

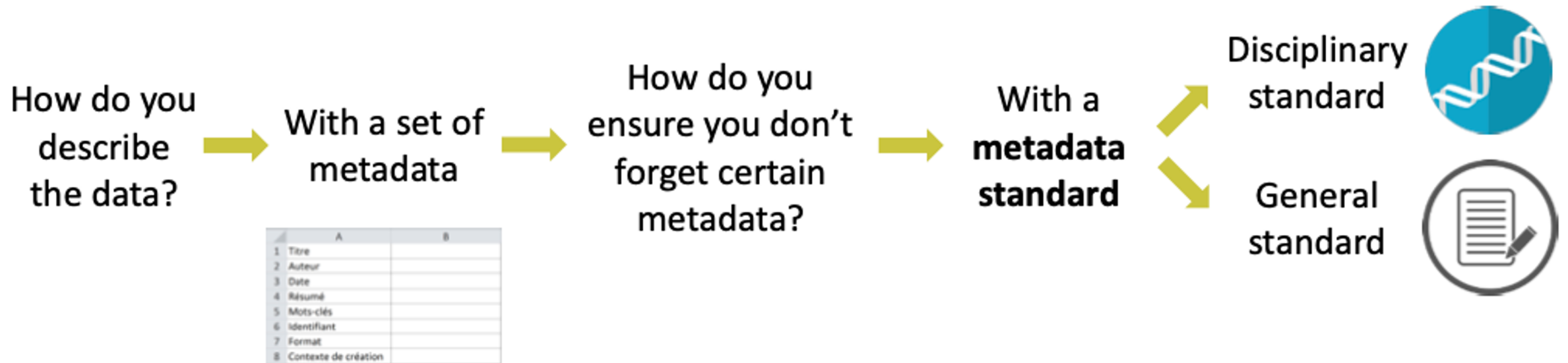


# Life science standards and ENA submission

[helene.chiapello@inrae.fr](mailto:helene.chiapello@inrae.fr) & [thomas.denecker@france-bioinformatique.fr](mailto:thomas.denecker@france-bioinformatique.fr)

# Metadata & standards in life sciences

# Metadata standards help describing data



Source: <https://www.pasteur.fr/fr/file/20615/download>

# Definition of a standard

In essence, a standard is an **agreed way of doing something**.

A standard provides the **requirements, specifications, guidelines or characteristics** that can be used for the **description, interoperability, citation, sharing, publication, or preservation** of all kinds of **digital objects** such as data, code, algorithms, workflows, software, or papers.

source: <https://fairsharing.org/educational/>

**Example of standard in biology : Gene Ontology**



# The standards concern both data and metadata

Why do I have to use a **data standard**?

- to analyse, compare and exchange data
- to publish datasets in international resources

And a **metadata standard**?

- To describe data richly and accurately, with the same vocabulary as the rest of your scientific community
- To make your metadata interoperable and to allow other systems to exploit them

The Gene Ontology is a **metadata** standard

Question: What do you know as standard in life sciences ?

*10 minutes to find an example (one for data and one for metadata) and write a note in*

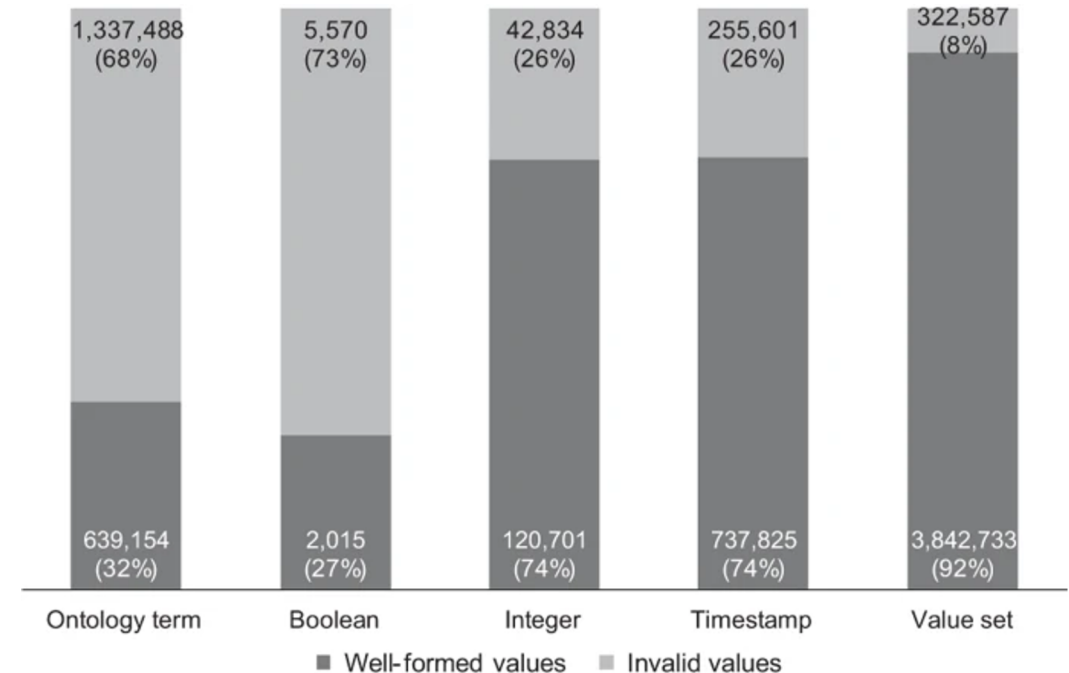
<https://scrumbler.ethibox.fr/standard>

# Metadata exhibit questionable quality in biology

Submission in public resources is often a complex task

Submission procedures are heterogeneous

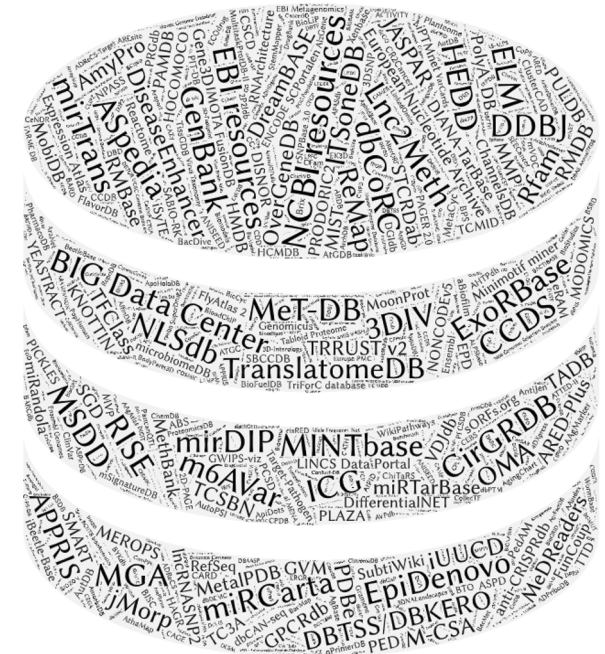
**Metadata are often incomplete, inconsistent, redundant or not enough informative**



Quality of dictionary attributes in NCBI BioSample according to their type, in [Gonçalves et al., 2019](#)

# Standard adoption and perenity

- There are thousand of databases, softwares and resources in biology with **unequal level of standard adoption**
- Is is not easy for Life scientists and bioinformaticians to identify and use the most appropriate standards



1641 databases in NAR Database 2021

[Rigden \*et al\*, 2021](#)

