



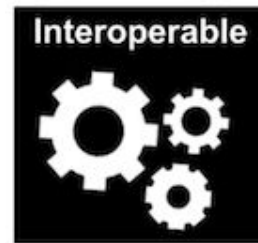
Data Collection: Metadata Management

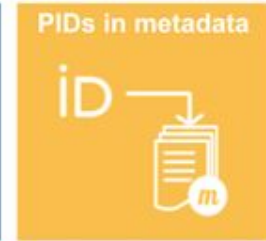
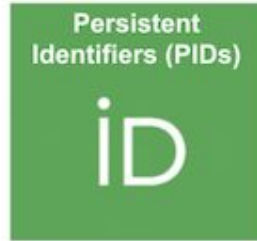
Speakers: Federico Bianchini (Centre for Bioinformatics UiO)

Moderator: Michal Torma / Rukaya Johaadein (UiO)

What is a metadata standard?

- How does a standard make data more FAIR
- What are the ingredients required for defining a standard
- Where to find metadata standards
- Which tools can be used in connection with standards

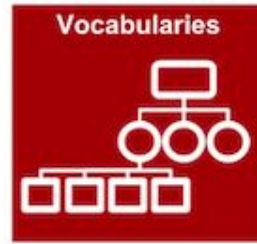




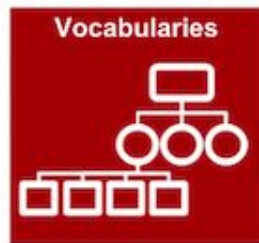
- A persistent identifier is required in the metadata
- Metadata standard compliant with repositories checklist
- Metadata fields used to identify/retrieve the data



- Persistency of metadata (also when the data is not available)



- Interoperability fully rely on metadata
- Vocabularies and ontologies ensure that standards are FAIR
- A well-defined standard can be linked with standards describing other type of data
- Focus on machine-actionability



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How many ways can you say “female”?

18-day pregnant females
2 yr old female
400 yr. old female
adult female
asexual female

female (lactating)
female (pregnant)
female (outbred)
female parent
female plant

individual female
lgb*cc females
mare
female (worker)
monosex female

worker caste (female)
sex: female
female, other
female child
femal

How many ways can you say “female”?

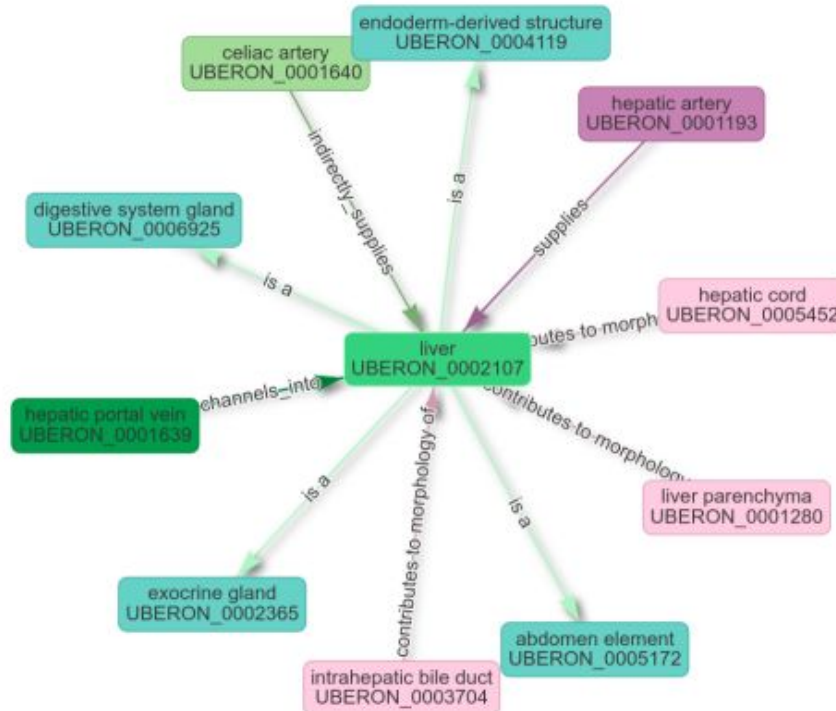
18-day pregnant females	female (lactating)	individual female	worker caste (female)
2 yr old female	female (pregnant)	lgb*cc females	sex: female
400 yr. old female	female (outbred)	mare	female, other
adult female	female parent	female (worker)	female child
asexual female	female plant	monosex female	femal
castrate female	female with eggs	ovigerous female	3 female
cf.female	female worker	oviparous sexual females	female (phenotype)
cystocarpic female	female, 6-8 weeks old	worker bee	female mice
dikaryon	female, virgin	female enriched	female, spayed
dioecious female	female, worker	pseudohermaphroditic female	femlale
diploid female	female(gynoeocious)	remale	metafemale
f	femele	semi-engorged female	sterile female
famale	female, pooled	sexual oviparous female	normal female
femal	femalen	sterile female worker	sf
female	females	strictly female	vitellogenic replete female
female - worker	females only	tetraploid female	worker
female (alate sexual)	gynoeocious	thelytoky	hexaploid female
female (calf)	healthy female	female (gynoeocious)	female (f-o)
hen	probably female (based on morphology)		

