



Preliminary Proof-of-Concept Catalogue Tool



Technical workshop on real-world metadata for regulatory purposes Virtual meeting, April 12, 2021

Presented by Prof Morris SwertzUniversity Medical Center Groningen





Outline

- The context: position in EMA MINERVA and its aims
- Approach & description of open-source software we plan to reuse
- A short demo of the proof of concept for the metadata access tool
- Any questions



MINERVA



Metadata for data discoverability aNd study rEplicability in obseRVAtional studies

- To define a list of criteria to identify relevant real-world data sources from which the data sources to be included in this study will be selected
- To identify a minimum of 10 data sources to use in the study
- To define a set of metadata that should be collected from real-world data sources
- To conduct an in-depth stakeholders' consultation on the metadata identified
- To define a process to collect the set of metadata for the data sources included in the study
- To collect the defined set of metadata for data sources included in the study
- To develop or provide a tool enabling access to the metadata collected (e.g., through a dynamic dashboard)
- To draft a good practice guide with the description of the metadata defined and recommendations on the
 use of metadata for the purpose of identifying real-world data sources for a specific study purpose



Catalogue tool

From the proposal:

We will deliver a proof-of-concept interactive catalogue and tools to test its functionality to access, search, and visualise metadata, including the metadata that can be collected as part of this project from the selected data sources

The catalogue will be a metadata inventory with searchability, dynamic dashboards, visualisation capabilities, and integration of different levels of access (public vs. confidential information)



Approach







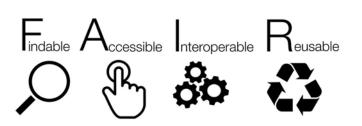


On top of MOLGENIS open source software

Data tools for scientific data

Application communities in

- cohorts & biobanks
- Rare disease
- Omics and imaging
- Large multi-center studies



Bulk data

Import your own data and metadata model using the EMX format. VCF. OBO



Data request

Find and request (biobank) data sets and items

4 🗌 🖟 Questionnaire Mental health ► □
B MINI version 1

Data explorer

Filter and download for further analysis

	pkP1050	pkP1101	pkP1103	pkP1052	egPE107
WSU1	-0.1892	-0.1892	0.231	-0.8379	-0.9186
W5U2	-0.012	-0.012	0.1026	-0.2283	-0.4022
WSU3	0.0637	0.0637	0.2153	-0.1182	-0.1068
WSU4	0.0136	0.0136	0.1208	-0.1924	-0.1909
WSUS	0.054	0.054	0.1649	-0.1768	-0.1621
WSU6	0.0873	0.0873	0.1452	-0.0902	-0.0322
WSUZ	-0.0529	-0.0529	-0.0248	0.0354	0.0405
WILLS	0.0629	0.0629	0.1488	-0.06	-0.1015

Genome browser

Data sharing and integration **DAS** protocol



Model registry

Metadata registry of models for biobanks and molecular data



molgenis



Annotators

Data integration for diagnostics personalized medicine



Use R data api to up/o data and integrate graphics



FAIR integration

Using ontologies to derive harmonization rule for data

Pipelines

Large scale computation on

pooling



Reports

Tailormade report functionality



App store

Add your own user interfaces and advanced tools.



Data capture

Questionnaires, forms. importer to easily add data to a running instance



Mostly funded via national and EU consortia since 2002; currently 27 active actions from:



