Two real use cases of FAIR maturity indicators in the life sciences

This manuscript was automatically generated on August 7, 2019.

Authors

· Serena Bonaretti

© 0000-0003-4264-1773 · ♥ sbonaretti · ❤ SerenaBonaretti

Department of Bioinformatics - BiGCaT, NUTRIM, Maastricht University, The Netherlands

• Egon Willighagen

© 0000-0001-7542-0286 · ♥ egonw · ♥ egonwillighagen

Department of Bioinformatics - BiGCaT, NUTRIM, Maastricht University, The Netherlands

Abstract

Data reuse is crucial to enhance scientific progress and maximize return on science investments. Given the incremented availability, manual and automatic retrieval of data for new research questions can be challenging. Among the guidelines created to enhance data retrieval, the FAIR (findable, accessible, interoperable, reusable) principles are increasingly adopted at an institutional and funding level. Metrics to assess FAIRness of data repositories are under study and contributions are highly encouraged. In this work, we propose two real use-cases of researchers retrieving data from two different repositories (Array Express and Gene Expression Omnibus) to answer their research questions. [The following part still requires some work] For each use case, we harvested data and metadata via application program interface (API) and we calculated FAIR metrics [...]. We found [...]. To conclude [...]

Keywords:

FAIR guidelines; FAIR Maturity indicators; Life sciences; Jupyter notebook

Introduction

Data sharing and data reuse are two complementary aspects of modern research activity. Researchers share their data for a sense of community, to demonstrate integrity of acquired data, and to enhance quality and reproducibility of research work [1]. In addition, data sharing is supported by the emerging citation system for datasets, scientific journals requirements, and funding agencies that want to maximize their return on science investments [2], [3]. At the same time, researchers are eager to reuse available data to integrate information that answer interdisciplinary research questions and to optimize use of fundings [4]. [The following part of this paragraph still requires some work] Although attitudes towards data sharing and reuse are increasingly favorable [12], data discovery and re-use remain difficult in practice [11]. Studies show that 40% of qualitative data sets were never downloaded, and about 25% of data is used just 1-10 times. In addition, data availability decreases 17% per year [10] due to... To happen, data sharing and reuse need appropriate data management, including quality, standardization, ethics, and security [cit]. (infrastructure) Data retrieval, the process of identifying and extracting data from a database using a query [5], is one of the main challenges of data reuse.

In 2016, the FORCE 11 group proposed guidelines to increase data reuse in the life sciences. These guidelines aimed to make data findable, accessible, interoperable, and reusable, and were summarized in the acronym FAIR [6] (principles fully listed in Table 2). In a short time the FAIR guidelines have gained remarkable popularity, and they are currently supported by funding agencies and political entities, such as the European Commission, the National Institutes of Health in the United States, and institutions in Africa and Australia [7]. In addition, academic and institutional initiatives were launched to promote and implement data FAIRness, such as GOFAIR and FAIRsharing. Although largely adopted, the FAIR principles do not specify any technical requirement as they are deliberately intended as aspirational [7]. The lack of practical specifications generated a large spectrum of interpretations and concerns and raised the need to define measurements of data FAIRness. Some of the authors of the seminal paper proposed a set of FAIR metrics [8], subsequently reformulated as FAIR maturity indicators [9]. At the same time, they invited consortia and communities to suggest and create alternative evaluators. The majority of the proposed tools are online questionnaires that researchers and repository curators can manually fill to assess the FAIRness of their data (Table 1). However, the FAIR metrics guidelines emphasize on the importance of creating "objective, quantitative, machine-interpretable" evaluators [8]. Following this criterion, two platforms have recently been developed to automatically compute FAIR maturity indicators: FAIR Evaluation Services and FAIRshake. The first platform offers evaluation of maturity indicators and compliance tests [9], whereas the second platform provides metrics, rubrics and evaluators for registered digital resources [10]. Both platforms provide use cases for FAIRness assessment, however they do not provide systematic analysis of evaluated datasets and repositories. In the literature, two studies report evaluation of FAIRness for large datasets. Dunning et al. [11] used a qualitative approach to investigate 37 repositories and databases. They assessed FAIRness using a traffic-light rating system that ranges from no to full compliance. Differently, Weber et al. [12] implemented a computational workflow to analyze the retrieval of more than a million images from five repositories. They proposed metrics specific for images, including time and place of acquisition to assess image provenance. The first study provides valuable concrete guidelines to assess data FAIRness, whereas the second study constitutes a solid example of computational implementation.

