

# BioSharing: data repositories, standards and policies in the life, biomedical and environmental sciences

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**All the chairs and the above adopters agree with and approve this document.**

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## Executive summary

This **draft report** provides a summary of the problems we address and their context, along with a description of the outputs of the joint RDA/Force11 BioSharing Working Group (WG), which was approved at the 6th RDA Plenary (September 2015). This report is open for community review, a phase of the RDA Recommendation Endorsement Process<sup>1</sup>.

In line with the objectives, this WG has delivered the following outputs:

1. a set of **recommendations** to guide users and producers of databases and content standards to select and describe them, or recommend them in data policies; and
2. a curated **registry**, which enacts the recommendations and assists a variety of end users, through the provision of well described, interlinked, and cross-searchable records on content standards, databases and data policies.

The intended target of these outputs are stakeholders in all sectors, those producing and using databases, content standards and data policies, and those who are involved in managing, serving, curating, preserving, publishing or regulating data and/or other digital objects, in particular datasets. Whether they are researchers, standard/database developers, funders, journal editors, librarians or data managers, the outputs from the BioSharing WG aim to enable end users to understand which standards and databases are mature and appropriate to their use case. By mapping the relationships between standards and the databases that implement them, or the policies that recommend them, the BioSharing registry enables them to make an informed decision as to which standard or database to use or endorse.

As of 28th of March 2017, the BioSharing registry<sup>2</sup> contains over 1639 manually curated and linked entries, split into over 868 database entries, over 675 data and metadata standards records, and over 96 data policy records, from journals, funders, societies and other organisations. The registry already has many adopters ranging from journal publishers, infrastructure programmes, to other organizations or projects (that in turn serve individual researchers or other stakeholders) - all use BioSharing in their activity in some way, and link back to the BioSharing portal from their webpages. A list of adopters can be found at the end of this document, with a continuously updated version on the BioSharing website.

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<sup>1</sup> <https://www.rd-alliance.org/groups/creating-and-managing-rda-groups/working-group-outputs.html>

<sup>2</sup> <https://www.biosharing.org>

BioSharing is maintained at the University of Oxford and is an ELIXIR Interoperability Platform resource. The registry will continue to evolve - as an element within an ecosystem of services - to support and enable the FAIR principles for reproducible research and open science.

## 1. The context

The growing movement for reproducible research and open science has, along with an overall increase in data generation, led to the development of many community-driven data repositories and standards. Among the latter, interoperability standards are essential to drive the operational processes underlying information exchange of information between different systems, to ensure data and all other digital research outputs are Findable, Accessible, Interoperable and Reusable, according to the FAIR principles<sup>3</sup>, to both human and machine. Interoperability requires standardized identifiers and descriptions (or metadata) for each digital object, including the accessibility level of the information and/or licence type, among other requirements.

Within the metadata standards there are content standards, which open all elements of a dataset to transparent interpretation, verification and exchange, so facilitating the integrative analysis and comparison of heterogeneous data from multiple sources, domains and disciplines. Content standards vary in depth and breadth but generally cover the what, who, when, where, how and why of a dataset. Using an example from the life sciences, content standards allow fundamental biological entities (e.g., samples, genes), experimental components (e.g., conditions, cell lines), complex concepts (such as tissues and diseases), analytical processes and mathematical models and their instantiation in computational simulations (spanning from the molecular level through to whole populations of individuals) to be harmonized with respect to structure, format and annotation, detailing the information on who produced the data, who funded it, where it is deposited, published, and so on.

The whole area of interoperability standards is being actively developed and - from the life sciences perspective - an overview of the different community efforts (their life cycle along with challenges and opportunities) is available in this Wellcome Trust review<sup>4</sup>.