computational

clusters, grids

and clouds







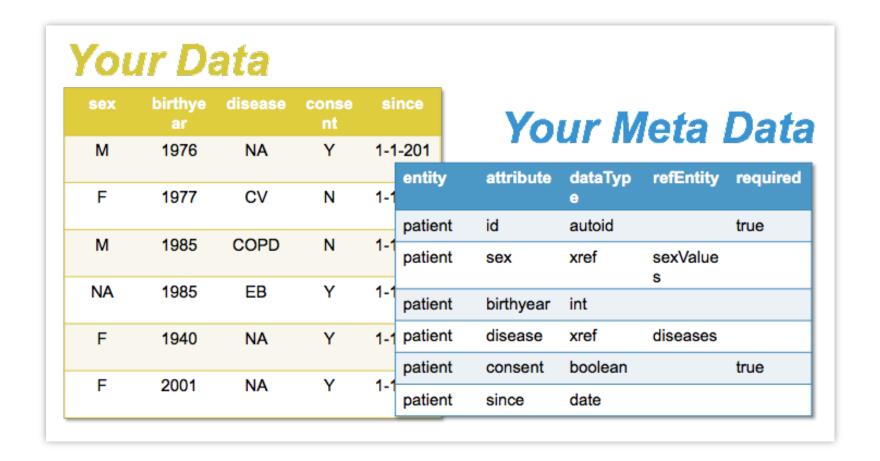




1. Configure the meta data items into a catalogue

Can change data model rapidly without coding

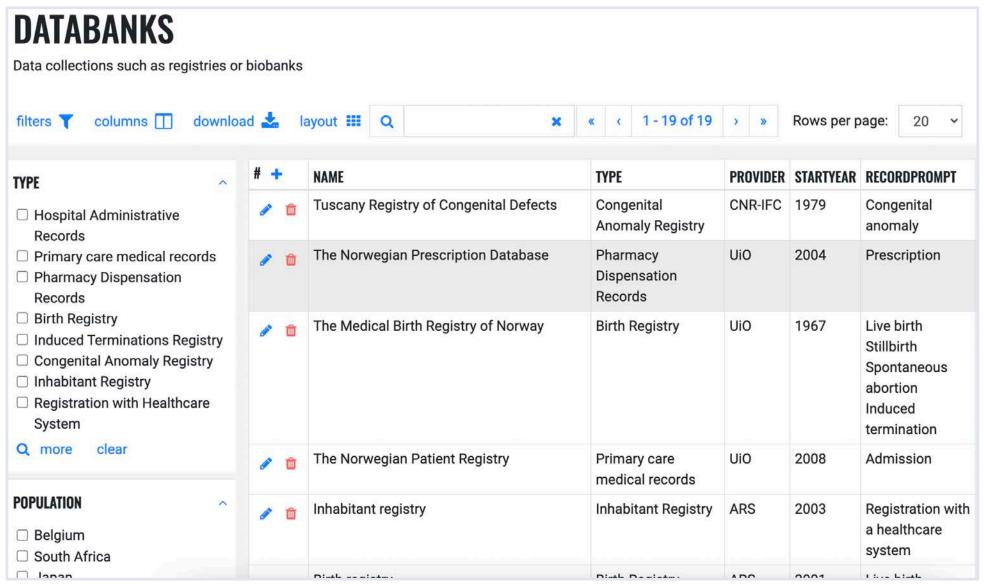
E.g. using the integrated EMX data model format & online metadata editor





2. Testagainstuse cases

E.g. using the integrated data entry forms & query /data explorer tools





3. Tune user experience

Reuse practices from existing catalogues

E.g. Databank overview

(example courtesy of BBMRI-ERIC directory of biobanks, MIABIS working group)

► COVID-19
▶ COVID-19 Services
▼ Diagnosis available
Type to search
▼ Materials
Satisfy all
Buffy Coat
CDNA / mRNA
Cell lines
O DNA
Feces microRNA
MICTORNA
<u> </u>
Not available

4 organisations with 770 collections matching the search criteria

REQUEST SAMPLES

⊞ Biobank Graz	Collection types: Cohort, Disease specific, Hospital, Image collection,
ISO-9001:2015 ✓	Longitudinal, Population-based, Sample collection, Prospective study, Case-
	Control, Rare disease collection, Cross-sectional, Birth cohort
*	Juridical person: Medical University of Graz
	Covid-19: Member COVID-19 Network, Proteomics studies including protein
	engineering and protein interactions, Screening tools for searching virus
	proteases inhibitors, Animal Testing Facility, Ability to set up clinical trials,
	Virus Sequencing Facility, BSL-2 laboratories available, BSL-3 laboratories
	available, Laboratories doing PCR-based diagnosis

Collection	Туре	Materials	Standards	#Samples
Ability to collect COVID-19 cases	Cohort, Disease specific, Hospital, Prospective study, Sample collection	Serum, Throat swab, Buffy Coat, Feces, Plasma		<10
Bio-UV 2017	Cohort, Disease specific, Hospital, Longitudinal, Sample collection	Serum, Plasma, Buffy Coat, Other		2838
BioPersMed Cohort	Cohort, Disease specific, Hospital, Image collection, Longitudinal,	Serum, Plasma, Buffy Coat, Urine	CEN/TS 16945:2016✔	260680

Biopreserv Biobank. 2016 Dec;14(6):559-562.



