



The ISA-model

Speakers: Korbinian Bösl (UiB)



Learning Objectives

In this talk, we will learn:

- The structure of ISA (Investigation, Study, Assay)



Session Take-Away

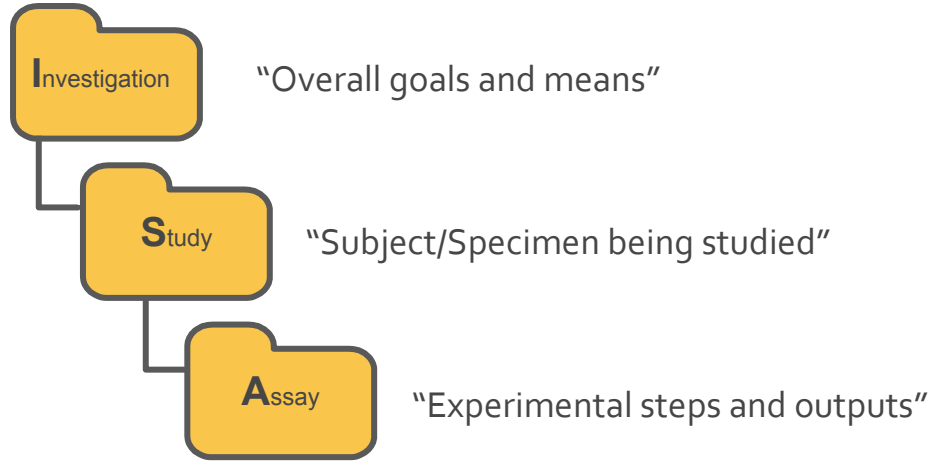
After completing this session, you will be:

- Able to understand the concept of ISA (Investigation, Study, Assay) Model
- Identify metadata schema with similar underlying concepts

