Why FAIR?



Enabling data intensive research !



SCIENTIFIC DATA

Open Access | Published: 15 March 2016

The FAIR Guiding Principles for scientific data management and stewardship

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Scientific Data 3, Article number: 160018 (2016) | Cite this article 130k Accesses | 1680 Citations | 1571 Altmetric | Metrics

In An Addendum to this article was published on 19 March 2019

Abstract

The machine knows what I mean

There is an urgent need to improve the infrastructure supporting the reuse of scholarly data. A diverse set of stakeholders—representing academia, industry, funding agencies, and scholarly publishers—have come together to design and jointly endorse a concise and measureable set of principles that we refer to as the FAIR Data Principles. The intent is that these may act as a guideline for those wishing to enhance the reusability of their data holdings. Distinct from peer initiatives that focus on the human scholar, the FAIR Principles put specific emphasis on enhancing the ability of machines to automatically find and use the data, in addition to supporting its reuse by individuals. This Comment is the first formal publication of the FAIR Principles, and includes the rationale behind them, and some exemplar implementations in the community.

Box 2: The FAIR Guiding Principles

To be Findable:

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

F2. data are described with rich metadata (defined by R1 below)

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

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

To be Accessible:

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

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

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

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

To be Interoperable:

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

I2. (meta)data use vocabularies that follow FAIR principles

13. (meta)data include qualified references to other (meta)data

To be Reusable:

R1. meta(data) are richly described with a plurality of accurate and relevant attributes

R1.1. (meta)data are released with a clear and accessible data usage license

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

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



Virus Outbreak Data Network (VODAN)

Home > Implementation Networks > Current Implementation Networks > Virus Outbreak Data Network (VODAN)

The VODAN Implementation Network is one of the joint activities carried out by **CODATA**, **RDA**, **WDS**, and **GO FAIR** (Link to the **Data Together Statement**). Read the full statement on **Data Together COVID-19 Appeal and Actions**.

Active GO FAIR Implementation Network

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









The end of data sharing





Fig.5



Fig.8

provenance Multiple different cardinal Assertions* with the same subject GUPRI CA1 CA2 → Knowlet form a -CA3 CA4

 $G\ensuremath{\mathsf{UPRI}}\xspace's$ and Provenance not depicted for simplicity reasons



Fig.10























Real-world observations

Figure 1. The essence of the STAYAHEAD approach: The combination of a rapid MS test to directly detect viral variants (WP2), as well as broader data on the host (WP3) with computational predictions of likely but still 'virtual' variants of high concern (WP4) would enable to stay ahead of the virus with early detection and pre-emptive vaccine strategies. The validation of predictions in vitro (WP5) traditional sequencing will be used to demonstrate the feasibility of this approach. All data stored as FAIR digital Twins will be made available for a wide range of AI applications (WP1)

