

# FAIR & FAIR Implementation Strategies



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[go-fair.org](http://go-fair.org)

# Automating F, A, I and R

## Box 2 | The FAIR Guiding Principles

<https://www.nature.com/articles/sdata201618>

### To be Findable:

- F1. (meta)data are assigned a globally unique and persistent identifier
- F2. data are described with rich metadata (defined by R1 below)
- F3. metadata clearly and explicitly include the identifier of the data it describes
- F4. (meta)data are registered or indexed in a searchable resource

### To be Accessible:

- A1. (meta)data are retrievable by their identifier using a standardized communications protocol
  - A1.1 the protocol is open, free, and universally implementable
  - A1.2 the protocol allows for an authentication and authorization procedure, where necessary
- A2. metadata are accessible, even when the data are no longer available

### To be Interoperable:

- I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles
- I3. (meta)data include qualified references to other (meta)data

### To be Reusable:

- R1. meta(data) are richly described with a plurality of accurate and relevant attributes
  - R1.1. (meta)data are released with a clear and accessible data usage license
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  - R1.3. (meta)data meet domain-relevant community standards

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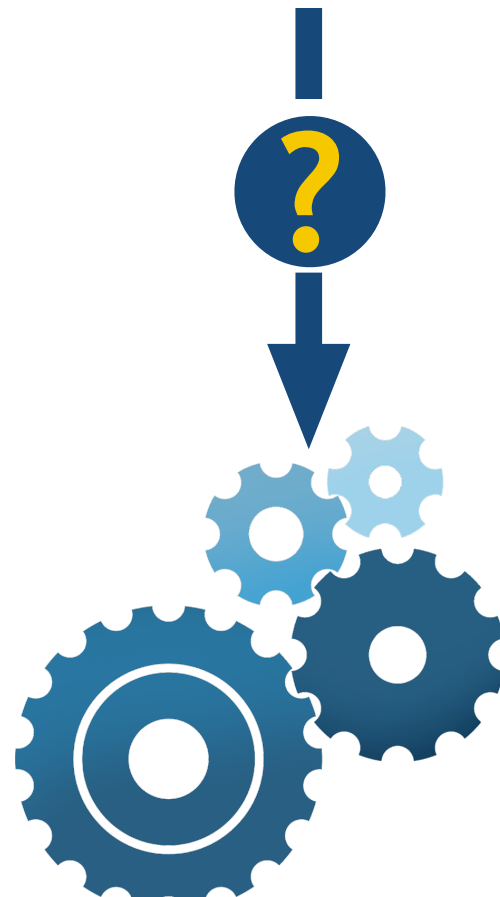
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FAIR Principles say nothing about FAIR implementation priorities, strategies, costs or choices.

FAIR Implementations

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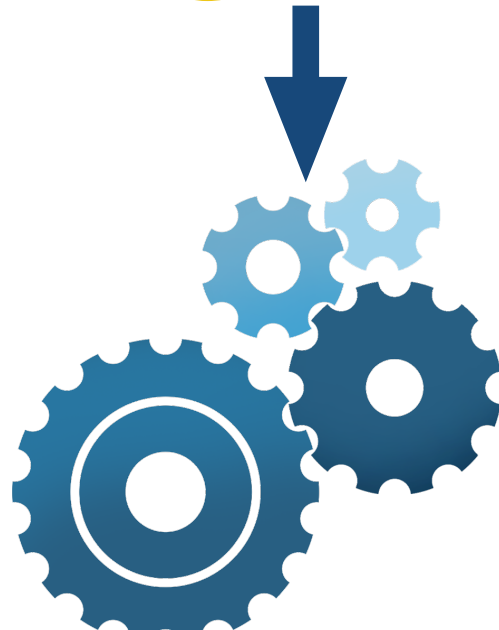
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Coordinating decision making to optimize FAIR Implementations.



FAIR Implementations



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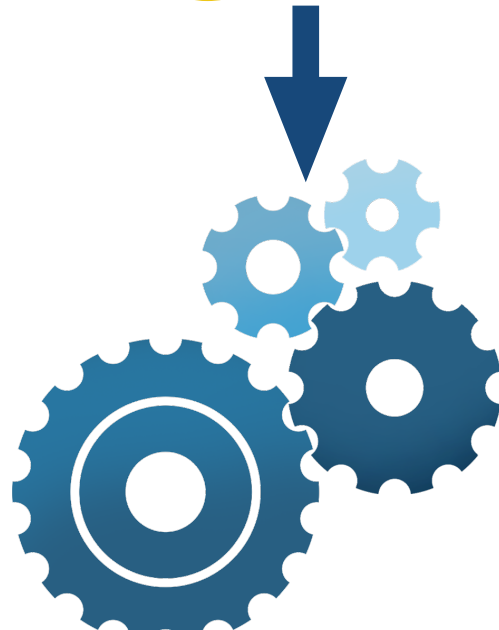
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**Maximize** reuse of existing solutions  
**Minimize** costs and needless reinvention  
**Maximize** interoperation.  
**Speed** discovery  
**Shorten** time to market



FAIR Implementations

# There is no FAIR data without machine-actionable metadata

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# Technical infrastructure (generic operations)

## Data/metadata (domain-specific content)

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# Technical infrastructure: Repository

## Data/metadata: biomedical, geological, historical...

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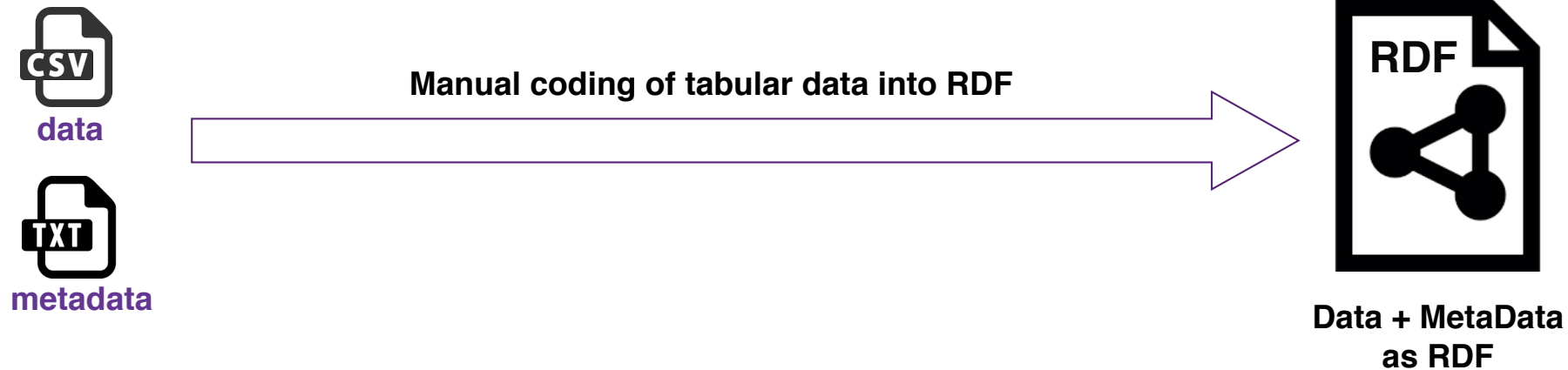
**For today:**

- **FAIR Data Point**
- **FAIR Implementation Profile**

# The FAIR Data Point:

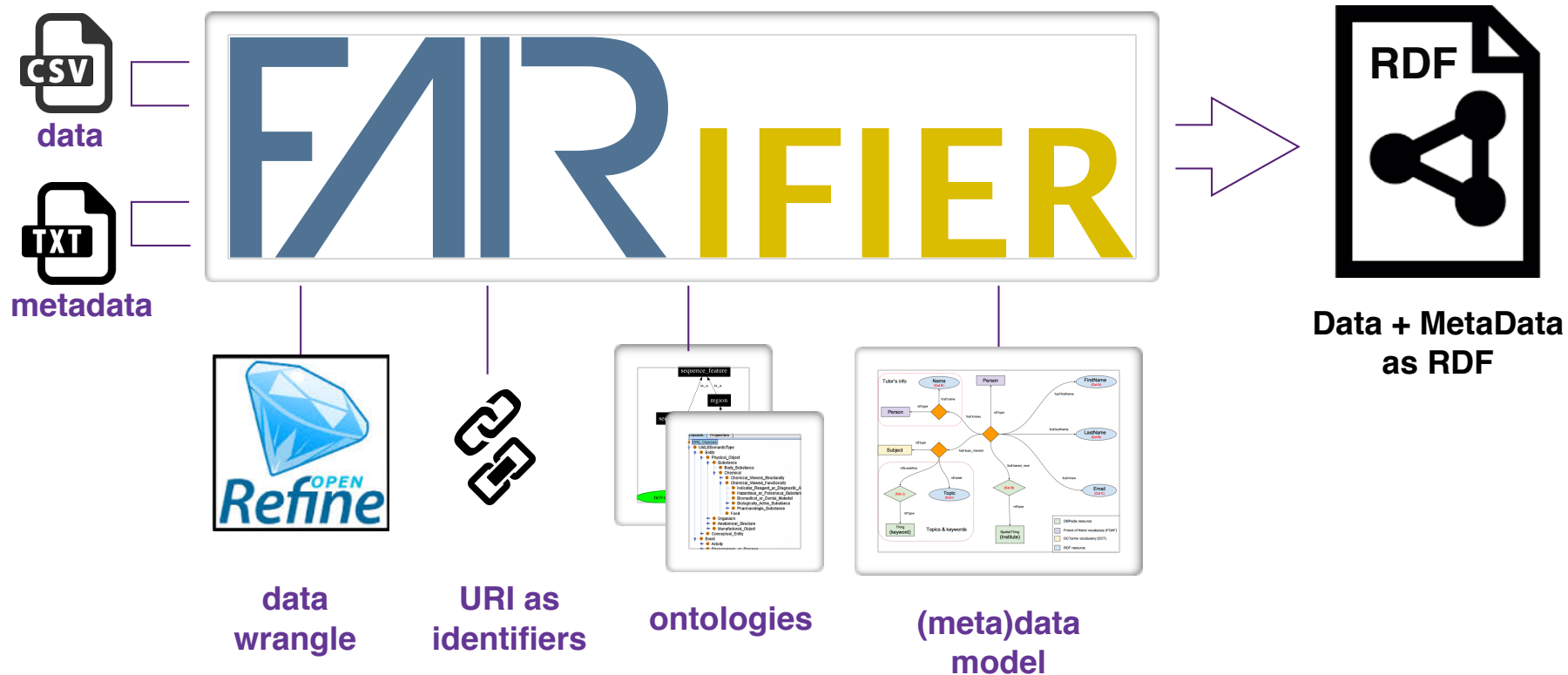
## A Reference Implementation of the 15 Principles to show how Data can be made FAIR for machines

