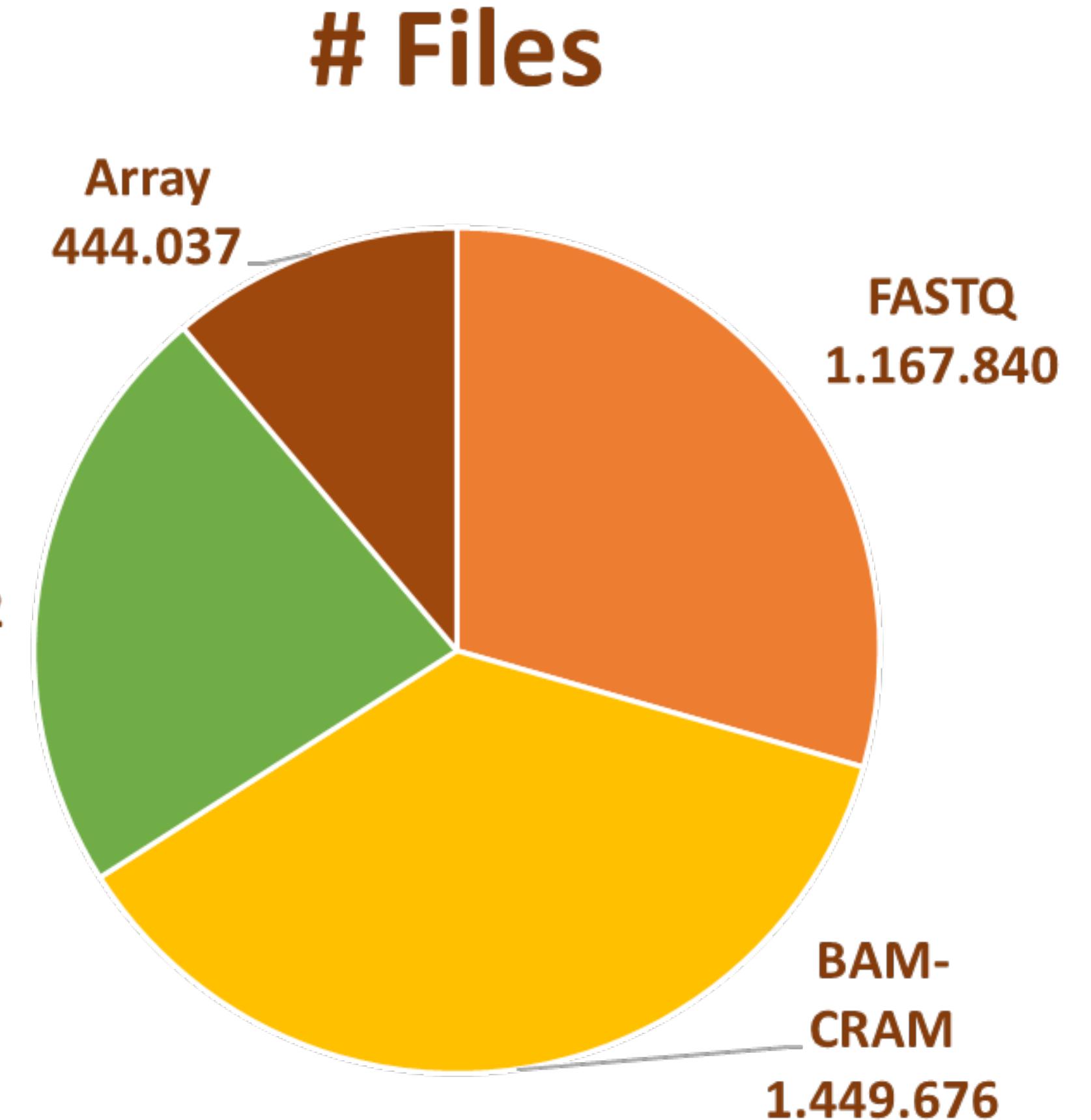
# The EGA



- EGA “owns” nothing; data controllers tell who is authorized to access ***their*** datasets
- EGA admins provide smooth “all or nothing” data sharing process

A screenshot of the EGA DAC interface. At the top, it shows 'My DACs - EGAC5000000005 - Requests' and 'HISTORY'. Below this, it says 'EuCanImage DAC' and 'This is a DAC for EuCanImage data'. It displays a list of requests with columns for Date, Requester, Dataset, and DAC Admin/Member. The requests listed are:

Date	Requester	Dataset	DAC Admin/Member
18 August 2022	gemma.milla@crg.eu	EGAD5000000032	Dr Lauren A Fromont
17 August 2022	Dr Teresa Garcia Lezana	EGAD5000000033	Dr Teresa Garcia Lezana
16 August 2022	Dr Teresa Garcia Lezana	EGAD5000000032	Dr Lauren A Fromont

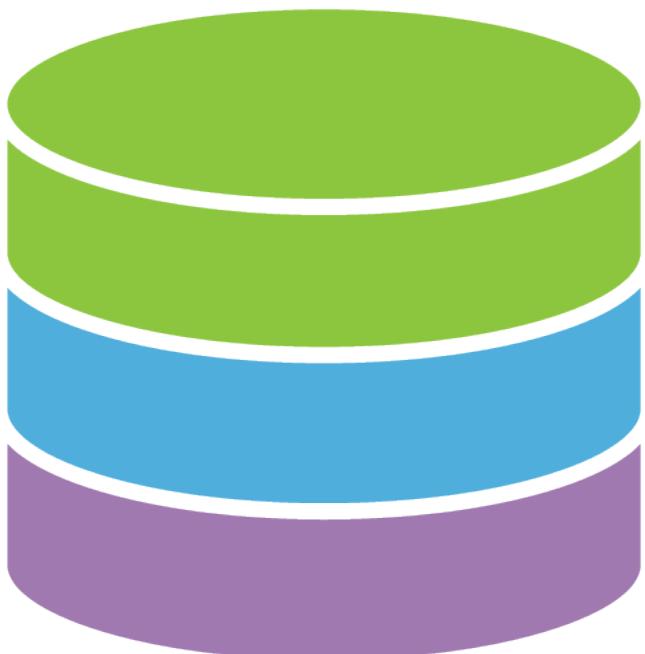
At the bottom right of the interface is a 'REQUESTS' button.

4,328 Studies released  
10,470 Datasets  
2,309 Data Access Committees

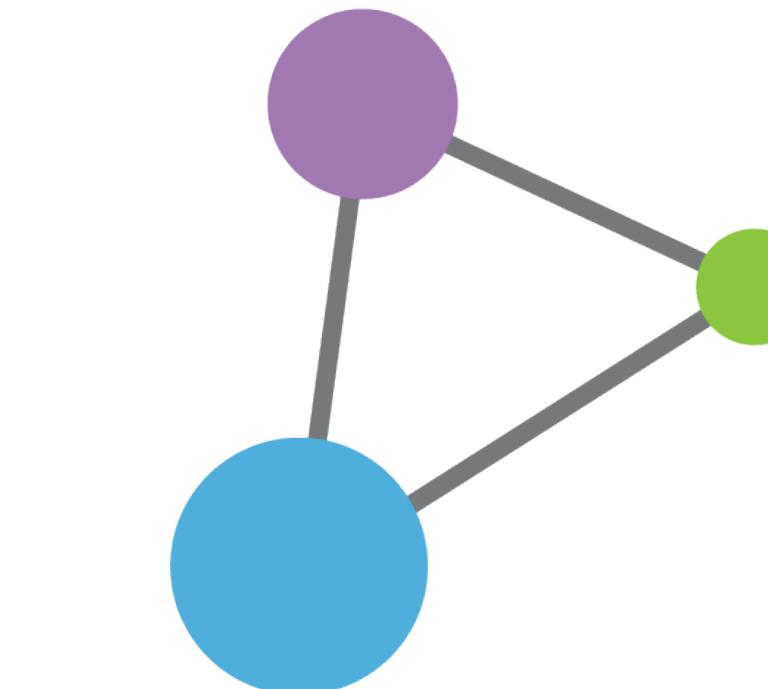
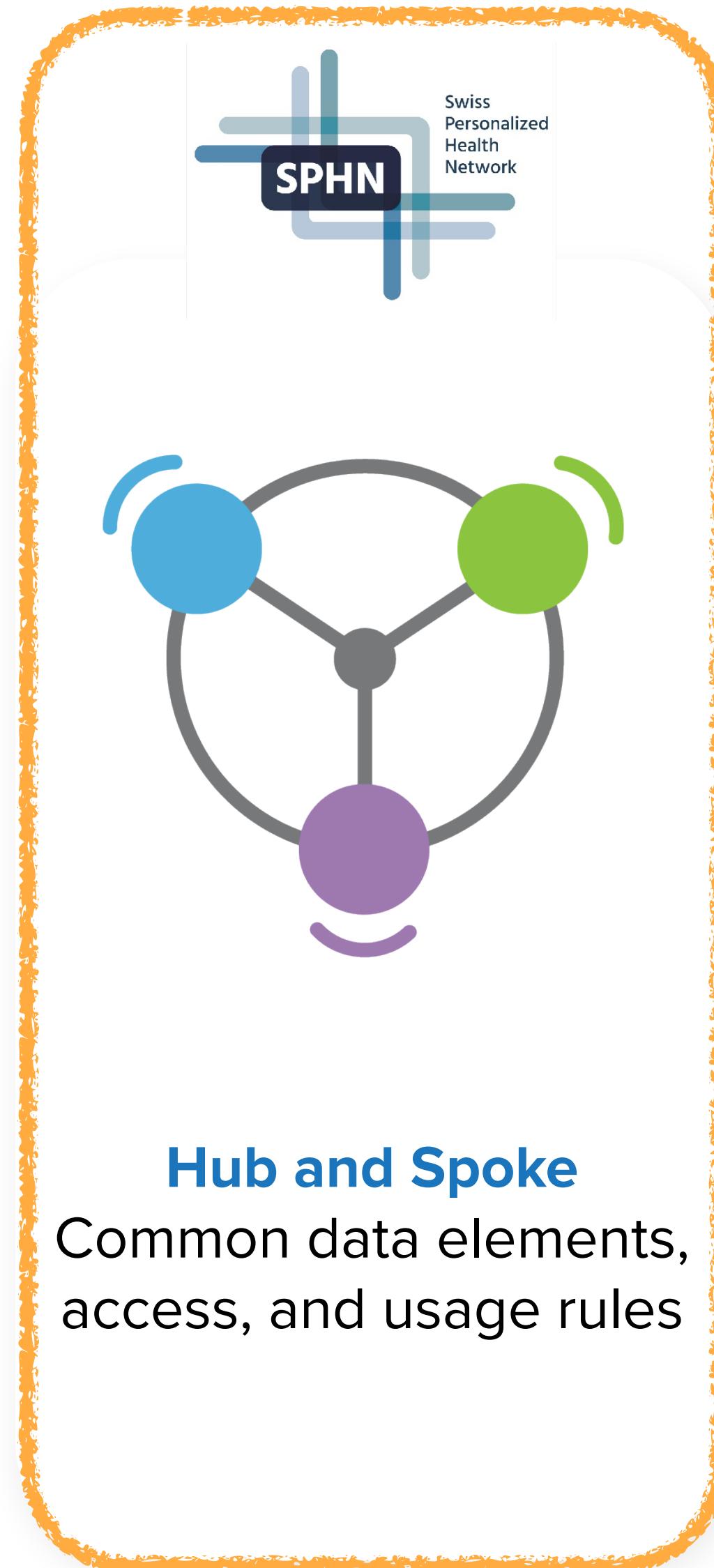
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**Centralized Genomic Knowledge Bases**

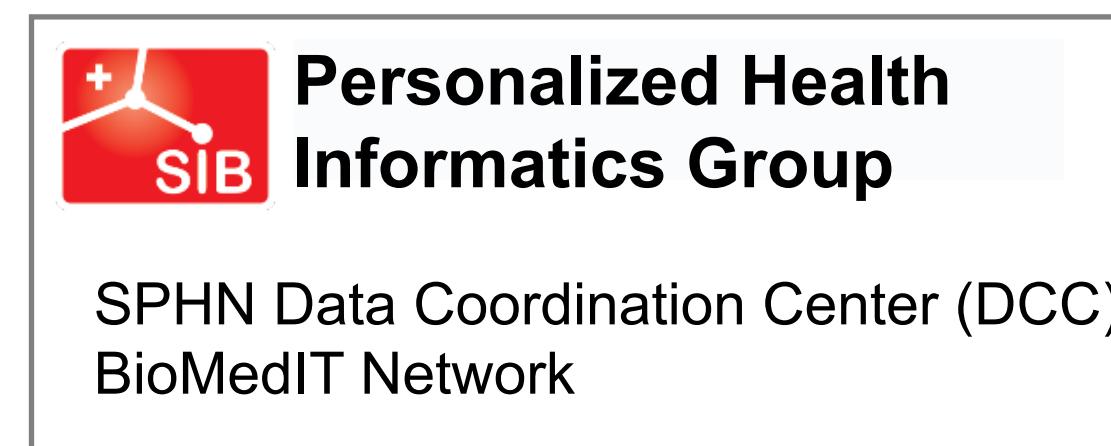
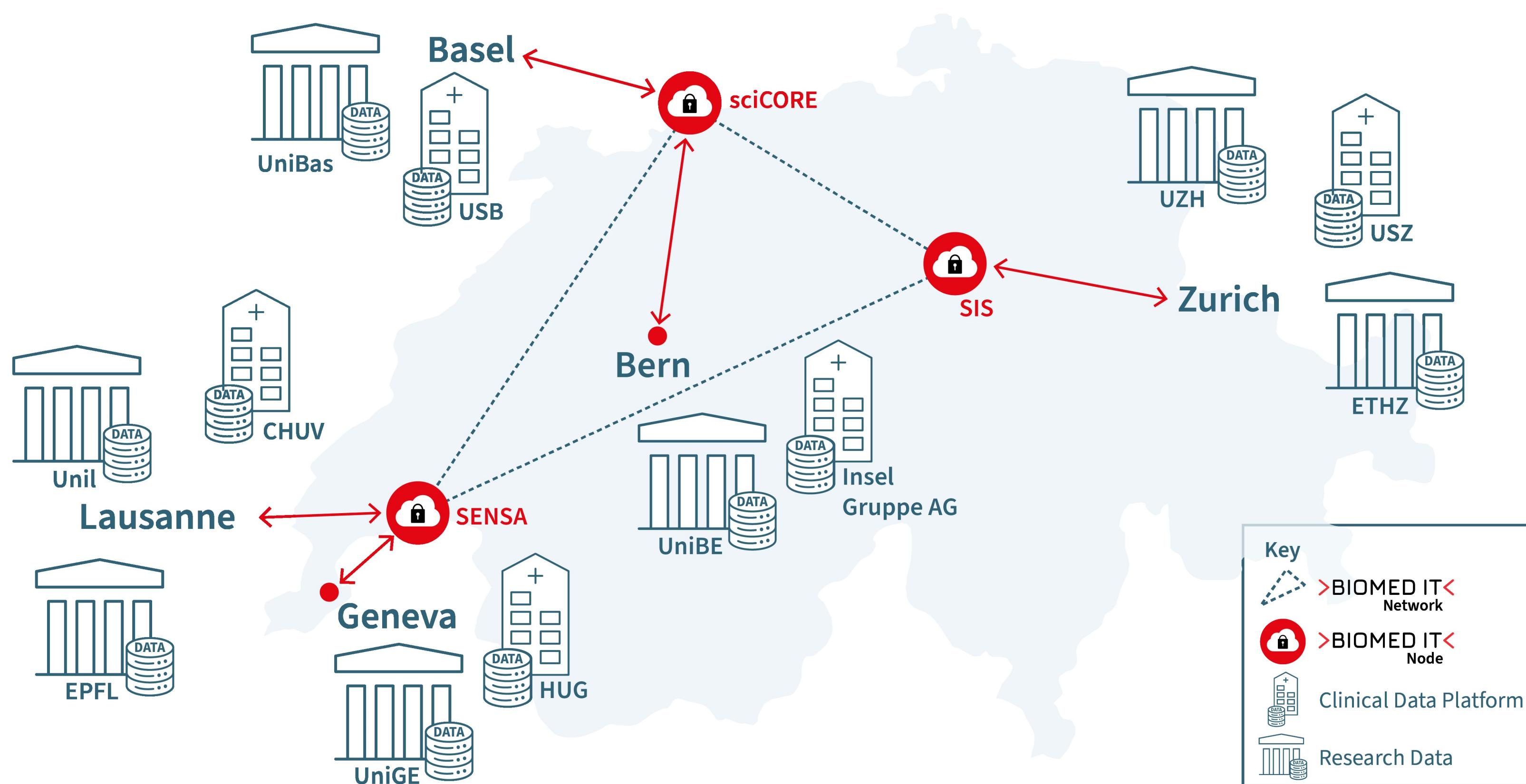


