F1000Research

F1000Research 2024, 12(ELIXIR):499 Last updated: 29 JUN 2024

OPINION ARTICLE

REVISED The ELIXIR Biodiversity Community: Understanding short- and long-term changes in biodiversity [version 2; peer review: 3 approved]

Robert M. Waterhouse[1], Anne-Françoise Adam-Blondon[2], Bachir Balech[3], Endre Barta[4], Physilia Ying Shi Chua[5], Valeria Di Cola[6], Katharina F. Heil[5], Graham M. Hughes[7], Lars S. Jermiin[8,9], Matúš Kalaš[10], Jerry Lanfear[5], Evangelos Pafilis[11], Patricia M. Palagi[6], Aristotelis C. Papageorgiou[12], Joana Paupério[13], Fotis Psomopoulos[14], Niels Raes[15], Josephine Burgin[13], Toni Gabaldón[16,17]

[1]Department of Ecology and Evolution, SIB Swiss Institute of Bioinformatics, Universite de Lausanne, Lausanne, Vaud, 1015, Switzerland
[2]INRAE, BioinfOmics, Plant Bioinformatics Facility, Universite Paris-Saclay, Gif-sur-Yvette, Île-de-France, 78026, France
[3]Istituto di Biomembrane, Bioenergetica e Biotecnologie Molecolari, Bari, 70126, Italy
[4]Institute of Genetics and Biotechnology, Magyar Agrar- es Elettudomanyi Egyetem, Gödöllő, Pest County, Hungary
[5]ELIXIR, Wellcome Genome Campus, Hinxton, England, CB10 1SD, UK
[6]SIB Swiss Institute of Bioinformatics, Lausanne, Vaud, 1015, Switzerland
[7]School of Biology and Environmental Science, University College Dublin, Dublin, Leinster, Ireland
[8]Systems Biology Ireland, School of Medicine, University College Dublin, Dublin, Leinster, Ireland
[9]School of Mathematical and Statistical Sciences, University of Galway, Galway, Ireland
[10]Department of Informatics, Universitetet i Bergen, Bergen, Hordaland, Norway
[11]Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, Heraklion, 71003, Greece
[12]Department of Molecular Biology and Genetics, Democritus University of Thrace, Alexandroupolis, Greece
[13]EMBL-EBI, Wellcome Genome Campus, Hinxton, England, CB10 1SD, UK
[14]Institute of Applied Biosciences, Centre for Research and Technology Hellas, Thessaloniki, Greece
[15]Naturalis Biodiversity Center, Leiden, South Holland, The Netherlands
[16]Institut de Recerca Biomedica, Barcelona, Catalonia, Spain
[17]Centro Nacional de Supercomputacion, Barcelona, Catalonia, Spain

v2 **First published:** 15 May 2023, **12**(ELIXIR):499
https://doi.org/10.12688/f1000research.133724.1
Latest published: 22 May 2024, **12**(ELIXIR):499
https://doi.org/10.12688/f1000research.133724.2

Abstract

Biodiversity loss is now recognised as one of the major challenges for humankind to address over the next few decades. Unless major actions are taken, the sixth mass extinction will lead to catastrophic effects on the Earth's biosphere and human health and well-being. ELIXIR can help address the technical challenges of biodiversity science, through leveraging its suite of services and expertise to

Open Peer Review

Approval Status ✓ ✓ ✓

	1	2	3
version 2 (revision) 22 May 2024	✓ view	✓ view	✓ view
version 1 15 May 2023	? view	✗ view	✗ view

enable data management and analysis activities that enhance our understanding of life on Earth and facilitate biodiversity preservation and restoration. This white paper, prepared by the ELIXIR Biodiversity Community, summarises the current status and responses, and presents a set of plans, both technical and community-oriented, that should both enhance how ELIXIR Services are applied in the biodiversity field and how ELIXIR builds connections across the many other infrastructures active in this area. We discuss the areas of highest priority, how they can be implemented in cooperation with the ELIXIR Platforms, and their connections to existing ELIXIR Communities and international consortia. The article provides a preliminary blueprint for a Biodiversity Community in ELIXIR and is an appeal to identify and involve new stakeholders.

Keywords
White Paper, ELIXIR Strategy, Community Roadmap, Biodiversity Networks, Biodiversity Informatics, Environmental Systems, Data Science

1. **Patrick Comer**, NatureServe, Arlington, USA
2. **Abigail Benson**, US Geological Survey, Colorado, USA
   Stephen Formel, U.S. Geological Survey, Colorado, USA
3. **Cher FY Chow**, University of St Andrews, St Andrews, UK

Any reports and responses or comments on the article can be found at the end of the article.

This article is included in the Ecology and Global Change gateway.

This article is included in the Bioinformatics gateway.

This article is included in the ELIXIR gateway.

