



ELIXIR Resources

Enabling life science researchers to access and analyse data

Peter Maccallum, ELIXIR Chief Technical Officer

European Biomedical Research Infrastructures' resources for
Researchers in Neurosciences, 1st Feb 2022

www.elixir-europe.org

ELIXIR Life Science Resources

ELIXIR is Europe's **Infrastructure for Life Science Data**.

- The concept was developed in close collaboration with the European Bioinformatics Institute and consultation with the EU
- Development has been aligned with the **European Strategy Forum on Research Infrastructures** (ESFRI) and ELIXIR has been an ESFRI 'landmark' since 2016

Life Science Data seems quite broad?

- Our core is the 'omics databases and tools
- In some topics - human data, imaging - other ESFRI partners have strengths and we collaborate
- Our early focus on Open Science and FAIR have made us significant contributors to FAIR toolkits and the **European Open Science Cloud** (EOSC)

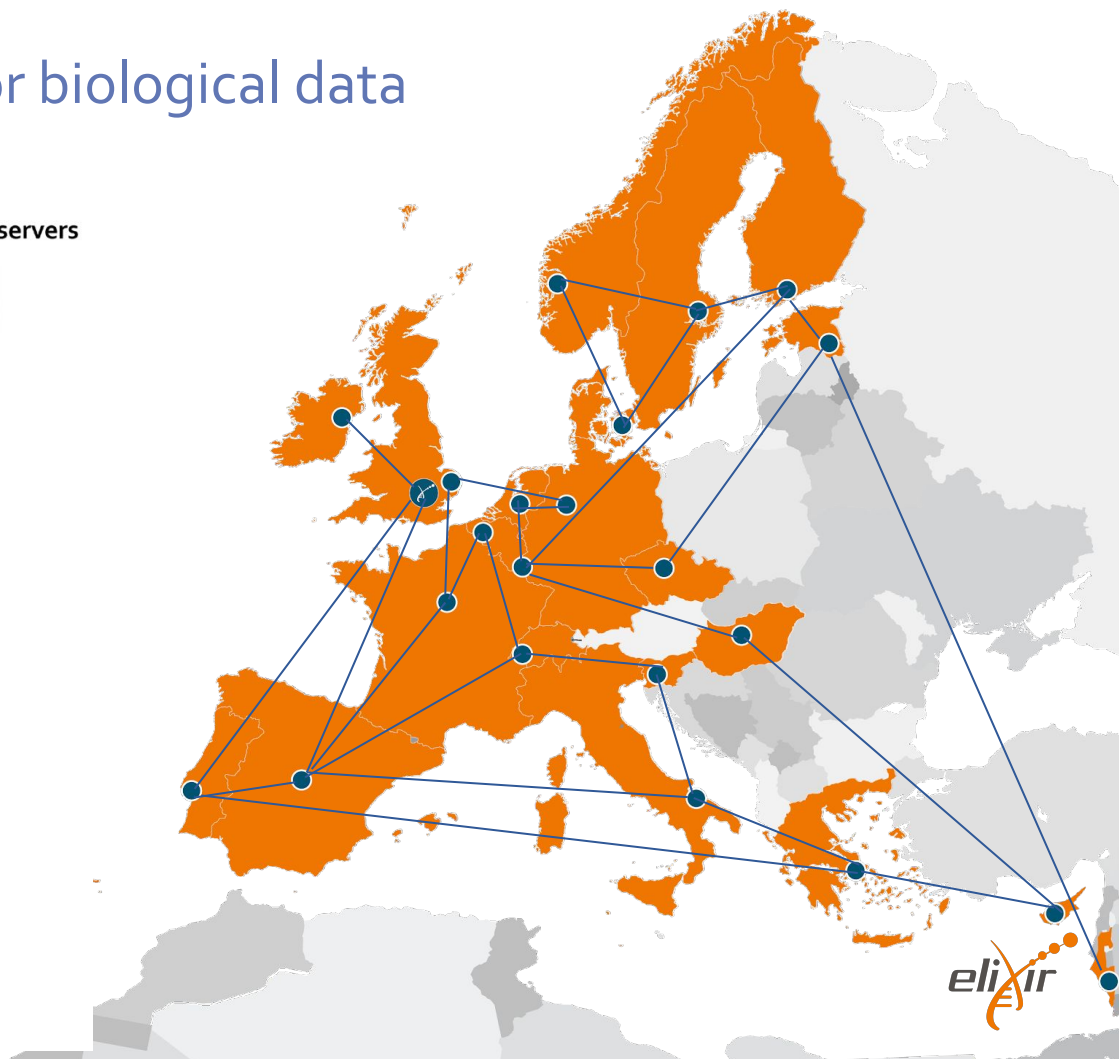


A sustainable infrastructure for biological data

ELIXIR Members



ELIXIR Observers



ELIXIR's Technical Framework - some terminology

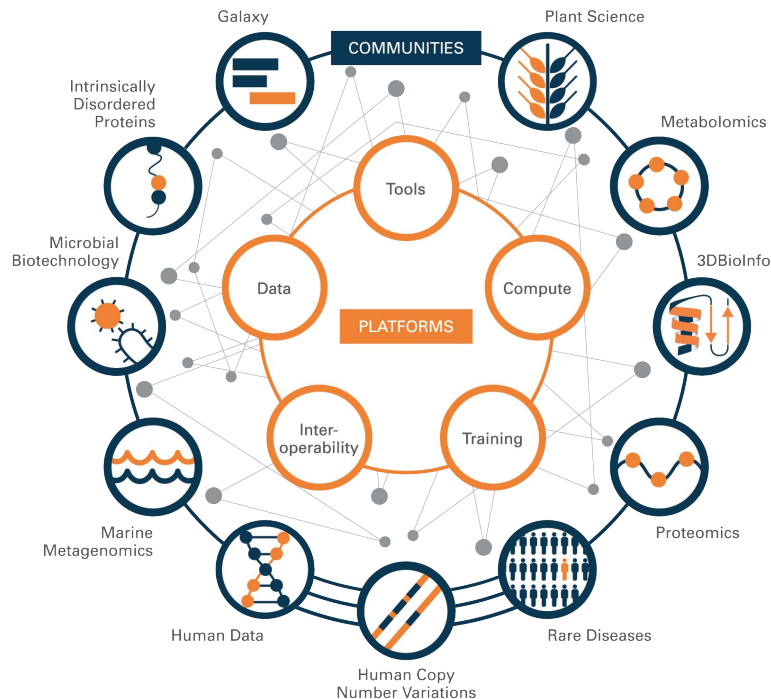
ELIXIR offers over 300 distinct services, from specialist tools to full research environments.

We group together technical aspects of these services through our **ELIXIR Platforms**

- Compute, Data, Interoperability, Tools and Training

We collect the driving use cases and specialist topics through the **ELIXIR Communities**

<https://elixir-europe.org/services/list>



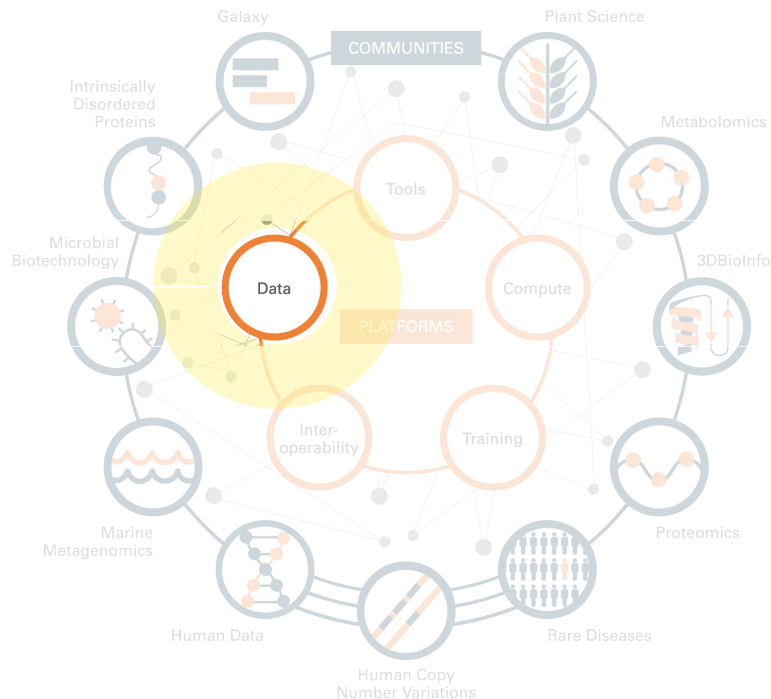
ELIXIR Data Platform - sustainable data resources

The goal of the **ELIXIR Data Platform** is to drive the use, re-use and value of life science data.

- for bioinformaticians and life science researchers
- users in academic and industrial settings
- sound governance, life cycle management, and long-term sustainability

Researchers need open access to technically and scientifically excellent data resources for effective data discovery, deposition, and re-use.

- Open Access as a core principle for publicly funded research.
- terms of use or a licence that enable the reuse and remixing of data (see **Open Definition**)