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<sup>3</sup> Wilkinson MD et al. The FAIR Guiding Principles for scientific data management and stewardship. *Sci Data*. 2016 Mar 15;3:160018. <http://dx.doi.org/10.1038/sdata.2016.18>

<sup>4</sup> Sansone, S-A and Rocca-Serra, P. Review: Interoperability standards. Wellcome Trust. *Figshare*. 2016 <https://doi.org/10.6084/m9.figshare.4055496.v1>

## 2. The problem we address

In the life, environmental and biomedical sciences there are almost a **thousand content standards** and **several thousand databases**, designed to assist the virtuous data cycle, from collection to annotation, through preservation and publication to subsequent sharing and reuse. This proliferation of community-developed content standards and data repositories brings with it massive sociological and technological challenges; for example there are duplications and gaps in coverage, and often their maturity and standing in the community is not obvious. Therefore it is essential that not just researchers but all stakeholders involved in managing, serving, curating, preserving, publishing or regulating data and/or other digital objects are able to select, use, implement and/or recommend the appropriate content standards and databases. Researchers should be able to select the relevant database(s) for data submission, to know which implement content standards to use to format their datasets and which databases and standards are recommended by a journal or funder. Another example is when a content standard is mature, and standard-compliant databases become available, these resources should be channelled to funder and journal editors who in turn can recommend them in their data policies.

To achieve this, we need to curate and cross-link information on databases, content standards and journal and funder policies, and serve this information in a searchable form to inform, educate and help researchers, standard/database developers, funders, journal editors, librarians, data managers and other stakeholders.

## 3. Goals and accomplishments

To address the problem, we have decided to focus on the life, environmental and biomedical domains, in the first instance. Firstly, because a wealth of standards and databases exists, along with a growing number of data policies by journals and funders, and secondly, because an initiative working to map these some of these resources, the MIBBI portal<sup>5</sup>, has been active since 2008. The BioSharing portal<sup>6</sup> is an evolution of its basic MIBBI predecessors, and was launched in 2011 by the same operational team.

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<sup>5</sup> Taylor C., et al. "Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project" *Nature Biotechnology* 26, 889 - 896 (2008)  
<http://dx.doi.org/10.1038/nbt.1411>

<sup>6</sup> McQuilton, P., et al. BioSharing: curated and crowd-sourced metadata standards, databases and data policies in the life sciences. *Database (Oxford)* 2016; 2016 baw075.  
<http://dx.doi.org/10.1093/database/baw075>

Therefore, building upon the existing BioSharing portal and its community has been a natural choice for the WG, which has reached out to more participants, users and collaborators via the RDA and the link to Force11 (a community of scholars, librarians, archivists, publishers and research funders that has arisen organically to help facilitate the move towards improved knowledge creation and sharing).

The overall goal of the BioSharing WG is to deliver: (i) a curated portal that inter-relates databases, content standards and data policies, to inform and educate a variety of stakeholders, along with (ii) a set of recommendations to guide users and producers of databases and content standards to select and describe them, or recommend them in data policies. Figure 1 illustrates some of the use cases and competency questions BioSharing addresses.

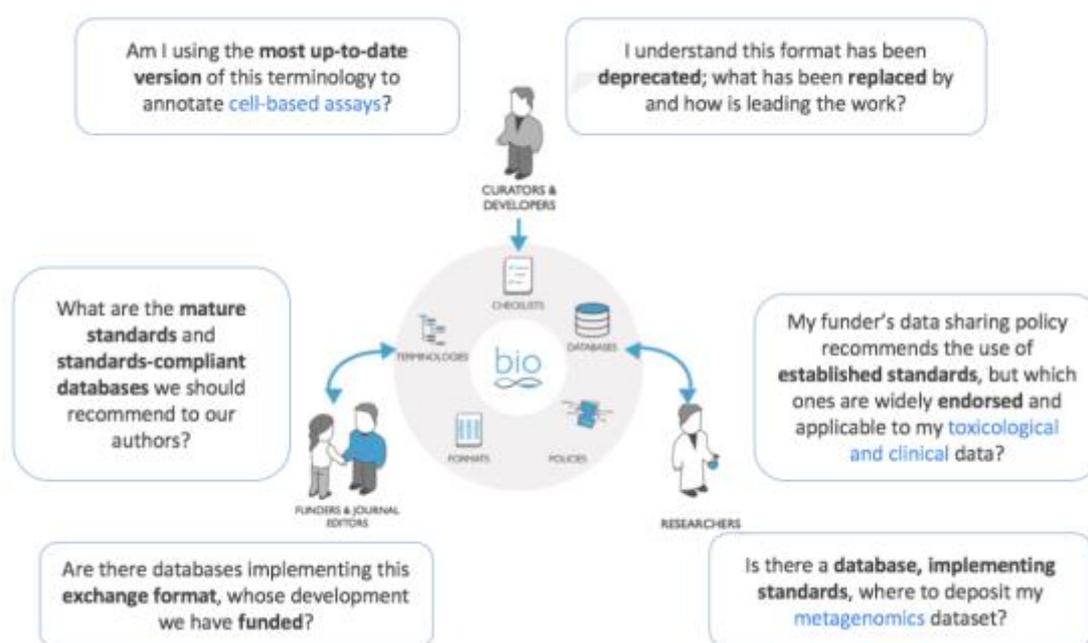


Figure 1. Some of the use cases and competency questions.