Corresponding author: Robert M. Waterhouse (robert.waterhouse@gmail.com)

Author roles: Waterhouse RM: Conceptualization, Project Administration, Writing – Original Draft Preparation, Writing – Review & Editing; **Adam-Blondon AF**: Writing – Review & Editing; **Balech B**: Writing – Review & Editing; **Barta E**: Writing – Review & Editing; **Ying Shi Chua P**: Writing – Review & Editing; **Di Cola V**: Writing – Review & Editing; **Heil KF**: Project Administration, Writing – Review & Editing; **Hughes GM**: Writing – Review & Editing; **Jermiin LS**: Writing – Review & Editing; **Kalaš M**: Writing – Review & Editing; **Lanfear J**: Conceptualization, Project Administration, Writing – Original Draft Preparation, Writing – Review & Editing; **Pafilis E**: Writing – Review & Editing; **Palagi PM**: Writing – Review & Editing; **Papageorgiou AC**: Writing – Review & Editing; **Paupério J**: Writing – Review & Editing; **Psomopoulos F**: Writing – Review & Editing; **Raes N**: Writing – Review & Editing; **Burgin J**: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing; **Gabaldón T**: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: The authors acknowledge the following grant support: Swiss National Science Foundation (SNSF) grant number PP00P3_202669 and Swiss State Secretariat for Education, Research and Innovation (SERI) contract numbers 22.00173 and 24.00054 to RMW. Institut Français de Bioinformatique (IFB) grant number ANR-11-INSB-0013 and French National Infrastructure of resources for Research in Agriculture (SOERE RARe) to AFAB; Green Fund, Hellenic Ministry of Environment and Energy, Funding Program "Natural Environment & Innovative Actions", Priority Axis 3 "Research and Implementation" Grant number 83078 to ACP.
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

How to cite this article: Waterhouse RM, Adam-Blondon AF, Balech B *et al.* **The ELIXIR Biodiversity Community: Understanding short- and long-term changes in biodiversity [version 2; peer review: 3 approved]** F1000Research 2024, **12**(ELIXIR):499 https://doi.org/10.12688/f1000research.133724.2

First published: 15 May 2023, **12**(ELIXIR):499 https://doi.org/10.12688/f1000research.133724.1

REVISED **Amendments from Version 1**

The article has been substantially revised to address the points raised by the three reviewers - the responses to the reviews contain also the main new texts that were added to the manuscript during revisions. This included the addition of several new references to support statements made throughout the text. It also included providing more context about ELIXIR and the role of ELIXIR Communities in general, as well as substantially extending the description of the structure and operational functioning and goals of the Biodiversity Community and a description of the Community's Implementation Study. Four authors were added as they contributed substantially to the manuscript revisions, especially the newly added parts about the Community goals and Implementation Study.

Any further responses from the reviewers can be found at the end of the article

Introduction

Biodiversity threats and challenges

Biological diversity—or biodiversity—refers to the variety and variability of life on Earth, encompassing genetic and species diversity at the levels of populations, communities, and ecosystems. Biodiversity reflects the ever-changing natural balance that has evolved over billions of years, sustaining communities of interdependent and interacting organisms. Those balances form the basis of a healthy Earth, including the ecosystem functions that support human well-being (*i.e.*, ecosystem services). With growing demands on nature due to human activities, the Anthropocene is upsetting this balance and is consequently witnessing an unprecedented loss of biodiversity globally (WWF, 2022; Johnson *et al.*, 2017). These declines pose a grave threat to humanity, the severity of which is increasingly recognised by international organisations, regional bodies, national governments, and society. The urgency to act is recognised particularly in the field of conservation biology, which has been described as a "discipline with a deadline" (Soulé & Wilcox, 1980).

Strategies to protect and restore biodiversity are wide-ranging in scope and scale, with policies and actions that require broad support to be feasible and effective *e.g.*, goals 12-15 of the 17 Sustainable Development Goals (SDGs) adopted by the United Nations (UN, 2015). Biodiversity research aimed at building the knowledge and resources that inform management practices and policy is equally wide-ranging, often bringing together researchers from different disciplines, such as taxonomists, ecologists, evolutionary biologists, and informaticians. This is particularly true for the growing field of interdisciplinary research taking advantage of molecular sequence data, which recognises the relevance of and advantages offered by genetic and genomic data in biodiversity assessment, monitoring, conservation, and restoration (Hoban *et al.*, 2021; Lewin *et al.*, 2022). Connecting such molecular sequence data with biodiversity research infrastructures (see *Extended Data* (Waterhouse, 2023)) and resources is a critical step towards facilitating exchange of knowledge, sharing, and interoperability of large and complex datasets (Waterhouse *et al.*, 2022).