[The following paragraph still requires some work] In this paper, we propose a computational approach to calculate FAIR maturity indicators in the life sciences. We followed the recommendations provided by the Maturity Indicator Authoring Group [9] and we created a visualization tool to summarize and compare FAIR maturity indicators across various datasets and repositories. We tested our approach on two real use cases of data retrieval to answer research questions in system biology.

We evaluated FAIRness for two repositories, i.e. ArrayExpress and Gene Expression Omnibus. Finally, we made our work open and reproducible by using the open language python in a Jupyter notebook/

Table 1: Online FAIR evaluators and studies in the literature assessing FAIRness of data repositories.

Authors	Questionnaire / Platform	Manual Assessment	Automatic Assessment			Data / Code Repository
			Code / Language	Metadata Format	Protocol / Library	
FAIRness evaluators						
Wilkinsons et al. [8]	-	x	-	-	-	<u>GitHub</u>
Australian Research Data Commons	FAIR self-assessment tool	x	-	-	-	-
Commonwealth Scientific and Industrial Research Organization	5 star data rating tool	x	-	-	-	-
Data Archiving and Networked Services	FAIR enough? and FAIR data assessment tool	x	-	-	-	-
GOFAIR consortium	FAIR ImplementationMatrix	x	-	-	-	Open Science Framework
EUDAT2020	How FAIR are your data?	x	-	-	-	Zenodo
Wilkinsons et al. [9]	FAIR evaluation services	-	Ruby on Rails	JSON, Microformat, JSSON-LD, RDFa	nanopublications	<u>GitHub</u>
Clark et al. [<u>10</u>]	<u>FAIRshake</u>	-	Django and python	RDF	Extruct	GitHub
Studies assessing FAIRness of repositories						
Dunning et al. [<u>11</u>]	-	x	-	-	-	Institutional repository
Weber et al. [<u>12</u>]	-	-	python	DataCite	OAI-PMH	GitLab
Our approach	-	x (partially)	Jupyter notebook with python	XML, JSON	request?	GitHub

Materials and methods

Use cases in the life sciences

We asked researchers in our department for cases where they looked for datasets in a scientific repository to answer a research questions. We selected two cases that involved different repositories. For each use case, name used throughout the paper, research question, and investigated repository are:

- *Parkinsons_AE*: What are the differentially expressed genes between normal subjects and subjects with Parkinson's diseases in the brain frontal lobe? To answer this question, the researcher looked for a dataset in the search engine of ArrayExpress, a repository for microarray gene expression data based at the European Bioinformatics Institute (EBI), United Kingdom [13];
- *NBIA_GEO*: What is the function of mutation of WDR45 protein in the brain? In this case, the researcher looked for a dataset to analyze in the search engine of Gene Expression Onmibus (GEO), a repository containing gene expression and other functional genomics data hosted at the National Center for Biotechnology Information (NCBI), United States [14].

What is data and what is metadata?

The FAIR guidelines recursively use the terminology *data*, *metadata*, and *(meta)data*. For our computational implementation, we needed precise definitions of these terms. Accordingly to the Merrian-Webster online dictionary, *data* are "information in digital form that can be transmitted or processed" [15] whereas *metadata* are "data that provide information about other data" [16]. Following these definitions, we considered the dataset that researchers analyzed to answer their research question as *data*, and the additional information provided in the database about *data* as *metadata*. In addition, we defined *(meta)data* as *data* for the principles R1, R1.1, and R1.2, as *metadata* for the principles I1, I3, and as both *data* and *metadata* for the principles F1, F4, A1. (add to table)

Finally, we specified the *metadata* to retrieve according to the requirements of the FAIR guidelines:

- F2: Information that allows researchers to find the dataset s/he looks for. It coincides with the keywords used in the search;
- F3: Identifier of the dataset in the repository;
- 13: Reference to other metadata;
- R1: Information about the dataset, other than the search keywords;
- R1.1: Data license:
- R1.2: Data provenance as publication title, author names, and one author's email address.

In all cases, we assumed that *data* and *metadata* were hosted in the same repository.