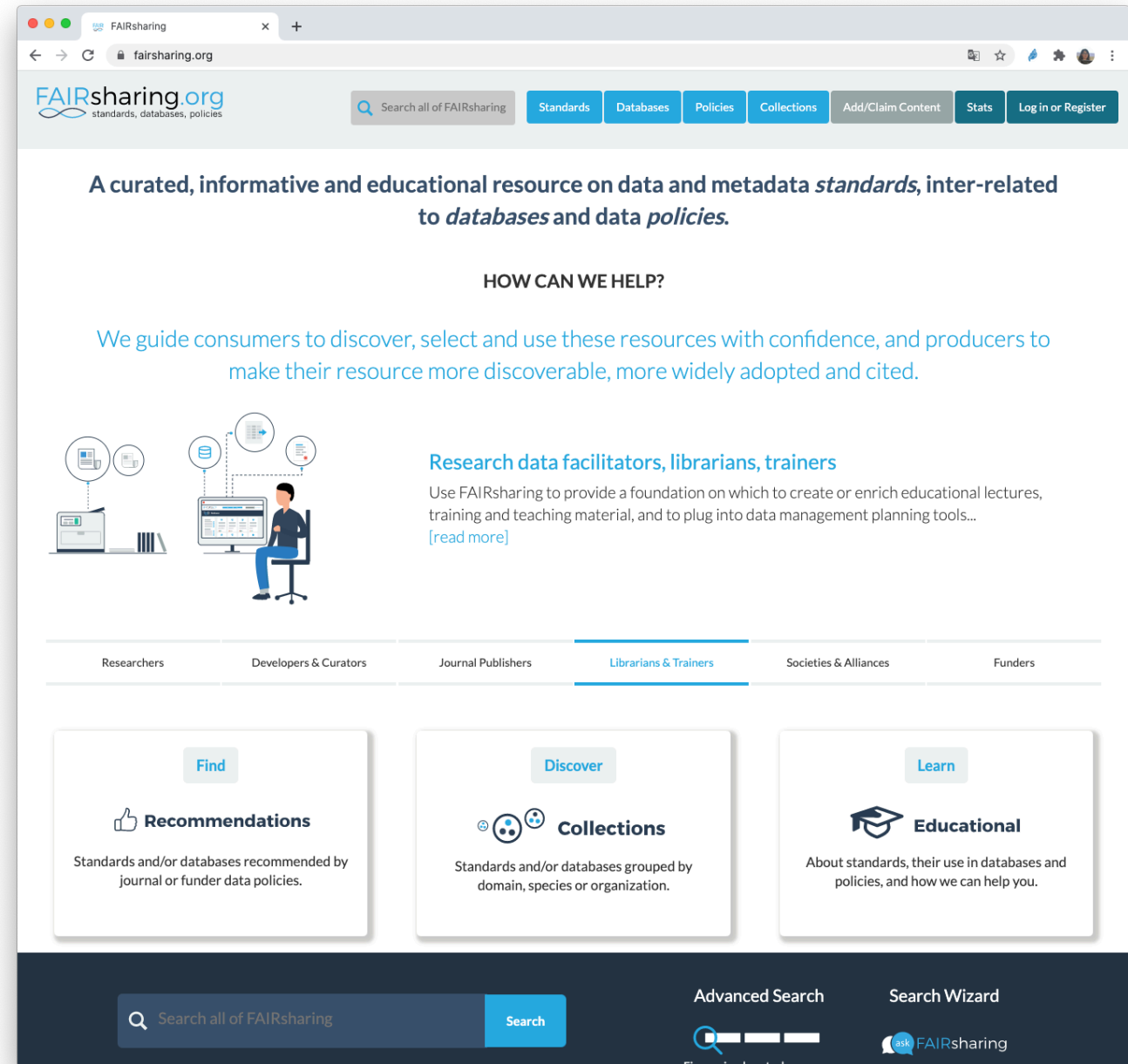
# How do I find the standard I need?

# The FAIRsharing portal

Sansone, *et al.* FAIRsharing as a community approach to standards, repositories and policies.

Nat Biotech. 2019

<https://doi.org/10.1038/s41587-019-0080-8>



<https://fairsharing.org>

# The FAIRsharing portal

Citable *DOI* for all records

Accessible via *API* or *web interface*

*Curation*

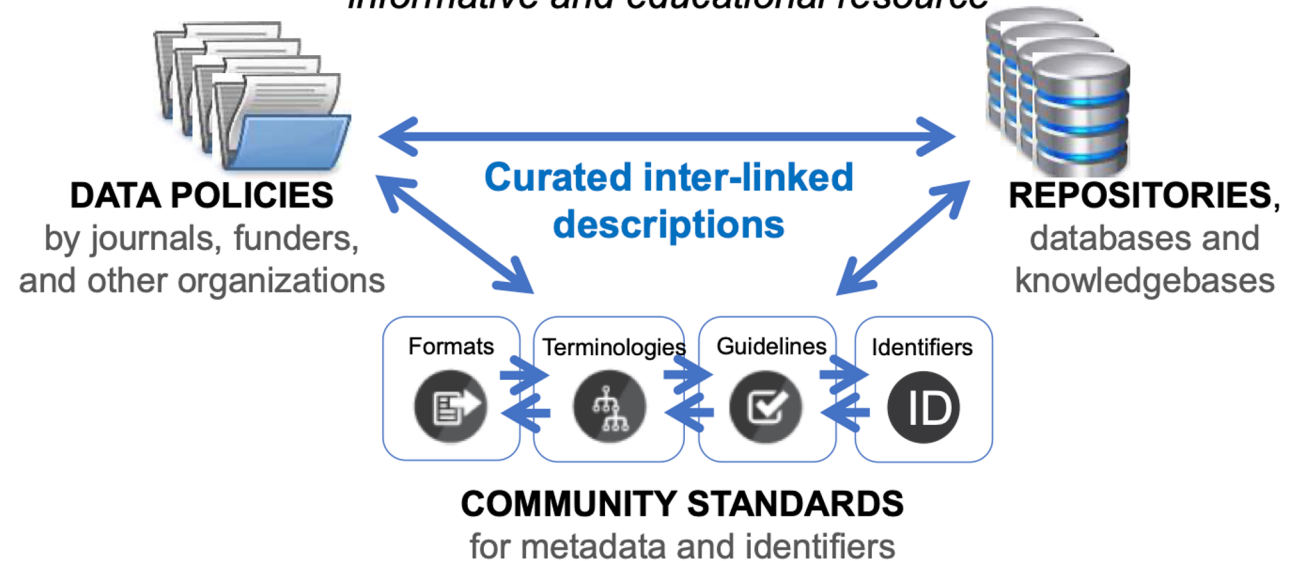
**RECORD  
STATUS**

- R** Ready for use, implementation, or recommendation
- Dev** In development
- U** Status uncertain
- D** Deprecated as subsumed or superseded

All records are manually **curated in-house**, verified and claimed by the community behind each resource