As a European life sciences infrastructure, ELIXIR strives to coordinate bioinformatics resources from across Europe to enable researchers to access and analyse life science data, to improve the value and impact of life science research on public health, the environment, and the economy. The need for informatics solutions to address key societal challenges inspires many scientists from across the ELIXIR Nodes to increasingly engage in different aspects of biodiversity research. This stems from a natural alignment with ELIXIR's overarching mission to support the management of public research data, integrate and coordinate life science resources, and foster the development of innovative services and technical solutions in Europe (Harrow *et al.*, 2021). Here we present the ELIXIR Biodiversity Community, comprised of researchers from different disciplines, united by a shared recognition of the main societal and informatics challenges, as well as key scientific and organisational opportunities; how these connect with ELIXIR Platforms and other ELIXIR Communities, as well as with the wider "ecosystem" of biodiversity projects and infrastructures; and set out our roadmap for building on ELIXIR expertise to grow the ELIXIR Biodiversity Community and engage with the development of resources and infrastructures to support biodiversity research.

Societal challenges and global responses

Biodiversity represents the variety of organisms on the planet at all taxonomic levels, a result of a long and complex evolutionary process. Biodiversity is essential for life itself, for the adaptation of populations, species, communities, and ecosystems towards rapid change in biotic and abiotic parameters, including climate change. From a human standpoint, biodiversity forms the foundation of ecosystem services that are indispensable for human well-being and a healthy planet, and has long been a source of adaptive solutions or innovations in several critical areas such as food production. Despite its importance, biodiversity has been declining at a mass-extinction-level rate (IPBES, 2019) over the last decades. The unsustainable human development model has increased pressures on biodiversity, through climate change (IPCC, 2022; Wezel *et al.*, 2020), invasive species, habitat loss and degradation, and the depletion of natural resources (IPBES, 2019). The decline of biodiversity at this rate often creates unpredictable threats and changes to ecological oscillations, such as the increased risk of new human diseases (Frumkin & Haines, 2019), the collapse of ecosystem services, the degradation of natural resources, and the increased possibility of a global food crisis (FAO, 2019).

At the same time, scientists and naturalists do not even know what is being lost, as around 80% of biodiversity at the species and population levels remains undescribed and/or underrepresented in inventories and databases (Mora *et al.*, 2011; Costello *et al.*, 2013; Moura & Jetz, 2021; Bispo *et al.*, 2022; Boekhout *et al.*, 2022; Chimeno *et al.*, 2022). Furthermore, most research and monitoring efforts tend to focus on a limited number of biodiversity levels or elements. While there is significant literature around biodiversity loss (*e.g.,* a Scopus query [13.09.2022] for "biodiversity loss" returns 33,324 documents), there is a very limited effort in reviewing biodiversity using high-throughput data (Scopus query [13.09.2022] for "Biodiversity loss" AND ("omics" OR "genomics" OR "metagenomics") returns only 1,795 documents). This clearly indicates a bias in reporting, which has repercussions on the decision-making process pertaining to biodiversity conservation efforts (Gadelha *et al.*, 2021). This brings forward an additional challenge of shifting perspectives from narrow, low-throughput efforts towards more holistic, high-throughput initiatives, including better citizen scientist contributions towards these efforts. Humanity may miss important solutions to key problems for its survival, such as the loss of important genetic variants among wild plants, animals, and microbes for agriculture (Nic Lughadha *et al.*, 2020) and for dealing with health issues (Marselle *et al.*, 2021).

Following the 1992 United Nations Convention on Biological Diversity (CBD), governments and international organisations have responded to the decline of biodiversity with policies, and restoration and protection strategies. However, the initial goals of these have not been reached and biodiversity decline continues accelerating (IPBES, 2019; Turvey & Crees, 2019; WWF, 2022). For the new targets set by the post-2020 global biodiversity framework (GBF, 2023) to succeed, research is considered to be key, especially the interaction between science, society, and policy makers (Blicharska *et al.*, 2019; Hermoso *et al.*, 2022; Nature, 2022), with net improvements by 2050 to achieve the CBD's vision of "living in harmony with nature by 2050". Today, scientists recognise the important roles that genetic and genomic data can play in biodiversity discovery, assessment, monitoring, conservation, and restoration, to ensure the long-term resilience of ecosystems (Hoban *et al.*, 2020; Gadelha *et al.*, 2021; Segelbacher *et al.*, 2022; Formenti *et al.*, 2022; Theissinger *et al.*, 2023). The contribution of genomics and bioinformatics towards these targets, and many of the associated technical and scientific challenges are described in Waterhouse *et al.* (2022), together with the possible contribution of the ELIXIR European Strategy Forum for Research Infrastructures to meet them.