Data for Life: Sustaining Europe's life science data infrastructure

Mission: drive long-term sustainability of life science data resources

ELIXIR Core Data Resources and Deposition Databases

- Resources of fundamental importance for the research community and the long-term preservation of life-science data.

- Basis for policy actions
- Basis for technical actions
- Capacity building
- Life cycle management

Core Data Resource	Data type
ArrayExpress	Functional Genomics Data from high-throughput functional genomics experiments.
BRENDA	Database of enzyme and enzyme-ligand information, across all taxonomic groups, manually extracted from primary literature and extended by text mining procedures, integration of external data and prediction algorithms.
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 vertebrate genomes
Europe PMC	Europe PMC books, papers
Human Protein Atlas	The Human protein-coding proteins database
The IMEx Consortium: represented by IntAct and MINT	IntAct provides molecular interaction data
Protein Data Bank	Functional annotation of protein structures

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
MetabolLights	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 data (protein expression information (FDR values) and the supporting	

<https://elixir-europe.org/core-data-resources>

<https://elixir-europe.org/recommended-deposition-databases>



The **BioModels** ELIXIR Deposition Database allows users to deposit and re-use physiologically and pharmaceutically relevant mechanistic models in standard formats

<https://www.ebi.ac.uk/biomodels/>



ELIXIR Interoperability Platform - FAIR and Open Science

The goal of the **ELIXIR Interoperability Platform** is to help people and machines to discover, access, integrate and analyse biological data.

It encourages the life science community to adopt

- standardised file formats,
- metadata,
- vocabularies and
- Identifiers

...and works internationally to achieve its goals.

Identifies and promotes interoperability best practices for data providers and data integrators.

Delivers the interoperability services that underpin ELIXIR **Communities** and **Platforms**.