### 3.1. Output 1: BioSharing registry

The BioSharing registry<sup>2</sup> is a manually curated, informative and educational resource on inter-related content standards, databases and data policies in the life, environmental and biomedical sciences. The data policies are further divided into those from journal publishers, funders and societies. The content standard are subdivided in three types:

- *Reporting guidelines* or checklists, outline the necessary and sufficient (or minimum) information that is vital for contextualizing and understanding a dataset (e.g. the ARRIVE<sup>7</sup> guidelines);
- *Terminology artefacts* or semantics, provide the unambiguous identification and definition of concepts within a scientific domain, encompassing lexica, dictionaries, vocabularies, taxonomies, thesauri and ontologies (e.g. Disease Ontology<sup>8</sup>);
- *Models/formats* or syntaxes, define the structure and interrelation of information from a conceptual model or schema, and the transmission format to facilitate data exchange between different systems (e.g. CellML<sup>9</sup>).

The BioSharing registry currently contains 1639 records that can be searched via a number of search and filter tools in the registry; the content is licensed via the Creative Commons Attribution ShareAlike license 4.0 (CC BY-SA 4.0). Each standard and database record in BioSharing contains over 40 metadata fields, split into three types - free text, controlled vocabularies/tags, and drop-down menus. Very often content standards are related as they need to be used in combination, or are implemented by one or more databases; these relations need to be made explicit, where appropriate. For example, a reporting guideline may suggest the use of a particular terminology and model/format, or a database may implement a number of standards in its schema. BioSharing shows the number of databases in which a standard is implemented, the type and number of community standards a database uses, and how many and which journal and funder data policies recommend the use of a resource (database or standard). By doing so, BioSharing provides users with simple indicators to assess community usage and adoption of a standard or database, empowering them to make an informed decision as to which standard(s) to use for their data and where it should be deposited.

The relationships between standards, databases and policies are not static but evolve over time, with new links being added and old links being removed as standards and databases are deprecated and superseded. Although BioSharing does not yet implement versioning, records are not deleted but their evolution is tracked and their status tagged, accordingly, like illustrated in Figure 2. To capture the status of a resource, be it a standard or database, BioSharing uses one of the following four options - 'R' for ready, i.e. for use or implementation - this is our most common status; 'Dev' for those resources which are still in development, but where the developers wish to list the resource on BioSharing to encourage community interaction; 'D' for deprecated, where a resource is designated as no longer

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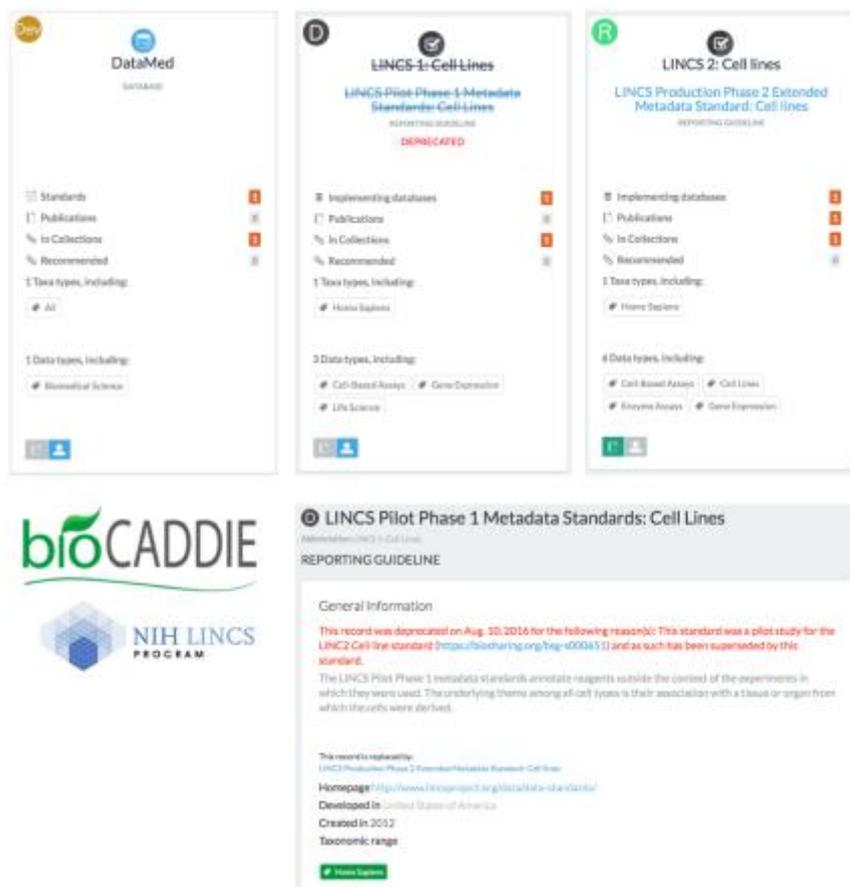
<sup>7</sup> <https://biosharing.org/bsq-s000035>

