WELCOME

SESSION 2

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FAIR DATA STEWARDSHIP AWARENESS COURSE

FAIR DATASTEWARDSHIP: AN INTRODUCTION

INTRODUCTION TO FAIR DATA STEWARDSHIP

FIRST THE FAIR DATA STEWARDSHIP PART

UCLA 1992

ERIK'S PHD PROJECT

TABLE 1. Phylogenetically and functionally representative compilation of ssRNA nucleotide composition.

RNA	Taxon	n^a	$\langle N \rangle^b$	$\langle G+C \rangle^c$	$\langle G+A \rangle^c$	$\langle G+U \rangle^c$
Comprehensive	—	2,800	287.0 ± 662.0	0.509 ± 0.200	0.516 ± 0.0310	0.523 ± 0.0462
23S rRNA	Archaea	15	2,968.9 ± 65.8	0.588 ± 0.0525	0.567 ± 0.00597	0.509 ± 0.0212
	Bacteria	39	2,915.6 ± 86.3	0.526 ± 0.0383	0.570 ± 0.00720	0.517 ± 0.0102
	Eucarya	33	3,615.0 ± 470.3	0.530 ± 0.0832	0.540 ± 0.0139	0.520 ± 0.0143
18S rRNA	Metazoa	20	1,821.0 ± 43.2	0.494 ± 0.0297	0.517 ± 0.0123	0.535 ± 0.0113
16S rRNA	Archaea	15	1,530.7 ± 184.9	0.611 ± 0.0427	0.562 ± 0.00500	0.507 ± 0.00681
	Bacteria	85	1,511.8 ± 30.9	0.550 ± 0.0387	0.568 ± 0.00770	0.520 ± 0.0118
	Eucarya	47	1,823.6 ± 57.8	0.486 ± 0.0255	0.524 ± 0.00671	0.527 ± 0.00955
5S rRNA	Archaea	26	124.5 ± 3.9	0.598 ± 0.0726	0.508 ± 0.0272	0.498 ± 0.0409
	Bacteria	123	117.6 ± 3.9	0.575 ± 0.0574	0.520 ± 0.0308	0.495 ± 0.0344
	Eucarya	234	119.3 ± 1.4	0.557 ± 0.0369	0.517 ± 0.0119	0.505 ± 0.0176
P RNA	Archaea	7	400.9 ± 62.0	0.644 ± 0.0966	0.564 ± 0.0140	0.469 ± 0.0296
	Bacteria	37	389.0 ± 39.7	0.569 ± 0.114	0.570 ± 0.0168	0.496 ± 0.0147
Group I ribozymes	—	13	757.15 ± 517.5	0.434 ± 0.105	0.561 ± 0.0302	0.492 ± 0.0268
Group II ribozymes	—	6	734.8 ± 853.8	0.355 ± 0.0933	0.566 ± 0.0259	0.495 ± 0.0276
HDV Ribozymes	—	2	43.5 ± 43.1	0.619 ± 0.00212	0.512 ± 0.0368	0.519 ± 0.0269
snRNA, U1	Eucarya	24	162.4 ± 4.2	0.557 ± 0.0228	0.487 ± 0.00957	0.548 ± 0.0152
snRNA, U2	Eucarya	16	187.8 ± 11.6	0.455 ± 0.0357	0.456 ± 0.0310	0.543 ± 0.0257
snRNA, U3	Eucarya	8	220.6 ± 14.6	0.468 ± 0.0684	0.477 ± 0.0417	0.561 ± 0.0207
snRNA, U4	Eucarya	11	143.6 ± 12.3	0.484 ± 0.0384	0.493 ± 0.0192	0.536 ± 0.0303
snRNA, U5	Eucarya	11	125.6 ± 29.7	0.411 ± 0.0345	0.448 ± 0.0279	0.531 ± 0.0220
snRNA, U6	Eucarya	14	101.5 ± 7.7	0.451 ± 0.0233	0.544 ± 0.0304	0.469 ± 0.0352
tRNA	Comprehensive	2,011	74.3 ± 6.3	0.496 ± 0.120	0.510 ± 0.0280	0.528 ± 0.0509
	Archaea	121	77.0 ± 4.2	0.633 ± 0.0457	0.503 ± 0.0215	0.516 ± 0.0351
	Bacteria	371	78.3 ± 5.2	0.580 ± 0.0522	0.506 ± 0.0222	0.522 ± 0.0317
	Eucarya	436	75.8 ± 4.2	0.572 ± 0.0438	0.510 ± 0.0282	0.544 ± 0.0365
	Chloroplast	291	75.6 ± 5.0	0.526 ± 0.0531	0.510 ± 0.0212	0.540 ± 0.0341
	Mitochondria	742	70.3 ± 6.4	0.372 ± 0.0939	0.514 ± 0.0328	0.519 ± 0.0685
Artificial ribozymes[d]	Class I					
	b1	1	274	0.471	0.511	0.493
	b1-207	1	119	0.513	0.546	0.445
	Class II					
	c2	1	271	0.568	0.535	0.546
	d1	1	273	0.487	0.502	0.524
	f1	1	273	0.546	0.524	0.502
	Class III					
	e3	1	272	0.529	0.511	0.563
	g1	1	274	0.544	0.522	0.518
Random	—	500	25	0.498 ± 0.104	0.495 ± 0.0979	0.494 ± 0.130
	—	500	74	0.500 ± 0.0560	0.502 ± 0.0587	0.498 ± 0.0548
	—	500	120	0.500 ± 0.0471	0.501 ± 0.0457	0.500 ± 0.0446
	—	500	400	0.501 ± 0.0260	0.501 ± 0.0247	0.500 ± 0.0254
	—	500	1,500	0.500 ± 0.0134	0.500 ± 0.0132	0.500 ± 0.0129
	—	500	3,000	0.500 ± 0.00924	0.500 ± 0.00954	0.500 ± 0.00888
	—	500	5,000	0.500 ± 0.00692	0.500 ± 0.00758	0.500 ± 0.00703

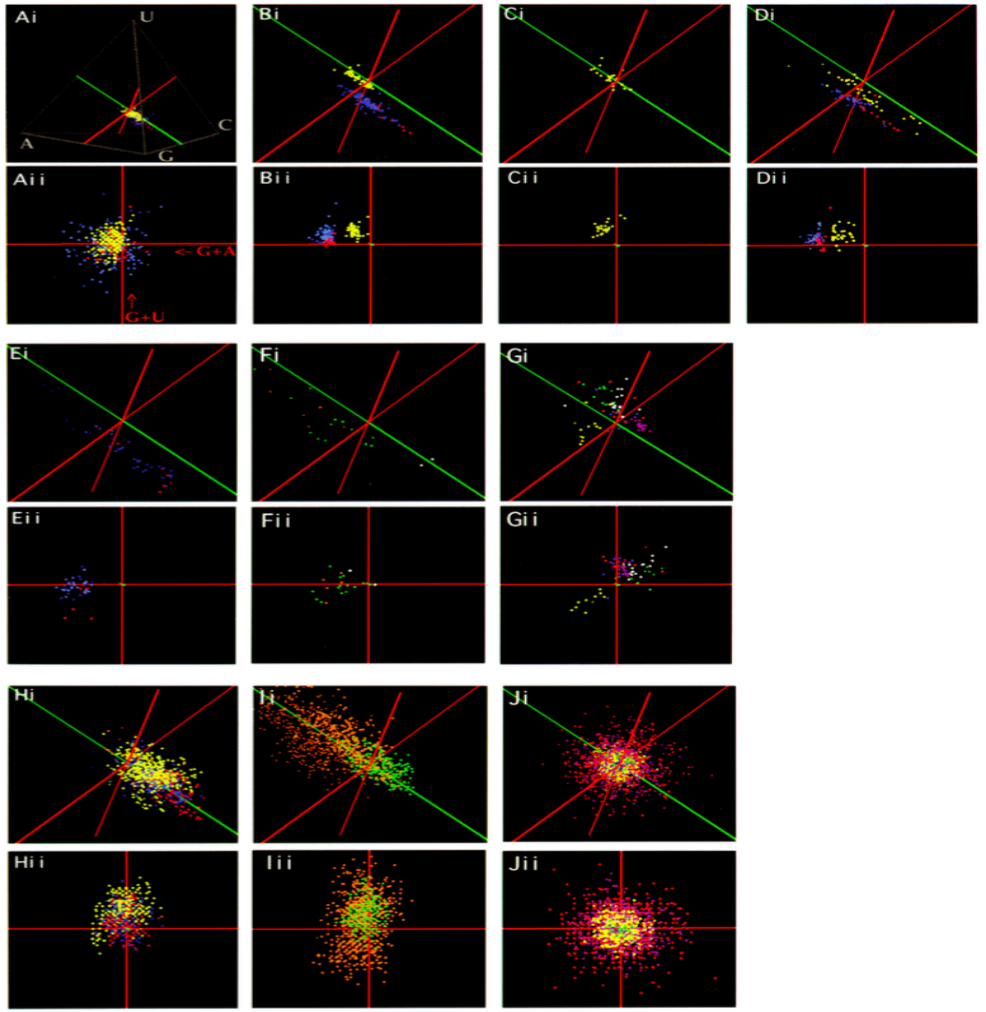

FIGURE 2. *(Legend on facing page.)*

ERIK'S PHD DATA STEWARDSHIP PLAN

ERIK'S PHD DATA STORAGE PLAN

ERIK'S PHD DATA STORAGE PLAN SPECIFIED LOCATION

EUREKA

MIT 1997

ERIK'S POST DOC RESEARCH

minus the background levels observed in the HSP in the control (Sar1-GDP–containing) incubation that prevents COPII vesicle formation. In the microsome control, the level of p115-SNARE associations was less than 0.1%.
46. C. M. Carr, E. Grote, M. Munson, F. M. Hughson, P. J. Novick, *J. Cell Biol.* **146**, 333 (1999).
47. C. Ungermann, B. J. Nichols, H. R. Pelham, W. Wickner, *J. Cell Biol.* **140**, 61 (1998).
48. E. Grote and P. J. Novick, *Mol. Biol. Cell* **10**, 4149 (1999).
49. P. Uetz *et al.*, *Nature* **403**, 623 (2000).
50. GST-SNARE proteins were expressed in bacteria and purified on glutathione-Sepharose beads using standard methods. Immobilized GST-SNARE protein (0.5 μM) was incubated with rat liver cytosol (20 mg) or purified recombinant p115 (0.5 μM) in 1 ml of NS buffer containing 1% BSA for 2 hours at 4°C with rotation. Beads were briefly spun (3000 rpm for 10 s) and sequentially washed three times with NS buffer and three times with NS buffer supplemented with 150 mM NaCl. Bound proteins were eluted three times in 50 μl of 50 mM tris-HCl (pH 8.5), 50 mM reduced glutathione, 150 mM NaCl, and 0.1% Triton X-100 for 15 min at 4°C with intermittent mixing, and elutes were pooled. Proteins were precipitated by MeOH/CH_3Cl and separated by SDS–polyacrylamide gel electrophoresis (PAGE) followed by immunoblotting using p115 mAb 13F12.
51. V. Rybin *et al.*, *Nature* **383**, 266 (1996).
52. K. G. Hardwick and H. R. Pelham, *J. Cell Biol.* **119**, 513 (1992).
53. A. P. Newman, M. E. Groesch, S. Ferro-Novick, *EMBO J.* **11**, 3609 (1992).
54. A. Spang and R. Schekman, *J. Cell Biol.* **143**, 589 (1998).
55. M. F. Rexach, M. Latterich, R. W. Schekman, *J. Cell Biol.* **126**, 1133 (1994).
56. A. Mayer and W. Wickner, *J. Cell Biol.* **136**, 307 (1997).
57. M. D. Turner, H. Plutner, W. E. Balch, *J. Biol. Chem.* **272**, 13479 (1997).
58. A. Price, D. Seals, W. Wickner, C. Ungermann, *J. Cell Biol.* **148**, 1231 (2000).
59. X. Cao and C. Barlowe, *J. Cell Biol.* **149**, 55 (2000).
60. G. G. Tall, H. Hama, D. B. DeWald, B. F. Horazdovsky, *Mol. Biol. Cell* **10**, 1873 (1999).
61. C. G. Burd, M. Peterson, C. R. Cowles, S. D. Emr, *Mol. Biol. Cell* **8**, 1089 (1997).
62. M. R. Peterson, C. G. Burd, S. D. Emr, *Curr. Biol.* **9**, 159 (1999).
63. M. G. Waters, D. O. Clary, J. E. Rothman, *J. Cell Biol.* **118**, 1015 (1992).
64. D. M. Walter, K. S. Paul, M. G. Waters, *J. Biol. Chem.* **273**, 29565 (1998).
65. N. Hui *et al.*, *Mol. Biol. Cell* **8**, 1777 (1997).
66. T. E. Kreis, *EMBO J.* **5**, 931 (1986).
67. H. Plutner, H. W. Davidson, J. Saraste, W. E. Balch, *J. Cell Biol.* **119**, 1097 (1992).
68. D. S. Nelson *et al.*, *J. Cell Biol.* **143**, 319 (1998).
69. We thank G. Waters for p115 cDNA and p115 mAbs; G. Warren for p97 and p47 antibodies; R. Scheller for rbet1, membrin, and sec22 cDNAs; H. Plutner for excellent technical assistance; and P. Tan for help during the initial phase of this work. Supported by NIH grants GM 33301 and GM42336 and National Cancer Institute grant CA58689 (W.E.B.), a NIH National Research Service Award (B.D.M.), and a Wellcome Trust International Traveling Fellowship (B.B.A.).

20 March 2000; accepted 22 May 2000

One Sequence, Two Ribozymes: Implications for the Emergence of New Ribozyme Folds

Erik A. Schultes and David P. Bartel*

We describe a single RNA sequence that can assume either of two ribozyme folds and catalyze the two respective reactions. The two ribozyme folds share no evolutionary history and are completely different, with no base pairs (and probably no hydrogen bonds) in common. Minor variants of this sequence are highly active for one or the other reaction, and can be accessed from prototype ribozymes through a series of neutral mutations. Thus, in the course of evolution, new RNA folds could arise from preexisting folds, without the need to carry inactive intermediate sequences. This raises the possibility that biological RNAs having no structural or functional similarity might share a common ancestry. Furthermore, functional and structural divergence might, in some cases, precede rather than follow gene duplication.

Related protein or RNA sequences with the same folded conformation can often perform very different biochemical functions, indicating that new biochemical functions can arise from preexisting folds. But what evolutionary mechanisms give rise to sequences with new macromolecular folds? When considering the origin of new folds, it is useful to picture, among all sequence possibilities, the distribution of sequences with a particular fold and function. This distribution can range very far in sequence space (*1*). For example, only seven nucleotides are strictly conserved among the group I self-splicing introns, yet secondary (and presumably tertiary) structure within the core of the ribozyme is preserved (*2*). Because these disparate isolates have the same fold and function, it is thought that they descended from a common ancestor through a series of mutational variants that were each functional. Hence, sequence heterogeneity among divergent isolates implies the existence of paths through sequence space that have allowed neutral drift from the ancestral sequence to each isolate. The set of all possible neutral paths composes a "neutral network," connecting in sequence space those widely dispersed sequences sharing a particular fold and activity, such that any sequence on the network can potentially access very distant sequences by neutral mutations (*3*–*5*).

Theoretical analyses using algorithms for predicting RNA secondary structure have suggested that different neutral networks are interwoven and can approach each other very closely (*3*, *5*–*8*). Of particular interest is whether ribozyme neutral networks approach each other so closely that they intersect. If so, a single sequence would be capable of folding into two different conformations, would have two different catalytic activities, and could access by neutral drift every sequence on both networks. With intersecting networks, RNAs with novel structures and activities could arise from previously existing ribozymes, without the need to carry nonfunctional sequences as evolutionary intermediates. Here, we explore the proximity of neutral networks experimentally, at the level of RNA function. We describe a close apposition of the neutral networks for the hepatitis delta virus (HDV) self-cleaving ribozyme and the class III self-ligating ribozyme.

In choosing the two ribozymes for this investigation, an important criterion was that they share no evolutionary history that might confound the evolutionary interpretations of our results. Choosing at least one artificial ribozyme ensured independent evolutionary histories. The class III ligase is a synthetic ribozyme isolated previously from a pool of random RNA sequences (*9*). It joins an oligonucleotide substrate to its 5′ terminus. The prototype ligase sequence (Fig. 1A) is a shortened version of the most active class III variant isolated after 10 cycles of in vitro selection and evolution. This minimal construct retains the activity of the full-length isolate (*10*). The HDV ribozyme carries out the site-specific self-cleavage reactions needed during the life cycle of HDV, a satellite virus of hepatitis B with a circular, single-stranded RNA genome (*11*). The prototype HDV construct for our study (Fig. 1B) is a shortened version of the antigenomic HDV ribozyme (*12*), which undergoes self-cleavage at a rate similar to that reported for other antigenomic constructs (*13*, *14*).

