

Using Standards for greater reuse of training material

Dr. Sonika Tyagi

Monash Bioinformatics Platform Manager

Training Coordinator EMBL-ABR

Chair Standards Committee GOBLET

Member Education sub-committee ABACBS



Why Standards ?

- In a digital world, **standards** of many types are essential for underpinning **interoperability** between **data**, computational **tools/software** that act on the data, and the **underlying infrastructure** that these tools/software use.
- Standards allow automated efficient exchange between tools and environment.

biosharing.org

The screenshot shows the biosharing.org website. At the top, there is a navigation bar with links for Standards, Databases, Policies, Collections, Add/Claim Content, Stats, and Log in or Register. The main heading reads "A curated, informative and educational resource on data and metadata standards, inter-related to databases and data policies." Below this are three main sections: "Find Recommendations" (standards and/or databases recommended by journal or funder data policies), "Discover Collections" (standards and/or databases grouped by domain, species or organization), and "Learn Educational" (about standards, their use in databases and policies, and how we can help you). A search bar is present with a "Search" button and a "Search Wizard" link. Below the search bar are checkboxes for Standards, Databases, Policies, and Collections/Recommendations. At the bottom, there are three columns of data: 702 Standards (Terminology Artifact: 345, Model/Format: 240, Reporting Guideline: 117), 975 Databases (Life Science: 733, Biomedical Science: 181, General Purpose: 10), and 97 Policies (Funder: 22, Journal: 68, Society: 3).

Oxford e-Research Centre & University of Oxford



biosharing.org : What it is?

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For researchers/curators looking for guidance

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For funders developing data policies

- To help refine policy by discovering which standards and databases are inter-related, more used and mature, or are funded by the organisation



biosharing.org : What is in it ?

STANDARDS

The standards in biosharing are manually curated from a variety of sources, including:

- [BioPortal](#) (repository of biomedical ontologies),
- [MIBBI](#) (repository of Minimum Information specifications for Biological and Biomedical Investigations)
- [Equator Network](#) (database of health research reporting guidelines)

Current content - 701 standards:

- [Terminologies](#) (ontology, controlled vocabulary, staging systems, etc) 344 (7 Aus)
- [Model/Format](#) (exchange formats, markup languages, RIF-CS, etc) 240 (11 Aus)
- [Reporting Guideline](#) (diagnostic reporting guidelines, minimum info specs, etc) 117 (10 Aus)



biosharing.org : What is in it ?

DATABASES

A catalogue of databases, described according to the [BioDBcore guidelines](#) (a community-defined, uniform, generic description of the core attributes of biological databases), along with the standards used within them; partly compiled with the support of Oxford University Press ([NAR Database Issue](#) and [DATABASE Journal](#)).

Current content - 975 databases:

- [Life Science](#) (non-human) 733 (20 Aus)
- [Biomedical Science](#) (human) 181 (5 Aus)
- [General Purpose](#) (incl. figshare, OSF, zenodo, wikidata, RDA, etc) 10 (1 Aus)



biosharing.org : What is in it ?

POLICIES

A catalogue of data preservation, management and sharing policies from international funding agencies, regulators and journals.

Current content - 97 Policies

- [Funder](#) 22 (1 Aus)
- [Journal](#) 68 (0 Aus)
- [Society](#) 3 (1 Aus)



biosharing.org : Who can contribute ?

Anyone can register to contribute content, or claim ownership of records created by a 3rd party



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Recently (2017) biosharing has become discipline agnostic:



FAIRsharing.org
standards, databases, policies

The logo for FAIRsharing.org features the word "FAIR" in blue, "sharing.org" in black, and a blue infinity symbol below "FAIR". The tagline "standards, databases, policies" is in black below the infinity symbol.

biosharing.org : Researcher attitude



2015/16 survey

BioSharing Survey - Summary, 19 May 2016

BioSharing Survey - Summary

Peter McQuilton¹, Pascale Gaudet² and Susanna-Assunta Sansone¹.