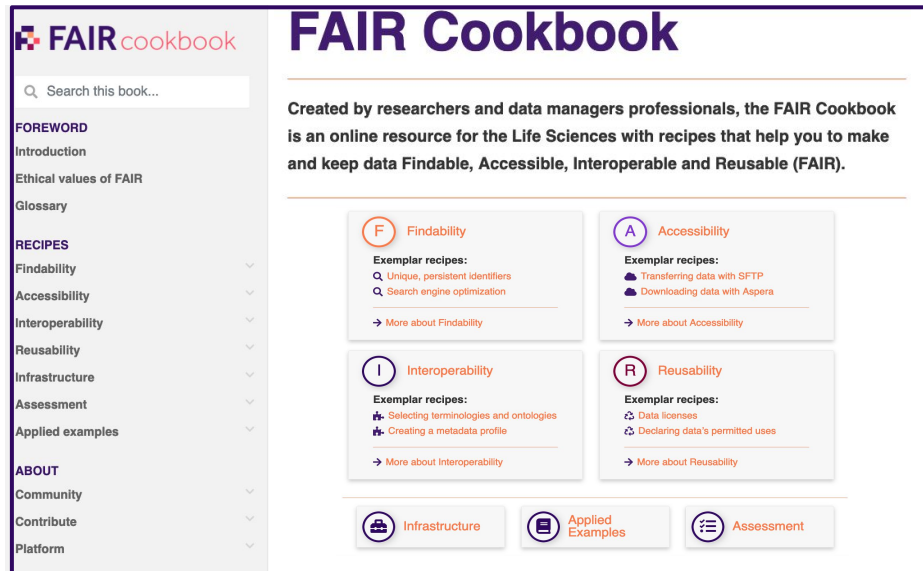


Interoperability - Recommended Interoperability Resources

- ELIXIR's **Recommended Interoperability Resources**.
- These are resources that:
 - Establish connections between resources
 - Acquire and expose metadata of different resources
 - Create the infrastructure needed to build integratable data collections
- They will help you **translate your data across databases** or resources or find the **best standards for your data**.

Resource	Description
FAIRsharing	A registry of the curated metadata of databases, policies and standards.
g:Profiler	A gene-centric data integrator with web UI and API services.
Identifiers.org	An identification and resolution system for life science, and a provider of compact identifiers and URLs.
InterMine	Framework to integrate life sciences data based on an extensible data model, providing web interface and RESTful web services.
ISA Framework	ISA (Investigation > Study > Assay) helps researchers to provide rich description of experimental metadata so that the resulting data and discoveries are reproducible and reusable.
Ontology Lookup Service	Repository for biomedical ontologies that aims to provide a single point of access to the latest ontology versions through web UI or RESTFUL API
3DBIONOTES API	A reusable platform-independent API call component for protein metadata alignment, annotation, and integration across major protein data resources.
BridgeDb	A combination of a software framework and an API for mapping identifiers for related objects in life sciences.
DisGeNET API	An API SPARQL Endpoint for genetic variants (https://disgenet.org/)
MOLGENIS	A software package to help researchers to integrate and analyze data from different sources. It supports data queries and data analysis.

Interoperability example: FAIR Cookbook



<https://fairplus.github.io/the-fair-cookbook>



IMI FAIRplus, private-public partnership:

- Addresses common FAIRification problems
- Uses data from other IMI projects: from clinical (observational & event based) to molecular data

FAIR Cookbook flagship output:

- 50+ recipes a- guidance, technical, hands-on & reviews
- 50+ contributors, incl many ELIXIR Nodes
- Part of ELIXIR FAIR services ecosystem: RDMkit, FAIRsharing, biotools
- Complementary to Pistoia Alliance FAIR Toolkit

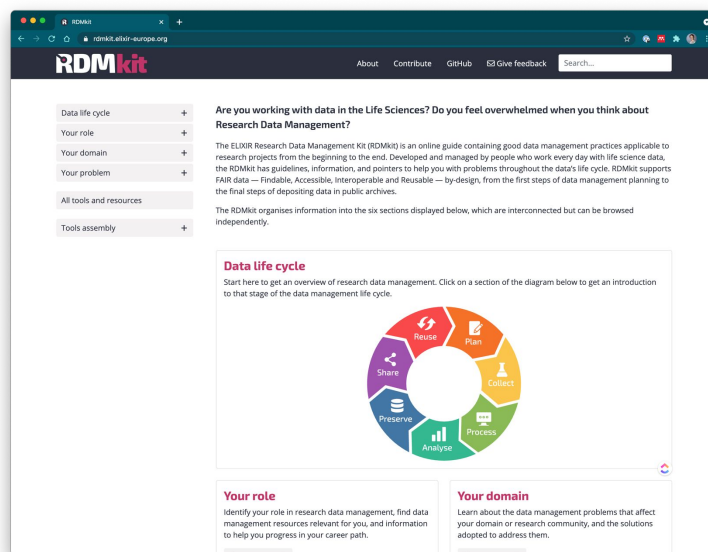
FAIR Cookbook already adopted by IMI in their RDM guidance