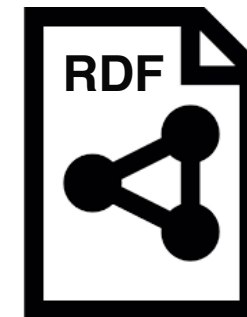
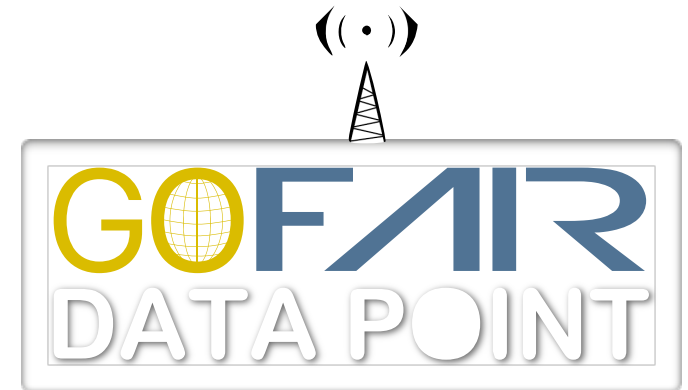
- FAIR-dICT project, DTL: <https://www.dtls.nl/fair-data/fair-dict/> (**2016-2017**)
- Interoperability and FAIRness through a novel combination of Web technologies, <https://peerj.com/articles/cs-110/>
- <https://github.com/DTL-FAIRData/FAIRDataPoint/wiki/FAIR-Data-Point-Specification>



# The FAIR Data Point: A Reference Implementation of the 15 Principles to show how Data can be made FAIR for machines

- FAIR-dICT project, DTL: <https://www.dtls.nl/fair-data/fair-dict/> (2016-2017)
- Interoperability and FAIRness through a novel combination of Web technologies, <https://peerj.com/articles/cs-110/>
- <https://github.com/DTL-FAIRData/FAIRDataPoint/wiki/FAIR-Data-Point-Specification>





Data + MetaData  
as RDF



data



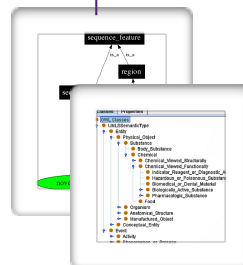
metadata



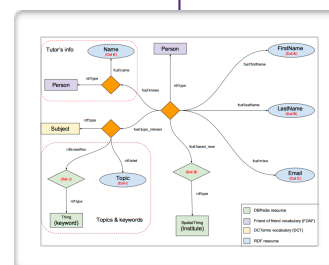
data  
wrangle



URI as  
identifiers

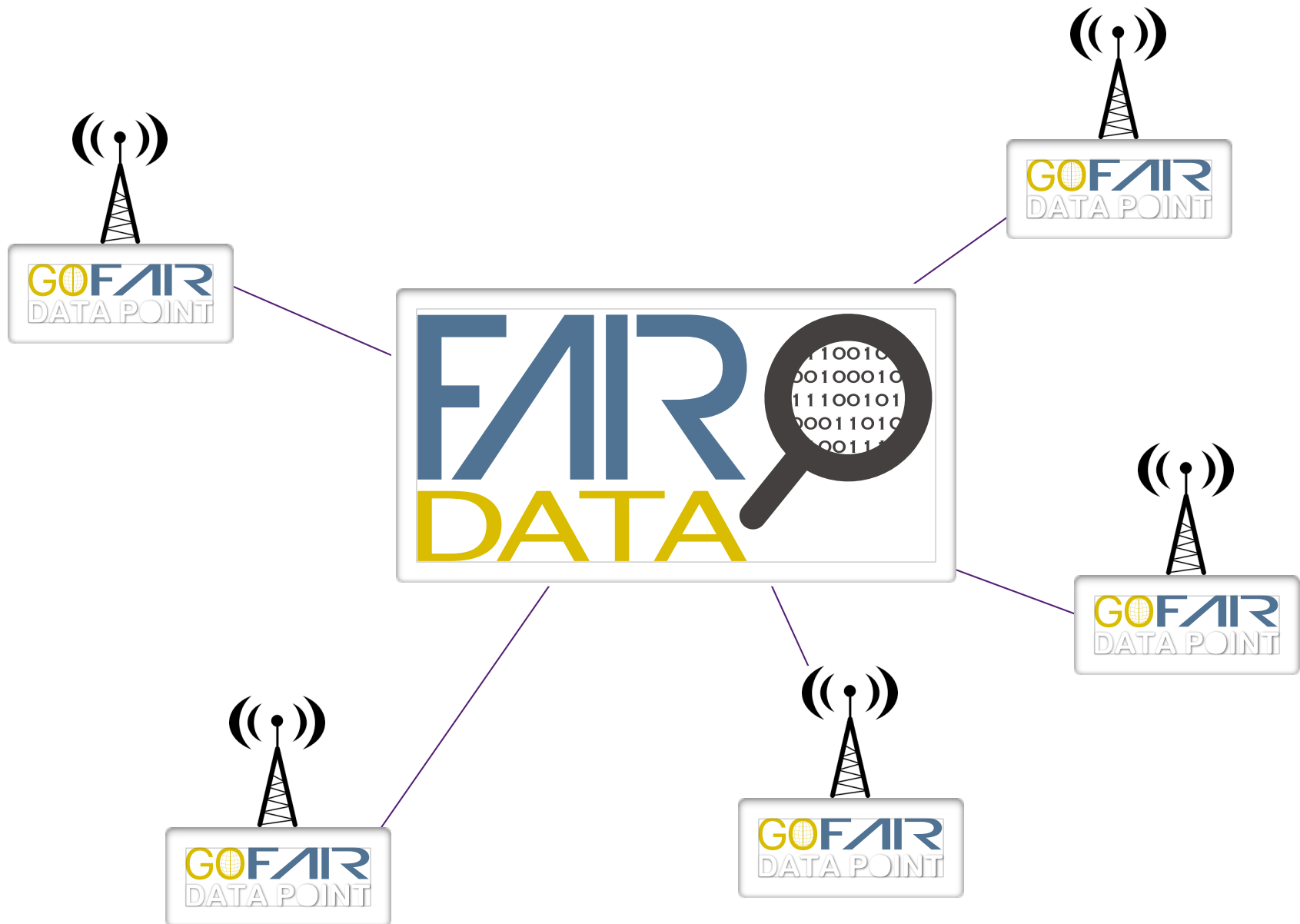


ontologies



(meta)data  
model





# FAIR Data Point

GET <URL>

<http://www.w3.org/TR/vocab-dcat/>

## Catalog 1

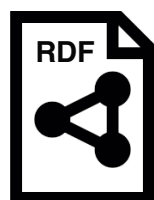
DATASET 1

DIST 1

DIST 2

DATASET 2

DIST 3



## Catalog 2

DATASET 3

DIST 4

DIST 5



Title	FDP of biosemantics group	
Metadata ID	fdp	
Description	This is a prototype FDP for hosting research and student projects datasets	
Issued	2017-05-23T09:43:15.57Z	
Modified	2018-08-20T13:09:55	
Version	1.0E0	
License	<a href="http://rdflicense.appspot.com/rdflicense/cc-by-nc-nd3.0">http://rdflicense.appspot.com/rdflicense/cc-by-nc-nd3.0</a>	
Access Rights	This resource has no access restriction	
Specification	<a href="http://rdf.biosemantics.org/fdp/shex/fdpMetadata">http://rdf.biosemantics.org/fdp/shex/fdpMetadata</a>	
Language	<a href="http://id.loc.gov/vocabulary/iso639-1/en">http://id.loc.gov/vocabulary/iso639-1/en</a>	
Publisher	Biosemantic group	
Metrics	Type	<a href="https://purl.org/fair-metrics/FM_F1A">https://purl.org/fair-metrics/FM_F1A</a>
	Value	<a href="https://www.ietf.org/rfc/rfc3986.txt">https://www.ietf.org/rfc/rfc3986.txt</a>
	Type	<a href="https://purl.org/fair-metrics/FM_A1.1">https://purl.org/fair-metrics/FM_A1.1</a>
	Value	<a href="https://www.wikidata.org/wiki/Q8777">https://www.wikidata.org/wiki/Q8777</a>
Catalogs	<a href="http://136.243.4.200:8087/fdp/catalog/Transcriptomics">http://136.243.4.200:8087/fdp/catalog/Transcriptomics</a>	
	<a href="http://136.243.4.200:8087/fdp/catalog/multiomics">http://136.243.4.200:8087/fdp/catalog/multiomics</a>	
	<a href="http://136.243.4.200:8087/fdp/catalog/textmining">http://136.243.4.200:8087/fdp/catalog/textmining</a>	
	<a href="http://136.243.4.200:8087/fdp/catalog/Biosamples">http://136.243.4.200:8087/fdp/catalog/Biosamples</a>	
	<a href="http://136.243.4.200:8087/fdp/catalog/Patient_Registries_1.0_998ccbcf-8714-426a-a28e-9335a86adb19">http://136.243.4.200:8087/fdp/catalog/Patient_Registries_1.0_998ccbcf-8714-426a-a28e-9335a86adb19</a>	
	<a href="http://136.243.4.200:8087/fdp/catalog/SCA3_HD_multi-omics_blood_data">http://136.243.4.200:8087/fdp/catalog/SCA3_HD_multi-omics_blood_data</a>	
Institution Country	<a href="http://lexvo.org/id/iso3166/NL">http://lexvo.org/id/iso3166/NL</a>	
Download RDF	ttl rdf+xml jsonld	

## Orphadata FAIR Data Point

FAIR Data Point to host free orphanet's dataset(s). These data sets are a partial extraction of the Orphanet data base, freely accessible at [www.orpha.net](http://www.orpha.net) (for consultation purposes only). The data sets are available in nine languages: English, French, German, Italian, Portuguese, Spanish, Dutch, Polish and Czech.

### Catalogs

#### Cross-referencing of rare diseases

Rare Diseases and Cross-referencing

Q929833

Q2330408

Datasets: 9 Issued: 27-11-2019 Modified: 27-11-2019

#### Genes associated with rare diseases

Table with ORPHA number of the disease linked to the associated genes, with a characterisation of the relationship between gene and disease (causative, modifier, susceptibility, or...

Q929833

Q7187

Datasets: 1 Issued: 27-11-2019 Modified: 27-11-2019

#### Phenotypes associated with rare diseases

Table with diseases listed in Orphanet annotated with HPO phenotypes. The alignment is characterised by frequency (obligatory, very frequent, frequent, occasional, very rare or exc...