FAIRsharing.org

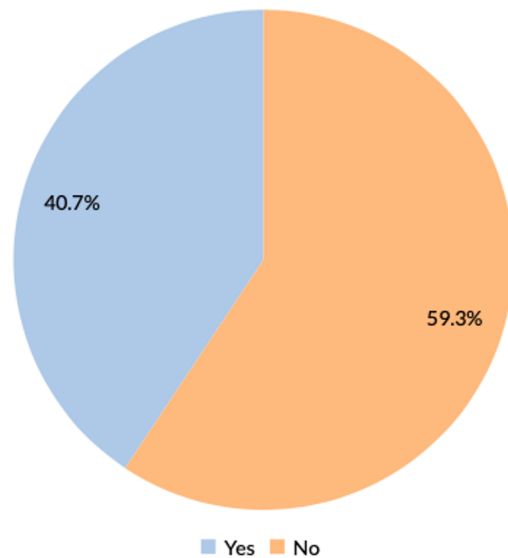
*informative and educational resource*



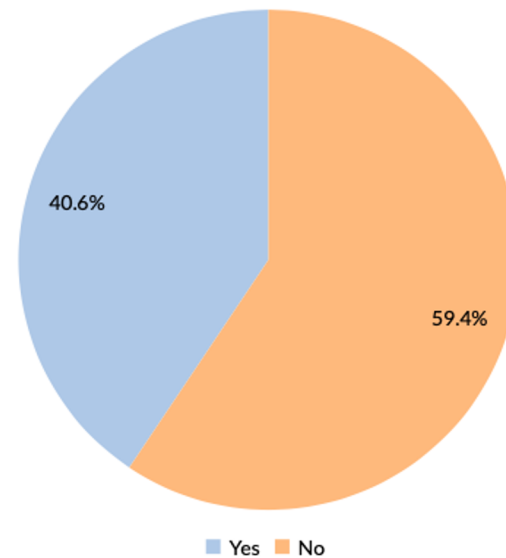
<https://fairsharing.org>

# Standard maintenance is a key point

Standard records that have maintainers



Standards that have a publication



59.3 % of standards have no maintainer

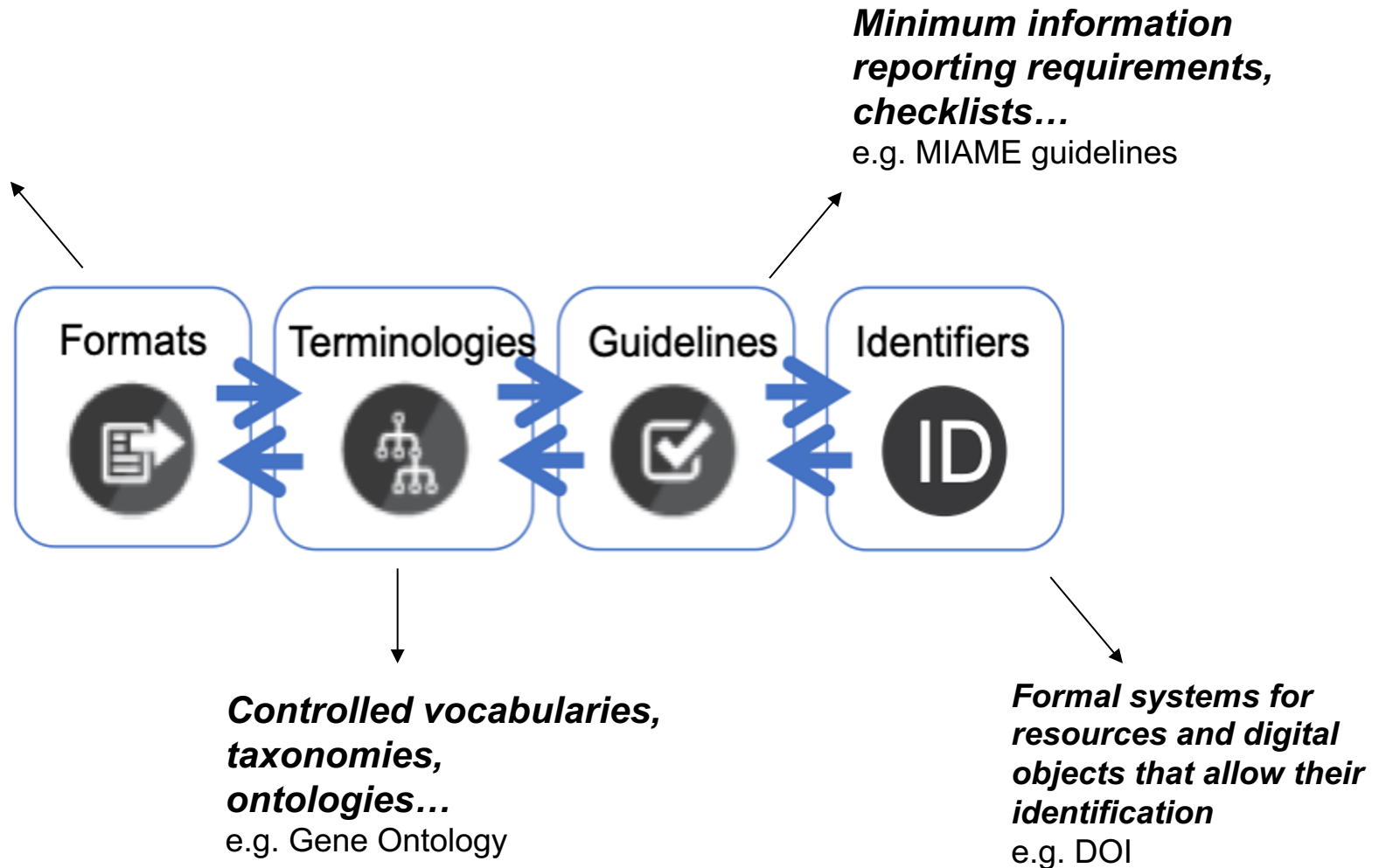
59.4% of standard has no publication

<https://fairsharing.org/summary-statistics/?collection=standards>

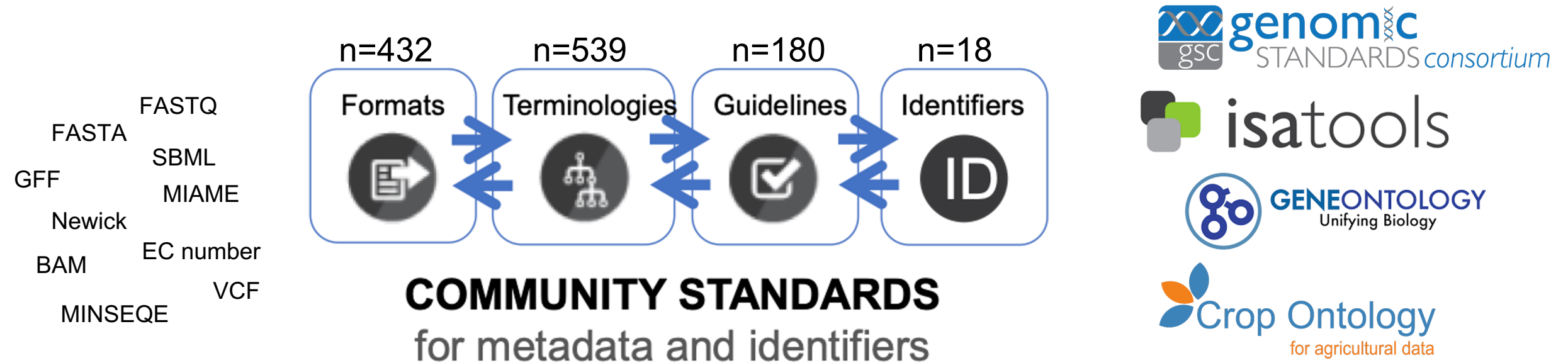


# Types of data standards

**Conceptual model, schema, exchange formats, etc...**  
e.g. FASTA



# The landscape of standards in life sciences



# Collections in the FAIRsharing portal

A *collection* include standards and/or databases *grouped by domain, species or organization*

