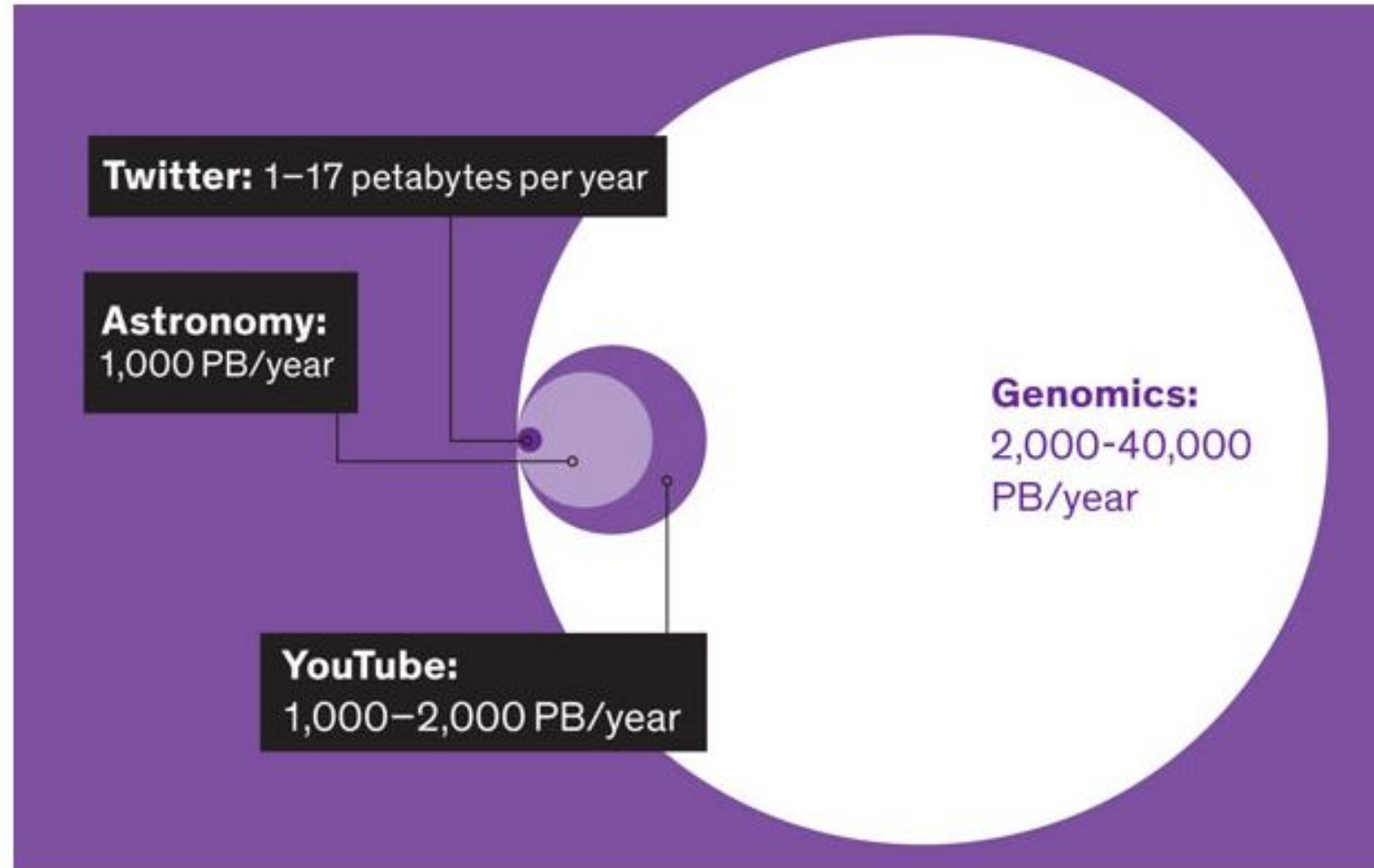


APPLICATIONS OF LINKED DATA IN THE LIFE SCIENCES

DR. JASPER J. KOEHORST - LABORATORY OF SYSTEMS AND SYNTHETIC BIOLOGY

JASPER.KOEHORST@WUR.NL

Projected annual storage in 2025



Source: ["Big Data: Astronomical or Genomical?"](#) PLoS Biology, 7 July 2015.

GENOMICAL AMOUNT OF DATA

- **Not only a lot of data**
- **Extremely diverse**
- **Interoperability problems: Inconsistencies in describing genomic information**
- **Current data standards are not sufficient.**
- **The process of FAIRification is complex and costly**
- **99.99% of information obtained is computationally predicted**

The Crazy-Ambitious Effort to Catalogue Every Microbe on Earth

It's the most macro study of the microscopic world ever published.

A CHINESE PROVINCE IS SEQUENCING ONE MILLION OF ITS RESIDENTS' GENOMES

THE PROJECT IS BEING ADVISED BY HARVARD GENETICIST GEORGE CHURCH.



NEWS • 02 NOVEMBER 2018

'Why not sequence everything?' A plan to decode every complex species on Earth

The Earth BioGenome Project aims to sequence 1.5 million genomes and will probably cost US\$4.7 billion.