**Data Commons**  
Trusted, controlled repository of multiple datasets

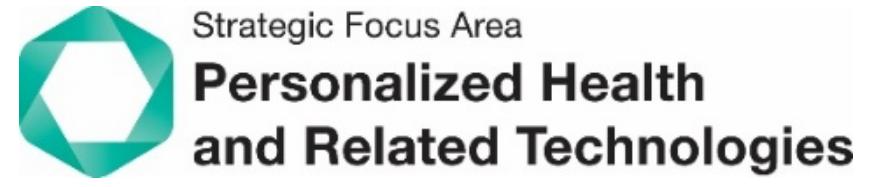


**Linkage of distributed and disparate datasets**

# The Swiss Personalized Health Network



**swissuniversities**



**ehealthsuisse**



**Personalized Health Alliance**  
Basel-Zurich

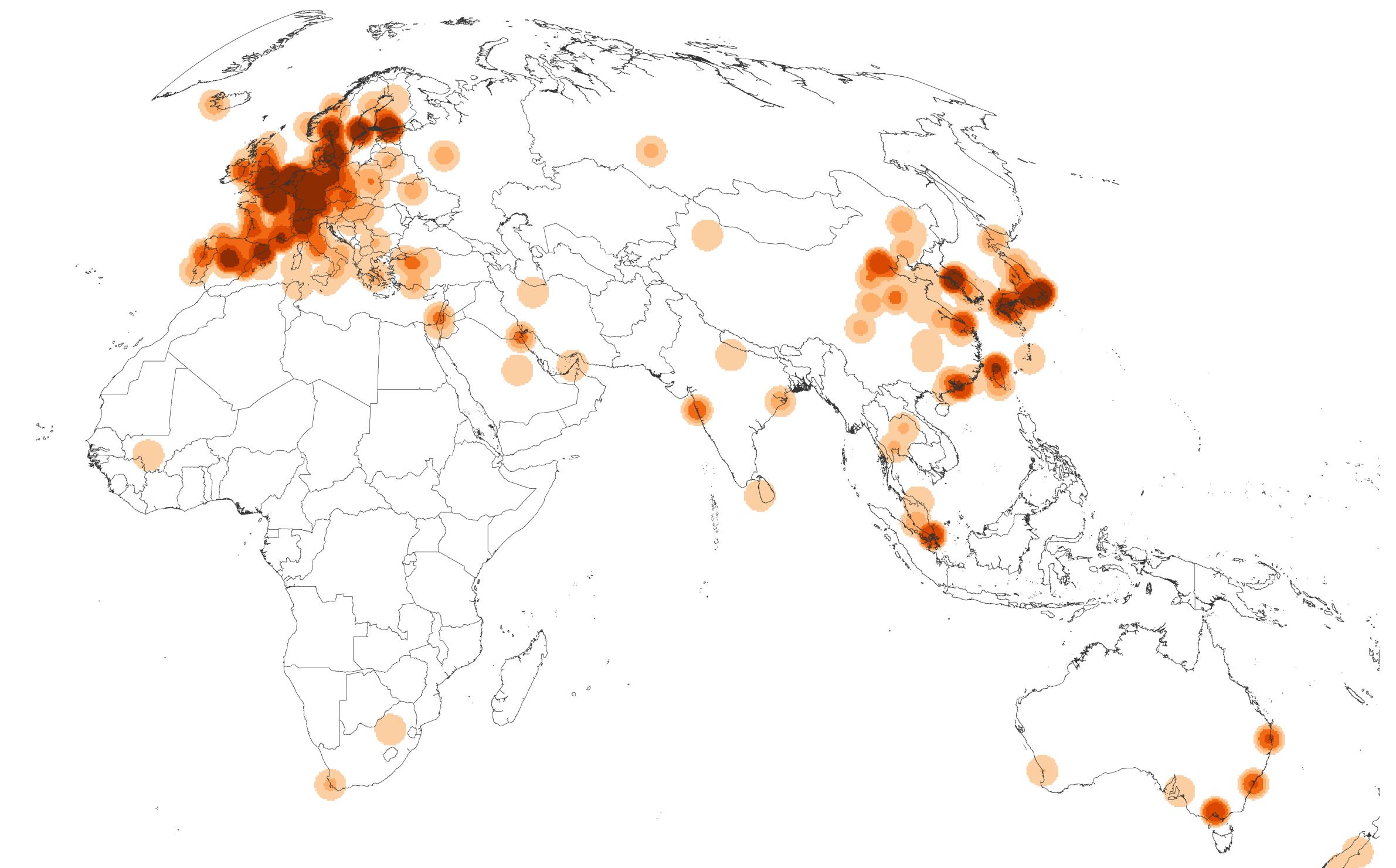
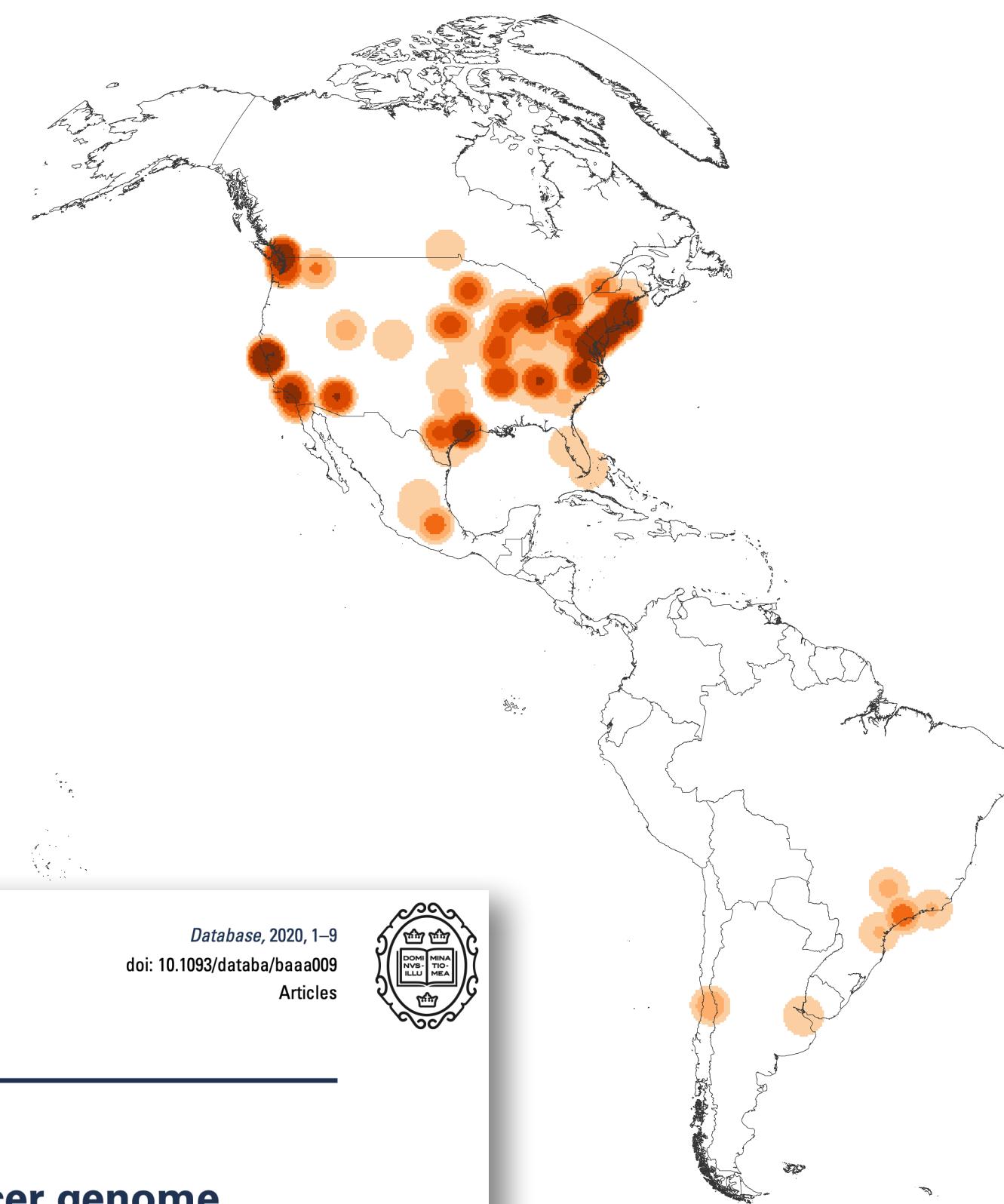
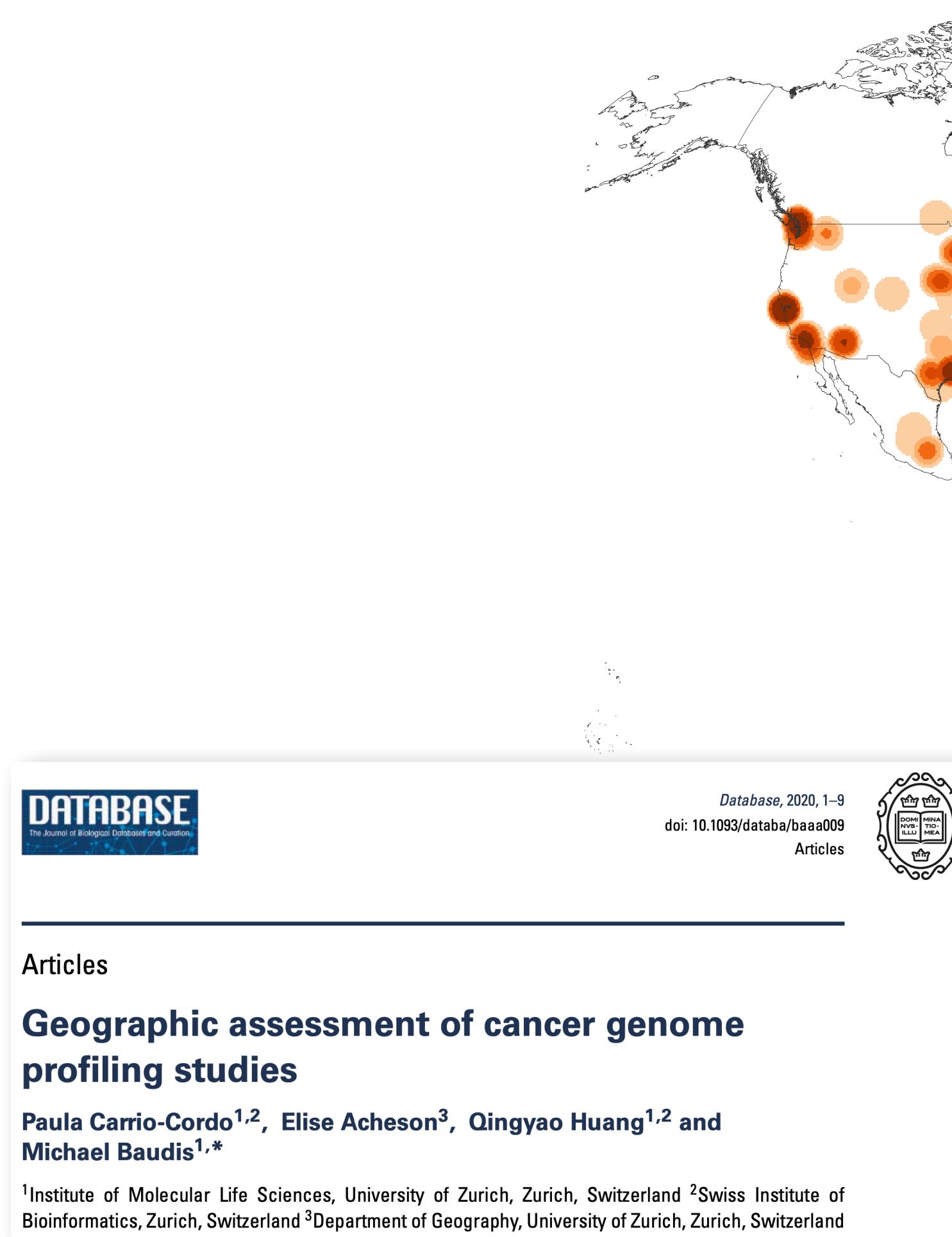


**life sciences  
cluster** basel



# Where Does Cancer Genomic Data Come From?

## Geographic bias in published cancer genome profiling studies



Map of the geographic distribution (by first author affiliation) of the 104'543 genomic array, 36'766 chromosomal CGH and 15'409 whole genome/exome based cancer genome datasets. The numbers are derived from the 3'240 publications registered in the Progenetix database.

# Different Approaches to Data Sharing



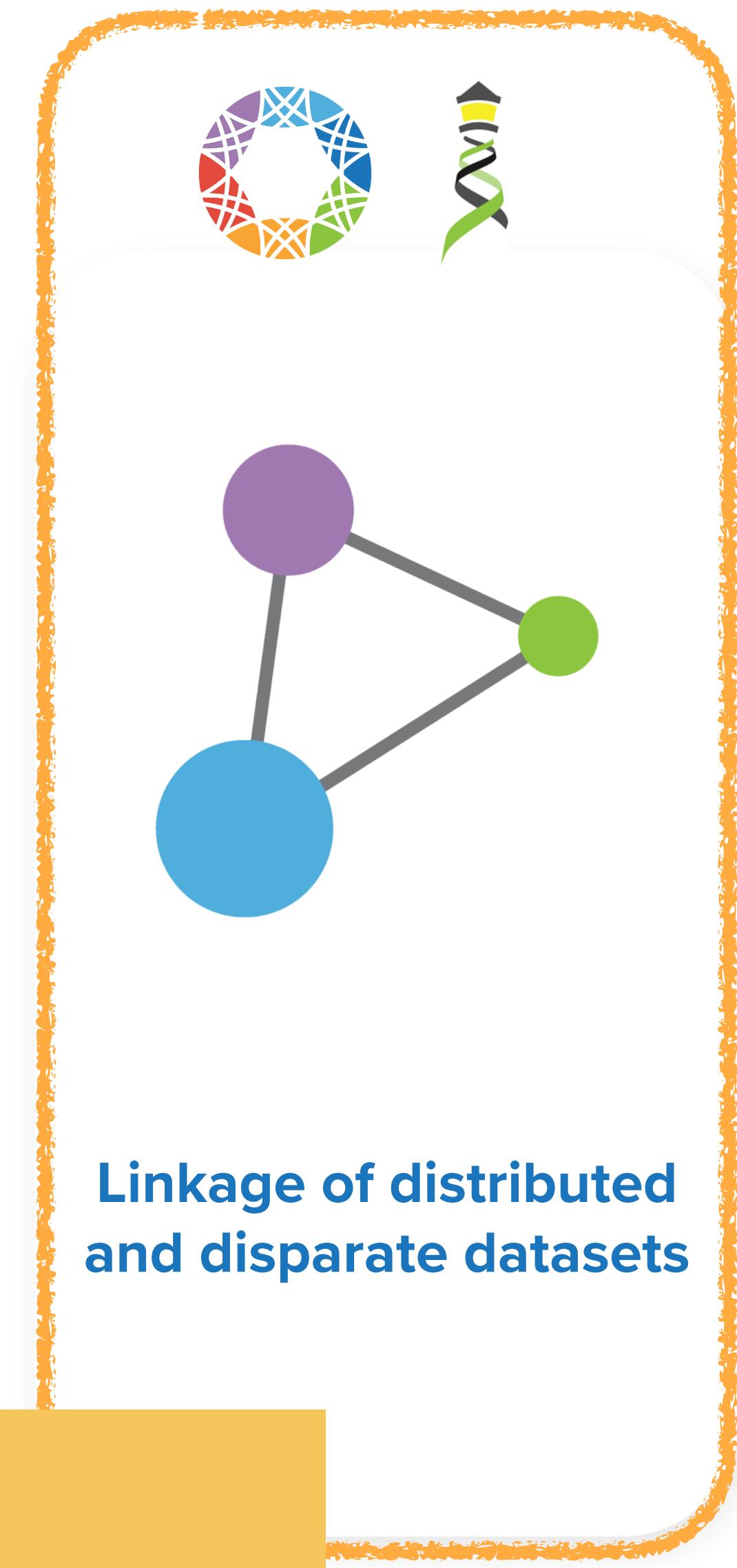
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Common data elements, access, and usage rules



**Linkage of distributed and disparate datasets**

**Federation**



# Global Alliance for Genomics & Health

Collaborate. Innovate. Accelerate.