female (note: this sample was originally provided as a \"male\" sample to us and therefore labeled this way in the brawand et al. paper and original geo submission; however, detailed data analyses carried out in the meantime clearly show that this sample stems from a female individual)

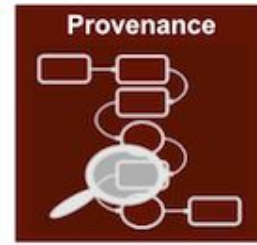
Courtesy of N. Silvester, European Nucleotide Archive, EMBL-EBI

Ontologies

Ontology a set of concepts and categories in a subject area or domain that shows their properties and the relations between them.



Relationship	Color	Visibility
Extended nodes (*)	<div></div>	-
is a	<div></div>	<input checked="" type="checkbox"/>
part of	<div></div>	<input type="checkbox"/>
develops from	<div></div>	<input type="checkbox"/>
contributes to morphology of	<div></div>	<input checked="" type="checkbox"/>
drains	<div></div>	<input type="checkbox"/>
supplies	<div></div>	<input checked="" type="checkbox"/>



- Richer metadata fields enhance reusability
- Metadata should describe data provenance
- Everything needs to follow community standards
 - Alignment with repository



MINSEQE
MIAME

...



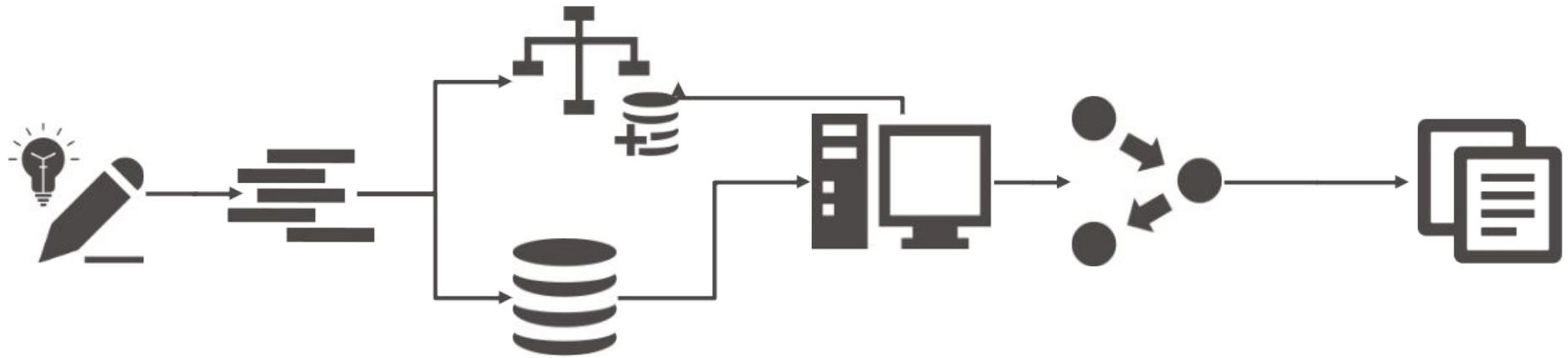
HUPO-PSI
TraML
MIAPE

...