Calculating FAIR maturity indicators

Because the FAIR guidelines stress on the importance of *data* and *metadata* being "machine-readable" [cit], we collected information about datasets and repositories via application programming interface (API) wherever possible. We queried three different sources:

• Data repositories (<u>ArrayExpress</u> and <u>Gene Expression Omnibus</u>): We programmatically queried each repository using the same keywords researchers had used in their manual query when

looking for a dataset. From the obtained metadata, we retrieved information to calculate maturity indicators for the principles F2, F3, I1, I3, R1, and R12;

- Registry of repository: We queried <u>re3data.org</u>, a registry containing information about more than 2000 data repositories from various disciplines [cit]. We used the retrieved information to computed the maturity indicators for the principles F1, A2, and R12;
- Searchable resource: We queried <u>Google Dataset Search</u>, an emerging search engine specific for datasets, to quantify the principle F4.

The output of queries consisted of information structured in xml. Details about the computation of each specific maturity indicator are in Table 2 and in our Jupyter notebook-link (interactive on binder-link). To the majority of the maturity indicators, we assigned value 1 if the criterion was satisfied and 0 in the opposite case. To the maturity indicator for F2 we assigned a number between 0 and 1 as we calculated it as the ratio between the number of keywords in the dataset metadata over the total number of keywords used by the researcher in the manual query. Similarly to what reported in the literature (Table 2), we did not evaluate maturity indicators for the principles I2 and R1.3.

Table 2: FAIR principles and corresponding evaluation criteria proposed by the Maturity Indicator Authoring Group [9], Dunning et al. [11], Weber et al. [12], and our approach. The criteria used in the first two works are extrapolated from their publication text, whereas the criteria by Weber et al. are from Table IV of their paper. The metrics Weber et al. developed are Q_{geo} for image location, Q_{time} for the time of picture acquisition, Q_{ret} when data is automatically downloadable only given its metadata and Q_{lic} for found license. In our approach, *dataset* metadata refers to metadata retrieved from ArrayExpress and Gene Expression Omnibus, whereas *registry* metadata consists of metadata retrieved from re3data. In addition, we indicate when we used *(meta)data* as (data) or (metadata), and an automatic (A) or manual (M) procedure for information retrieval. Acronyms: GUID = Globally Unique IDentifier, DOI = Digital Object Identifier.

FAIR principle [6]	Wilkinson et al. [9]	Dunning et al. [11]	Weber et al. [<u>12</u>]	Our approach
F1: (meta)data are assigned a globally unique and persistent identifier	The GUID matches a scheme that is globally unique and persistent in FAIRsharing	Persistent identifier is DOI or similar	Pass (embedded in DataCite)	"doi" icon is enabled in www.re3data.org (data) (M)
F2: data are described with rich metadata (defined by R1 below)	Metadata contains "structured" elements (micrograph, JSON) or linked data (JSON-LD, RDFa)	Title, creator, date, contributors, keywords, temporal and spatial coverage	Q geo ^{, Q} chrono	Search keywords are in <i>dataset</i> metadata (A)
F3: metadata clearly and explicitly include the identifier of the data it describes	Metadata contains both its own GUID and the data GUID	DOI of data is in metadata	Pass (embedded in DataCite)	Dataset metadata contains dataset ID (A)
F4: (meta)data are registered or indexed in a searchable resource	The digital resource can be found using web-based search engines	Dataset title found in google.com or duckduckgo.com	Pass	Dataset title found in Google Dataset Search (data) (M)
A.1 (meta)data are retrievable by their identifier using a standardized communications protocol	N/A	HTTP request returns 200	Q _{ret}	HTTP request returns 200 (data) (A)
A1.1 the protocol is open, free, and universally implementable	The resolution protocol is universally implementable with an open protocol	Accomplished if protocol is HTTP	Q _{ret}	Accomplished if protocol is HTTP (A)
A1.2 the protocol allows for an authentication and authorization procedure, where necessary	The resolution protocol supports authentication and authorization for access to restricted content	Accomplished if protocol is HTTP	Q _{ret}	Accomplished if protocol is HTTP (A)
A2. metadata are accessible, even when the data are no longer available	There is a policy for metadata	Repository has a clear policy statement	N/A	"data availability policy" is filled in <i>registry</i> metadata (A)
I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation	If hash-style metadata (e.g. JSON) or Linked Data are found, pass	Metadata is structured (e.g. Dublin Core)	Pass (embedded in DataCite)	Dataset metadata is structured (e.g. xml) (metadata) (M)
I2. (meta)data use vocabularies that follow FAIR principles	(meta)data uses vocabularies that are, themselves, FAIR	N/A	N/A	N/A
l3. (meta)data include qualified references to other (meta)data	Metadata contain links that are not from the same source (domain/host)	Links to publications and terms definitions	N/A	Dataset metadata includes reference to other dataset IDs (metadata) (M)

