ELIXIR Europe

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ELIXIR Services

Data deposition:
ENA, EGA, PDBe, EuropePMC, …

Data management:
Genome annotation
Data management plans

Data access :
UniProt, Ensembl, OrphaNet, …

Data Interoperability:
Standards, Identifiers, FAIR, Ontologies

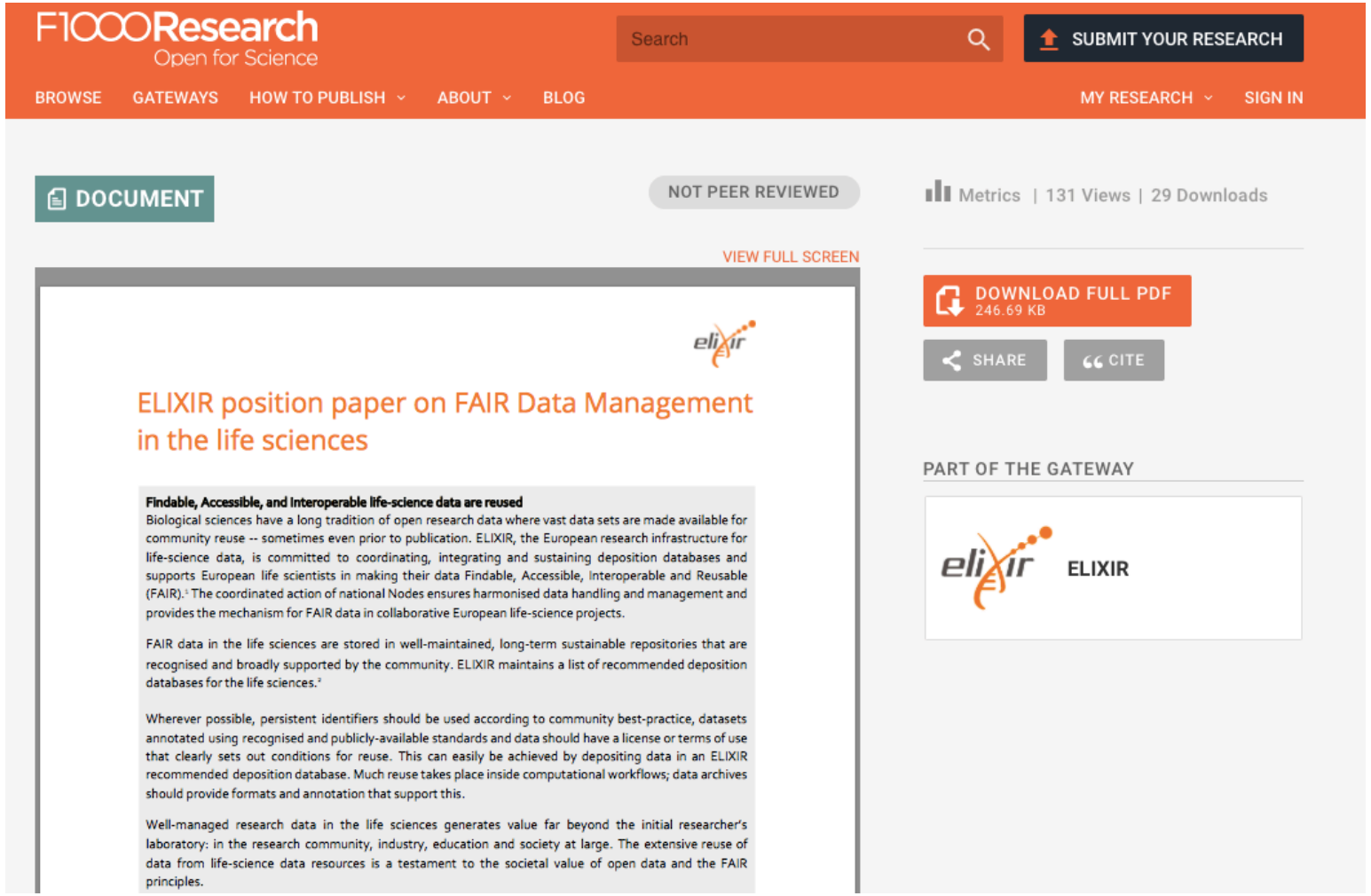
Compute:
Secure data transfer, cloud computing, AAI

Bioinformatics tools:
Bio.tools

Industry:
Innovation and SME programme
Bespoke collaborations

Training:
TeSS, Data Carpentry, eLearning

ELIXIR position on FAIR Data Management



ELIXIR position on FAIR Data Management

- Open sharing of research data is a core principle for publicly-funded research and ELIXIR encourages all funders to adopt Open Data mandates.
- Data Management is crucial part of good scientific practice and research excellence.
- Whenever possible, biological research data should be submitted to the recommended community deposition databases.
- All data submitted to Open Data archives must be annotated in accordance with community-defined standards.
- ELIXIR Nodes are the national implementation of a harmonised FAIR Data Management programme for the life sciences.
- FAIR data management requires professional skills and adequate resources.
- Good research data management requires appropriate funding for data infrastructures.