*Graph view* to visualize relationship links between resources

<https://fairsharing.org/collections/>

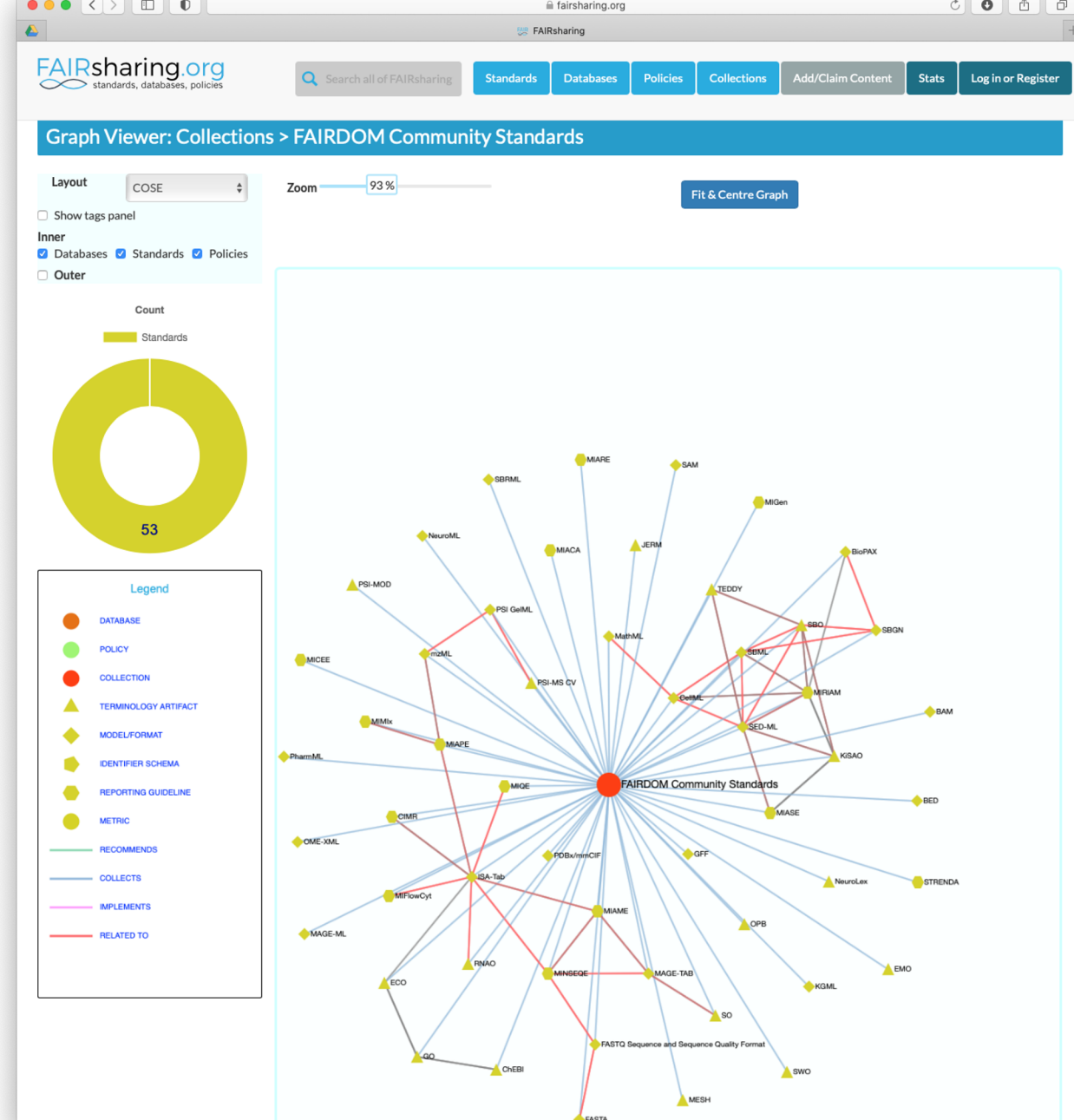
The screenshot displays the FAIRsharing.org interface for a collection titled "COVID-19 Resources". The page features a navigation bar with tabs for Standards, Databases, Policies, Collections, Add/Claim Content, Stats, and Log in or Register. Below the navigation, there are subject filters (Biomedical Science, Clinical Studies, Epidemiology, Global Health, Health Science, Preclinical Studies, Public Health, Virology) and user-defined tags (Respiratory Disease). A "View as Graph" button is visible, along with a "Compare with collection/recommendation (Beta)" dropdown menu. The main content area shows "General collection/recommendation statistics" for "COVID-19 Resources (bsg-c000070)" with a "Show Stats" button. A table of records is displayed, showing 1-50 of 80 records. The table has columns for Registry Name, Abbreviation, Type, Subject, Domain, Taxonomy, Related Database, Related Standard, and Related Policy. The first record is "American Type Culture Collection Database" with Abbreviation "ATCC", Type "Database", Subject "Virology", "Uk Health", and "Genetics", Domain "Genetics", Taxonomy "Genetics", and Related Database "None".

# Collections in Life Sciences

63 collections related to Life Science standards in FAIRsharing

Example 1: the *FAIRdom community Standards collection* (System biology)

<https://fairsharing.org/collection/FAIRDOME>



# Some collections are recent

## Example 2: The *Covid-19* collection

FAIRsharing.org  
standards, databases, policies

Search all of FAIRsharing

Standards Databases Policies Collections Add/Claim Content Stats Log in or Register

Graph Viewer: Collections > COVID-19 Resources

Layout COSE Zoom 93% Fit & Centre Graph

Show tags panel

Inner  
 Databases  Standards  Policies

Outer

Count

- 4 Policies
- 5 Standards
- 70 Databases

Legend

- DATABASE
- POLICY
- COLLECTION
- ▲ TERMINOLOGY ARTIFACT
- ◆ MODEL/FORMAT
- ◆ IDENTIFIER SCHEMA
- REPORTING GUIDELINE
- METRIC
- RECOMMENDS
- COLLECTS
- IMPLEMENTS
- RELATED TO

Registry	Name	Abbreviation	Type	Subject	Domain	Taxonomy	Related Database	Related Standard	Related Policy	In Collection?
American Type Culture Collection database	ATCC	Database	Microbiology	Microbiology	Microbiology	Microbiology	None	None	Springer Nature Medicine - Availability of Data and materials	Yes
Australian New Zealand Clinical Trials Registry	ANZCTR	Database	Health Services	Health Services	Health Services	Health Services	ClinicalTrials.gov	None	None	Yes
BBMRI-ERIC Directory	BBMRI-ERIC Directory	Database	Health Services	Health Services	Health Services	Health Services	ERIC-CoRe	None	None	Yes

<https://fairsharing.org/collection/COVID19Resources>

FAIRsharing.org  
standards, databases, policies

Search all of FAIRsharing

Standards Databases Policies Collections Add/Claim Content Stats Log in or Register

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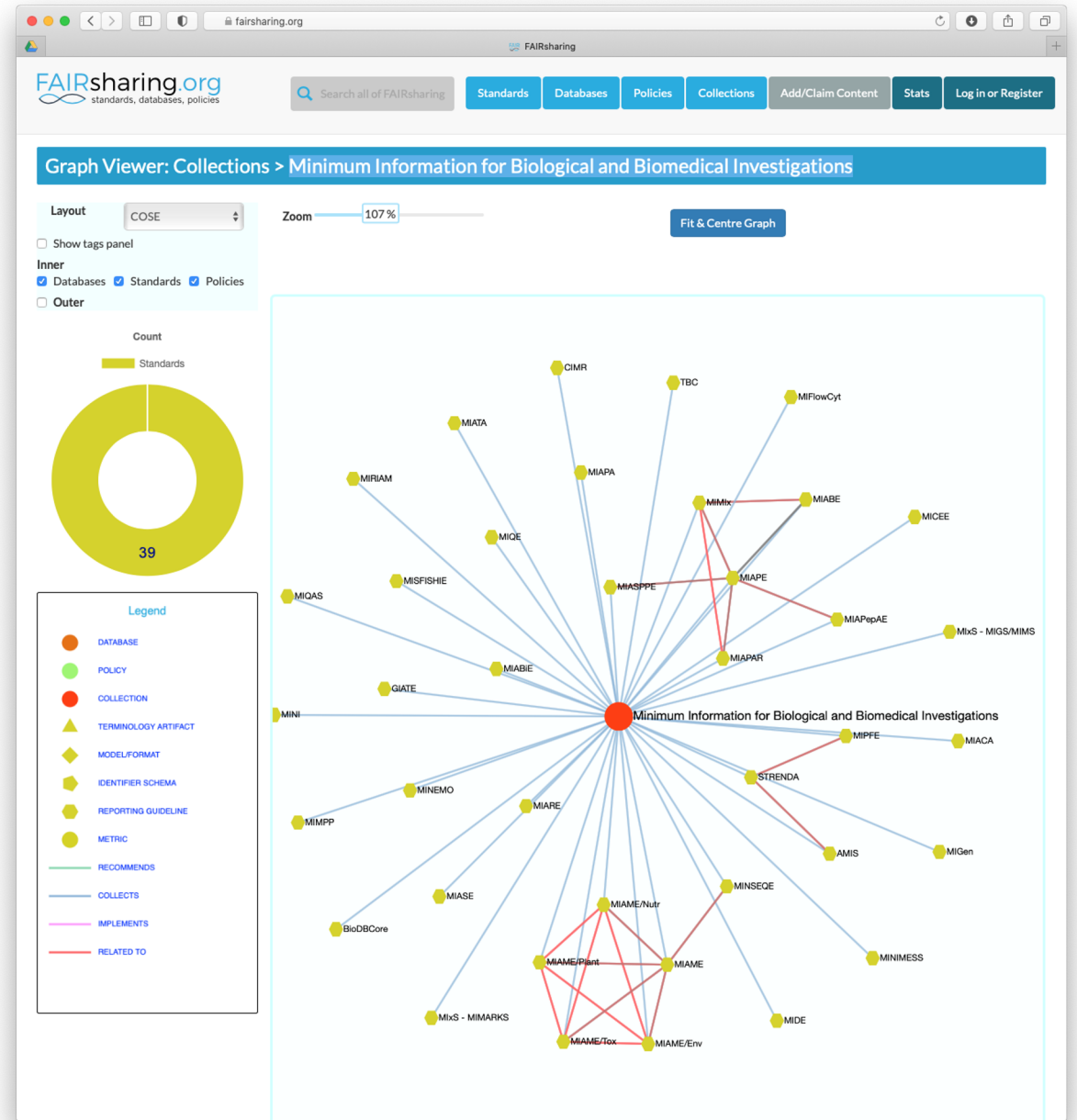
- DATABASE
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- REPORTING GUIDELINE
- METRIC
- RECOMMENDS
- COLLECTS
- IMPLEMENTS
- RELATED TO