FAIR principle [6]	Wilkinson et al. [9]	Dunning et al. [11]	Weber et al. [12]	Our approach
R1. meta(data) are richly described with a plurality of accurate and relevant attributes	N/A	Metadata provide information on how to reuse a dataset	Q geo ^{, Q} chrono	Dataset metadata contain more information than search keywords (F2) (metadata) (A)
R1.1. (meta)data are released with a clear and accessible data usage license	Metadata contains a pointer to the data license	Metadata license is present	Q _{lic}	"datalicensename" and "datalicenseulr" are filled in <i>reg</i> istry metadata (data) (A)
R1.2. (meta)data are associated with detailed provenance	N/A	Documentation on how data was created	N/A	"authors", "email" and "title" are filled in <i>dataset</i> metadata (data) (A)
R1.3. (meta)data meet domain- relevant community standards	N/A	N/A	N/A	N/A

Visualizing FAIR maturity indicators

To summarize and compare the outputs of our calculation, we created a customized balloon plots using the R library ggplot2 [17]. In the graph, each row corresponds to a user-case and each column to a FAIR maturity indicator. The size of each shape is the value of a specific FAIR maturity indicator for a particular dataset. Squares represent maturity indicators determined manually, circles depict maturity indicators established automatically, and crosses illustrate the maturity indicators we did not compute. Finally, colors represent the group of principles in the acronym: blue for findable, red for accessible, green for interoperable, and orange for reusable.

Results

For both use cases, metadata contained all keywords used in the manual search (F2), dataset unique identifiers (F3), and additional information for data reuse (R1). In addition, they were structured in xml format (I1) and were released with a clear usage license (R11). The protocol used to retrieved all information was HTTP, which is standardized (A1), open, free and universally implementable (A11), and allows for authentication where needed (A12). In both cases, dataset metadata were not assigned a persistent identifiers (F1) and did not reference to other metadata (I3). Finally, the dataset of the use case *Parkinson_AE* was listed in Google Dataset Search (F4) and had detailed provenance (R12), whereas the dataset *NBIA_GEO* did not. Comparative summary of results is in Figure 1, whereas details of findings are in Table 3.

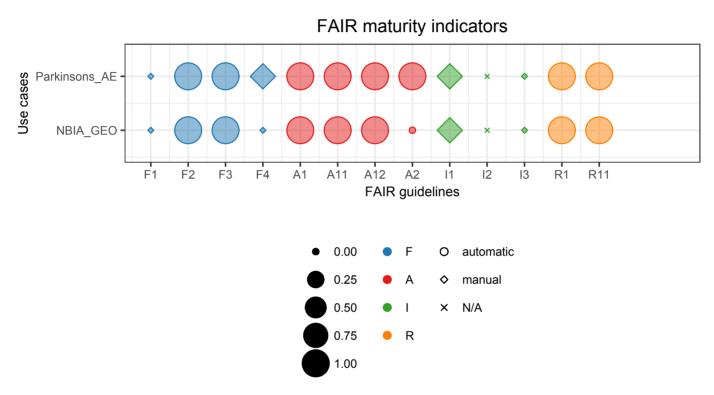


Figure 1: Comparative summary of FAIR maturity indicators for the two use cases evaluated in this work. Shape size corresponds to the numerical value of mutual indicators, colors represent FAIR categories, and shapes illustrate the way we retrieved information (N/A = not

Table 3: Comparison of API systems and FAIR maturity indicators for the two uses cases analyzed in this work. For each maturity indicator, we indicate the outcome in natural language and in numbers (1 for pass and 0 for fail).

Use case	Parkinsons_AE	NBIA_GEO			
Repository / Database	Array Express	Gene Expression Omnibus			
Search output on browser	link	link			
API	API				
Туре	REST	REST			
Documentation	link	link			
Output format	XML	XML			
FAIR maturity indicators					
F1 (Persistent identifier)	No (0)	No (0)			
F2 (Findable metadata)	Parkinson's disease, normal, homo sapiens, transcription profiling by array, raw data, frontal lobe, male, female (1)	nbia, homo sapiens, expression profiling by array (1)			
F3 (Unique identifier)	219251 (1)	200070433 (1)			
F4 (Google Dataset Search)	Yes (1)	No (0)			