The prototype class III and HDV ribozymes have no more than the 25% sequence identity expected by chance and no fortuitous structural similarities that might favor an intersection of their two neutral networks. Nevertheless, sequences can be designed that simultaneously satisfy the base-pairing requirements

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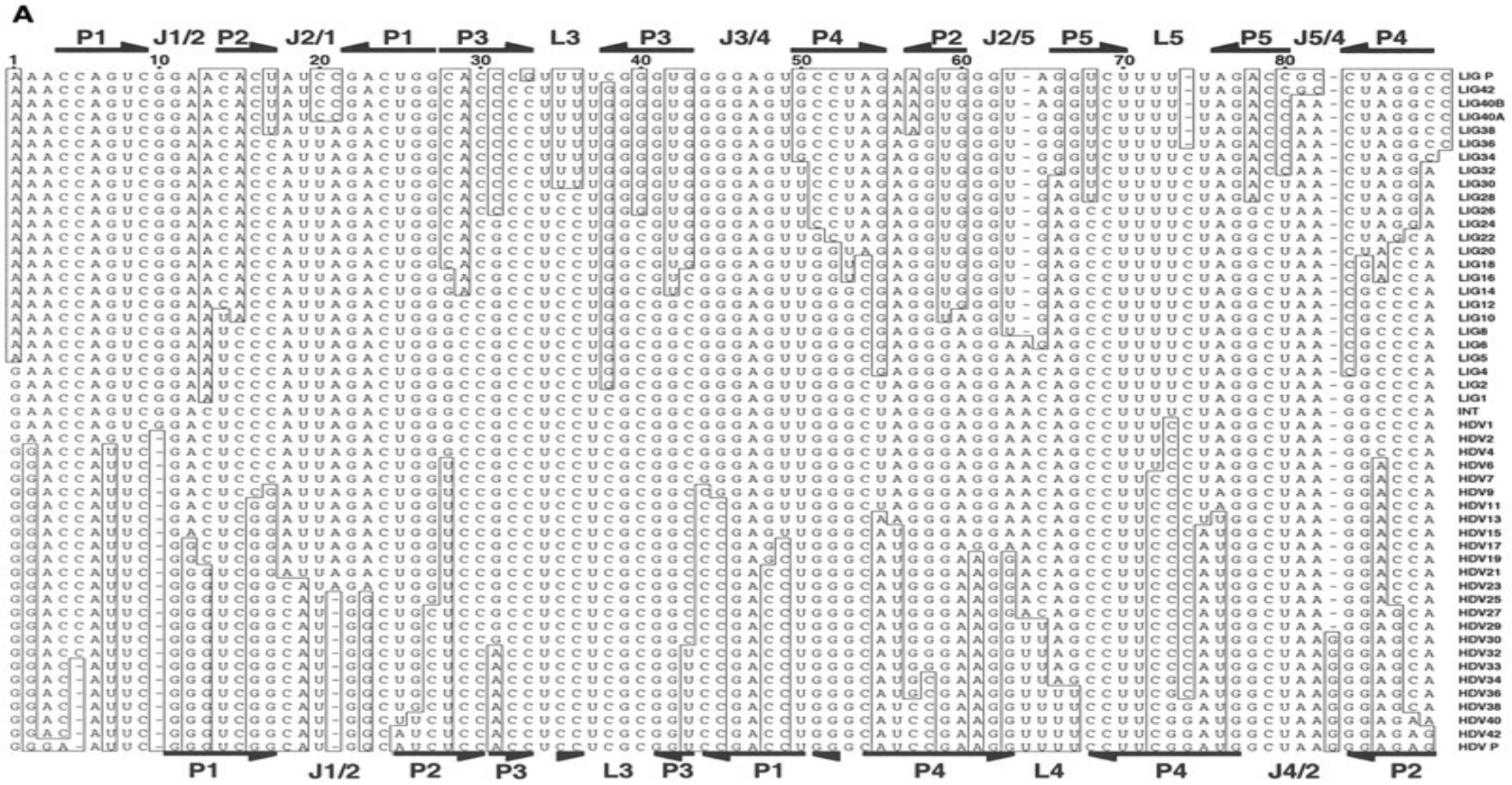
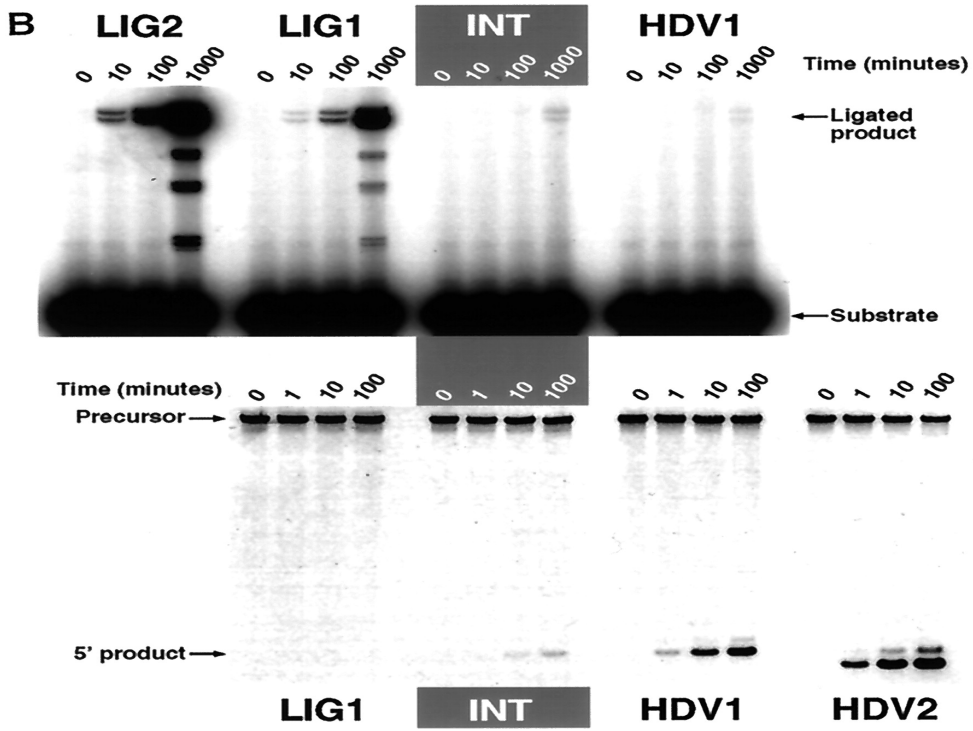


AND IMAGES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LIG2
LIG1
INT
HDV1
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Ligated product
Substrate
Time (minutes)
0 1 10 100
Precursor
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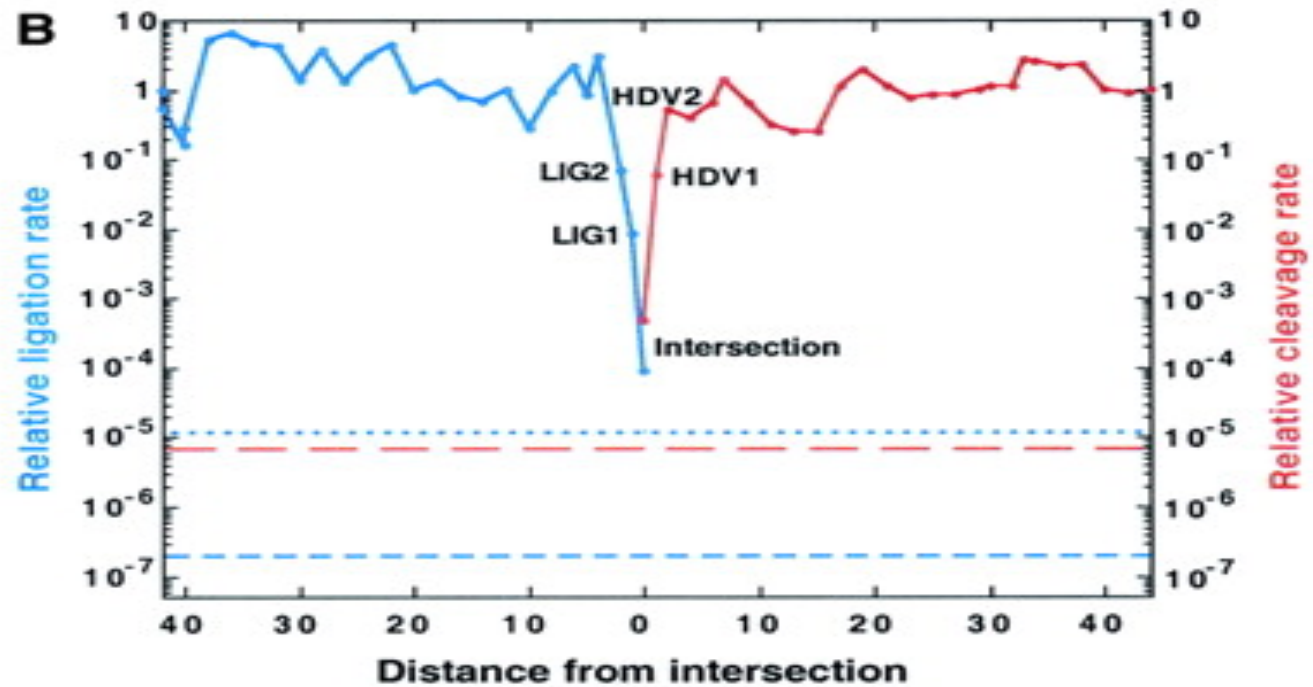
LIG1
INT
HDV1
HDV2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LIG2
HDV1
LIG1
Intersection
Relative ligation rate
Relative cleavage rate
Distance from intersection
40 30 20 10 0 10 20 30 40

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AND EVEN AVAILABLE ONLINE!

24. M. A. Tanner and T. R. Cech, *RNA* **2**, 74 (1996).
25. Supplemental data showing the predicted secondary structures of each construct (Fig. 3) and explaining the ligation activity of truncated ribozymes (Fig. 2B) are available at *Science* Online at www.sciencemag.org/feature/data/1050240.shl.
26. J. Maynard Smith, *Nature* **225**, 563 (1970).
27. The Intersection Theorem (*5*) states that there exists at least one intersection sequence for every pair of RNA secondary structures (usually as suboptimal conformations).
28. S. Ohno, *Evolution by Gene Duplication* (Springer-Verlag, New York, 1970).
29. D. L. Minor Jr. and P. S. Kim, *Nature* **380**, 730 (1996).
30. M. H. J. Cordes, N. P. Walsh, C. J. McKnight, R. T. Sauer, *Science* **284**, 325 (1999).
31. X. Ye *et al.*, *Chem. Biol.* **6**, 657 (1999).

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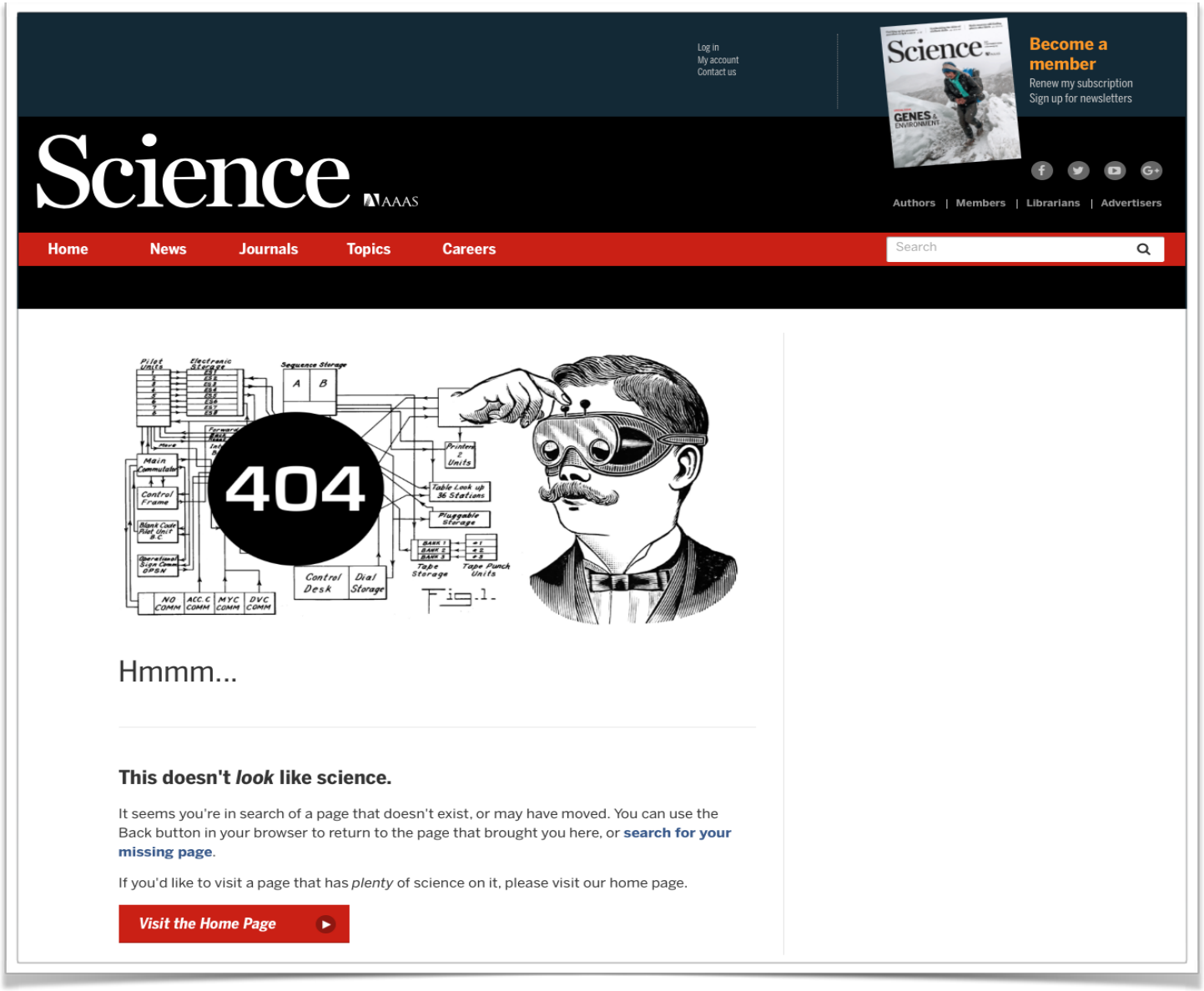
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It seems you're in search of a page that doesn't exist, or may have moved. You can use the Back button in your browser to return to the page that brought you here, or search for your missing page.
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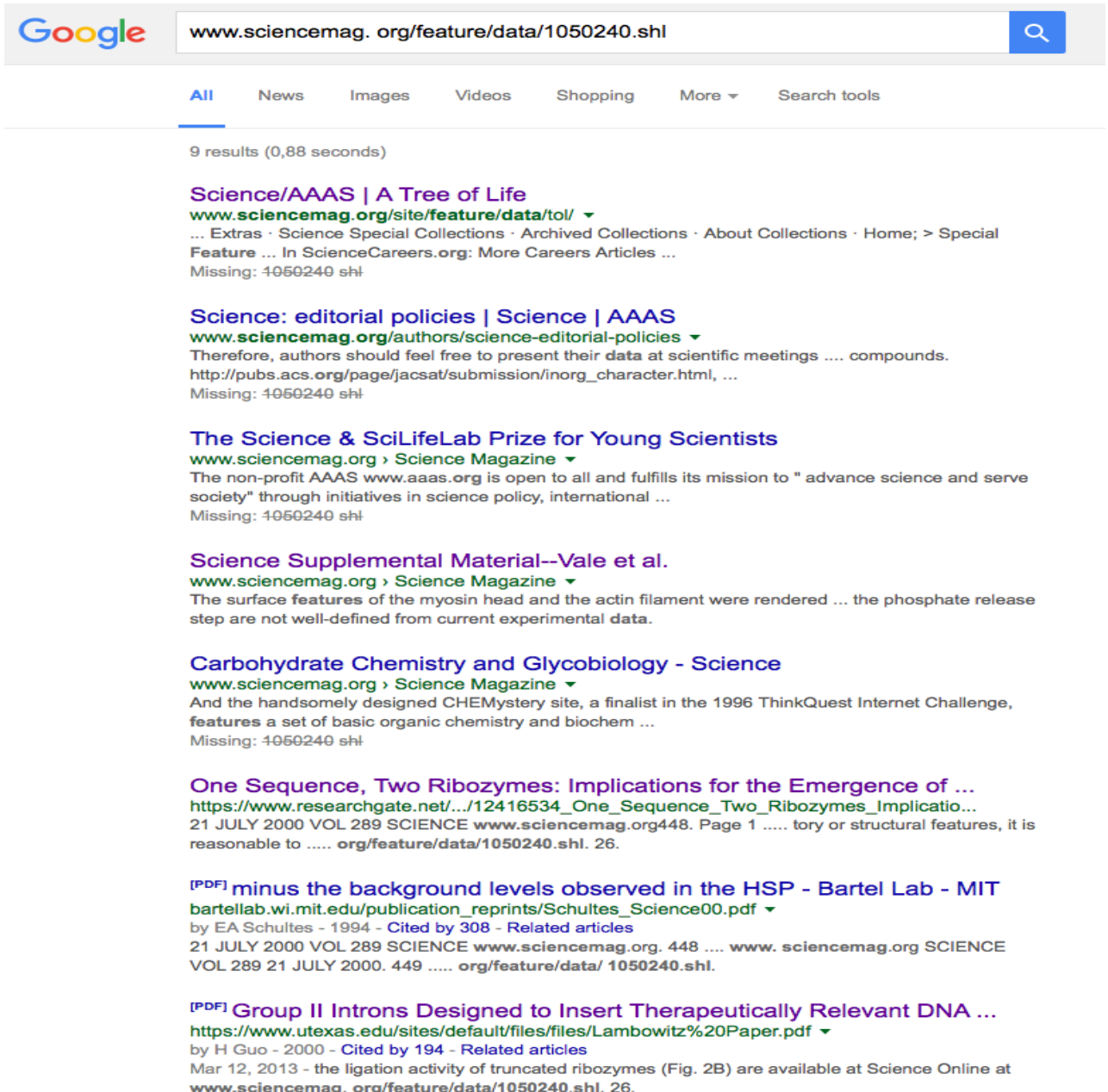
BUT THERE IS GOOGLE NOW



SCIENCE MUST HAVE THEIR ACT TOGETHER?

From: **Erik Schultes** erik.schultes@dtls.nl
Subject: Supplemental Data
Date: October 1, 2016 at 11:20 AM
To: science_editors@aaas.org

ES

To whom it may concern -

I authored this article in 2000:
http://science.sciencemag.org/content/289/5478/448.article-info

At the time, we had submitted Supplemental Data.

However, on the webpage supporting the paper, I no longer see a link to the Supplemental Data.

In endnote 25 of the paper, I see this link to the Supplemental Data:
www.sciencemag.org/feature/data/l050240.shl

However, this link appears to be broken, and redirects to a 404 page:
http://www.sciencemag.org/feature/data/l050240.shl

So I have a few questions:

(1) Is it possible, one way or another, to obtain or access the original Supplemental Data ?

(2) My immediate interest is not so much at the content level, but more at the 'Data Stewardship' level. Recently, my colleagues and I conducted a LERU Summer School on Data Stewardship (in Leiden, the Netherlands, see http://www.dtls.nl/fair-data/fair-data-training/leru-summer-school/). I actually used this 'broken link' as a case study for the kinds of problems we all face in scholarly data stewardship. So I'm wondering, can you tell me when and why the link was broken ? It is instructive for us to better understand the challenges that publishers face these days.

Many thanks in advance,

Best regards,

Erik

--
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FAIR Data Scientific Projects Lead

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NO REPLY TO DATE!

ABSTRACT FULL TEXT

One Sequence, Two Ribozymes: Implications for the Emergence of New Ribozyme Folds

Erik A. Schultes and David P. Bartel

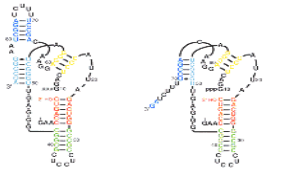
Supplementary Material

Supplemental Figure 1. Secondary structures of the ribozyme variants aligned in Fig. 3A. Accumulated changes from the intersection sequence are indicated (red and blue residues, with blue identifying residues changed at the step indicated by an arrow; dashes mark sites of point deletions). Self–ligation and self–cleavage rates (min^{-1}) are listed below the name of each construct.