Scientific opportunities in biodiversity research

Biodiversity researchers are increasingly realising the potential offered by modern technologies, particularly in genomics, to create new opportunities for developing tools and resources that will transform the field. These opportunities lie primarily in the types of scientific applications that are becoming more feasible and scalable through continued advances in genomics technologies alongside enhanced data management systems. A long-term vision sees a future where sequence-based biodiversity monitoring at scale becomes a default and provides the means for ecosystem biodiversity characterisation in space and time, complemented and enhanced by other biomonitoring technologies. In support of realising these opportunities, ongoing global and regional efforts are building capacity to generate catalogues of reference DNA barcodes (International Barcode of Life, iBOL) (Hobern, 2021) and genomes by the Earth BioGenome Project (EBP) (Lewin *et al.*, 2018, 2022) as well as the European Reference Genome Atlas (ERGA, 2023), or both by the Biodiversity Genomics Europe (BGE, 2023; Mazzoni *et al.*, 2023) project. Along with this increased production, concurrent development of the necessary tools and resources will greatly enhance our abilities to:

- Maintain and query increasingly comprehensive reference DNA barcode and genome catalogues, improving taxonomic coverage and differentiation (including of cryptic species), and coordinating the efforts of various initiatives under global and regional umbrellas *e.g.*, McGee *et al.* (2019);

- Connect and integrate these molecular resources with other biodiversity data (traits, observations, literature, *etc.*) *e.g.*, König *et al.* (2019), using an increasingly standardised and harmonised taxonomic framework as the common backbone;

- Use these integrated resources for applied data-driven science to understand the diversity of extant life on Earth, how that diversity functions and interacts, and how it responds to changing environmental pressures (Pereira *et al.*, 2012);

- Implement monitoring of lesser-known or complex ecosystems, including for enhancing understanding of species interactions and dynamics, as well as for species discovery and exploration of "dark taxa" *e.g.*, Rahman *et al.* (2022);

- Include assessments of within-species, population-level genetic diversity to support characterisations of their evolutionary histories and predictions of their future prospects in the face of ongoing climatic changes (Pearman *et al.*, 2024);

- Operationalise the assessment of Essential Biodiversity Variables (EBVs) across taxa and spatiotemporal scales, focusing on species distribution and abundance (Kissling *et al.*, 2018; Jetz *et al.*, 2019);

- Engage with naturalists and citizen scientist groups through the use of new technologies that help build a democratised monitoring framework and improve characterisation of ecosystem biodiversity in space and time (Robinson & Peres, 2021);

- Evaluate biodiversity declines, as well as population-level adaptation and migration processes, in the context of anthropogenic activities (*e.g.*, climate change and urbanisation consequences, (Finn *et al.*, 2023)), and understand key aspects necessary to restore ecosystem functions (Breed *et al.*, 2019) to help prioritise biodiversity conservation, restoration, and "rewilding" efforts (*e.g.,* particularly relevant to at-risk biodiversity hotspots).

Organisational opportunities and ELIXIR's roles

The field of biodiversity assessment and research, from an organisational context, is broad, complex, and distributed. There are a multitude of organisations that operate across international borders, within countries, and at a local level (see *Extended Data* (Waterhouse, 2023)). This landscape is further demarcated along scientific and technical lines, with organisations that focus on taxonomies, ecology, molecular sciences, and method development (necessitated by the increasingly large and complex amount of data being generated). ELIXIR, perhaps uniquely, stands as a hub for the molecular sciences and bioinformatics at an international and national level across many scientific disciplines (Waterhouse *et al.*, 2022). Biodiversity research and infrastructures increasingly rely on molecular data (Karp *et al.*, 1997; Porter & Hajibabaei, 2018), so ELIXIR is well placed to lead organisational alignments and collaborations: from a core set of partners across Europe mainly within the field of molecular sciences, to an expanding variety of partner organisations that focus on other biodiversity-related research and resources (see below for examples from the ecosystem of biodiversity projects, resources, and infrastructures). Importantly, this extends beyond the data themselves as FAIR-ification of digital research objects (Wilkinson *et al.*, 2016), championed by ELIXIR's Services and Platforms, is increasingly recognised as essential in biodiversity research (Wetzel *et al.*, 2018; Lannom *et al.*, 2020). Opportunities to help coordinate and align organisational activities in the biodiversity domain arise naturally from ELIXIR's established European-wide "network of networks" approach, connecting to existing initiatives at both the national and international levels. With ELIXIR's strengths in molecular sciences, a "hub and spokes" model would help augment opportunities to connect molecular-focused bioinformatics tools, protocols, and resources with the many other biodiversity-related infrastructure and stakeholder organisations. Building on these strengths in data science and a connected network across Europe, ELIXIR can contribute to coordinated efforts designed to support and grow the many existing initiatives in the domains of biomonitoring, ecosystem health, and biodiversity research.

