

Common Infrastructure for National Cohorts in Europe, Canada, and Africa

Bringing it all together: human cohort standards, tools and applications

Presenter: Dr. Melanie Courtot, Ontario Institute for Cancer Research (OICR)

Host: Vera Matser (EMBL-EBI)

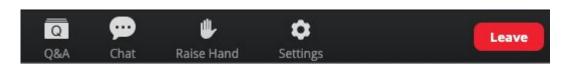


About this webinar

This webinar is being recorded and will be disseminated afterwards



After the presentation we will address the questions posted by the audience using the Q&A function





Common Infrastructure for National Cohorts in Europe, Canada and Africa

The vision:

Accelerating disease research and improving health by facilitating transcontinental human data exchange

Stay informed

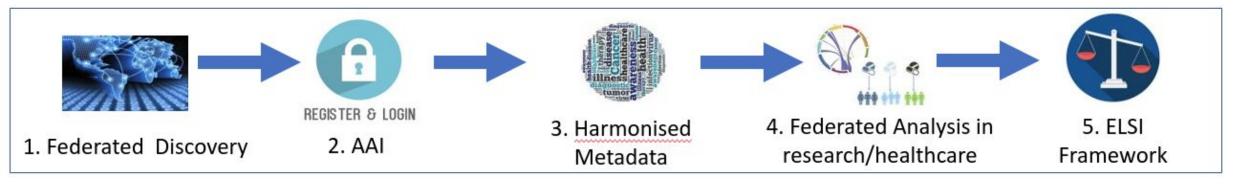




www.cineca-project.eu



The challenges:







Today's presenter

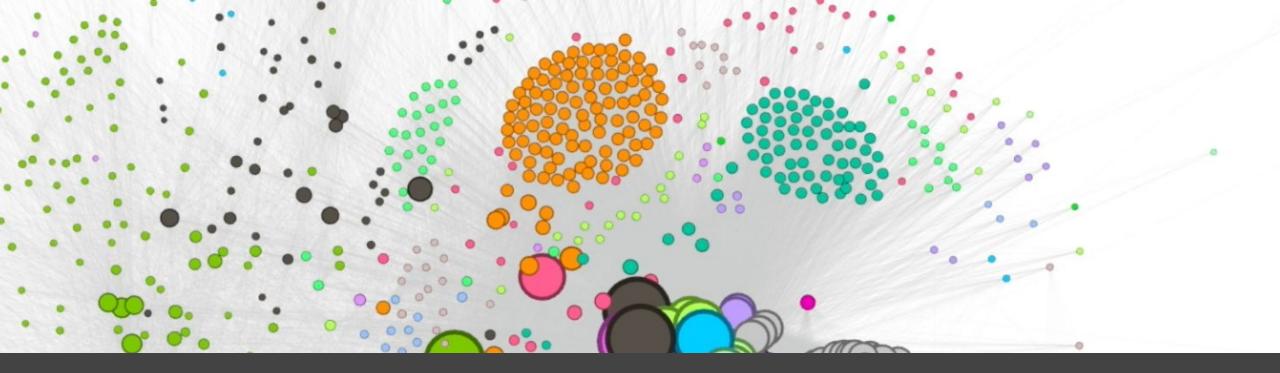


Dr. Melanie Courtot is Director of Genome Informatics and incoming Principal Investigator at the Ontario Institute for Cancer Research (OICR). Her team develops new software, databases and other necessary components to store, organize and compute over the large and complex datasets being generated by OICR's cancer research programs.

Dr Courtot is passionate about translational informatics - building intelligent systems to gain new insights and impact human health.

She co-leads the Data Use and Cohort representation groups for the Global Alliance for Genomics and Health (GA4GH), as well as cohort harmonization efforts for Common Infrastructure for National Cohorts in Europe, Canada, and Africa (CINECA), the International HundredK+ Cohorts Consortium (IHCC) and the Davos Alzheimer's Collaborative.

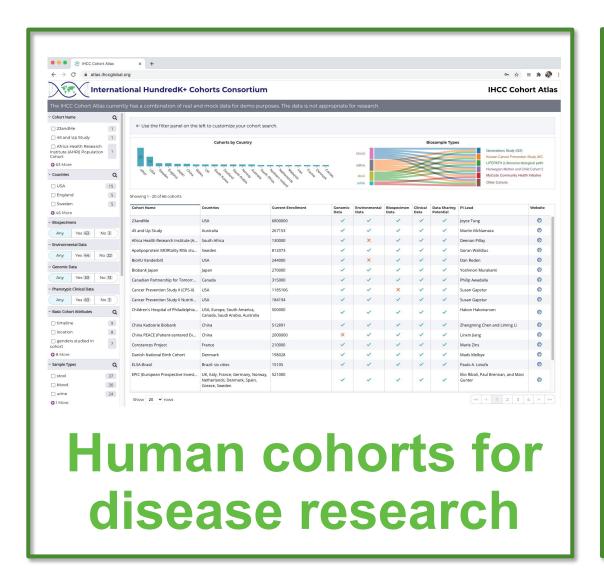
Melanie can be found twitter, @mcourtot, where she often posts about science, equity and diversity, food and silly things she or her children do.



Bringing it all together: human cohort standards, tools and applications

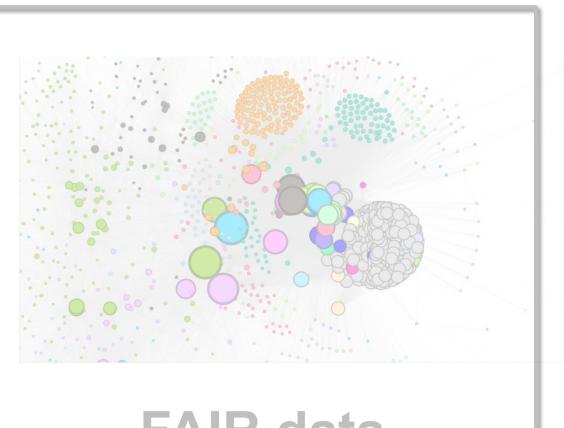
Mélanie Courtot, PhD
Ontario Institute for Cancer Research
mcourtot@oicr.on.ca
@mcourtot







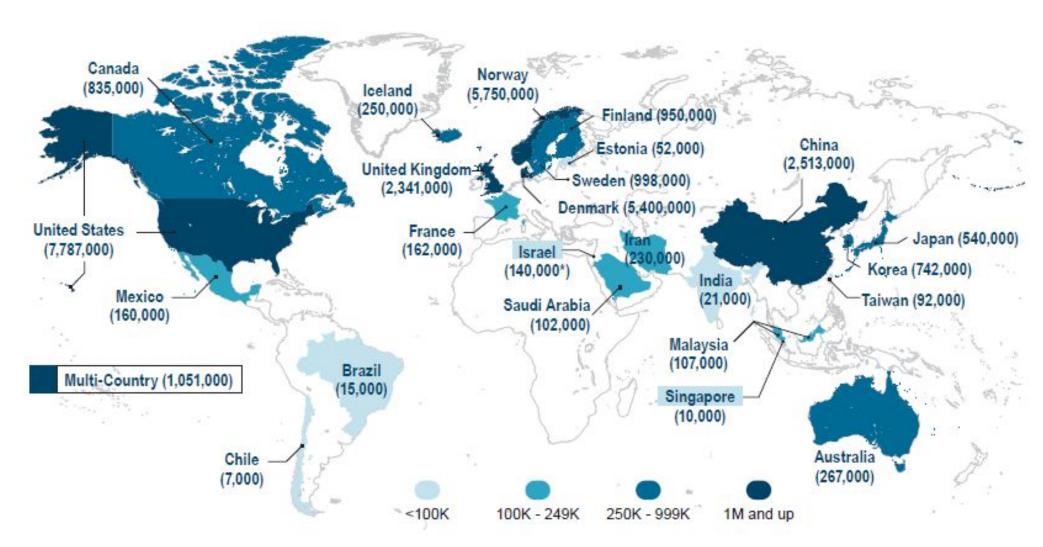




FAIR data management



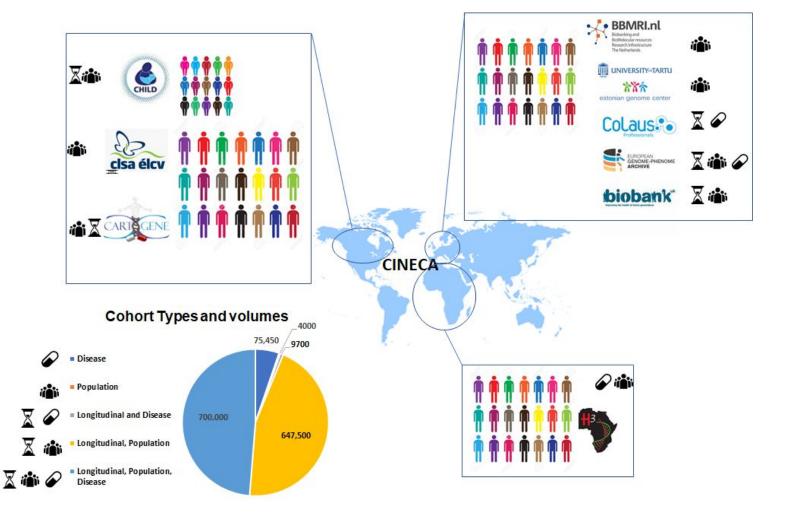
International HundredK+ Cohort consortium



Global Alliance for Genomics and Health (GA4GH)



Common Infrastructure for National **Cohorts in** Europe, Canada, and **Africa** (CINECA)



Use cases for care providers and patients

Does anybody else have the same disease phenotype?