Interoperability example: RDMkit — supporting FAIR-by-design

Designed to enable data
lifecycle management



Website focal point for guidance,
information, best practice, examples

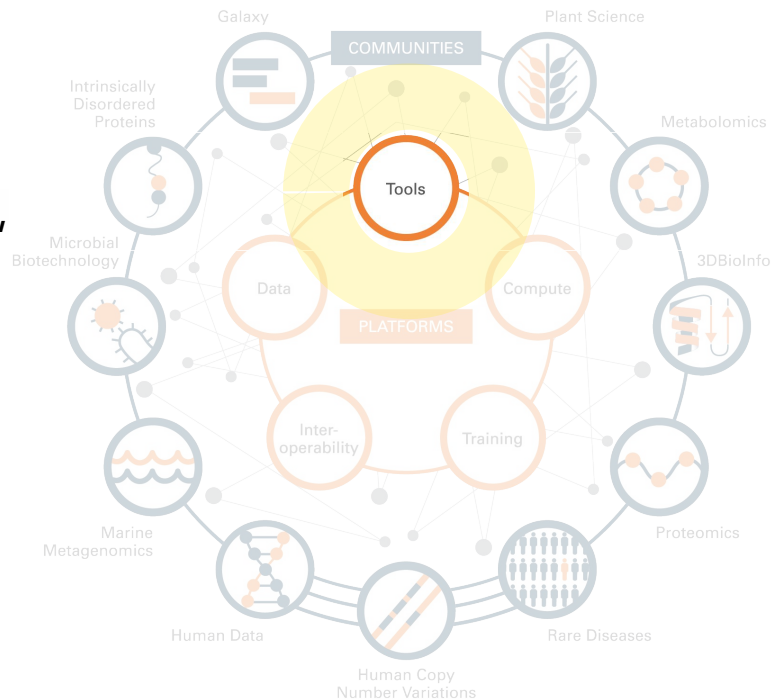


ELIXIR Tools Platform - an ecosystem for analysis

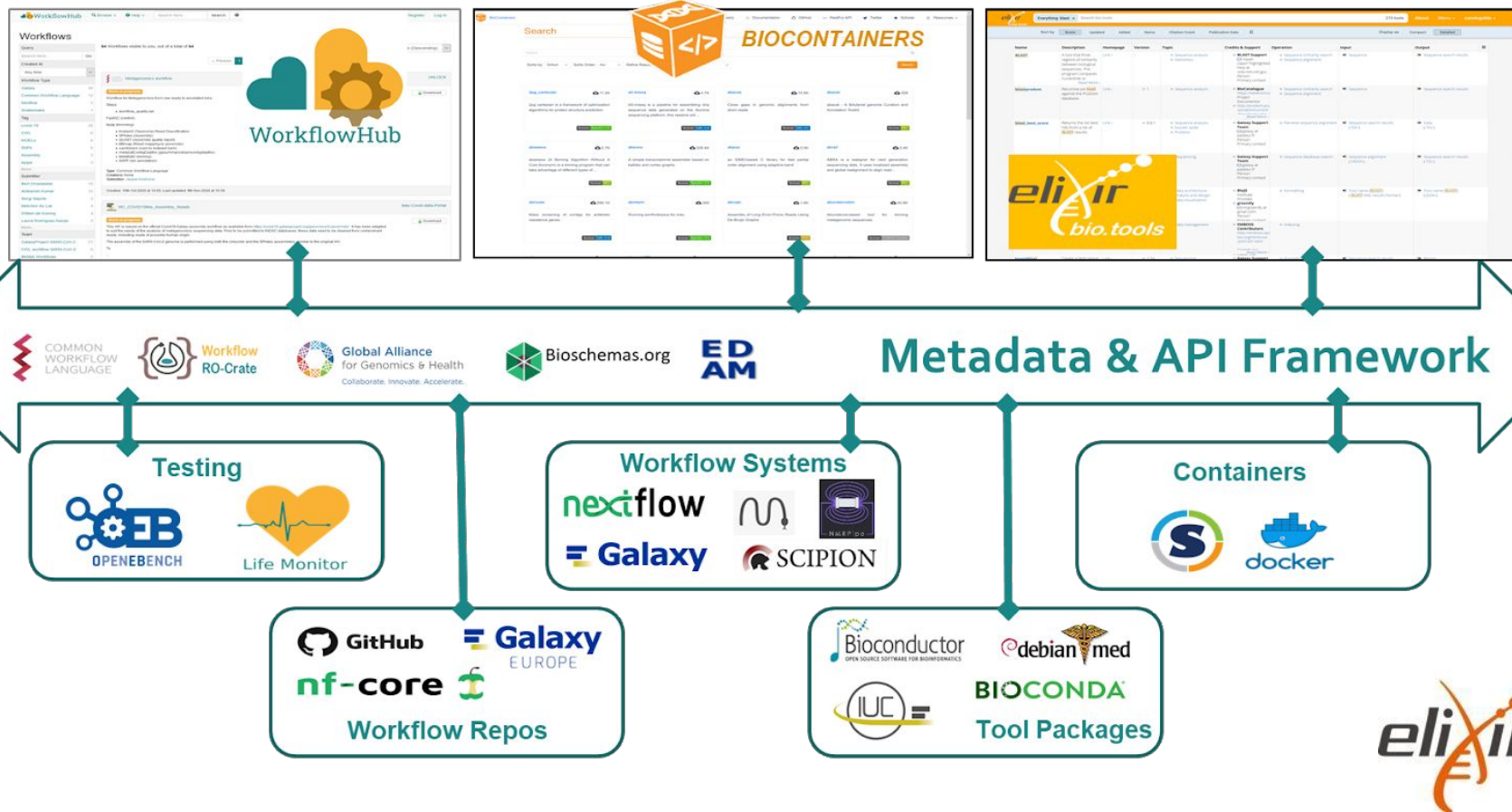
The **ELIXIR Tools Platform** helps communities find, register and benchmark software tools. These tools help researchers access, analyse and integrate biological data, and so drive scientific discovery across the life sciences.

We maintain information standards for these tools, and produce, adopt and promote best practices for their development. We also:

- connect tools and data services
- link tools to training materials
- make it easy to download, deploy, and benchmark tools
- put tools in the context of workflows, including container technologies and Galaxy.



Tool and Workflow Registries



Tools example: bio.tools

Bio.tools is a discovery portal for bioinformatics software information, providing a **curated, annotated description** of tools and data services.

'a comprehensive registry of software and databases,

- ...simple command-line tools and online services,*
- ...databases and complex, multi-functional analysis workflows*
- ...described in a rigorous semantics and syntax,*
- ...concise, consistent and therefore comparable information.'*

The **EDAM Ontology** of bioscientific data analysis and **data management** enables the search and comparison.