Larger, segmented version of this image (new window – 160K JPEG images) | Full version of this image (827K JPEG file)] | Download PDF of this image (9MB)

Explanation of the ligation activity of truncated ribozymes.
For LIG2, LIG1, INT, and HDV1, the ligation products are represented by two bands in Fig. 2B (top panel), due to unanticipated ligation activity of truncated ribozyme molecules in addition to the activity of full–length RNA. On lower percentage gels, the faster–migrating product band resolves into seven distinct bands, corresponding to a loss of 9 to 15 nucleotides at the ribozyme 3′ terminus. These truncated ribozymes appear to adopt a class III–like fold as evidenced by the following: (i) They produce 2′–linkages. (ii) Nucleotide substitutions known to favor the class III ligase function and fold (C13A and C38G) lead to parallel increases in the activity of the truncated RNAs (Fig 2). (iii) Constructs LIG2, LIG1, INT, and HDV1 have fortuitous potential base pairing between segments corresponding to G51–U55 and A66–U70 in Fig. 2A. For the truncated molecules, this base pairing would lead to a fold that has all the class III features except the P4 stem–loop (Web fig. 2). The fortuitous potential pairing is not present in the original class III ligase isolates or in the constructs of the ligase neutral path (LIG4–LIG P in Fig. 3), explaining why only one product band was observed for LIG4–LIG P. (iv) The Pb(II)–cleavage pattern of the ligation product of truncated LIG2 was consistent with the formation of G51–U55:A66–U70 pairing, whereas probing of full–length LIG2, LIG1, and INT products confirmed formation of the anticipated P4 and P5 stems. None of the fortuitous pairs are present in the HDV secondary structure, and thus the alternative ligase fold, like the prototype ligase fold, has no base pairs in common with the HDV fold. The 3′ truncations contaminating the ribozyme preparations of LIG2, LIG1, INT, and HDV1 can generate over half of the ligated product (Fig. 2B), even though they compose only a minor fraction of the ribozyme preparation (presumably arising from RNA degradation or premature transcription termination). For these truncated molecules, a more optimal P5 might more than offset the loss of P4.

Supplemental Figure 2. The intersection sequence and a truncated form of this sequence assuming the class III ligase fold and the class III ligase–like fold, respectively.



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Science. ISSN 0036–8075 (print), 1095–9203 (online)

FIRST: THE DATA STEWARDSHIP PART

Stewardship is an ethic that embodies the responsible planning and management of resources. Can be applied to nature, economics, health, property, information, theology, etc.

https://en.wikipedia.org/wiki/Stewardship

Data Stewardship: A plan for maximizing the re-use of data.

- exposing versus publishing data
- hiding versus securing data
- open versus closed data
- licensing and fees
- authors versus owners (eg patient privacy)
- who paid for the data ?
- big data scaling: storage, compute
- serving (e.g. 24/7) versus archiving
- machine interoperation (ontology engineering, data modeling)
- human interoperation (24 EU languages)

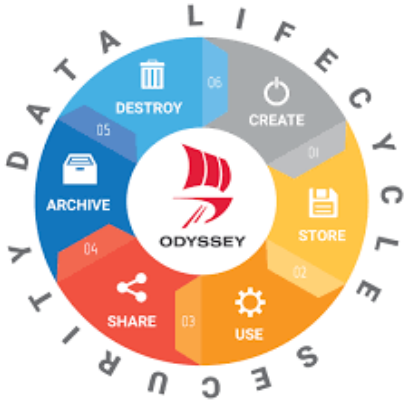
Data Stewardship: A plan for maximizing the re-use of data.

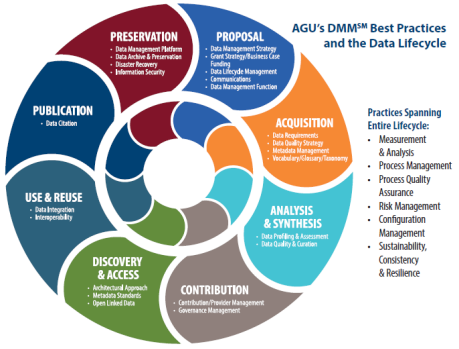
Requires:

- Systematic organisational changes (policy, mandates, budgets
- New Technologies
- Training for new profession

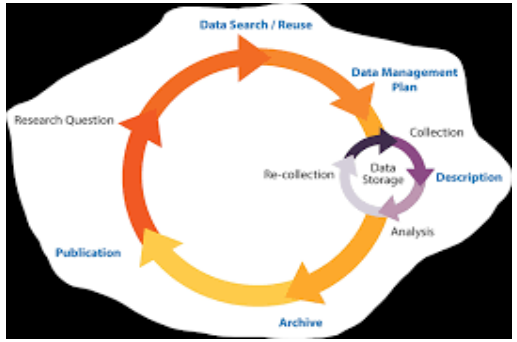
Data Stewardship: A plan for maximizing the re-use of data.

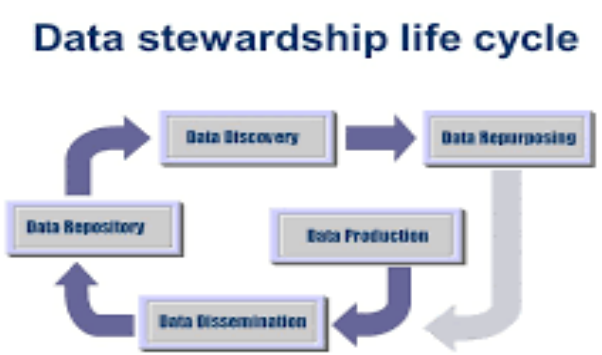
DATA STEWARDSHIP: GETTING SYSTEMATIC

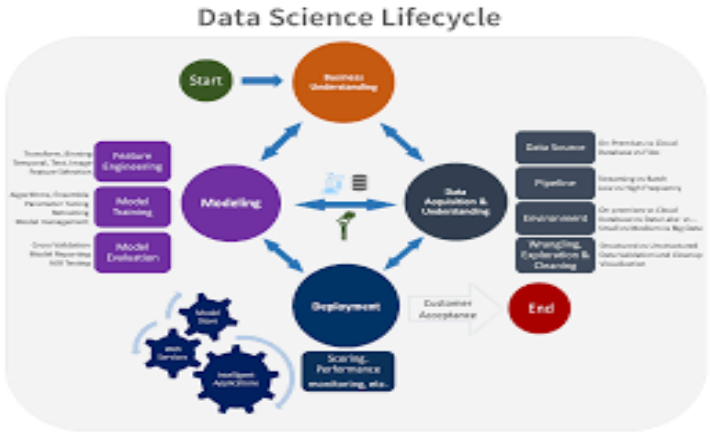


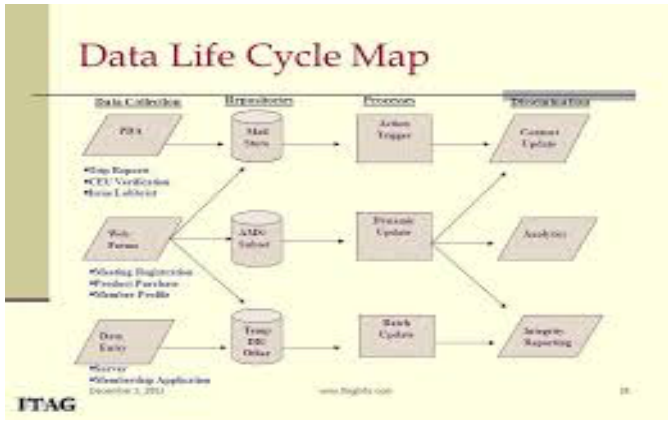


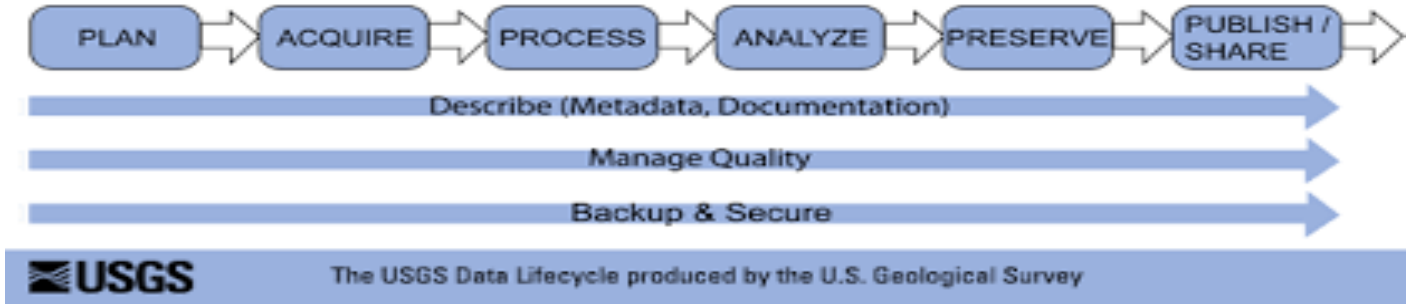
DATA STEWARDSHIP: GETTING SYSTEMATIC

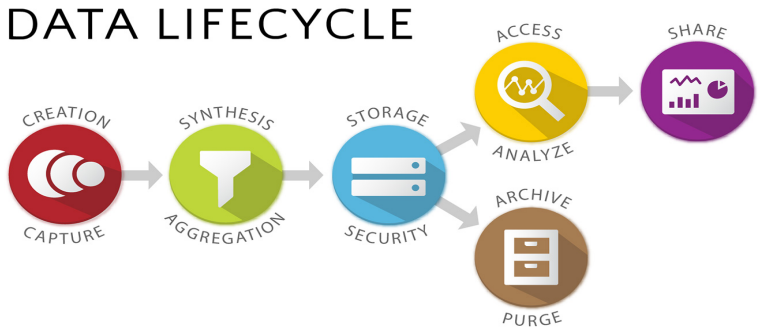




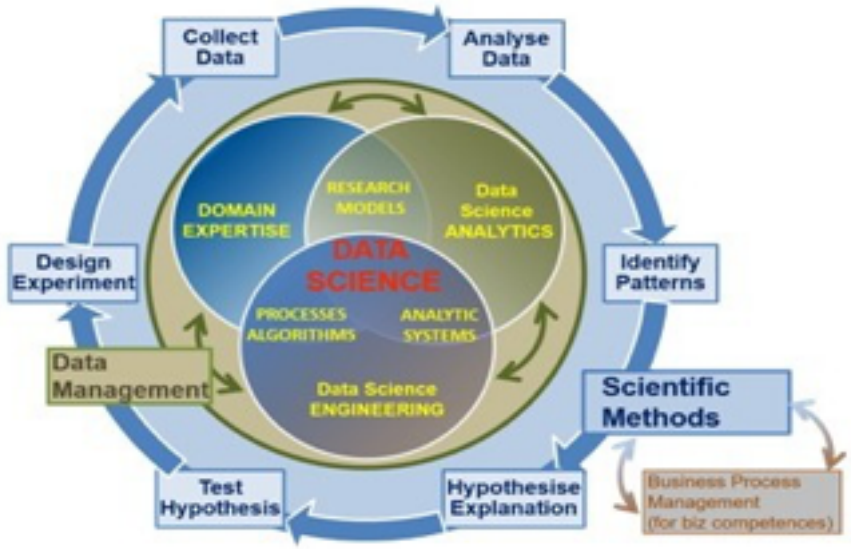


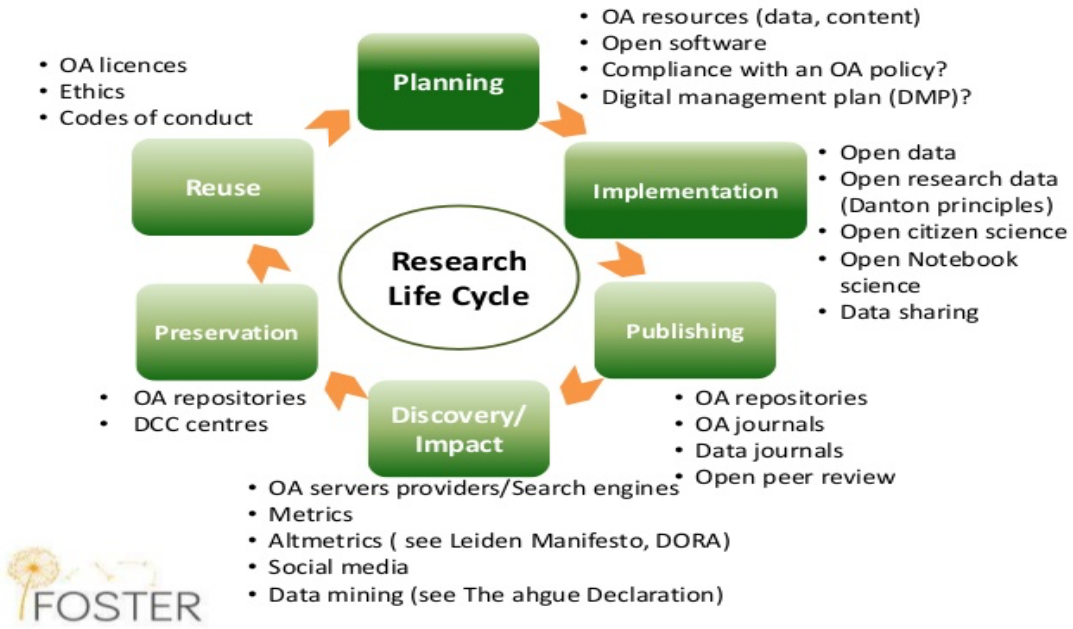






DATA STEWARDSHIP: GETTING SYSTEMATIC





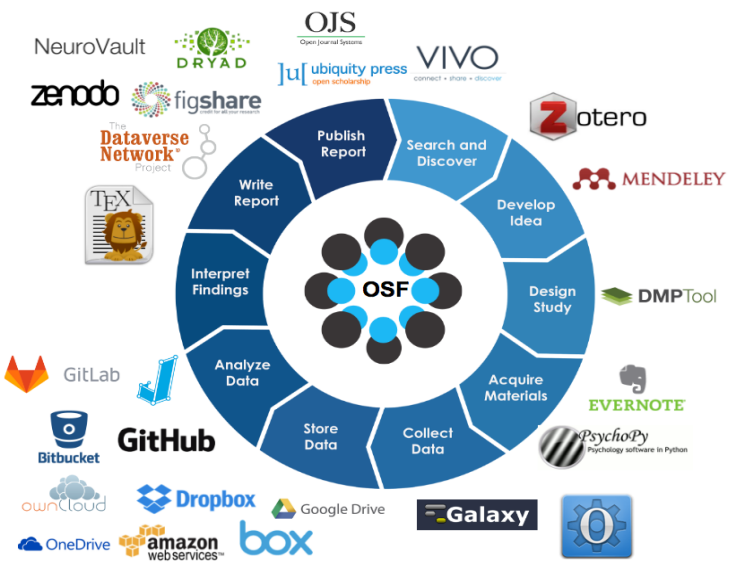
FOSTER: practical implementation of Open Science in Horizon 2020 and beyond

https://www.fosteropenscience.eu/

EDISON Data Science Framework to define the Data Science Profession

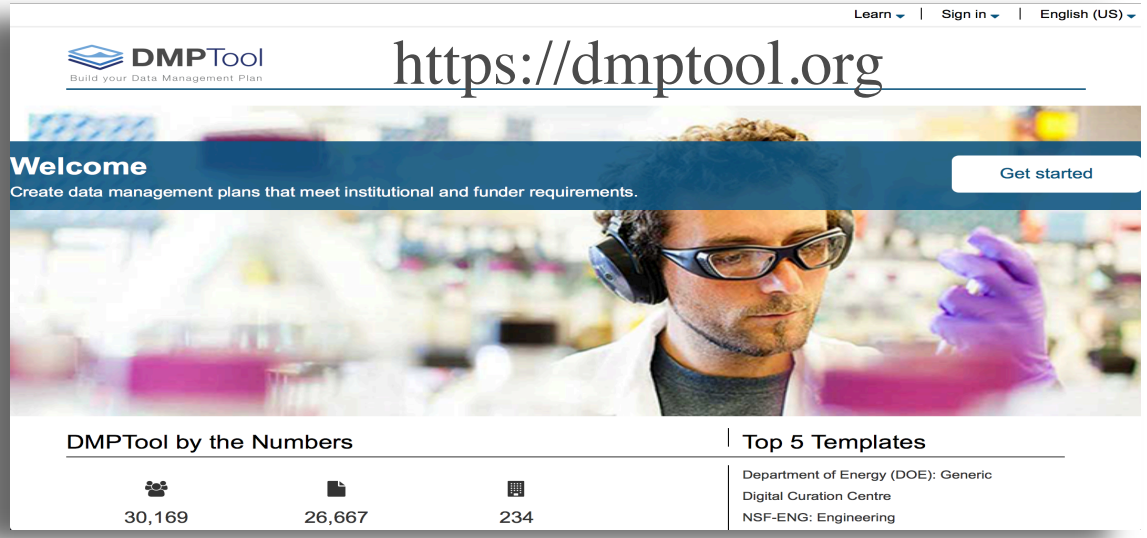
http://edison-project.eu/edison

DATA STEWARDSHIP: GETTING SYSTEMATIC

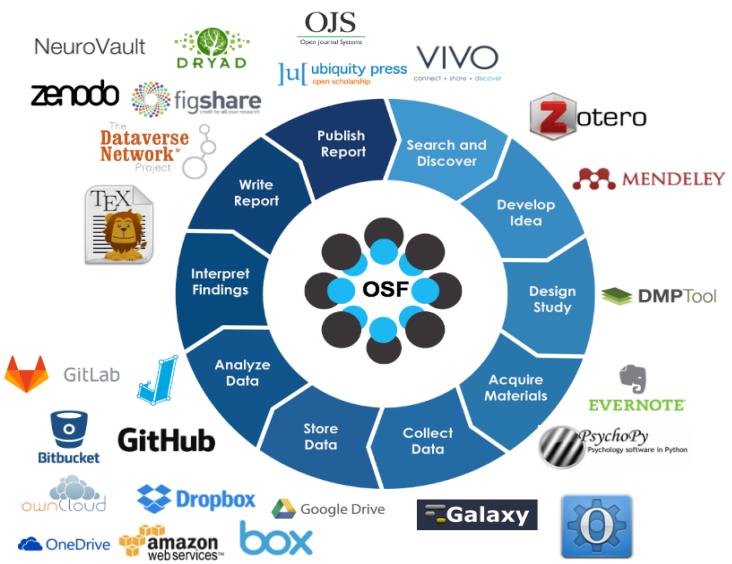


Center of Open Science, providing tools, training, support and advocacy for changes in incentives to make research investment go farther, faster.