What is the prognosis for this rare disease?

What's a person's cancer risk based on their medical history?

Can we better monitor individuals with Parkinson?

Should we give radiation therapy to this child?



Which drugs will be most effective in this individual?

Use cases for researchers, pharma and HealthTech



Can we use wearable to predict disease before symptoms?

Can we develop diagnosis tests eg prenatal?

Which molecular pathway is involved in LMNA-mediated obesity?



Given parameters X, what is the COVID-19 excess mortality?

What is the best crop in those conditions for yield and nutritional value?

Is there a known drug target involved in this disease?



What are cellular responses during virus infection to this drug?

Building the IHCC cohort atlas

350,000

Cohort presentation and display

IHCC Cohort Atlas

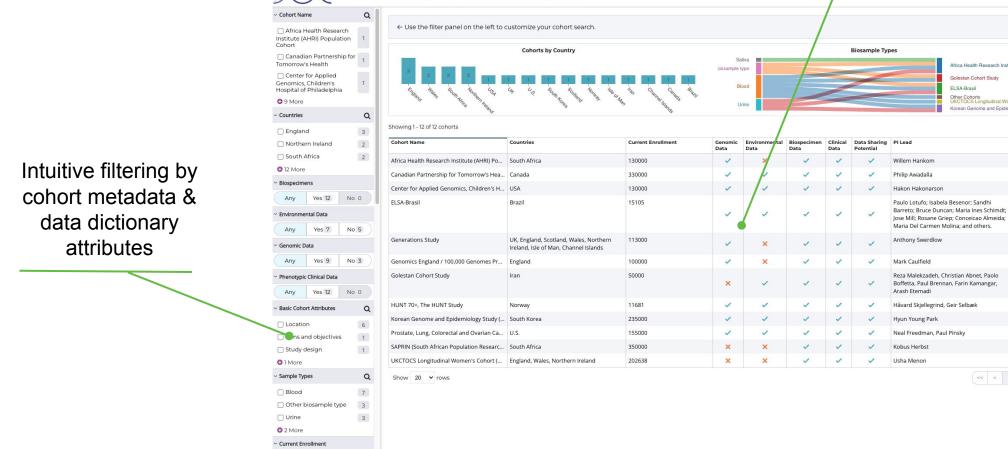
Website

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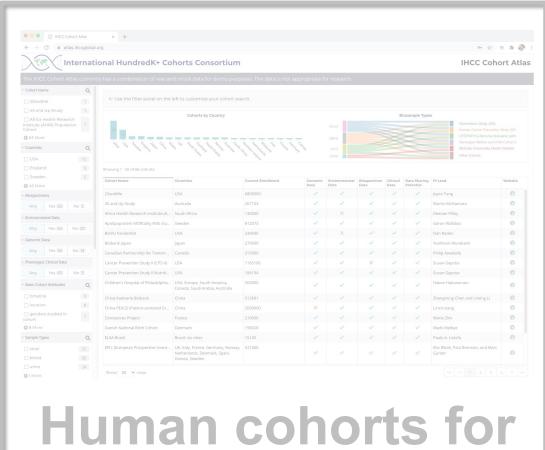
Golestan Cohort Study

ELSA-Brasil

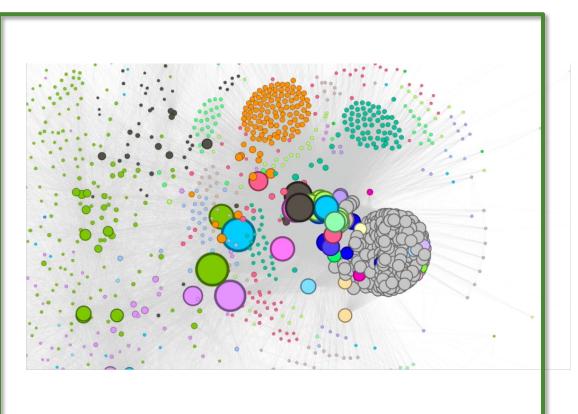


International HundredK+ Cohorts Consortium

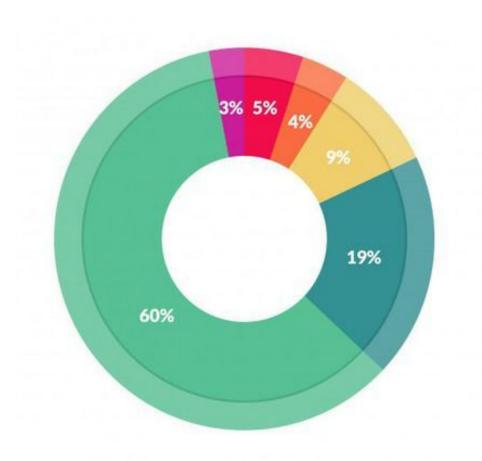
Reference to external cohort sites



Human cohorts for disease research

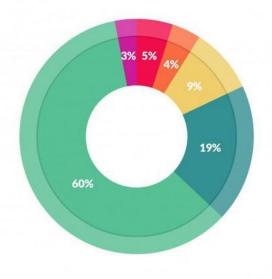


FAIR data management



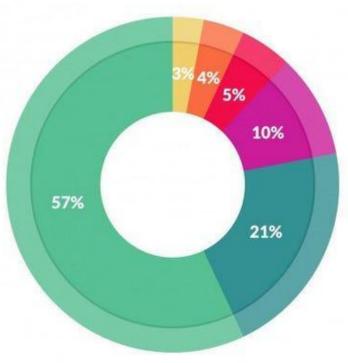
What data scientists spend the most time doing

- Building training sets: 3%
- Cleaning and organizing data: 60%
- Collecting data sets; 19%
- Mining data for patterns: 9%
- Refining algorithms: 4%
- Other: 5%



What data scientists spend the most time doing

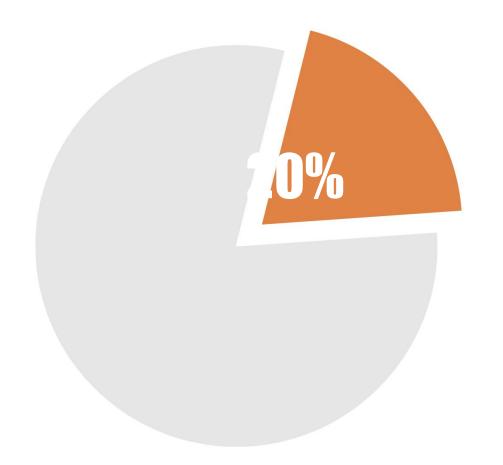
- Building training sets: 3%
- Cleaning and organizing data: 60%
- Collecting data sets; 19%
- Mining data for patterns: 9%
- Refining algorithms: 4%
- Other: 5%



What's the least enjoyable part of data science?

- Building training sets: 10%
- Cleaning and organizing data: 57%
- Collecting data sets: 21%
- Mining data for patterns: 3%
- Refining algorithms: 4%
- Other: 5%

"Sometimes it's easier to rewrite genetics than update Excel"

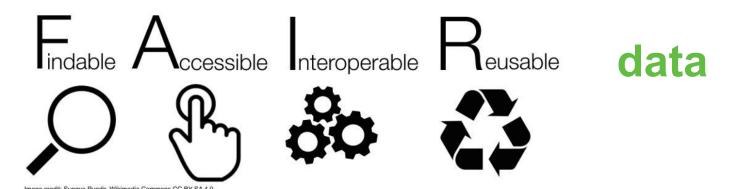


Symbols that affect data handling and retrieval. For example, all symbols that autoconverted to dates in Microsoft Excel have been changed (for example, *SEPT1* is now *SEPTIN1*; *MARCH1* is now *MARCHF1*); tRNA synthetase symbols that were also common words have been changed (for example, *WARS* is now *WARS1*; *CARS* is now *CARS1*).



Sambavisan et al.

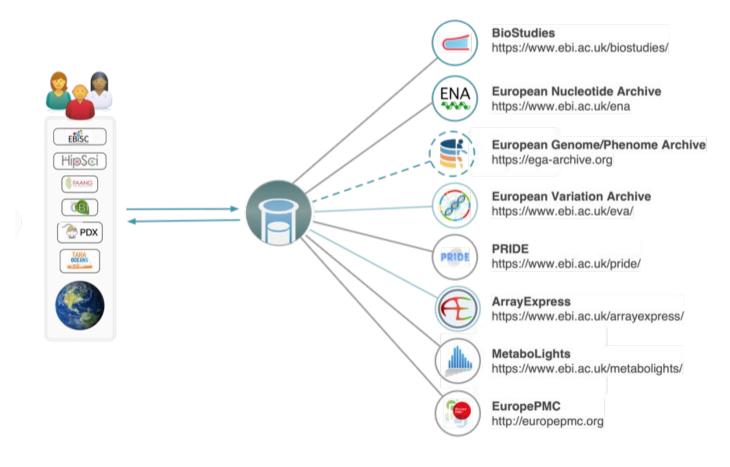
The importance of



- More data resources than ever before
- Combining data from "federated" data repositories for analysis is becoming increasingly common
- The impact of AI and machine learning is rapidly growing, and require data that computers can understand
- Current data generation efforts do not support this level of reuse