Issued

27-11-2019

Modified

27-11-2019

Version

1.0

License

legalcode

Access Rights

The resource may have some access restrictions

Specification

fdpMetadata

Language

en

Publisher

Orphadata

Download RDF

ttl rdf+xml jsonld



**Google Search**

**I'm Feeling Lucky**



| inhibitors p65

**Google Search**

**I'm Feeling Lucky**



inhibitors p65



All

Images

Shopping

Videos

News

More

Settings

Tools

About 544.000 results (0,51 seconds)

### RelA/NFkB p65 Inhibitors: Novus Biologicals

<https://www.novusbio.com/inhibitors/rela-nfkb-p65> ▼

RelA/NFkB **p65 Inhibitors** available through Novus Biologicals. Browse our RelA/ NFkB **p65 Inhibitor** catalog backed by our Guarantee+.

### Inhibiting NF-κB Activation by Small Molecules As a Therapeutic ...

<https://www.ncbi.nlm.nih.gov> › NCBI › Literature › PubMed Central (PMC)

by SC Gupta - 2010 - Cited by 345 - Related articles

May 21, 2010 - ... pathway (Fig 3). Table 1. A list of small molecules as **inhibitors** of NF-κB pathway .... Blocking NF-κB activation by **inhibitors** of **p65** acetylation.

### Suppression of p65 phosphorylation coincides with inhibition of ... - NCBI

<https://www.ncbi.nlm.nih.gov/pubmed/16163708>

by J Hu - 2005 - Cited by 26 - Related articles

Mol Carcinog. 2005 Dec;44(4):274-84. Suppression of **p65** phosphorylation coincides with **inhibition** of IkappaBalpha polyubiquitination and degradation.

### Identification of a p65 peptide that selectively inhibits NF-kappa B ...

<https://www.ncbi.nlm.nih.gov/pubmed/14711835>

by Y Takada - 2004 - Cited by 157 - Related articles

Jan 7, 2004 - Identification of a **p65** peptide that selectively **inhibits** NF-kappa B activation



inhibitors p65



All

Images

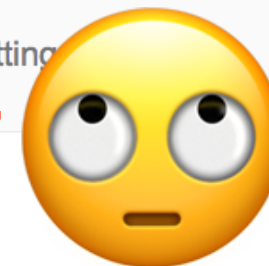
Shopping

Videos

News

More

Settings



About 544.000 results (0,51 seconds)

Mostly narrative articles, in PDF

RelA/NFkB p65 Inhibitors: Novus Biologicals

<https://www.novusbio.com/inhibitors/rela-nfkb-p65>

RelA/NFkB p65 Inhibitors available through Novus Biologicals. Browse our RelA/ NFkB p65 Inhibitor catalog backed by our Guarantee+.

Inhibiting NF-κB Activation by Small Molecules As a Therapeutic ...

[https://www.ncbi.nlm.nih.gov/NCBI/Literature/PubMed Central \(PMC\)](https://www.ncbi.nlm.nih.gov/NCBI/Literature/PubMedCentral(PMC))

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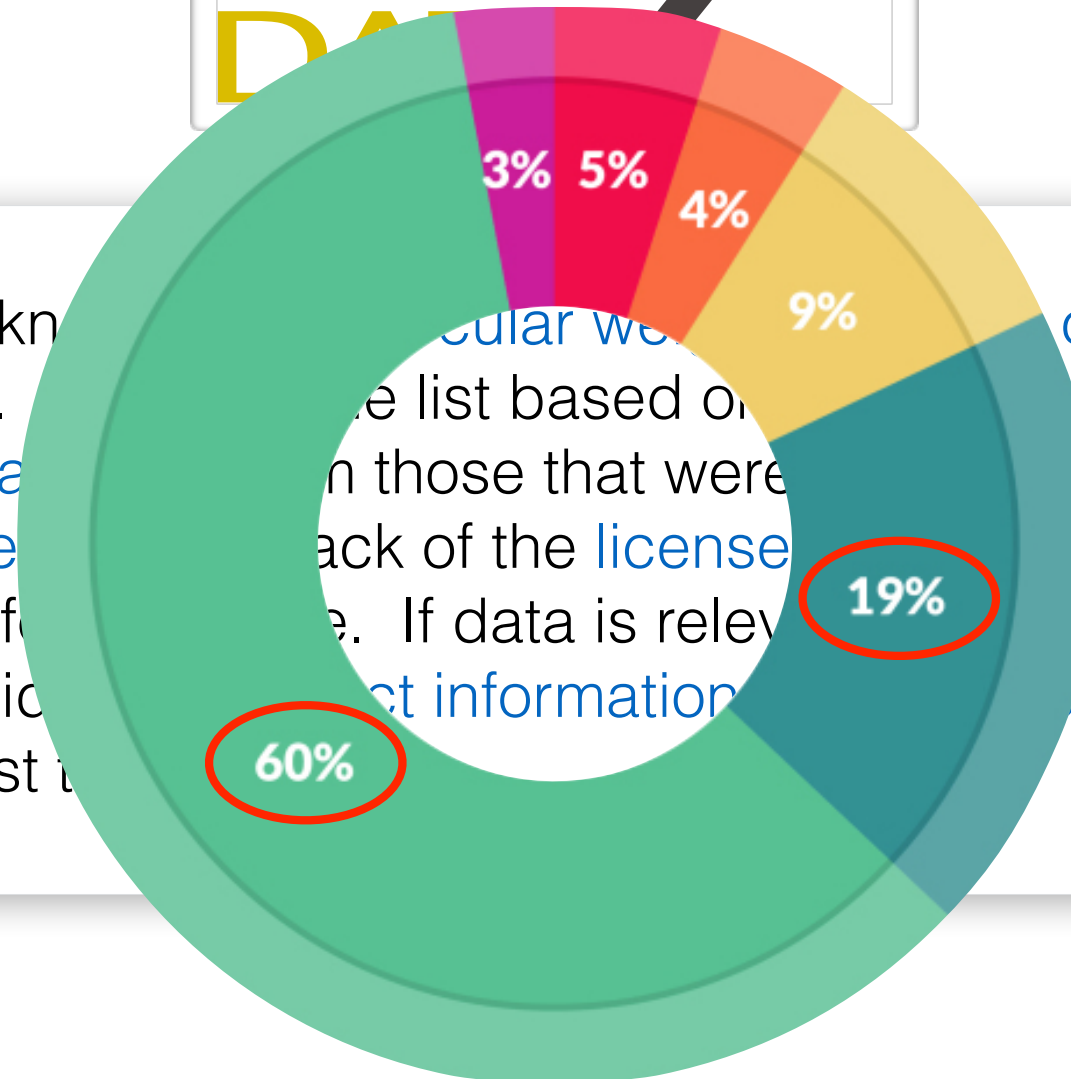
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Find me [all](#) known [low molecular weight](#) inhibitors of the Human p65 Protein. Separate the list based on those that were [found in curated databases](#), from those that were [found in self-deposited data archives](#). Keep track of the [license and citation information](#) for each one. If data is relevant, but [not public](#), please provide the [contact information for the person](#) I need so I can request the data.



Find me [all known](#)  
[p65 Protein](#).  
[curated data](#)  
[data archive](#)  
[information](#) for  
please provide  
I can request to

[molecular weight](#)  
the list based on  
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September 5, 2018

# Google Dataset Search Beta

Search for Datasets



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September 5, 2018

# Google Dataset Search Beta

Biosemanantics Group LUMC



Try [boston education data](#) or [weather site:noaa.gov](#)



## Gene disease association (LUMC)



semlab1.liacs.nl

### Dataset provided by

Biosemanantics group leiden

### License

[Attribution-NonCommercial-NoDerivs 3.0 Unported \(CC BY-NC-ND 3.0\)](#)

### Available download formats from providers

HTML




Gene disease  
association (LUMC)

semlab1.liacs.nl

### Description

Gene disease association dataset from LUMC

 http://136.243.4.200:8087/fdp/dataset/gene\_disease\_association

NEW TEST



```
1 <!DOCTYPE html>
2 <html>
3   <head>
4     <!-- Latest compiled and minified CSS -->
5     <link rel="stylesheet" href="https://stackpath.bootstrapcdn.com/bootstrap/4.1.0/css/bootstrap.min.css"
      integrity="sha384-9gVQ4dYFwWSjIDZnLEWnxCjeSWFphJiwGPx1jddIhOegui1FwO5qRGvFXOdJZ4" crossorigin="anonymous">
6
7     <title>
8       Gene disease association (LUMC)
9     </title>
10
11     <script type="application/ld+json">
12       {
13         "@graph":
14           [{ "@id": "http://136.243.4.200:8087/fdp/dataset/gene_disease_association", "@type": "http://schema.org/Dataset", "http://schema.org/creator": { "@id": "http://biosemantics.org", "http://schema.org/description": "High-throughput experimental methods such as medical sequencing and genome-wide association studies (GWAS) identify increasingly large numbers of potential relations between genetic variants and diseases. Both biological complexity (millions of potential gene-disease associations) and the accelerating rate of data production necessitate computational approaches to prioritize and rationalize potential gene-disease relations. Here, we use concept profile technology to expose from the biomedical literature both explicitly stated gene-disease relations (the explicitome) and a much larger set of implied gene-disease associations (the implicitome). Implicit relations are largely unknown to, or are even unintended by the original authors, but they vastly extend the reach of existing biomedical knowledge for identification and interpretation of gene-disease associations. The implicitome can be used in conjunction with experimental data resources to rationalize both known and novel associations. We demonstrate the usefulness of the implicitome by rationalizing known and novel gene-disease associations, including those from GWAS. To facilitate the re-use of implicit gene-disease associations, we publish our data in compliance with FAIR Data Publishing recommendations [https://www.force11.org/group/fairgroup] using nanopublications. An online tool (http://knowledge.bio) is available to explore established and potential gene-disease associations in the context of other biomedical relations.", "http://schema.org/distribution": [{ "@id": "http://136.243.4.200:8087/fdp/distribution/gene_disease_association_html", { "@id": "http://136.243.4.200:8087/fdp/distribution/gene_disease_association_nquads_gzip", { "@id": "http://136.243.4.200:8087/fdp/distribution/gene_disease_association_csv_gzip" } } ], "http://schema.org/keywords": [ "The Explicitome", "The Implicitome", "Text mining", "Gene disease association (LUMC)", "GDA", "LWAS" ], "http://schema.org/name": "Gene disease association (LUMC)" }, { "@id": "http://biosemantics.org", "@type": "http://schema.org/Thing", "http://schema.org/name": "Biosemantic group" } ], "@context": { "rdf": "http://www.w3.org/1999/02/22-rdf-syntax-ns#", "rdfs": "http://www.w3.org/2000/01/rdf-schema#", "dc": "http://www.w3.org/ns/dc/terms", "xsd": "http://www.w3.org/2001/XMLSchema#", "owl": "http://www.w3.org/2002/07/owl#", "dcterms": "http://purl.org/dc/terms/", "fdp": "http://rdf.biosemantics.org/ontologies/fdp-0#", "r3d": "http://www.re3data.org/schema/3-0#", "lang": "http://id.loc.gov/vocabulary/iso639-1/" } }
15     </script>
16
17     <style>
18       /* Sticky footer styles
19       ----- */
20
21       html {
22         position: relative;
23         min-height: 100%;
24       }
25
26       body {
27         /* Margin bottom by footer height */
28         margin-bottom: 60px;
29       }
30     </style>
31
32   </head>
33   <body>
34
35   </body>
36 </html>
```