<https://bio.tools/>

<https://edamontology.org/page>

The screenshot displays the bio.tools website interface. At the top, there is a search bar with the text 'Everything: 'Neuron' x' and a search icon. To the right of the search bar, it says '59 tools'. Further right are links for 'Explore', 'Login', and 'Sign-up'. Below the search bar, there are tabs for sorting results: 'Sort by', 'Score', 'Updated', 'Added', 'Name', 'Citation Count', and 'Publication Date'. To the right of these tabs are options for 'Display as' with 'Compact' and 'Detailed' buttons. A cookie notice banner is visible below the sorting options. The main content area shows two tool entries. The first entry is for 'Neuron', which includes a description: 'Stimulates a neuron and monitor what happens. Pause, rewind, and move forward in time in order to observe the ions as they move across the neuron membrane.' Below the description are several category tags: 'Cell biology', 'Neurobiology', 'Simulation experiment', 'Molecular dynamics simulation', and 'Desktop application'. The second entry is for 'LFPy', with a description: 'Python package for calculation of extracellular potentials from multicompartments neuron models. It relies on the NEURON simulator and uses the Python interface it provides.' Below this description are tags: 'Neurobiology', 'Neurology', 'Biophysics', 'Calculation', 'Network simulation', 'Library', and 'GPL-3.0'. The third entry is for 'NeuronSubtypeTranscriptomes', with a description: 'Genome-wide analysis of differential gene expression and splicing in excitatory neurons and interneuron subtypes. Transcriptomics of cortical excitatory and inhibitory neurons'. Below this description are tags: 'Transcriptomics', 'Gene transcripts', 'Small molecules', 'RNA splicing', 'RNA-Seq', 'Essential dynamics', 'Splicing model analysis', 'Differential gene expression analysis', 'Expression analysis', and 'Web application'.

Tools example: WorkflowHub

Developed though the **EOSC-Life** project, **WorkflowHub** adds a registry for workflows to the ELIXIR Tools Ecosystem.

- *'describing, sharing and publishing scientific computational workflows.'*
- *supports any workflow in its native repository.*
- *use of open standards and tools, including Common Workflow Language (CWL), RO-Crate, BioSchemas and (GA4GH) Tools Registry Service'*

<https://workflowhub.eu/>

The screenshot shows the WorkflowHub interface for a workflow titled "Automatic Ligand parameterization for GROMACS" (Version 1). The interface includes a search bar, navigation tabs for "Overview" and "Files", and a description of the workflow's purpose: "This workflow performs the process of ligand parameterization for a small molecule, step by step, using the BioExcel Building Blocks library (biobb). The parameters generated are topologies for GROMACS." A workflow diagram is displayed, showing a sequence of steps: "step1_biobb_minimize_input", "step2_biobb_minimize_input", "step3_biobb_minimize_output", "step4_biobb_minimize_output", "step5_biobb_minimize_output", "step6_biobb_minimize_output", "step7_biobb_minimize_output", "step8_biobb_minimize_output", "step9_biobb_minimize_output", "step10_biobb_minimize_output", "step11_biobb_minimize_output", "step12_biobb_minimize_output", "step13_biobb_minimize_output", "step14_biobb_minimize_output", "step15_biobb_minimize_output", "step16_biobb_minimize_output", "step17_biobb_minimize_output", "step18_biobb_minimize_output", "step19_biobb_minimize_output", "step20_biobb_minimize_output", "step21_biobb_minimize_output", "step22_biobb_minimize_output", "step23_biobb_minimize_output", "step24_biobb_minimize_output", "step25_biobb_minimize_output", "step26_biobb_minimize_output", "step27_biobb_minimize_output", "step28_biobb_minimize_output", "step29_biobb_minimize_output", "step30_biobb_minimize_output", "step31_biobb_minimize_output", "step32_biobb_minimize_output", "step33_biobb_minimize_output", "step34_biobb_minimize_output", "step35_biobb_minimize_output", "step36_biobb_minimize_output", "step37_biobb_minimize_output", "step38_biobb_minimize_output", "step39_biobb_minimize_output", "step40_biobb_minimize_output", "step41_biobb_minimize_output", "step42_biobb_minimize_output", "step43_biobb_minimize_output", "step44_biobb_minimize_output", "step45_biobb_minimize_output", "step46_biobb_minimize_output", "step47_biobb_minimize_output", "step48_biobb_minimize_output", "step49_biobb_minimize_output", "step50_biobb_minimize_output", "step51_biobb_minimize_output", "step52_biobb_minimize_output", "step53_biobb_minimize_output", "step54_biobb_minimize_output", "step55_biobb_minimize_output", "step56_biobb_minimize_output", "step57_biobb_minimize_output", "step58_biobb_minimize_output", "step59_biobb_minimize_output", "step60_biobb_minimize_output", "step61_biobb_minimize_output", "step62_biobb_minimize_output", "step63_biobb_minimize_output", "step64_biobb_minimize_output", "step65_biobb_minimize_output", "step66_biobb_minimize_output", "step67_biobb_minimize_output", "step68_biobb_minimize_output", "step69_biobb_minimize_output", "step70_biobb_minimize_output", "step71_biobb_minimize_output", "step72_biobb_minimize_output", "step73_biobb_minimize_output", "step74_biobb_minimize_output", "step75_biobb_minimize_output", "step76_biobb_minimize_output", "step77_biobb_minimize_output", "step78_biobb_minimize_output", "step79_biobb_minimize_output", "step80_biobb_minimize_output", "step81_biobb_minimize_output", "step82_biobb_minimize_output", "step83_biobb_minimize_output", "step84_biobb_minimize_output", "step85_biobb_minimize_output", "step86_biobb_minimize_output", "step87_biobb_minimize_output", "step88_biobb_minimize_output", "step89_biobb_minimize_output", "step90_biobb_minimize_output", "step91_biobb_minimize_output", "step92_biobb_minimize_output", "step93_biobb_minimize_output", "step94_biobb_minimize_output", "step95_biobb_minimize_output", "step96_biobb_minimize_output", "step97_biobb_minimize_output", "step98_biobb_minimize_output", "step99_biobb_minimize_output", "step100_biobb_minimize_output".