## GENOMICS

*A federated ecosystem for  
sharing genomic, clinical data*

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

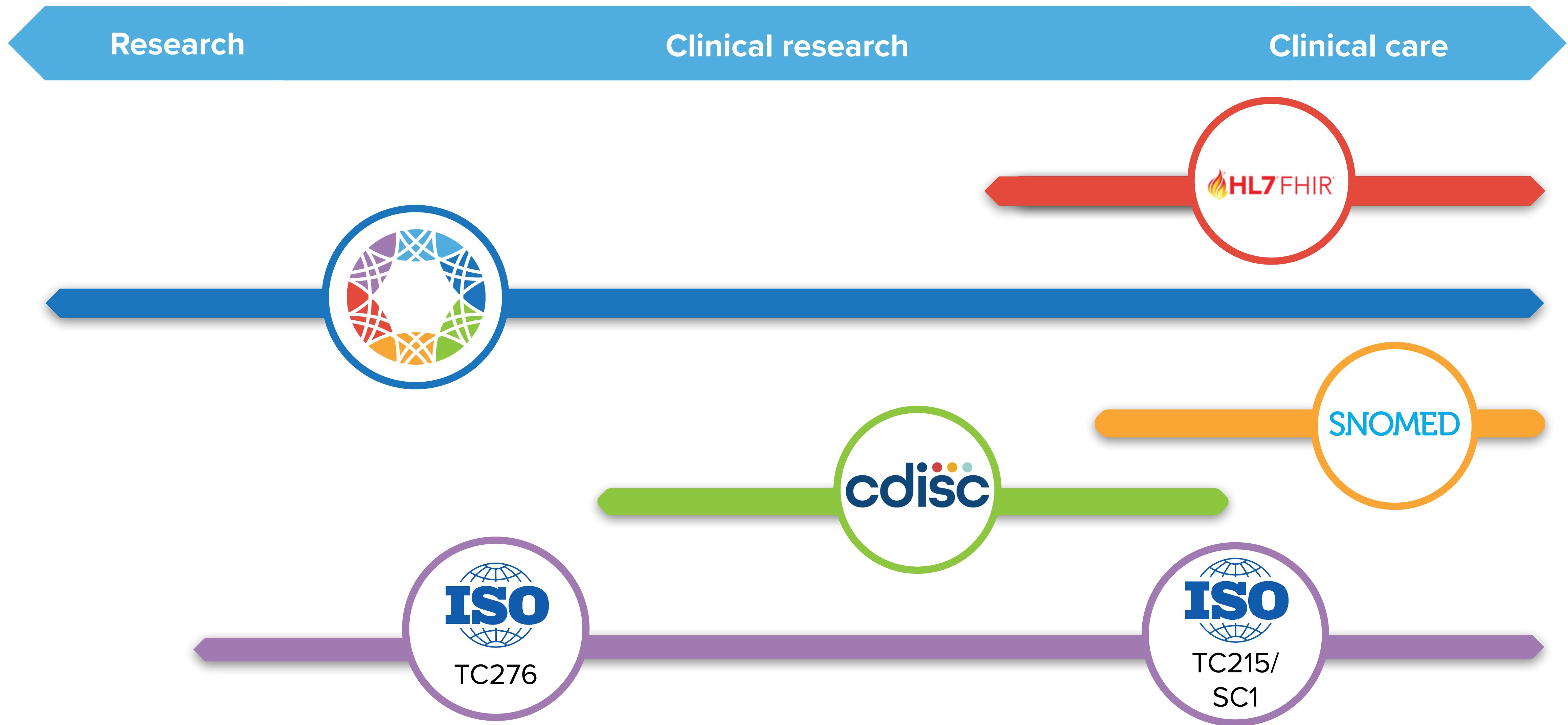
The Global Alliance for Genomics  
and Health\*

SCIENCE 10 JUNE 2016 • VOL 352 ISSUE 6291

## Alignment with other standards organizations



Global Alliance  
for Genomics & Health



# Our funders, partners, and Driver Projects

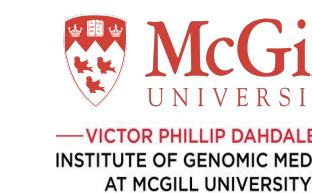


Global Alliance  
for Genomics & Health

## Core Funders



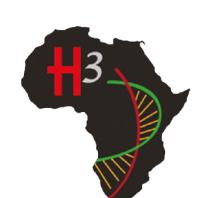
## Host Institutions



## Assigned Expert Funders/Employers



## Strategic Partner



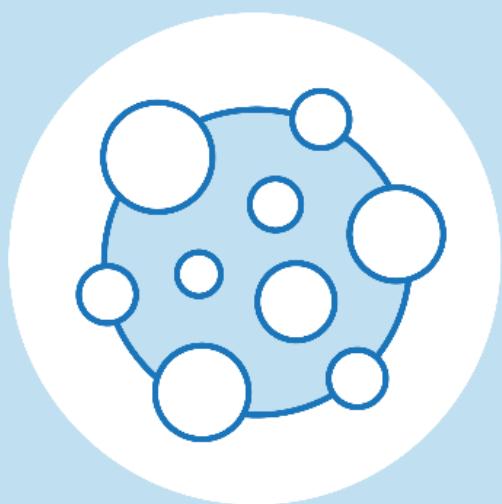
GDI is funded by the European Commission under the Digital Europe Programme under grant agreement number 101081813 and through co-funding from participating Member States.

# Driver Project areas of focus

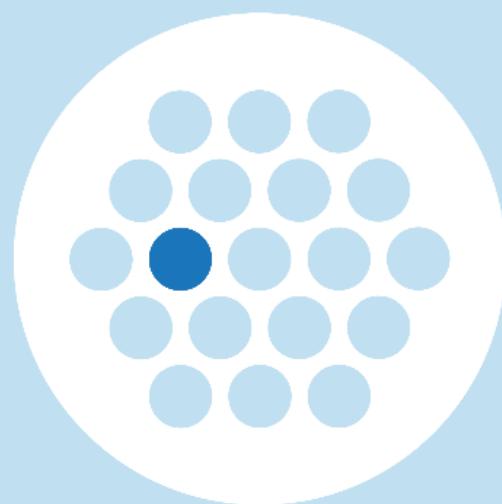


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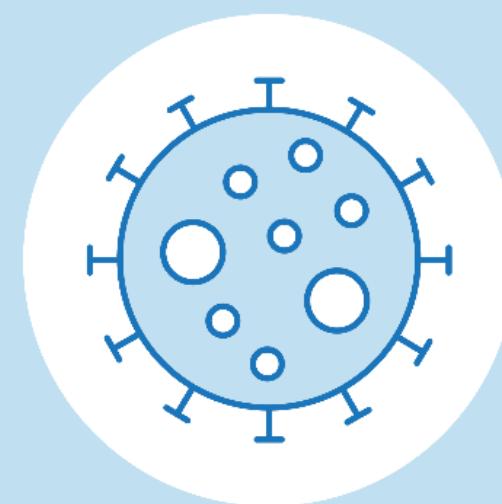
## DRIVER PROJECT AREAS OF FOCUS



17 Driver Projects  
focus on **cancer**



19 Driver Projects  
focus on **rare disease**



12 Driver Projects  
focus on **infectious disease**



15 Driver Projects  
focus on **common disease**

## TYPES OF DRIVER PROJECTS



23 Driver Projects  
in **academic research**



19 Driver Projects  
in **clinical research**



14 Driver Projects  
in **industry**



7 Driver Projects  
in **government**

# GA4GH Driver Projects



Global Alliance  
for Genomics & Health



All of Us Research Program



Autism Sharing Initiative



European Joint Programme - RD



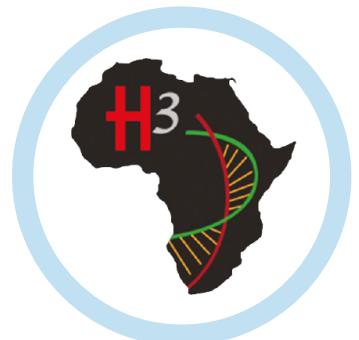
ClinGen



CanDIG



European Genome-phenome Archive



H3Africa



Genomics England



Australian Genomics



Variant Interpretation for  
Cancer Consortium



Human Cell Atlas



ELIXIR Beacon Project



ELIXIR Cloud & AAI



NCI CRDC



Matchmaker Exchange



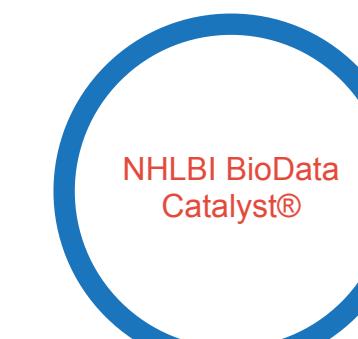
Epishare



ICGC ARGO



Monarch Initiative



NHLBI BioData Catalyst®



Biomedical Research Hub



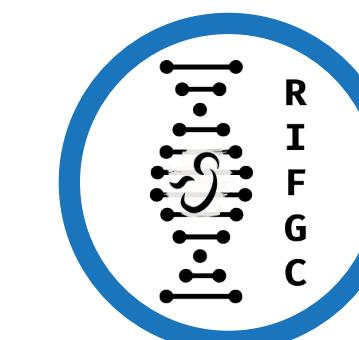
imCORE®



Human Pangenome Project



International Precision Child  
Health Partnership



Repository of the International  
Fetal Genomics Consortium



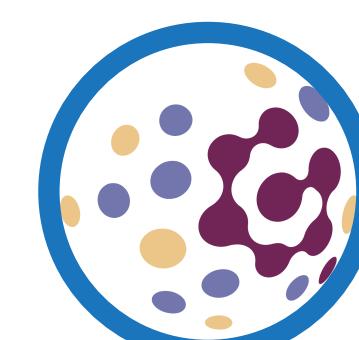
NIH Cloud Platform  
Interoperability effort



Qatar Genome Program



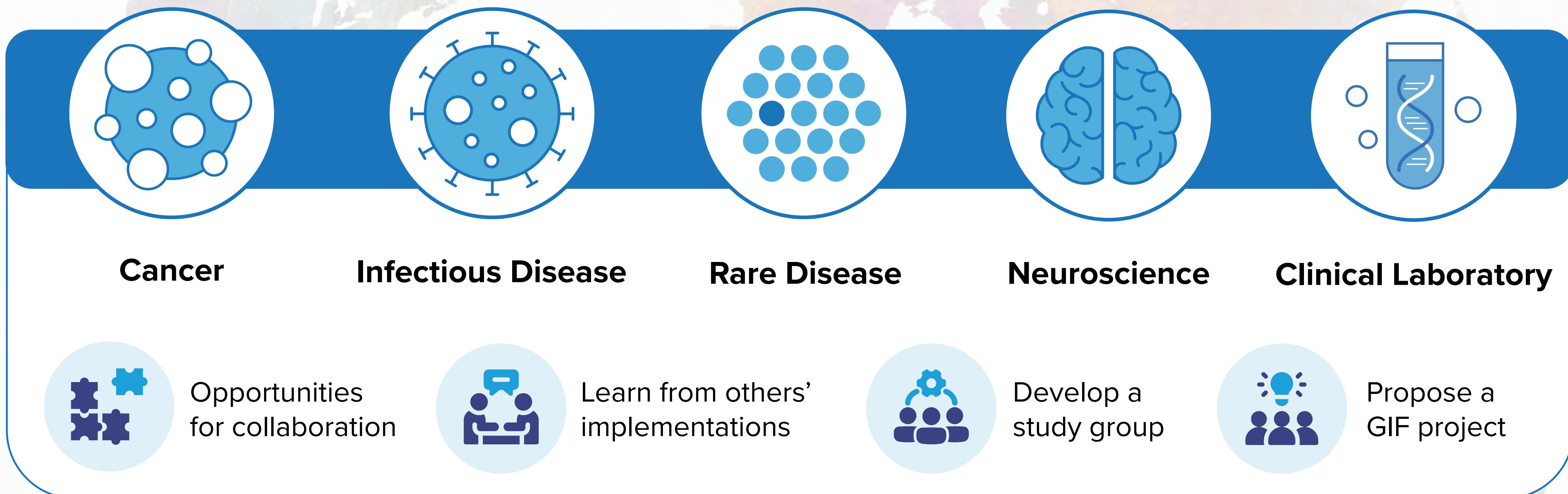
EOSC4Cancer



Genomic Data Infrastructure



Domain-specific groups promoting global cooperation, data sharing and collaborative research through identifying the need for new standards, and implementing existing GA4GH standards.



## INFORMATICS

### Beacon v2 and Beacon networks: federated data discovery in biome

#### Commentary

### International federation of genomic medicine databases using GA4GH standards

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# Cell Genomics

## Technology

### The GA4GH Variation Representation Specification A computational framework for variation representation and federated identification

Alex H. Wagner,<sup>1,2,25,\*</sup> Lawrence Babb,<sup>3,\*</sup> Gil Alterovitz,<sup>4,5</sup> Michael Baudis,<sup>6</sup> Matthew Brush,<sup>7</sup> Daniel L. Cameron,<sup>8,9</sup> Melissa Cline,<sup>10</sup> Malachi Griffith,<sup>11</sup> Obi L. Griffith,<sup>11</sup> Sarah E. Hunt,<sup>12</sup> David Kreda,<sup>13</sup> Jennifer M. Lee,<sup>14</sup> Stephanie Li,<sup>15</sup> Javier Lopez,<sup>16</sup> Eric Moyer,<sup>17</sup> Tristan Nelson,<sup>18</sup> Ronak Y. Patel,<sup>19</sup> Kevin Riehle,<sup>19</sup> Peter N. Robinson,<sup>20</sup> Shawn Rynearson,<sup>21</sup> Helen Schuilenburg,<sup>12</sup> Kirill Tsukanov,<sup>12</sup> Brian Walsh,<sup>7</sup> Melissa Konopko,<sup>15</sup> Heidi L. Rehm,<sup>3,22</sup> Andrew D. Yates,<sup>12</sup> Robert R. Freimuth,<sup>23</sup> and Reece K. Hart<sup>3,24,\*</sup>