Informatics challenges facing biodiversity infrastructures and resources

The variety of existing biodiversity data infrastructures and resources is a testament to the long-standing recognition by multiple stakeholders of their importance, currently reflected in the growing European and global commitments to prevent further biodiversity decline and ensure the long-term health of ecosystem services. This heterogeneity, however, gives rise to many challenges, both technical in terms of data analysis (due to inadequacies of existing methodologies), data integration and data interaction, and at the level of the scientific community, which faces a heterogeneous landscape of infrastructures and resources that can be difficult to navigate (Blaxter & Floyd, 2003; Huang *et al.*, 2012; Levin *et al.*, 2014). The methodological and logistical challenges range from scaling up (needed to be able to process the increasing amounts of complex molecular data) to the management of these data and working on connecting them to other biodiversity research infrastructures (Waterhouse *et al.*, 2022). The biodiversity research community needs to proactively seek common solutions that enable molecular technologies to advance biodiversity research. A key part of this is the building of distributed infrastructures for life-science data that avoid or minimise unnecessary duplication of effort to be able to advance efficiently towards common goals. To this end, informatics solutions will need to be developed to address the practicalities of common challenges, such as:

- The need to constantly incorporate knowledge-based updates and resolve conflicts to maintain standardised taxonomies that serve as a dynamic framework that facilitates interoperability across research infrastructures;

- Building data and metadata brokering services that support coordinated community engagement to ensure good data management through technical infrastructures for aiding and automating data submission;

- Developing the means, through text mining and curation, to identify and liberate in digital form invaluable historical or baseline data trapped in the literature (including those published in non-English sources), or in museum and other natural history collections;
- Improving the accessibility of research results through publications (*e.g.,* by making published traits, tables, treatments, specimens, figures *etc.*), citable and reusable (*e.g.,* through nanopublications), and including identifiers of cited elements (genes, specimens, taxonomic names, treatments);
- Improving and harmonising currently highly heterogeneous metadata collection standards to promote the adoption of community best practices that will maximise findability, accessibility, interoperability, and reusability of digital research objects (*i.e.*, drive biodiversity research towards FAIR compliance);
- Scaling up of services for data and metadata management to keep pace with and accommodate the increases in data production (*e.g.,* genomics) and collection (*e.g.*, Essential Biodiversity Variables);
- Developing frameworks that deliver an increasingly integrated and interconnected landscape of biodiversity research infrastructures, utilising developments in application programming interfaces and Semantic Web services;
- Ensuring widespread access to high-performance computing (HPC) and HPC-deployable software and data-management systems, including containers and workflows, to enable decentralised efforts while promoting standardisation.

The ELIXIR Biodiversity Community: An “ecosystem” of projects

ELIXIR Communities are groups of experts across ELIXIR Nodes and beyond that represent a scientific or technological theme which drives the development of standards, services, and/or training in and across services offered by ELIXIR, thereby connecting the infrastructure services to research domains (Heil & Garrard, 2024). The ELIXIR Biodiversity Community was first launched in 2019 as a Focus Group to develop and coordinate ELIXIR Nodes’ tools, resources, and research work connected to the biodiversity domain. As part of the process of maturing from a Focus Group to a Community, members initiated activities including: (1) cataloguing ELIXIR Services that support biodiversity research; (2) developing and publishing their “Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR” (Waterhouse *et al.*, 2022); (3) coordinating ELIXIR Node participation in Horizon Europe project proposals - The Biodiversity Community Integrated Knowledge Library (BiCIKL) and Biodiversity Genomics Europe (BGE); and (4) beginning to establish connections with key external partners/projects in the biodiversity domain (such as those listed in Table 1); leading to the formal recognition in 2022 as an ELIXIR Community (Waterhouse *et al.*, 2023).

Table 1. Summaries of a selection of transnational and national biodiversity-related projects in which ELIXIR Nodes are involved.

Project	Node/Funder	Summary details/description
ARISE	Netherlands	ARISE (Authoritative and Rapid Identification System for Essential biodiversity information) is a digital infrastructure with a mission to provide semi-automated identification of all multicellular species in the Netherlands (van Ommen Kloeke *et al.*, 2022).
BiCIKL	E.C. (coordinated by Pensoft)	BiCIKL (Biodiversity Community Integrated Knowledge Library) will catalyse a culture change in the way biodiversity data is identified, linked, integrated and re-used across the research cycle. We will cultivate a more transparent, trustworthy and efficient research ecosystem.
Biodiversity Genomics Europe (BGE)	E.C. (coordinated by Naturalis Biodiversity)	By bringing together Europe’s key practitioners in two fundamental DNA-based technologies - DNA barcoding and genome sequencing - the BGE consortium aims to streamline the rollout of these methods across Europe.