Science

Contents ▾

News ▾

Careers ▾

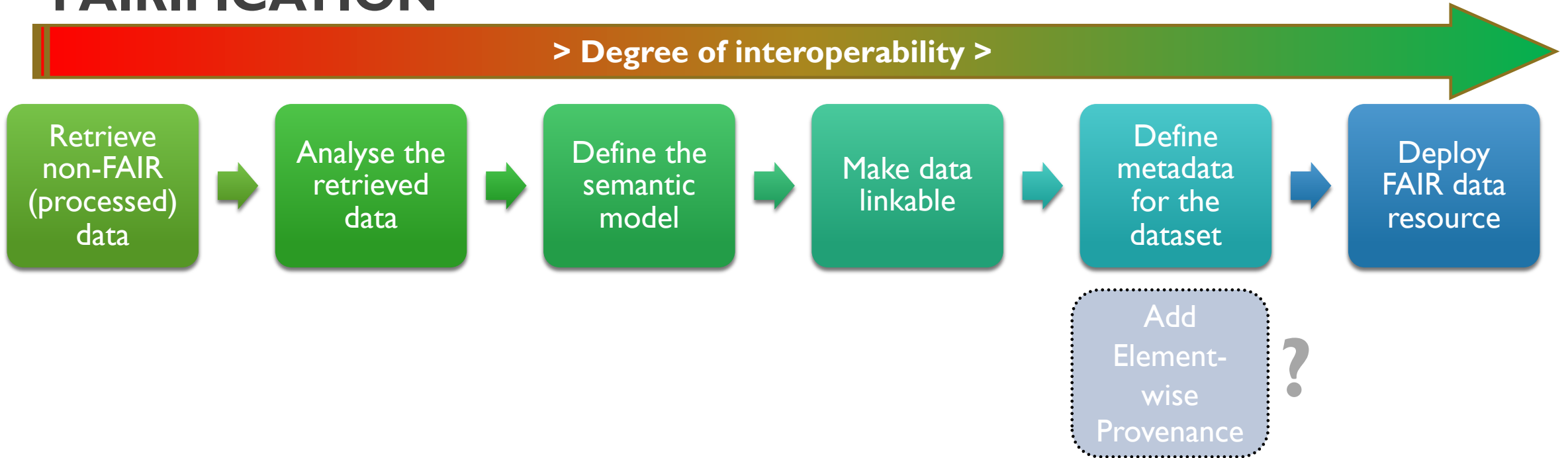
Journals ▾

Researchers launch plan to sequence 66,000 species in the United Kingdom. But that's just a start

By Erik Stokstad | Nov. 1, 2018, 3:15 PM

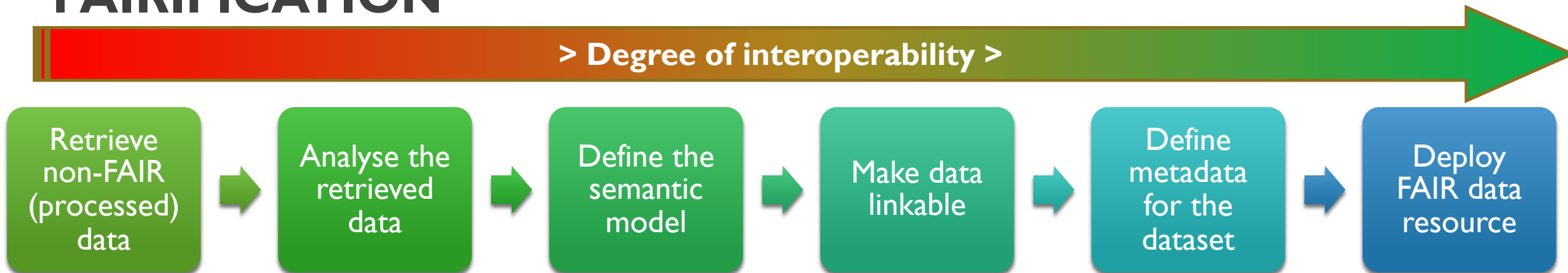
FAIRIFICATION

> Degree of interoperability >

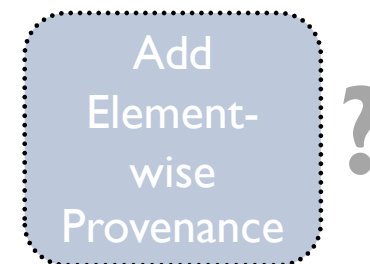
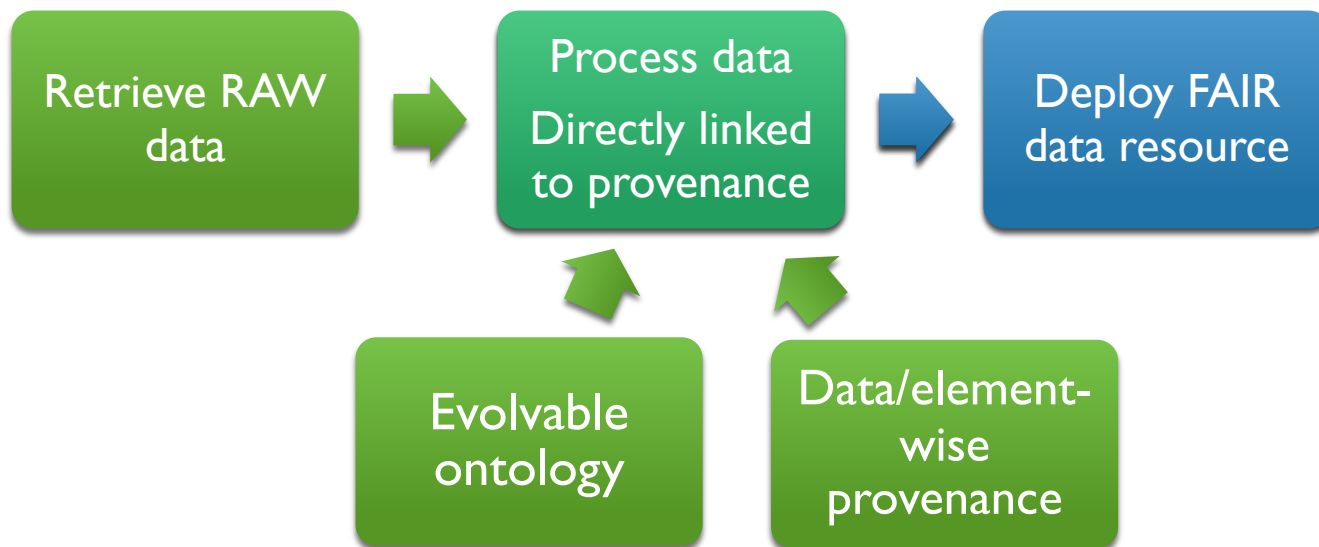