https://cos.io



DATA STEWARDSHIP: GETTING SYSTEMATIC



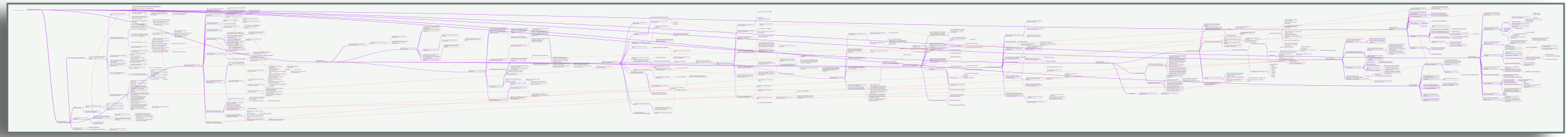
Center of Open Science, providing tools, training, support and advocacy for changes in incentives to make research investment go farther, faster.

https://cos.io

The Data Stewardship Mind Map

Rob Hooft

DTL
DUTCH TECHCENTRE FOR LIFE SCIENCES



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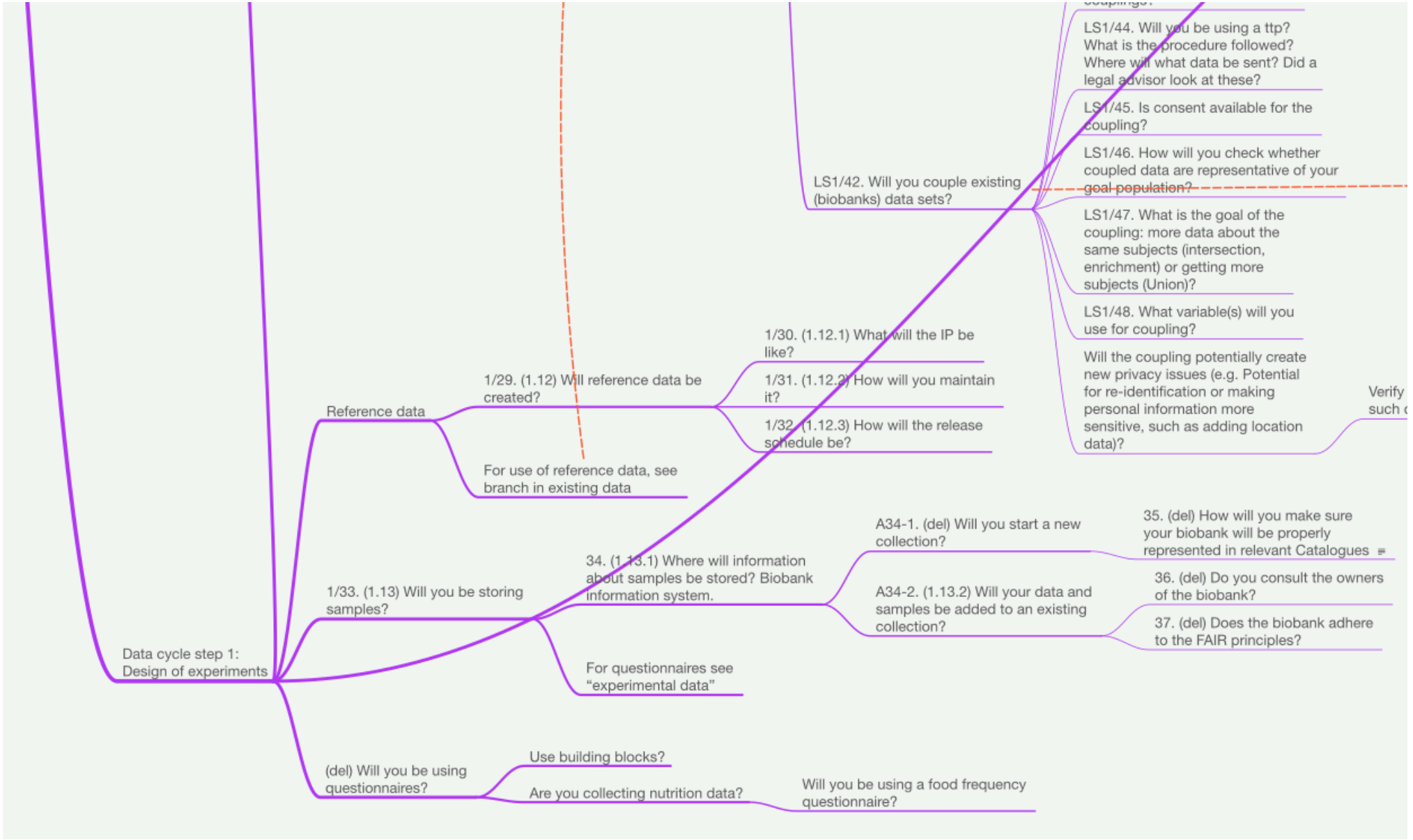
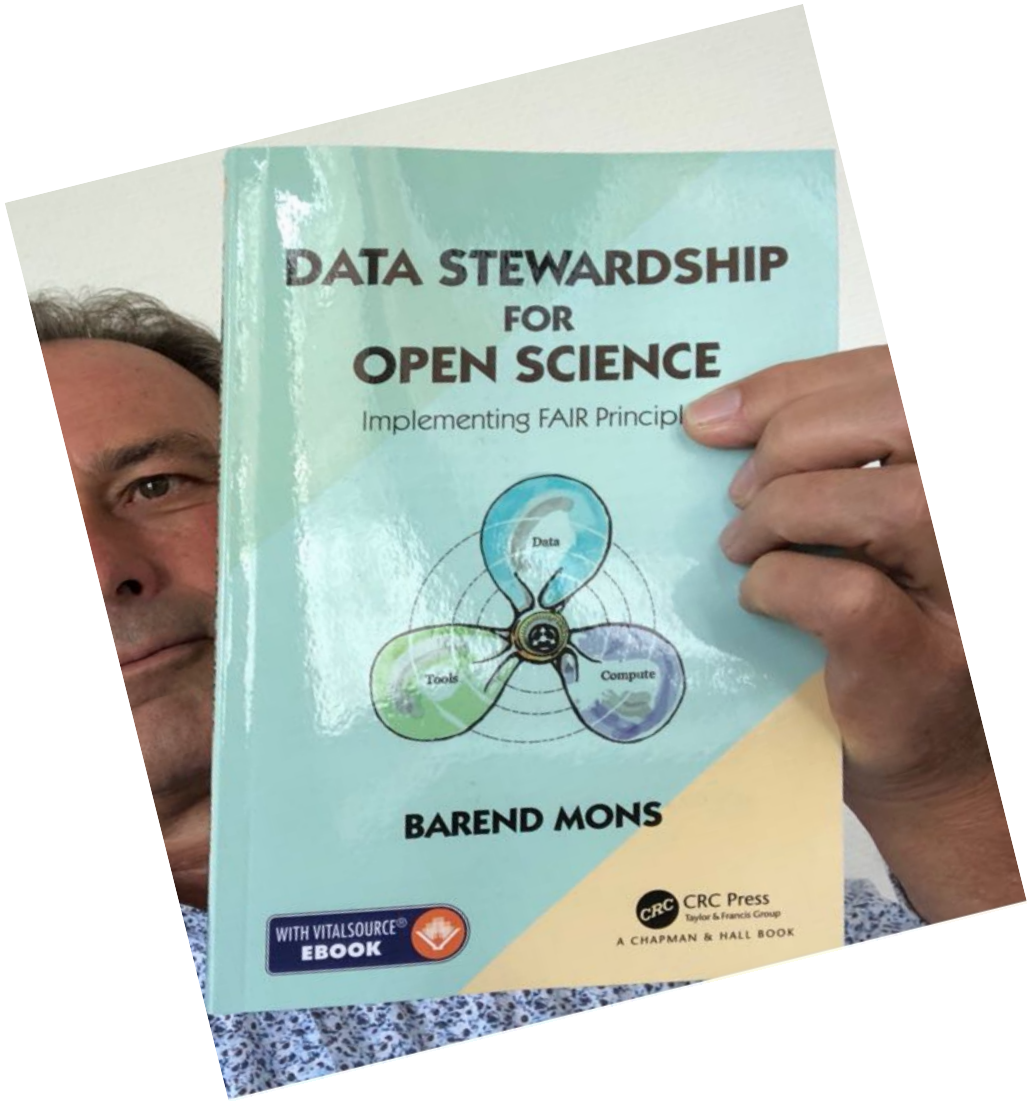
THE DATA STEWARDSHIP MIND MAP



Rob Hooft

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP



Data Cycle Step 1: Design of Experiment

Data Cycle Step 2: Data Design and Planning

Data Cycle Step 3: Data Capture (Equipment)

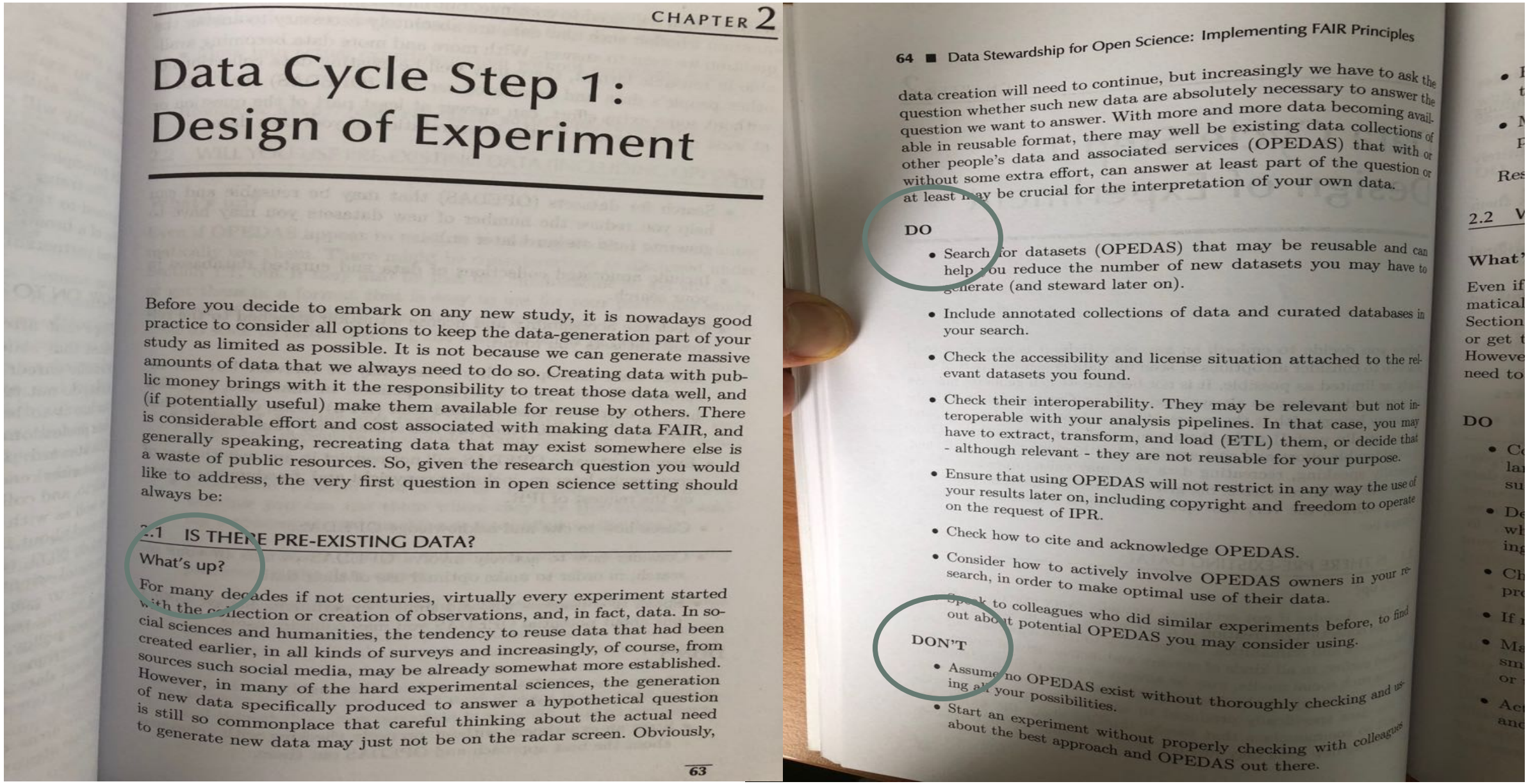
Data Cycle Step 4: Data Processing and Curation

Data Cycle Step 5: Data Linking and Integration

Data Cycle Step 6: Data Analysis and Interpretation

Data Cycle Step 7: Publishing

DATA STEWARDSHIP: PLANNING TOOLS



CHAPTER 2

Data Cycle Step 1: Design of Experiment

Before you decide to embark on any new study, it is nowadays good practice to consider all options to keep the data-generation part of your study as limited as possible. It is not because we can generate massive amounts of data that we always need to do so. Creating data with public money brings with it the responsibility to treat those data well, and (if potentially useful) make them available for reuse by others. There is considerable effort and cost associated with making data FAIR, and generally speaking, recreating data that may exist somewhere else is a waste of public resources. So, given the research question you would like to address, the very first question in open science setting should always be:

2.1 IS THERE PRE-EXISTING DATA?

What's up?

For many decades if not centuries, virtually every experiment started with the collection or creation of observations, and, in fact, data. In social sciences and humanities, the tendency to reuse data that had been created earlier, in all kinds of surveys and increasingly, of course, from sources such social media, may be already somewhat more established. However, in many of the hard experimental sciences, the generation of new data specifically produced to answer a hypothetical question is still so commonplace that careful thinking about the actual need to generate new data may just not be on the radar screen. Obviously,

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64 ■ Data Stewardship for Open Science: Implementing FAIR Principles

data creation will need to continue, but increasingly we have to ask the question whether such new data are absolutely necessary to answer the question we want to answer. With more and more data becoming available in reusable format, there may well be existing data collections or other people's data and associated services (OPEDAS) that with or without some extra effort, can answer at least part of the question or at least may be crucial for the interpretation of your own data.

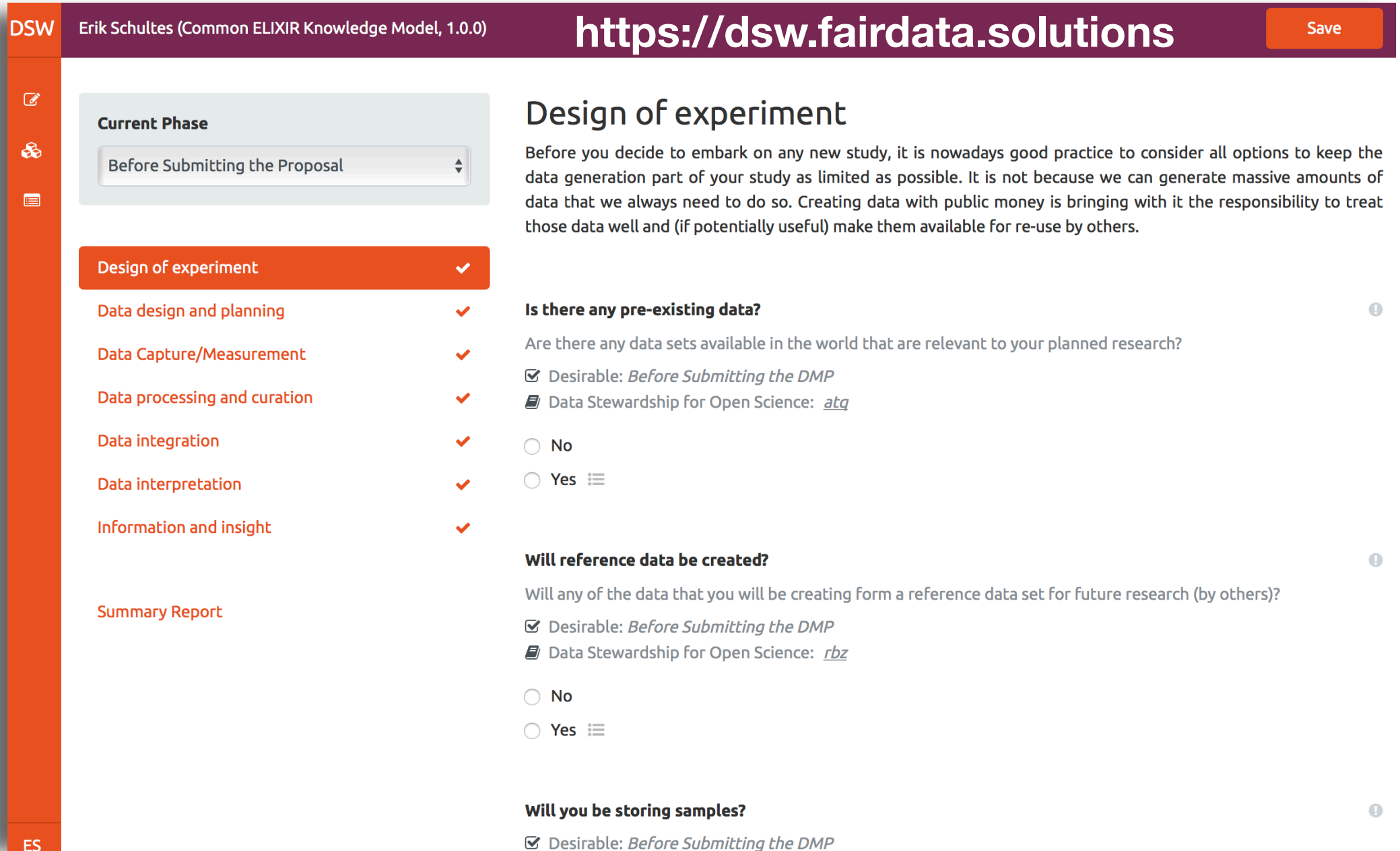
DO

- Search for datasets (OPEDAS) that may be reusable and can help you reduce the number of new datasets you may have to generate (and steward later on).
- Include annotated collections of data and curated databases in your search.
- Check the accessibility and license situation attached to the relevant datasets you found.
- Check their interoperability. They may be relevant but not interoperable with your analysis pipelines. In that case, you may have to extract, transform, and load (ETL) them, or decide that - although relevant - they are not reusable for your purpose.
- Ensure that using OPEDAS will not restrict in any way the use of your results later on, including copyright and freedom to operate on the request of IPR.
- Check how to cite and acknowledge OPEDAS.
- Consider how to actively involve OPEDAS owners in your research, in order to make optimal use of their data.
- Speak to colleagues who did similar experiments before, to find out about potential OPEDAS you may consider using.

DON'T

- Assume no OPEDAS exist without thoroughly checking and using all your possibilities.
- Start an experiment without properly checking with colleagues about the best approach and OPEDAS out there.