EMBL-EBI BioSamples : a metadata hub

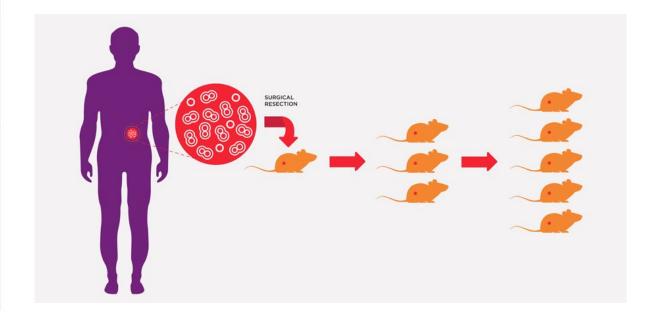
- Archive of information about biological materials
- From internal and external sources, and directly from submitters.
- Enables technology independent linking between assay data and sample metadata



https://www.ebi.ac.uk/biosamples/

Linking Samples through relationships

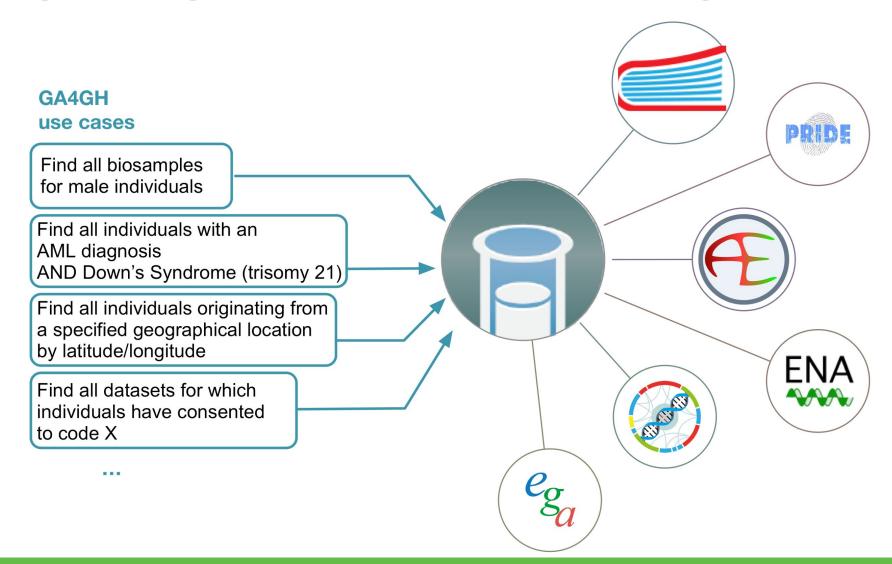
Relationship types	Reverse relationships	Description
derived from	derived from (reverse)	Sample A is derived from Sample B. E.g Tissue samples derived from donor samples - Cell line samples derived from tissue samples - Viral samples separated from saliva samples - Organoid samples cultured from tissue samples
same as	same as	Sample A is the same as Sample B. This can be used to link duplicated samples
has member	has member (reverse)	Sample A is a member of Sample group G. BioSamples create a sample group for each sampleTab submission*. It's also possible to put patient samples as a sample group.
child of	child of (reverse)	Sample A is the child of Sample B. E.g - Patient A is the child of Patient B



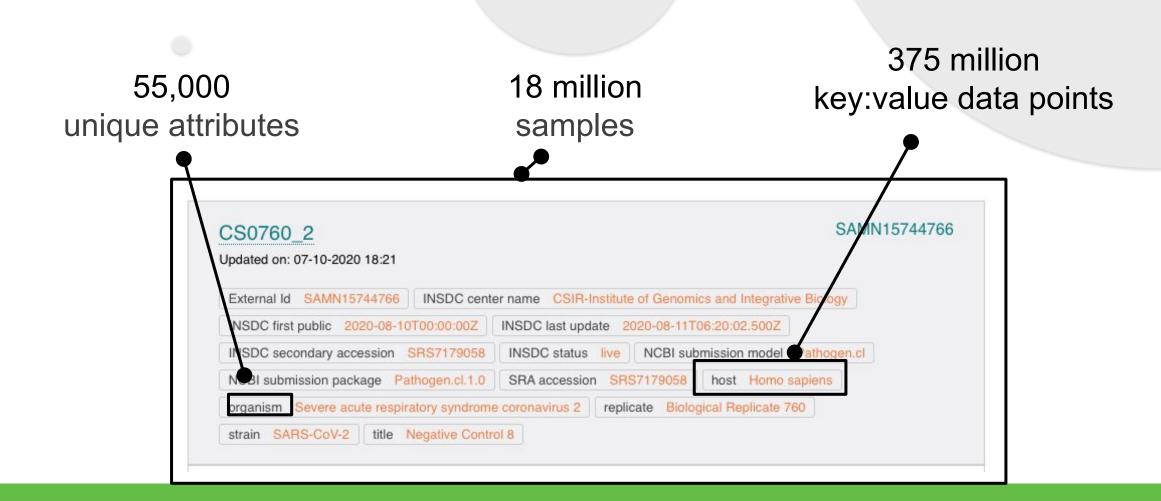
https://www.ebi.ac.uk/biosamples/docs/guides/relationships

Related patient-derived xenografts(PDX) samples

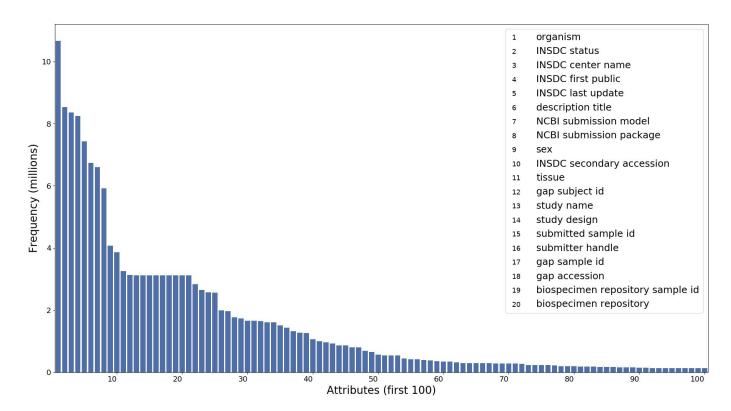
Finding the right data is hard without good metadata



BioSamples dataset size



Metadata curation



Redundancy and inconsistency in real life data



60% of attributes cover only 5% of key:value pairs



I need to find all COVID related samples



Covid 19-related attributes in BioSamples:

- severe acute respiratory syndrome
- COVID19
- novel coronavirus pneumonia
- nCoV pneumonia
- COVID-19
- Coronavirus infected disease-19 (COVID-19)

Metadata curation

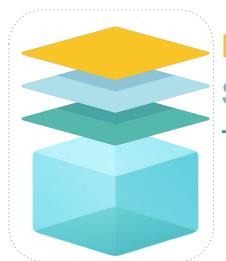
- Text curation
- Semantic annotation

Common challenges in sample metadata

- Special characters (COVID19 vs COVID-19)
- Acronyms (T2D for diabetes)
- Typo
- Synonyms

Text curation and semantic annotation

- Automatic curation by pipelines
- Manual curation by experts
- Curation tool based on manual curation and machine learning



Manual curation
Semantic annotation
Text curation
Raw metadata



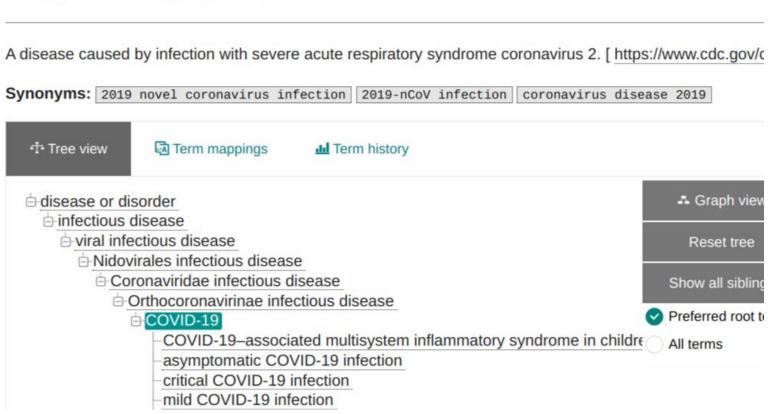




to access and visualize

COVID-19

The Ontology Lookup Service (OLS) is repository for biomedical ontologies providing access to up-to-date ontology resources (UI + API)





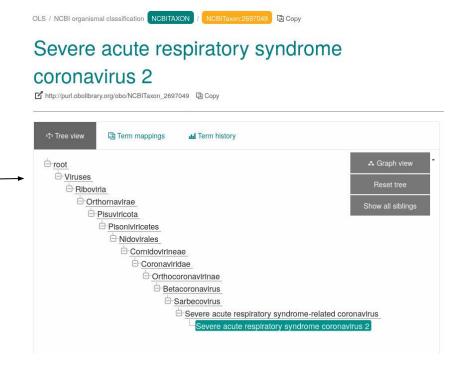
for automated ontology annotation

MOITATAMA VSA IGTIMA

- An annotation service mapping ontology terms to free text
- Stores known rules
 (e.g., manual curation)
 to guide future
 annotations