Workflow Type: Common Workflow Language
Stable

SEEK ID: <https://workflowhub.eu/workflows/2557>
version=1

DOI: [10.48546/workflowhub.workflow.255.1](https://doi.org/10.48546/workflowhub.workflow.255.1)

Inputs

ID	Name	Description	Type
step2_babel_minimize_config	n/a	n/a	string
step2_babel_minimize_input_path	n/a	n/a	File
step2_babel_minimize_output_path	n/a	n/a	string
step3_acpype_params_gmx_config	n/a	n/a	string

Creators and Submitter

Creators

- Adam Hospital, Genis Bayarri

Submitter

- Genis Bayarri

Discussion Channels

- BioExcel Workflows
- Tutorial
- Documentation
- Launch on MyBinder

Citation

Copy

Bayarri, G., & Hospital, A. (2022). Automatic Ligand parameterization for GROMACS. WorkflowHub. <https://doi.org/10.48546/WOF>

American Psychologica

ELIXIR Compute Platform - data-centric computing solutions

The **ELIXIR Compute Platform** was established to build and integrate **cloud, compute, storage** and **access services** for the life-science research community.

Downloading and analysing data locally is no longer viable due to both the data size and scope of the analysis activities.

- data needs to be managed as a federation
- data providers work as a single infrastructure
- researchers can bring their analysis to where the data is located

The objective is to combine all components of the ELIXIR Compute services into a seamless workflow.



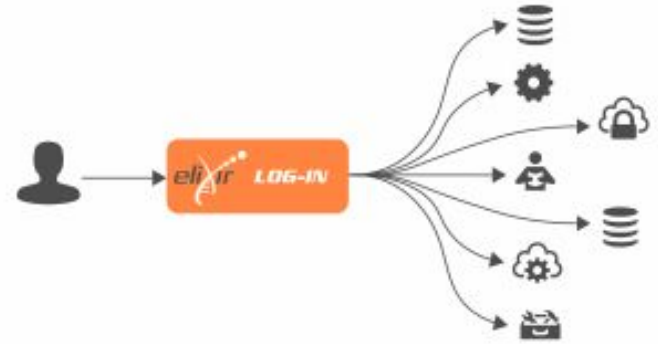
Compute example: Authentication & Authorisation

- Majority of life science services are openly accessible but may require researchers to sign in using a username and password
- Sensitive data and licensed resources of course require strong security for access
- Researchers quickly become overloaded with having to remember numerous login credentials

ELIXIR Authorisation and Authentication Infrastructure (AAI)

- Enables **researchers** to use their home organisation credentials - or community or commercial identities (e.g. ORCID, LinkedIn) - to sign in and access data and services they need
- allows **service providers** to control and manage the access rights of their users and create different access levels for research groups or international projects

Look for the 'elixir LOG-IN' logo on services.



Compute example : EBI Embassy Cloud

Compute Platform services include **Data-centric Cloud** environments in Nodes.

'Embassy Cloud users (tenants) have direct access to the EMBL-EBI data, services and compute. This is a practical and cost-effective alternative to replicating services and downloading vast, public datasets locally. Tenants can access their workspace from anywhere in the world, reducing the need for capital investments in hardware and related operational costs.'

<https://www.embassycloud.org/>

EMBL-EBI

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EMBASSY cloud

ANALYSE YOUR LIFE-SCIENCE DATA FASTER IN THE EMBL-EBI CLOUD

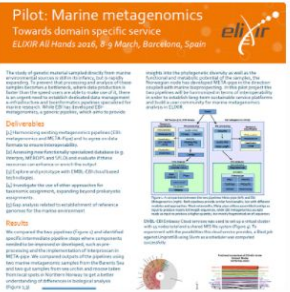
Big data may be a goldmine for discovery, but analysis can be a bottleneck without the right infrastructure. Embassy Cloud provides a solution: private, secure, virtual-machine-based workspaces within the EMBL-EBI infrastructure, where collaborators can make optimal use of their own customised workflows, applications and datasets.



About
Learn more about the Embassy cloud



My workspace
What do I get?



More
Use cases & more information

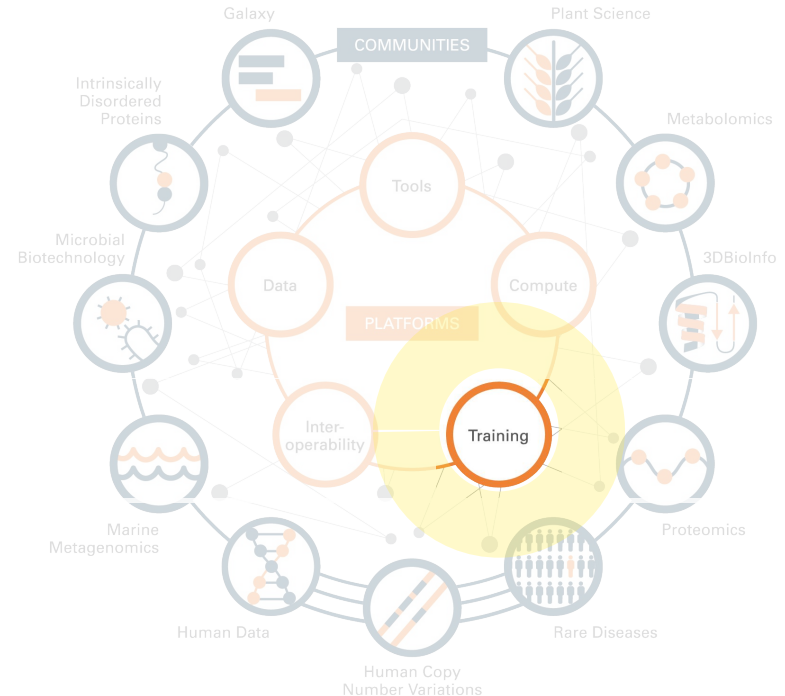
ELIXIR Training Platform

The **ELIXIR Training Platform** was established to develop a training community that spans all ELIXIR member states (see the [list of Training Coordinators](#)). It aims to:

- strengthen national training programmes,
- grow bioinformatics training capacity and competence across Europe, and
- empower researchers to use ELIXIR's [services and tools](#).