<sup>8</sup> <https://biosharing.org/bsq-s000093>

<sup>9</sup> <https://biosharing.org/bsq-s000050>

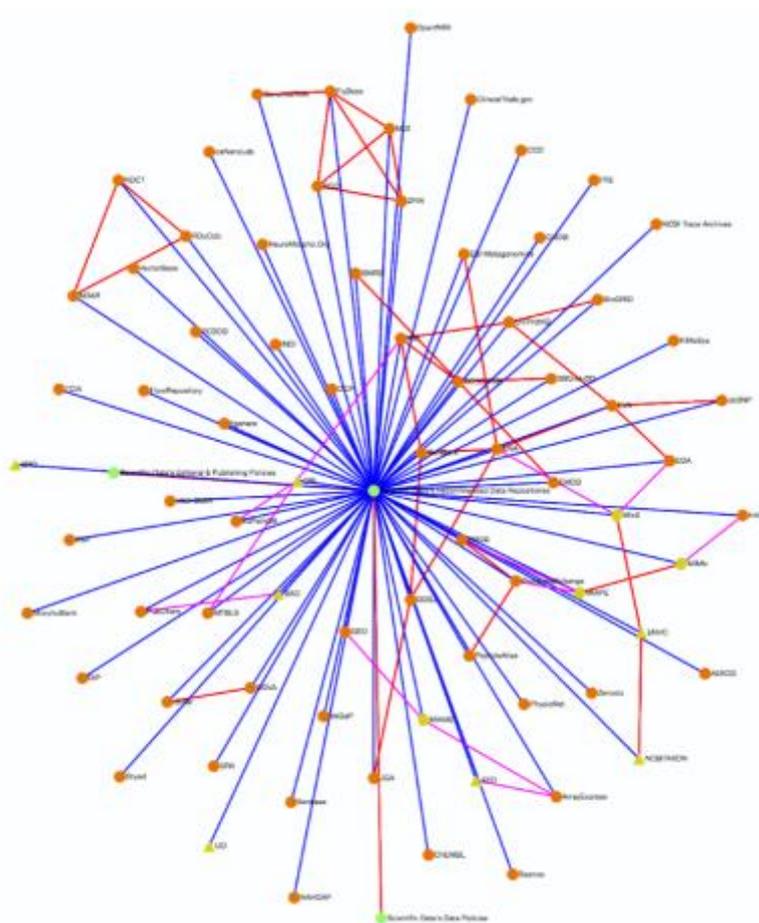
active or maintained - where appropriate, we provide links to resources that supersede the deprecated resource, to provide alternatives for users; 'U' for uncertain - where we simply don't have enough information to know whether a resource is ready 'R', 'Dev', or 'D'. This last status is really a request for help from our community to provide more information on the resource so we can assign the appropriate status.

One of the many features that make BioSharing unique is the ability for users to claim a record, so granting them not only exposure and credit for the resource they are maintaining, but also the ability to update the record for that resource. All records are checked by a BioSharing curator/knowledge engineer. If a user updates a record, those updates will be assessed against our curation guidelines to ensure they are an accurate representation of the resource. Likewise, if a record is updated by a BioSharing curator, an email notification is sent to the record claimant, so providing a data cross-check to reduce the introduction of inaccuracies.