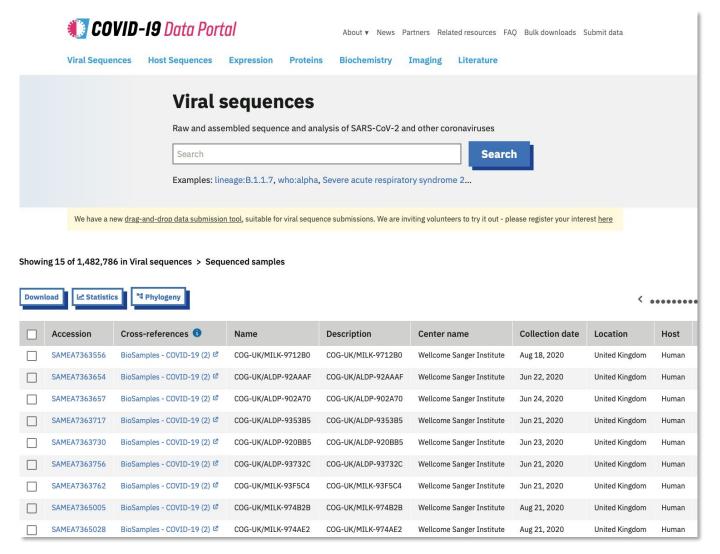
SARS-CoV-2 related values

- SARS-CoV2
- Wuhan coronavirus
- Human coronavirus 2019
- SARS-CoV-2
- 2019-nCoV
- COVID-19 virus



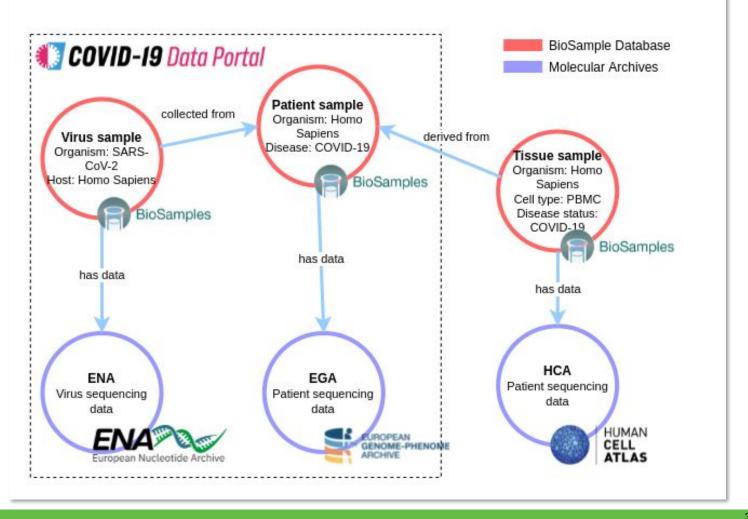
https://www.ebi.ac.uk/spot/zooma/

~5 Million samples in the EMBL-EBI COVID-19 Data Portal (March 2022)



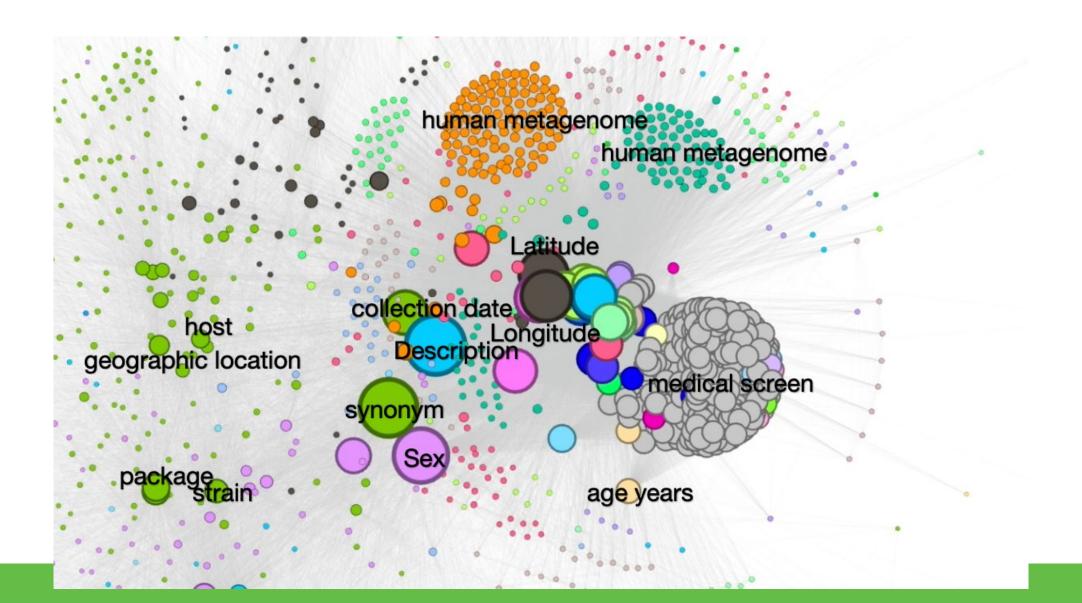
Graph search across archives

As a researcher, I Researchers want to find the immunotyping data of all lung samples from COVID19 patients and corresponding genome sequencing data of the viral isolate, to study how the immune systems response to viral infection.



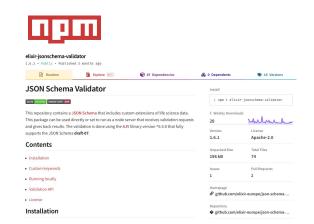
Connecting attributes for recommendation

Connecting attributes for recommendation





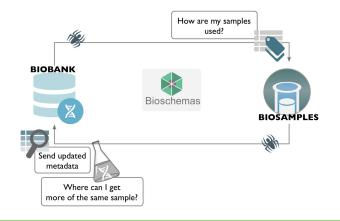
Semantic based validation



https://www.npmjs.com/pa ckage/elixir-jsonschema-v alidator



Structured schema annotation



https://bioschemas.org/types/B ioSample/0.1-RELEASE-2019 06 19/



Structured phenotype exchange



id: "UBERON_0001256"
label: "wall of urinary bladder"
ageOfIndividualAtCollection:
age: "P52Y2M" When?
histologicalDiagnosis:
id: "NCIT:C39853"
label: "Infiltrating Urothelial C..."
tumorProgression:
id: "NCIT:C84509"
label: "Primary Malignant Neo..."

what?

biosamples:

- sampledTissue:

https://phenopacket-schema.rea dthedocs.io/en/latest/biosample. html

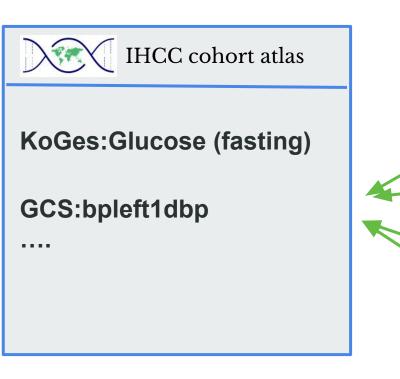


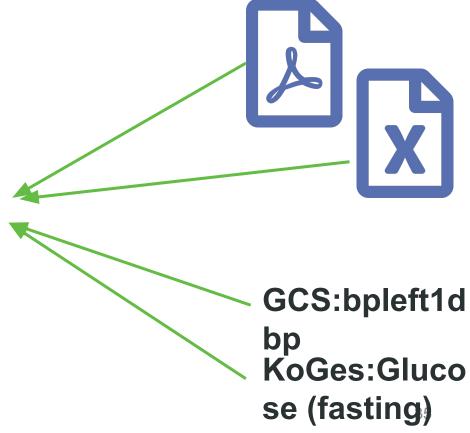


Use case: As a researcher, I am looking for cohorts with XXX data

I am looking for cohorts with 'blood measurement' data







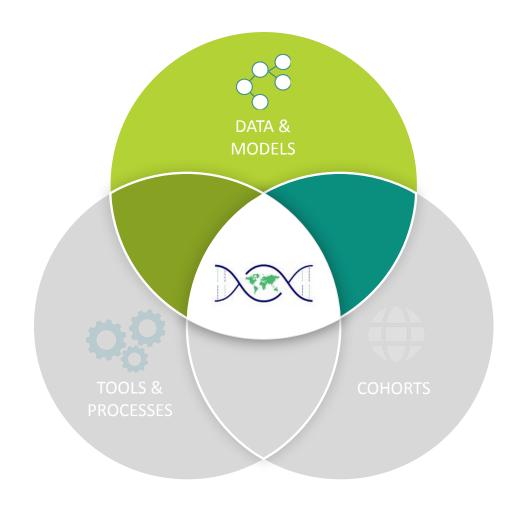


Bringing cohort data together





- Data models to represent both access conditions and cohort data
- 2. Tools and processes for implementations
- Deployment over clinical cohorts





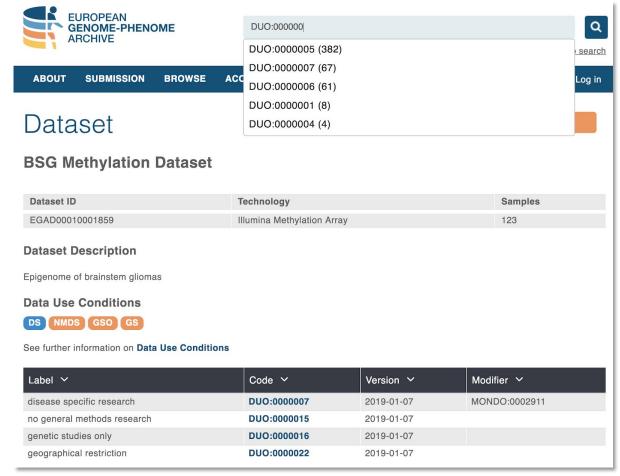




Use Ontology GA4GH Data Use Ontology



- Vocabulary describing permitted data uses and modifiers
- "General research use",
 "disease-specific research",
 "not for profit only"...