FAIRIFICATION

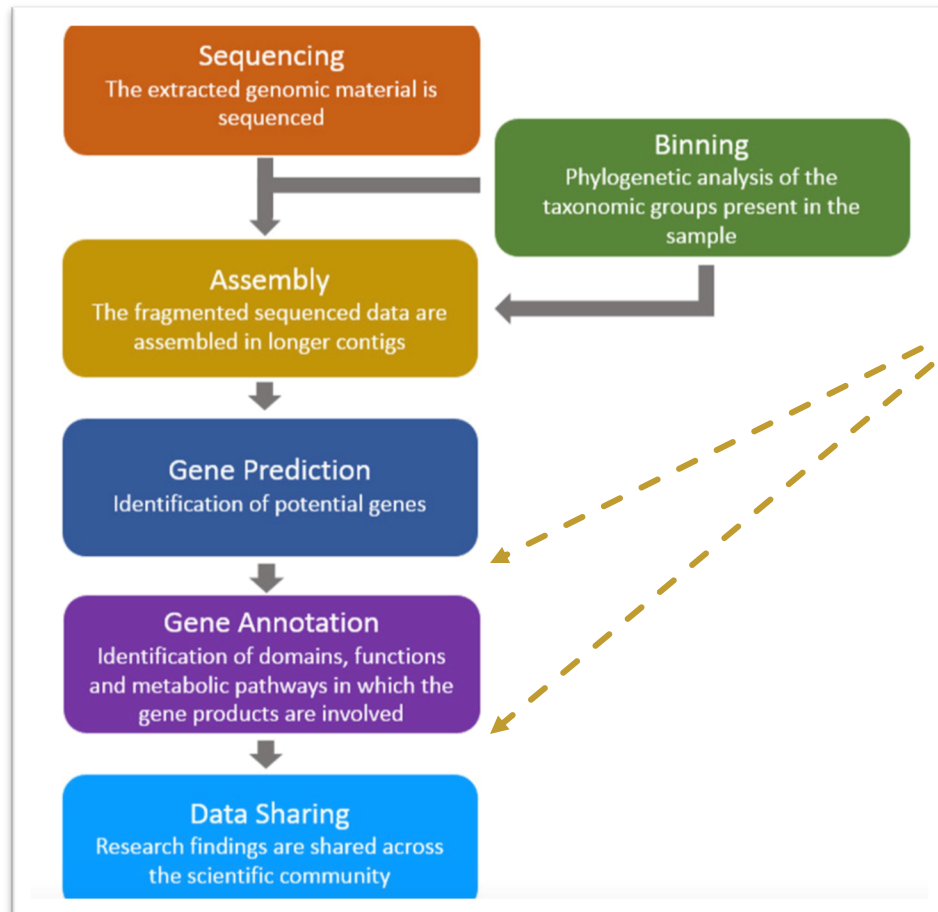
> Degree of interoperability >



FAIR BY DESIGN



CLASSICAL ANALYSIS WORKFLOW: **DATA MEETS THE TOOL**

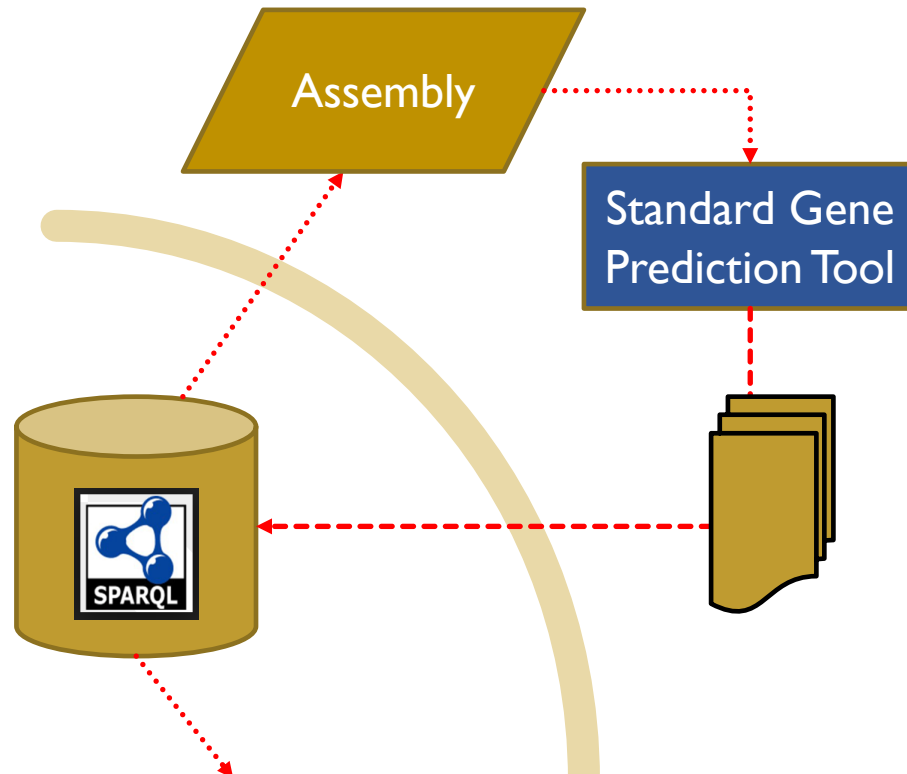


IN EACH STEP A DECISION IS MADE BASED ON A PRE-DEFINED THRESHOLD

THE ACTUAL ELEMENT-WISE PROVENANCE

- E.G CONFIDENCE SCORES - IS LOST
- NO STATISTICAL ANALYSIS ON METADATA POSSIBLE
- CHANGING THE THRESHOLD VALUE = **RECOMPUTE**

FAIR BY DESIGN SEMANTIC ANALYSIS WORKFLOW: TOOL MEETS THE DATA



FAIR Data Sharing – Linked Data
Triple store can be queried with
SPARQL

**DATA/ELEMENT-WISE PROVENANCE
AUTOMATICALLY AND DIRECTLY
LINKED TO THE PREDICTION**

Algorithm = ..

Version = ..

Run date = ..

.....

Genomic location

Confidence score

.....