Use case	Parkinsons_AE	NBIA_GEO
A1 (Communication protocol)	request status code = 200 (1)	request status code = 200 (1)
A11 (Open and free protocol)	Yes (1)	Yes (1)
A12 (Communication protocol)	Yes (1)	Yes (1)
A2 (Metadata always accessible)	Yes: https://www.ebi.ac.uk/arrayexpress/help/data_availability.html (1)	No (0)
I1 (Language representation)	XML (1)	XML (1)
I2 (FAIR vocabularies)	Not evaluated (None)	Not evaluated (None)
I3 (Reference to other metadata)	No (0)	No (0)
R1 (Metadata for reuse)	56 metadata fields (1)	58 metadata fields (1)
R1.1 (License)	name: other url: https://www.ebi.ac.uk/arrayexpress/help/ data_availability.html (1)	name: other url: http://www.ncbi.nlm.nih.gov/geo/info/disclaimer.html (1)
R1.2 (Provenance)	Authors: Garcia-Esparcia P, Schlüter A, Carmona M, Moreno J, Ansoleaga B, Torrejón-Escribano B, Gustincich S, Pujol A, Ferrer I Email: aschluter@idibell.org Title: Functional genomics reveals dysregulation of cortical olfactory receptors in parkinson disease: novel putative chemoreceptors in the human brain (1)	No (0)
R1.3 (Community standards)	Not evaluated (None)	Not evaluated (None)

Discussion

Heavily work in progress

In this study, we proposed an approach to calculated FAIR maturity indicators in the life science. We tested our method on two real use cases from our Department. We created a reproducible pipeline using Jupter notebook.

Our implementation builds on the shoulders of the implementations by the Maturity Indicator Authoring Group [], Dunning et al. [], and Weber et al []. Specifically:

- *Findable* For F1 we all agree that there has to be a DOI, and similarty for F3 F2 is the metric that allows for the largest interpretation that goes from structure data, metrics of time and compliance F3 is fine for everybody F4 different searchable resources
- Accessible We retrieved our data using the HTTP protocol, which is free, open and allows for
 authentication. However, differently from what specified by the guideline, we did not retrieve data
 and metadata by their identifiers, but by the search keywords researchers used when manually
 querying the repository because the repository we investigated do not provide globally unique and
 persistent identifiers. Both dataset top scored in the A1 and sub-principles, however NBIA_GEO did
 not have an automatically retrievable policy from re3data (which does not imply that the policy is
 automatically or manually retrievable somewhere. If data is on a local excel file or database, then
 we need a different implementation
- Interoperable I1: Similarly to Wilkinson et al, we passed metadata structured in a formal file format, such as xml. However Dunning et al and Weber et al. suggest using a more strict criteria such as that metadata have to have a standardized schema, such as <u>Dublin Core</u> or <u>DataCite</u>. Similarly to dunning and weber, we did not evaluate FAIRness of vocabulary as it is not clear to us... Finally, we manually looked for reference to other dataset identifiers in the metadata Both use cases scored the same way because they both had structured metadata (e.g. not a plain text) and did contain references to other datasets
- Reusable The Maturity Indicator Authoring group does not provide any guideline, weber uses the same metadata as F2. We followed the separation by dunning of dividing findable from reusable keywords. However, we calculated that just as a difference between the total amount of metadata and the search keywords The license presence is pretty straight-forward, there is accordance among Studies Wherease for provenance we propose specifically authors email and title of publication Finally, non of the work in the literature nor the guidelines have evaluated community standards, most likely because they do not exist Our use cases scored similarly well for the two first maturity indicators as they both had a large number of metadata and a license retrievable in re3data, however the case NBIA_GEO did not have authors in the metadata

The largest similarities among studies to calculate maturity indicators are for more precise guidelines, such as F1, whereas the a range of different implementations are for the F2, I1 Comparison with other papers - create graph for dunning? - Comments on the findings

We assessed FAIR maturity indicators using a mixed manual and automatic approach. In the literature, Dunning at al. used a fully manual approach, although the guidelines recommend an automatic one. On the other side, Weber et al. used a fully automatic approach, but they could calculate only 10 out of 15 metrics. A mixed approach allowed us to assess automatically the metrics that were easily retrievable, and to complement manually with the ones that were not retrievable via

API, hoping that in the future it will be possible to retrieve them automatically Both our manual and automatic implementations required knowledge of data schema. Specifically, we had to know in advance some keywords, such as "author", "email" Similarly, we had to know the fields in re3data, such as "data availability policy" for A2 "datalicensename" and "datalicenseurl" for R1.1 In addition, we had to implement a manual change For example, when assessing criteria F2 (keywords are in metadata), we had to change the keyword "true" that we used for data retrieval into "rawdata" This is different from what Wilkinsons et al propose with the new FAIR maturity indicators, where the approach is fully automatic. However, their workflow start with a globally unique identifier (GUID). However, when researchers look for data they do not know already the identifiers, they do not simulate what researchers do. In addition, this workflow would preclude the analysis of our two repositories as they do not provide GUIDs (F1).