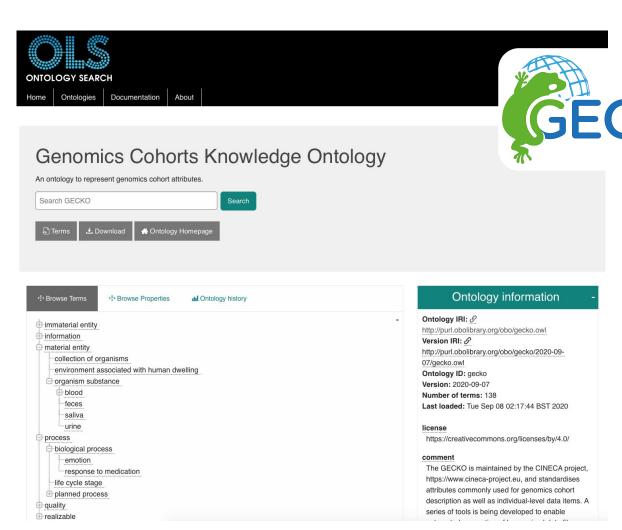
https://www.ebi.ac.uk/ols/ontologies/duo https://github.com/EBISPOT/DUO

https://ega-archive.org/datasets/EGAD00010001859

Semantic harmonisation

To promote and publish it, the CINECA model was formalised as an ontology

- using World Wide Web Consortium standards
- Adopting OBO Foundry best practices
- Leverages (and contributes) to existing resources for maximal interoperability
- Available publicly (CC-BY)



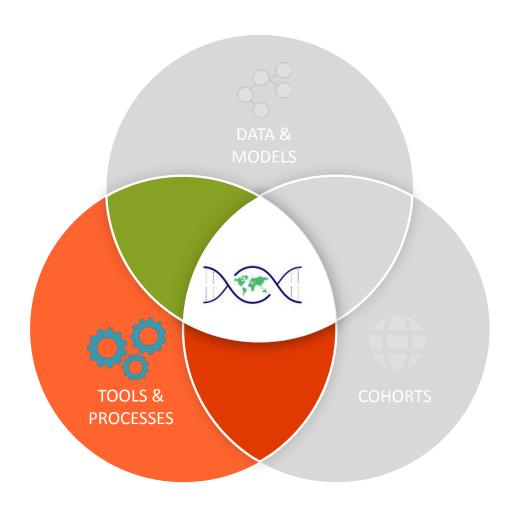
Genomics Cohorts Knowledge Ontology

- Commonly used attributes to describe cohort metadata
- "Medication", "sample type", "genomics datatypes"...

https://www.ebi.ac.uk/ols/ontologies/gecko https://github.com/IHCC-cohorts/GECKO



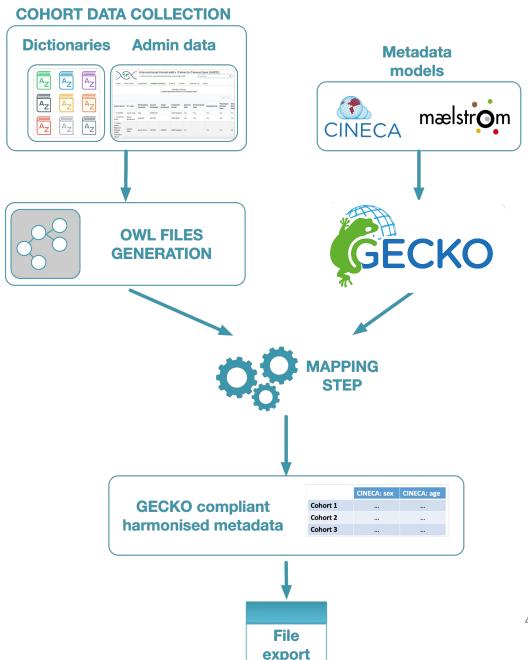




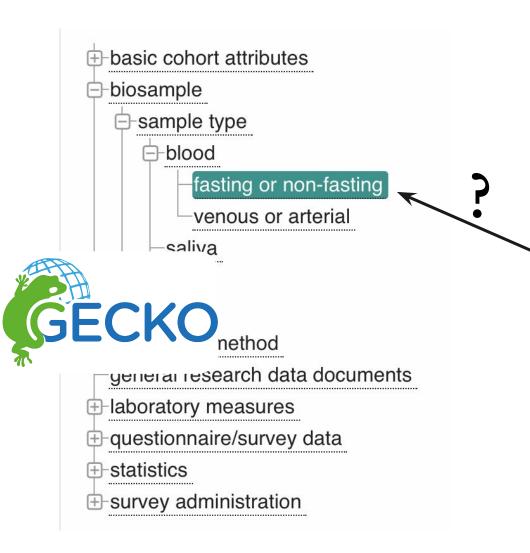
Harmonization process

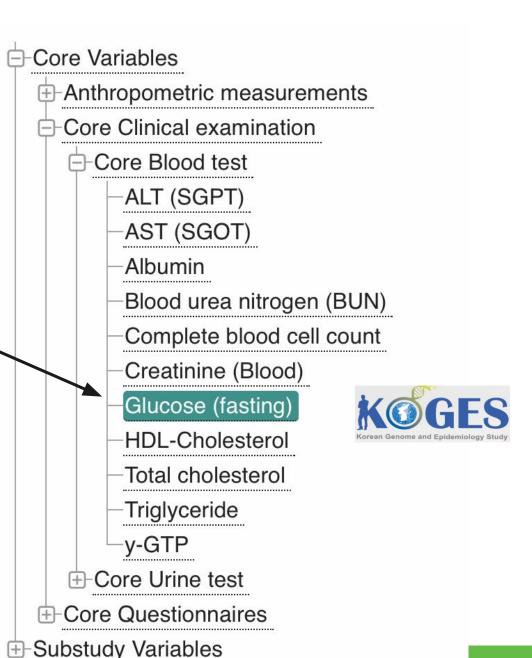
Data harmonisation process:

- Data collection
- 2. Metadata model design
- 3. Harmonisation

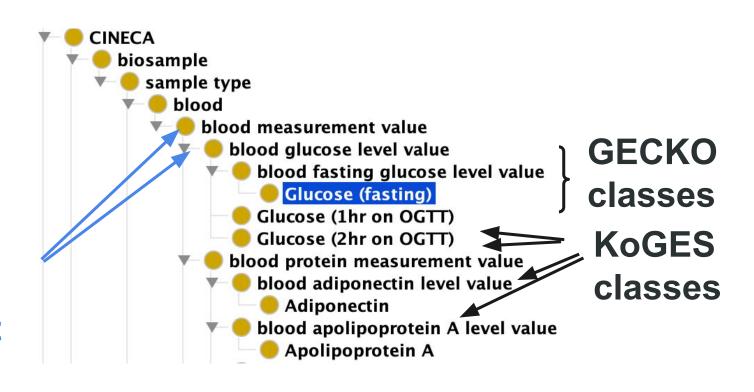


Harmonisation example



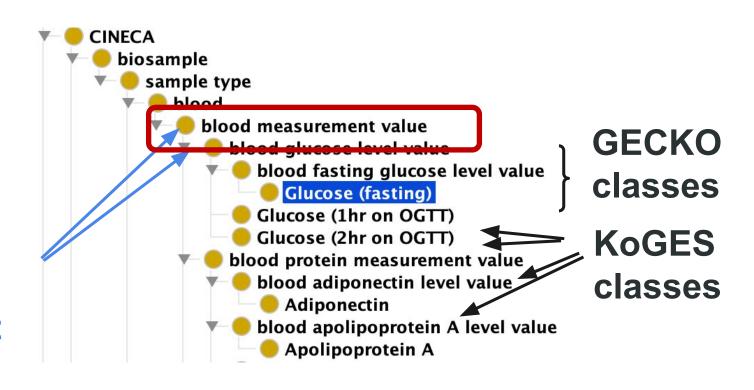


Harmonisation example



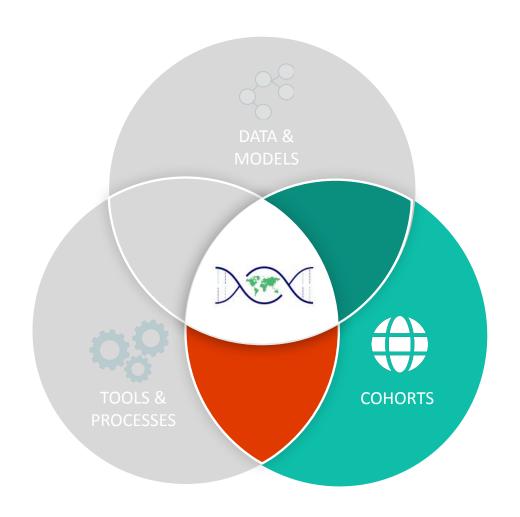
Clinical Measurement Ontology

Harmonisation example



Clinical Measurement Ontology





Applying these techniques to clinical cohorts...