## Dataset

0 ERRORS 0 WARNINGS ^

ID: http://136.243.4.200:8087/fdp/dataset/gene\_disease\_association

@type	Dataset
@id	http://136.243.4.200:8087/fdp/dataset/gene_disease_association
description	High-throughput experimental methods such as medical sequencing and genome-wide association studies (GWAS) identify increasingly large numbers of potential relations between genetic variants and diseases. Both biological complexity (millions of potential gene-disease associations) and the accelerating rate of data production necessitate computational approaches to prioritize and rationalize potential gene-disease relations. Here, we use concept profile technology to expose from the biomedical literature both explicitly stated gene-disease relations (the explicitome) and a much larger set of implied gene-disease associations (the implicitome). Implicit relations are largely unknown to, or are even unintended by the original authors, but they vastly extend the reach of existing biomedical knowledge for identification and interpretation of gene-disease associations. The implicitome can be used in conjunction with experimental data resources to rationalize both known and novel associations. We demonstrate the usefulness of the implicitome by rationalizing known and novel gene-disease associations, including those from GWAS. To facilitate the re-use of implicit gene-disease associations, we publish our data in compliance with FAIR Data Publishing recommendations [https://www.force11.org/group/fairgroup] using nanopublications. An online tool (http://knowledge.bio) is available to explore established and potential gene-disease associations in the context of other biomedical relations.
keywords	The Explicitome
keywords	The Implicitome
keywords	Text mining
keywords	Gene disease association (LUMC)
keywords	GDA
keywords	LWAS
name	Gene disease association (LUMC)
creator	
@type	Thing
@id	http://biosemantics.org/
name	Biosemantic group
distribution	
@type	DataDownload
@id	http://136.243.4.200:8087/fdp/distribution/gene_disease_association_html
distribution	
@type	DataDownload
@id	http://136.243.4.200:8087/fdp/distribution/gene_disease_association_nquads_gzip
distribution	
@type	DataDownload
@id	http://136.243.4.200:8087/fdp/distribution/gene_disease_association_csv_gzip

# Virus Outbreak Data Network (VODAN)

[Home](#) › [Implementation Networks](#) › [Current Implementation Networks](#) › Virus Outbreak Data Network (VODAN)

## Active GO FAIR Implementation Network

The spread of the virus causing the COVID-19 outbreak is far from over. During this epidemic and in earlier occasions, we have seen severely suboptimal data management and data reuse. Moreover, access to the immensely valuable data of past and current epidemics is not always equally accessible for different affected populations and countries. For instance, the data from the past Ebola epidemics are very difficult to find, to access, and if accessible, they are not interoperable, *let alone reusable*. In the case of Ebola this is even more harrowing and ironic as the data are *least available* to the population that were *most affected* by the disaster. Under the urgent need to harness machine-learning and future AI approaches to discover meaningful patterns in epidemic outbreaks, we need to do better and ensure that data are FAIR (in this sense also meaning **F**ederated, **AI**-Ready).

## Purpose of the Implementation Network

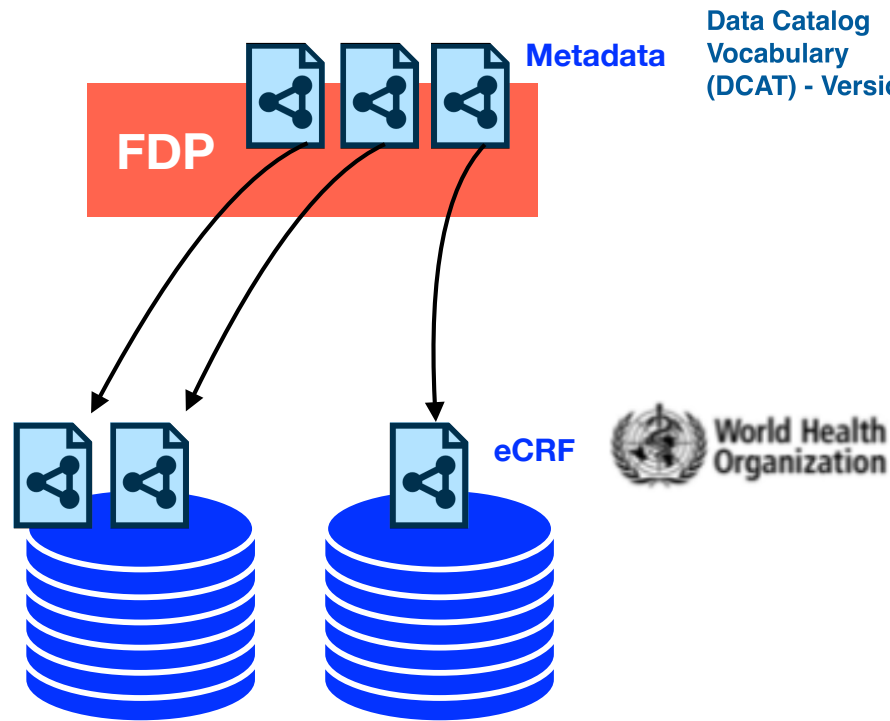
**This time, we can do better.** We now have the technical ability, as well as the commitment from experts in a series of affected countries, to make the SARS CoV-2 virus data FAIR, meaning that they are Findable, Accessible, Interoperable and thus Reusable by both humans and machines, during this epidemic of COVID-19. The technical components that make this possible can remain in place, waiting in the ready state *for potential future infectious disease outbreaks*.

**With a sense of urgency driven by the rapid developments on COVID-19 we come together to launch** a GO FAIR Implementation Network to address the current and immediate challenges. For this epidemic, unfortunately, we have to 'FAIRify' COVID-19 data '*after the fact*' and use Chinese, Dutch, Swedish, etc. and English electronic (or even hand-written) health records to create proper FAIR data. The FAIRification will initially focus on the Clinical Research Form (CRF) model following the WHO standards. Multiple IN partners will create input forms that make it easy for local caregivers to create FAIR-CRF data in real time as a first step. As a second step, we will jointly develop (via online work sessions) localized FAIR Data Points (FDP). FDP is a FAIR data repository with 'docking' capabilities as a 'station' for 'trains' (virtual machines (VMs)) that come to 'visit' the data locally, with a specific question to ask. The local data custodian (frequently a hospital or centre for disease control and prevention type of institution) grants permission to VMs to ask the question / run analyses. As the personal data of patients never leaves the underlying database of the local institution, GDPR issues are largely accommodated and in this way data can be 'shared' or rather 'visited' without violating any patient rights and, in the case of a disease outbreak, also governed by the laws and policies of the individual jurisdictions in which the outbreak manifests.

# The VODAN FAIR Data Point

(Enables data visiting)

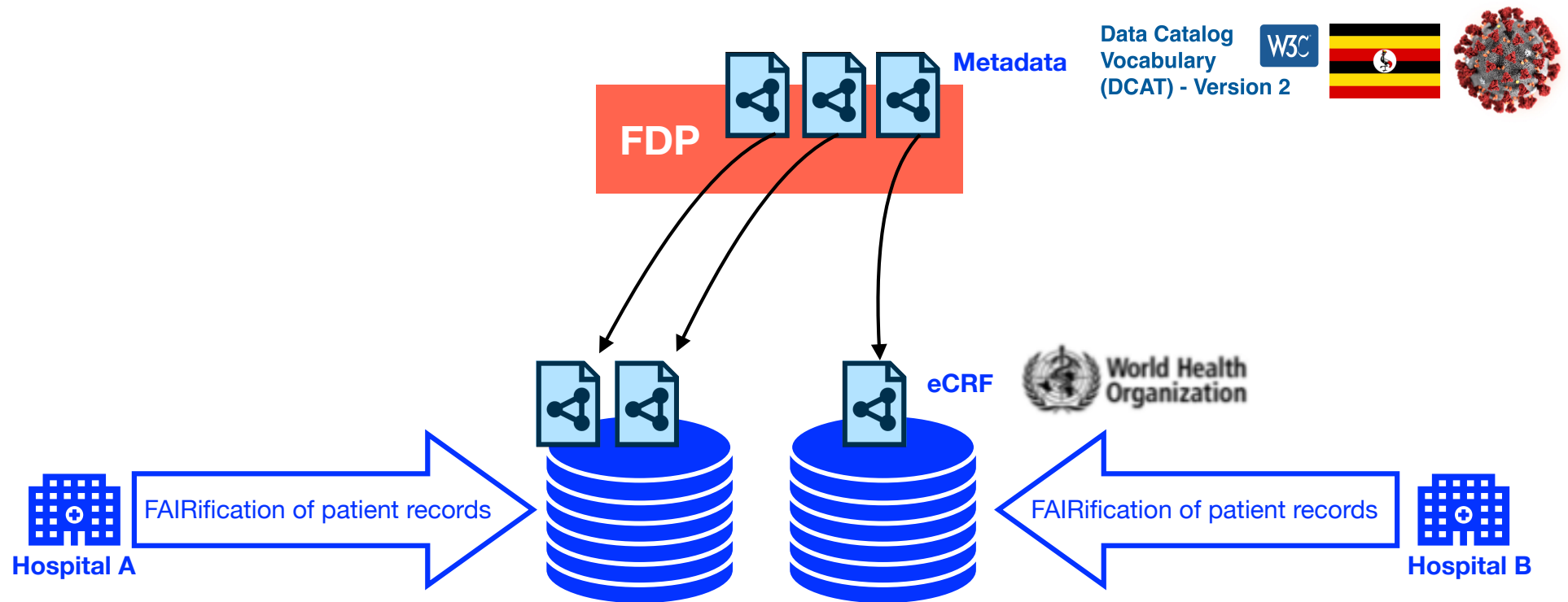
- Ethiopia: Addis Ababa University
- Ethiopia: Mekelle University
- Uganda: KIU
- Zimbabwe: GZU
- Nigeria: Data Science group
- Kenya: Westlands