Investigation Study Assay structure

Investigation Study Assay structure

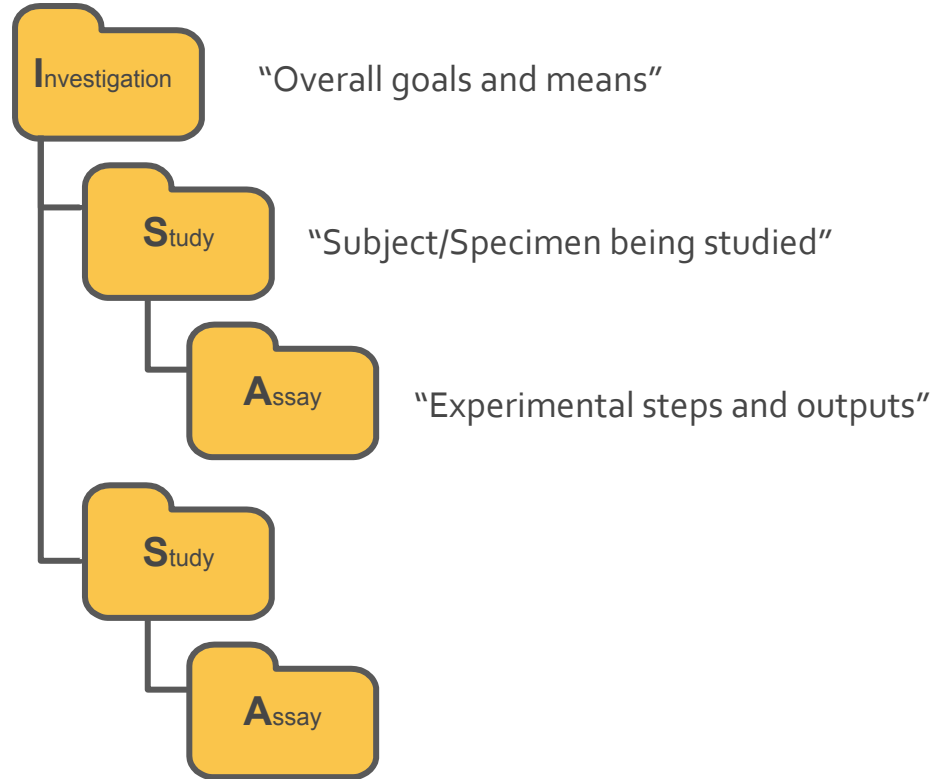
Hierarchical



Investigation Study Assay structure

Hierarchical

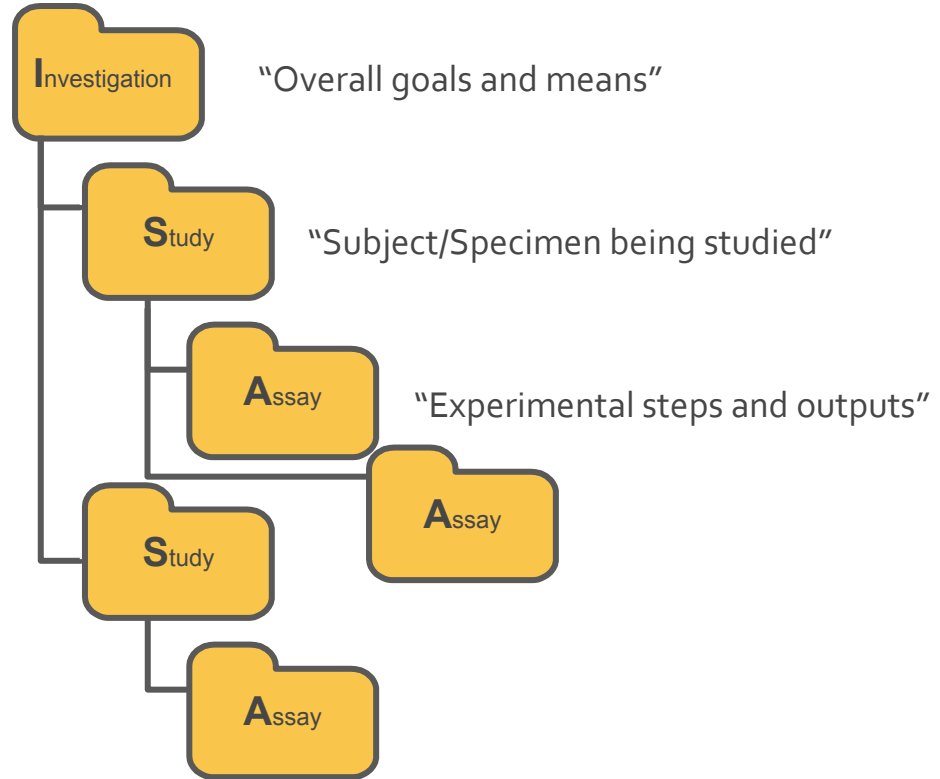
Extendable



Investigation Study Assay structure

Hierarchical

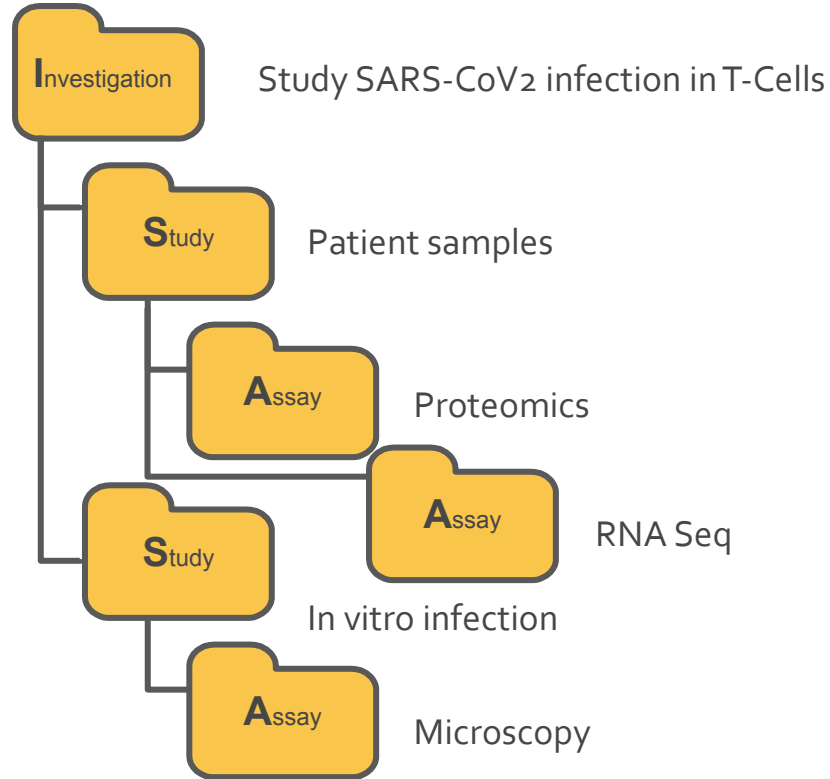
Extendable



Investigation Study Assay structure

Hierarchical

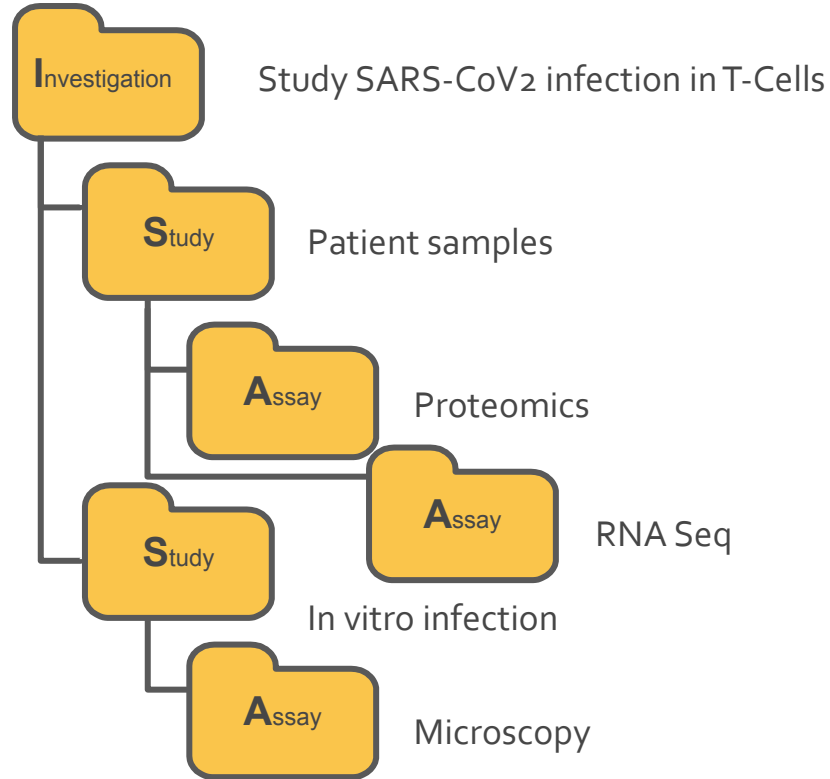
Extendable



Background

Hierarchical

Extendable



The First RSBI (ISA-TAB) Workshop: “Can a Simple Format Work for Complex Studies?”

Susanna-Assunta Sansone, Philippe Rocca-Serra, Marco Brandizi, Alvis Brazma, Dawn Field, Jennifer Fostel, Andrew G. Garrow, Jack Gilbert, Federico Goodsaid, Nigel Hardy, Phil Jones, Allyson Lister, Michael Miller, Norman Morrison, Tim Rayner, Nataliya Sklyar, Chris Taylor, Weida Tong, Guy Warner, Stefan Wiemann, and and Members of the RSBI Working Group

Published Online: 19 Jun 2008 | <https://doi.org/10.1089/omi.2008.0019>

“(...) a simple format that can easily be created, viewed,
and edited by researchers with little or no
bioinformatics support (...)”

(...) a general purpose framework with which to
collect and communicate complex metadata
(i.e. sample characteristics, technologies used,
type of measurements made) from
'omics-based' experiments (...)