Use case: As a researcher, I am looking for cohorts with XXX data

I am looking for cohorts with 'blood measurement' data





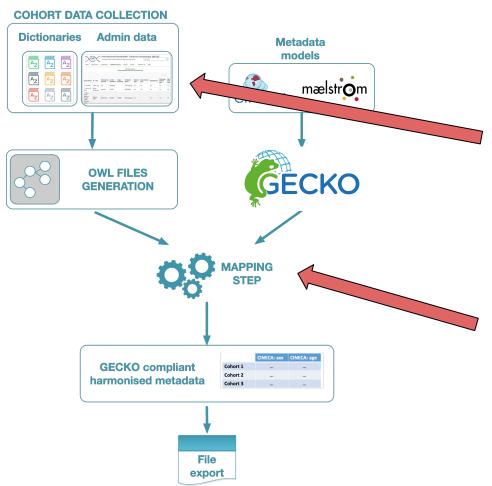
IHCC cohort atlas

KoGes:Glucose (fasting) is a subtype of Blood glucose level value: defined in OWL as 'blood measurement value' and ('has target' some glucose)

GCS:bpleftldbp is a subtype of diastolic blood pressure value, subtype of blood pressure measurement value

••••

Automating the process

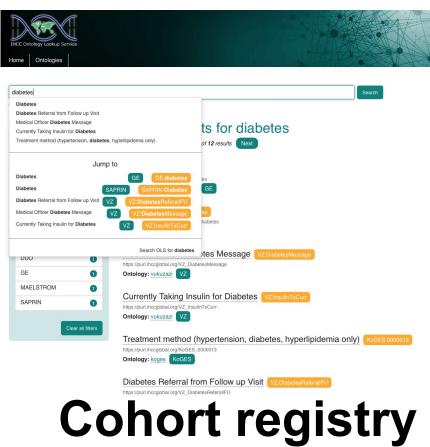


Refine import pipeline to (semi) automatically ingest data dictionaries provided as CSV files

Develop automated mapping using existing tooling and text-mining processes

Automated mapping pipeline for cohort owners





Cohort registry

Deploy cohort registry

- Provide dereferencing for human readability, e.g., http://purl.obolibrary.org/obo/GECKO_0000068
 returns a human readable page describing tobacco history in GECKO
- Include versioning and change detection for reupload

Built-in interoperability with mapping/curation tools





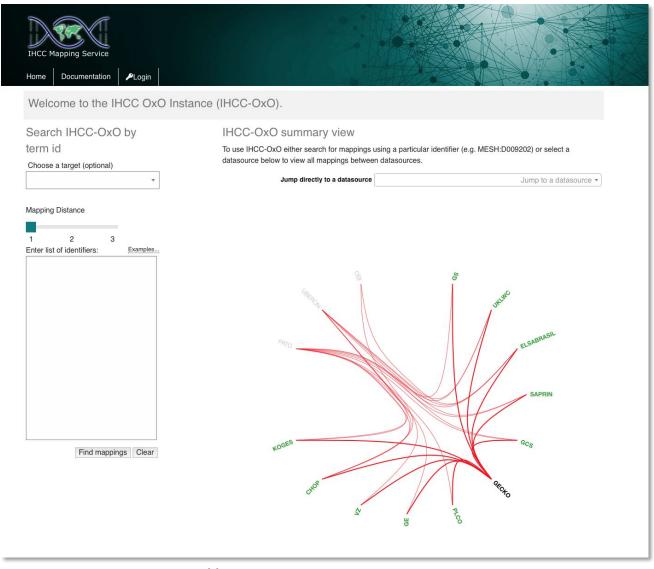






IHCC cohort mappings

- Stores mapping between GECKO and cohort terms
- Accessible through APIs
- Parameter to bridge between mappings: If A ⇔ B and B ⇔
 C then can infer A⇔ C



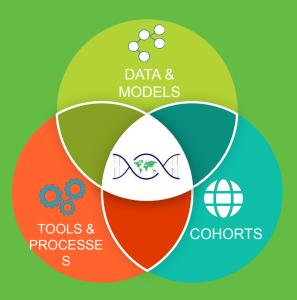
https://mapping.ihccglobal.app







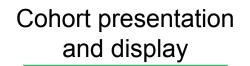
IHCC Cohort Atlas



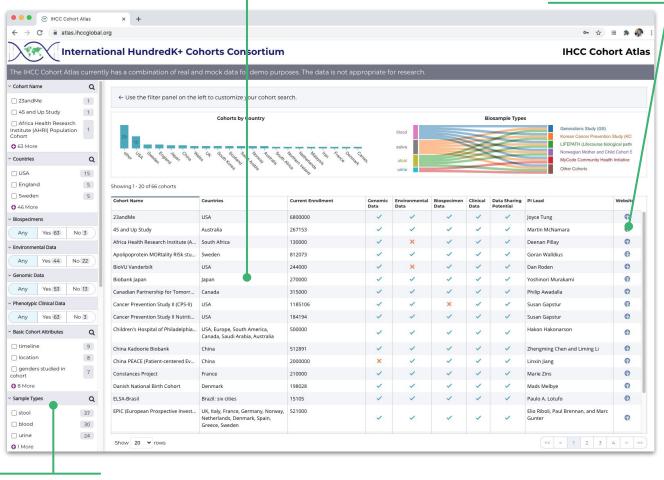
User interface and search API leverage the reusable modules from



- 12 cohorts deployed
- In the process of adding more cohorts



Reference to external cohort sites



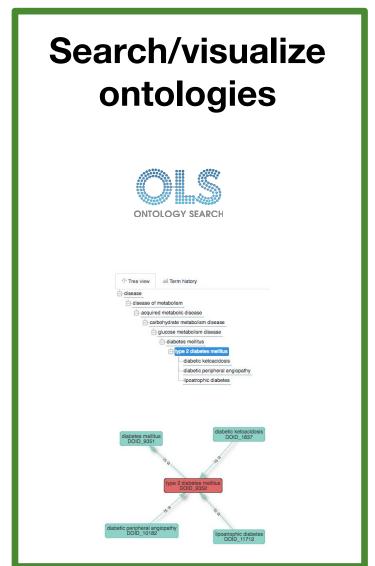
Intuitive filtering by cohort metadata & data dictionary attributes

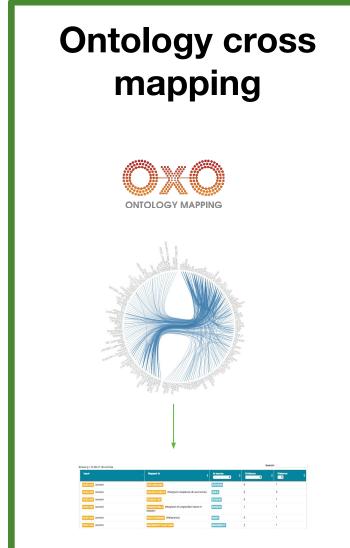
https://atlas.ihccglobal.org

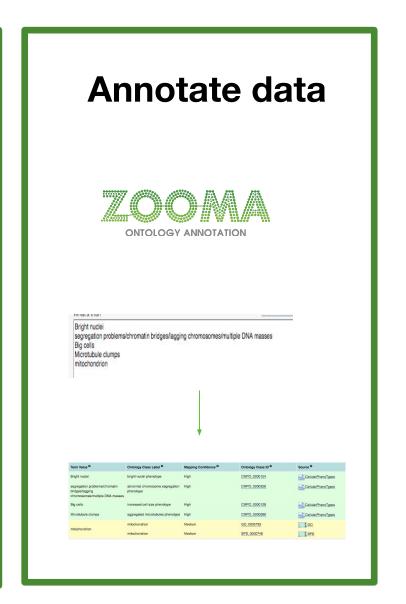


Summary: bringing it together

EMBL-EBI semantic toolkit







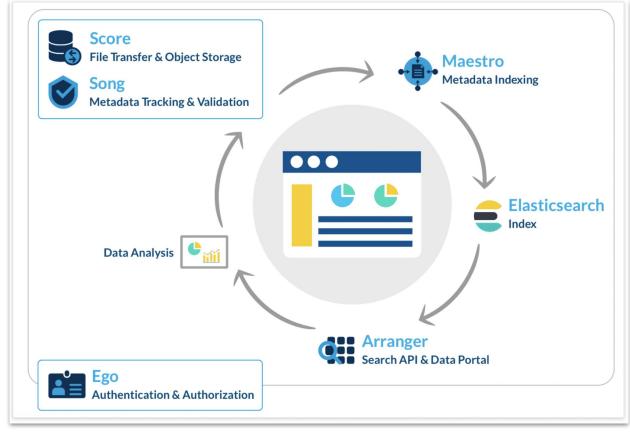
The Overture suite

- Flagship product powering
 Software Engineering team
 projects
- Interoperability with community standards e.g., Global Alliance for Genomics and Health (GA4GH)