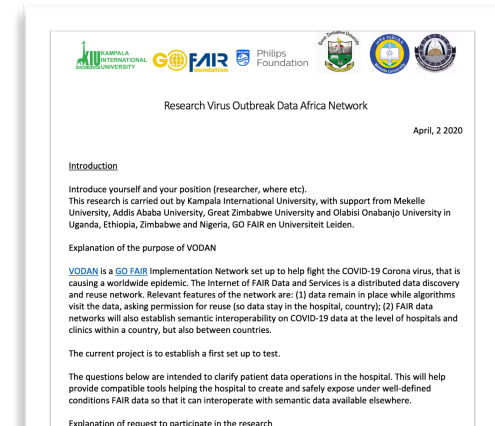
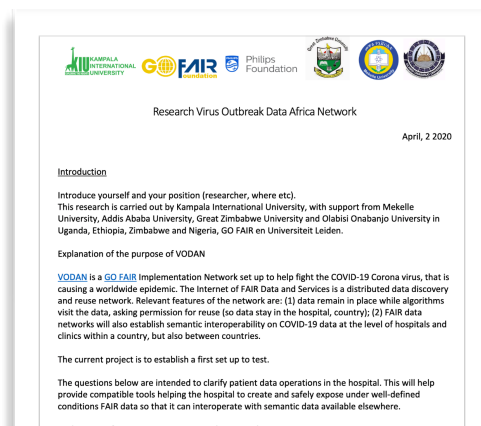
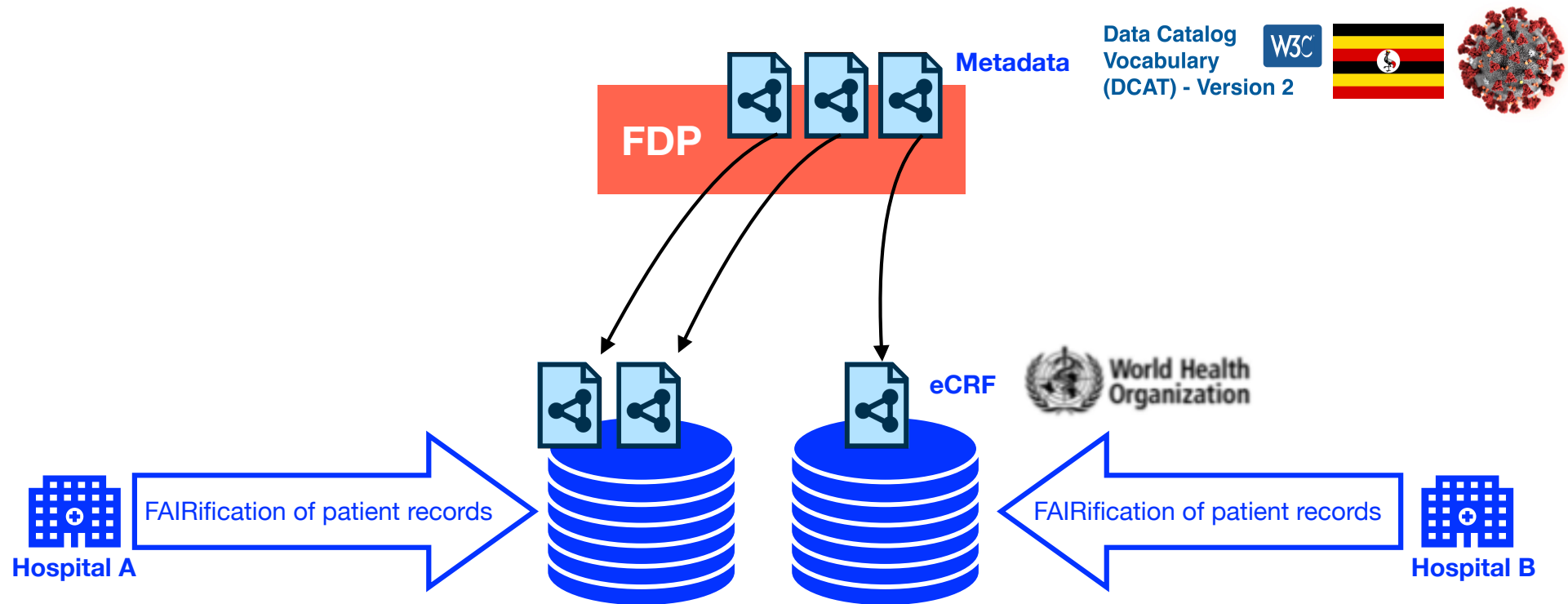
# The VODAN FAIR Data Point

(Enables data visiting)



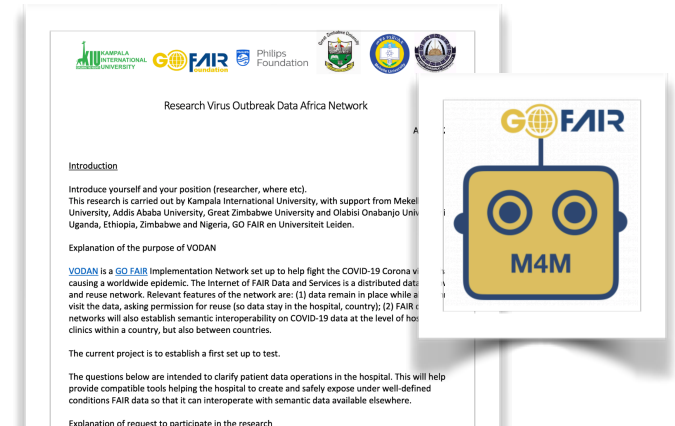
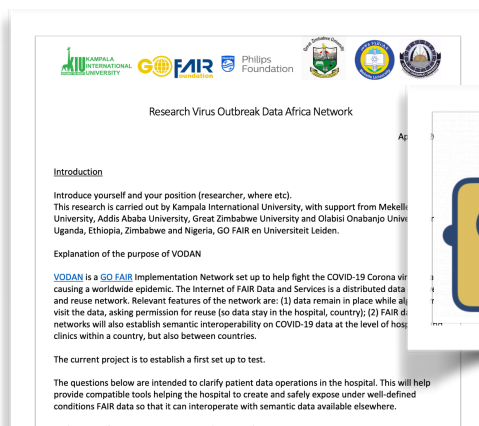
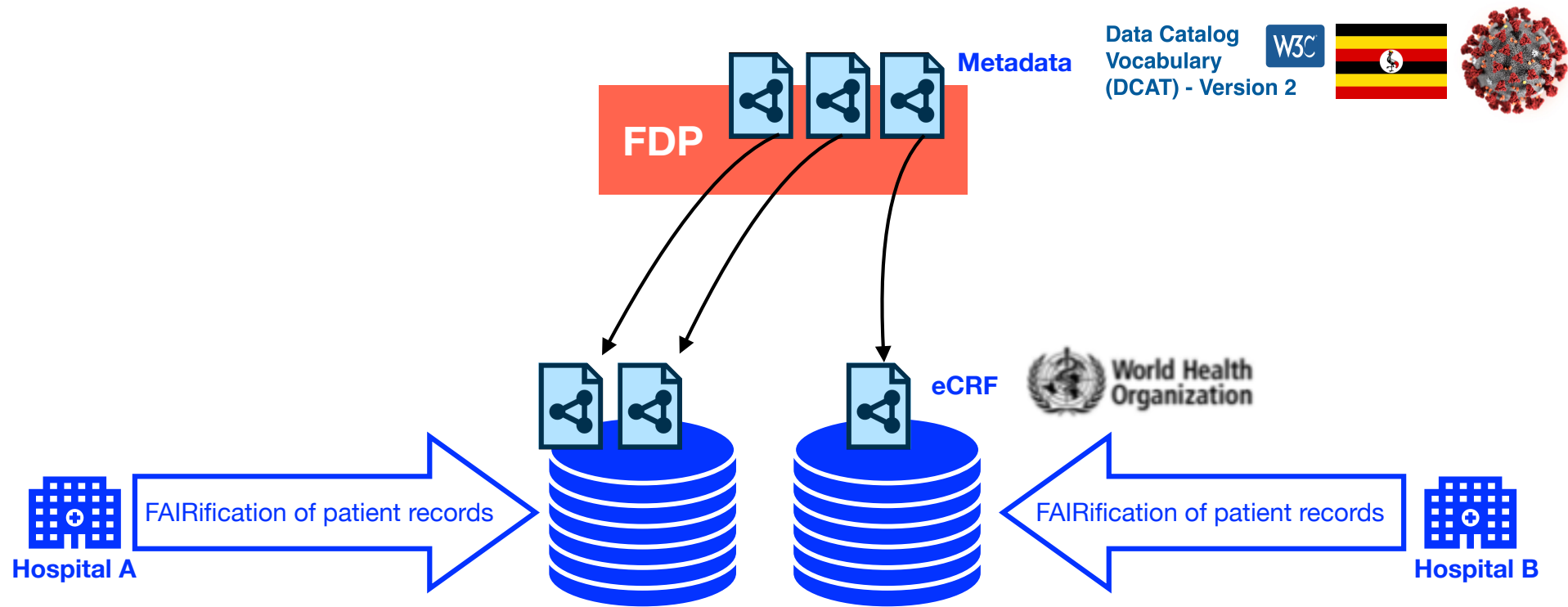
# The VODAN FAIR Data Point

(Enables data visiting)