1. Oxford e-Research Centre, University of Oxford, UK
2. CALIPHO, Swiss Institute of Bioinformatics, CH

EXECUTIVE SUMMARY

A 10-question survey was conducted from the 18th December 2015 to 22nd February 2016 to gather users' views on which features and content they need to make informed decisions, e.g. on how to best select standards and understand their maturity, or to find the databases that implement them. A link to the questions can be found here: <https://bd2kccc.org/2016/01/15/biosharing-standards-registry-survey>.

https://figshare.com/articles/New_draft_item/3795810



biosharing.org : Researcher attitude

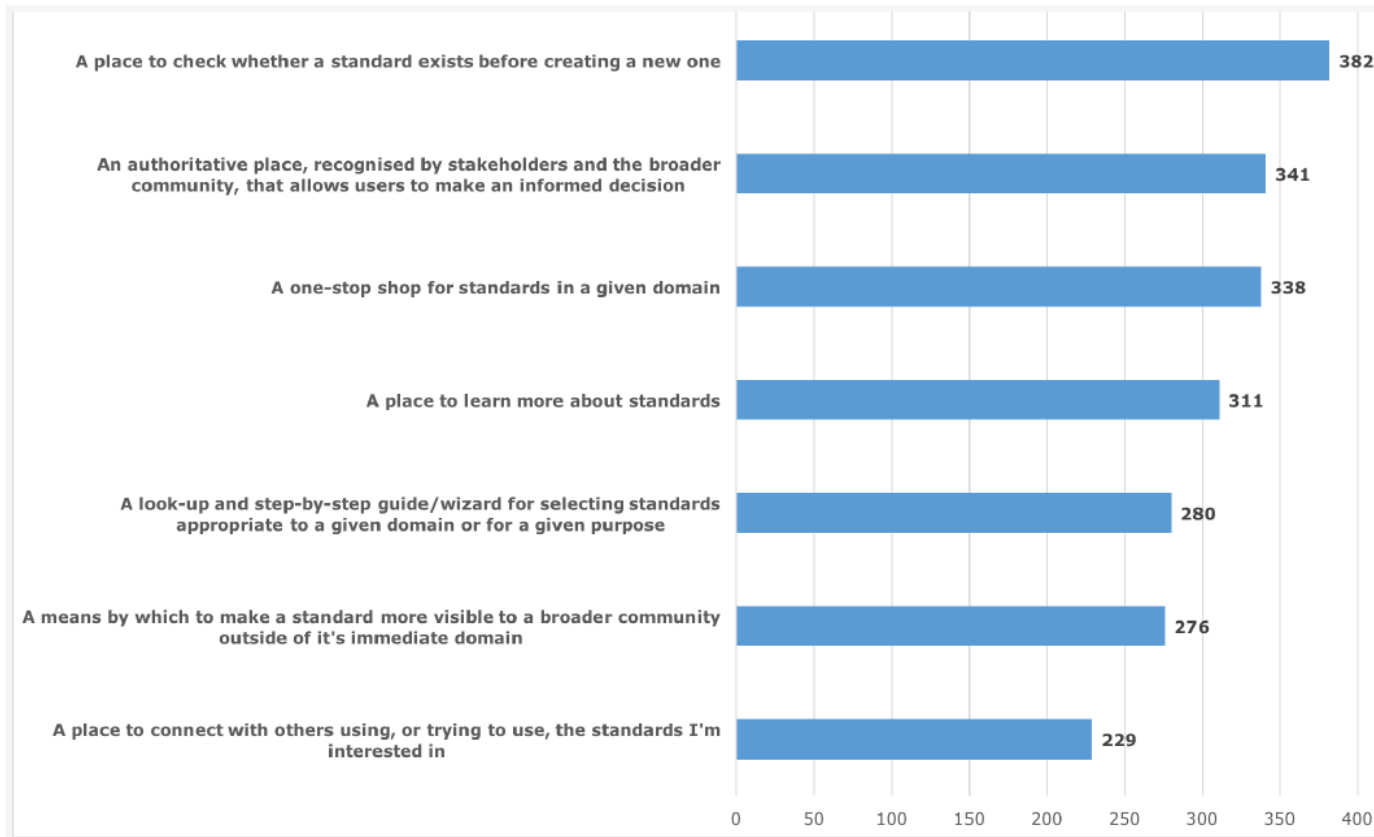
2015/16 survey - 3 months, 533 respondents