Because good research needs good data

<https://www.dcc.ac.uk/resources/metadata-standards/isa-tab>

Related models

MAGE-TAB

MINSEQE



MIAPE



MIAPPE

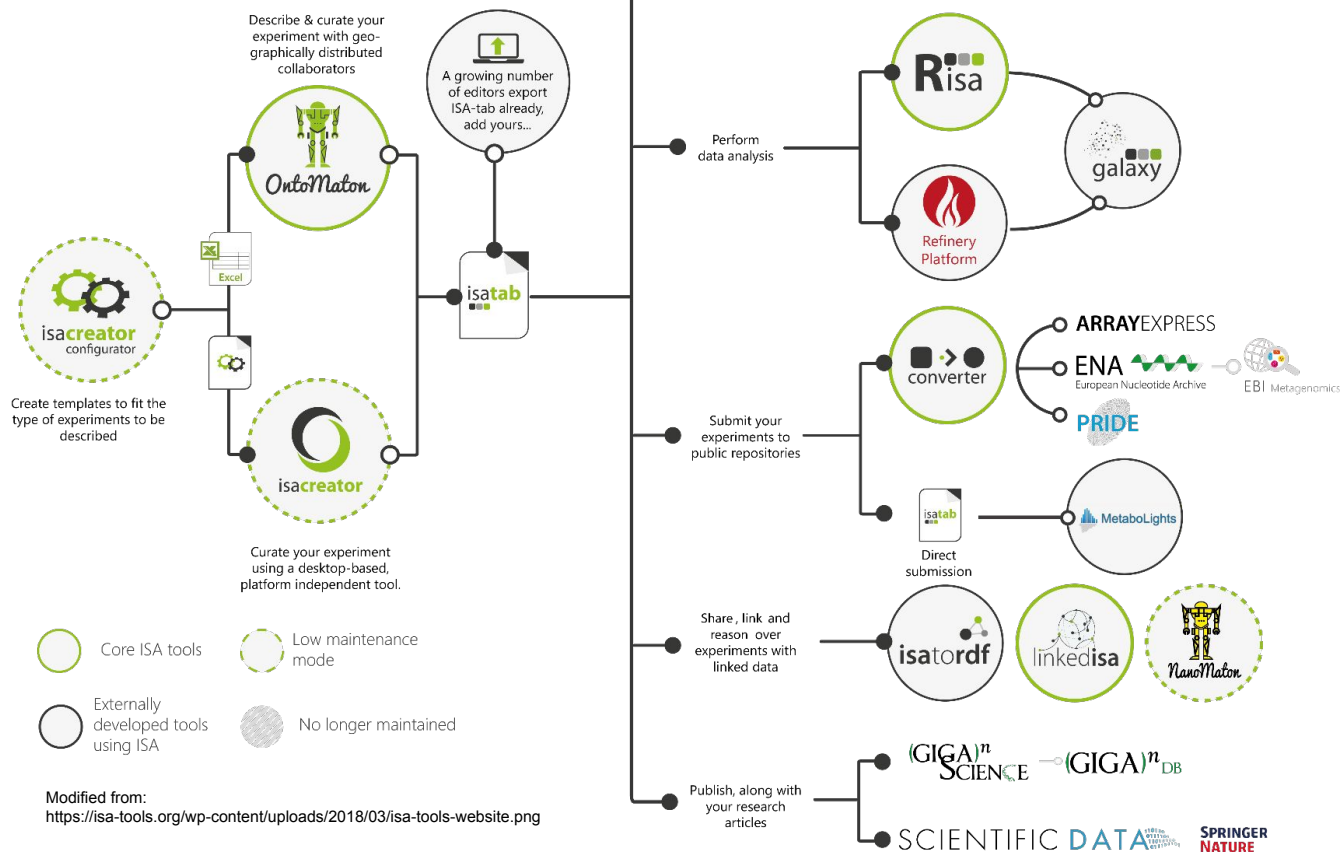