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP



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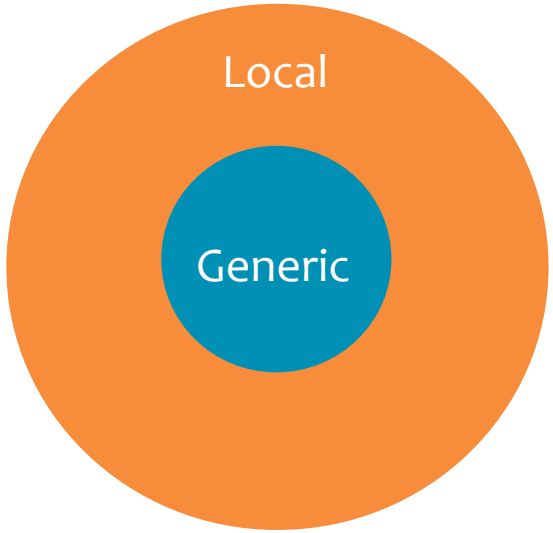
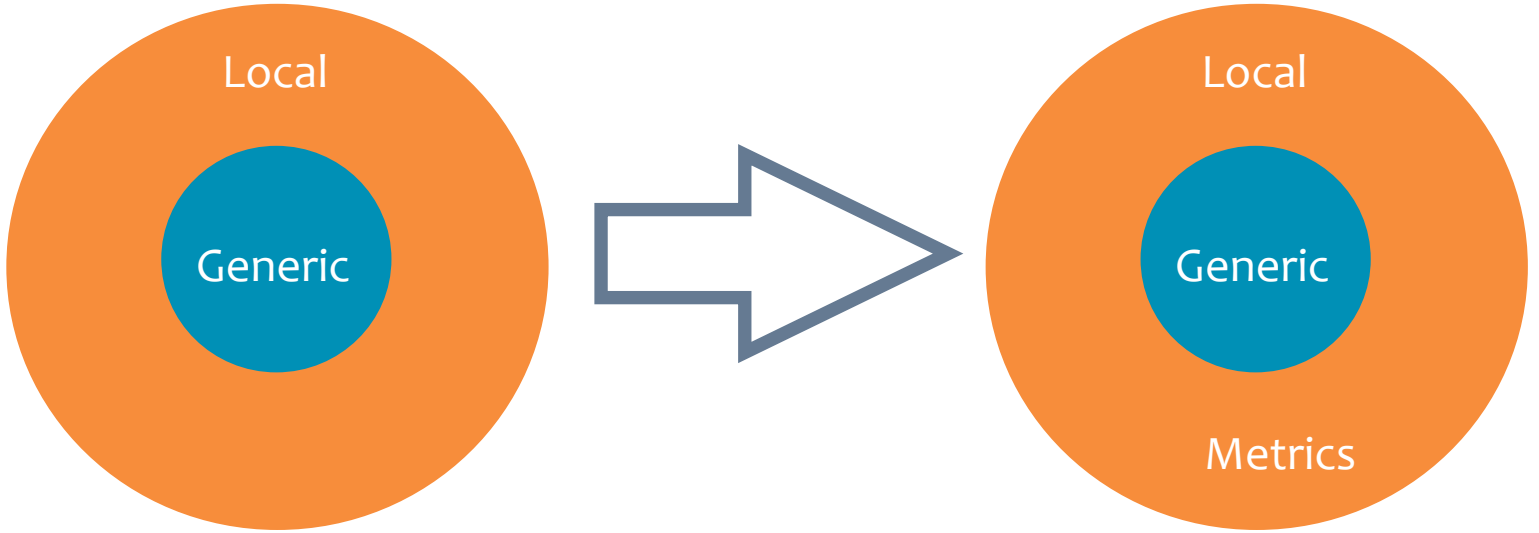


ELIXIR Data Stewardship Knowledge Model

https://github.com/DataStewardshipWizard/ds-km

DS Wizard + Metrics Hackathon, Leiden, July 2-4



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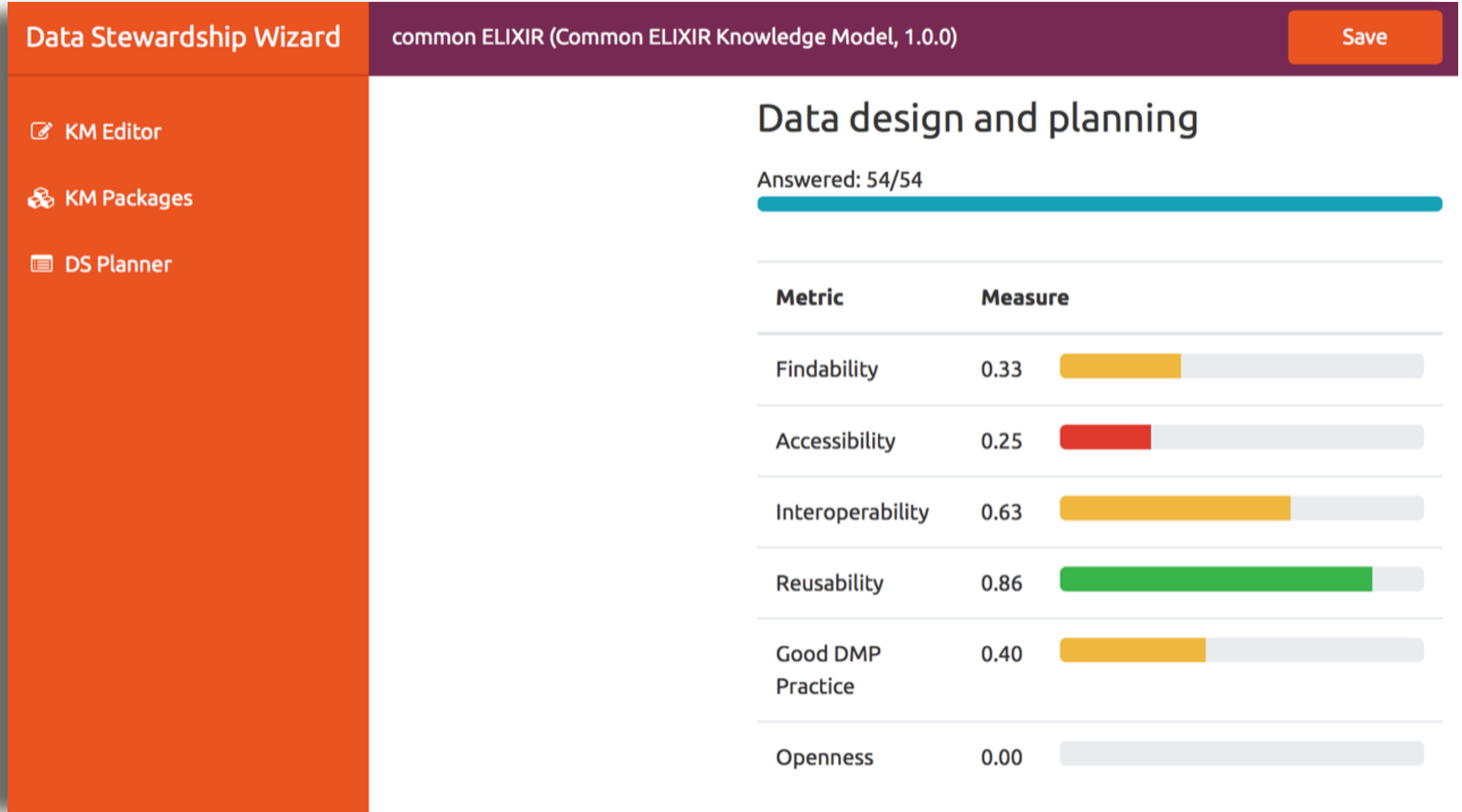

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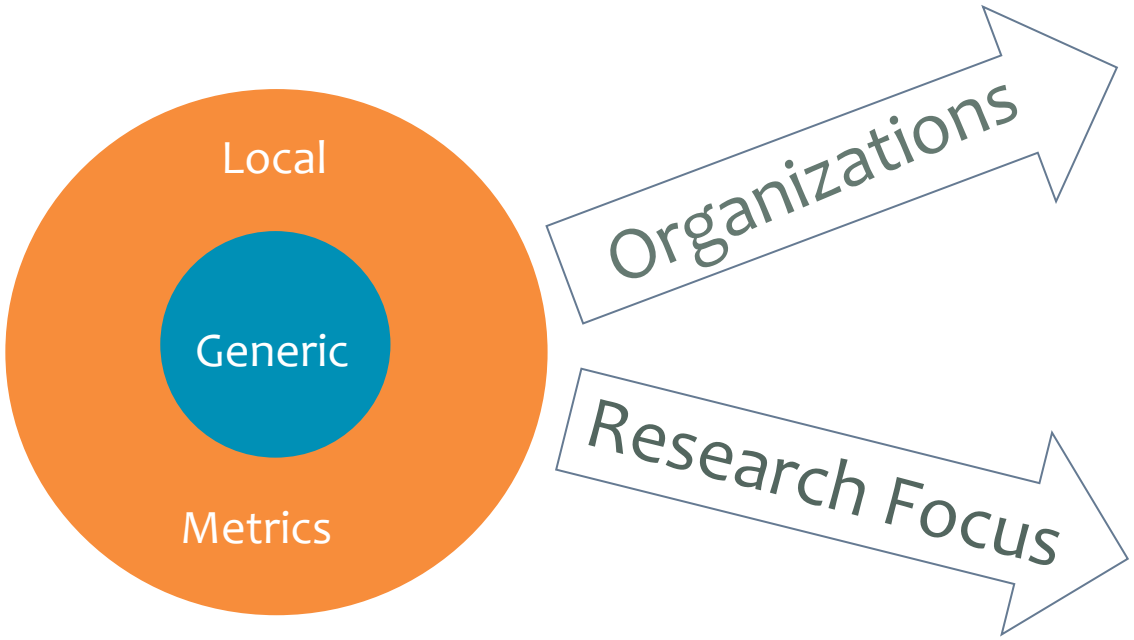

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GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP

Findable:

F1 (meta)data are assigned a globally unique and persistent identifier;

F2 data are described with rich metadata;

F3 metadata clearly and explicitly include the identifier of the data it describes;

F4 (meta)data are registered or indexed in a searchable resource;

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;

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;

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;

R1.2 (meta)data are associated with detailed provenance;

R1.3 (meta)data meet domain-relevant community standards;

Measuring FAIRness
http://fairmetrics.org

Framework for authoring FAIR Metrics

FAIR Metrics

The FAIR Metrics Group took-on the challenge of designing a framework for evaluating "FAIRness".

Discoverability and reusability are not abstract concepts, but imply concrete behaviors and properties that must hold true for the fulfillment of the FAIR objectives. Given this, it must therefore be possible to precisely define a measurable set of properties and behaviors that assess FAIRness. Over the short 1 month lifespan of the FAIR Metrics Working Group, we have created a cogent framework for developing FAIR metrics manifested as a simple form with 8 questions that structures fruitful conversations about proposed metrics.

Our approach recognizes that the diversity in opinion must play a key role in crafting fair and effective FAIR guidelines. Communities must not only understand what is meant by FAIR, but must also be able to monitor the FAIRness of their digital resources, in a realistic, but quantitative manner. We recognize that what is considered FAIR in one community may be quite different from FAIRness in another community - different community norms and practices make this a certainty! As such, our approach focuses on the mechanism by which metrics can be created by community members themselves, rather than attempting to create a set of one-size-fits-all metrics to apply to every resource.

FAIR Metrics GitHub

FAIR Metrics Paper

Metrics Process

Metrics Authoring Framework

Metrics Form

About Us

Measuring FAIRness
http://fairmetrics.org

Framework for authoring FAIR Metrics

www.nature.com/scientificdata

SCIENTIFIC DATA

OPEN

Comment: A design framework and exemplar metrics for FAIRness

Mark D. Wilkinson[1], Susanna-Assunta Sansone[2], Erik Schultes[3], Peter Doorn[4], Luiz Olavo Bonino da Silva Santos[5,6] & Michel Dumontier[7]

Received: 28 November 2017
Accepted: 9 May 2018

The FAIR Principles[1] (https://doi.org/10.25504/FAIRsharing.WWI10U) provide guidelines for the publication of digital resources such as datasets, code, workflows, and research objects, in a manner that makes them Findable, Accessible, Interoperable, and Reusable (FAIR). The Principles have rapidly been

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP

Measuring FAIRness
http://fairmetrics.org

FM	Question	Dataverse	Dryad	Nano-pub	Zenodo	Yale ISPS	Figshare	Broad's SCP	SeaData Net's CDI	Wikidata
IRI Exists	1	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI
F1A	2	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI
F1B	3	IRI	IRI	IRI	NRP	none	IRI	IRI	IRI	IRI
F2A	4A	IRI	IRI	IRI	IRI	none	none	IRI	IRI	IRI
F2A	4B	IRI	none	IRI	IRI	"Multiple"	none	IRI	IRI	IRI
F3	5A	IRI	IRI	IRI	IRI	none	NRP	IRI	IRI	IRI
F3	5B	IRI	IRI	IRI	IRI	IRI	IRI	IRI	none	IRI
F4	6A	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI
F4	6B	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI
A1.1	7A	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI	IRI
A1.1	7B	true	true	true	true	true	true	true	true	true
A1.1	7C	true	true	true	true	true	true	true	true	true
A1.2	8A	false	false	false	false	false	false	false	true	false
A1.2	8B	N/A	N/A	N/A	N/A	NRP	NRP	NRP	link	N/A
A2	9	IRI	IRI	none	IRI	none	IRI	none	IRI	NRP
I1	10	IRI	IRI	IRI	IRI	none	none	NRP	IRI	IRI
I2	11	IRI	IRI	IRI	none	none	none	IRI	IRI	IRI
I3	12	NRP	IRI	IRI	none	none	none	NRP	NRP	IRI
R1.1	13	IRI	IRI	IRI	IRI	IRI	IRI	NRP	IRI	IRI
R1.2	14A	IRI	IRI	IRI	IRI	none	none		NRP	NRP

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP

New Results

Previous Next

Evaluating FAIR-Compliance Through an Objective, Automated, Community-Governed Framework

Mark D Wilkinson, Michel Dumontier, Susanna-Assunta Sansone, Luiz Olavo Bonino da Silva Santos, Mario Prieto, Julian Gautier, Peter McQuilton,

Posted September 16, 2018.

14 CORE METRICS

Findable:

FM-F1A FM-F1B

F1 (meta)data are assigned a globally unique and persistent identifier;

FM-F2

F2 data are described with rich metadata;

FM-F3

F3 metadata clearly and explicitly include the identifier of the data it describes;

FM-F4

F4 (meta)data are registered or indexed in a searchable resource;

Accessible:

A1 (meta)data are retrievable by their identifier using a standardized communications protocol;

FM-A1.1

A1.1 the protocol is open, free, and universally implementable;

FM-A1.2

A1.2 the protocol allows for an authentication and authorization procedure, where necessary;

FM-A2

A2 metadata are accessible, even when the data are no longer available;

Interoperable:

I1 (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.

FM-I1

FM-I2

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FM-I3

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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;

FM-R1.1

R1.2 (meta)data are associated with detailed provenance;

FM-R1.2

R1.3 (meta)data meet domain-relevant community standards;

FM-R1.3

Sci. Data 3:160018 doi: 10.1038/sdata.2016.18 (2016)

http://fairmetrics.org

https://github.com/FAIRMetrics/Metrics/blob/master/ALL.pdf

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP

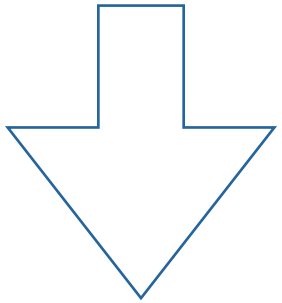
The FAIR Metrics Template

FIELD	*DESCRIPTION*
Metric Identifier	FM-F1B: `https://purl.org/fair-metrics/FM_F1B`
Metric Name	Identifier persistence
To which principle does it apply?	F1
What is being measured?	Whether there is a policy that describes what the provider will do in the event an identifier scheme becomes deprecated.
Why should we measure it?	The change to an identifier scheme will have widespread implications for resource lookup, linking, and data sharing. Providers of digital resources must ensure that they have a policy to manage changes in their identifier scheme, with a specific emphasis on maintaining/redirecting previously generated identifiers.
What must be provided?	A URL that resolves to a document containing the relevant policy.
How do we measure it?	Use an HTTP GET on URL provided.
What is a valid result?	Present (a 200,202,203 or 206 HTTP response after resolving all and any prior redirects. e.g. 301 -> 302 -> 200 OK.) or Absent (any other HTTP code)
For which digital resource(s) is this relevant?	All
Comments	A first version of this metric would focus on just checking a URL that resolves to a document. We can't verify that