**Figure 2.** Examples of status indicators for a database, in development 'Dev', of two standards: one deprecated 'D' and the one that has superseded it, marked as ready 'R'. In this case, working with the maintainer of the standards, the BioSharing curator has also been able to add a note explaining the reason why the standard has been deprecated.

A further feature which has proved popular with our adopters, is the ability to collate or group resources into Collections<sup>10</sup>, where they are related to a particular group or initiative, or Recommendations<sup>11</sup>, where the grouping is based on a data policy from a journal, society or funder. An example of a journal policy that recommends a variety of databases and standards is provided in Figure 3. Collections and recommendations can be viewed on BioSharing as a table, grid or as an interactive network graph, via our ExploreBioSharing tool. In the graph, each node is clickable and provides some minimal information about the resource, along with a link to the main BioSharing record for that resource. The network graph can also be filtered by domain or species and can be expanded to include a further level of related databases and standards.



**Figure 3.** An example of an ExploreBioSharing network graph, representing the repositories (orange dots) and data standards (yellow dots) recommended by the *Scientific Data* journal data policy (the green dot in the centre of the graph)<sup>12</sup>

<sup>10</sup> <https://biosharing.org/collections>

<sup>11</sup> <https://biosharing.org/recommendations>

<sup>12</sup> <https://biosharing.org/recommendation/ScientificData>

## 3.2. Output 2: Recommendations

Presented here with a CC0 license, are recommendations to guide users and producers of databases and content standards to select and describe them, or recommend them in data policies. Recommendations have been grouped according to the target community, where possible, and provided along with explanation of the benefits. For the life, biomedical and environmental sciences, the recommendations alone would not be usable without the portal. However, the recommendations are easily generalizable or customizable to other areas of sciences and humanities. These recommendations should be considered as a ***strawman draft that will be extended and refined using the feedback and comments from the open RDA community review process*** (scheduled to last for 4 weeks, starting on April 5th 2017 when the 9th RDA Plenary begins).

### **For developers and maintainers of standards and databases**

- Register or claim your resource in BioSharing to make your work more visible and discoverable, provide or vet the tags indicating its status of maturity, and get credit for maintaining the record.
  - This provides the resource with increased exposure outside of your immediate community, particularly to journals, funders, librarians, researchers curators or data managers, who could recommend it to their community or use it themselves. The more adopted a resource is, the greater its visibility in BioSharing. For example, if your standard is implemented by a database, these two records will be interlinked; thus if someone is interested in that database they will also be able to look at the standards used. And vice-versa for databases. Once your resource is registered, as the content grows and it is progressively interlinked, your database(s) and/or standard(s) could also be recommended in a data policy by journals, funders or other organizations. When this is the case, your resource gets a 'recommended' ribbon, which is clearly visible in the search results.
- Create your own collection of standards and/or databases or a combination of these resources to help promote their relations.
  - This personalized collection page is customisable with your community name and logo and can be linked to/from your website. A collection can help you to e.g. showcase the standards developed by the same standard developing organization, and the databases implementing them.

### **For journal and funder data policy editors**

- Create clear, time-stamped and up to date data policies, detailing where you recommend authors or fundees should deposit their data, and where possible which content standards to use and/or is used by the recommended databases.
  - All journals and funders who do not have such statements should develop them to ensure all data relating to an article or project are as FAIR as possible.
- Register your data policy in BioSharing, and then link it to an interrelated list of database and standards that correspond to the resources you recommend.
  - This personalized recommendation page is customisable with your policy publisher's name and logo and can be linked to/from your website. The content of your recommendations is searchable and can be viewed on BioSharing as a table, grid or as an interactive network graph, via our ExploreBioSharing tool.

**For researchers, curators and data managers (supporting researchers)**

- Search in BioSharing to identify the database(s) and standard(s) appropriate to your data and study types, before experiments commence, in order to make the data more easily submittible and useful in the future.
  - For example, when creating a data management plan, ensure you identify the most appropriate reporting guidelines, formats and terminologies, wherever these exist for your data and study types. The content standards used should also be clearly identified in the metadata associated with your dataset(s).
- Select resources starting with those recommended by journals and funders data policies and those grouped in collections, and use the indicators of status provided in each BioSharing record for further guidance.
  - Use a combination of the search functionalities provided by BioSharing, and look especially for databases implementing standards and vice-versa.