<https://fairsharing.org/graph/#/collection/bsg-c000070>

# What about the minimum required metadata in biology?

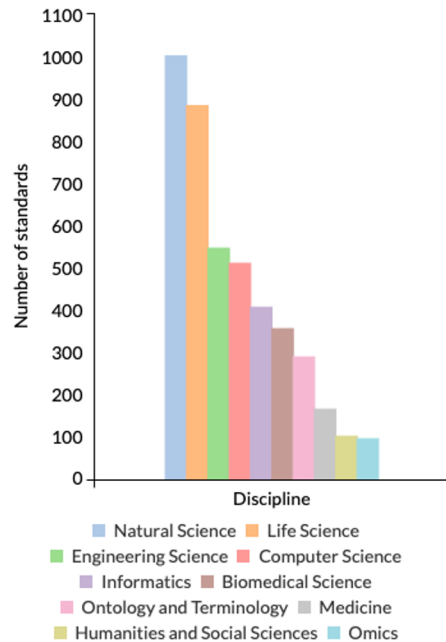
Example 3: the *Minimum Information for Biological and Biomedical Investigations* collection

<https://fairsharing.org/collection/MIBBI>

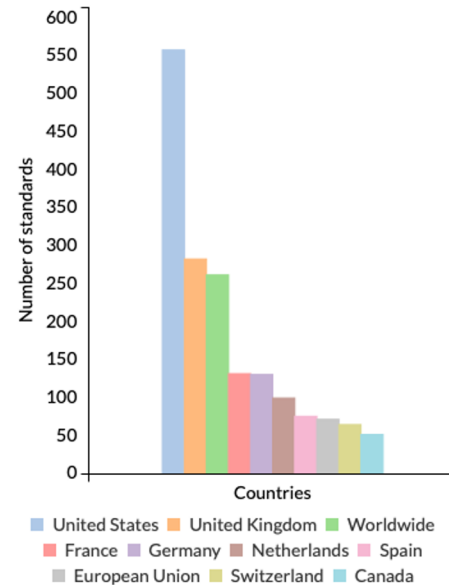


# Summary statistics about standards

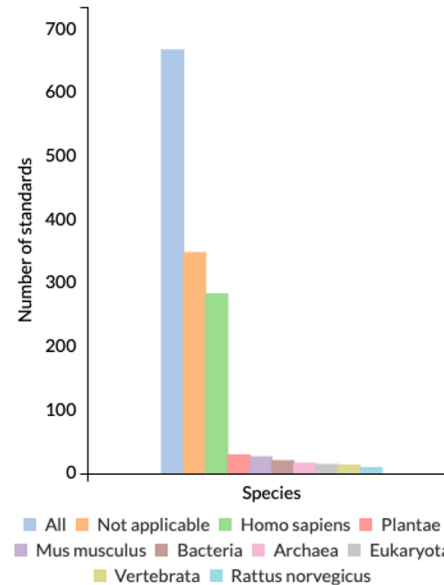
Top 10 disciplines covered by standards



Top 10 standard producing countries



Top 10 species covered by standards



**Life Science is one of the best covered discipline**

US and UK are the main standards producers

**Human species is the best covered species**

<https://fairsharing.org/summary-statistics/?collection=standards>



# Practice

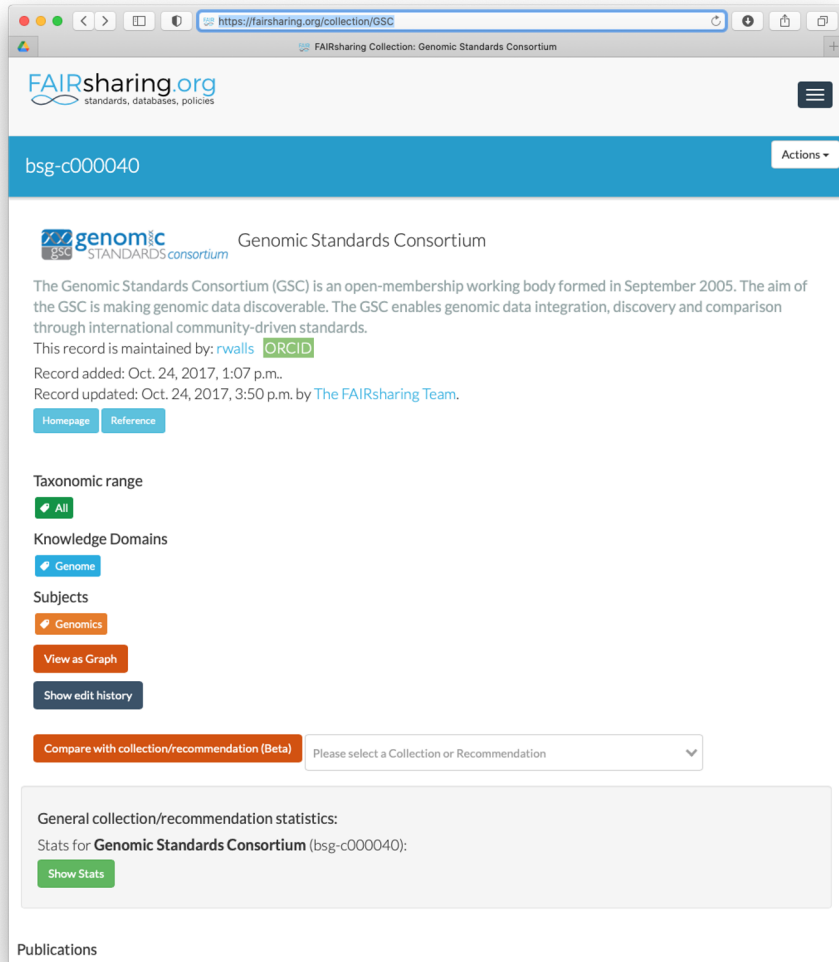
Find the *Genomics Standard Consortium (GSC)* used by both ENA and SRA databases in the FAIRsharing resource

Use both the record summary and the Graph visualization to interpret and answer the questions in zoom:

1. How many records (*i.e.* standards) are associated to the GSC ?
2. What type of standard is *Minimum Information about any (x) Sequence (MiXS)* ?
3. What is the record status of the GAZ record ?