Researcher	323
Tool/database developer	274
Standard Developer/maintainer	206
Data Curator	151
Data Manager	150
Journal Publisher/Editor	31
Librarian	20
Funding Agency	20

- 25% assoc. with Elixir (EU)
- 21% assoc. with NIH BD2K (US)
- 65% aware of biosharing
- 30% had used biosharing

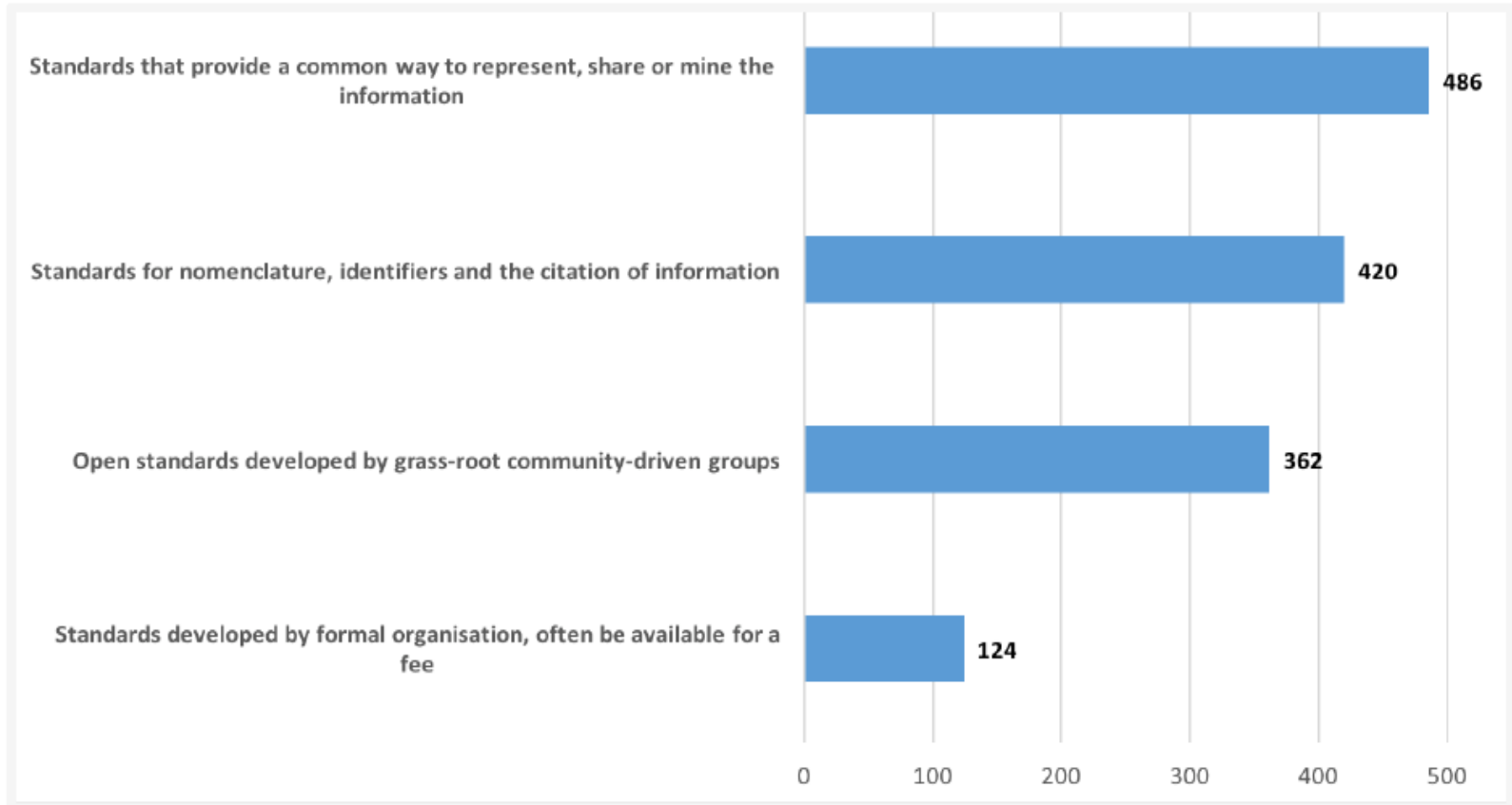


2015/16 survey : What do you need from a standards registry?