Metadata format chosen could be <u>DataCite</u>, which provides a standard for metadata for publication and citation of research data, or <u>schema.org</u>, which provide more generic schemas for structured data on the Internet. Both are community-based initiative aiming at

We extracted information about the repositories from re3data. These information were about DOI, availability policy of metadata when data are not available, and data license. We selected only one registry (re3data) and one search engine(Google Dataset search). In the first case, alternative can be FAIRshare, however it still does not provide an open API. on the other side, we could have choose a generic search engine, like google, but we considered pertinent to look for a dataset specifically in a dataset search engine. We chose re3data as it provides an API for queries. Other registries, such as FAIRshare, do not provide open API yet. Similarly, Google Dataset Search does not provide any API, so we did a manual search.

Similarly to Dunning et al. and to Weber et al. we did not computer two principles. The first isthe principle I2. i.e. presence of a fair metadata vocabulary. The difficulty raises from the fact that The second is R13, which is that metadata follow community standards at those have not been formally established yet.

comparison with dunning: mainly the criteria expecially difference between metadata for findable and reusable. comparison with Weber: re3data, comparison with Wilkinson: assumes that the GUID is already know thus skipping the finding of the dataset - this is not compatible with our findable criteria

Before calculating the metrics we decided to simulate dataset retrieval via API. We assumed that a researcher does not know a priori the. Sometimes you dont get only 1 datasets

- We chose python as it is a language that is used in various scientific communities and thus could potentially provide extension and reuse of our work.
- We chose to use Jupyter notebooks for reproducibility of our results. However, databases change
 but they do not provide versions. Therefore, we can just declare the time stamps when our query
 was done. In addition, Jupyter notebooks are both machine and human readable, and easier to
 export to other domains that do not use specifically programming languages designed for the web
 To be fully reproducible, ideally repositories and registries should have a version of their database
 or provide a doi of metadata

To summarize and compare the FAIRness evaluation we used a visualization that embeds principles, scores, and type of information retrieval (manual, automatic, not assessed).

We created a visualization plot to summarize FAIR evaluation and compare results of various datasets.

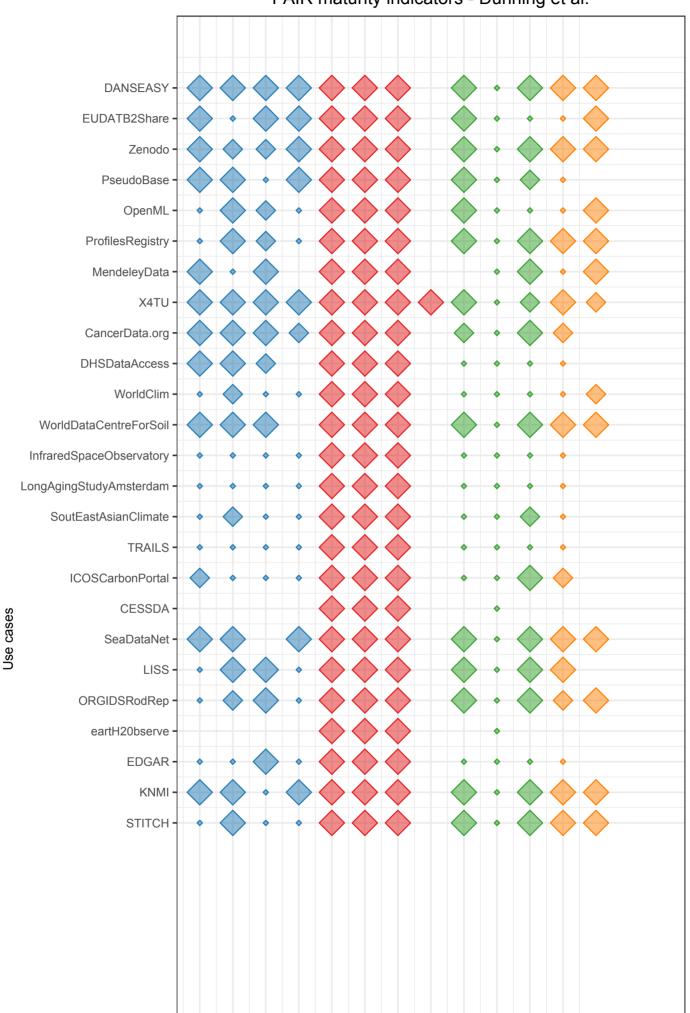
and implementations. We chose not to create a final score in accordance (to uniform) with the recommendations for the FAIR guidelines that want to keep suggestions and not to assign a score. The summary of metrics is provided by the fact the we exploited shapes, colors, and sizes to put all possible information. On the other side, the fact that each row represent a dataset allows for comparison among datasets