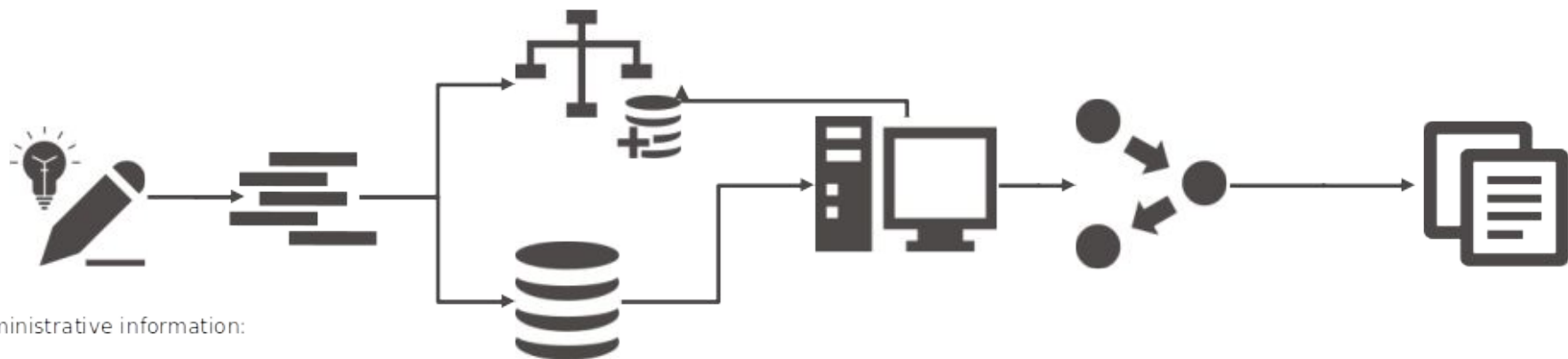


SRA-XML

MINSEQE



MINSEQE



Administrative information:

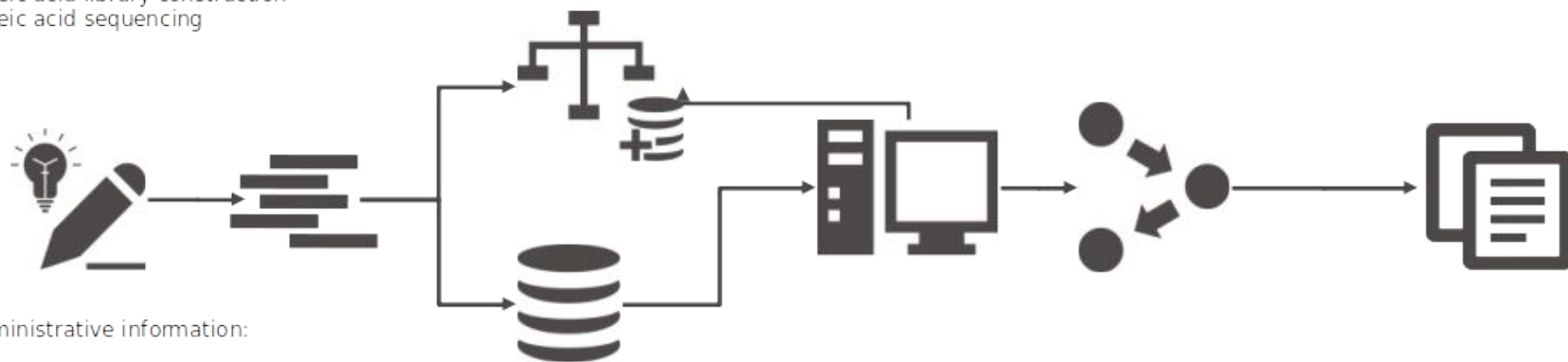
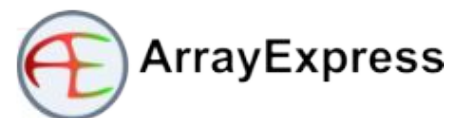
Persons
Organizations
Publications