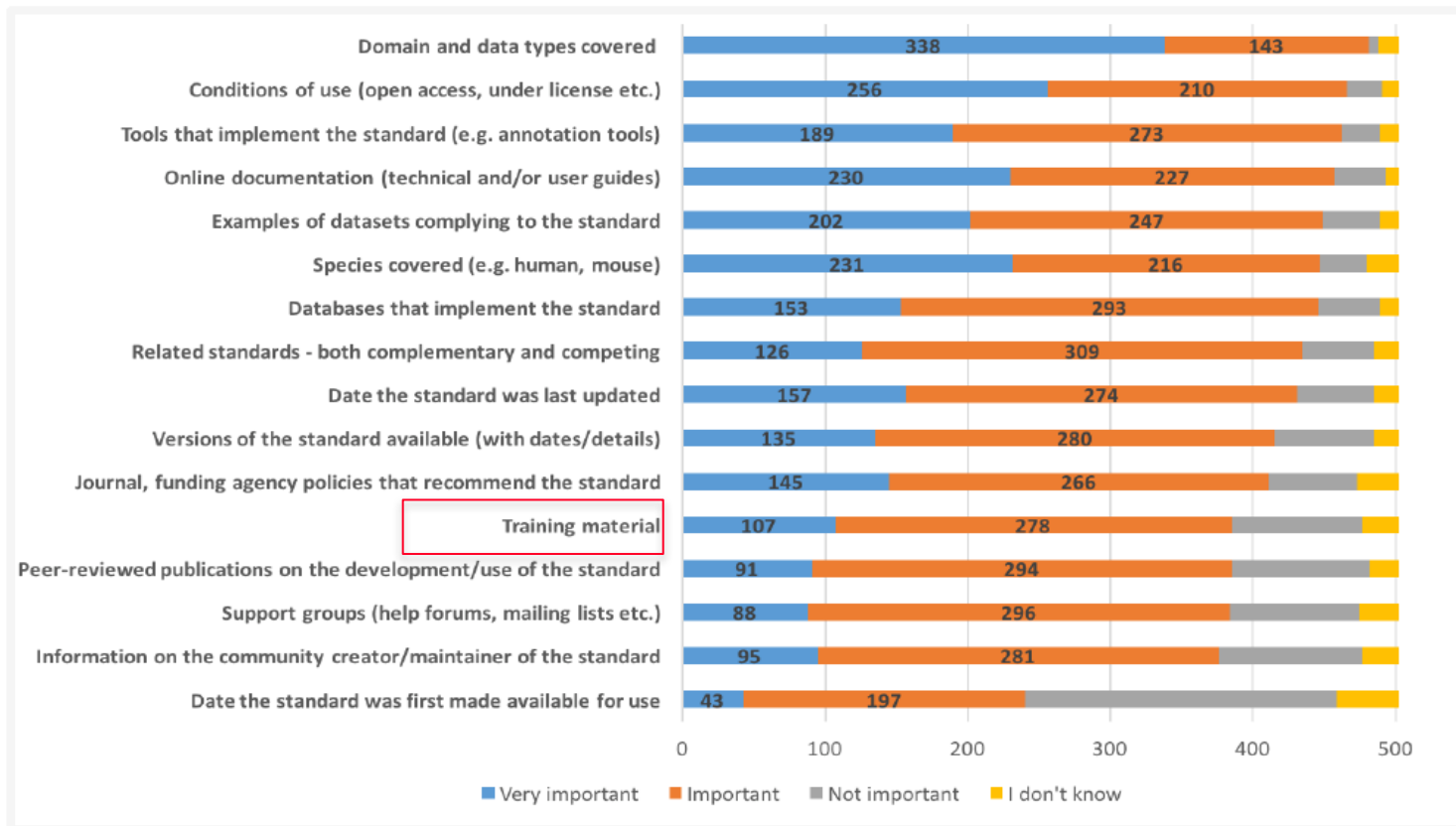
biosharing.org : Researcher attitude

2015/16 survey: What types of standards would you like to see in the registry?



biosharing.org : Researcher attitude

2015/16 survey: What information should a standards registry capture about a standard?



biosharing.org: Awareness in Australian Bioscience community



How aware is Australia's bioscience community of Standards?

EMBL-ABR + GOBLET Standards Key Area: 2017 Survey into Standards

- Is interest in and/or understanding of standards by biology and bioinformatics researchers in Australia therefore low?
- Awareness and Education is required ?

Overall, there is confusion between file formats and standards for metadata and annotation. Most respondents are unable to name an ontology or are unaware of how to find one. As yet, we have received limited responses relating to training material standards; however, this was listed amongst the top priority standards to be developed



Bioschemas

- to improve **data interoperability** in life sciences.
 - By using **schema.org** to add semantic markup to webpages for consistently structured information.
 - makes it easier to discover, collate and analyze distributed data.
- a collection of specifications that provide guidelines to facilitate a more consistent adoption of **schema.org** markup within the life sciences.

The IEEE 1484.12.1 – 2002 Standard for Learning Object Metadata