**For all the stakeholders above, and research data support teams, training and educational organizations**

- Promote the education of researchers in data management and organize and develop training and educational tools and resources, including using BioSharing.
- Create your own BioSharing collection of standards and/or databases or a combination of these resources for data and study types.
- Encourage data producers to license their data with the most open licence possible (e.g. CC0), and pay attention to the licences associated with the databases you recommend.

- *Promote the use of persistent identifiers for databases and standards, and also for researchers (ORCID), citations (PMIDs) and funders (FundRef) to uniquely and unambiguously identify objects. Where possible, authors/researchers should add RRIDs<sup>13</sup> to their papers and include concise data statements in research papers which should contain information about the availability, location and format of data, and where possible, use permanent identifiers.*
  - *Note: we acknowledge that many activities on identifiers are work in progress and several different efforts exists to identify and cite resources, including databases and standards. BioSharing records also have a unique, persistent identifier, which can be used for citation purpose. However, our recommendations around this specific point will be reviewed and refined during this RDA open review phase and consolidated as the WG recommendation are finalized.*

### 3.3. Links and collaborations with other systems

No other system exists that connects all three aspects of data deposition: the content standards one should use, which particular database to deposit data into, and which standards and repositories are recommended by a particular funder or journal. However, other resources exist that are either complementary or contain a subset of the resources found in BioSharing. Through our joint RDA/Force11 WG and other interactions, we collaborate with a wide variety of communities and other registries and portals. Without trying to be exhaustive, for example, the BioSharing portal has: (i) integrated data from the JISC journal policy project<sup>14</sup>, which maps journal data policies with data standards and repositories; (ii) initiated a database records exchange project with the Japanese National Bioscience Center Integbio database<sup>15</sup> (funded by the UK-Japan BBSRC International Partnering Award); (iii) created links with other ELIXIR-related resources and activities, such as the ELIXIR TeSS<sup>16</sup> training and events platform, Identifiers.org catalogue<sup>17</sup> of directly resolvable identifiers in the life sciences, schema.org<sup>18</sup> and Bioschemas<sup>19</sup> to enhance discoverability by major search engines, and the USA NIH-funded BioPortal<sup>20</sup>; (iv) initiated

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<sup>13</sup> <https://www.force11.org/group/resource-identification-initiative>

<sup>14</sup> <https://www.jisc.ac.uk/rd/projects/journal-research-data-policy-registry-pilot>

<sup>15</sup> <http://integbio.ip/en>

<sup>16</sup> <https://tess.elixir-europe.org>

<sup>17</sup> <http://identifiers.org>

<sup>18</sup> <https://schema.org>

<sup>19</sup> <http://bioschemas.org>

<sup>20</sup> <https://biportal.bioontology.org>

discussions with the re3data registry<sup>21</sup> of data repositories, the RDA Metadata Standards Directory WG<sup>22</sup>, and data management tools, such as DMPOnline/DMPTool<sup>23</sup> and the nascent ELIXIR Data Stewardship wizard.

## 4. Maintenance and outreach

BioSharing is embedded in several UK, EU and USA National Institutes of Health's Big Data to Knowledge (BD2K) projects and activities, which fund the operational team at the University of Oxford. BioSharing has also an active and dynamic International Advisory Board, drawn from the worlds of publishing, data management, national funders, research and infrastructure projects, who guide our team of developers and knowledge engineers. See the BioSharing communities page for more information.

BioSharing will continue to be developed also as a resource of the Interoperability Platform of ELIXIR (<https://www.elixir-europe.org/platforms/interoperability>), which works to coordinate, integrates and sustain Europe's leading bioinformatics resources, to enable users in academia and industry to access services that are vital for their research activities.

Planned activities, include opening up the BioSharing data for sharing and linking across a number of other resources, which will allow the information entered into BioSharing to not only be of more use to the community but also to be more sustainable. This could reduce the chances of both BioSharing and the information therein being lost to the community.