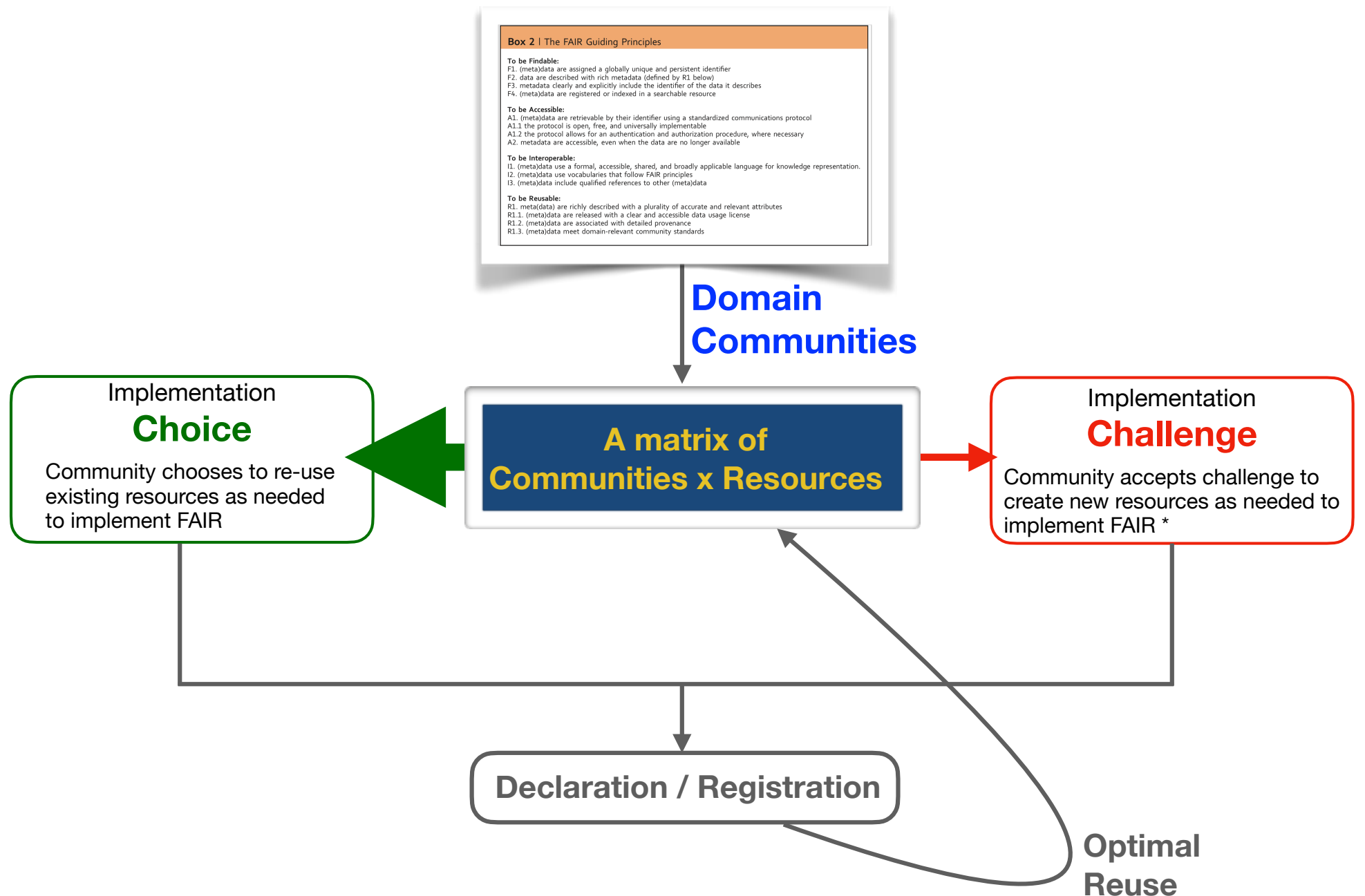
# The VODAN FAIR Data Point

(Enables data visiting)