Recommended Deposition Databases

ELIXIR Deposition Database list

Deposition Database	Data type	International collaboration framework [1]
ArrayExpress	Functional genomics data. Stores data from high-throughput functional genomics experiments.	
BioModels	Computational models of biological processes.	
EGA	Personally identifiable genetic and phenotypic data resulting from biomedical research projects.	European Bioinformatics Institute and the Centre for Genomic Regulation
ENA	Nucleotide sequence information, covering raw sequencing data, contextual data, sequence assembly information and functional and taxonomic annotation.	International Nucleotide Sequence Database Collaboration
IntAct	IntAct provides a freely available, open source database system and analysis tools for molecular interaction data.	The International Molecular Exchange Consortium
MetaboLights	Metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments.	
PDBe	Biological macromolecular structures.	
PRIDE	Mass spectrometry-based proteomics da… protein expression information (… values) and the suppor…	

- "Whenever possible, biological research data should be submitted to the recommended community deposition databases"

https://elixir-europe.org/platforms/data/elixir-deposition-databases

ELIXIR Core Data Resources

ELIXIR Core Data Resource list

Core Data Resource	Data type
ArrayExpress	Functional Genomics Data from high-throughput functional genomics experiments.
CATH	A hierarchical domain classification of protein structures in the Protein Data Bank.
ChEBI	Dictionary of molecular entities focused on 'small' chemical compounds.
ChEMBL	Database of bioactive drug-like small molecules, it contains 2-D structures, calculated properties and abstracted bioactivities.
EGA	Personally identifiable genetic and phenotypic data resulting from biomedical research projects.
ENA	Nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation.
Ensembl	Genome browser for vertebrate genomes that supports research in comparative genomics, evolution, sequence variation and transcriptional regulation.
Ensembl Genomes	Comparative analysis, data mining and visualisation for the genomes of non-vertebrate species.
Europe PMC	Europe PMC is a repository, providing [illegible] books, patents and clinical [illegible]

- A sub-set of critical databases to the functioning of life sciences
- 5 indicators
  - Scientific focus
  - Impact
  - Governance
  - Quality
  - Community
- See "Identifying ELIXIR Core Data Resources"

https://www.elixir-europe.org/platforms/data/core-data-resources

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OPINION ARTICLE

Four simple recommendations to encourage best practices in research software [version 1; referees: 3 approved]

Rafael C. Jiménez[1], Mateusz Kuzak[2], Monther Alhamdoosh[3], Michelle Barker[4], Bérénice Batut[5], Mikael Borg[6], Salvador Capella-Gutierrez[7], Neil Chue Hong[8], Martin Cook[1], Manuel Corpas[9], Madison Flannery[10], Leyla Garcia[11], Josep Ll. Gelpí[12,13], Simon Gladman[10], Carole Goble[14], Montserrat González Ferreiro[11], Alejandra Gonzalez-Beltran[15], Philippa C. Griffin[10], Björn Grüning[5], Jonas Hagberg[6], Petr Holub[16], Rob Hooft[17], Jon Ison[18], Daniel S. Katz[19-22], Brane Leskošek[23], Federico López Gómez[1], Luis J. Oliveira[24], David Mellor[25], Rowland Mosbergen[26], Nicola Mulder[27], Yasset Perez-Riverol[11], Robert Pergl[28], Horst Pichler[29], Bernard Pope[10], Ferran Sanz[30], Maria V. Schneider[10], Victoria Stodden[20], Radosław Suchecki[31], Radka Svobodová Vařeková[32,33], Harry-Anton Talvik[34], Ilian Todorov[35], Andrew Treloar[36], Sonika Tyagi[10,37], Maarten van Gompel[38], Daniel Vaughan[11], Allegra Via[39], Xiaochuan Wang[40], Nathan S. Watson-Haigh[31], Steve Crouch[41]

Author details

Grant information

elixir This article is included in the ELIXIR gateway .

- Make source code publicly accessible from day one
- Make software easy to discover by providing software metadata via a popular community registry
- Adopt a license and comply with the license of third-party dependencies
- Define clear and transparent contribution, governance and communication processes

excelerate

Thank you

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