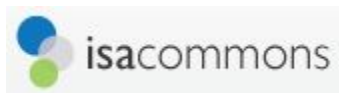
PAGE



ISA



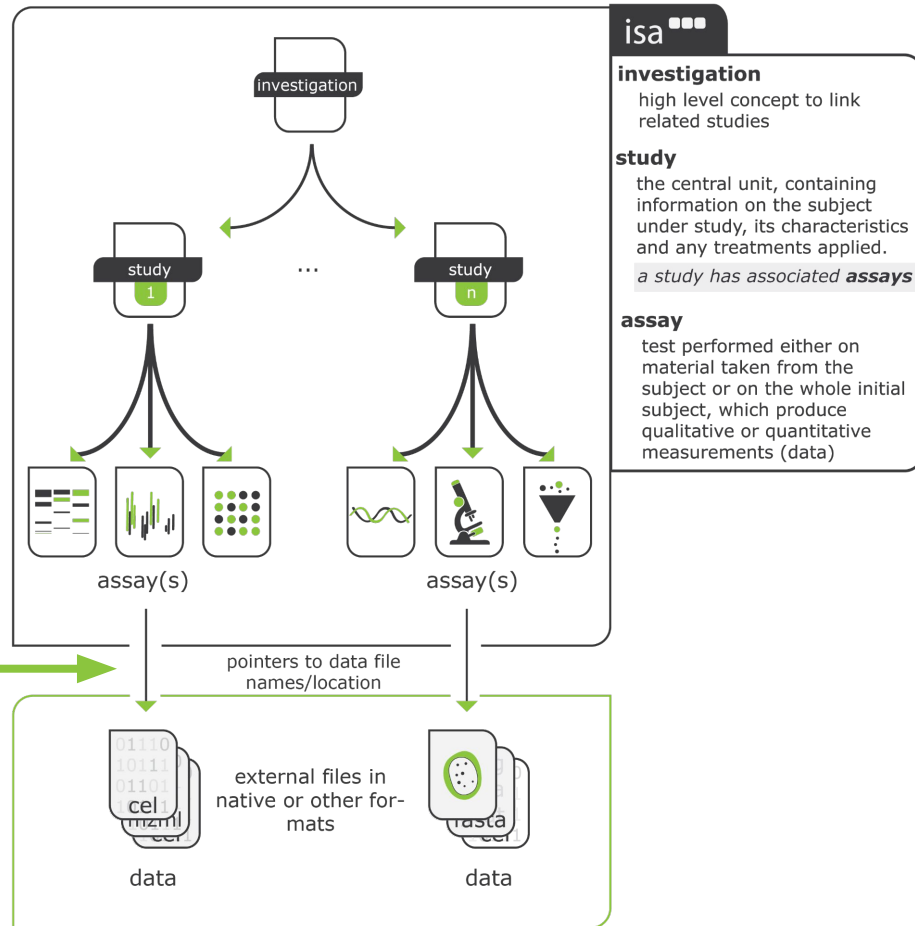


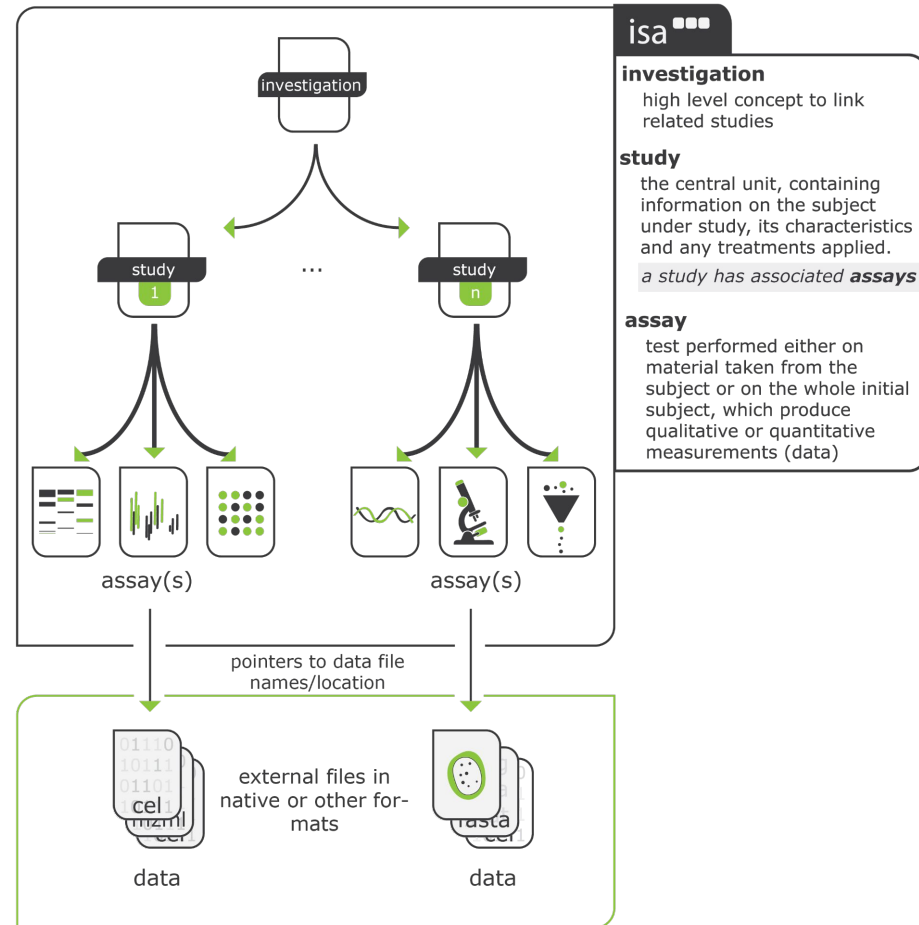
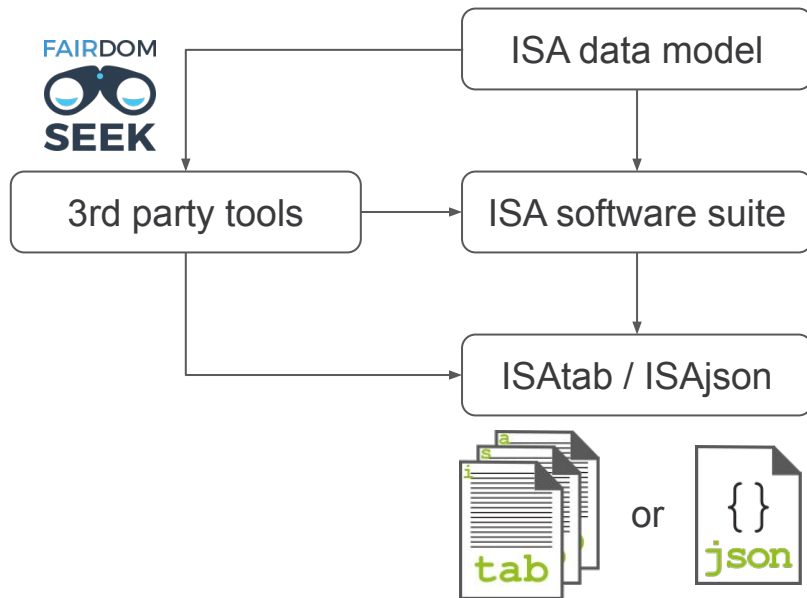