A visual approach Visualizing results for summary and comparison is an approach taken also by FAIRshake. They created *insignas*, which FAIRness using a color gradient from blue (satisfactory) to red (unsatisfactory). The platform FAIRshake provide visualizations that can dinamically expand to fit scores calculated using different metrics.

Differently, we chose a static approach because these the FAIRshake insignias do not allow for comparison has implemented visualizations called "insignas", where they use color gradents

- We chose to plot our results instead of providing a final score to avoid negative connotations (see FAIR metrics vs. maturity indicators). However, we wanted to be able to compare our results, so we used balloon plots, usually used for categorical data visualization and comparison. (FAIR shake uses visualizations too but they are not comparable)
- NO final score because

FAIR maturity indicators - Dunning et al.



Difficulty / Limitations

Some limitations must be acknowledged. First, our approach requires an a-priori knowledge of metadata structure.

Different repositories use different data structure. Automatization occurs after a lot of manual investigation

- We had to adapt the code based on API type and response schema. Our implementation requires specific knowledge of the database structure and thus it is difficult to directly generalize it to various databases
- We considered use cases where all queries provided one final dataset. In real practice, researchers
 often need to compare subset of retrieved datasets manually because there are not enough
 information to discriminate them computationally (the information is present, but not machinereadable)
 - Our implementation requires specific knowledge of the database structure and thus it is difficult to directly generalize it to various databases.
 - Different repositories use different html tags to define their
- Database APIs do not allow to retrieve all the information that the user interface allows (example 1: ChEBI does not allow to retrieve information about reactions; example 2: Array Express has some metadata in tables that must be downloaded locally before being queried

Limitations of current implementation - Limitations: A1, A11, A12: retrieve information only via HTTP, so they are all true. If data is on a local excel file or database, then we need a different implementation + Retrieval is not via identifier but keywords - Repositories not databases

General considerations All the information needed are retrieved from metadata, not from data. We did not investigate databases, but only repositories

In conclusion, we have proposed a computational implementation to calculate FAIR maturity indicators in the life sciences. Similarities and differences with the other criteria Conclusion: - it would be great if all repos had similar schema - it would be great if we could access everything via API

Acknowledgments

This work received funding from from the European Union's Horizon 2020 research and innovation programme via NanoSolvelT Project under grant agreement No 814572 and via RiskGONE Project under grant agreement No 814425. We would like to thank Nasim B. Sangani, Gwen Keulen, and Friederike Ehrhart for the use cases, Tobias Weber for the insightful discussion about data retrieval, and Lauren Dupuis for revising our manuscript.

We created this manuscript using manubot [18].

References

1. Attitudes and norms affecting scientists' data reuse

Renata Gonçalves Curty, Kevin Crowston, Alison Specht, Bruce W. Grant, Elizabeth D. Dalton *PLOS ONE* (2017-12-27) https://doi.org/gcrjn3

DOI: 10.1371/journal.pone.0189288 · PMID: 29281658 · PMCID: PMC5744933

2. Credit data generators for data reuse

Heather H. Pierce, Anurupa Dev, Emily Statham, Barbara E. Bierer

Nature (2019-06) https://doi.org/gf3j9t

DOI: 10.1038/d41586-019-01715-4 · PMID: 31164773

3. Who Shares? Who Doesn't? Factors Associated with Openly Archiving Raw Research Data

Heather A. Piwowar

PLoS ONE (2011-07-13) https://doi.org/cqvpdd

DOI: 10.1371/journal.pone.0018657 · PMID: 21765886 · PMCID: PMC3135593

4. Exploring visual representations to support data re-use for interdisciplinary science

Andrea Wiggins, Alyson Young, Melissa A. Kenney

Proceedings of the Association for Information Science and Technology (2018) https://doi.org/gf5shc