As the BioSharing RDA/Force11 WG comes to an end, we foresee that the work will be maintained under the ELIXIR Bridging Force IG and evolve as part of the new Data Policy Standardisation and Implementation IG and Active Data Management Plans IG. Furthermore, the WG co-chairs will continue their active participation and further integration with relevant RDA, Force11, International Society for Biocuration and CODATA activities, along with other open science projects such as the EOSC Open Science Policy Platform and the nascent GO-FAIR ecosystem.

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<sup>21</sup> <http://re3data.org>

<sup>22</sup> <https://www.rd-alliance.org/groups/metadata-standards-directory-working-group.html>

<sup>23</sup> <https://dmponline.dcc.ac.uk/roadmap>

## 5. Current adopters

As of March 2017, the BioSharing portal has already a large number of high-caliber adopters, which are also listed on the respective RDA and Force11 webpages for the WG and on the BioSharing community webpage<sup>24</sup>

Adopter	Type	Associated BioSharing Record
Biotechnology and Biological Sciences Research Council (BBSRC)	Resource list <a href="http://www.bbsrc.ac.uk/funding/application-guidance/justification-resources/resources">http://www.bbsrc.ac.uk/funding/application-guidance/justification-resources/resources</a>	-
BioMedCentral (BMC)	Journal Data Policy <a href="http://www.biomedcentral.com/getpublished/editorial-policies#DataandMaterialRelease">http://www.biomedcentral.com/getpublished/editorial-policies#DataandMaterialRelease</a>	Recommendation <a href="https://biosharing.org/recommendation/BMC">https://biosharing.org/recommendation/BMC</a>
EMBO Press	Journal Data Policy <a href="http://msb.embopress.org/authorguide#datadeposition">http://msb.embopress.org/authorguide#datadeposition</a>	Recommendation <a href="https://biosharing.org/recommendation/EMBOPress">https://biosharing.org/recommendation/EMBOPress</a>
Faculty of 1000 (F1000)	Journal Data Policy <a href="https://f1000research.com/for-authors/data-guidelines">https://f1000research.com/for-authors/data-guidelines</a>	Recommendation <a href="https://biosharing.org/recommendation/F1000ResearchRecommendedRepositories">https://biosharing.org/recommendation/F1000ResearchRecommendedRepositories</a>
GigaScience	Journal Data Policy <a href="https://academic.oup.com/gigascience/pages/instructions-to-authors#Preparing%20Supporting%20Information">https://academic.oup.com/gigascience/pages/instructions-to-authors#Preparing%20Supporting%20Information</a>	Recommendation <a href="https://biosharing.org/recommendation/GigaScience">https://biosharing.org/recommendation/GigaScience</a>
Scientific Data	Journal Data Policy <a href="http://www.nature.com/sdata/policies/repositories">http://www.nature.com/sdata/policies/repositories</a>	Recommendation <a href="https://biosharing.org/recommendation/ScientificData">https://biosharing.org/recommendation/ScientificData</a>
Springer Nature	Journal Data Policy <a href="http://www.springernature.com/gp/group/data-policy/repositories">http://www.springernature.com/gp/group/data-policy/repositories</a>	-
Wellcome Open Research	Journal Data Policy <a href="https://wellcomeopenresearch.org/for-authors/article-guidelines">https://wellcomeopenresearch.org/for-authors/article-guidelines</a>	Recommendation <a href="https://biosharing.org/recommendation/WellcomeOpenResearch">https://biosharing.org/recommendation/WellcomeOpenResearch</a>
ELIXIR Europe	Infrastructure <a href="https://www.elixir-europe.org/platforms/interoperability">https://www.elixir-europe.org/platforms/interoperability</a>	Collection <a href="https://biosharing.org/collection/ELIXIR">https://biosharing.org/collection/ELIXIR</a>