Table 1. *Continued*

Project	Node/Funder	Summary details/description
Biodiversity Digital Twin (BioDT)	E.C. (coordinated by CSC – IT CENTER FOR SCIENCE LTD.)	The Biodiversity Digital Twin prototype will provide advanced models for simulation and prediction capabilities, through practical use cases addressing critical issues related to global biodiversity dynamics.
Curated collections of DNA barcode marker	Italy	A reference collection of COXI mitochondrial DNA genes based on the integration of sequence and taxonomy data of BOLD and ENA (Balech *et al.*, 2022).
e-BioDiv	Switzerland	Open Biodiversity FAIR-ification Services for Biospecimens stored in Swiss Natural History Museums
Earlham Institute Barcoding the Broads	UK	A Wellcome-funded programme of public engagement events and activities to explore biodiversity on the Norfolk Broads, led by the Earlham Institute as part of the work on the Darwin Tree of Life project.
ELIXIR Norway	Norway	Dedicated national ELIXIR Node funding (2022-2026) includes a focus on biodiversity and connections to other biodiversity infrastructures and projects in Norway (*e.g.*, the Earth BioGenome Project Norway: EBP-Nor).
Establishment of an ELIXIR Contextual Data Clearinghouse	ELIXIR (Implementation study)	The objective is to develop and deploy an "ELIXIR Contextual Data Clearinghouse" for extending, correcting and improving publicly available annotations on records in sample and sequencing data resources.
Molecular Biodiversity Greece Community (MBGC)	Greece	Greece is a biodiversity hotspot and to this end, a network of networks covering different disciplines of molecular biodiversity research has been developed. MBGC aims to channel the flow of information amongst researchers, institutions, policy makers, stakeholders and local communities, remaining aligned to all relevant initiatives and infrastructures, at the national, European, and global level.
NFDI4Biodiversity	Germany	Network of diverse biodiversity data (not only molecular). Data are provided by research organisations and projects (*e.g.*, GBOL), public authorities, professional societies and citizen initiatives. Data Management oriented. The production of the data itself is done through use cases.
Phylogenetic methodology	Ireland	A range of analytical tools is being developed to augment the bioinformatics tool kit for comparative genome analysis.
Pole National de Données de Biodiversité	France	National centre of data on biodiversity: the data are provided by the same diversity of channels as in Germany and the role of PNDB is to support FAIR data management.

Operationally, monthly online meetings coordinated by the Community co-leads with support from the ELIXIR Hub serve as the primary forum for interactions, complemented by discussions and notifications on the ELIXIR Slack Workspace's Biodiversity Community channel. These include sharing information on members' participation in ongoing or planned biodiversity-related projects and initiatives, including the Community-led Implementation Study "Biodiversity Networks for ELIXIR". The online meetings also feature presentations on tools and services developed by ELIXIR Nodes as well as hosting invited speakers representing key external partners/projects. The Community's Implementation Study encompasses four key areas of work to drive Community activities: (1) to survey and catalogue Research Data Management (RDM) elements relevant to the biodiversity domain, with a focus on molecular data; (2) to catalogue, review, and categorise tools, services, and analytical workflows currently in use by ELIXIR Nodes and the wider community, that process and analyse biodiversity-related data; (3) to describe the landscape of stakeholders ELIXIR is working with or needs to better engage with to establish a "network of networks" for biodiversity research and services;

and (4) to leverage the strengths of ELIXIR's training experience to help support the growth of the Biodiversity Community through network-driven sharing of training experiences and knowledge transfer and materials. Together, these actions are serving to enhance ELIXIR's network of networks in helping to deliver connected data to advance biodiversity research.

Tackling the biodiversity crisis at a general level is not going to be resolved through a single action, but instead requires a complex set of interacting actions that are co-dependent but usually funded separately. ELIXIR can assume a key leading role in a subset of those actions, focused on data management and the molecular sciences, where even at the level of ELIXIR, there are a multitude of funded projects at a transnational, national, and local level. In terms of informatics solutions connected to such projects, the ELIXIR Biodiversity Community is guided by themes emerging from surveying approaches by which molecular technologies are helping to inform understanding of biodiversity (Waterhouse *et al.*, 2022): biodiversity-related and informatics infrastructures need to develop close and strategic collaborations; work on taxonomy needs to be better aligned and standardised across different infrastructures and fields of study; metadata urgently needs harmonisation and common approaches to research data management must be widely adopted; current data science solutions need to be scaled up to address the rapidly accumulating amounts of molecular data; bioinformatics support for biodiversity research needs to be made widely available and properly maintained; user training on biodiversity research tools, services, and infrastructures needs to be prioritised; and community initiatives need to be collaborative, proactive, and solution-driven. These themes come together in a complex network of interacting projects that have distinct but related aims, usually focused on establishing communities and connections and/or building new technical solutions to help with data access, storage, or analysis. ELIXIR can serve a critical function here, as a fundamental aspect of its mission is to make connections and coordinate across complex activities. Table 1 lists a subset of ongoing projects across Europe and within ELIXIR member states that illustrate the breadth of activities underway.