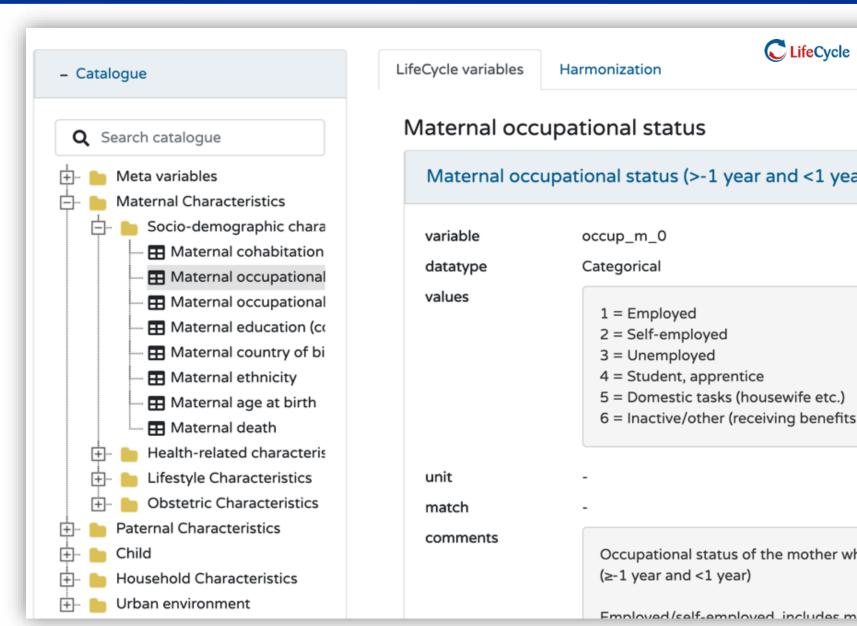


3. Tune user experience

Reuse practices from existing catalogues

E.g. Data items available

(example courtesy LifeCycle project)







3. Tune user experience

Reuse practices from existing catalogues

E.g. **Mapping to standards**

(example courtesy LifeCycle project)

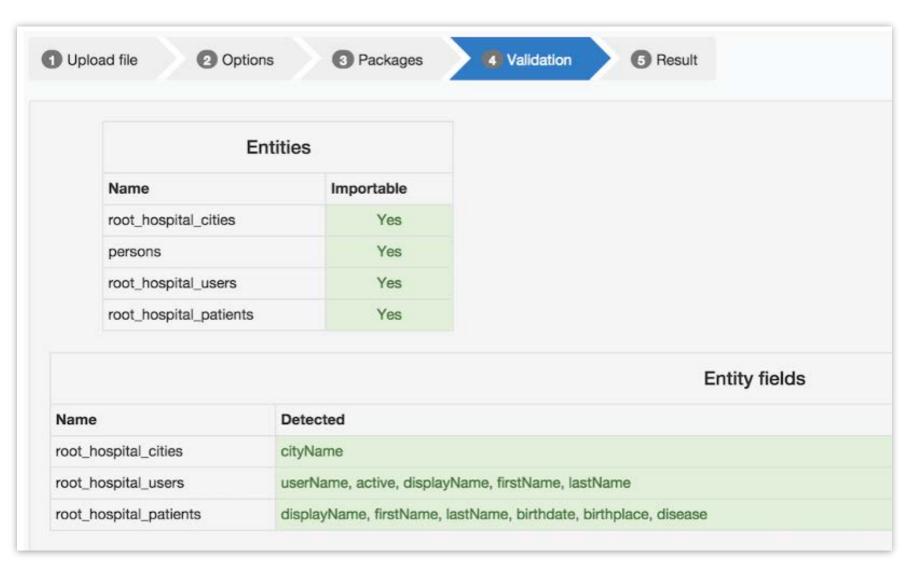
Cohort	occup_m_0	occup_m_1	occup_m_2	occup_m_3	occup_m_4	occup_m_5
ALSPAC 12/18	•	0	Ø	Ø		Ø
BIB 18 / 18	②	②	②	②	0	Ø
CHOP 18/18	Ø					
DNBC 18/18	Ø					
EDEN 18/18	•	•	•	•	•	•
ELFE 18/18	Ø	•	Ø			
GECKO 18/18	Ø					Ø
GenR 18/18	Ø	•	•	•	•	Ø
INMA 18/18	②	0	0	0	0	0