<sup>24</sup> <https://biosharing.org/communities>

ELIXIR UK	Infrastructure <a href="http://www.elixir-uk.org/resources/biosharing">http://www.elixir-uk.org/resources/biosharing</a>	-
JISC, UK	Infrastructure <a href="https://www.jisc.ac.uk/rd/projects/journal-research-data-policy-registry-pilot">https://www.jisc.ac.uk/rd/projects/journal-research-data-policy-registry-pilot</a>	-
Cell Migration Standardisation Organisation (CMSO)	Organisation <a href="https://cmso.science">https://cmso.science</a>	Collection <a href="https://biosharing.org/collection/CellMigrationStandardisationOrganisation">https://biosharing.org/collection/CellMigrationStandardisationOrganisation</a>
Clinical Data Interchange Standards Consortium (CDISC)	Organisation <a href="https://www.cdisc.org/standards">https://www.cdisc.org/standards</a>	Collection <a href="https://biosharing.org/collection/ClinicalResearchCDISC">https://biosharing.org/collection/ClinicalResearchCDISC</a>
EMBL-Australia Bioinformatics Resource (EMBL-ABR), AU	Organisation <a href="https://www.embl-abr.org.au/standards/">https://www.embl-abr.org.au/standards/</a>	Collection <a href="https://biosharing.org/collection/EMBLABR">https://biosharing.org/collection/EMBLABR</a>
Taxonomic Databases Working Group (TDWG)	Organisation <a href="http://www.tdwg.org/standards">http://www.tdwg.org/standards</a>	Collection <a href="https://biosharing.org/collection/TDWGBiodiversity">https://biosharing.org/collection/TDWGBiodiversity</a>
FAIRDOM, EU	Project <a href="https://fair-dom.org/knowledgehub/community-standards">https://fair-dom.org/knowledgehub/community-standards</a>	Collection <a href="https://biosharing.org/collection/FAIRDOM">https://biosharing.org/collection/FAIRDOM</a>
Euro-BiolImaging, EU	Project <a href="https://www.eurobioimaging-interim.eu/image-data-resource.html">https://www.eurobioimaging-interim.eu/image-data-resource.html</a>	Collection <a href="https://biosharing.org/collection/EuroBioImaging">https://biosharing.org/collection/EuroBioImaging</a>
Innovative Medicine Initiative (IMI) eTRIKS	Project <a href="https://www.etriks.org/standards-starter-pack">https://www.etriks.org/standards-starter-pack</a>	Collection <a href="https://biosharing.org/collection/eTRIKS">https://biosharing.org/collection/eTRIKS</a>
NIH LINCS Program, USA	Project <a href="http://www.lincsproject.org">http://www.lincsproject.org</a>	Collection <a href="https://biosharing.org/collection/LINCSPROJECT">https://biosharing.org/collection/LINCSPROJECT</a>
Stanford University, USA	Research Data Management <a href="http://library.stanford.edu/research/data-management-services/share-and-preserve-research-data/domain-specific-data-repositories">http://library.stanford.edu/research/data-management-services/share-and-preserve-research-data/domain-specific-data-repositories</a>	-
University of Cambridge, UK	Research Data Management <a href="http://www.data.cam.ac.uk/data-management-guide/organising-your-data">http://www.data.cam.ac.uk/data-management-guide/organising-your-data</a>	-
University of Oxford, UK	Research Data Management <a href="http://researchdata.ox.ac.uk/home/tools-services-and-training/browse-subject/science-">http://researchdata.ox.ac.uk/home/tools-services-and-training/browse-subject/science-</a>	-

## 6. Get involved and become an adopter

To provide feedback on this document, join the **BioSharing RDA WG email list**<sup>25</sup>; or contact us via the **Force 11 WG email list**<sup>26</sup>. To become a signatory of the final document, you need to be an adopter.

Adopters are representatives of journal publishers, infrastructure programmes, institutions and other organizations or projects (that in turn serve and guide individual researchers or other stakeholders). Adopters use BioSharing to inform their data policy and create a Recommendation, or to create a Collection around a given domain of interest, and link back to them from their webpages.

If you are a producer or maintainer of standards and/or databases, you can add a record to BioSharing for the resource. If a record for the resource already exists in BioSharing, you can claim that record, which allows you to edit and update the record to ensure it is as accurate as possible, as well as providing a contact point for BioSharing users should they wish to contact you to find out more about your resource.

More information on how to create and claim records can be found on a dedicated BioSharing webpage<sup>27</sup>. For any enquire on how use or submit to BioSharing, contact the team<sup>28</sup>.

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<sup>25</sup> <https://www.rd-alliance.org/group/biosharing-registry-connecting-data-policies-standards-databases-life-sciences.html>

<sup>26</sup> <https://www.force11.org/group/biosharingwg>

<sup>27</sup> <https://biosharing.org/new>

<sup>28</sup> [biosharing-contact-us@lists.sf.net](mailto:biosharing-contact-us@lists.sf.net)