GBOL ontology for
Interoperable
genome annotation

**DYNAMIC THRESHOLD SELECTION (AFTERWARDS)
MULTIPLE (SIMILAIR) TOOLS CAN BE COMPARED**

FROM FAIRIFICATION TO FAIR BY DESIGN



RAW DATA



ONTOLOGIES



APPLICATION
PROGRAMMING
INTERFACE

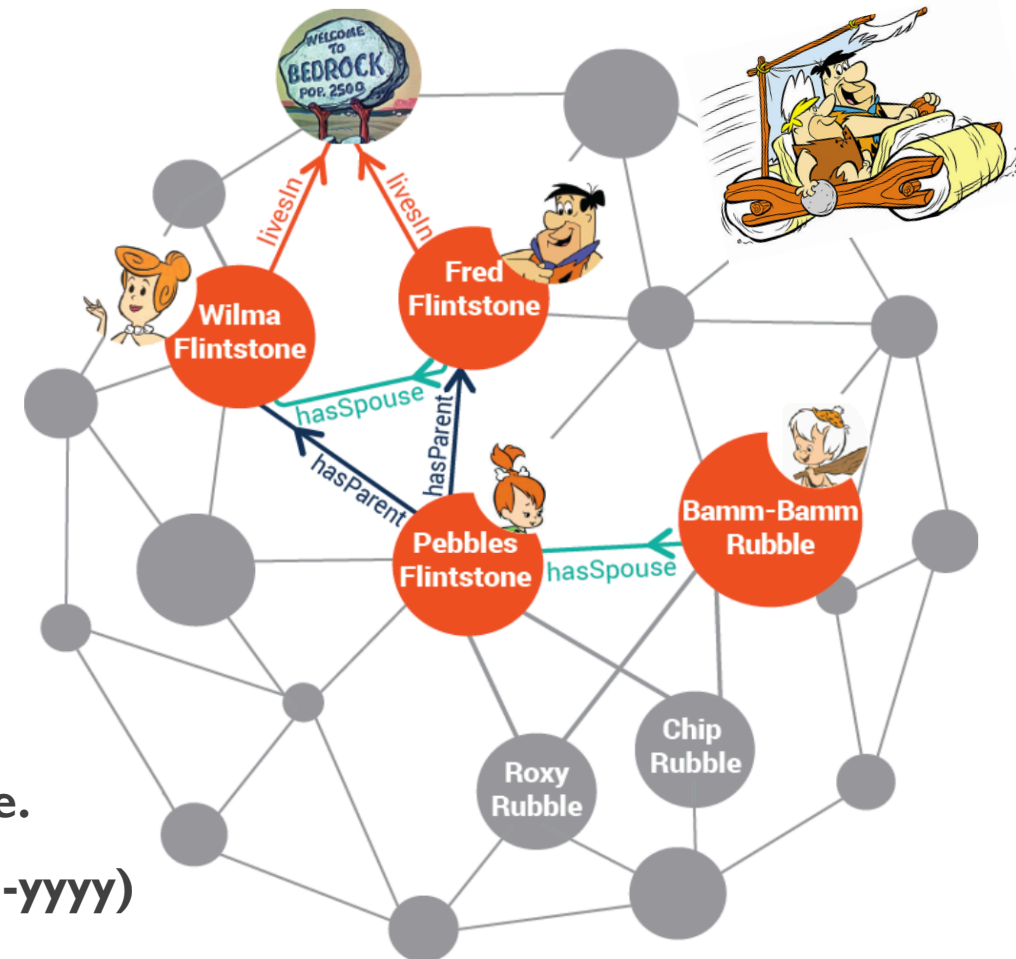
SEMANTIC FRAMEWORK & LINKED (RDF) DATA MODEL

HOW TO ENSURE A HIGH DEGREE OF INTEROPERABILITY USING A GENOMICAL AMOUNTS OF DATA: **ONTOLOGIES**



- **DEFINITIONS, DEFINITIONS AND MOST IMPORTANTLY DEFINITIONS**
 - MINIMAL INFORMATION MODEL REQUIRED FOR INTEROPERABILITY
 - ONTOLOGY AND CONSTRAINED RELATIONS
 - SHEX DEFINITION (a language for validating and describing the RDF data according to the ontology)

```
<cartoonfigureShape> {  
  :name xsd:string+;  
  :birthdate xsd:date?  
}  
# A cartoonfigure (e.g Fred) has:  
# one or more names  
# and optionally a (single) birthdate.  
# in a specific format (e.g. dd-mm-yyyy)
```