Experimental conditions/design

protocols:

treatment
sample collection
growth
nucleic acid extraction
conversion
nucleic acid library construction
nucleic acid sequencing

MINSEQE



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Experimental conditions/design

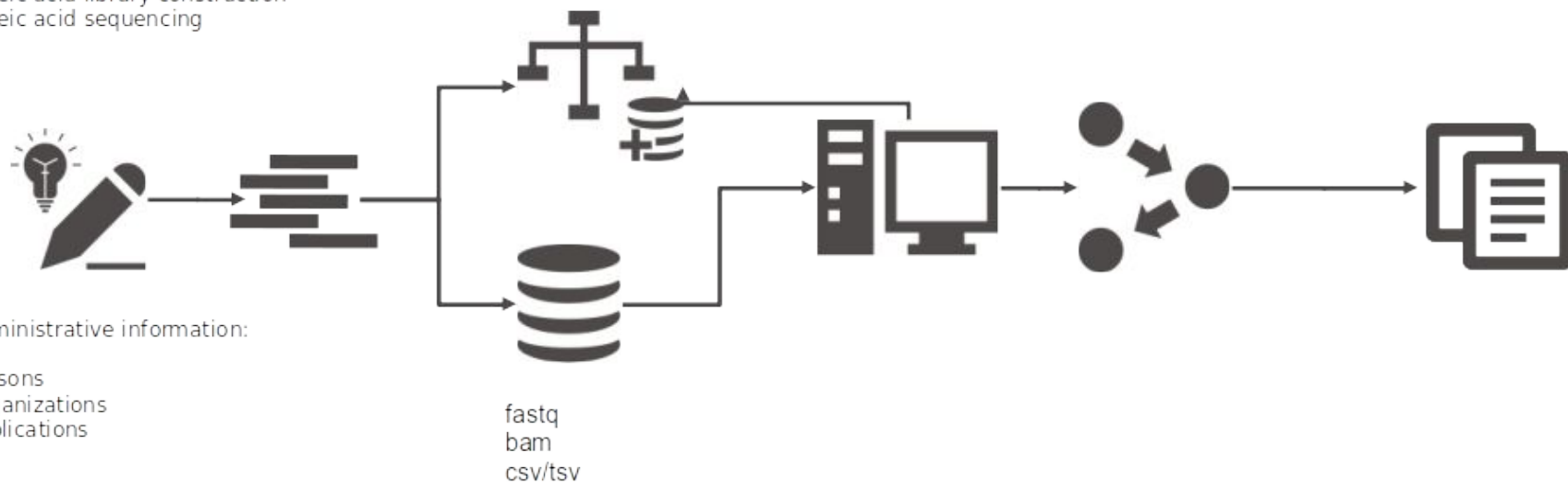
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MINSEQE

protocols:

high throughput sequence alignment
normalization data transformation



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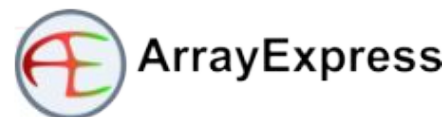
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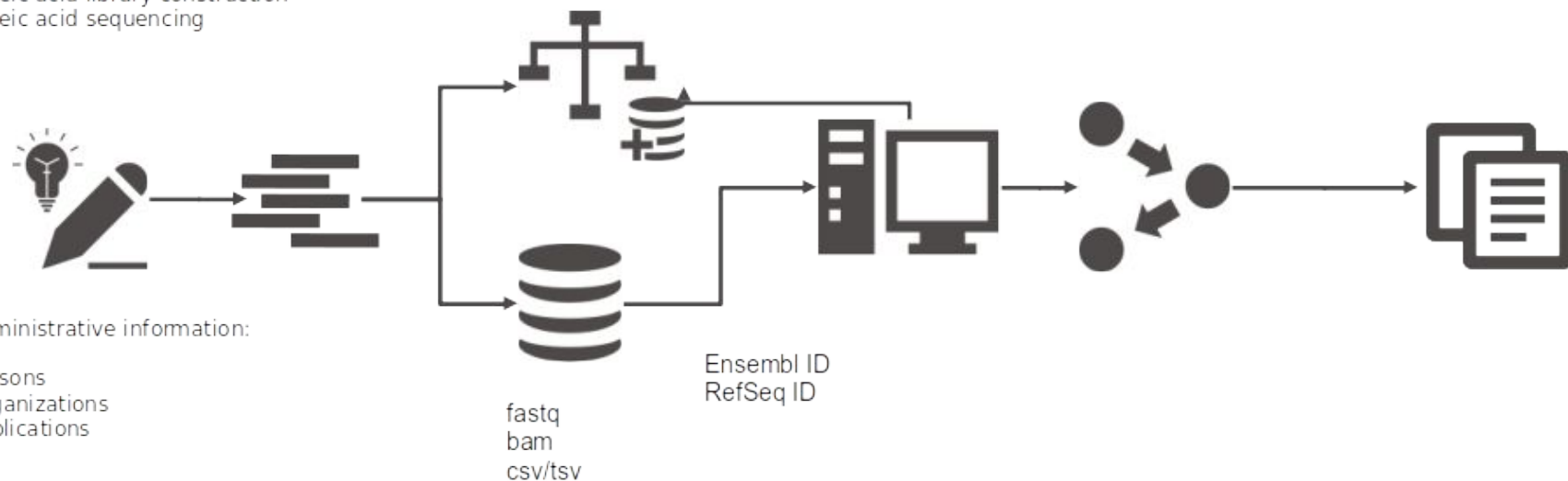
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Taxonomy



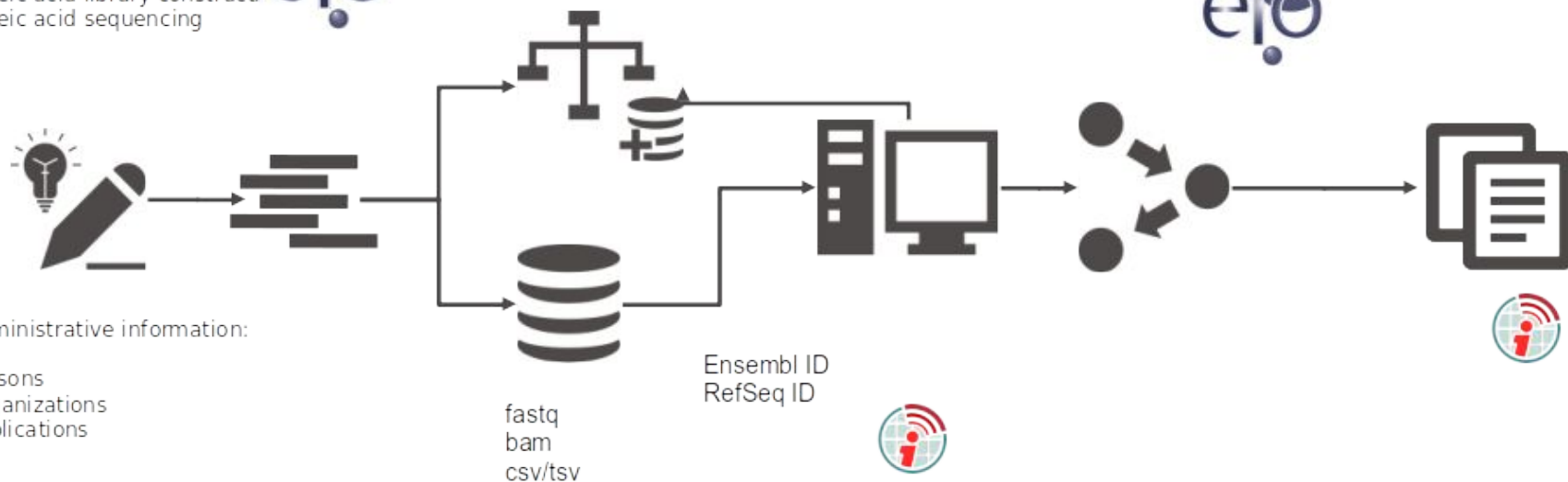
MINSEQE

protocols:

high throughput sequence alignment
normalization data transformation



ArrayExpress



Experimental conditions/design

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Taxonomy



MINSEQE

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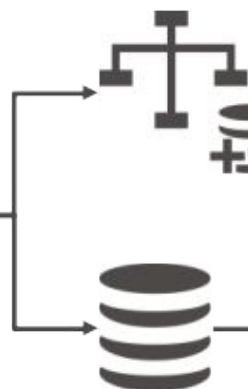