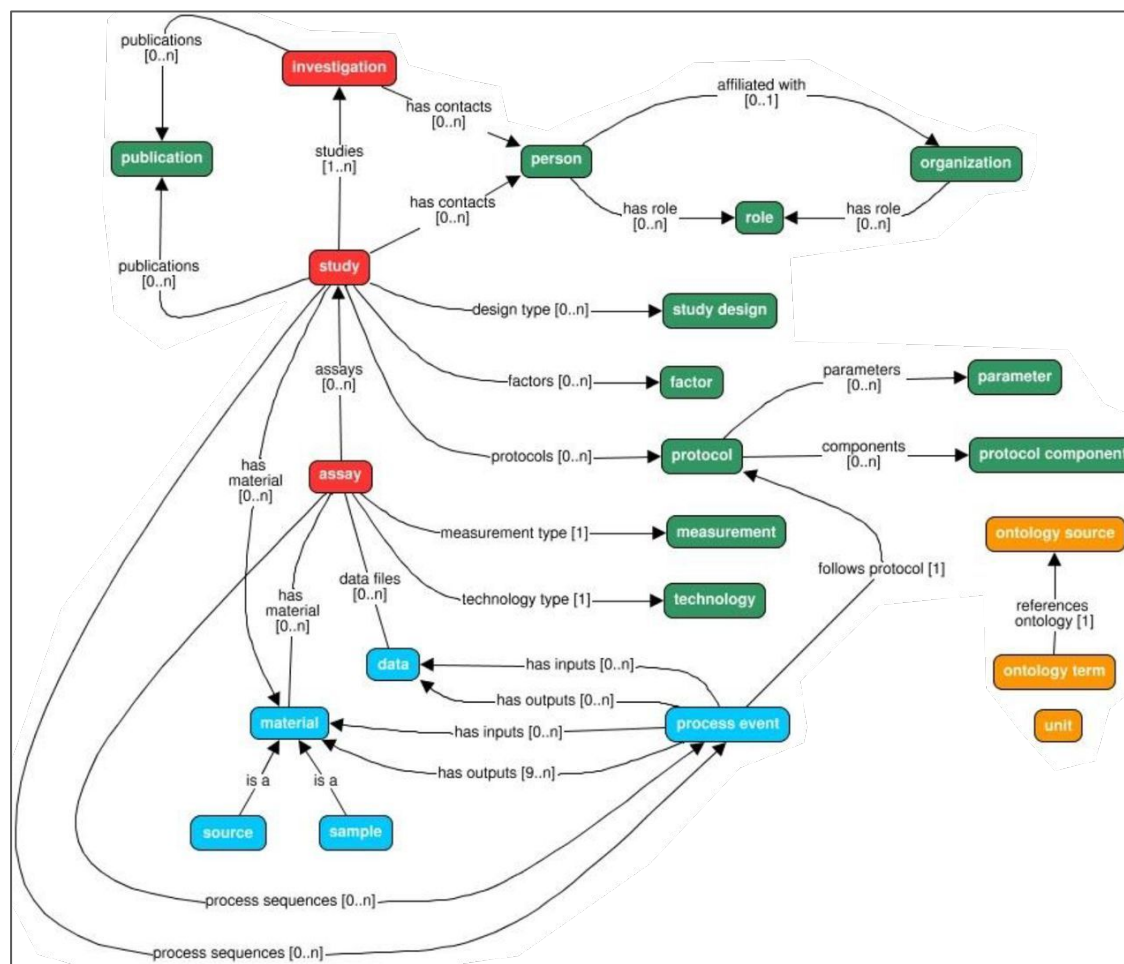
ISA data model

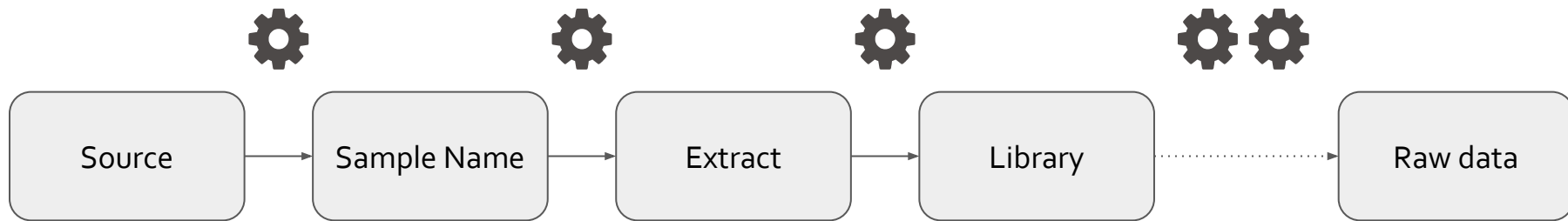
ISA software

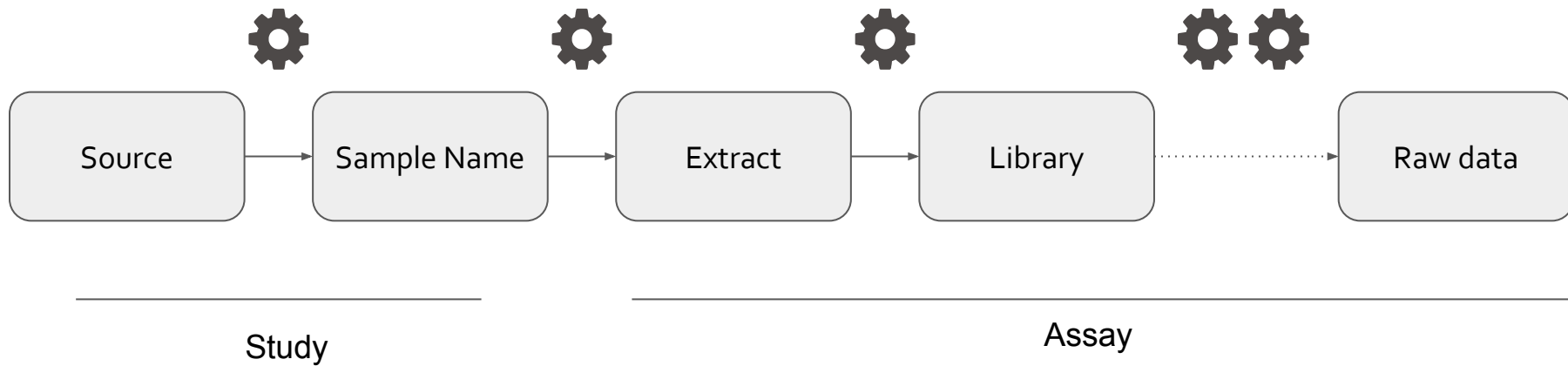
Access to files not
necessary

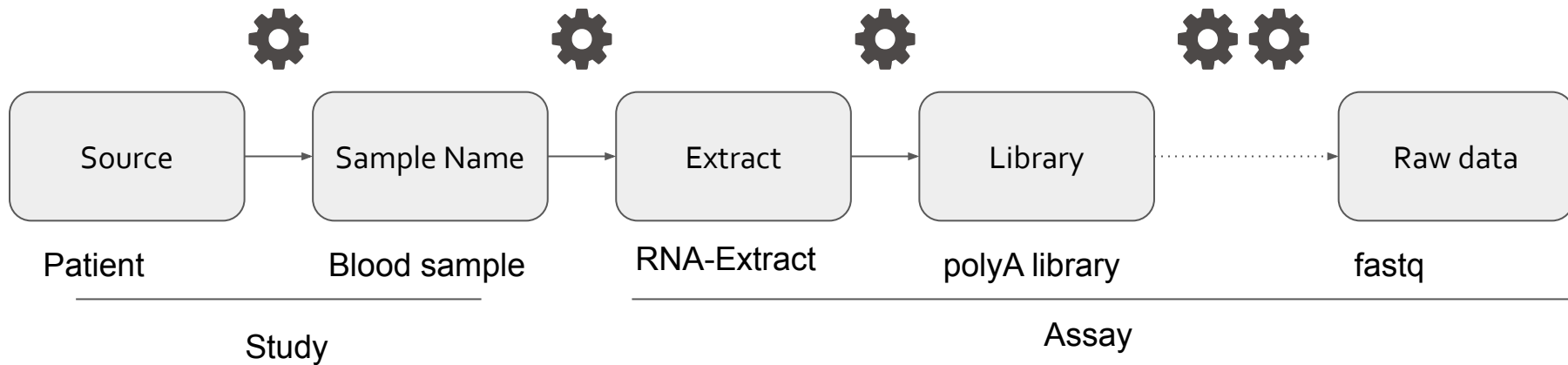


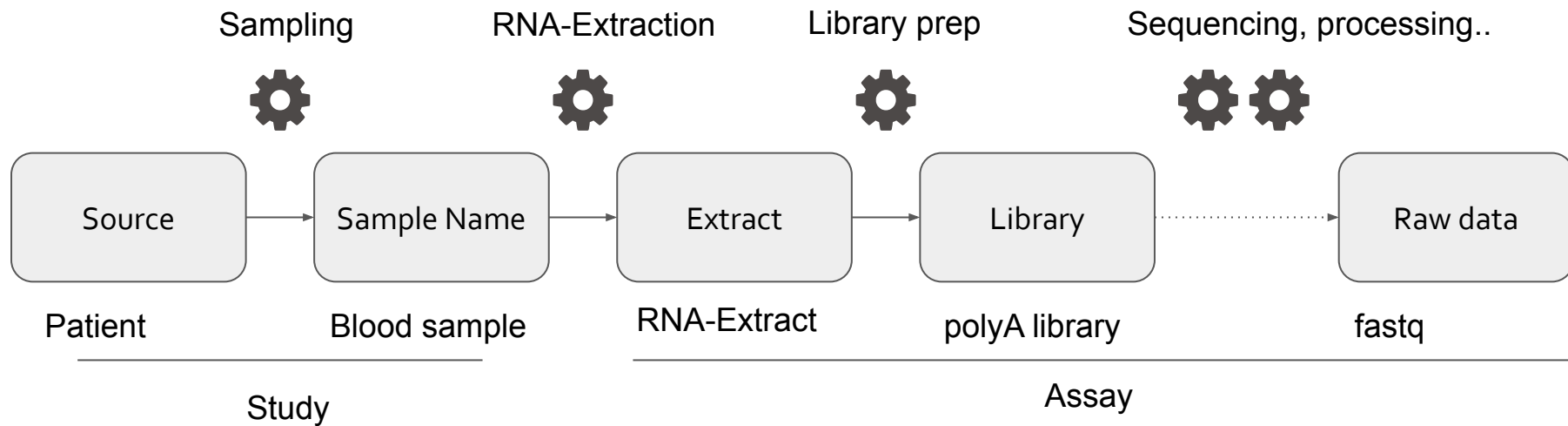




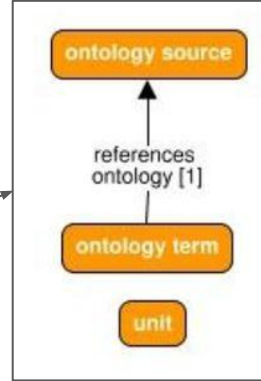
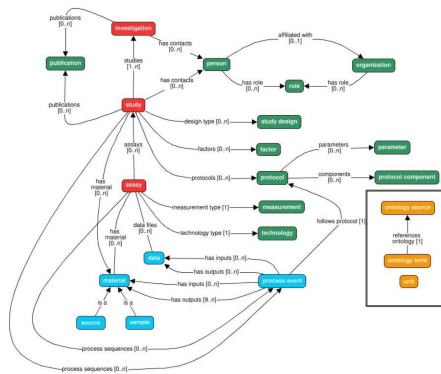








Ontologies



"ISA Data Model objects can be qualified with ontology terms (Ontology Annotations) that are linked to a declared description of the source of the terms (Ontology Sources)"

<https://doi.org/10.1101/2020.11.13.382119>



```

1  {
2    "submissionDate": "2007-04-30",
3  >   "people": [...],
76  ],
77  >   "publications": [...],
89  ],
90   "description": "Background Cell growth underlies many key cellular and developmenta
91  >   "studies": [...],
26164 ],
26165 "publicReleaseDate": "2009-03-10",
    "ontologySourceReferences": [...],
26209 ],
26210 >   "comments": [...],
26219 ],
26220 "identifier": "BII-I-1",
26221 "title": "Growth control of the eukaryote cell: a systems biology study in yeast"
26222 }
```