Connections with ELIXIR Platforms and Communities

ELIXIR as a Research Infrastructure is structured around (technological) Platforms as well as (user) Communities. Both of these interact on an ongoing basis, mutually supporting each other's efforts. The ELIXIR Biodiversity Community is already collaborating with some of these and aims to broaden interactions to fully leverage the available potential and resources. Some examples of current and future interactions with ELIXIR Platforms (Tools, Compute, Data, Training, and Interoperability) are:

- The Tools Platform provides services for finding software tools and web portals (Bio.tools (Ison *et al.*, 2019), including the https://biodiversity.bio.tools subdomain to be populated by the ELIXIR Biodiversity Community), software containers (BioContainers (da Veiga Leprevost *et al.*, 2017)), and workflows (WorkflowHub (Goble *et al.*, 2021)); for assessing tools (OpenEBench (Capella-Gutierrez *et al.*, 2017)); and the best practices in providing research software (Jiménez *et al.*, 2017)). EDAM ontology enables annotation and search of tools and other research objects by application domain, task, or data (Black *et al.*, 2022); and an extended coverage of biodiversity research concepts could be achieved *via* engagement with the Biodiversity Community.

- Specifically for the Compute Platform: User accessible compute, potentially controlled user access *via* Authentication and Authorisation Infrastructure (AAI).

- Community data-management support, and integration with ELIXIR Core and Deposition Data resources. The European Nucleotide Archive (ENA) is a critical data deposition resource for biodiversity genomics data. A concrete example of metadata management workflow is that developed between biodiversity scientists, the Data Platform, and the Biodiversity Community Integrated Knowledge Library (BiCIKL) project (Penev *et al.*, 2021, 2022): a metadata management workflow employs the PlutoF tool for biodiversity data and metadata management (Abarenkov *et al.*, 2010), and the ELIXIR Data Platform services.

- Networks of tool/infrastructure users and developers to augment the Training Platform offerings (*e.g.*, with specific courses covering aspects such as: genome annotation, meta-data brokering, *etc.*) and more complete learning paths, covering entire workflows (*e.g.,* from sequencing to annotation, possibly covered *via* Galaxy).

- A growing necessity in the biodiversity field towards connected data, as championed by the Interoperability Platform, concretely touching on resources like: RO-Crate and link to specimens, RDMkit, FAIRsharing, Bioschemas and the FAIRcookbook. The ELIXIR Biodiversity Community aims to bring together researchers producing the data, in all their varied forms, with informaticians developing interoperability solutions, to help overcome the challenges of data heterogeneity in the field.

Table 2. **Examples of links between the ELIXIR Biodiversity Community and other ELIXIR Communities.**

Community	Shared activities
Food & Nutrition	Conceptualisation and implementation of interoperability data models able to integrate, standardise and harmonise data from different disciplines: metagenomics, metabolomics and transcriptomics.
Galaxy	Thousands of tools, including hundreds for biodiversity and microbial/microbiome analysis, are ready to be used on publicly-accessible HPC resources, together with workflows for data processing, which can be versioned, annotated, and shared for reuse. The European Galaxy server (https://usegalaxy.eu) offers access to 2700+ tools and workflows. Galaxy-Ecology is its subdomain piloted by the French ELIXIR Node. A training material repository (https://training.galaxyproject.org) is open for everyone to use and contribute to, providing slides, hands-on tutorials, and other material on using Galaxy to analyse data, with 260+ tutorials in 20+ topics including ecology, microbiome, and climate. Integration of PlutoF and other biodiversity tools into Galaxy could be carried out together with the Biodiversity Community in the near future.
Microbiome	Meta-genomic workflows and data archiving. Marine sample metadata annotation guidelines.
Plant Science	Taxonomy framework; coherent/consistent metadata standards for samples (see also interoperability PF (platform), MIAPPE (Minimum Information About Plant Phenotyping Experiments)). Alignment between the MIAPPE standard and exchange formats and the relevant TDWG (Biodiversity Information Standards) standards and exchange formats. Integration and linking different plant data types.

Regarding links between the ELIXIR Biodiversity Community and other ELIXIR Communities, these are already foreseen, and a number of synergies have been clearly identified. Some examples can be found in Table 2.