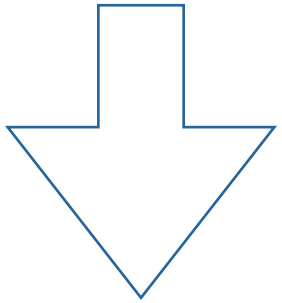
FAIR Metrics Upgrades

Example: FM-F1B, Identifier Persistence

v1.0 **checks** for HTTP 200 return



v2.0 **validates** a standard RDF persistence policy



v3.0 **scores** multiple parameters of persistence policy

The “15th” FAIR Metric

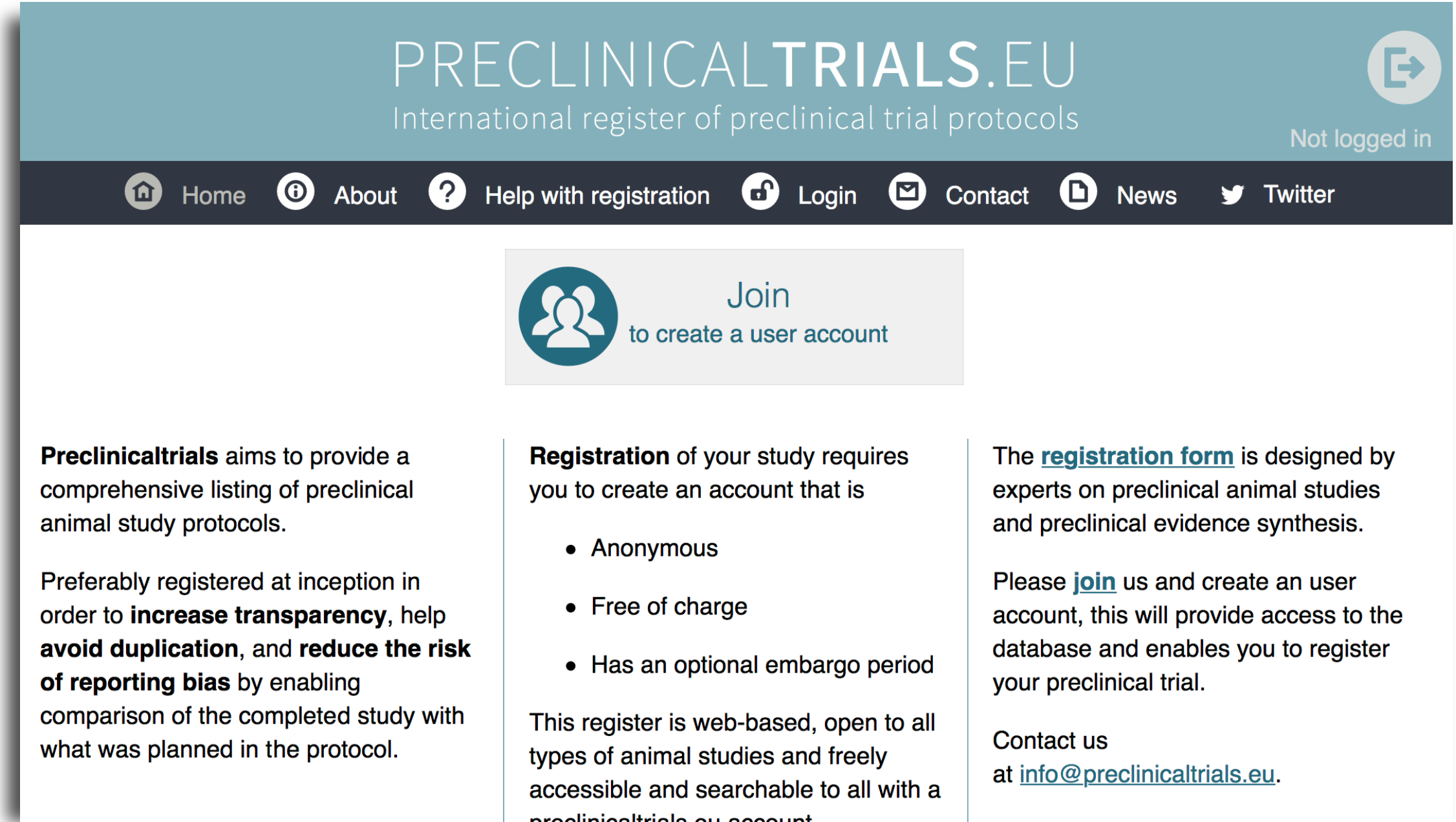
ZonMw

FAIR data and a new approach for data management
September 21 2018
Den Haag

Nicoline Smit, Project Manager at Netherland Heart Institute
Mira van der Naald, Department of Cardiology, UMC Utrecht

https://preclinicaltrials.eu

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP



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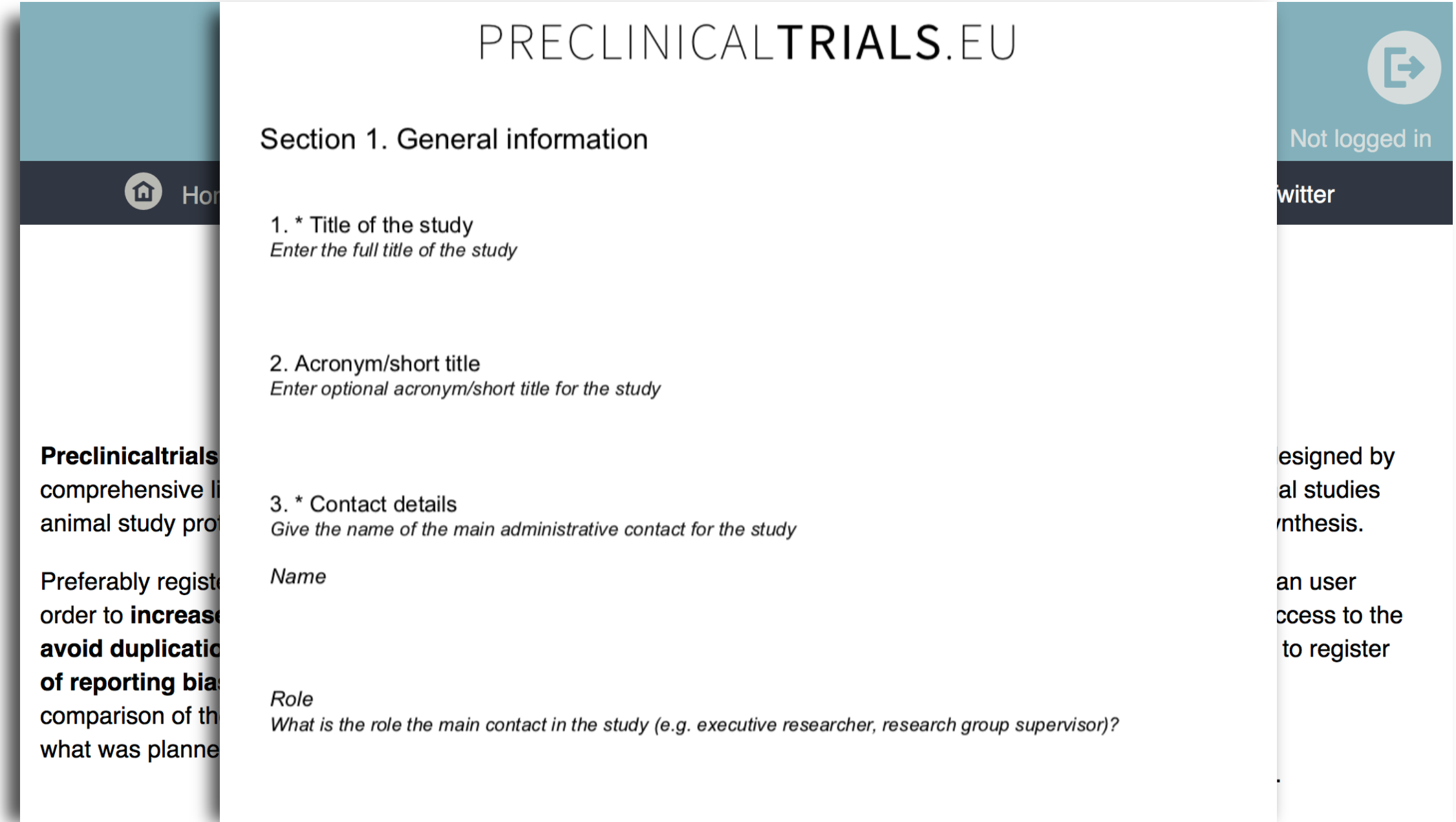


PRECLINICALTRIALS.EU

Section 1. General information

1. * Title of the study
Enter the full title of the study

2. Acronym/short title
Enter optional acronym/short title for the study

3. * Contact details
Give the name of the main administrative contact for the study

Name

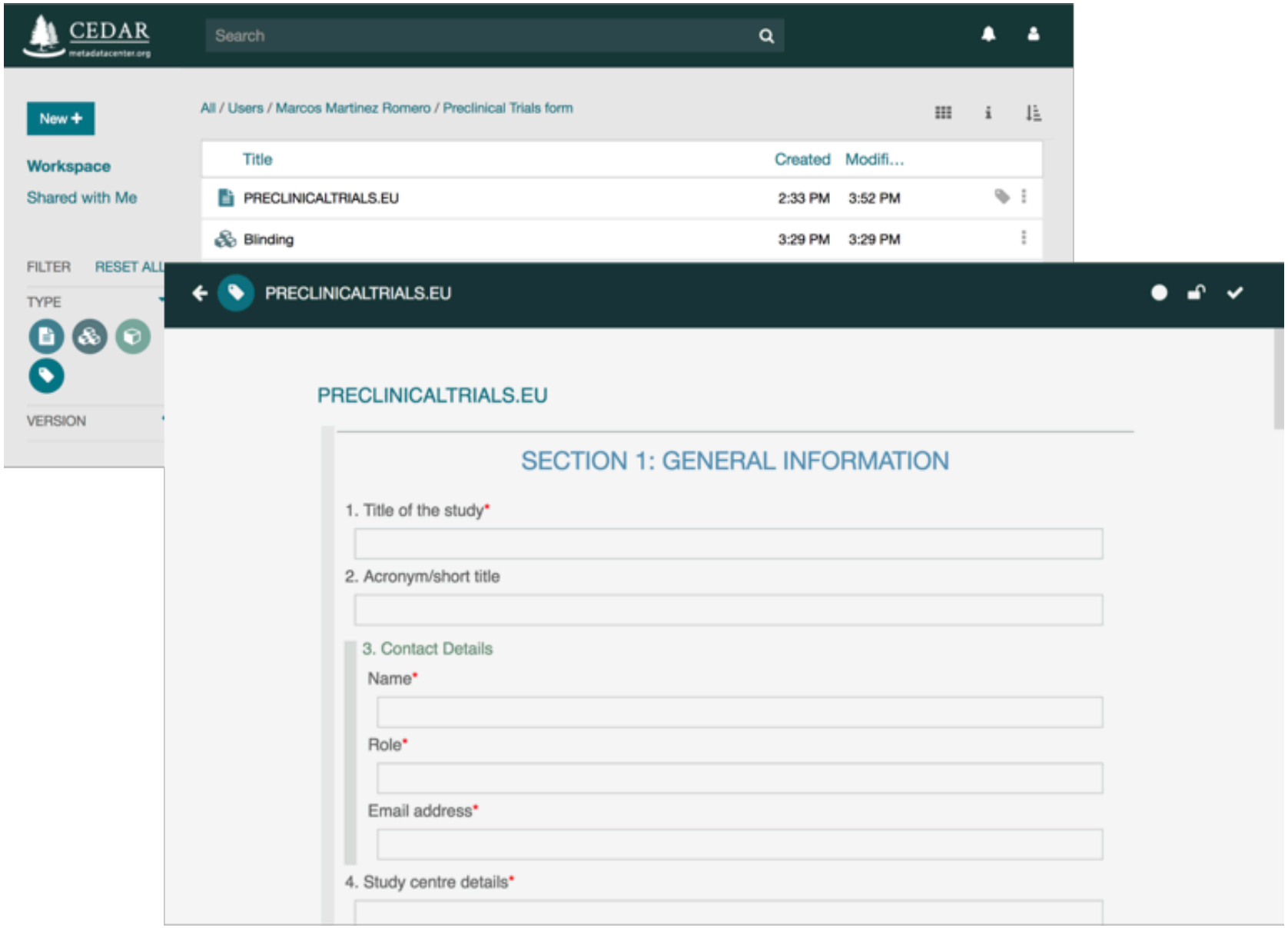
Role
What is the role the main contact in the study (e.g. executive researcher, research group supervisor)?

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP

The "15th" FAIR Metric

Metric Identifier	FM-CT1 (FAIR Metric Clinical Trail 1)
Metric Name	Preregistration
To which principle does it apply?	R1.2 (meta)data are associated with detailed provenance
What is being measured?	The existence of clinical trail preregistration
Why should we measure it?	Preregistration is important for Increased transparency and reduced risk of bias and help avoid duplication.
What must be provided?	A URL to the preclinical registration document
How do we measure it?	Use HTTP GET on URL provided.
What is a valid result?	HTTP 200 (now); Validted RDF file (later)
For which digital resource(s) is this relevant?	preclinicaltrails.eu

GETTING SYSTEMATIC ABOUT FAIR DATA STEWARDSHIP



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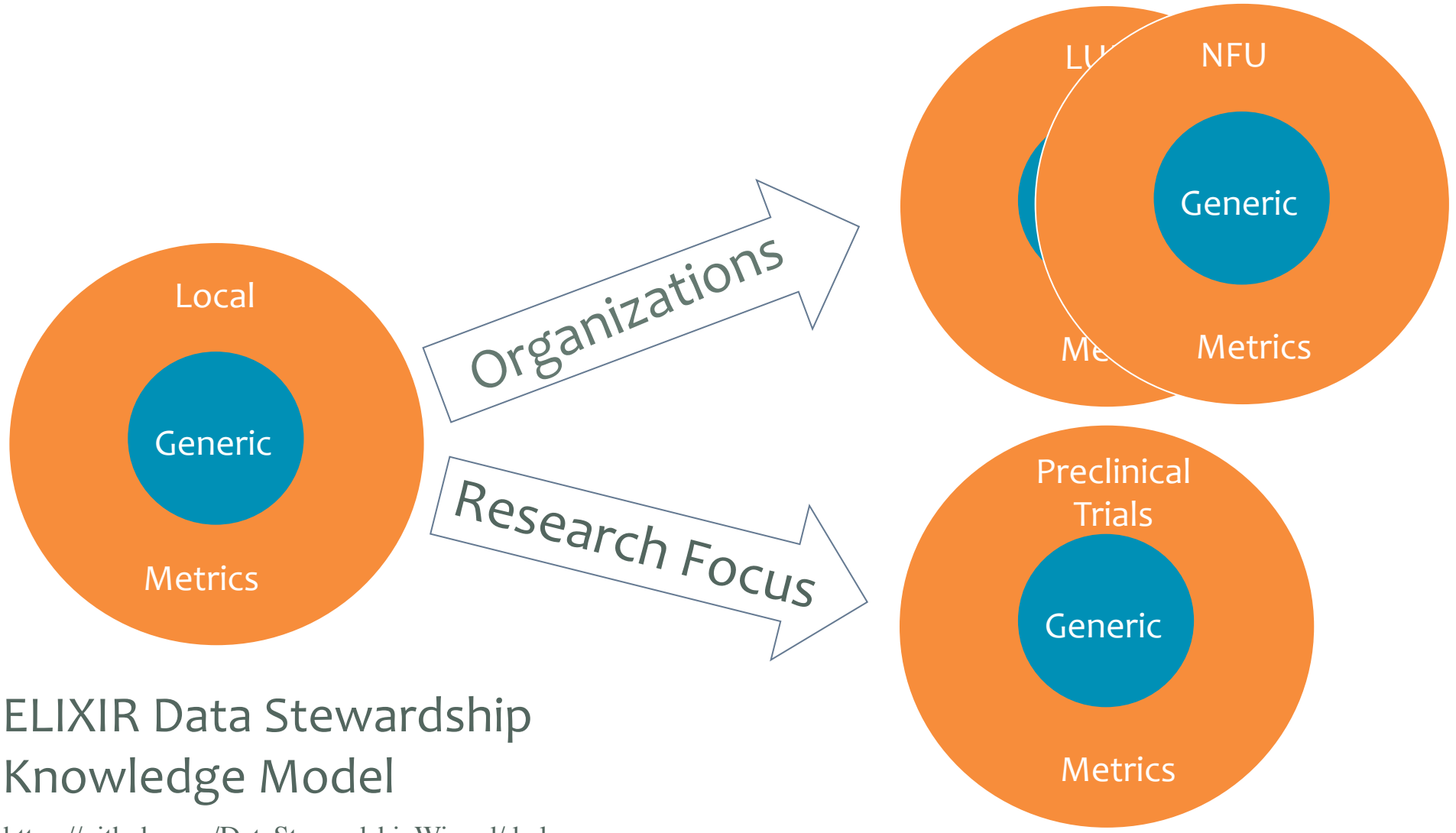

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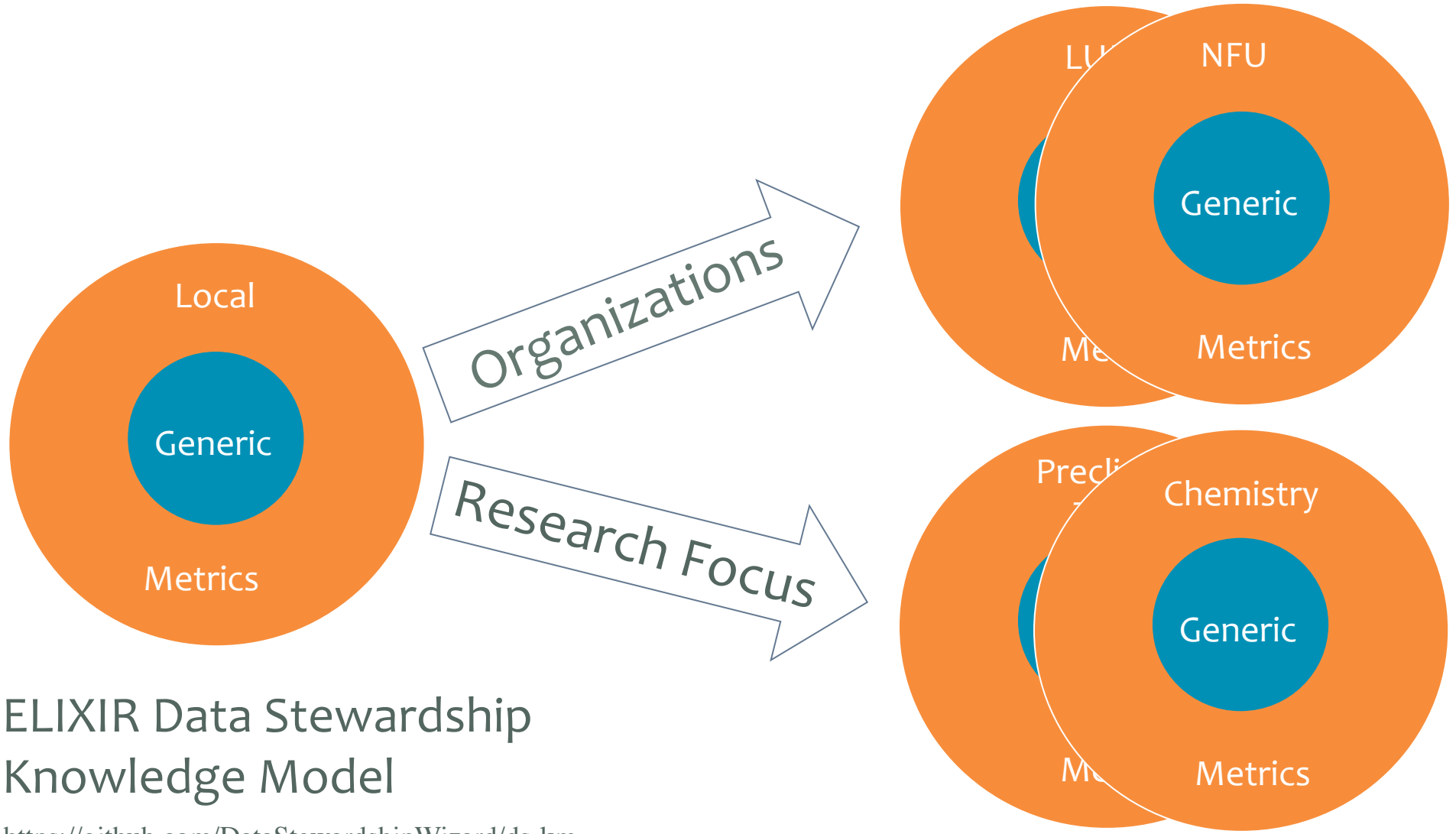