Ontologies

“ISA Data Model objects can be qualified with ontology terms (Ontology Annotations) that are linked to a declared description of the source of the terms (Ontology Sources)”

<https://doi.org/10.1101/2020.11.13.382119>

Items qualifiable with Ontology in ISA-JSON:

1. People's roles
2. Status of Publication
3. Study Design Descriptors
4. Units
5. Measurement Type
6. Technology Type
7. Factor (Attribute title)
8. Factor Value (Input value)
9. Characteristic (Attribute title)
10. Characteristics value (Input value)
11. Parameter Value (Attribute title)
12. Parameter Value value (Input value)
13. Protocol Type
14. Component Type (of Protocol)

Ontology Sources

```
"ontologySourceReferences": [  
  {  
    "file": "https://bioportal.bioontology.org/ontologies/UO,"  
    "description": "Units of Measurement Ontology",  
    "name": "UO",  
    "version": "2020-03-10"  
  },  
]
```

Ontology Annotations (example for a Unit)

```
{  
  "@id": "#Unit/hour",  
  "termAccession": "http://purl.obolibrary.org/obo/UO_0000032",  
  "annotationValue": "hour",  
  "termSource": "UO"  
}
```

Experimental conditions/design

protocols:

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



Taxonomy



MINSEQE

protocols:

high throughput sequence alignment
normalization data transformation

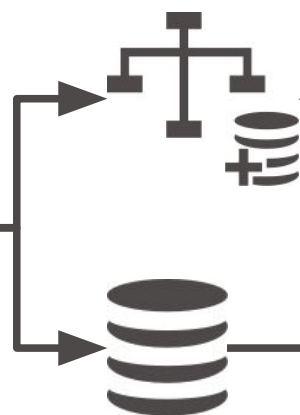


ArrayExpress



Administrative information:

Persons
Organizations
Publications



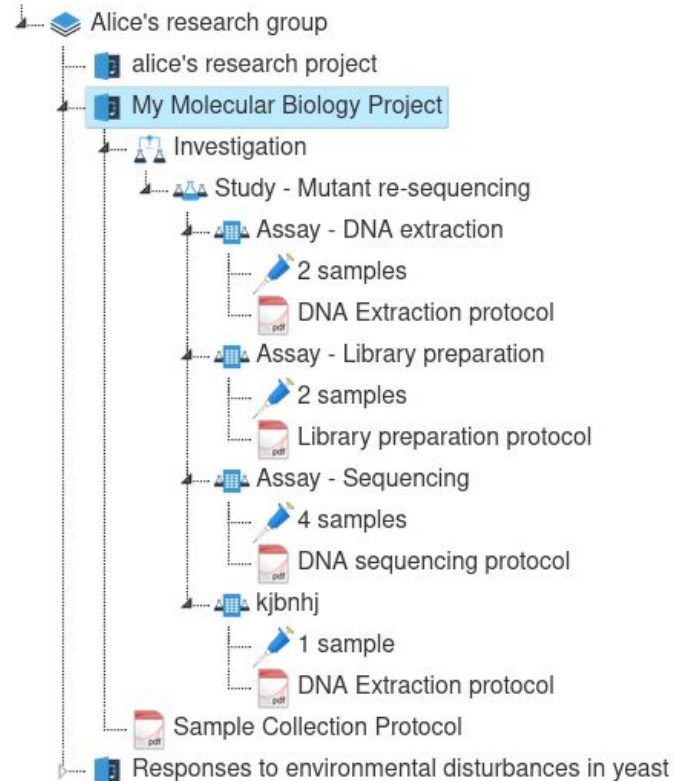
fastq
bam
csv/tsv

Ensembl ID
RefSeq ID



Interlinking with other resources

SEEK



SEEK



Ontology

You can, optionally, populate the terms from an ontology available from the [Ontology Lookup Service](#). To do so, select the ontology below, and then choose the root term - from which itself and its children will be added to the terms. You can choose the root term by following the link provided to browse the ontology. Then click Fetch to populate the terms below. Note that for a large tree this can take several minutes. Afterwards you can remove or tweak individual terms, or add additional terms. If you wish to generate a Controlled Vocabulary for an ontology that isn't available on the Ontology Lookup Service, then please contact us using the [Feedback Form](#).

Ontology

Human Disease Ontology

No Ontology

Agronomy Ontology

Allotrope Merged Ontology Suite

Amphioxus Development and Anatomy Ontology (AMPHX)

An ontology of core ecological entities

Anatomical Entity Ontology

Animal Trait Ontology for Livestock

Antibiotic Resistance Ontology

Apollo Structured Vocabulary (Apollo-SV)

Ascomycete Phenotype Ontology (APO)

Bambara groundnut ontology

Banana ontology

Barley ontology

Basic Formal Ontology

Beet Ontology ontology

BioAssay Ontology

Bioinformatics operations, data types, formats, identifiers and topics

Biological Collections Ontology

Biological Imaging Methods Ontology

Biological Spatial Ontology

Create

Our ambition:



Follow up from
Staff exchange
DE UK BE NO