ArrayExpress



Administrative information:

Persons
Organizations
Publications



fastq
bam
csv/tsv

Ensembl ID
RefSeq ID



Interlinking with other resources

Experimental conditions/design

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protocols:

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ArrayExpress



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fastq
bam
csv/tsv

Ensembl ID
RefSeq ID



Interlinking with other resources

Which metadata standard?

FAIRsharing

Demo



The ISA model

Investigation

- Persons
- Organizations
- Publications

Study(s)

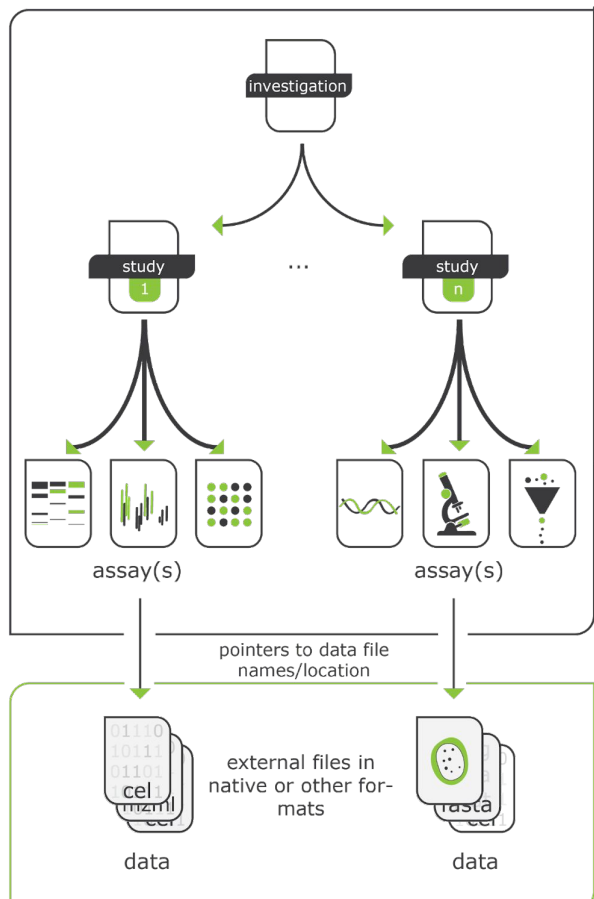
- Design
- Factor
- Protocol

Domain-agnostic standard with typical metadata fields for a project in the life sciences

Possibility of semantic annotations

Assay(s)

- Measurement
- Technology
- Materials
- Data



Metadata tracking platforms

Domain specific:

- COPO for plant sciences
- MOLGENIS for biobanking
- Omero for imaging data



Customisable (domain expertise required)

- Proprietary ELNs/LIMS -
 - often poor support for ontologies
- openBIS - open source ELN/LIMS
- FAIRDOM SEEK



<https://copo-project.org/>

<https://www.molgenis.org/>

<https://openbis.ch/>

<https://seek4science.org/>

Sample type was successfully created.

Editing Sample Type

Title *

Apple Pie

Description

baking an apple pie

Projects ·

The following projects are associated with this sample type:

Default Project [\[remove\]](#)

Select Project ...

Tags

Attributes

Re-arrange attributes by clicking and dragging the button on the left-hand side of each row.

Order	Name	Required?	Title?	Type	Unit	
1	Bake ID	*	*	String		Remove
2	Date of bake			String		Remove
3	Cooking temperature			String		Remove
4	Cooking time			String		Remove
5	Type of Apple			String		Remove

FAIRDOM SEEK

The [SEEK](#) platform is a web-based resource for sharing heterogeneous scientific research datasets, models or simulations, processes and research outcomes. It preserves associations between them, along with information about the people and organisations involved.