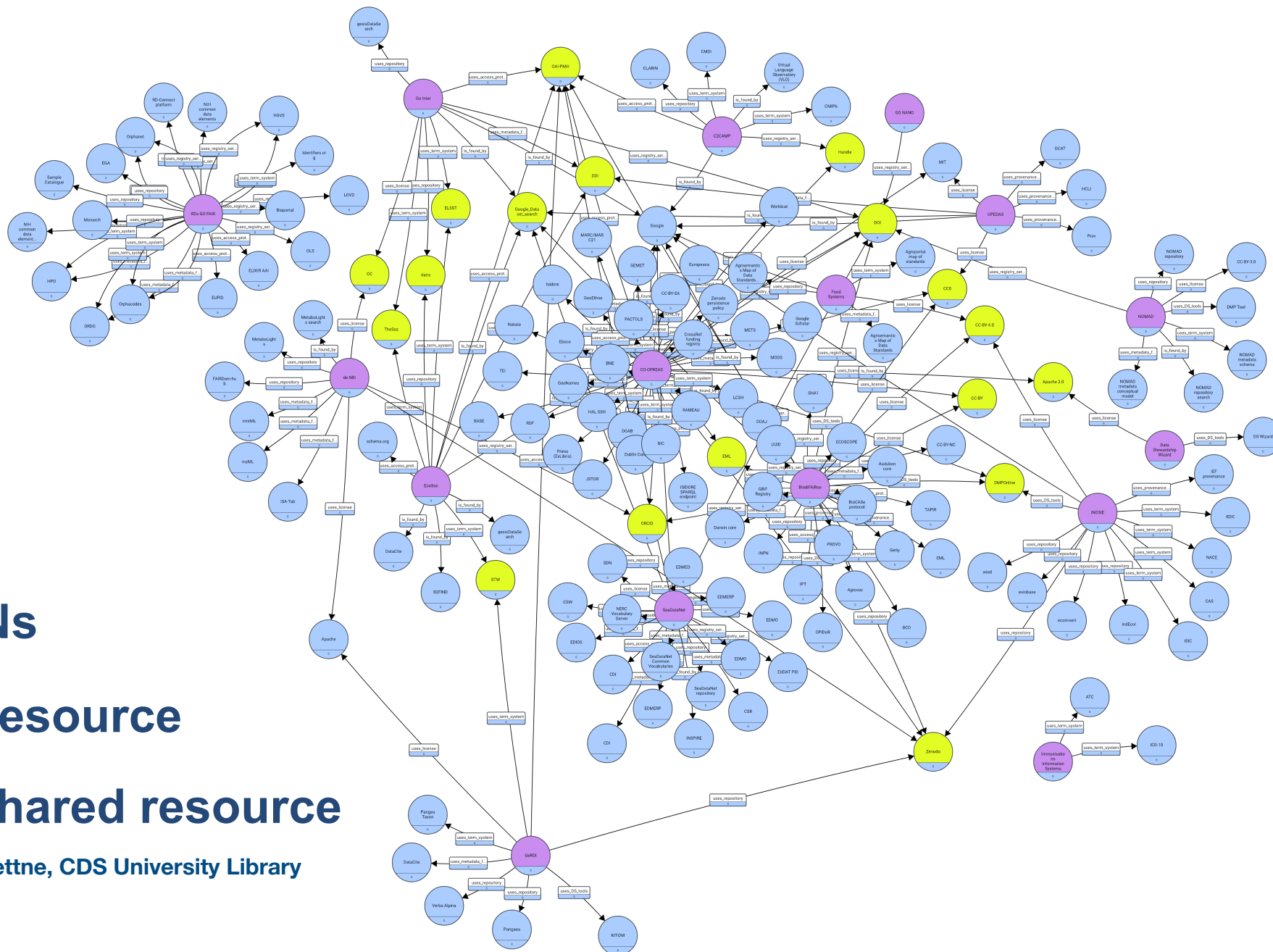
# **The FAIR Implementation Profile**

# FAIR Implementation Profiles



*\* every “choice” was once a “challenge”*

# FAIR Implementation Profiles

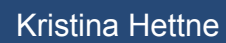


**INS**

## Resource

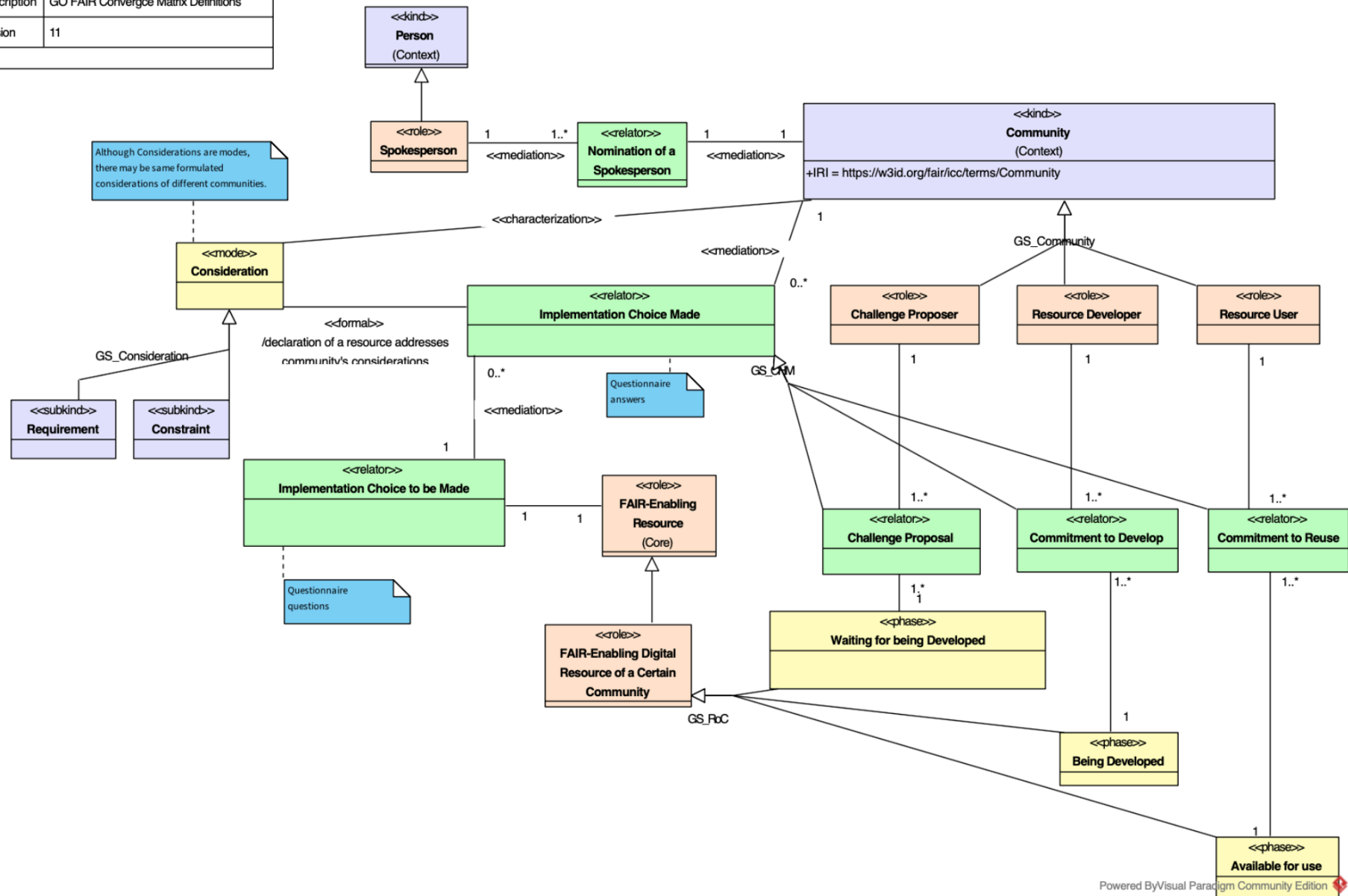
 **Shared resource**

**Kristina Hettne, CDS University Library**



# Core ontology

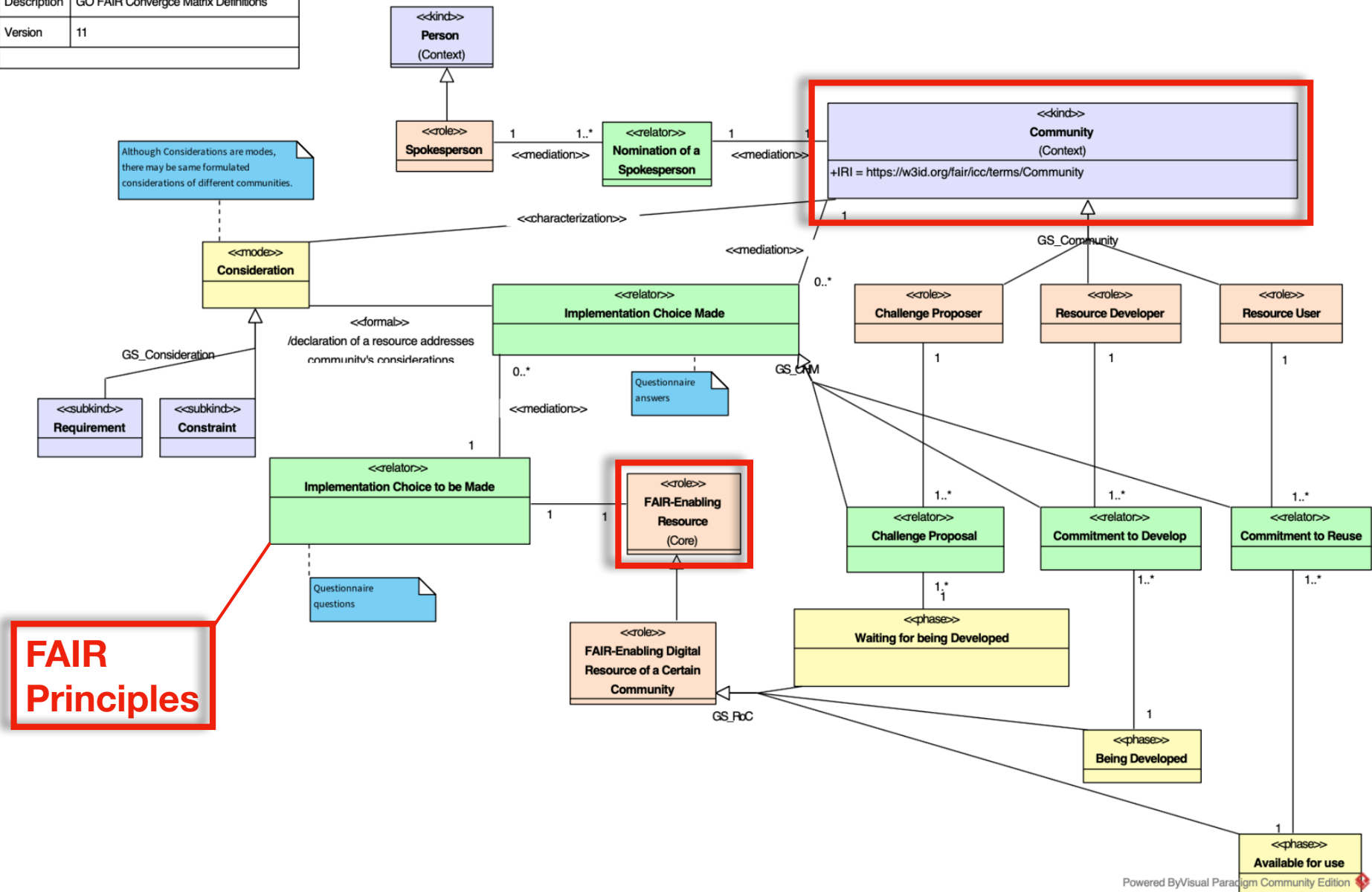
Name	Convergence Matrix
Description	GO FAIR Convergee Matrix Definitions
Version	11





# Core ontology

Name	Convergence Matrix
Description	GO FAIR Convergee Matrix Definitions
Version	11



# v3 Questionnaire


[illegible]

# FAIR Convergence Matrix

<https://fair-matrix.ds-wizard.org/>

Email: "guest@example.com"

Password: "guest"



Knowledge Models

Questionnaires

?

Help

FIP (FAIR Implementation Profile, 1.3.1)

(unsaved changes)DiscardSave

Chapters

General Information about Survey

General Information about Participant

III. Findability

IV. Accessibility

V. Interoperability

VI. Reusability

More

Summary Report

III. Findability

Chapter text

1 F1 What globally unique, persistent, resolvable identifiers do you use for metadata records?

1.a.1 Choose your answer from FAIRsharing

1.a.2 Add your resource description here

+ Add

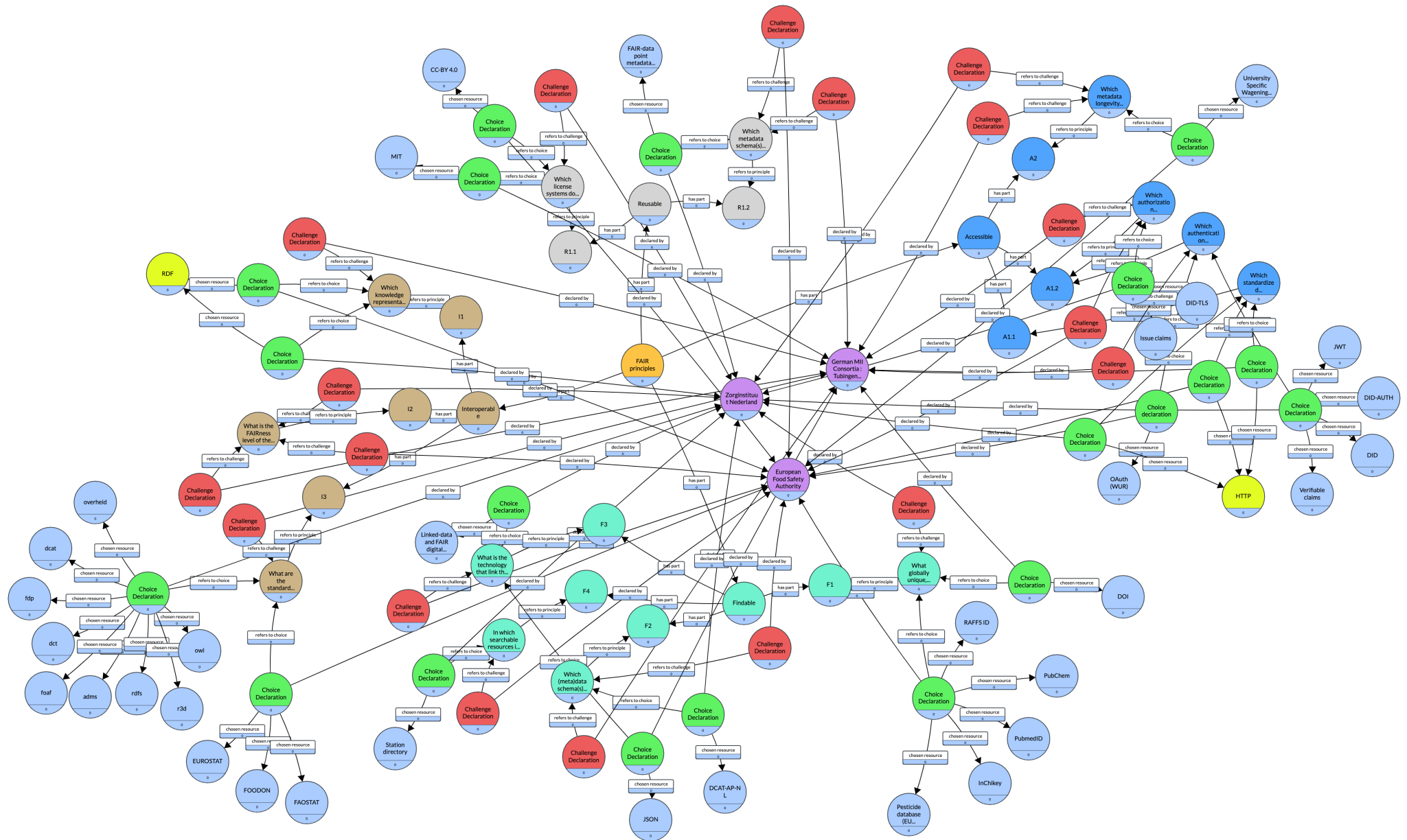
2 F1 What globally unique, persistent, resolvable identifiers do you use for datasets?

+ Add

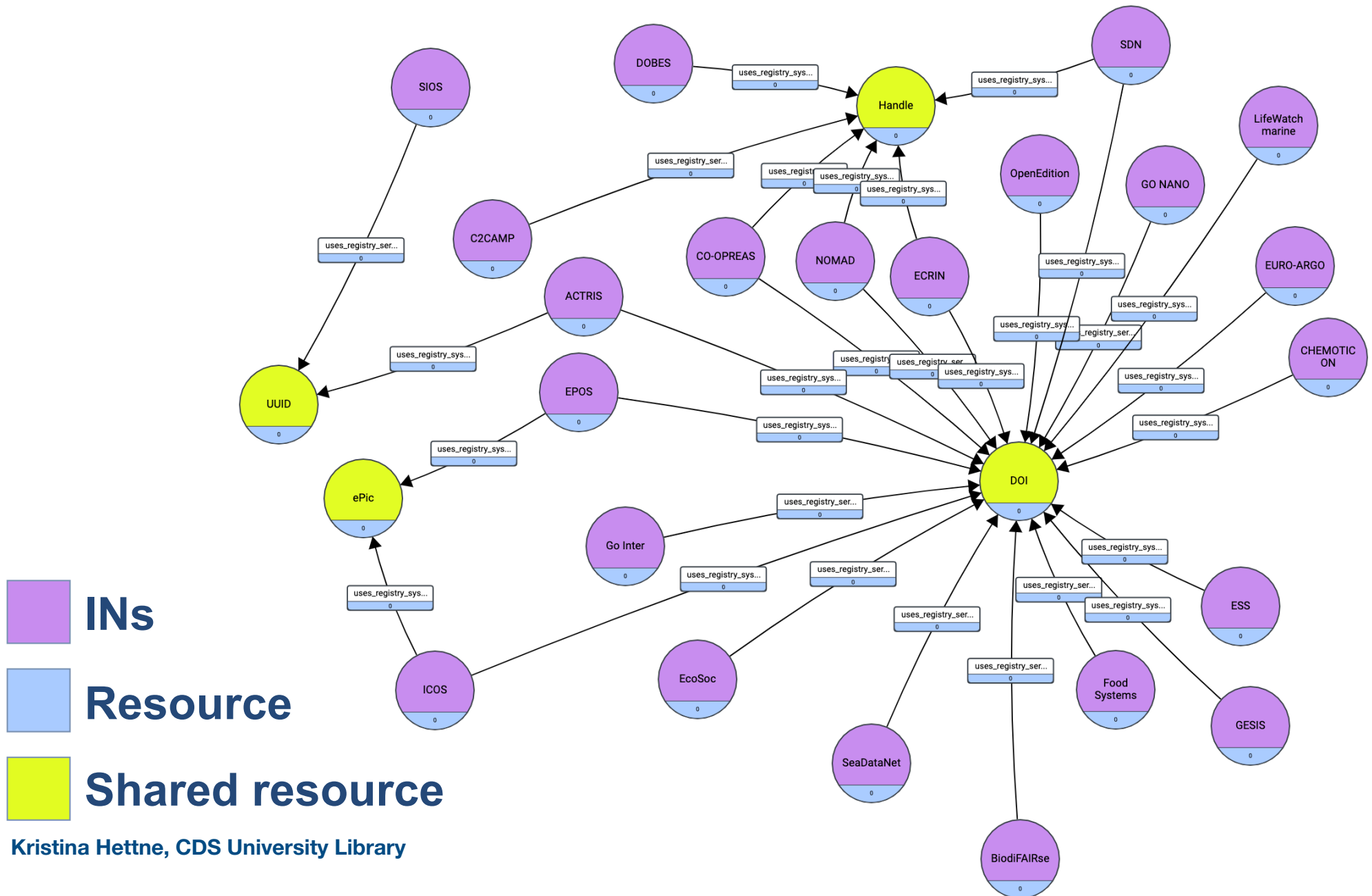
3 F2 Which metadata schema(s) are you using for findability?