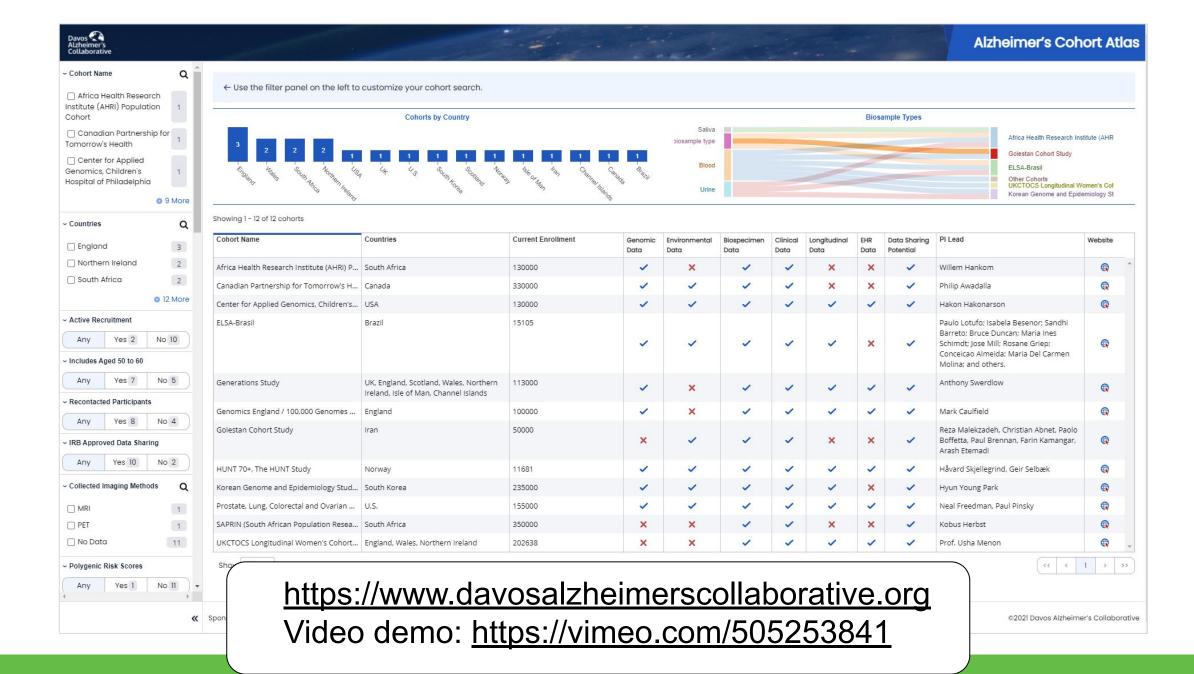
Next steps:

- Provide simple self-installer to make the product more accessible
- Enable further front-end customization by 3rd party

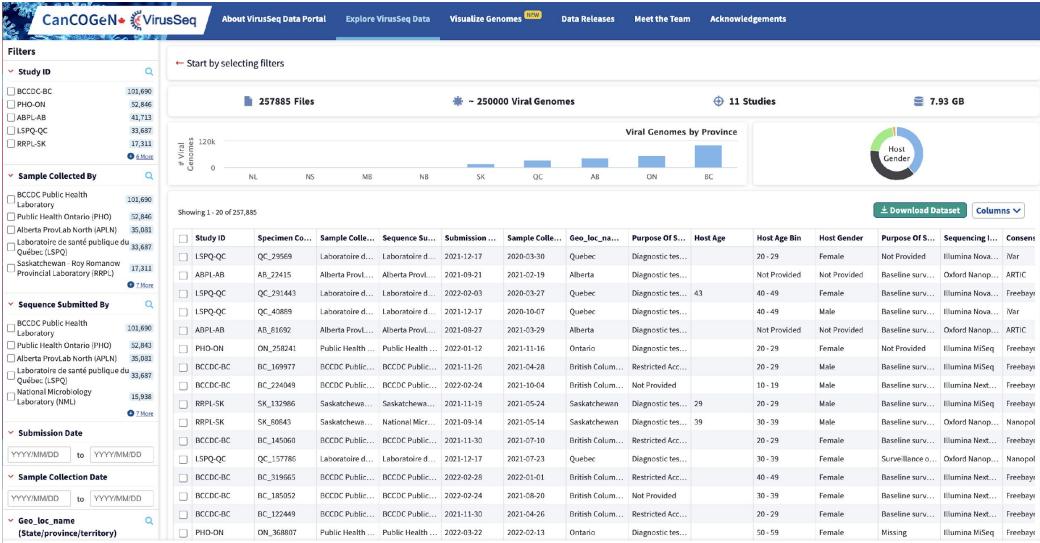




https://www.overture.bio/



VirusSeq data portal

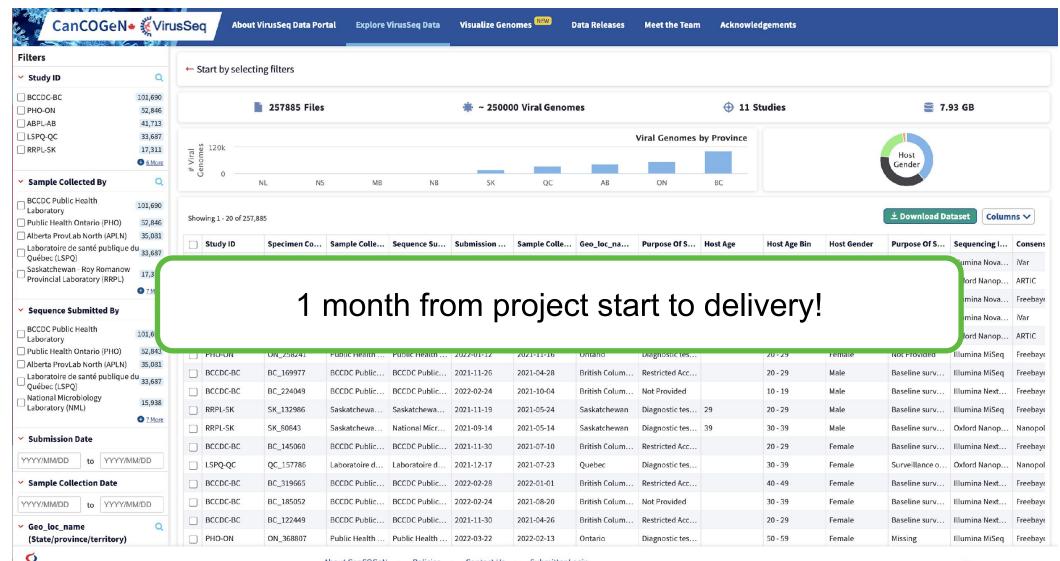


Submitter Login

nae lives.

GenomeCanada

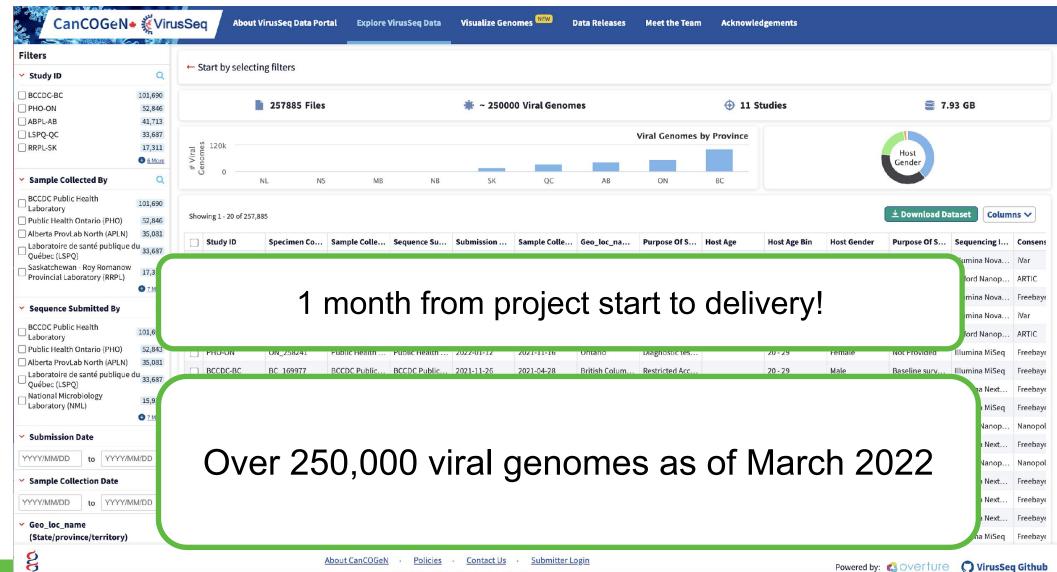
VirusSeq data portal



nae lives.

GenomeCanada

VirusSeq data portal



GenomeCanada

Community engagement is key

















Global Alliance for Genomics & Health

Collaborate. Innovate. Accelerate.















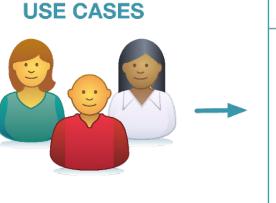


>200,000 datasets annotated with the Data Use Ontology

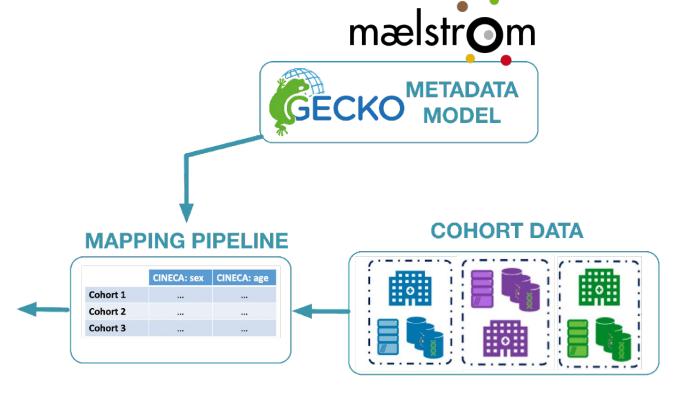




SHARED FRAMEWORK FOR DISCOVERY AND ACCESS







Cohort Representation - Use Cases



Pain Points:

Lack of interoperability

Demographic variables not standardized

Hard to perform analyses when there are different baseline measures/descriptions

Values for each individual often not available/shareable

Requirements:

Have an interoperable computable cohort definition standard that goes across OMOP / FHIR / HL7 CQL etc.

Provide a "computational" description of the cohort, e.g., one that could be run as a query on the baseline population

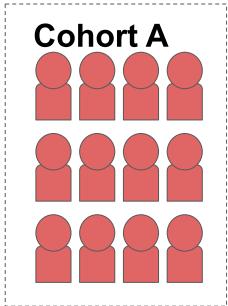
Allow for model representation of different sources, including annotation linking to semantic definitions (data elements, vocabularies, ontologies). Ability to create, share and use mappings.