# Cell Genomics

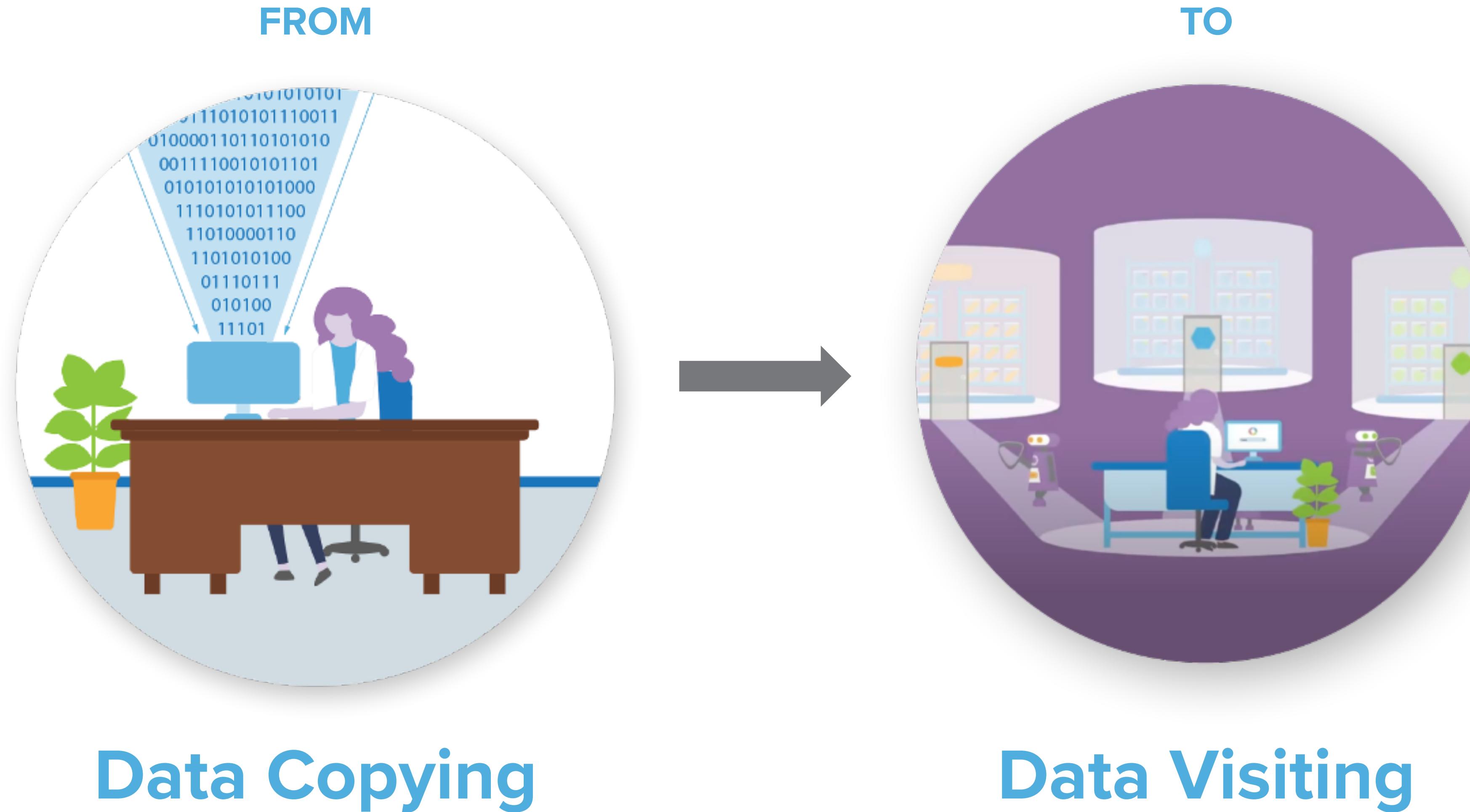
#### Perspective

### GA4GH: International policies and standards for data sharing across genomic research and healthcare

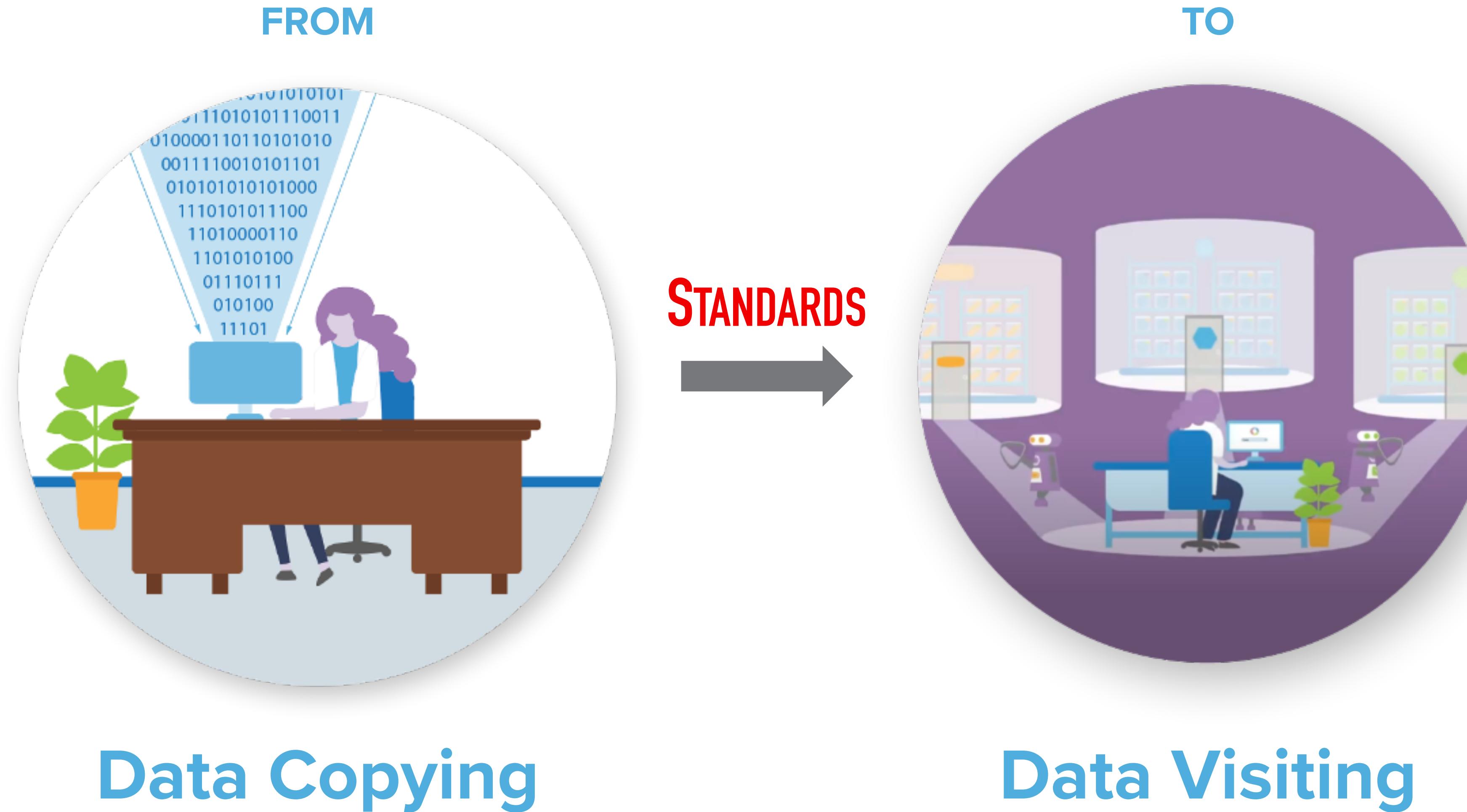
Heidi L. Rehm,<sup>1,2,47</sup> Angela J.H. Page,<sup>1,3,\*</sup> Lindsay Smith,<sup>3,4</sup> Jeremy B. Adams,<sup>3,4</sup> Gil Alterovitz,<sup>5,47</sup> Lawrence J. Babb,<sup>1</sup> Maxmillian P. Barkley,<sup>6</sup> Michael Baudis,<sup>7,8</sup> Michael J.S. Beauvais,<sup>3,9</sup> Tim Beck,<sup>10</sup> Jacques S. Beckmann,<sup>11</sup> Sergi Beltran,<sup>12,13,14</sup> David Bernick,<sup>1</sup> Alexander Bernier,<sup>9</sup> James K. Bonfield,<sup>15</sup> Tiffany F. Boughtwood,<sup>16,17</sup> Guillaume Bourque,<sup>9,18</sup> Sarion R. Bowers,<sup>15</sup> Anthony J. Brookes,<sup>10</sup> Michael Brudno,<sup>18,19,20,21,38</sup> Matthew H. Brush,<sup>22</sup> David Bujold,<sup>9,18,38</sup> Tony Burdett,<sup>23</sup> Orion J. Buske,<sup>24</sup> Moran N. Cabili,<sup>1</sup> Daniel L. Cameron,<sup>25,26</sup> Robert J. Carroll,<sup>27</sup> Esmeralda Casas-Silva,<sup>123</sup> Debyani Chakravarty,<sup>29</sup> Bimal P. Chaudhari,<sup>30,31</sup> Shu Hui Chen,<sup>32</sup> J. Michael Cherry,<sup>33</sup> Justina Chung,<sup>3,4</sup> Melissa Cline,<sup>34</sup> Hayley L. Clissold,<sup>15</sup> Robert M. Cook-Deegan,<sup>35</sup> Mélanie Courtot,<sup>23</sup> Fiona Cunningham,<sup>23</sup> Miro Cupak,<sup>6</sup> Robert M. Davies,<sup>15</sup> Danielle Denisko,<sup>19</sup> Megan J. Doerr,<sup>36</sup> Lena I. Dolman,<sup>19</sup>

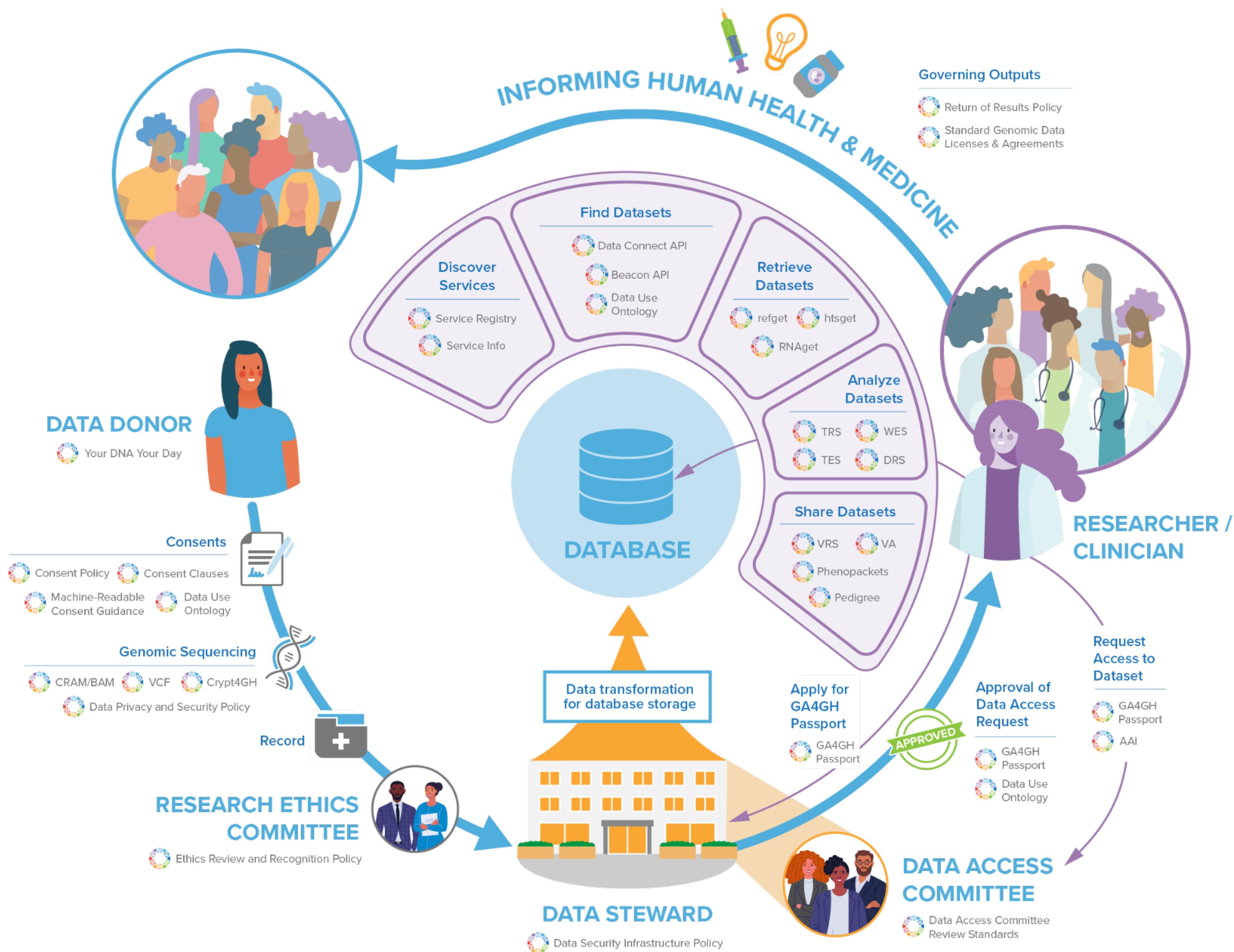
(Author list continued on next page)