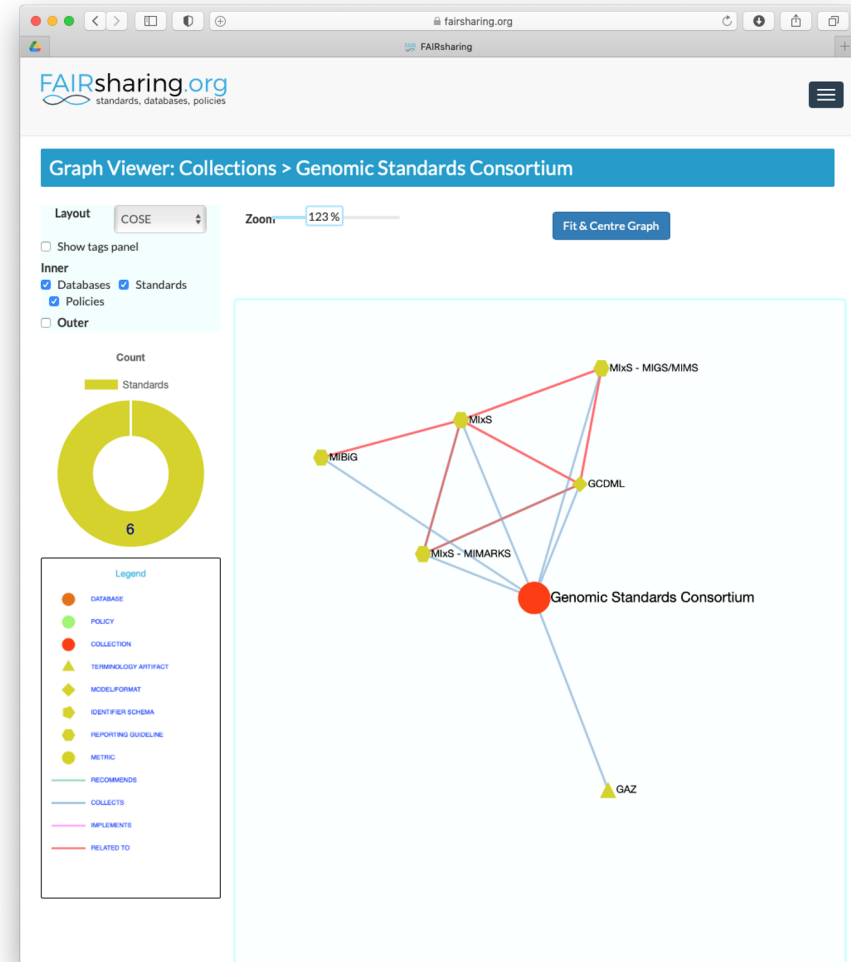


# The Genomics Standard Consortium (GSC)



The screenshot shows the FAIRsharing.org interface for the collection 'bsg-c000040'. The header includes the FAIRsharing.org logo and the collection ID. Below the header, there is a section for the 'Genomic Standards Consortium' with a description: 'The Genomic Standards Consortium (GSC) is an open-membership working body formed in September 2005. The aim of the GSC is making genomic data discoverable. The GSC enables genomic data integration, discovery and comparison through international community-driven standards. This record is maintained by: rwalls ORCID'. It also lists record dates and a link to the FAIRsharing Team. There are buttons for 'Homepage' and 'Reference'. A 'Taxonomic range' section shows 'All' selected. 'Knowledge Domains' includes 'Genome'. 'Subjects' includes 'Genomics'. There are buttons for 'View as Graph' and 'Show edit history'. A 'Compare with collection/recommendation (Beta)' section has a dropdown menu. At the bottom, there is a 'General collection/recommendation statistics' section with a 'Show Stats' button.

<https://fairsharing.org/collection/GSC>



The screenshot shows the FAIRsharing.org Graph Viewer for the collection 'bsg-c000040'. The header includes the FAIRsharing.org logo and the collection ID. Below the header, there is a 'Graph Viewer: Collections > Genomic Standards Consortium' section. The layout is set to 'COSE' with a zoom of 123%. There are checkboxes for 'Show tags panel', 'Inner' (with 'Databases' and 'Standards' checked), and 'Outer'. A donut chart shows a count of 6 for 'Standards'. A network graph shows connections between 'Genomic Standards Consortium' (red circle) and other entities: 'MIBIG' (green circle), 'MixS' (green circle), 'MixS - MIMARKS' (green circle), 'MixS - MIGS/MIMS' (green circle), 'GCDML' (green circle), and 'GAZ' (yellow triangle). A legend identifies the symbols: red circle for DATABASE, green circle for POLICY, red circle for COLLECTION, yellow triangle for TERMINOLOGICAL ARTIFACT, green diamond for MODELFORMAT, green diamond for IDENTIFIER SCHEMA, green circle for REPORTING GUIDELINE, green circle for METRIC, green line for RECOMMENDS, blue line for COLLECTS, pink line for IMPLEMENTS, and red line for RELATED TO.

<https://fairsharing.org/graph/#/collection/bsg-c000040>

# The Genomics Standard Consortium (GSC)

Genomic data integration, and comparison through international community-driven standards

Producer of the *Minimum Information Standards (Checklists)* used by **ENA (EBI) & SRA (NCBI)**

Ex: **MIxS** : Minimum Information about any (x) Sequence

Specification projects	MIGS					MIMS	MIMARKS		New checklists
Checklists	EU	BA	PL	VI	ORG	metagenomes	survey	specimen	e.g., pan-genomes
Shared descriptors	collection date, environmental package, environment (biome), environment (feature), environment (material), geographic location (country and/or sea, region), geographic location (latitude and longitude), investigation type, project name, sequencing method, submitted to INSDC								
Checklist-specific descriptors	assembly, estimated size, finishing strategy, isolation and growth condition, number of replicons, ploidy, propagation, reference for biomaterial						target gene		
Applicable environmental packages (measurements and observations)	Air Host-associated Human-associated Human-oral Human-gut Human-skin Human-vaginal					Microbial mat/biofilm Miscellaneous natural or artificial environment Plant-associated Sediment Soil Wastewater/sludge Water			

[Yilmaz et al, 2011](#)