“Reusability of learning objects, to aid discoverability, and to facilitate their interoperability, usually in the context of online [learning management systems](#)”

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The term "**schema**" refers to the organization of data as a blueprint of how the **database** is constructed.

The schemas are a set of 'types', each associated with a set of properties. The types are arranged in a hierarchy. e.g. '**Event**' is a type that has properties like '**startDate**', '**endDate**' and '**description**'.

Standards for Training material ?



Training specification is under development. It is being written by a multi-institutional team from [ELIXIR](#), [Pistoia Alliance](#), [GOBLET](#), [TeSS](#), [BioSharing](#), [EMBL-ABR](#) and [BBMRI](#).

You can find more about the project and similar projects on the [bioschemas GitHub pages](#).

Standards for Training material ?



Standards committee:

- started to test how to make easier sharing bioinformatics events and training materials using schema.org
- minimum information and vocabularies which are important in our community.
 - Minimum descriptors to define training material
 - <http://tiny.cc/TrainingStandards>
 - Bioschema mapping
 - <http://tiny.cc/bioschemaMapping>

Acknowledgements

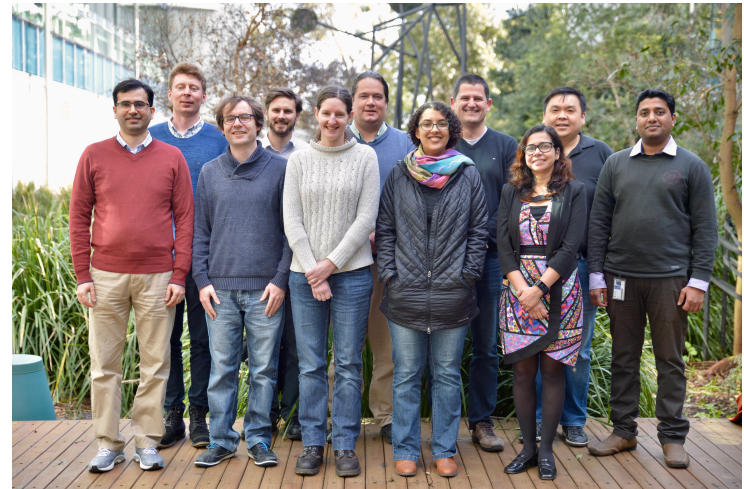


Jeff Christiansen (EMBL-ABR Data Coordinator)