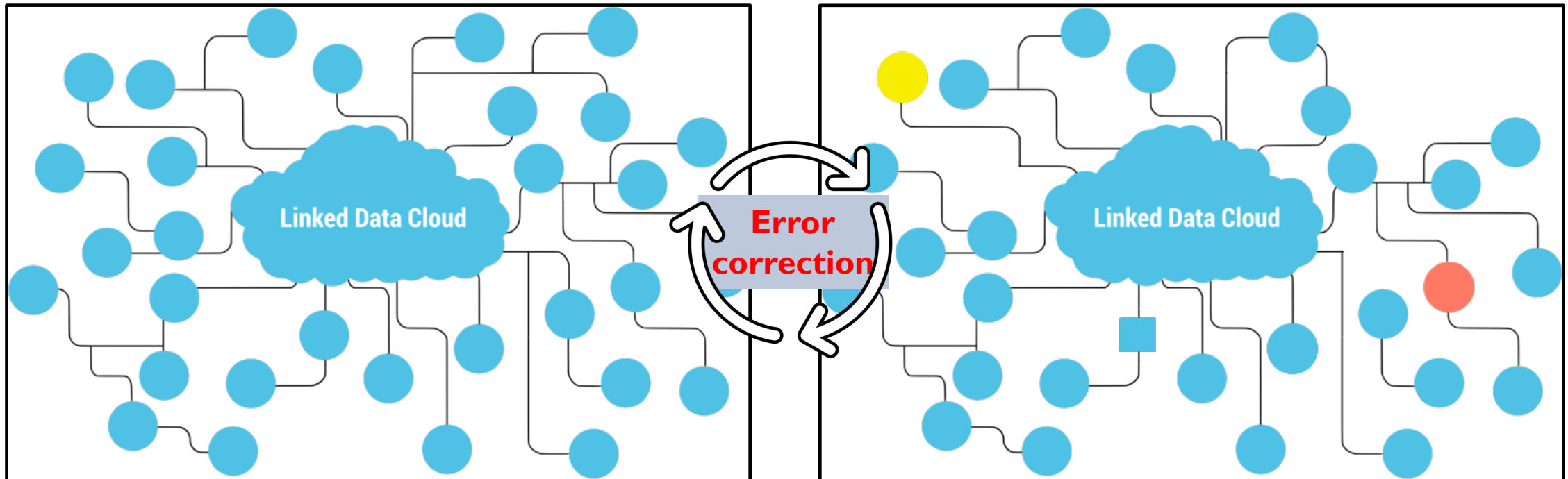






THE DYNAMIC NATURE

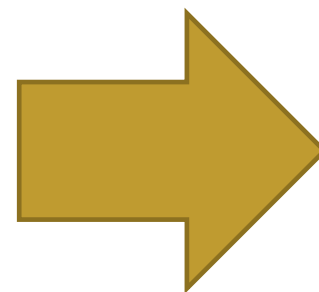
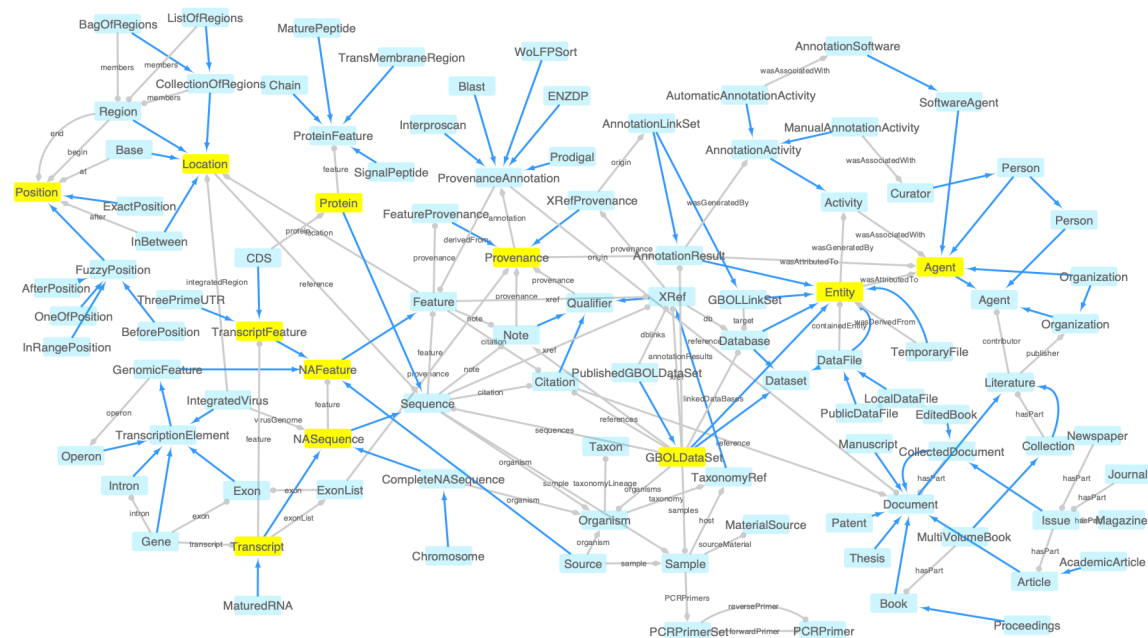
OF SEMANTIC WEB