+ Add

### 3 Communities devoted to distributed learning



# FIPs for 32 European Research Infrastructures



# FAIR Implementation Profiles

		Communities									
		A	B	C	D	E	F	G	H	I	J
Resources	<b>F</b> Resource 1	0	1	0	0	0	0	0	0	0	0
	Resource 2	1	1	1	0	1	1	1	1	1	0
	<b>A</b> Resource 3	1	1	0	0	0	0	0	0	1	0
	Resource 4	0	0	1	1	1	1	1	1	1	1
	<b>I</b> Resource 5	1	0	0	0	0	0	0	0	1	0
	Resource 6	0	1	1	0	1	1	1	1	1	0
	<b>R</b> Resource 7	1	0	0	0	0	0	0	0	0	0
	Resource 8	1	0	1	0	1	1	1	1	1	0

# FAIR Implementation Profiles

		Communities									
		A	B	C	D	E	F	G	H	I	J
Resources	<b>F</b> Resource 1	0	1	0	0	0	0	0	0	0	0
	Resource 2	1	1	1	0	1	1	1	1	1	0
	<b>A</b> Resource 3	1	1	0	0	0	0	0	0	1	0
	Resource 4	0	0	1	1	1	1	1	1	1	1
	<b>I</b> Resource 5	1	0	0	0	0	0	0	0	1	0
	Resource 6	0	1	1	0	1	1	1	1	1	0
	<b>R</b> Resource 7	1	0	0	0	0	0	0	0	0	0
	Resource 8	1	0	1	0	1	1	1	1	1	0

# FAIR Implementation Profiles


		Communities									
		A	B	C	D	E	F	G	H	I	J
Resources	<b>F</b> Resource 1	0	1	0	0	0	0	0	0	0	0
	Resource 2	1	1	1	0	1	1	1	1	1	0
	<b>A</b> Resource 3	1	1	0	0	0	0	0	0	1	0
	Resource 4	0	0	1	1	1	1	1	1	1	1
	<b>I</b> Resource 5	1	0	0	0	0	0	0	0	1	0
	Resource 6	0	1	1	0	1	1	1	1	1	0
	<b>R</b> Resource 7	1	0	0	0	0	0	0	0	0	0
	Resource 8	1	0	1	0	1	1	1	1	1	0

FAIR Implementation Profile for Community C = {0,1,0,1,0,1,0,1}



# FAIR Implementation Profiles

		Communities									
		A	B	C	D	E	F	G	H	I	J
Resources	<b>F</b> Resource 1	0	1	0	0	0	0	0	0	0	0
	Resource 2	1	1	1	0	1	1	1	1	1	0
	<b>A</b> Resource 3	1	1	0	0	0	0	0	0	1	0
	Resource 4	0	0	1	1	1	1	1	1	1	1
	Resource 5	1	0	0	0	0	0	0	0	1	0
	<b>I</b> Resource 6	0	1	1	0	1	1	1	1	1	0
	<b>R</b> Resource 7	1	0	0	0	0	0	0	0	0	0
	Resource 8	1	0	1	0	1	1	1	1	1	0



FAIR Implementation Profile for Community C = {0,1,0,1,0,1,0,1}

Community E-I have reused the FIP of (trusted) Community C

# FAIR Implementation Profiles

		Communities									
		A	B	C	D	E	F	G	H	I	J
Resources	<b>F</b> Resource 1	0	1	0	0	0	0	0	0	0	0
	Resource 2	1	1	1	0	1	1	1	1	1	0
	<b>A</b> Resource 3	1	1	0	0	0	0	0	0	1	0
	Resource 4	0	0	1	1	1	1	1	1	1	1
	<b>I</b> Resource 5	1	0	0	0	0	0	0	0	1	0
	Resource 6	0	1	1	0	1	1	1	1	1	0
	<b>R</b> Resource 7	1	0	0	0	0	0	0	0	0	0
	Resource 8	1	0	1	0	1	1	1	1	1	0

**FAIR Implementation Profile for Community C = {0,1,0,1,0,1,0,1}**

**Community E-I have reused the FIP of (trusted) Community C**

- Save time on FAIR implementation
- Maximize reuse
- Maximize interoperability

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## FAIR Convergence Matrix: Optimizing the Reuse of Existing FAIR-Related Resources



Hana Pergl Sustkova , Kristina Maria Hettne, Peter Wittenburg, Annika Jacobsen, Tobias Kuhn, Robert Pergl, Jan Slifka, Peter McQuilton, Barbara Magagna, Susanna-Assunta Sansone, Markus Stocker, Melanie Imming, Larry Lannom, Mark Musen, Erik Schultes  hidden

DOI: 10.1162/dint\_a\_00038



439 | 43 | 0

### Abstract & Keywords



**Abstract:** The FAIR Principles articulate the behaviors expected from digital artifacts that are Findable, Accessible, Interoperable and Reusable by machines and by people. Although by now widely accepted, the FAIR Principles by design do not explicitly consider actual implementation choices enabling FAIR behaviors. As different communities have their own, often well-established implementation preferences and priorities for data reuse, coordinating a broadly accepted, widely used FAIR implementation approach remains a global challenge. In an effort to accelerate broad community convergence on FAIR implementation options, the GO FAIR community has launched the development of the FAIR Convergence Matrix. The Matrix is a platform that compiles for any community of practice, an inventory of their self-declared FAIR implementation choices and challenges. The Convergence Matrix is itself a FAIR resource, openly available, and encourages voluntary participation by any self-identified community of practice (not only the GO FAIR Implementation Networks). Based on patterns of use and reuse of existing resources, the Convergence Matrix supports the transparent derivation of strategies that optimally coordinate convergence on standards and technologies in the emerging Internet of FAIR Data and Services.

**Keywords:** FAIR Implementation Choices and Challenges; Convergence; FAIR Communities

### Acknowledgments



### References



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## FAIR Convergence Matrix: Optimizing the Reuse of Existing FAIR-Related Resources



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DOI: 10.1162/dint\_a\_00038

439 | 43 | 0

### Abstract & Keywords

**Abstract:** The FAIR Principles and Reusable by machines consider actual implementation preferences. This approach remains a global challenge. The GO FAIR community has any community of practice, Matrix is itself a FAIR resource practice (not only the GO Convergence Matrix support technologies in the emerging

**Keywords:** FAIR Implementation

### Acknowledgments

### References

## Reusable FAIR Implementation Profiles as Accelerators of FAIR Convergence

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GO FAIR International Support and Coordination Office, Leiden, The Netherlands

[ORCID](#) 0000-0001-8888-635X

Version 2.0 DRAFT: DO NOT CIRCULATE

December 11, 2019

On OSF: <https://osf.io/8sv5f/>

### Abstract

There are now powerful incentives driving the adoption of FAIR practices among a broad cross section of public and private sector organizations<sup>1</sup>. This adoption process requires considerations on both domain-specific and infrastructural resources. Together, these considerations compose a potentially very large number of decisions on the use and reuse of standards and technologies. Many of the relevant factors in these considerations are likely to exceed the knowledge and experience of individual domain specialists and data stewards. For communities adopting FAIR practices, the collection of their implementation choices compose their *FAIR Implementation Profile* (FIP). The FIPs of numerous communities can be systematically acquired from the FAIR Convergence Matrix<sup>2</sup> and used as the basis to optimize the reuse of existing resources and interoperation within and between domains. Ready-made and well-tested FIPs created by trusted community authorized representatives could find widespread reuse and thus vastly accelerate well informed

# What is the FIP for your repository ?

Data Service Portal Aila, SND, DataDOI, SEAD, UiT Open Research Data Dataverse, CESSDA DC, CLARIN-DK, CLARINO Bergen Center repository, Språkbanken, TROLLing, tekstlab, NIRD Archive, ICOS, DDA, Kansanperinteen arkisto (Folkline archives), QsarDB, JYX, Kielipankki, Bolin Centre Database, GERDA, GEUS, HPA, DNBC, UNITE, PlutoF, FinBIF, CELR META-SHARE, MIDAS, SSRI, DTU data

## FAIR Convergence Matrix

<https://fair-matrix.ds-wizard.org/>

Email: "guest@example.com"

Password: "guest"

# What is the FIP for your repository ?

Data Service Portal Aila, SND, DataDOI, SEAD, UiT Open Research Data Dataverse, CESSDA DC, CLARIN-DK, CLARINO Bergen Center repository, Språkbanken, TROLLing, tekstlab, NIRD Archive, ICOS, DDA, Kansanperinteen arkisto (Folklore archives), QsarDB, JYX, Kielipankki, Bolin Centre Database, GERDA, GEUS, HPA, DNBC, UNITE, PlutoF, FinBIF, CELR META-SHARE, MIDAS, SSRI, DTU data

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Email: "guest@example.com"

Password: "guest"