Standards Committee

- Sonika Tyagi (Acting chair) (Monash, Aus)
 - Sarah Morgan (EBI, UK)
 - Michael Charston (UTAS, Aus)
 - Patricia Palagi (Swiss Institute of Bioinformatics)
 - Anette McGrath (CSIRO, Aus)
 - Gabriella Rustici (Cambridge University, UK)
 - Judit Kumuthini (H3BioNet South Africa)
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- Saravanan Dayalan (EMBL-ABR Standards Coordinator)



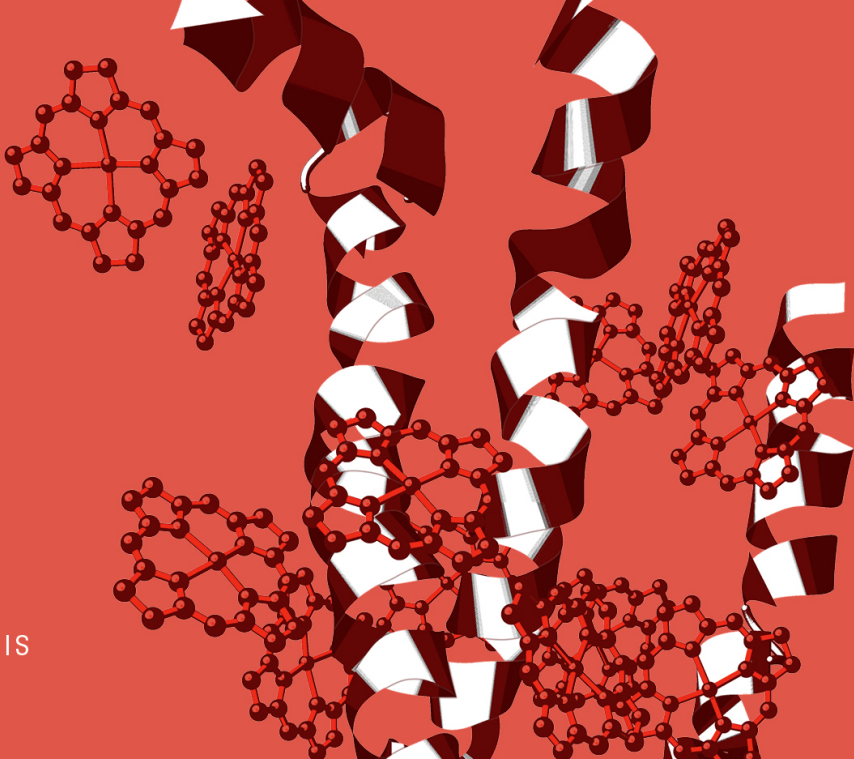
Monash Bioinformatics Platform team

Group exercises

1. Go to <https://fairsharing.org/standards/> and find out if there are existing standards for training material?
2. How many standards are there for the term 'expression' ? What different sub-types exist?
3. Go to <http://schema.org/docs/schemas.html> and look at 'CreativeWork' type and see if you can use some of the properties to 'training material' ? [hint: look at examples here <http://schema.org/docs/gs.html>]

Registrations are extended till the ABACBS17 week!

We are hosting BioinfoSummer 2017



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BIOINFO
SUMMER **17**




A SYMPOSIUM IN BIOINFORMATICS

4–8 DECEMBER 2017
MONASH UNIVERSITY, CAULFIELD CAMPUS

THEMES:
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PROTEOMICS & METABOLOMICS DATA
RNA-SEQ THEORY & PRACTICE
SINGLE-CELL GENOMICS
VISUALISATION, MODELLING & ANALYSIS

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