EXPECTED

OBSERVED

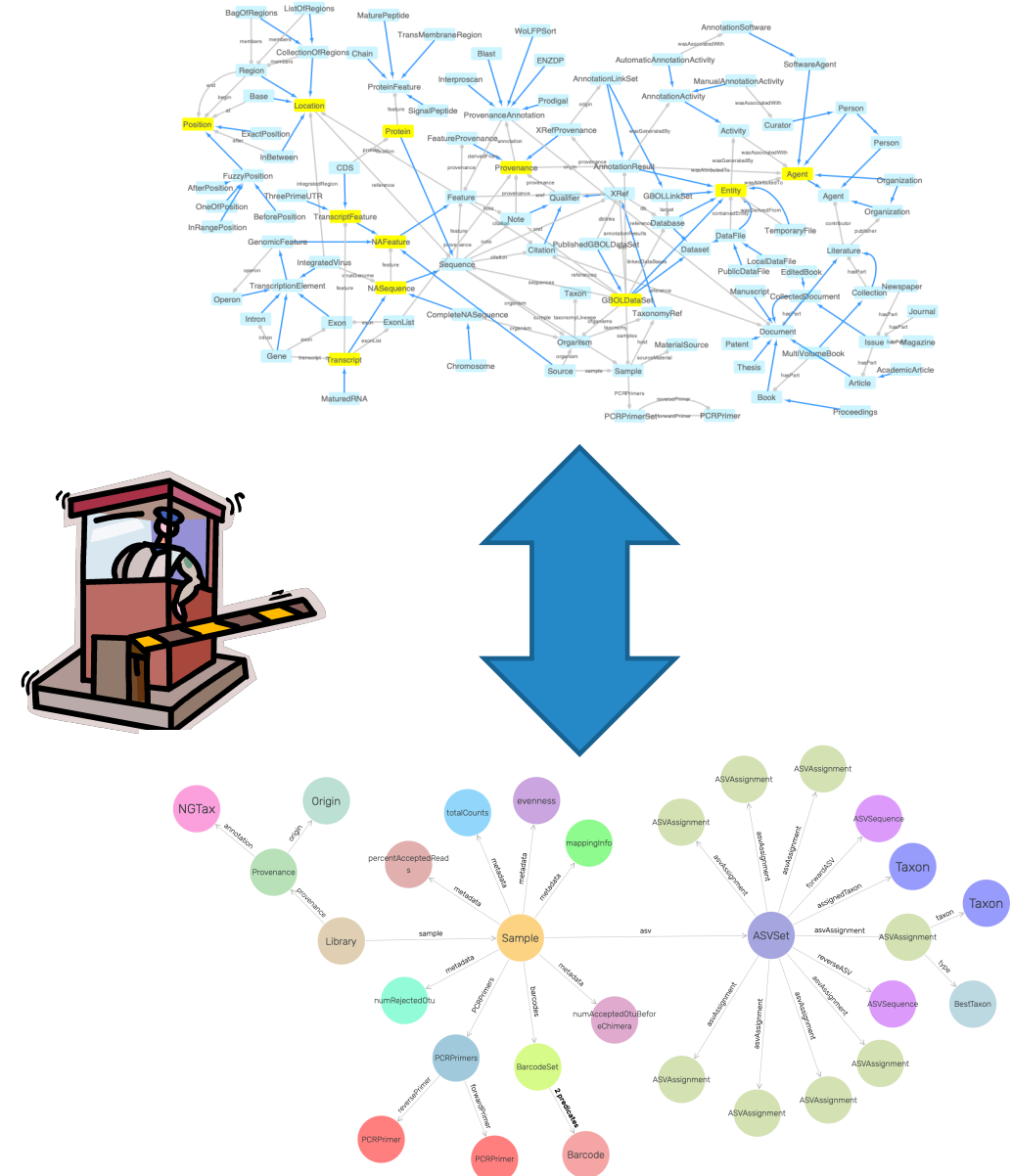
EMPUSA: ONTOLOGY VALIDATOR & CODE GENERATOR



APPLICATION
PROGRAMMING
INTERFACE

EMPUSA GENERATES THE CODE THAT CAN ACT AS A GATEKEEPER FOR FAIR LINKED DATA GENERATION

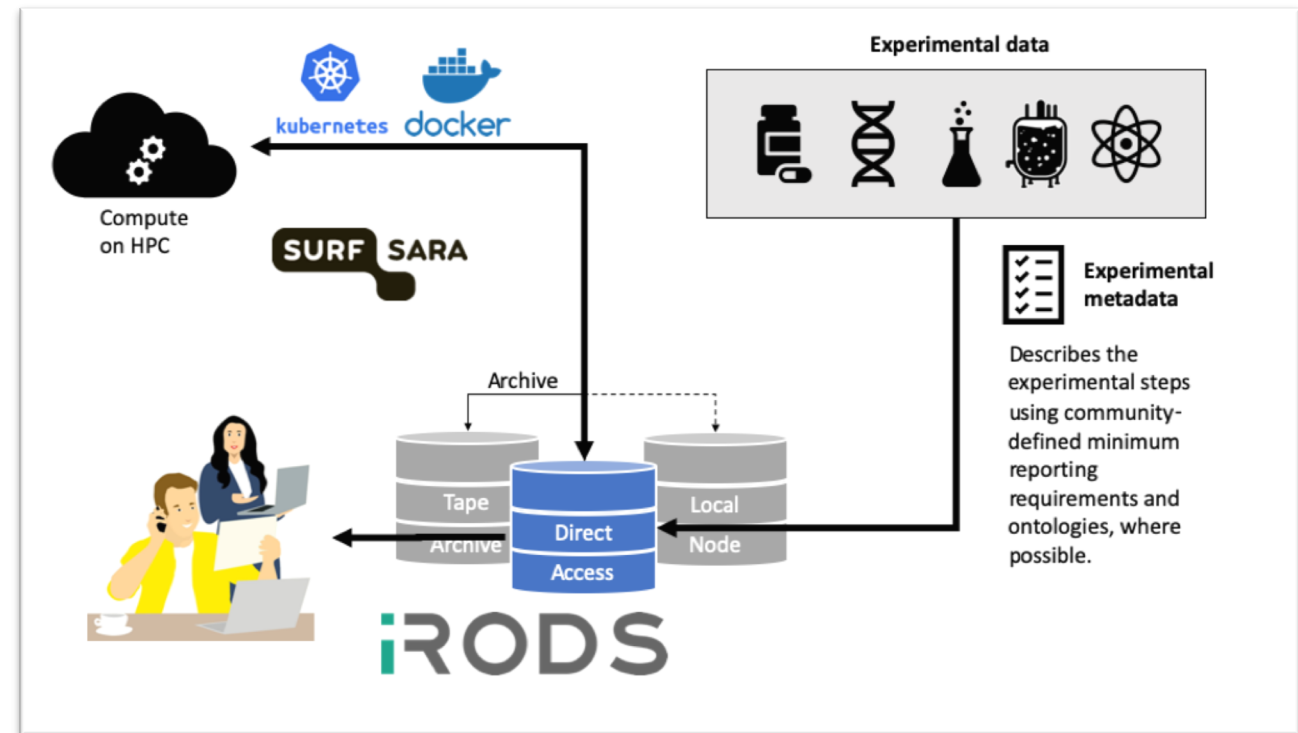
FAIR BY DESIGN FROM DATA TO LINKED DATA



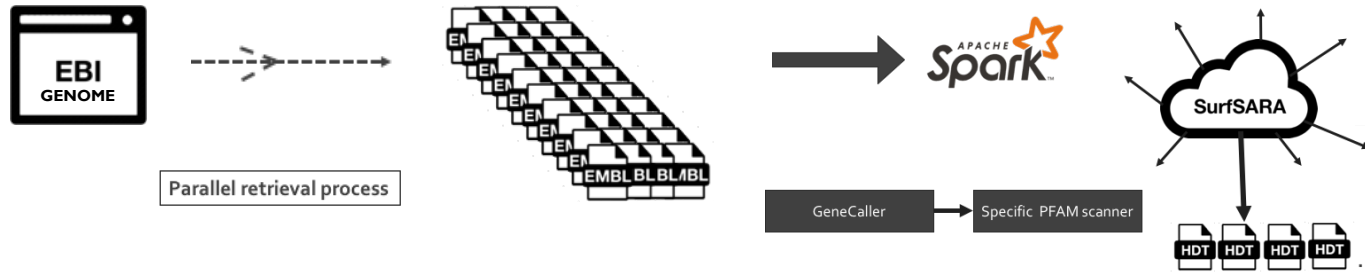
Validated linked (meta-)dataset

APPLICATION: PROJECT MANAGEMENT

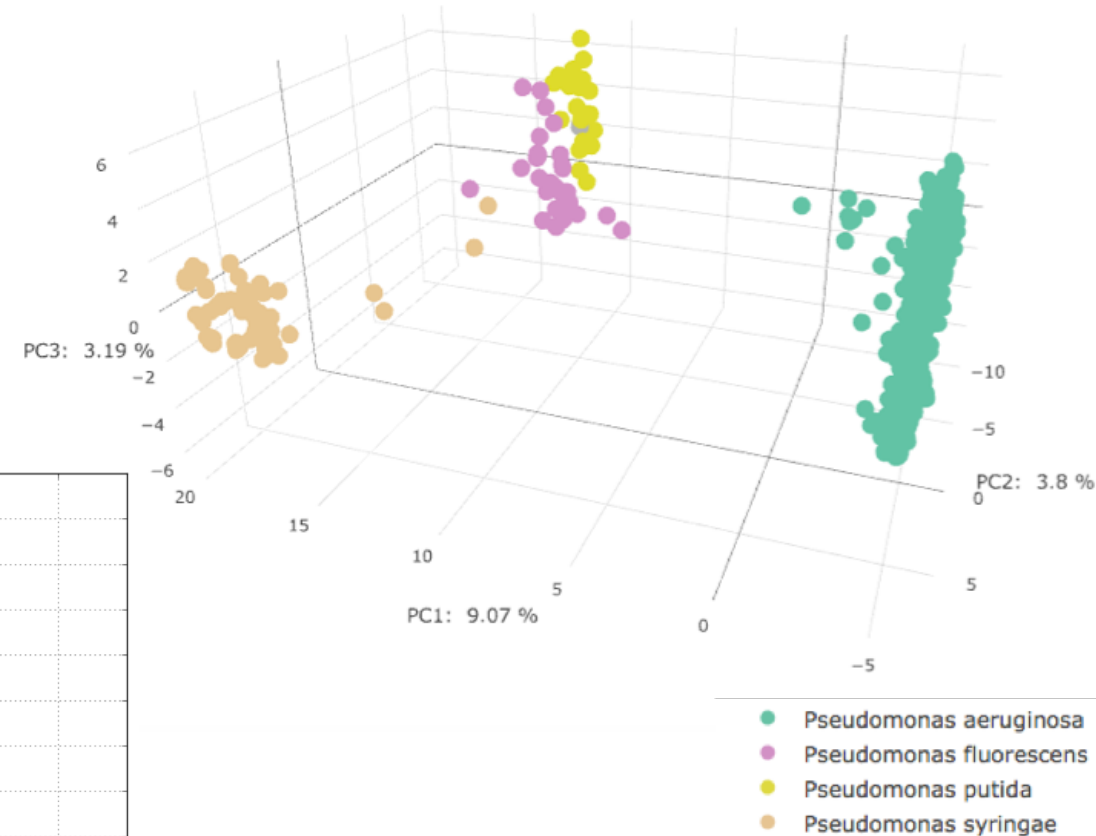
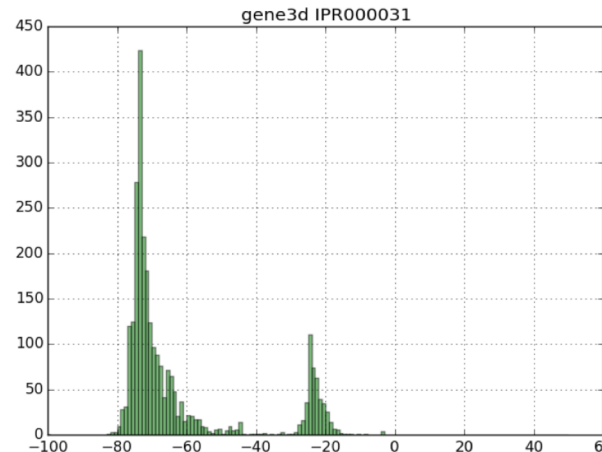
- According to the P-ISA principles
 - Project, Investigation, Study, Assay
 - All (meta-)data is available as linked data