# A New Paradigm for Data Sharing

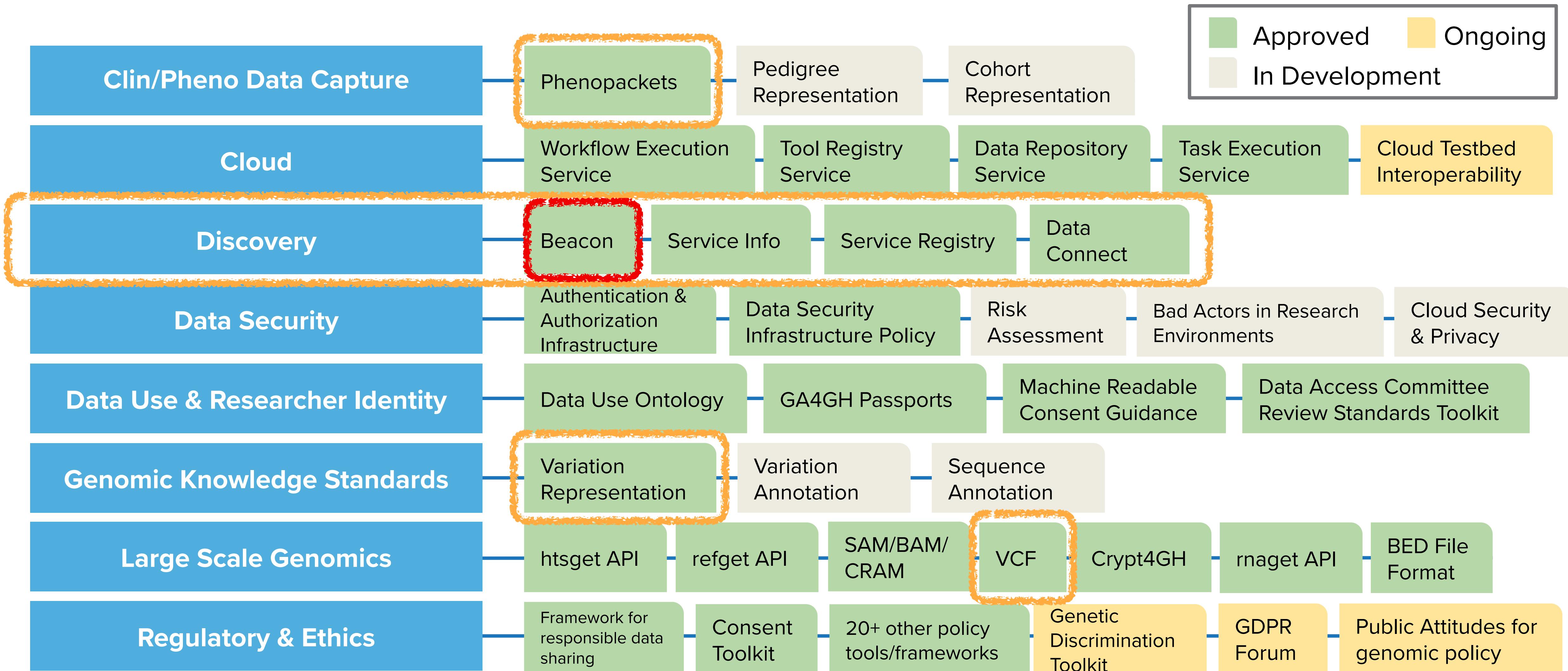


# A New Paradigm for Data Sharing



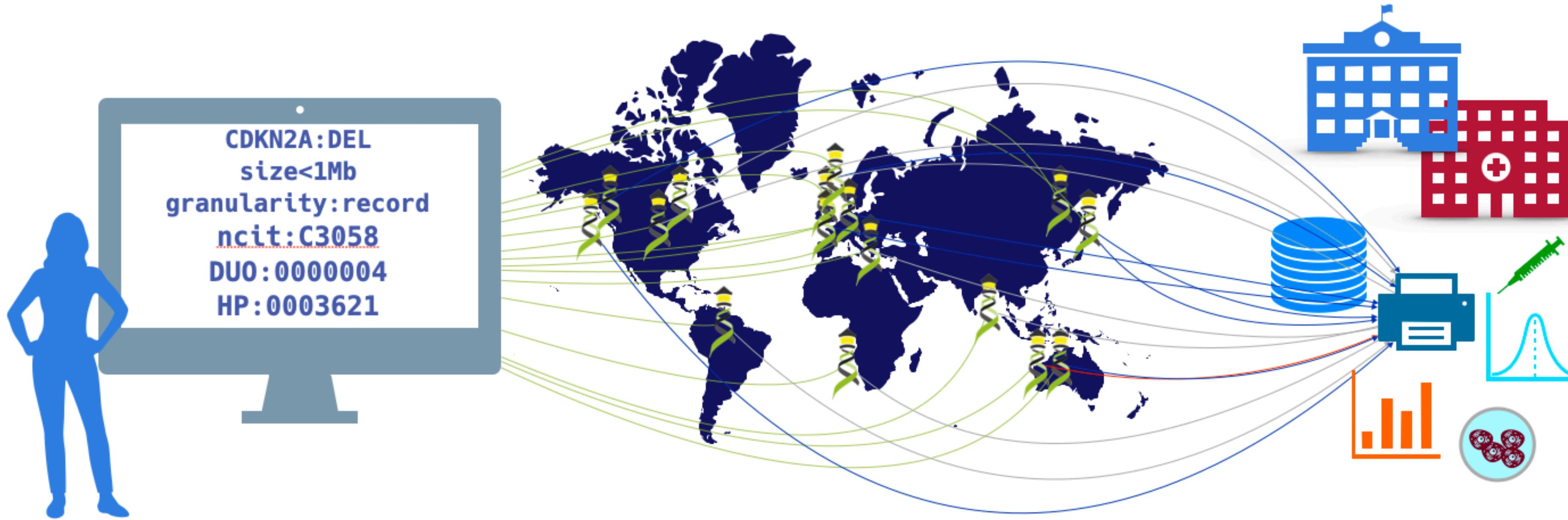


# Overview of GA4GH standards and frameworks



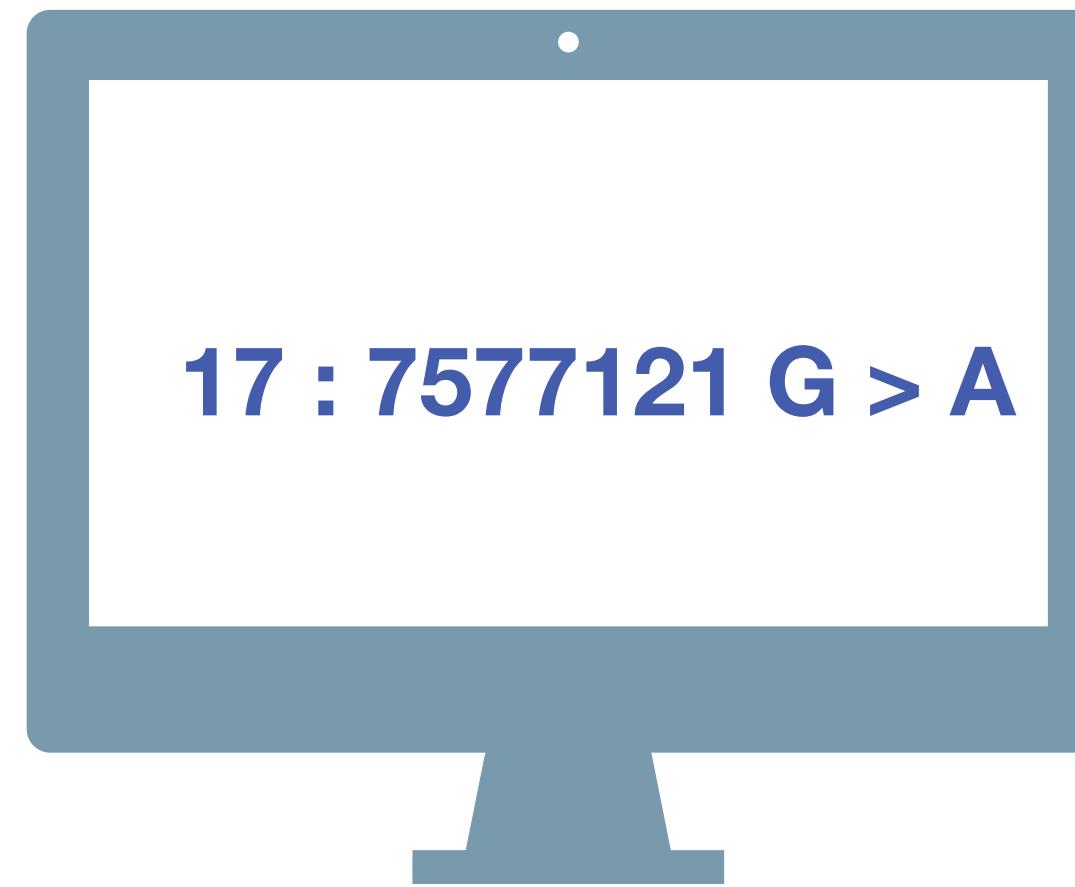


**Global Alliance**  
for Genomics & Health  
Collaborate. Innovate. Accelerate.



# The GA4GH Beacon Protocol

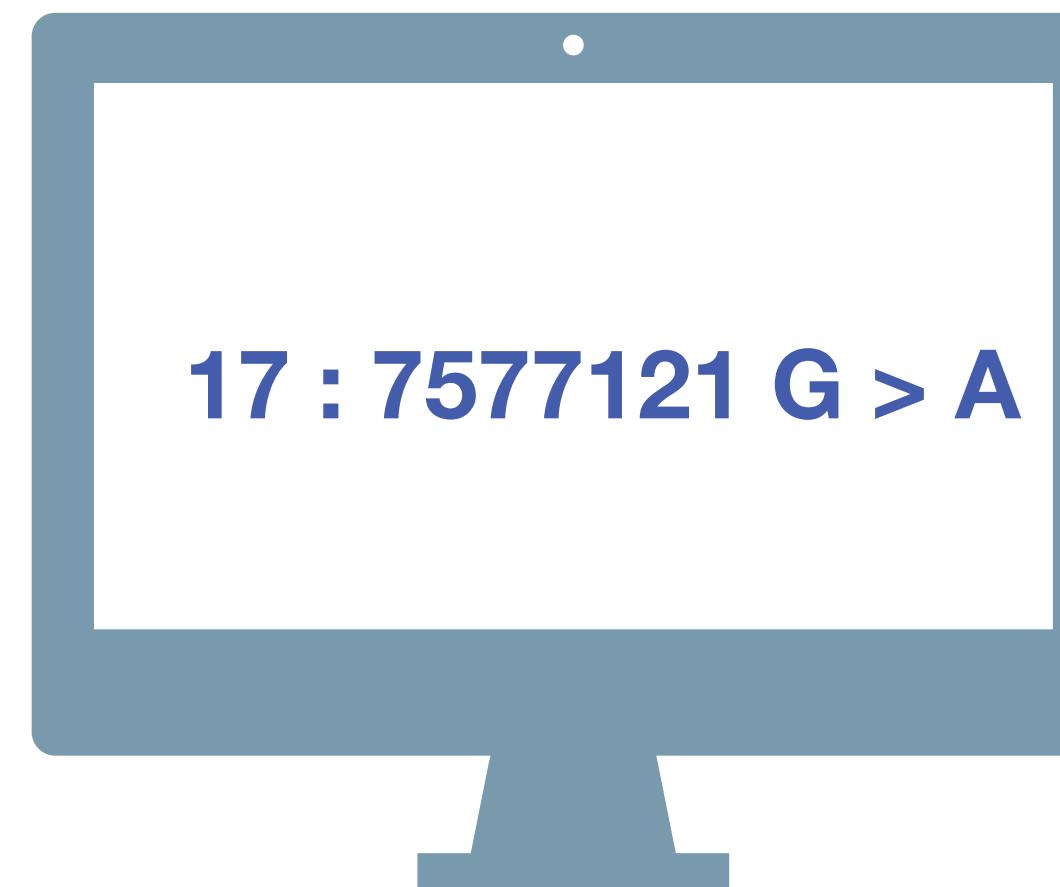
## Federating Genomic Discoveries



# 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**.

# Beacon Project in 2016

An open web service that tests the willingness of international sites to share genetic data.



Beacon Network

Search Beacons

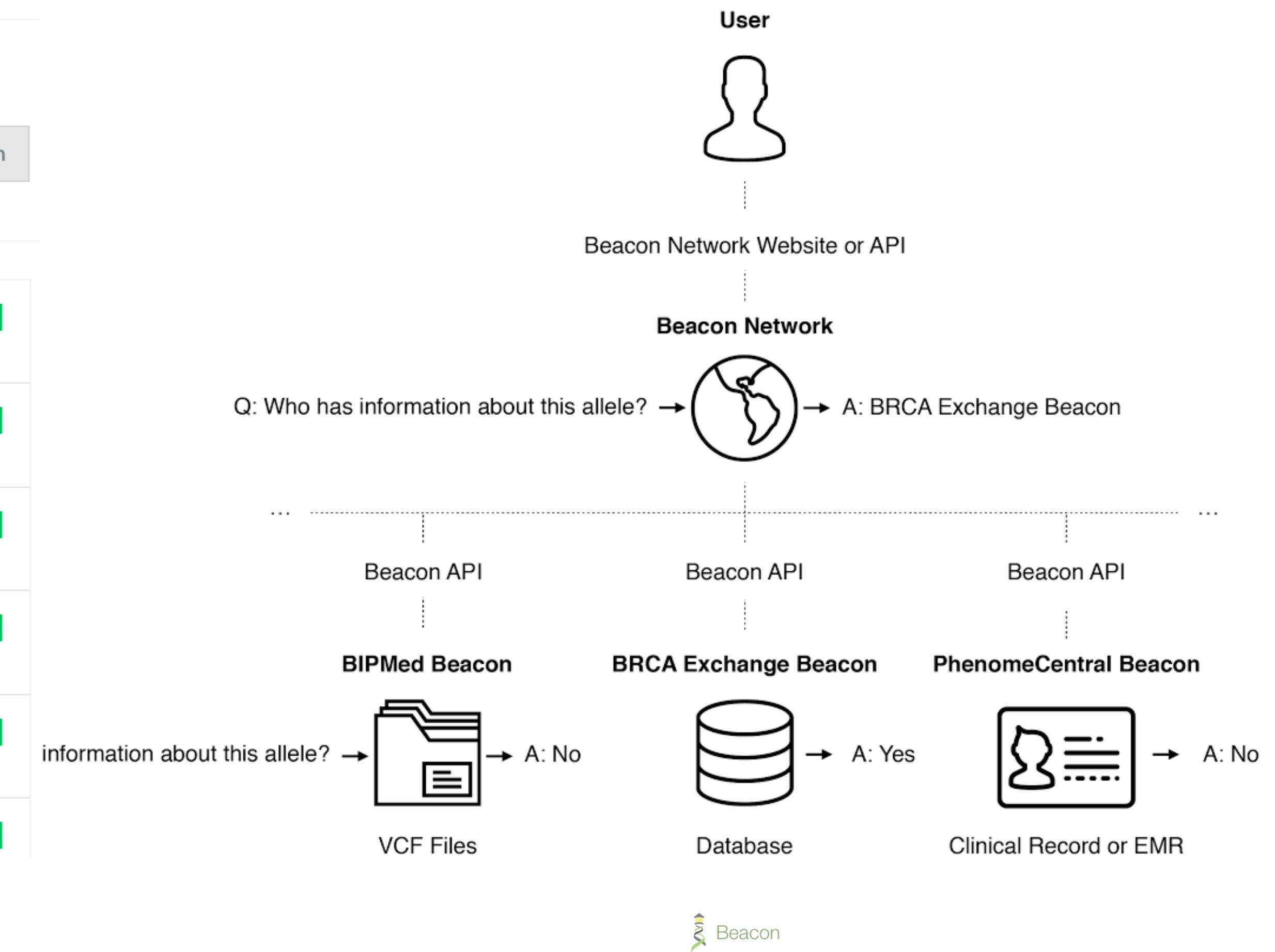
Search all beacons for allele

GRCh37 ▾ 10:118969015 C / CT Search

Response All None  
 Found 16  
 Not Found 27  
 Not Applicable 22

Organization All None  
 AMPLab, UC Berkeley  
 BGI  
 BioReference Laborato...  
 Brazilian Initiative on ...  
 BRCA Exchange  
 Broad Institute  
 Centre for Genomic R...  
 Centro Nacional de A...  
 Curoverse  
 EMBL European Bio...  
 Global Alliance for G...  
 Google  
 Institute for Systems ...  
 Instituto Nacional de ...

BioReference	Hosted by BioReference Laboratories	Found
Catalogue of Somatic Mutations in Cancer	Hosted by Wellcome Trust Sanger Institute	Found
Cell Lines	Hosted by Wellcome Trust Sanger Institute	Found
Conglomerate	Hosted by Global Alliance for Genomics and Health	Found
COSMIC	Hosted by Wellcome Trust Sanger Institute	Found
dbGaP: Combined GRU Catalog and NHLBI Exome Seq...		Found



35+ Organizations 90+ Beacons 200+ Datasets

100K+ Releases

Date	Tag	Title
2018-01-24	v0.4.0	Beacon
2016-05-31	v0.3.0	Beacon

## Beacon v1 Development

2014

GA4GH founding event; Jim Ostell proposes Beacon concept including "more features ... version 2"

2015

- beacon-network.org aggregator created by DNAstack

2016

- Beacon v0.3 release
- work on queries for structural variants (brackets for fuzzy start and end parameters...)

2017

- OpenAPI implementation
- integrating CNV parameters (e.g. "startMin, statMax")

2018

- Beacon v0.4 release in January; feature release for GA4GH approval process
- GA4GH Beacon v1 approved at Oct plenary

2019

- ELIXIR Beacon Network

2020



2021

## Beacon v2 Development

- Beacon<sup>+</sup> concept implemented on progenetix.org
- concepts from GA4GH Metadata (ontologies...)
- entity-scoped query parameters ("individual.age")

- Beacon<sup>+</sup> demos "handover" concept

- Beacon hackathon Stockholm; settling on "filters"
- Barcelona goes Zurich developers meeting
- Beacon API v2 Kick off
- adopting "handover" concept

- "Scouts" teams working on different aspects - filters, genomic variants, compliance ...
- discussions w/ clinical stakeholders

- framework + models concept implemented
- range and bracket queries, variant length parameters
- starting of GA4GH review process

- further changes esp. in default model, aligning with Phenopackets and VRS
- unified beacon-v2 code & docs repository
- Beacon v2 approved at Apr GA4GH Connect

2022

## Related ...

- ELIXIR starts Beacon project support

- GA4GH re-structuring (workstreams...)
- Beacon part of Discovery WS

- new Beacon website (March)

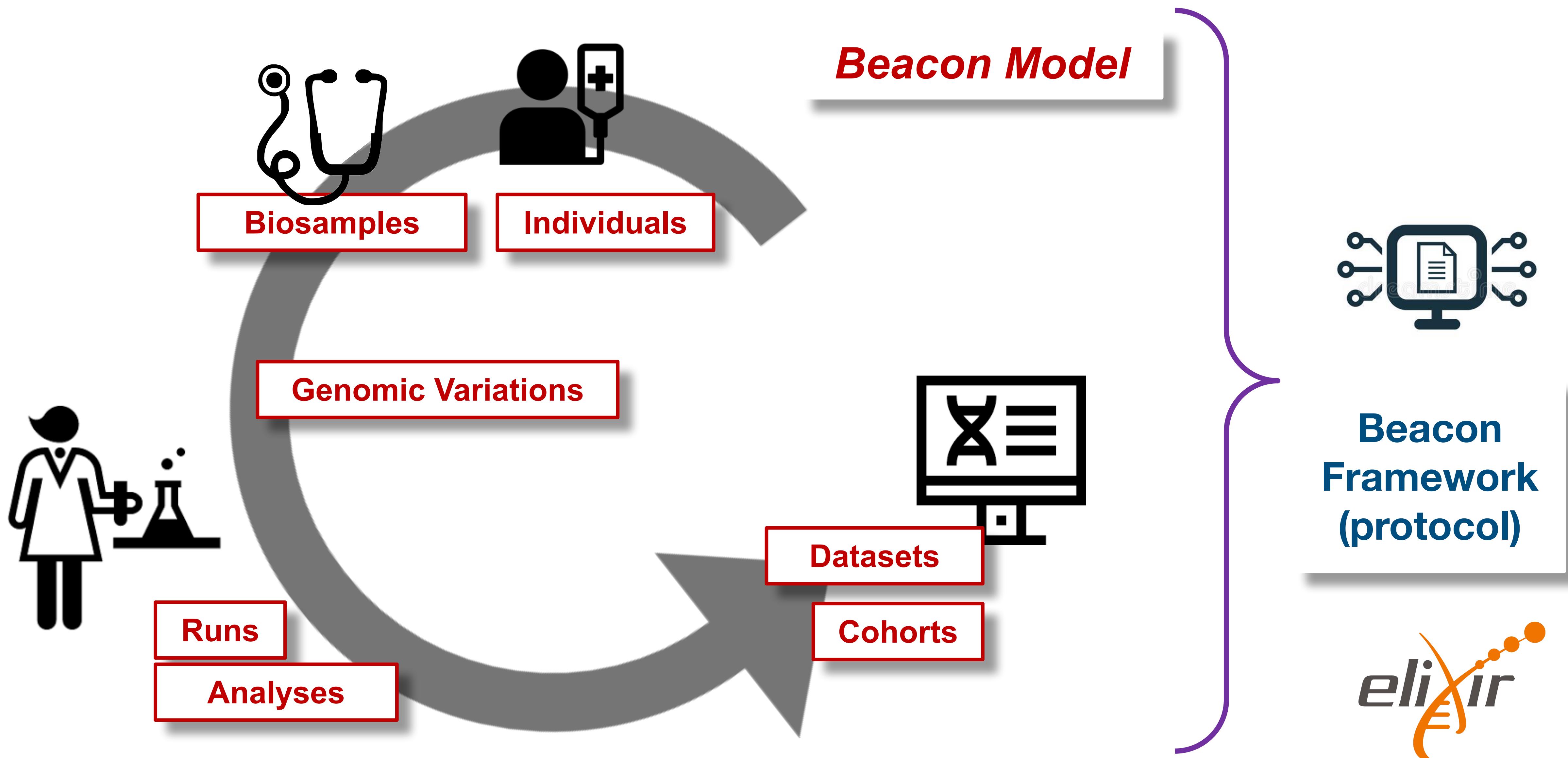
- Beacon publication at Nature Biotechnology

- Phenopackets v2 approved

- [docs.genomebeacons.org](https://docs.genomebeacons.org)