Source: <https://gensc.org>

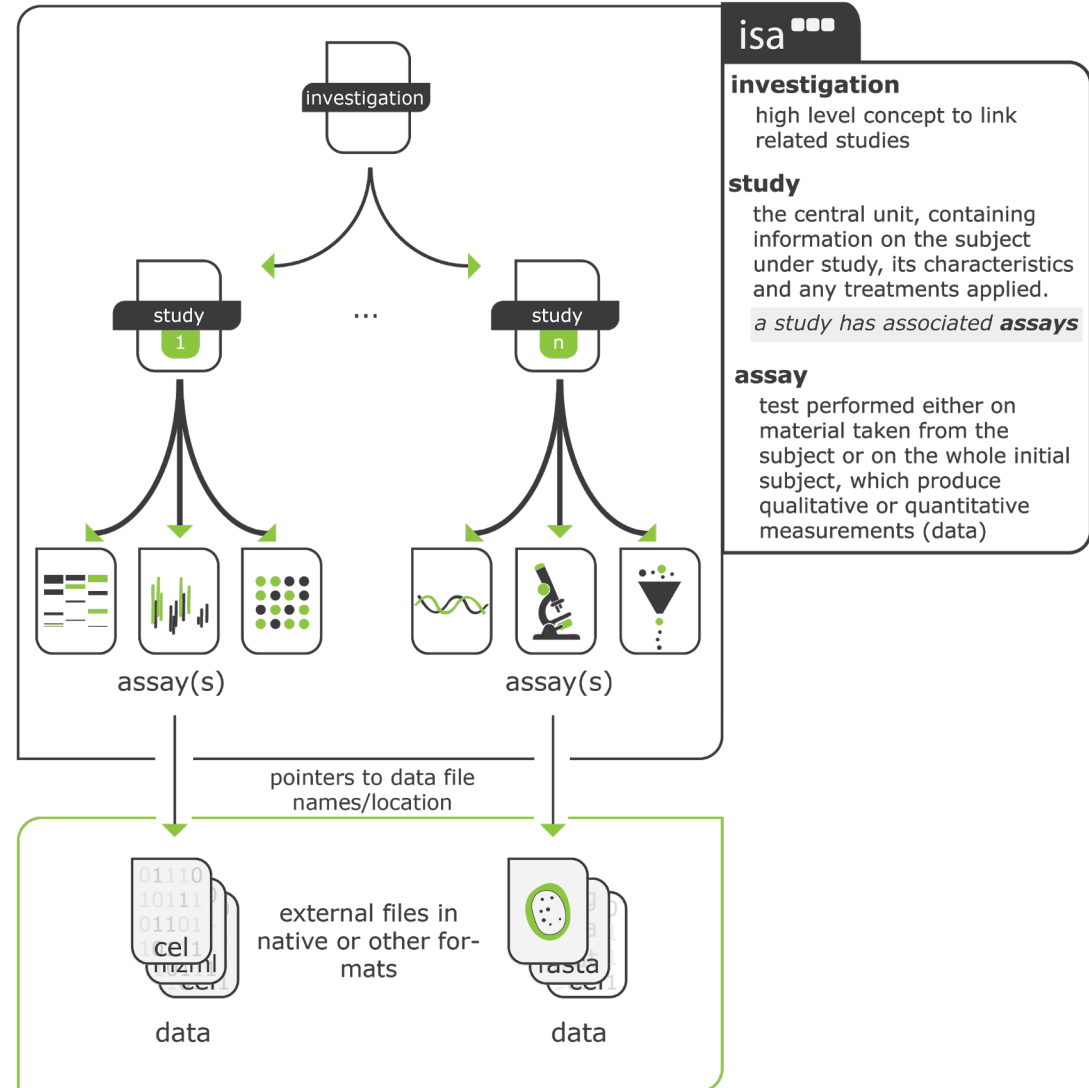
# The ISA model

## A standard for Life ScienceData

A model to capture **experimental metadata** through **3 core entities**:

- **Investigation**: the project context
- **Study**: an experimentation in one location
- **Assay**: a specific measurement that targets a trait with a method and a scale

ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level. Rocca-Serra P et al. **Bioinformatics** 2010. <https://doi.org/10.1093/bioinformatics/btq415>



Sources: <https://isa-tools.org> and : <https://isa-specs.readthedocs.io/en/latest/isamodel.html>

# European Nucleotide Archive (ENA) submission

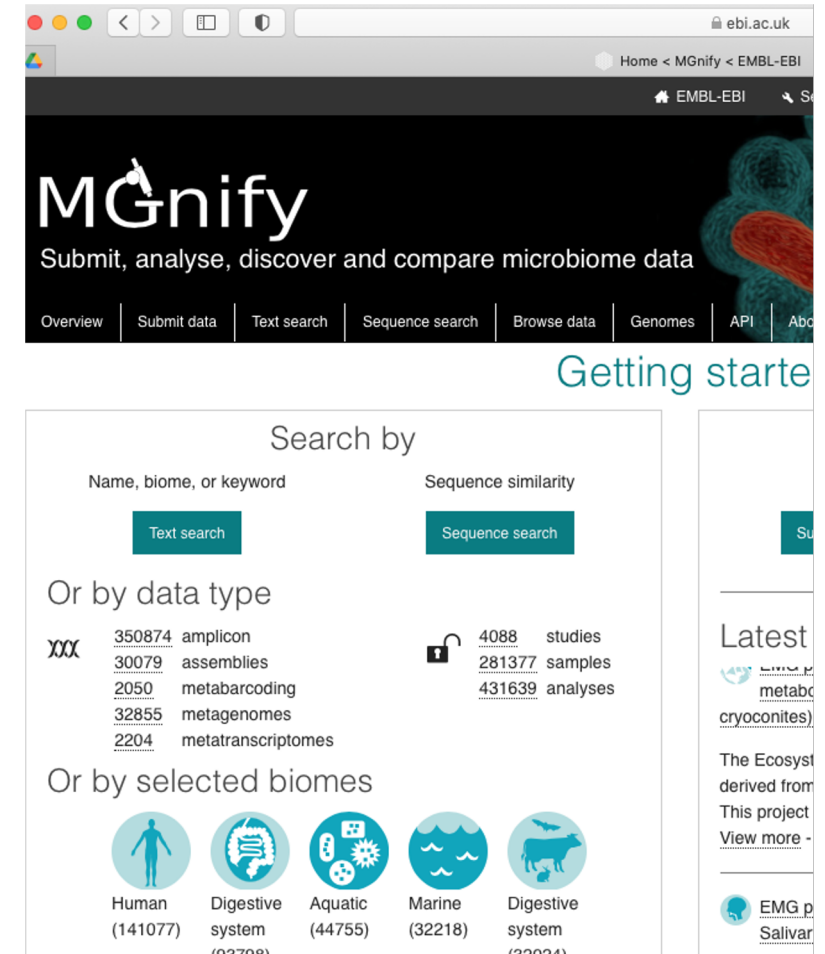


EMBL-EBI



# Why do I need to submit my data and metadata to ENA ?

- Open Science and reproducibility of experiments
- 3<sup>rd</sup> party access
- Archival
- Publication
- Analyses, example: [MGinify](https://mgify.ebi.ac.uk/)



The screenshot shows the MGnify website interface. The header includes the MGnify logo and the tagline "Submit, analyse, discover and compare microbiome data". Below the header is a navigation menu with options: Overview, Submit data, Text search, Sequence search, Browse data, Genomes, API, and About. A "Getting started" link is also visible. The main content area is titled "Search by" and features two search buttons: "Text search" and "Sequence search". Below these buttons, there are two sections: "Or by data type" and "Or by selected biomes".

Or by data type	
350874	amplicon
30079	assemblies
2050	metabarcoding
32855	metagenomes
2204	metatranscriptomes

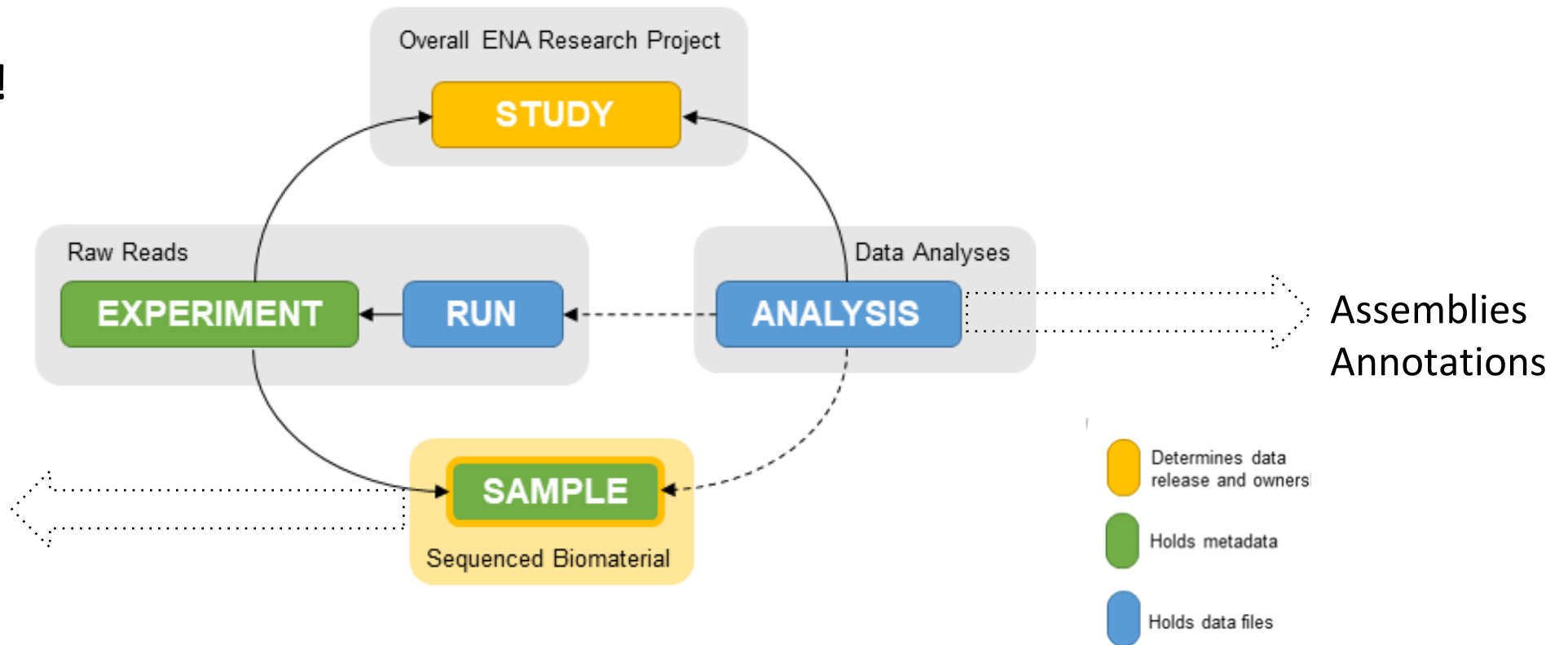
Or by selected biomes				
Human (141077)	Digestive system (42702)	Aquatic (44755)	Marine (32218)	Digestive system (32024)