 - Assay: compute results and provenance translated to RDF and embedded in the system



APPLICATIONS: SAPP, FUNCTIONAL GENOME ANNOTATION & COMPARATIVE FUNCTIONAL GENOMICS OF THOUSANDS OF SPECIES

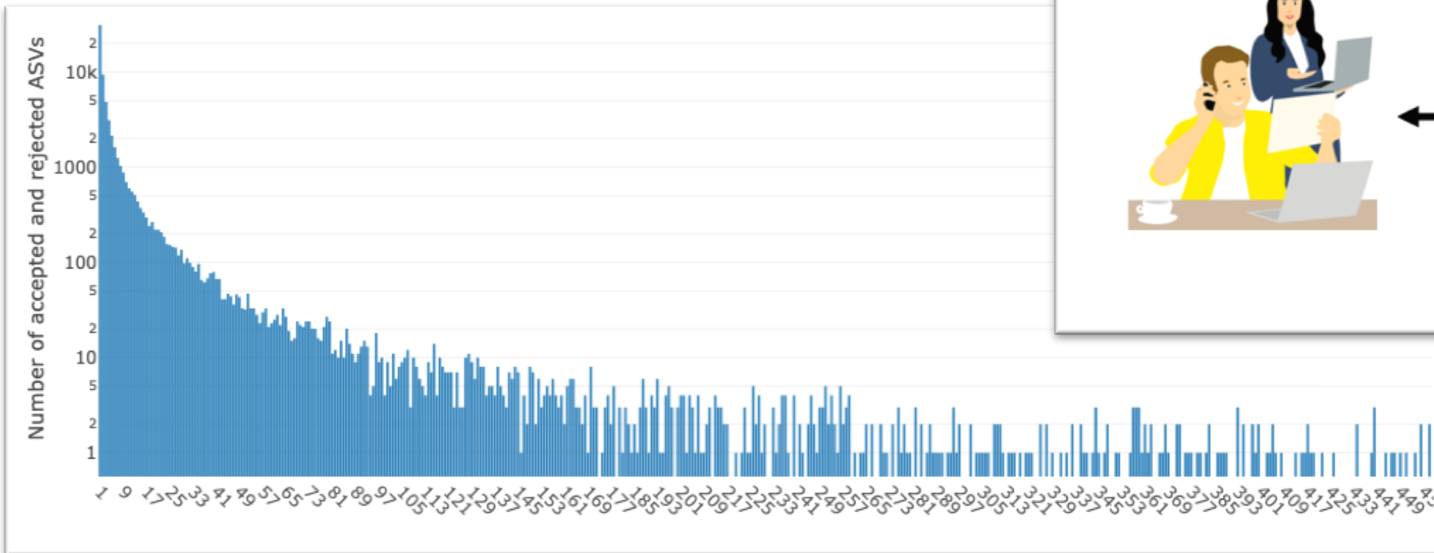


```
1 PREFIX gbol: <http://gbol.life/0.1/>
2 SELECT ?sample ?accession ?db
3 WHERE {
4   ?sample a gbol:Sample .
5   ?dnaobject gbol:sample ?sample .
6   ?dnaobject gbol:feature ?gene .
7   ?gene gbol:transcript ?transcript .
8   ?transcript gbol:feature ?cds .
9   ?cds gbol:protein ?protein .
10  ?protein gbol:feature ?domain .
11  ?domain gbol:xref ?xref .
12  ?xref gbol:db <http://gbol.life/0.1/db/pfam> .
13  ?xref gbol:accession ?accession .
14 } LIMIT 10
```