DOI: 10.1002/pra2.2018.14505501060

5. What is Data Retrieval? - Definition from Techopedia

Techopedia.com

https://www.techopedia.com/definition/30140/data-retrieval

6. The FAIR Guiding Principles for scientific data management and stewardship

Mark D. Wilkinson, Michel Dumontier, IJsbrand Jan Aalbersberg, Gabrielle Appleton, Myles Axton, Arie Baak, Niklas Blomberg, Jan-Willem Boiten, Luiz Bonino da Silva Santos, Philip E. Bourne, ... Barend Mons

Scientific Data (2016-03-15) https://doi.org/bdd4

DOI: <u>10.1038/sdata.2016.18</u> · PMID: <u>26978244</u> · PMCID: <u>PMC</u>4792175

7. Cloudy, increasingly FAIR; revisiting the FAIR Data guiding principles for the European Open Science Cloud

Barend Mons, Cameron Neylon, Jan Velterop, Michel Dumontier, Luiz Olavo Bonino da Silva Santos, Mark D. Wilkinson

Information Services & Use (2017-03-07) https://doi.org/gfkrrv

DOI: 10.3233/isu-170824

8. A design framework and exemplar metrics for FAIRness

Mark D. Wilkinson, Susanna-Assunta Sansone, Erik Schultes, Peter Doorn, Luiz Olavo Bonino da Silva Santos, Michel Dumontier

Scientific Data (2018-06-26) https://doi.org/gfkrrt

DOI: <u>10.1038/sdata.2018.118</u> · PMID: <u>29944145</u> · PMCID: <u>PMC6018520</u>

9. Evaluating FAIR Maturity Through a Scalable, Automated, Community-Governed Framework

Mark D Wilkinson, Michel Dumontier, Susanna-Assunta Sansone, Luiz Olavo Bonino da Silva Santos, Mario Prieto, Dominique Batista, Peter McQuilton, Tobias Kuhn, Philippe Rocca-Serra, Mercè Crosas, Erik Schultes

Cold Spring Harbor Laboratory (2019-05-28) https://doi.org/gf492b

DOI: 10.1101/649202

10. FAIRshake: toolkit to evaluate the findability, accessibility, interoperability, and reusability of research digital resources

Daniel J. B. Clarke, Lily Wang, Alex Jones, Megan L. Wojciechowicz, Denis Torre, Kathleen M. Jagodnik, Sherry L. Jenkins, Peter McQuilton, Zachary Flamholz, Moshe C. Silverstein, ... Avi Ma'ayan *Cold Spring Harbor Laboratory* (2019-06-03) https://doi.org/gf4cm8

DOI: 10.1101/657676

11. Are the FAIR Data Principles fair?

Alastair Dunning, Madeleine De Smaele, Jasmin Böhmer International Journal of Digital Curation (1970-01-01) https://doi.org/gf4bnb

DOI: 10.2218/ijdc.v12i2.567

12. How FAIR Can you Get? Image Retrieval as a Use Case to Calculate FAIR Metrics

Tobias Weber, Dieter Kranzlmuller

2018 IEEE 14th International Conference on e-Science (e-Science) (2018-10) https://doi.org/gf4bm9

DOI: 10.1109/escience.2018.00027

13. ArrayExpress-a public repository for microarray gene expression data at the EBI

A. Brazma

Nucleic Acids Research (2003-01-01) https://doi.org/fvff5t

DOI: <u>10.1093/nar/gkg091</u> · PMID: <u>12519949</u> · PMCID: <u>PMC165538</u>

14. Gene Expression Omnibus: NCBI gene expression and hybridization array data repository

R. Edgar

Nucleic Acids Research (2002-01-01) https://doi.org/fttpkn

DOI: <u>10.1093/nar/30.1.207</u> · PMID: <u>11752295</u> · PMCID: <u>PMC99122</u>

15. **Definition of DATA**https://www.merriam-webster.com/dictionary/data

16. **Definition of METADATA**https://www.merriam-webster.com/dictionary/metadata

17. ggplot2

Hadley Wickham

Springer New York (2009) https://doi.org/djmzjq

DOI: <u>10.1007/978-0-387-98141-3</u>

18. Open collaborative writing with Manubot

Daniel S. Himmelstein, Vincent Rubinetti, David R. Slochower, Dongbo Hu, Venkat S. Malladi, Casey S. Greene, Anthony Gitter

PLOS Computational Biology (2019-06-24) https://doi.org/c7np

DOI: 10.1371/journal.pcbi.1007128 · PMID: 31233491