- National users (via Digital Life):

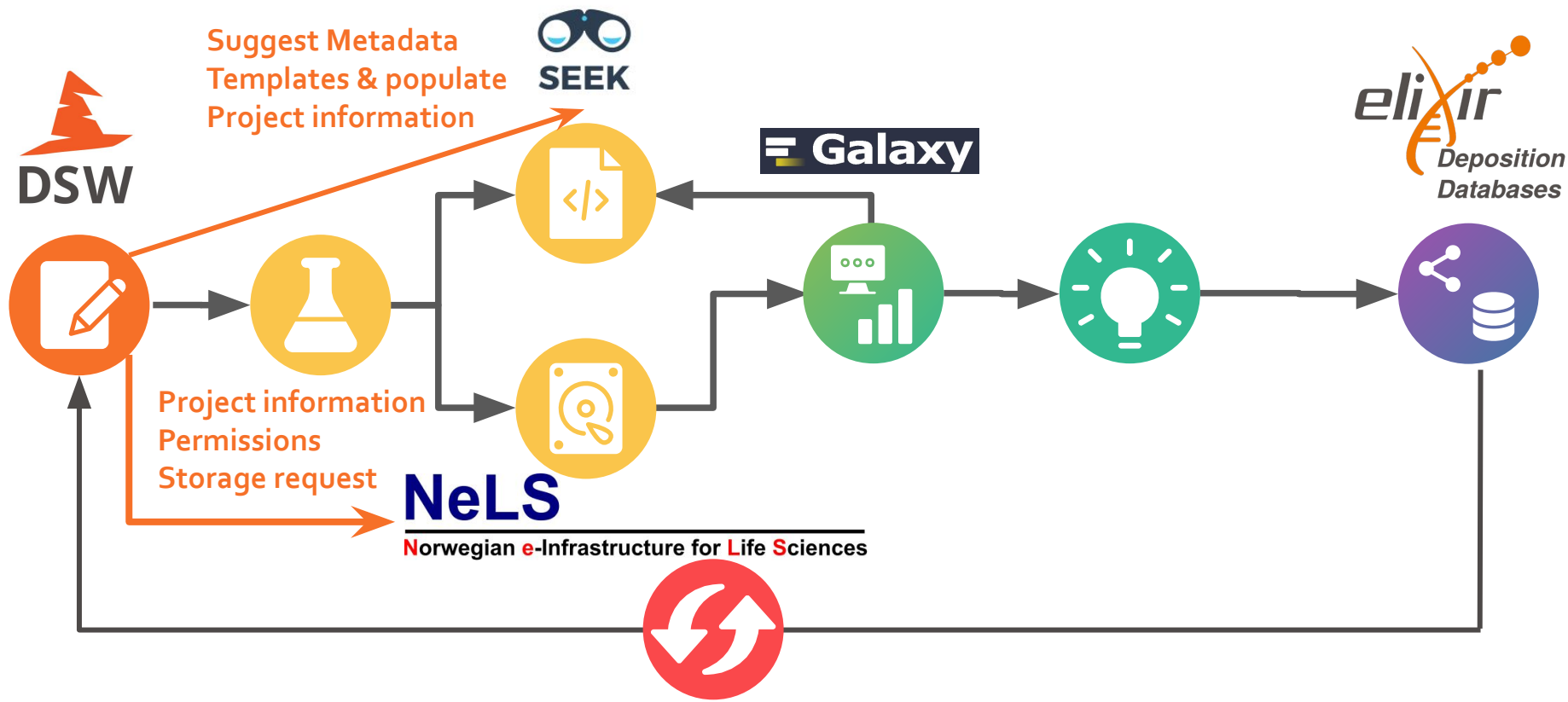


- Target new users (via ELIXIR)



Plans for further integration

K Bosl "NeLS (Norwegian e-Infrastructure for Life Sciences) tool assembly" originally presented at ELIXIR All Hands meeting 2022



Thank you!



elixir-norway.org



@elixirnorway



contact@bioinfo.no



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