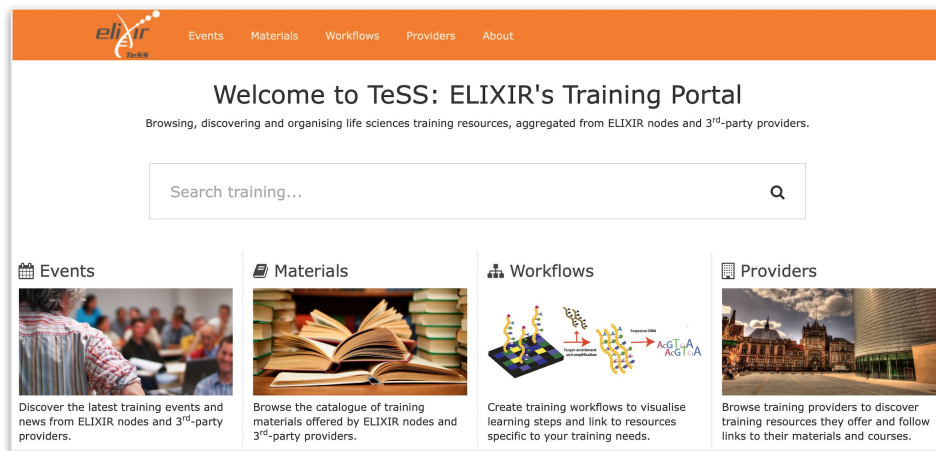
The Platform:

- establishes and implements best practices in bioinformatics training through a training Toolkit
- supports training providers across Europe in creating and delivering training for developers, researchers and trainers
- builds a sustainable training infrastructure



Training example: TeSS

- Need to find training courses or materials?
- ELIXIR's **Training e-Support System (TeSS)** Platform enables you to search, share & package training **resources, training materials and events**
- Any content providers can upload and include training courses or content



Search for events held near you...

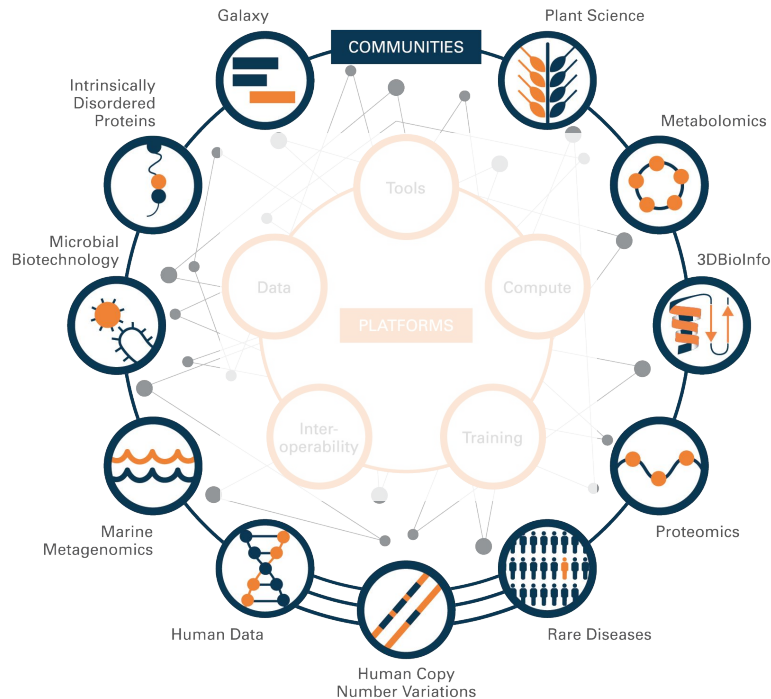


<https://tess.elixir-europe.org>



ELIXIR Communities

- Formed around domain experts in **ELIXIR Nodes** (including non-ELIXIR partners)
- Provide a mechanism for long-term collaborations with other ESRIs and large-scale initiatives
- Drive service developments in the **ELIXIR Platforms**
- Provide framework to develop and maintain community standards



ELIXIR Proteomics, Metabolomics Communities

The goal of the **ELIXIR Proteomics Community** is to develop and maintain sustainable proteomics tools and data resources.

- An essential part of the development will also be the 'FAIRification' of the resources.

The goal of the **ELIXIR Metabolomics Community** is to work with experimental scientists and developers to provide the resources, analysis tools and infrastructure that will help metabolite identification.

- The community will establish an infrastructure of services, standards and datasets.