4. Automate data ingest

E.g. using the integrated batch file formats, data validation and error reporting tools

In collaboration with task on 'process'





5. FAIR interfaces

Enables automated up- and downloads

E.g. using the integrated interoperability interfaces into linked data, FAIR data point, REST, JavaScript, Python, R, CSV, etc.

(courtesy of GO-FAIR / VODAN)

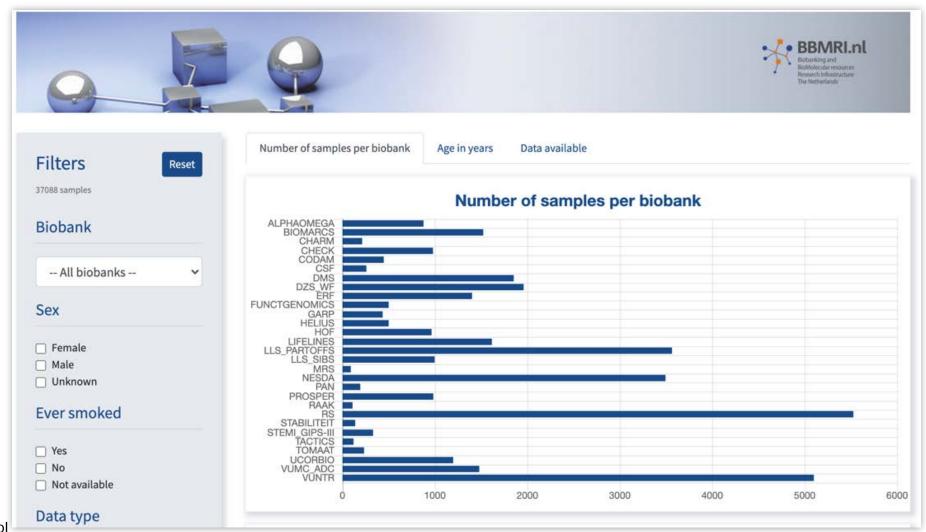
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      <http://www.w3.org/ns/dcat#Resource>;
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   <http://purl.org/dc/terms/hasVersion> "1.0";
   <http://purl.org/dc/terms/publisher> "http://molgenis.org";
   <http://purl.org/dc/terms/title> "test";
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   <http://rdf.biosemantics.org/ontologies/fdp-o#metadataModified> "2020-09-22T22:22:00";
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   <http://purl.org/dc/terms/publisher> "http://molgenis.org";
   <http://purl.org/dc/terms/title> "catl";
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   <http://purl.org/dc/terms/publisher> "http://molgenis.org";
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   <http://rdf.biosemantics.org/ontologies/fdp-o#metadataModified> "2020-09-22T22:22:00" .
```



6. Add dashboards

To enable catalogue users to compare contents of the databanks or timepoints

(example courtesy of BBMRI-NL)





DEMO of PROOF OF CONCEPT





Thank you!

For any question on this presentation, please contact: Malgorzata.Durka-Grabowska@ema.europa.eu Official address Domenico Scarlattilaan 6 • 1083 HS Amsterdam • The Netherlands Address for visits and deliveries Refer to www.ema.europa.eu/how-to-find-us Send us a question Go to www.ema.europa.eu/contact Telephone +31 (0)88 781 6000