# Beacon v2

docs.genomebeacons.org



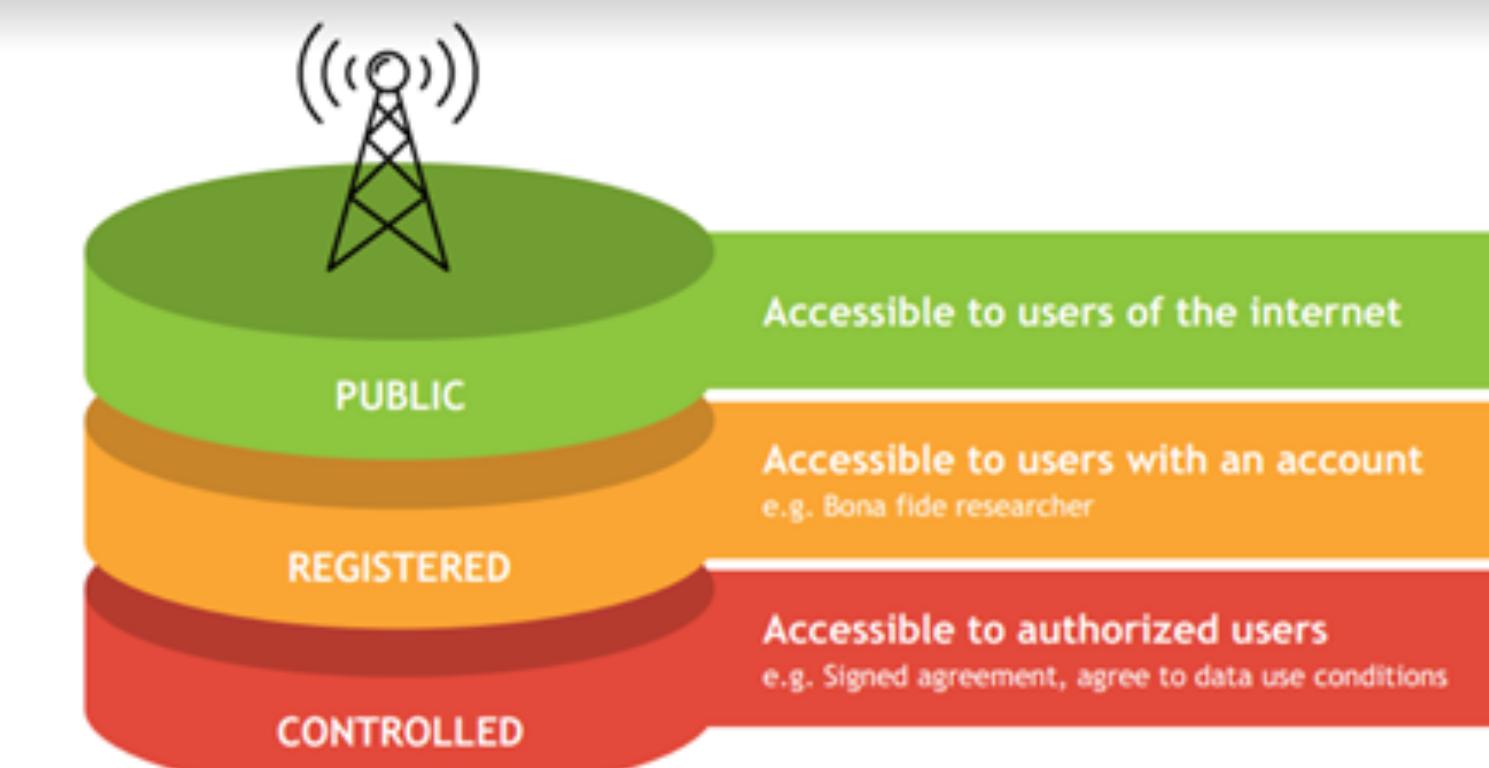
**Beacon  
Framework  
(protocol)**

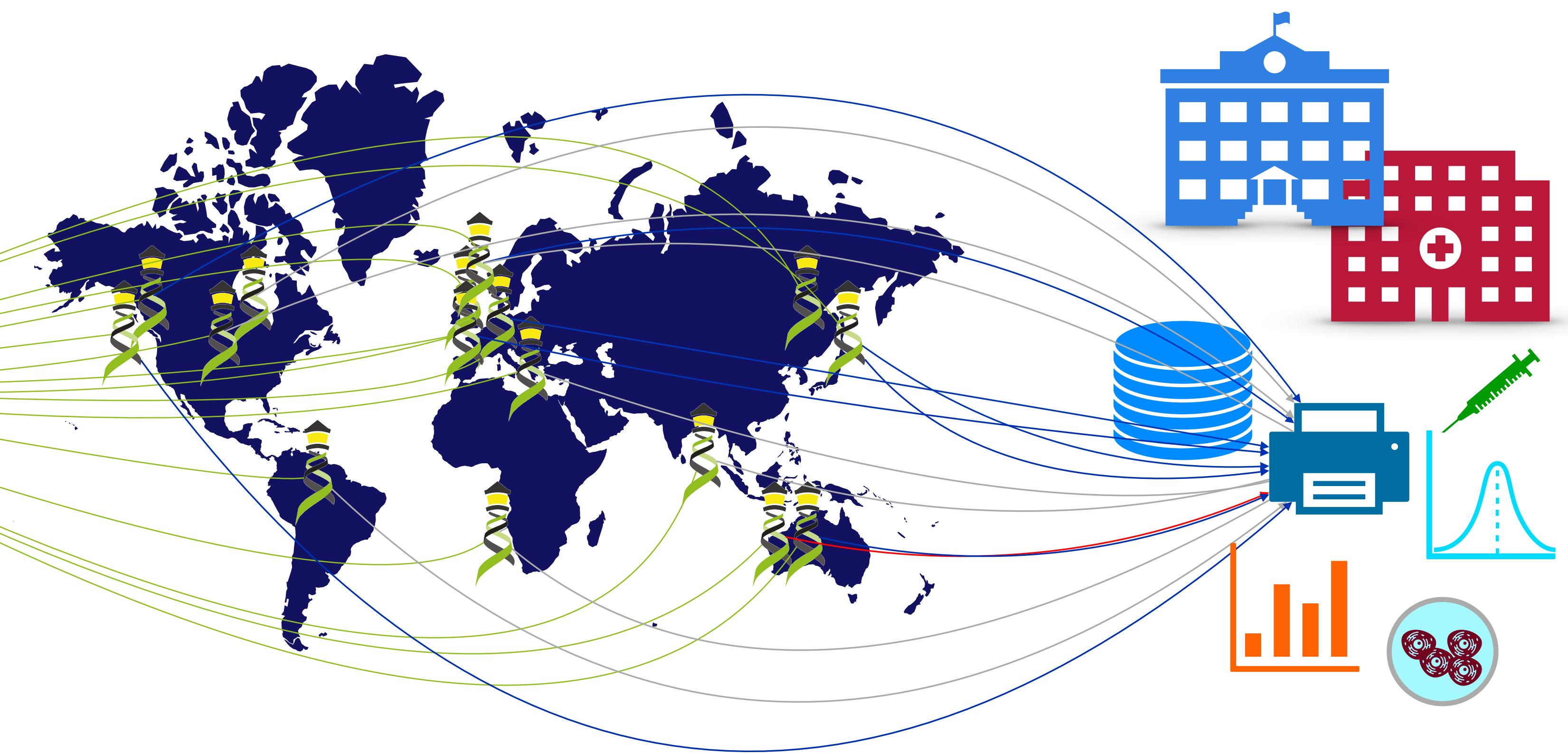


# Beacon Security

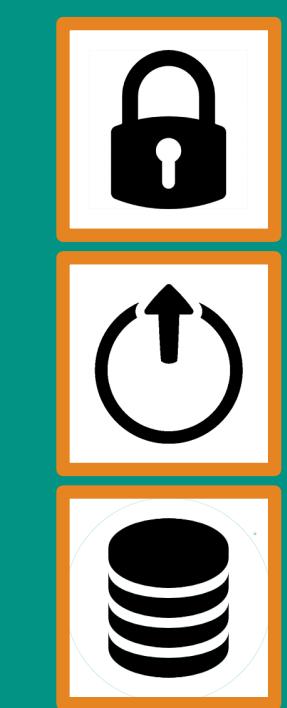
## Security by Design ... if Implemented in the Environment

- the beacon API specification does not implement explicit security (e.g. checking user authentication and authorization)
- the framework implements different levels of response granularity which can be mapped to authorization levels (**boolean** / **count** / **record** level responses)
- implementations can have beacons running in secure environments with a **gatekeeper** service managing authentication and authorization levels, and potentially can filter responses for escalated levels
- the backend can implement additional access reduction, on a user <-> dataset level if needed





Can you provide data about focal deletions in CDKN2A in Glioblastomas from juvenile patients with unrestricted access?

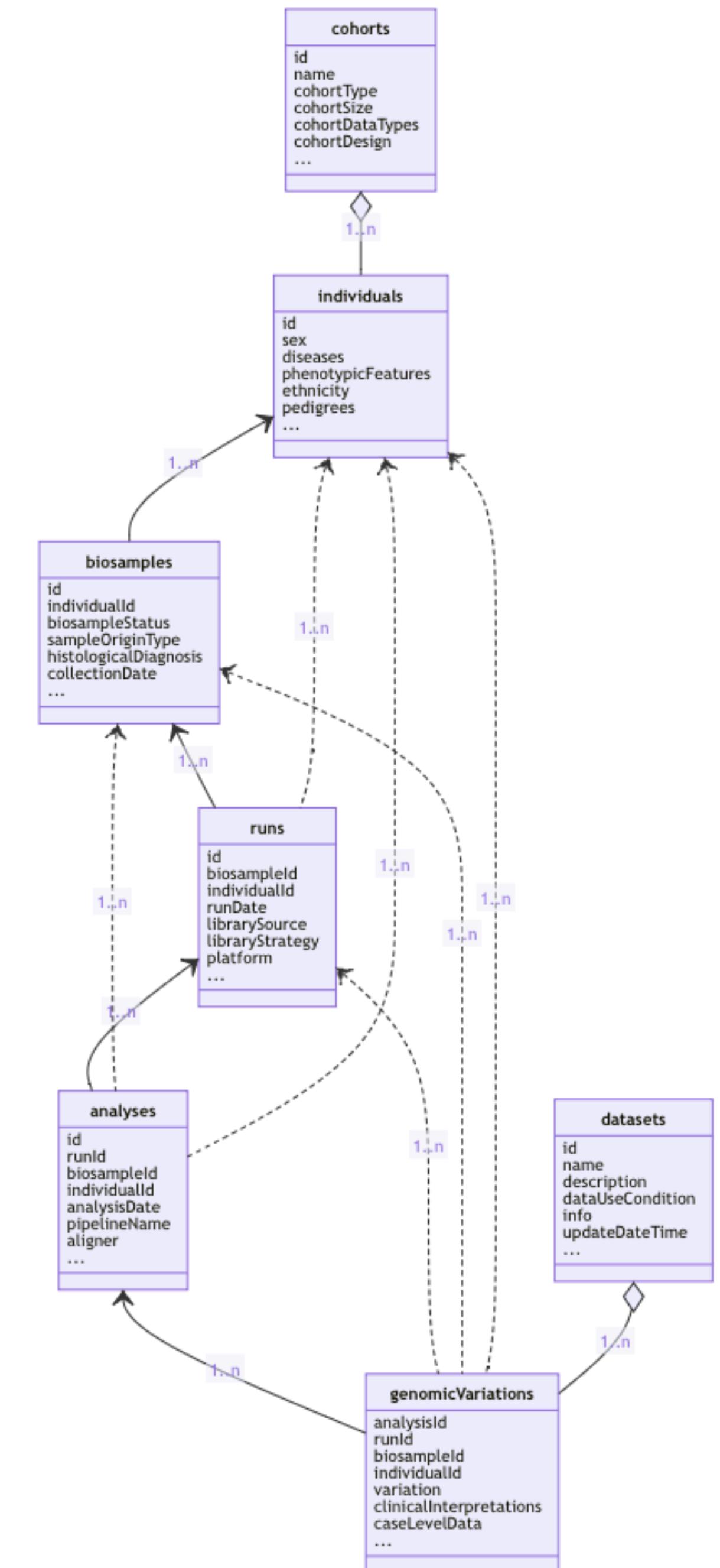


## Beacon v2 API

The Beacon API v2 represents a simple but powerful **genomics API** for **federated** data discovery and retrieval

# Beacon Default v2 Model

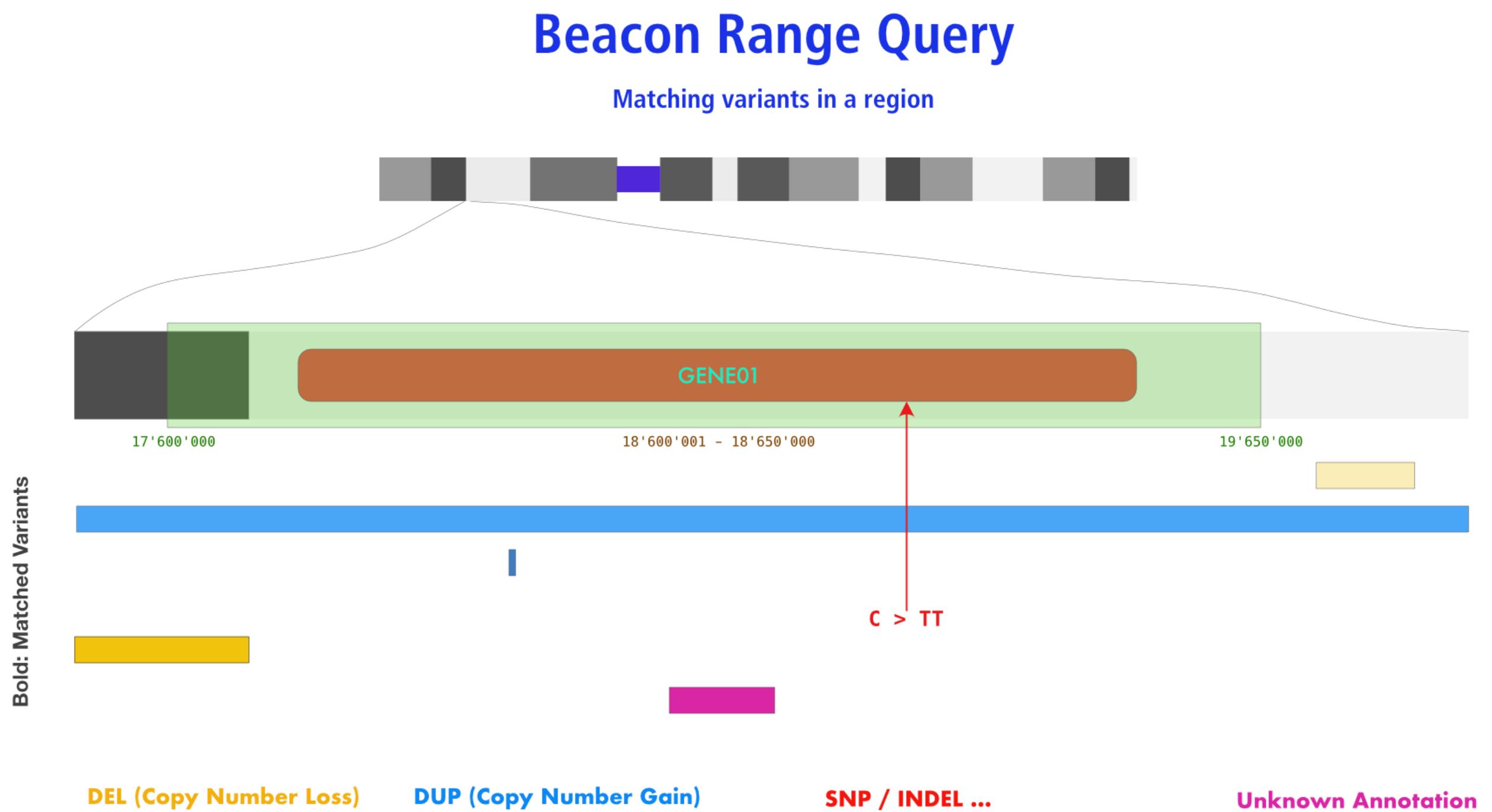
- The Beacon **framework** describes the overall structure of the API requests, responses, parameters, the common components, etc.
- Beacon **models** describe the set of concepts included in a Beacon, like individual or biosample, and also the relationships between them.
- Besides logical concepts, the Beacon **models** represent the schemas for data delivery in “record” granularity
- Beacon explicitly allows the use of *other models* besides its *version specific default*.
- Adherence to a shared **model** empowers federation
- Use of the **framework** w/ different models extends adoption



# Variation Queries

## Range ("anything goes") Request

- defined through the use of 1 start, 1 end
- any variant... but can be limited by type etc.



## Beacon Query Types

Sequence / Allele   CNV (Bracket)   **Genomic Range**   Aminoacid   Gene ID   HGVS   Sam

Dataset: Test Database - examplez

Chromosome: 17 (NC\_000017.11)

Variant Type: SO:0001059 (any sequence alteration - S...)

Start or Position: 7572826

End (Range or Structural Var.): 7579005

Reference Base(s): N

Alternate Base(s): A

Select Filters: Chromosome 17

Query Database

Form Utilities: Gene Spans, Cytoband(s)

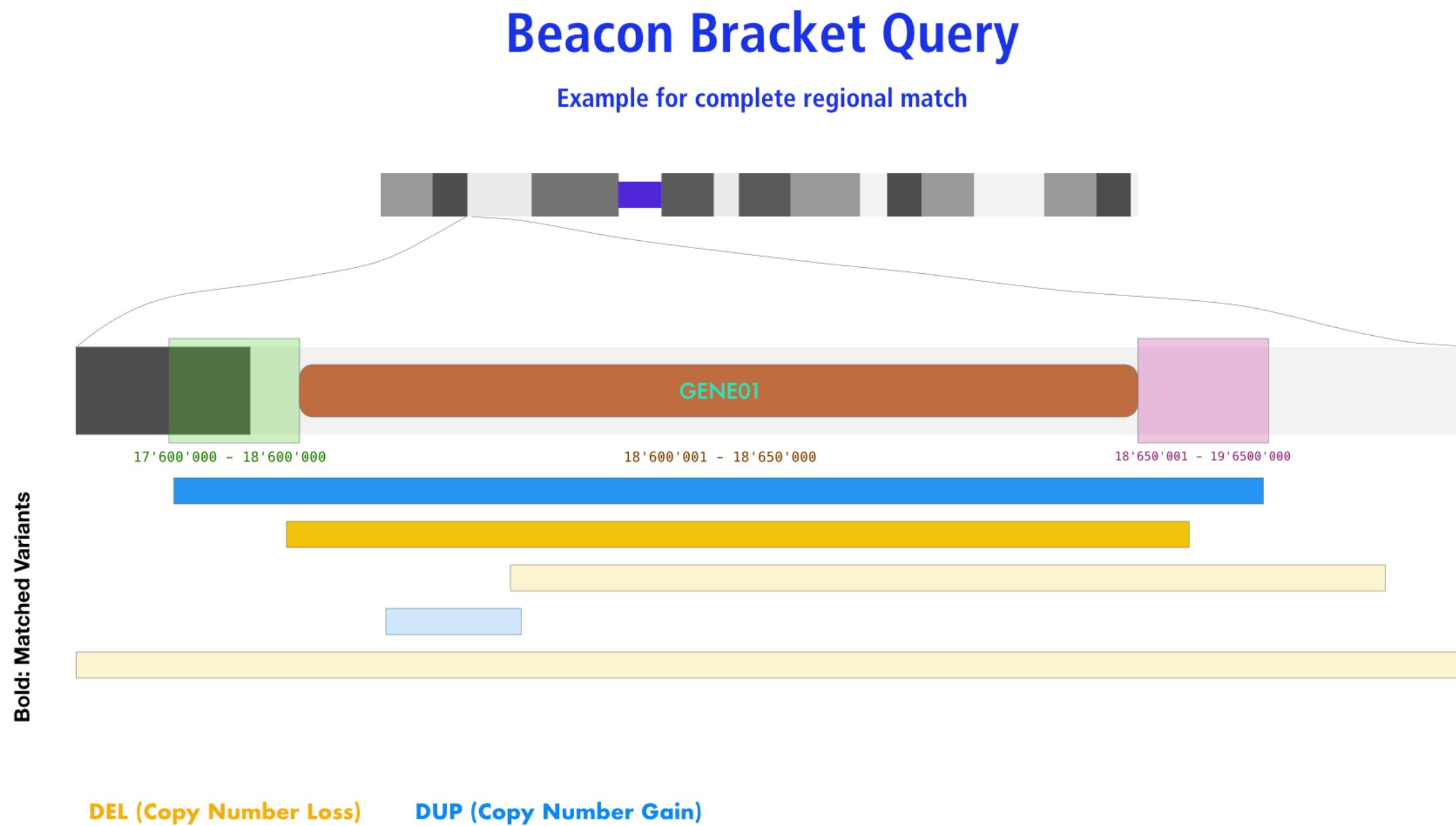
Query Examples: CNV Example, SNV Example, Range Example, Gene Match, Aminoacid Example, Identifier - HeLa

As in the standard SNV query, this example shows a Beacon query against mutations in the EIF4A1 gene in the DIPG childhood brain tumor dataset. However, this range + wildcard query will return any variant with alternate bases (indicated through "N"). Since parameters will be interpreted using an "AND" paradigm, either Alternate Bases OR Variant Type should be specified. The exact variants which were being found can be retrieved through the variant handover [H->O] link.