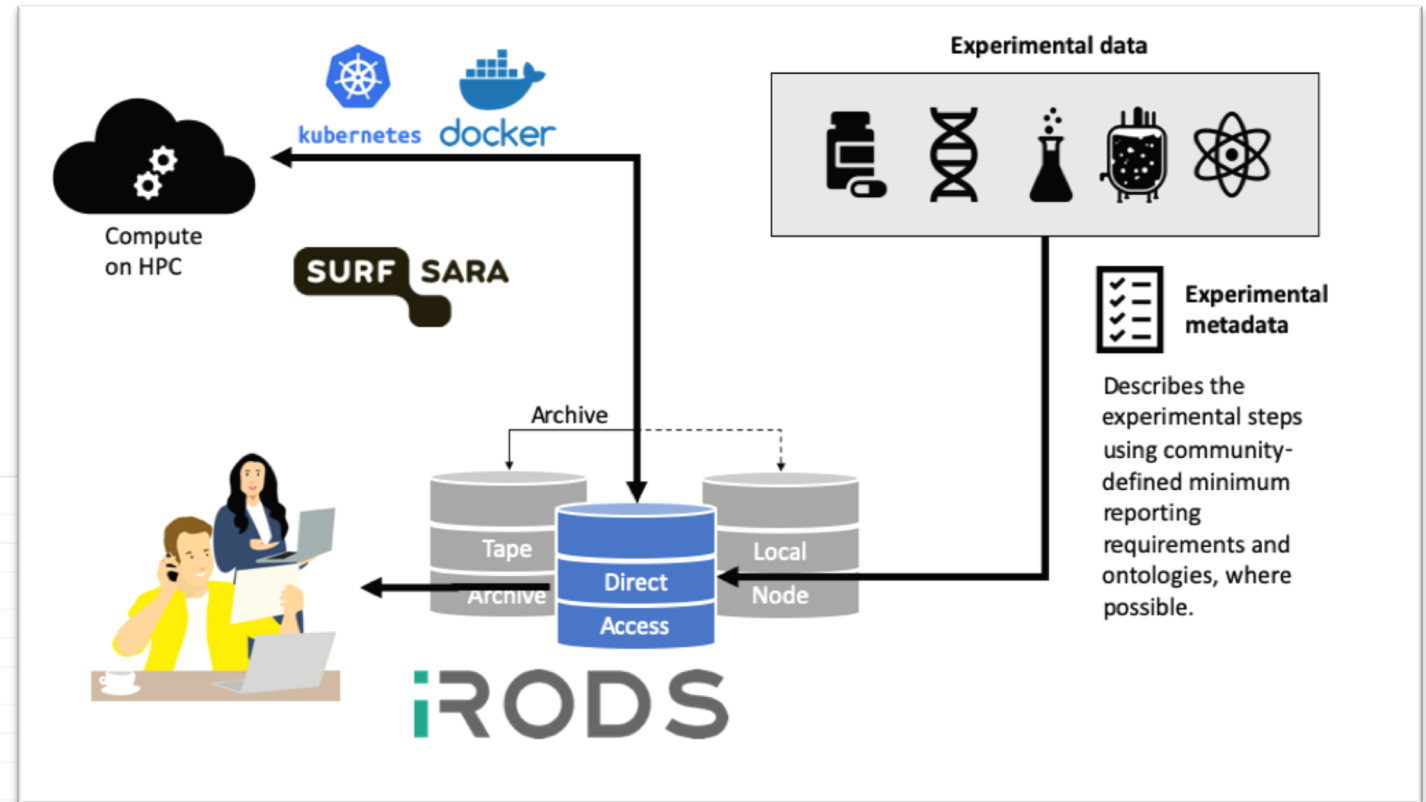


APPLICATIONS: NGTAX 2.0 HIGH THROUGHPUT AMPLICON ANALYSIS

- TRACK & TRACE EACH SPECIES
- SEQUENCE MAPPING ACROSS SAMPLES
- LINKED METADATA
 - AGE, GENDER, DIET, ...



NUMBER OF ASVs SHARED BETWEEN ~1800 SAMPLES



ANY OMICS CAN BE ANALYSED
USING THE SAME PRINCIPLES

SOFTWARE - AVAILABILITY

- GENOME BIOLOGY ONTOLOGY LANGUAGE (GBOL)
[HTTP://GBOL.LIFE](http://GBOL.LIFE)
- EMPUSA, THE CODE GENERATOR
[HTTP://EMPUSA.ORG](http://EMPUSA.ORG)
- SAPP, SEMANTIC GENOME ANNOTATION
[HTTP://SAPP.GITLAB.IO](http://SAPP.GITLAB.IO)
- PROJECT MANAGEMENT
[HTTP://M-UNLOCK.NL](http://M-UNLOCK.NL)
- NGTAX 2.0, AMPLICON ANALYSIS
[HTTP://WURSSB.GITLAB.IO/NGTAX/](http://WURSSB.GITLAB.IO/NGTAX/)



WDCC