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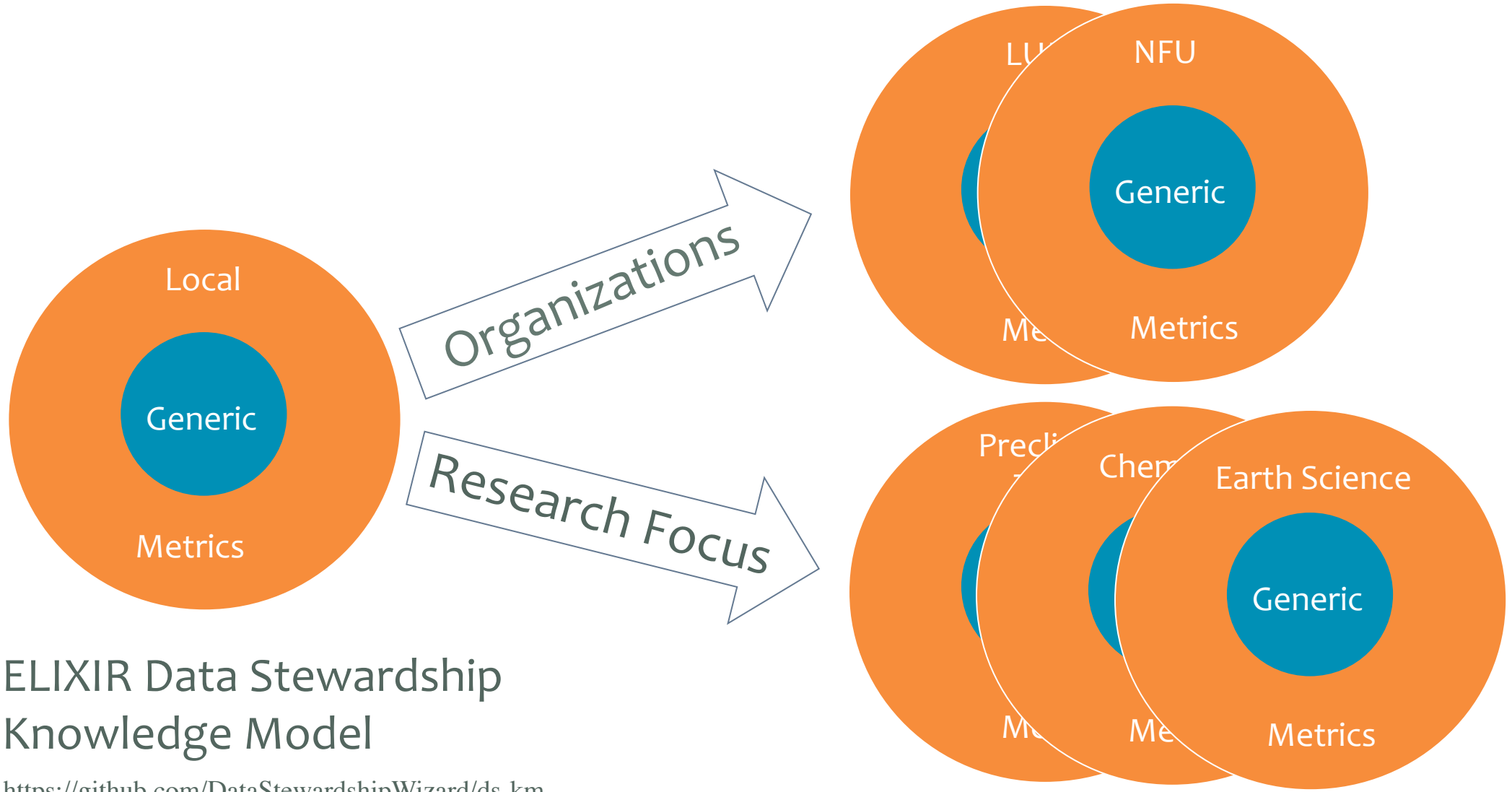

ELIXIR Data Stewardship Knowledge Model

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Metadata for Machines

Making it easy for humans to make metadata for machines

https://www.go-fair.org/resources/go-fair-workshop-series/

Metadata for Machines

First M4M: October 15-16, Leiden
Co-organizers: Wittenburg & Schultes

https://digitalscholarshipleiden.nl/articles/metadata-4-machines-help-you-find-and-reuse-relevant-research-data

Metadata for Machines

- Vehicle for Community Decision Making

- Likely Stakeholders:
  - Data steward
  - Researcher / Research community
  - University / organziations (NFU)
  - Funder
  - Publisher
  - Repository
  - FAIR tools and services
  - Instrumentation and other 3rd parties

GO FAIR Meta Data for Machines Pilot

GO FAIR M4M PILOT

Research Communities
- preclinical research
- chemistry
- earth science

GO FAIR M4M PILOT

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- preclinical research
- chemistry
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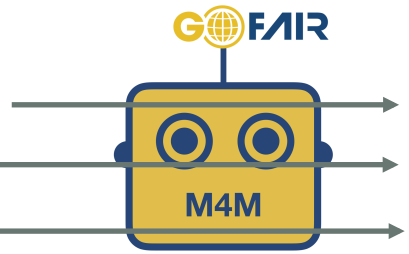

Metadata Templates
FAIR Metrics

GO FAIR M4M PILOT

Research Communities
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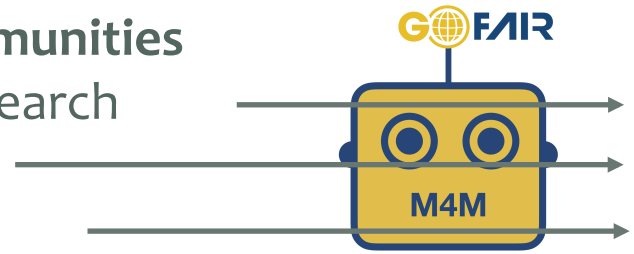
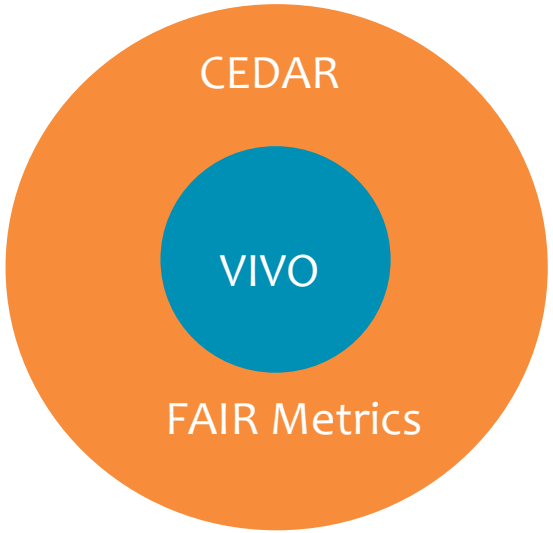
- chemistry
- earth science



Metadata Templates
FAIR Metrics

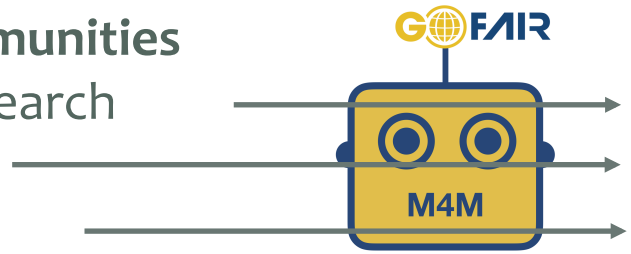
ZonMW composes program calls



DS Wizard

GO FAIR M4M PILOT

Research Communities
- preclinical research
- chemistry
- earth science



Metadata Templates
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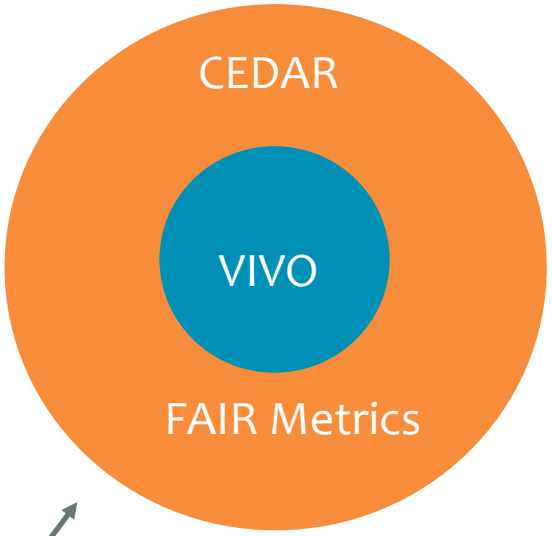

DS Wizard

Applicants
Write DS Plan

GO FAIR M4M PILOT

Research Communities
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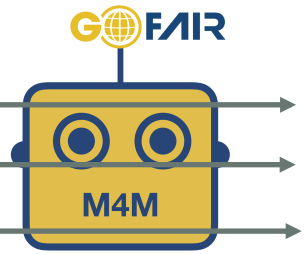

Metadata Templates
FAIR Metrics

ZonMW composes program calls

CEDAR
VIVO
FAIR Metrics

DS Wizard

Do the research

Castor

Data

Applicants
Write DS Plan

GO FAIR M4M PILOT

Research Communities
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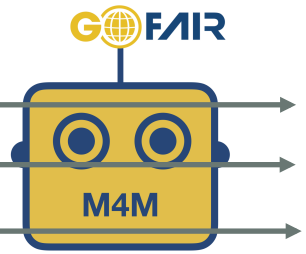

Metadata Templates
FAIR Metrics

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CEDAR
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Do the research

Castor

Data

Automated FAIRness Complaince

Trusted 3rd party
FAIR Metrics
Certification

Applicants
Write DS Plan

GO FAIR M4M PILOT

Research Communities
- preclinical research
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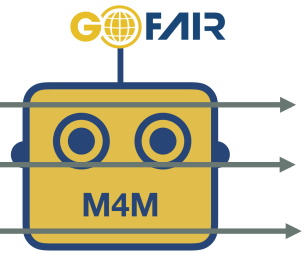
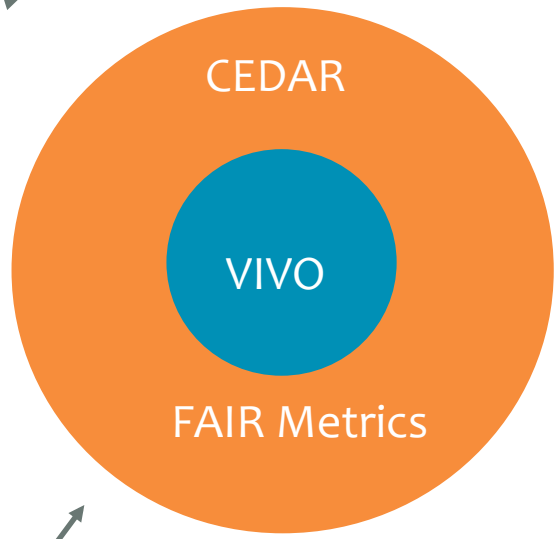


Metadata Templates
FAIR Metrics

ZonMW composes
program calls

Do the research

Castor



DS Wizard

Data

Automated FAIRness
Complaince

Trusted 3rd party
FAIR Metrics
Certification

Applicants
Write DS Plan

INTRODUCTION TO FAIR DATA STEWARDSHIP

SECOND: THE FAIR PART

WHAT IS FAIR DATA: MORE DETAIL

**“Data and services that are findable,
accessible,
interoperable,
re-usable
for machines and for people”**

The FAIR Guiding Principles for scientific data management and stewardship, Scientific Data (2016), https://www.nature.com/articles/sdata201618

WHAT IS FAIR DATA: MORE DETAIL

“Data and services that are findable, accessible, interoperable, re-usable for machines (and sometimes, in rare circumstances, may be even for people.”

The FAIR Guiding Principles for scientific data management and stewardship, Scientific Data (2016), https://www.nature.com/articles/sdata201618

WHAT IS FAIR DATA: MORE DETAIL ON THE PRINCIPLES

GO FAIR

News Contact

GO FAIR Initiative | Implementation Networks | FAIR Principles | Technology | Training | Certification

FAIR Principles

Home › FAIR Principles

FAIR Principles

- F1: (meta) data are assigned globally unique and persistent identifiers
- F2: Data are described with rich metadata
- F3: Metadata clearly and explicitly include the identifier of the data it describes

On March 15th, 2016, a group has published "**The FAIR Guiding Principles for scientific data management and stewardship**" comment on Nature's Scientific Data. The authors aimed for the principles to act as guidelines for those willing to improve findability, accessibility, interoperability and reuse of their digital assets. With the increase on volume, complexity and creation speed of data, humans are more and more relying on computational support for dealing with data. The principles were, therefore, defined with the focus on machine-actionability, i.e., the capacity of computational systems to find, access, interoperate and reuse data with none or minimal human intervention.

Findable: the first obstacle for someone willing to (re)use data is to find them. Metadata and data should be easy to find by both humans and computers. Machine-readable

FAIR DATA PRINCIPLES

Findable:

F1. (meta)data are assigned a globally unique and persistent identifier;

F2. data are described with rich metadata;

F3. metadata clearly and explicitly include the identifier of the data it describes;

F4. (meta)data are registered or indexed in a searchable resource;

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;

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;

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;

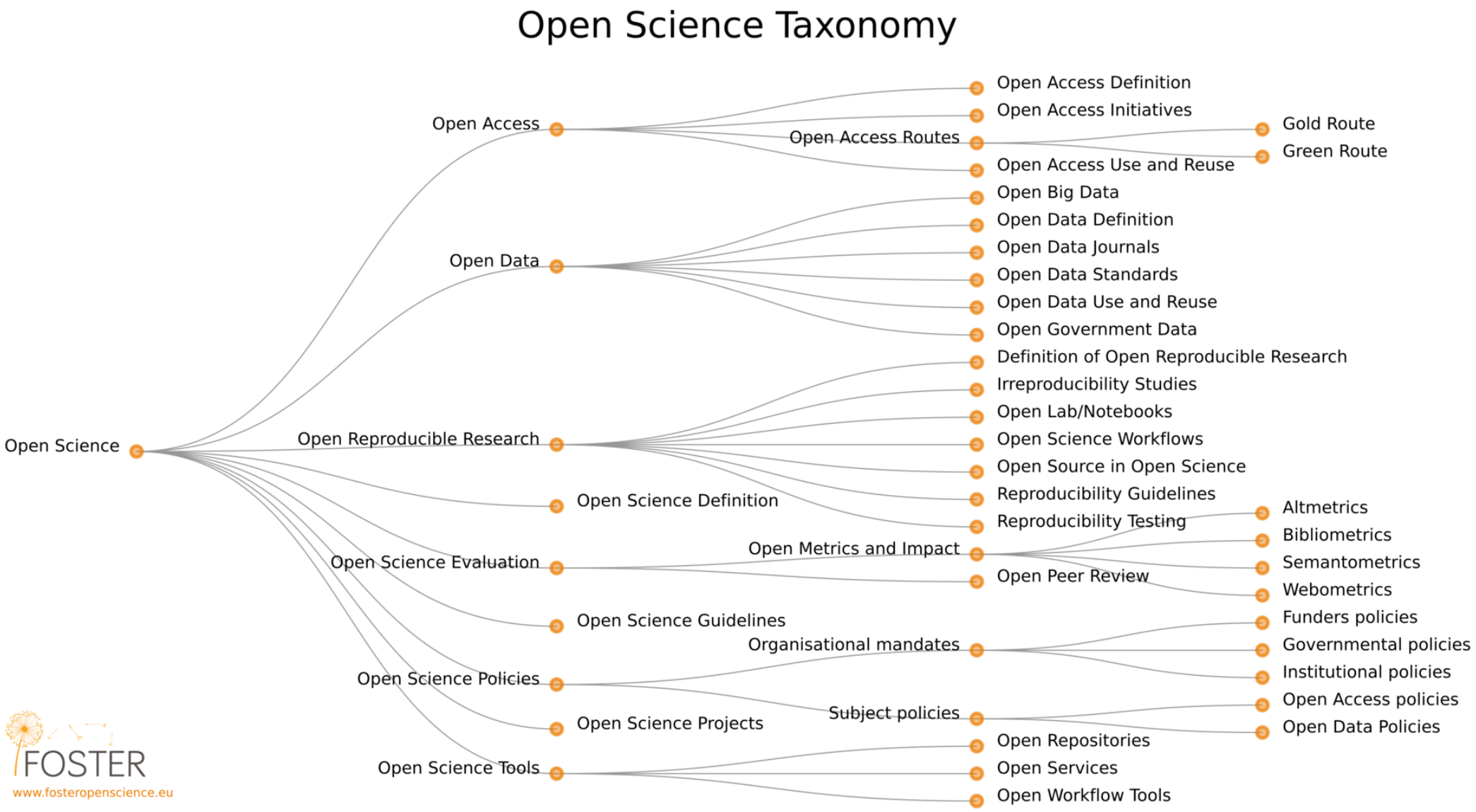
R1.2. (meta)data are associated with detailed provenance;

R1.3. (meta)data meet domain-relevant community standards;

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

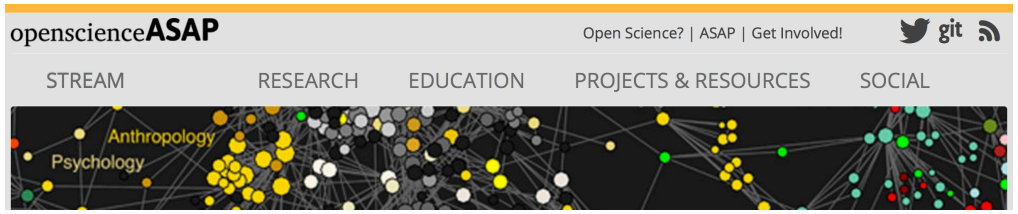
Sci. Data 3:160018 doi: 10.1038/sdata.2016.18 (2016)