# Variation Queries

## Bracket ("CNV") Query

- defined through the use of 2 start, 2 end
- any contiguous variant...



### Beacon Query Types

Sequence / Allele   **CNV (Bracket)**   Genomic Range   Aminoacid   Gene ID   HGVS   Sam

#### Dataset

Test Database - examplez X | ▼

#### Chromosome

9 (NC\_000009.12) | ▼

#### Variant Type

EFO:0030067 (copy number deletion) | ▼

#### Start or Position

21000001-21975098

#### End (Range or Structural Var.)

21967753-23000000

#### Select Filters

NCIT:C3058: Glioblastoma (100) X | ▼

#### Chromosome 9

21000001-21975098



### Query Database

#### Form Utilities

Gene Spans

Cytoband(s)

#### Query Examples

[CNV Example](#)

[SNV Example](#)

[Range Example](#)

[Gene Match](#)

[Aminoacid Example](#)

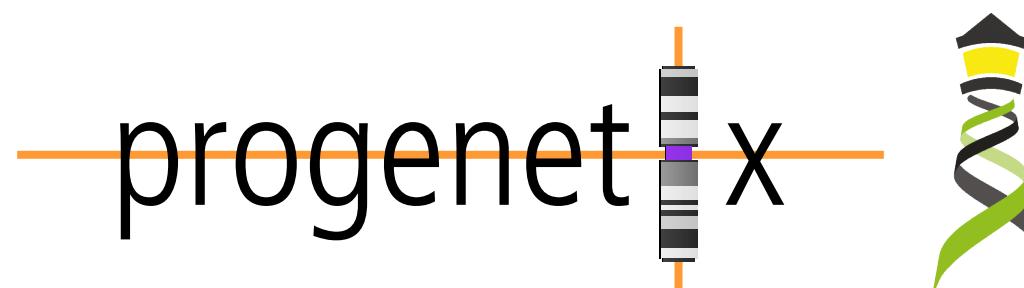
[Identifier - HeLa](#)

This example shows the query for CNV deletion variants overlapping the CDKN2A gene's coding region with at least a single base, but limited to "focal" hits (here i.e.  $\leq \sim 2\text{Mbp}$  in size). The query is against the examplez collection and can be modified e.g. through changing the position parameters or data source.

# Beacon v2 Filters

# **Example: Use of hierarchical classification systems (here NCI I neoplasm core)**

- Beacon v2 relies heavily on "filters"
    - ontology term / CURIE
    - alphanumeric
    - custom
  - Beacon v2 "filters" assumes inclusion of child terms when using hierarchical classifications
    - implicit *OR* with otherwise assumed *AND*
  - implementation of hierarchical annotations overcomes some limitations of "fuzzy" disease annotations



Beacon<sup>+</sup> specific: Multiple term selection with OR logic

<input checked="" type="checkbox"/>	> <a href="#">NCIT:C4914: Skin Carcinoma</a>	213
<input type="checkbox"/>	> <a href="#">NCIT:C4475: Dermal Neoplasm</a>	109
<input checked="" type="checkbox"/>	> <a href="#">NCIT:C45240: Cutaneous Hematopoietic and Lymphoid Cell Neoplasm</a>	310

**Filters:** NCIT:C4914, NCIT:C4819, NCIT:C9231, NCIT:C2921, NCIT:C45240, NCIT:C6858, NCIT:C3467, NCIT:C45340, NCIT:C7195, NCIT:C3246, NCIT:C7217

progenetix

Variants: 0    *f*alleles: 0    Callsets Variants ↗    UCSC region ↗    Calls: 0    Legacy Interface ↗    Samples: 523    [Show JSON Response](#)

Results    [Biosamples](#)

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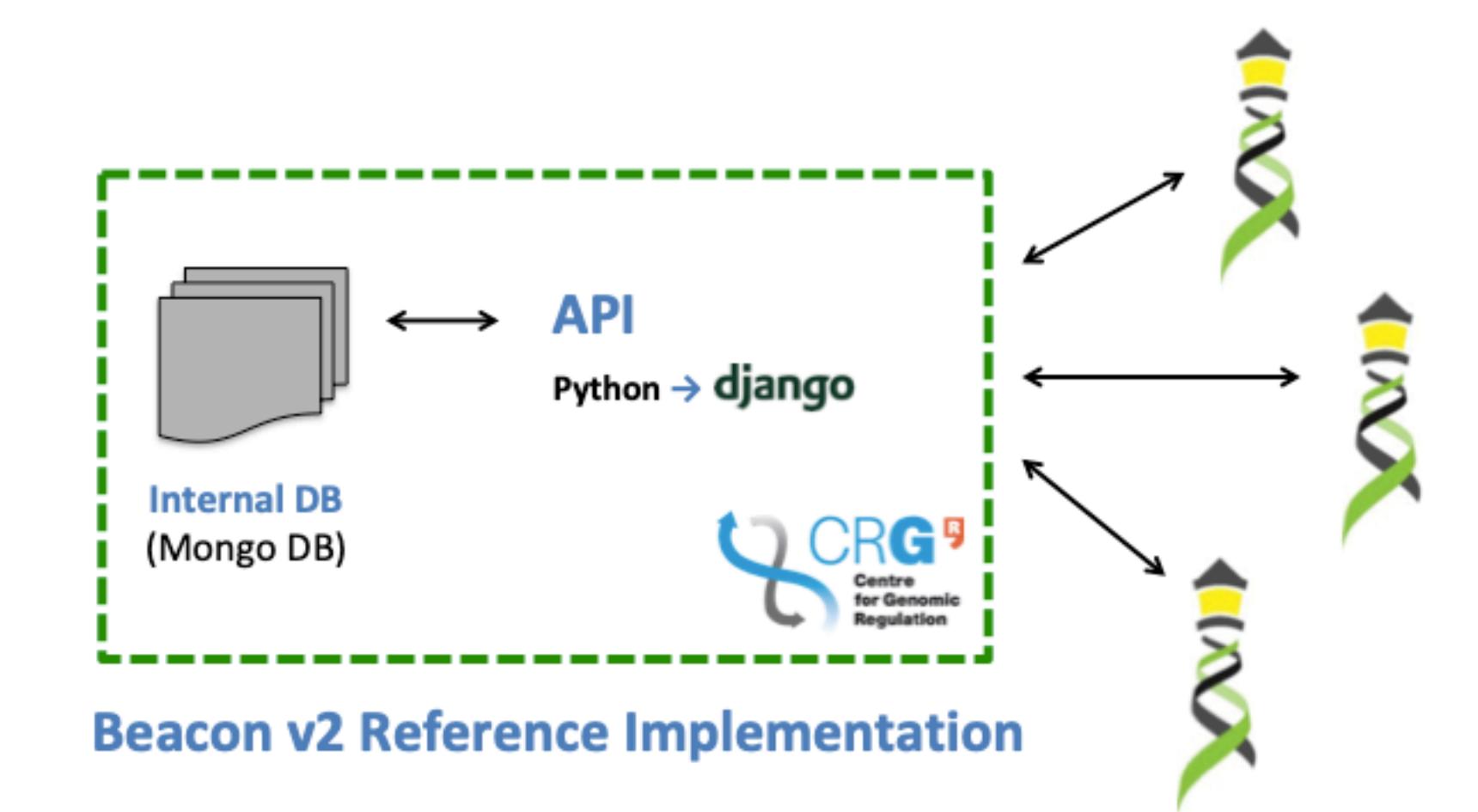
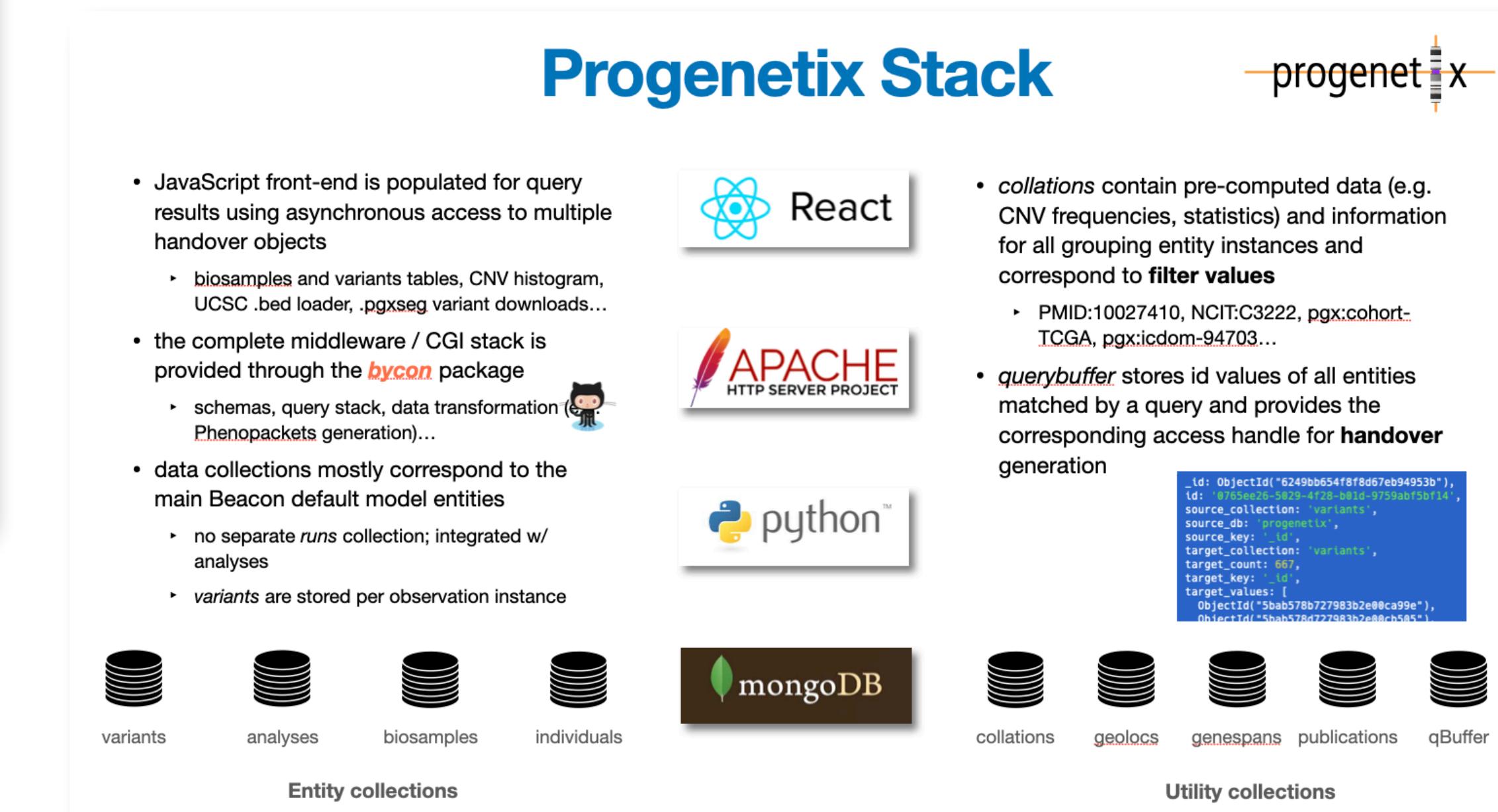
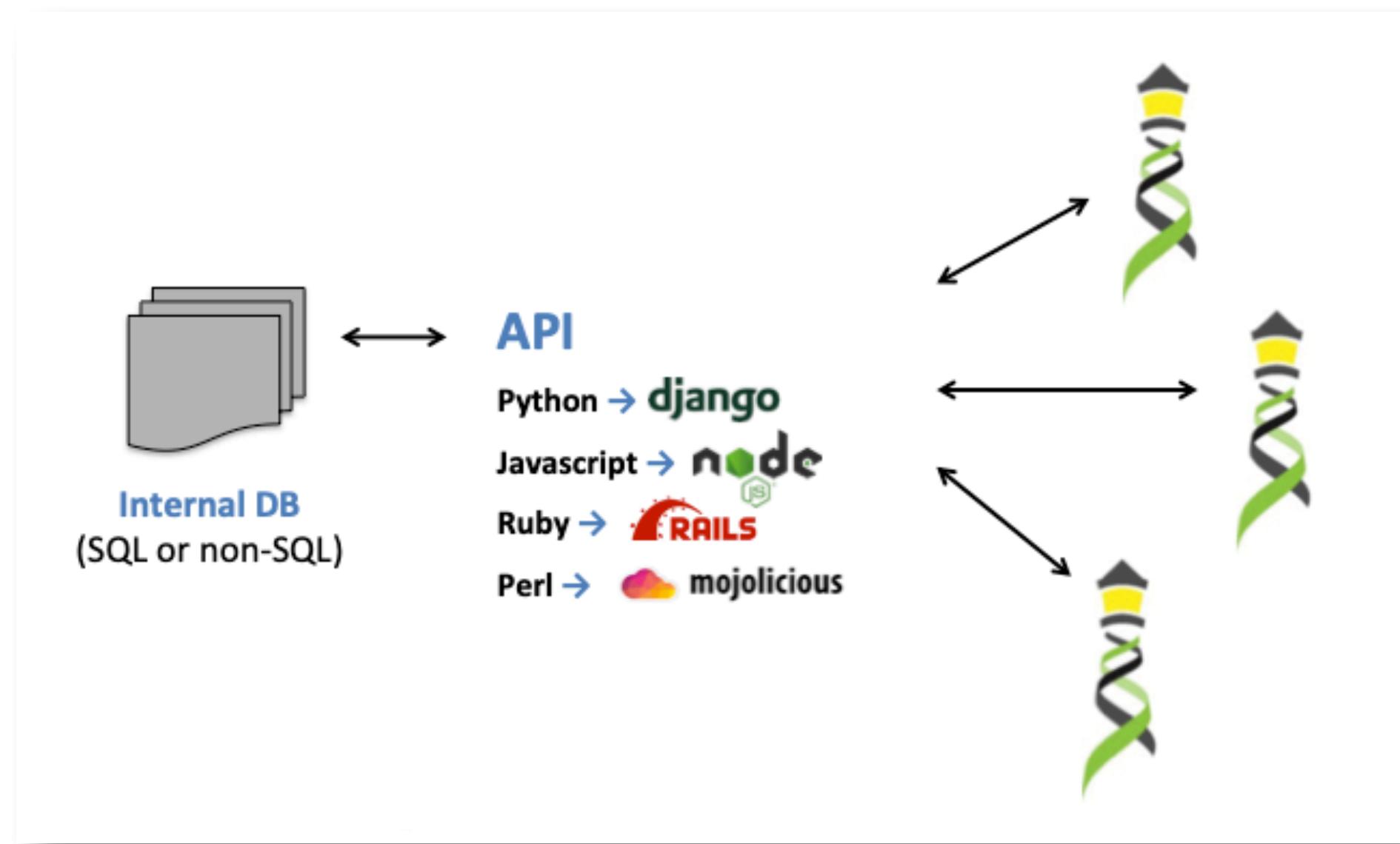
<b>Id</b>	<b>Description</b>	<b>Classifications</b>	<b>Identifiers</b>	<b>DEL</b>	<b>DUP</b>	<b>CNV</b>
PGX_AM_BS_MCC01	Merkel cell carcinoma	<a href="#">icdot-C44.9</a> Skin, NOS <a href="#">icdom-82473</a> Merkel cell carcinoma <a href="#">NCIT:C9231</a> Merkel Cell Carcinoma	<a href="#">PMID:9537255</a>	0.116	0.104	0.22
PGX_AM_BS_MCC02	Merkel cell carcinoma	<a href="#">icdot-C44.9</a> Skin, NOS <a href="#">icdom-82473</a> Merkel cell carcinoma <a href="#">NCIT:C9231</a> Merkel Cell Carcinoma	<a href="#">PMID:9537255</a>	0.154	0.056	0.21
PGX_AM_BS_MCC03	Merkel cell carcinoma	<a href="#">icdot-C44.9</a> Skin, NOS <a href="#">icdom-82473</a> Merkel cell carcinoma <a href="#">NCIT:C9231</a> Merkel Cell Carcinoma	<a href="#">PMID:9537255</a>	0.137	0.21	0.347
PGX_AM_BS_MCC04	Merkel cell carcinoma	<a href="#">icdot-C44.9</a> Skin, NOS <a href="#">icdom-82473</a> Merkel cell carcinoma <a href="#">NCIT:C9231</a> Merkel Cell Carcinoma	<a href="#">PMID:9537255</a>	0.158	0.056	0.214
PGX_AM_BS_MCC05	Merkel cell carcinoma	<a href="#">icdot-C44.9</a> Skin, NOS <a href="#">icdom-82473</a> Merkel cell carcinoma <a href="#">NCIT:C9231</a> Merkel Cell Carcinoma	<a href="#">PMID:9537255</a>	0.107	0.327	0.434

« < > »

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# Implementing Beacon v2

... its just code \\_(\_ツ)\_/



# *bycon* for GA4GH Beacon

## Implementation driven development of a GA4GH standard

# bycon Beacon

## Implementation driven standards development

- Progenetix' Beacon+ has served as implementation driver since 2016
- the *bycon* package is used to prototype advanced Beacon features such as
  - structural variant queries
  - data handovers
  - Phenopackets integration
  - variant co-occurrences
  - ...