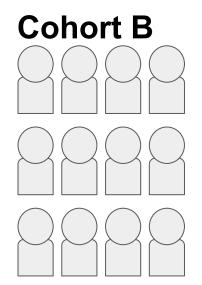
Cohort Identification



I am looking for cohorts with 'blood measurement' data"

Found it!





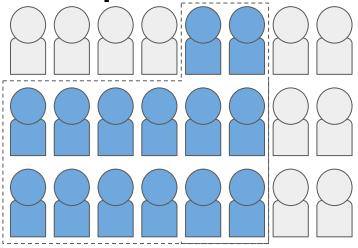
Cohort Discovery



I am looking for **female** Asthmatic patients with **creatinine** > **0.9**

Found it!

Participants



Cohort Registry Discovery



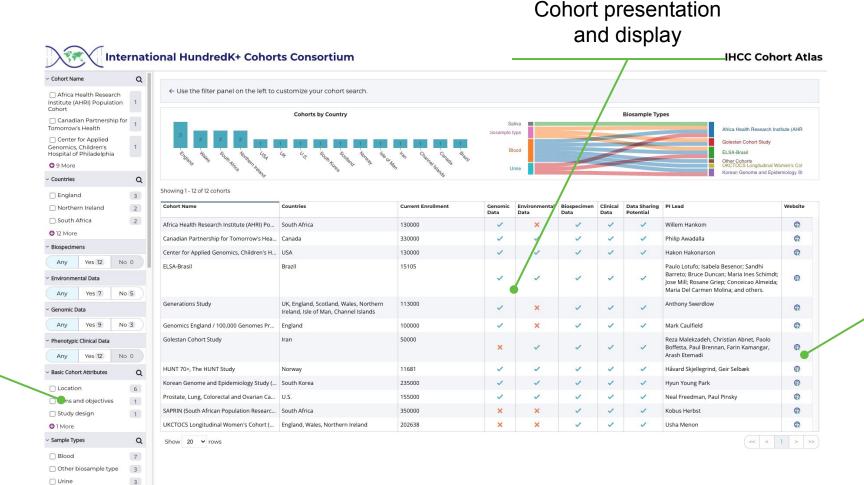


I am looking for cohorts with 'blood measurement' data"

Cohort Name	Country	Bio Specimens	Sample Type	 Enrollment
Cohort 1	South Africa	Yes	Blood (fasting)	 11,681
Cohort 2	England	No	Urine	 350,000
Cohort 3	Northern Ireland	Yes	Creatinine	2,856

. . .

The IHCC cohort atlas for cohort discovery



Intuitive filtering by cohort metadata & data dictionary attributes

• 2 More

Current Enrollment

350,000

Reference to

external cohort

sites

Computable Cohort Discovery





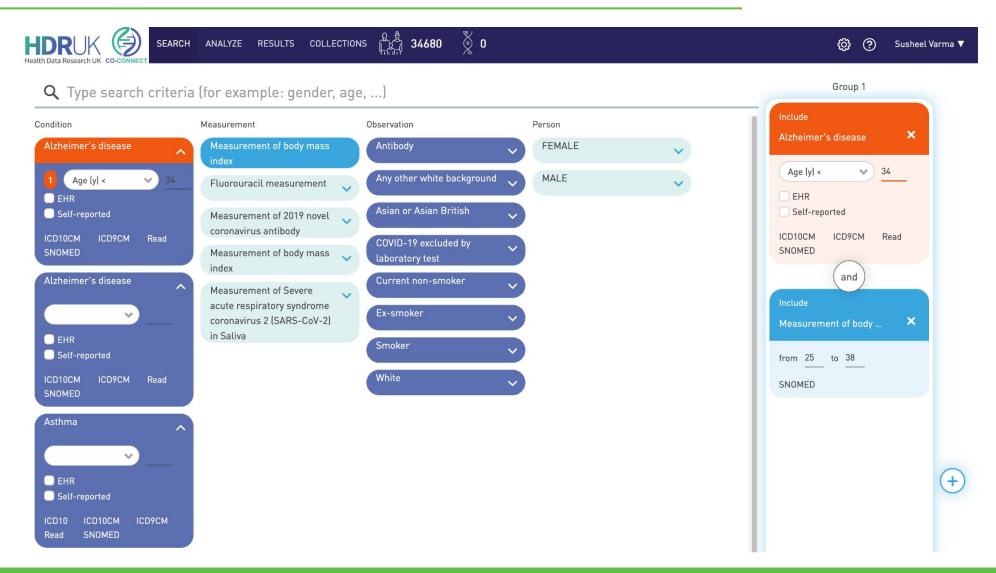
I am looking for **female** Asthmatic patients with **creatinine** > **0.9**

Patient ID	Age	Gender	 Lab Result (Creatinine)	•••	Diagnosis
1	34	M	 0.72		SNCT(26929004)
2	45	F	 1.13		ICD10CM(J45)
3	61	F	 0.81		

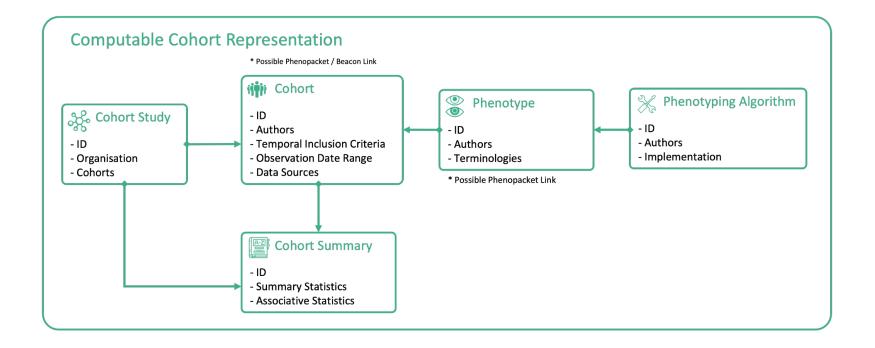
...

Computable Cohort Discovery





Computable Cohort Representation



- Minimum Information About Computable Cohorts (MIACC)
- Reuse Existing Standards:
 - GECKO / BBMRI / Registry Alignment
 - FHIR CQL / OMOP Cohort Query Alignment
 - Phenopackets Payload alignment
 - Beacons API Alignment



PID: hjmg45-2344-jnm2b34-2w34@0.0.3

Name: Asthma & Diabetic Patients

Description:

Authors: Susheel Varma, ...

Version: 0.0.3

Revisions: 0.0.1, 0.0.2

Changelog: []

Parents []: kj67-2321-3452mn-243234

Created: 2021-04-14 12:01:00 Updated: 2021-04-14 13:01:00 Cohort Type: Study | User

Projects: hg345-234j-2343,...

Entry_date: Exit_date:

Interval Type: Closed | Open

Criteria_Groups: [

{query criteria inclusion exclusion}

Collection Events: []

- Event Type: Incident | Prevalent | Other
- Entry Type: Single | Multiple

Datasets: []

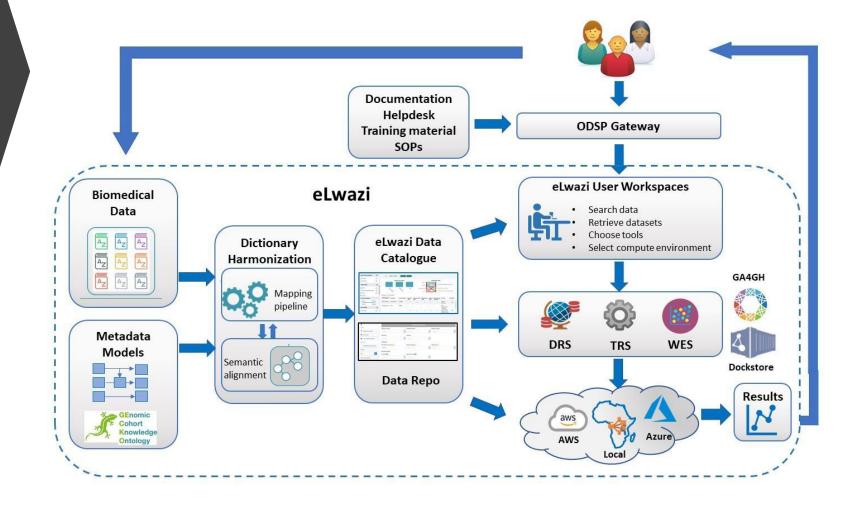
- Name
- ID
- Count:
- DUO Code (Restrictions & Limitations)

NOA September 2021

NIH RFA-RM-20-018 on Harnessing Data Science for Health Discovery and Innovation in Africa (DS-I Africa) Open Data Science Platform and Coordinating



Nicky Mulder



Acknowledgements



















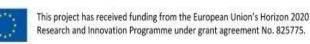
















Funding provided by the Government of Ontario.

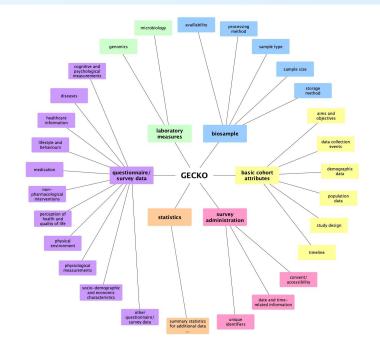




Questions?

Please write your questions using the Q&A button





Bringing it all together: human cohort standards, tools and applications

Presenter: Dr. Melanie Courtot (OICR)