OPEN SCIENCE TAXONOMY



FOSTER
www.fosteropenscience.eu

OPEN SCIENCE



Die 6 Prinzipien

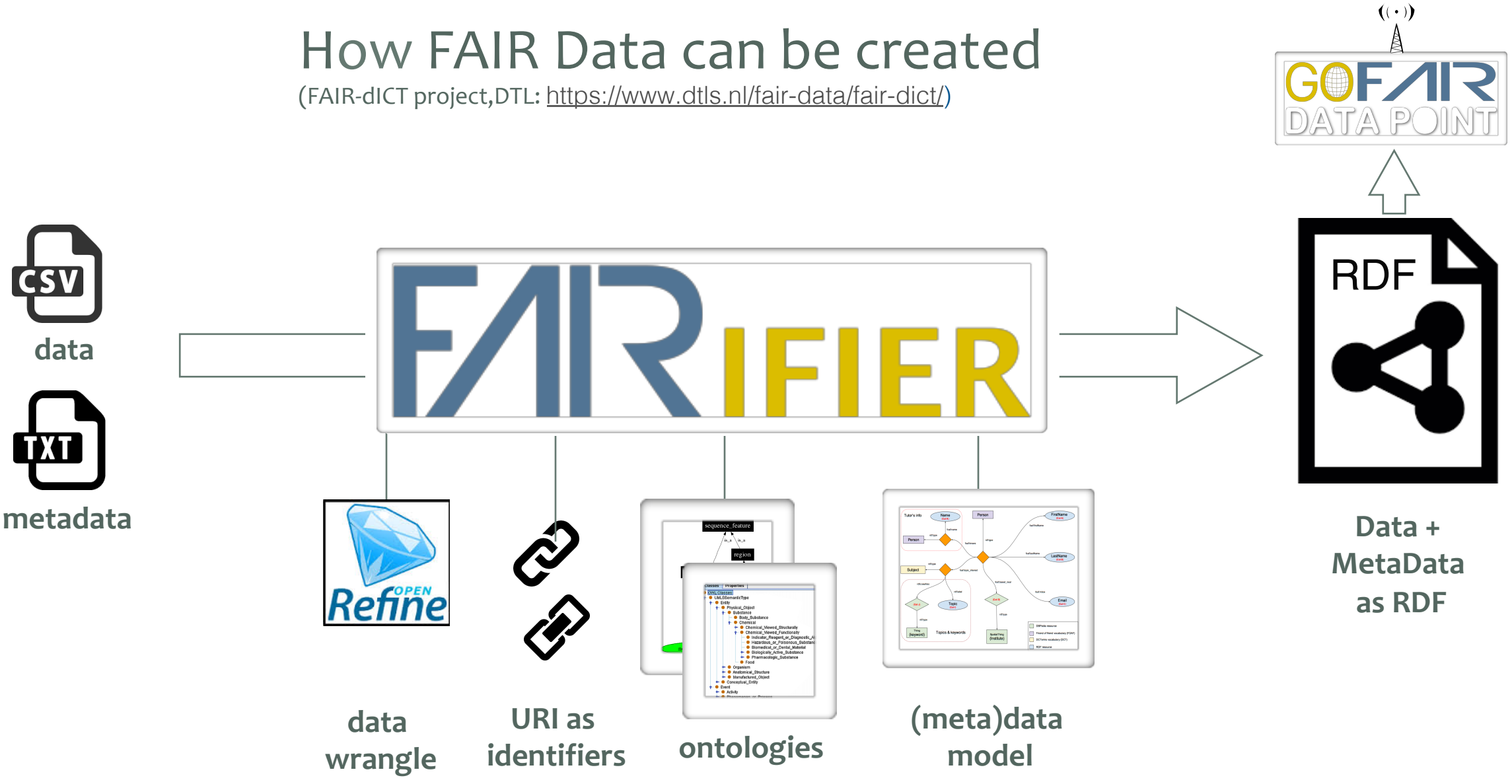
Offene Wissenschaft basiert auf sechs Prinzipien, um Teilschritte und -ergebnisse eines wissenschaftlichen Prozesses zu öffnen. Die ersten vier Prinzipien basieren auf dem Paper "The Case for an Open Science in Technology Enhanced Learning" (Kraker 2011). Open Peer Review und Open Educational Resources sind zwei weitere wichtige Aspekte von Wissenschaft. Die "Open Definition" erklärt, was "offen" in diesem Kontext bedeutet.

- **Open Methodology:** das Anwenden von Methoden sowie den gesamten Prozess dahinter soweit praktikabel und relevant dokumentieren
- **Open Source:** Quelloffene Technologie (Soft- und Hardware) verwenden und eigene Technologien öffnen
- **Open Data:** Erstellte Daten frei zur Verfügung stellen
- **Open Access:** In einer offenen Art publizieren, und für jedeN nutzbar und zugänglich machen (s. Budapest Initiative (eng))
- **Open Peer Review:** Transparente und nachvollziehbare Qualitätssicherung durch offenen Peer Review
- **Open Educational Resources:** Freie und offene Materialien für Bildung und in der universitären Lehre verwenden

A REFERENCE IMPLEMENTATION OF THE 15 PRINCIPLES

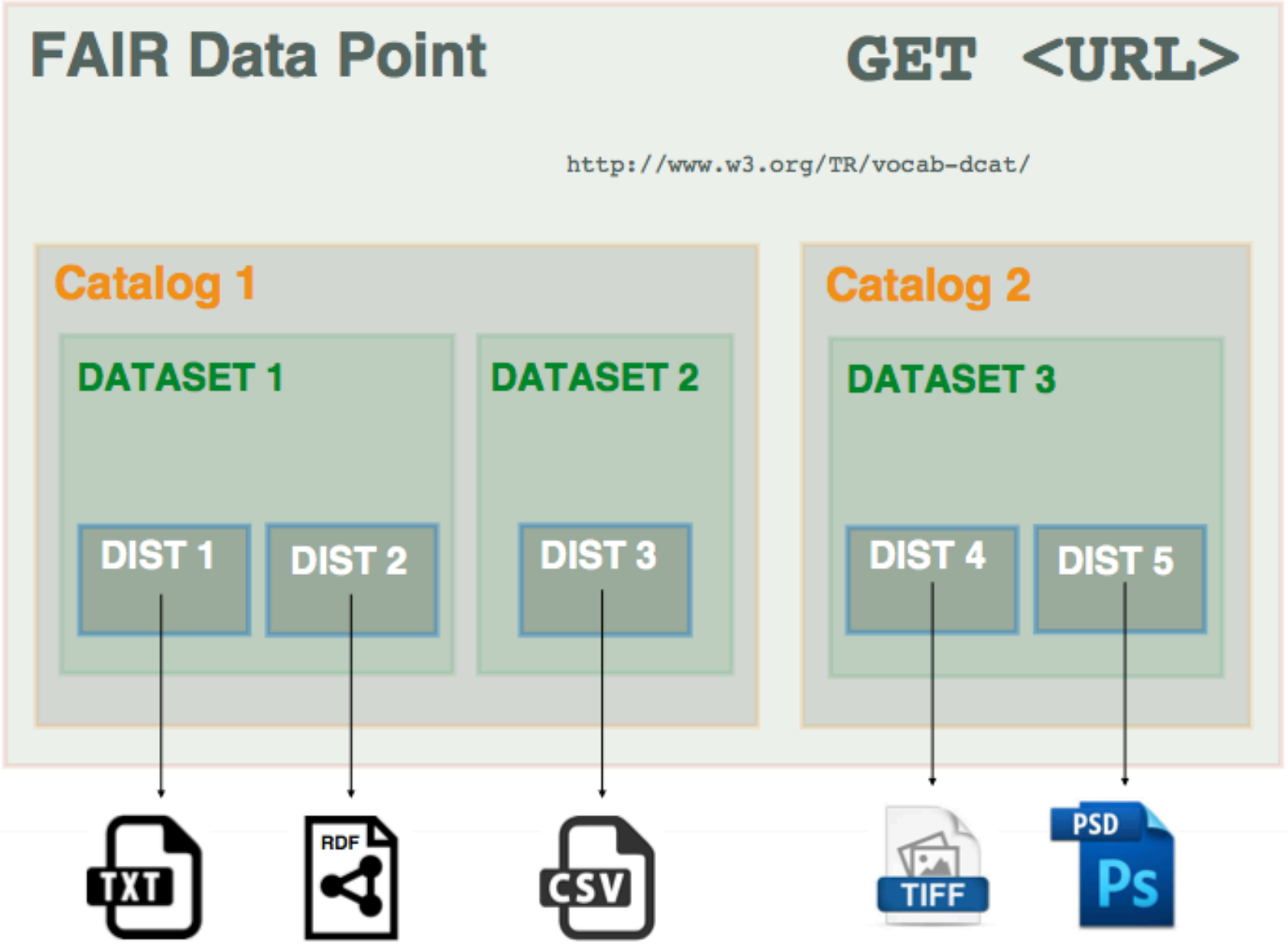
How FAIR Data can be created

(FAIR-dICT project,DTL: https://www.dtls.nl/fair-data/fair-dict/)



A REFERENCE IMPLEMENTATION OF THE 15 PRINCIPLES

FAIR DATA POINT



FAIR META DATA

FAIR metadata

Title	FDP of lorentz.fair-dtls.surf-hosted.nl
Metadata ID	3e77134d-9338-482a-a4f7-8e6933b47469
Description	FDP of lorentz.fair-dtls.surf-hosted.nl
Issued	2017-05-12T12:11:36.343Z
Modified	2017-05-12T12:11:36.355Z
License	license
Catalogs	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/wur
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/DvBC1
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/PKD_2.0
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/AGIS
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/PKD_1.0
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/Kenya.2017
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/test_example_number_2_2.0
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/post_example_2.0
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	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/post-test_1.0
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/testcatalog_1.0
	https://lorentz.fair-dtls.surf-hosted.nl/fdp/catalog/FAIR_in_Africa_0001

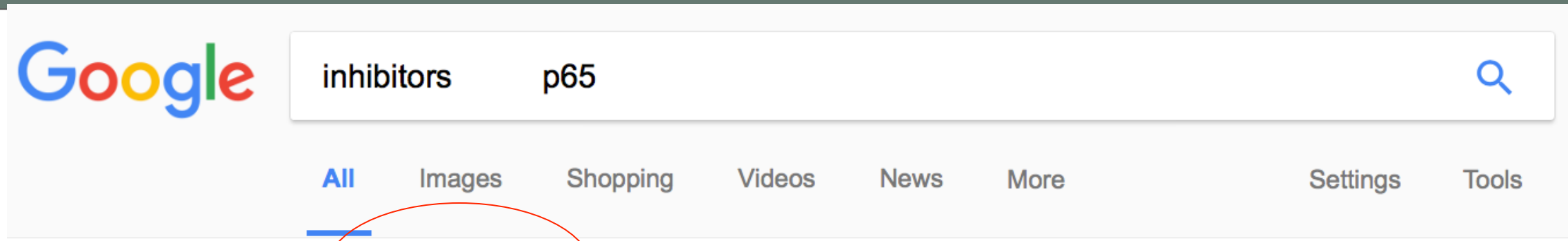
SEARCH

inhibitors p65

Google Search I'm Feeling Lucky

Mark D. Wilkinson
CBGP-UPM/INIA, Madrid

SEARCH


Google
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-kB 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

SEARCH

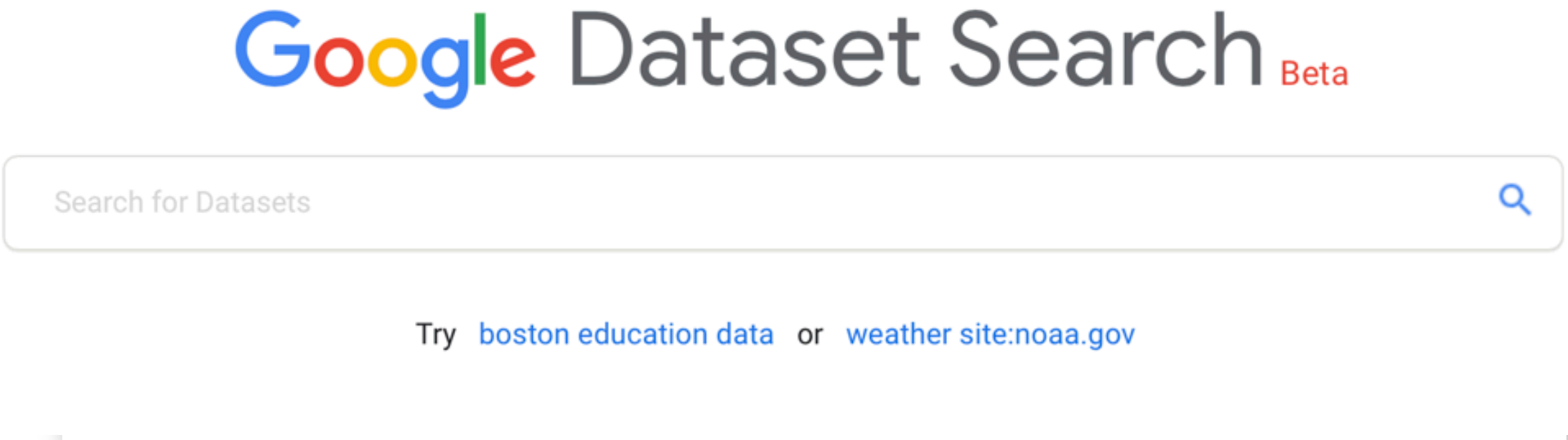
Mark D. Wilkinson
CBGP-UPM/INIA, Madrid

FAIR META DATA SEARCH

Find me all know… …nhibitors of the Human p65 P… …ased on those that were fou… …om those that were found i… …chives. Keep track of the license an… …tion for each one. If data is relevant, bu… …, please provide the contact information fo… …person I need so I can request the data.

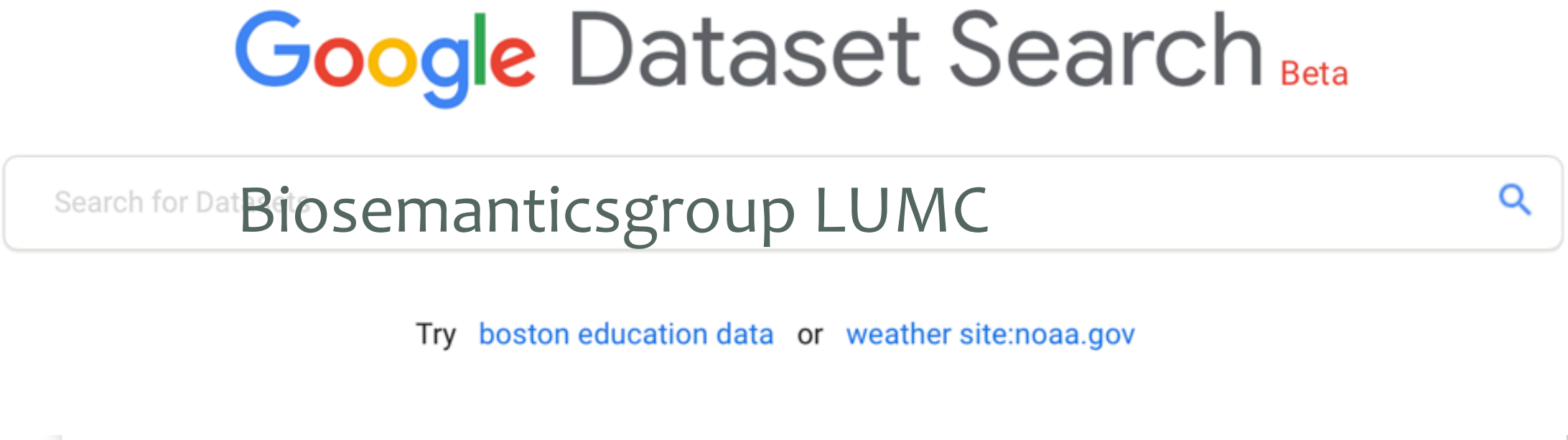
GOOGLE DATA SET SEARCH

5 September 2018

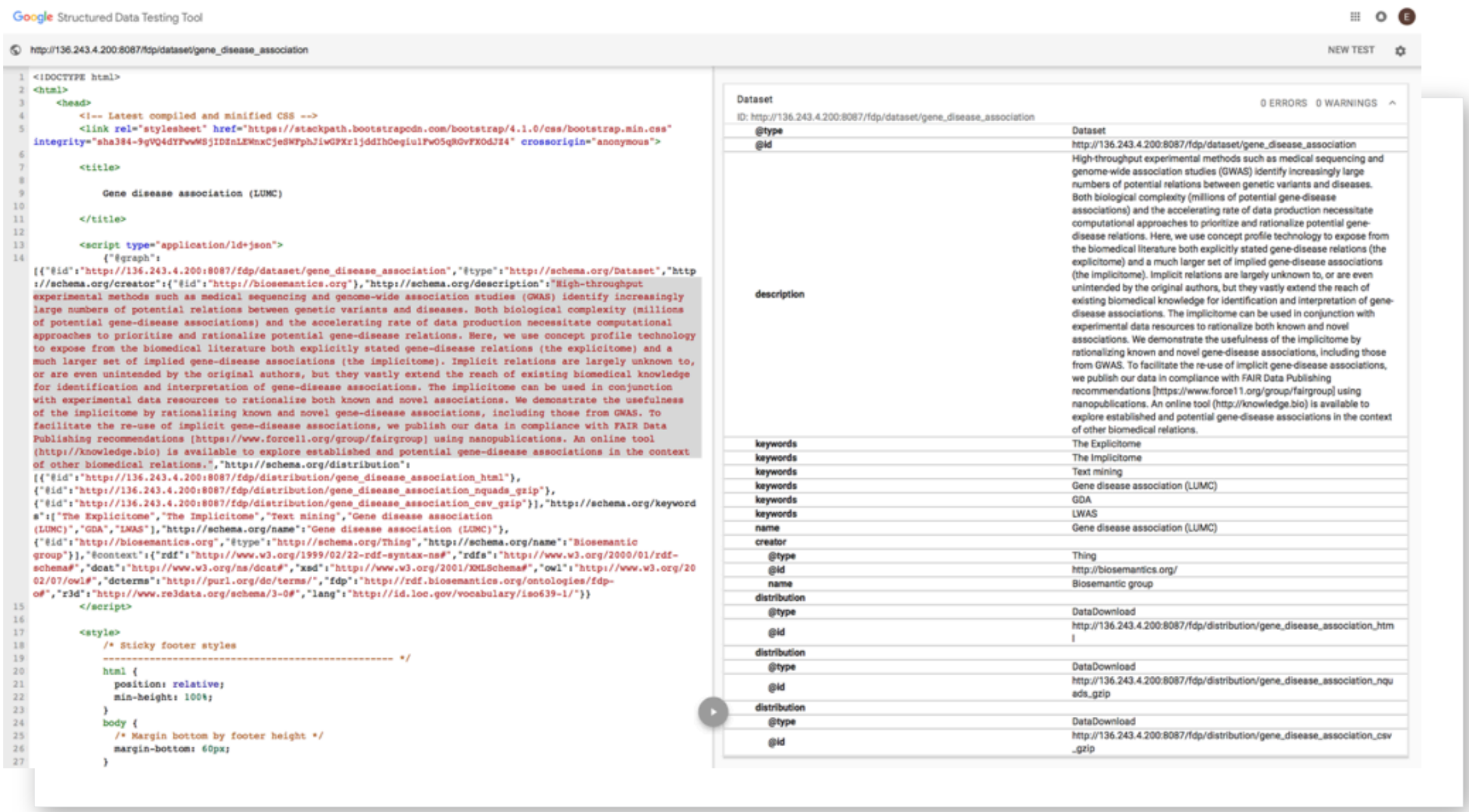


GOOGLE DATA SET SEARCH

5 September 2018



GOOGLE DATA SET SEARCH



FAIR DATA POINTS AND EXISTING REPOSITORIES

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Luiz Bonino, FigShare webinar State of the Open Data 2018
https://figshare.com/articles/Digital_Science_Webinar_The_State_of_Open_Data_2018/7257221