Beacon protocol response verifier at time of GA4GH approval Spring 2022

Beacon v2 GA4GH Approval Registry

Beacons:    

Category	EGA	progenetix	Theoretical Cytogenetics and Oncogenomics group at UZH and SIB
BeaconMap	Green	Green	Green
Bioinformatics analysis	Green	Green	Green
Biological Sample	Green	Green	Green
Cohort	Green	Green	Green
Configuration	Green	Green	Green
Dataset	Green	Green	Green
EntryTypes	Green	Green	Green
Genomic Variants	Green	Green	Green
Individual	Green	Green	Green
Info	Green	Green	Green
Sequencing run	Green	Green	Green

Category	cnag	University of Leicester
BeaconMap	Green	Green
Bioinformatics analysis	White	White
Biological Sample	Red	White
Cohort	White	White
Configuration	Green	White
Dataset	Red	White
EntryTypes	Green	White
Genomic Variants	White	White
Individual	Red	White
Info	White	White
Sequencing run	White	White

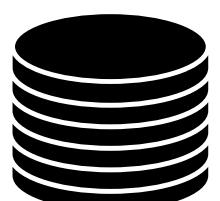
Green: Matches the Spec, Red: Not Match the Spec, White: Not Implemented



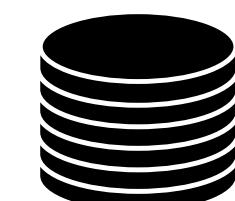
# *bycon* based Progenetix Stack



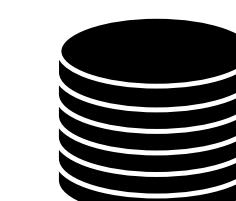
- JavaScript front-end is populated for query results using asynchronous access to multiple handover objects
  - ▶ biosamples and variants tables, CNV histogram, UCSC .bed loader, .pgxseg variant downloads...
- the complete middleware / CGI stack is provided through the *bycon* package
  - ▶ schemas, query stack, data transformation (Phenopackets generation)...
- data collections mostly correspond to the main Beacon default model entities
  - ▶ no separate *runs* collection; integrated w/ analyses
  - ▶ *variants* are stored per observation instance



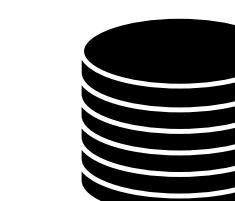
variants



analyses



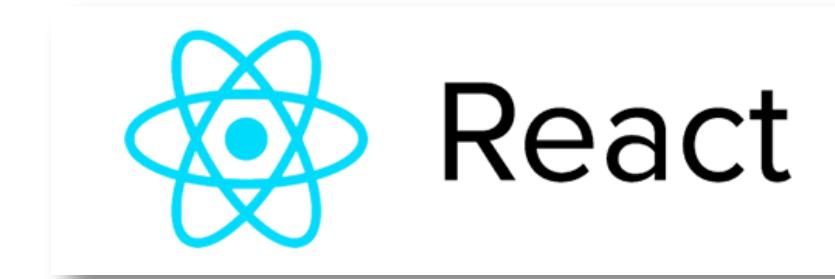
biosamples



individuals

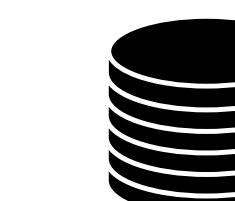


Entity collections

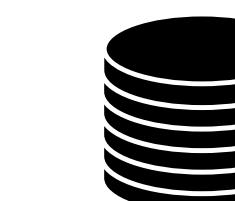


- *collations* contain pre-computed data (e.g. CNV frequencies, statistics) and information for all grouping entity instances and correspond to **filter values**
  - ▶ PMID:10027410, NCIT:C3222, pgx:cohort-TCGA, pgx:icdom-94703...
- *querybuffer* stores id values of all entities matched by a query and provides the corresponding access handle for **handover** generation

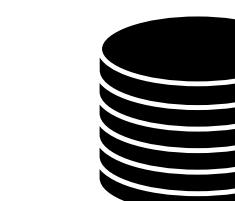
```
_id: ObjectId("6249bb654f8f8d67eb94953b"),
id: '0765ee26-5029-4f28-b01d-9759abf5bf14',
source_collection: 'variants',
source_db: 'progenetix',
source_key: '_id',
target_collection: 'variants',
target_count: 667,
target_key: '_id',
target_values: [
  ObjectId("5bab578b727983b2e00ca99e"),
  ObjectId("5bab578d727983b2e00cb505")]
```



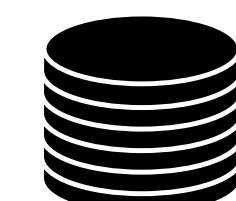
collations



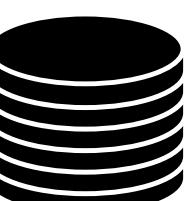
geolocs



genespans



publications



qBuffer

Utility collections

progenetix / byconaut

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byconaut Public

Edit Pins Unwatch 2 Fork 1 Star 0

bycon.progenetix.org  
github.com/progenetix/bycon/

progenetix / beaconplus-web

Type ⌘ to search

Code Pull requests Actions Projects Security Insights Settings

mbaudis get\_plot\_parameters

bin docs exports imports local rsrc services tmp .gitignore LICENSE README.md \_\_init\_\_.py install.py install.yaml mkdocs.yaml

2 branches

main

beaconplus-web Public forked from progenetix/progenetix-web

main 1 branch 0 tags

This branch is 44 commits ahead, 24 commits behind progenetix:main.

beaconplus.progenetix.org  
.../progenetix/beaconplus-web/

progenetix / bycon

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mbaudis 1.3.6 ... be19a12 3 days ago 852 commits

File	Commit	Date
.github/workflows	Create mk-bycon-docs.yaml	8 months ago
bycon	1.3.6	3 days ago
docs	1.3.6	3 days ago
local	1.3.5 preparation	2 weeks ago
.gitignore	Update .gitignore	3 months ago
LICENSE	Create LICENSE	3 years ago
MANIFEST.in	major library & install disentanglement	9 months ago
README.md	#### 2023-07-23 (v1.0.68)	4 months ago
install.py	1.3.6	3 days ago
install.yaml	v1.0.57	5 months ago
mkdocs.yaml	1.1.6	3 months ago
requirements.txt	1.3.6	3 days ago
setup.cfg	...	10 months ago
setup.py	1.3.6	3 days ago
updev.sh	1.3.6	3 days ago

About

Bycon - A Python Based Beacon API (beacon-project.io) implementation leveraging the Progenetix (progenetix.org) data model

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bycon.progenetix.org  
github.com/progenetix/bycon/

# pgxRpi

## An interface API for analyzing Progenetix CNV data in R using the Beacon+ API

GitHub: <https://github.com/progenetix/pgxRpi>

README.md

### pgxRpi

Welcome to our R wrapper package for Progenetix REST API that leverages the capabilities of [Beacon v2](#) specification. Please note that a stable internet connection is required for the query functionality. This package is aimed to simplify the process of accessing oncogenomic data from [Progenetix](#) database.

You can install this package from GitHub using:

```
install.packages("devtools")
devtools::install_github("progenetix/pgxRpi")
```

For accessing metadata of biosamples/individuals, or learning more about filters, get started from the vignette [Introduction\\_1\\_loadmetadata](#).

For accessing CNV variant data, get started from this vignette [Introduction\\_2\\_loadvariants](#).

For accessing CNV frequency data, get started from this vignette [Introduction\\_3\\_loadfrequency](#).

For processing local pgxseg files, get started from this vignette [Introduction\\_4\\_process\\_pgxseg](#).

If you encounter problems, try to reinstall the latest version. If reinstallation doesn't help, please contact us.

Bioconductor

### pgxRpi

platforms all rank 2218 / 2221 support 0 / 0 in BioC devel only  
build ok updated < 1 month dependencies 144

DOI: [10.18129/B9.bioc.pgxRpi](https://doi.org/10.18129/B9.bioc.pgxRpi)

This is the **development** version of pgxRpi; to use it, please install the [devel version](#) of Bioconductor.

### R wrapper for Progenetix

Bioconductor version: Development (3.19)

The package is an R wrapper for Progenetix REST API built upon the Beacon v2 protocol. Its purpose is to provide a seamless way for retrieving genomic data from Progenetix database—an open resource dedicated to curated oncogenomic profiles. Empowered by this package, users can effortlessly access and visualize data from Progenetix.

Author: Hangjia Zhao [aut, cre] , Michael Baudis [aut] 

Maintainer: Hangjia Zhao <[hangjia.zhao@uzh.ch](mailto:hangjia.zhao@uzh.ch)>

Citation (from within R, enter `citation("pgxRpi")`):

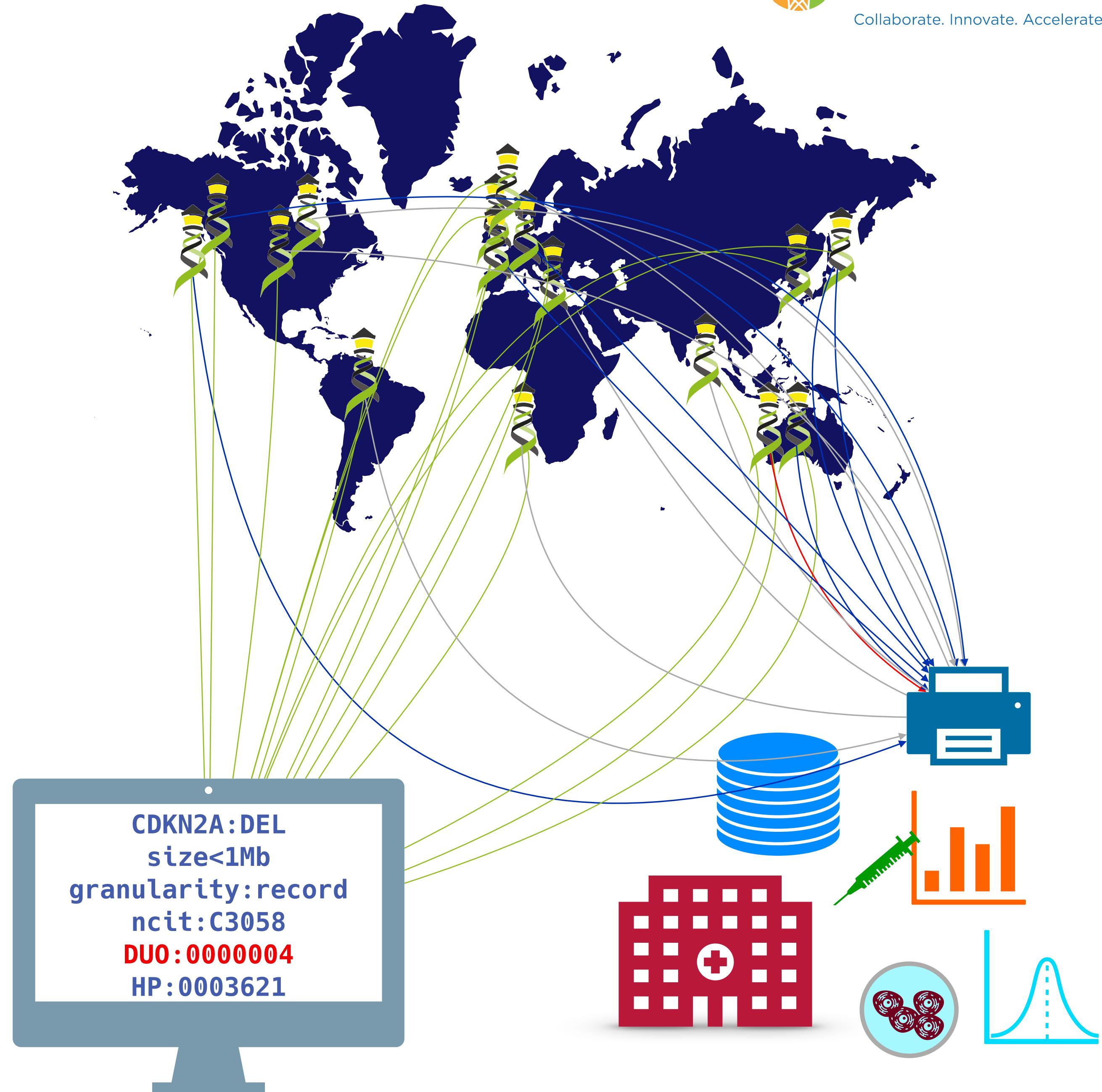
Zhao H, Baudis M (2023). *pgxRpi: R wrapper for Progenetix*. [doi:10.18129/B9.bioc.pgxRpi](https://doi.org/10.18129/B9.bioc.pgxRpi), R package version 0.99.9, <https://bioconductor.org/packages/pgxRpi>.

# What Can You Do?

- implement procedures and standards supporting **data discovery** (FAIR principles) and federation approaches using Beacon
- promote forward looking consent and data protection models (**ORD** principle "as secure as necessary, as open as possible")
- **support** and/or get involved with international **data standards** efforts and projects



**Collaborate!**

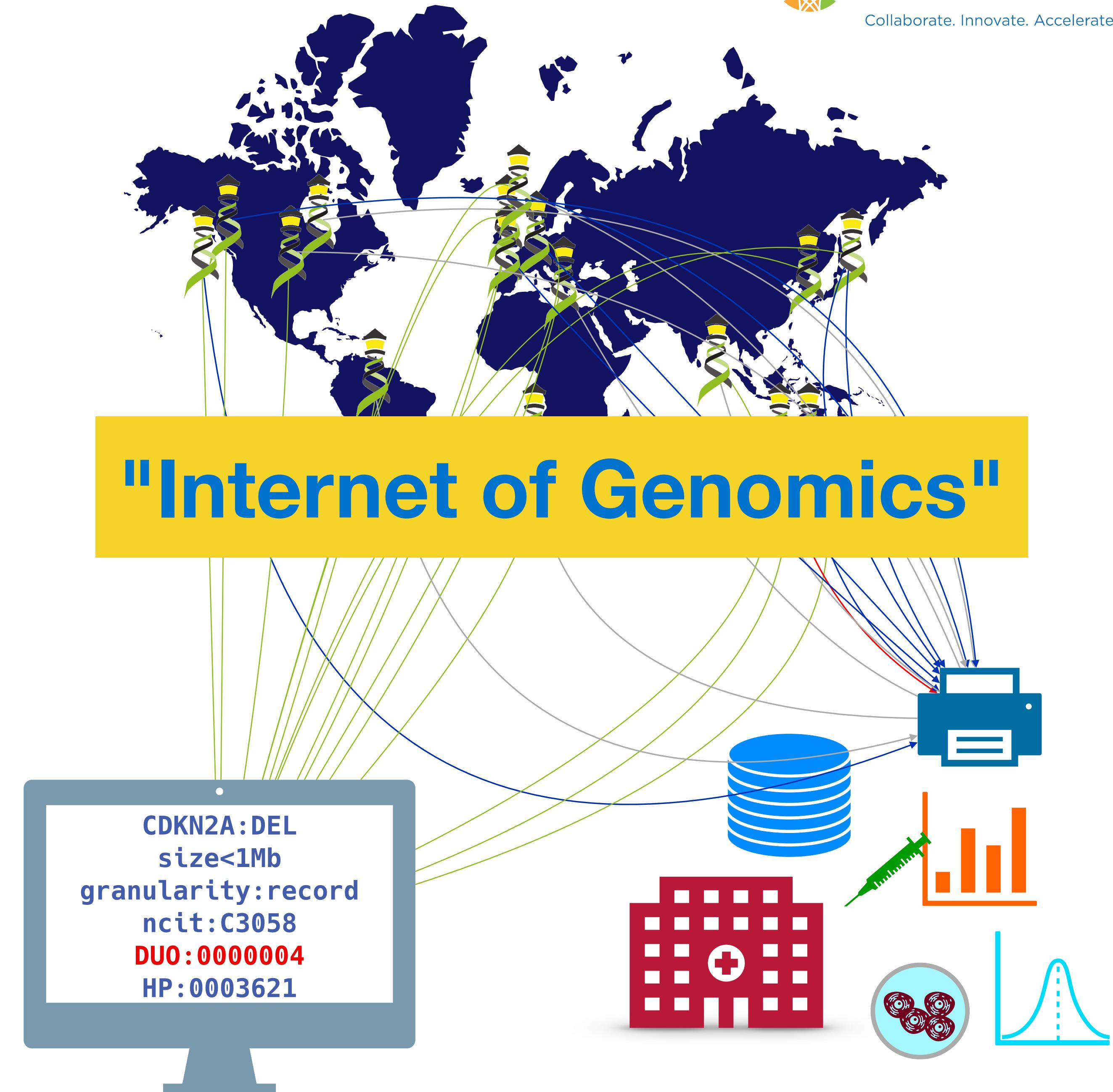


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## Universal Declaration of Human Rights (1948)

27(1)

### “The Right to Science”

“Everyone has the right freely to participate in the cultural life of the community, to enjoy the arts and **to share in scientific advancement and its benefits.**”

27(2)

### “The Right to Recognition”

“Everyone has the right to the protection of the moral and material interests resulting from any scientific, literary or artistic production of which he is the author.”



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Arcadi Navarro  
Roberto Ariosa  
Manuel Rueda  
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# The Beacon team through the ages



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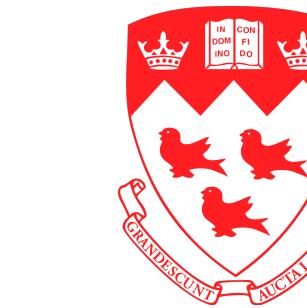
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