ELIXIR Research

F1000Research 2017, 6:875 Last updated: 21 JAN 2022



OPINION ARTICLE

A community proposal to integrate proteomics activities in ELIXIR [version 1; peer review: 2 approved]

Juan Antonio Vizcarra¹,
Wout Bittremieux²,
Myriam Ferro⁴, Al
Lydie Lane^{10,11}, Kr
Petr Novak¹⁵, Ma
Veit Schwämmle⁶,
Jiri Vondrasek⁹, M
Oliver Kohlbacher¹⁷

¹European Molecular Biology
²ELIXIR Hub, Cambridge, CB
³Department of Mathematics
⁴French Proteomics Infrastru
de Toulouse, CNRS, UPS), Str
⁵ProteoRed, Proteomics Unit
⁶Biomolecular Mass Spectro
Pharmaceutical Sciences, Un
⁷Netherlands Proteomics Ce
⁸Analytical Biochemistry, Dep
⁹Institute of Organic Chemis
¹⁰CALIPHO Group, SIB Swiss
¹¹Department of Human Pro
¹²National Bioinformatics Ini
62, Sweden
¹³Proteome Informatics Gro
¹⁴Computer Science Departm
¹⁵Institute of Microbiology, C
¹⁶Center for Proteomics and
¹⁷Department of Biomedical
¹⁸Center for Biotechnology, I
¹⁹Department of Biochemis
²⁰Interuniversity Institute for
²¹Center for Proteomics, Uni
²²Applied Bio & Molecular Sy
²³Netherlands Metabolomics
²⁴Dutch Techcentre for Life S
²⁵Medical Bioinformatics, Me
²⁶VIB-Ugent Center for Medi

ELIXIR Research

F1000Research 2017, 6(ELIXIR):1649 Last updated: 21 JAN 2022



OPINION ARTICLE

REVIEWED The future of metabolomics in ELIXIR [version 2; peer review: 3 approved]

Merlijn van Rijswijk^{1,2}, Charlie Beirnaert^{10,3}, Christophe Caron⁴,
Marta Cascante⁵, Victoria Dominguez^{10,4}, Warwick B. Dunn⁶,
Timothy M. D. Ebbels⁷, Franck Giacomoni⁸, Alejandra Gonzalez-Beltran^{10,9},
Thomas Hankemeier^{2,10}, Kenneth Haug^{10,11}, Jose L. Izquierdo-Garcia^{12,13},
Rafael C. Jimenez^{10,14}, Fabien Jourdan¹⁵, Namrata Kale^{10,11}, Maria I. Klapa^{10,16},
Oliver Kohlbacher^{10,17-19}, Kairi Koort^{20,21}, Kim Kultima²², Gildas Le Corguillier^{10,4,23},
Pablo Moreno¹¹, Nicholas K. Moschonas^{10,16,24}, Steffen Neumann²⁵,
Claire O'Donovan¹¹, Martin Reczko²⁶, Philippe Rocca-Serra⁹, Antonio Rosato^{10,27},
Reza M. Salek^{10,11}, Susanna-Assunta Sansone^{10,9}, Venkata Satagopam^{10,28},
Daniel Schober^{10,25}, Ruth Shimmo^{20,21}, Rachel A. Spicer^{10,11}, Ola Spjuth^{10,29},
Etienne A. Thévenot^{10,30}, Mark R. Viant⁶, Ralf J. M. Weber⁶,
Egon L. Willighagen^{10,31}, Gianluigi Zanetti³², Christoph Steinbeck^{10,33}

¹ELIXIR-NL, Dutch Techcentre for Life Sciences, Utrecht, 3503 RM, The Netherlands

²Netherlands Metabolomics Center, Leiden, 2333 CC, The Netherlands

³ADReM, Department of Mathematics and Computer Science, University of Antwerp, Antwerp, 2020, Belgium

⁴ELIXIR-FR, French Institute of Bioinformatics, Gif-sur-Yvette, F-91198, France

⁵Department of Biochemistry and Molecular Biomedicine, Faculty of Biology, Universitat de Barcelona, Barcelona, 08028, Spain

⁶School of Biosciences, Phenome Centre Birmingham and Birmingham Metabolomics Training Centre, University of Birmingham, Birmingham, B15 2TT, UK

⁷Computational and Systems Medicine, Department of Surgery and Cancer, Imperial College London, London, SW7 2AZ, UK

⁸INRA, UNH, Human Nutrition Unit, PFEM, Metabolism Exploration Platform, MetaboHUB-Clermont, Clermont Auvergne University, Clermont-Ferrand, F-63000, France

Galaxy Community ([web](#))



Mission/Vision

Fosters a **Galaxy community in Europe**, together with Galaxy resources and training.

Monitors and fosters the use of Galaxy in ELIXIR.



Goals

- Build a **European network** of Galaxy communities
- Extend Galaxy **training** provision
- Create a **Galaxy cloud** infrastructure across Europe
- Make it easier to **access and transfer data**
- **Improve** tools and data integration
- Promote FAIR principles in Galaxy

Some ELIXIR nodes already offer a centralised instance of Galaxy

- [IFB](#), France
- [de.NBI](#), Germany
- [usegalaxy.be](#), Belgium

→ collaboration with the **Galaxy Core Team**: launched [usegalaxy.eu](#) (2018), hosted in Freiburg (de.NBI)

→ Aim to expand this into a network of Galaxy instances worldwide, guaranteeing a base level of compatibility and enabling all **training materials** of the Galaxy Training Network.



Acknowledgements & contacts

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- Jonathan Tedds on behalf of the ELIXIR Compute Platform
- Katharina Heil on behalf of the ELIXIR Training Platform and the Proteomics, Metabolomics, and Galaxy ELIXIR Communities
- Andy Smith & the ELIXIR Hub

Follow **ELIXIR**:

- Post job vacancies here: <https://elixir-europe.org/about-us/vacancies>
- Follow us on social media - Twitter: @ELIXIREurope
- BioHackathon Europe: <https://biohackathon-europe.org>
- ELIXIR Webinars: <https://elixir-europe.org/events>
- Any post-meeting questions - peter.maccallum@elixir-europe.org