On the right side of the interface, there is a "Latest" section with a "View more" link and a logo for "EMG p Salivar".

# The ENA metadata model

ISA compliant !

All **samples** submitted to ENA must conform to a **Checklist**



Source: <https://ena-docs.readthedocs.io/en/latest/submit/general-guide/metadata.html>

# THE ENA Checklists

- A **checklist** defines the **minimum and optional metadata** expected to describe biological samples
- ENA are based on the **Genomic Standards Consortium (GSC)** recommendations
- The **most suitable checklist** depends on the type of the sample:  
<https://www.ebi.ac.uk/ena/browser/checklists>
- All ENA checklist are defined by an **access number** like ERCxxx (Ena R Checklist xxx)
  - example: GSC MIxS plant associated  
<https://www.ebi.ac.uk/ena/browser/view/ERC000020>

# Data brokering at IFB



# Why developing data brokering at IFB?

## Observations:

- Submissions are often complex and difficult to perform by individual teams
- Metadata are often poorly understood resulting in incomplete, redundant and inconsistent submissions
- ENA asks that IFB becomes the French national broker

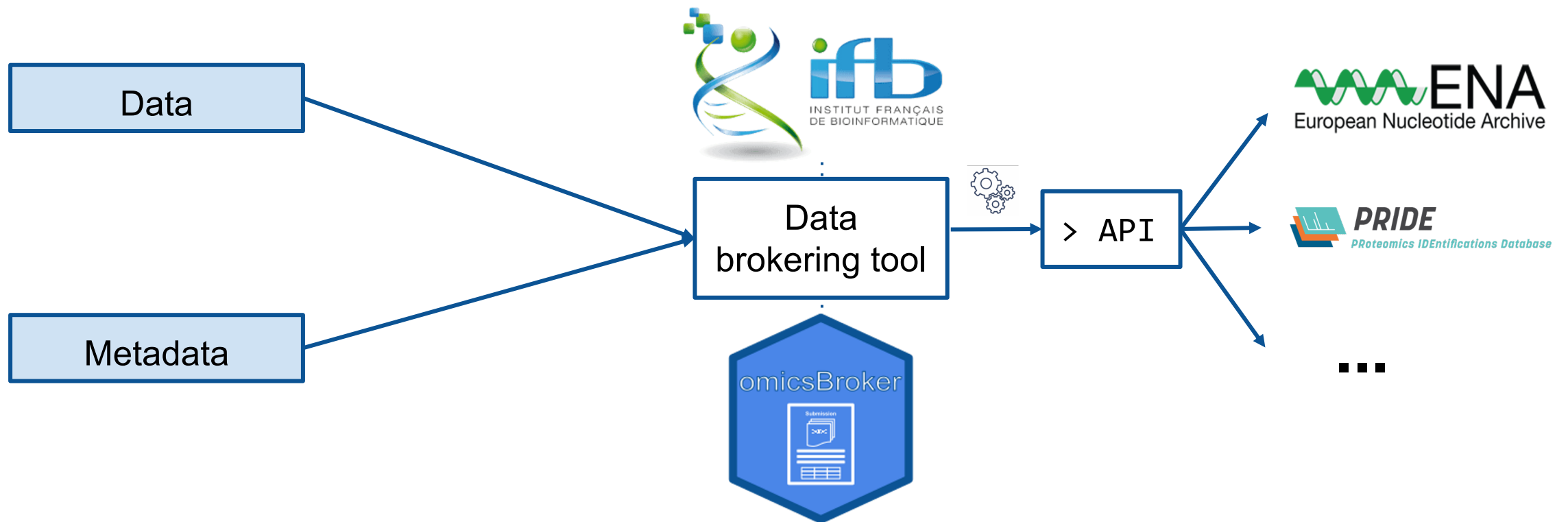
**Main idea:** offer a national service of **data brokering at IFB** to simplify and rationalize data exchange between international resources and the french Elixir node IFB.

**Brokering include 3 types of activities:** tools development, training and support to users

# Data Brokering service developed by IFB

*IFB services to manage and centralize data and metadata of a project*

*IFB services to submit data and metadata of a project to international resources*





# The omicsBroker tool

- **omicsBroker** is a tool to easily annotate and submit **omics data** to **international repositories**
- For now, only available as a **PROTOTYPE**
  - based on **R Shiny** technology
  - allowing to test submission of genomic and transcriptomic samples and reads to **ENA test instance**
- The final tool will be developed using Django technology and will **manage data and metadata from different sources** to make submission to international resources easier

<https://github.com/IFB-ElixirFr/omicsBroker>

# Practice

Use omicsBroker prototype ([134.158.247.213:443](http://134.158.247.213:443)) to test submission of samples to ENA

Use information of the corresponding DMP to associate relevant metadata to data <https://dmp.opidor.fr>

3 groups

- bacterial genome ([IFB\\_Training\\_salivarius](#))
- plant transcriptome ([IFB Training : Sars-CoV-2](#))
- SARS-Cov2 genome ([IFB\\_Training\\_plant](#))

[https://ifb-elixirfr.github.io/IFB-FAIR-data-training/sequences/module3\\_sequence3\\_tp.html](https://ifb-elixirfr.github.io/IFB-FAIR-data-training/sequences/module3_sequence3_tp.html)

# To conclude: sources & useful links

Description	Name	URL
A curated, informative and educational resource on data and metadata standards, inter-related to databases and data policies.	FAIRsharing portal	<a href="https://fairsharing.org">https://fairsharing.org</a>
Investigation, Study, Assay (ISA) ressource: A standard model an a set of tools to capture experimental data in life sciences	ISAtools	<a href="https://isa-tools.org">https://isa-tools.org</a>
Genomics Standard Consortium (GSC): An international consortium developing standards and checklists in genomics	GSC	<a href="https://gencsc.org">https://gencsc.org</a>
European National Archive Checklists	ENA Checklists	<a href="https://www.ebi.ac.uk/ena/browser/checklists">https://www.ebi.ac.uk/ena/browser/checklists</a>
European National Archive submission documentation	ENA submission guide	<a href="https://ena-docs.readthedocs.io/en/latest/submit/general-guide.html">https://ena-docs.readthedocs.io/en/latest/submit/general-guide.html</a>
A prototype to test submission of samples and DNaseq or RNAseq reads to ENA	omicsBroker	<a href="https://github.com/IFB-ElixirFr/omicsBroker">https://github.com/IFB-ElixirFr/omicsBroker</a>

# Thanks



Paulette Lieby



Jean-François Dufayard



Frédéric de Lamotte