A global network of biodiversity projects and infrastructures

ELIXIR entered the European Strategy Forum for Research Infrastructure's (ESFRI) first roadmap in 2006 and reached its Landmark status in 2016 (ELIXIR, 2021). As a distributed research infrastructure, ELIXIR coordinates, integrates, and sustains bioinformatics resources across European countries and helps address the Grand Challenges across life sciences, from marine research, *via* plants and agriculture, to health research, medical sciences, and biodiversity informatics. ELIXIR provides services in seven scientific domains including "Evolution and phylogeny" and "Genes and genomes" (https://elixir-europe.org/services) that link the activities of the ELIXIR community to the wider landscape of life-science research infrastructures (RIs) and international projects. As RIs mature and FAIRness has become the standard to achieve interoperability between RIs, it is opportune to outline the global network of interrelated projects and infrastructures, in which ELIXIR operates to maximise synergy and to avoid redundancy.

The relationships between different aspects of biodiversity data are well captured by the biodiversity knowledge graph of Roderic Page (Figure 1). The key activities of ELIXIR are captured by the molecular domain; the biodiversity knowledge graph clearly indicates how molecular data are related to the wider spectrum of biodiversity data that are targeted by other RIs and projects. The ELIXIR Biodiversity Community benefits from connections to RIs and projects in the biodiversity domain, an overview of which can build on the landscape analyses of the ESFRI roadmaps of ESFRI 2018 (ESFRI, 2018) and 2021 (ESFRI, 2021), the partners of the Alliance for Biodiversity Knowledge, and the research infrastructure contact zones analysis between 10 biodiversity infrastructures, including ELIXIR (Smith *et al.*, 2022). Additional to the data types considered by Page (Figure 1), the contact zones analysis considers 'observations' and 'collections', or groups of specimens, as elements of the biodiversity data domain. This recognition of the variety of types of biodiversity data and the importance of integration has been key to the establishment of many RIs and research projects, for example: the Alliance for Biodiversity Knowledge; Biodiversity Genomics Europe; Biodiversity Heritage Library; Biodiversity Community Integrated Knowledge Library; iBOL BIOSCAN; Biodiversity Literature Repository; Catalogue of Life; Data Observation Network for Earth; Distributed System of Scientific Collections; Earth BioGenome Project; European Marine Biological Resource Centre; Environmental Research Infrastructures; Encyclopedia of Life; European Open Science Cloud; European Reference Genome Atlas; Europa Biodiversity Observation Network; Global Biodiversity Information Facility; Global Earth Observation System of Systems; Global Soil Biodiversity Initiative; International Barcode of Life; iNaturalist; LifeWatch ERIC; Long-Term Ecosystem Research in Europe; Microbial Resource Research Infrastructure; National Ecological Observatory Network; Open Traits Network; Plazi; Pôle national de données de biodiversité; Swiss Institute for bioinformatics Literature Services; Soil Biodiversity Observation Network; Treatment-Bank; World Register of Marine Species.

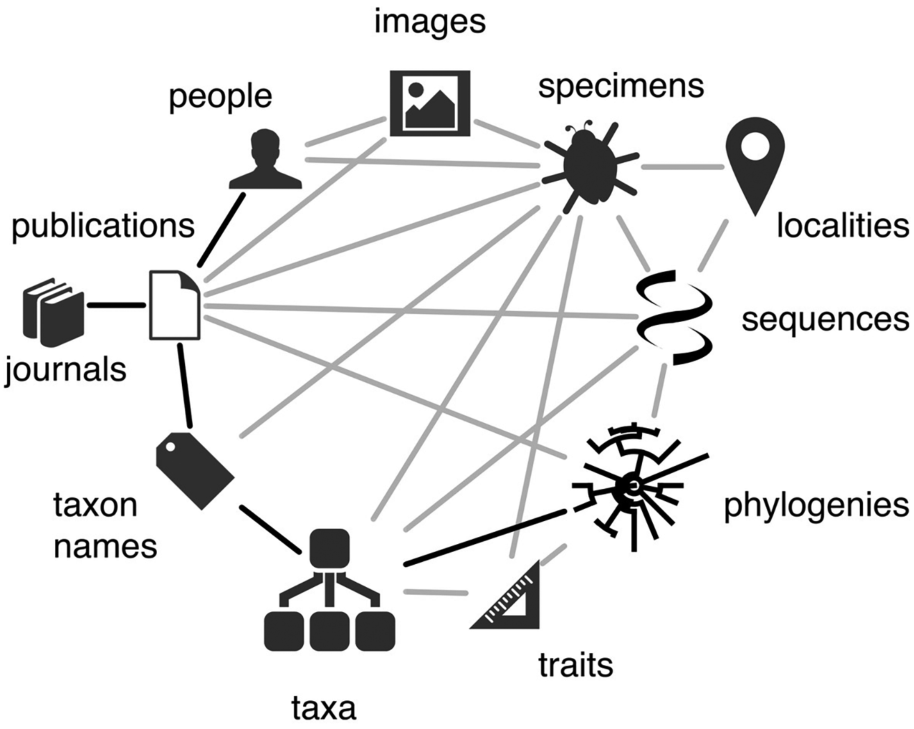

Figure 1. The biodiversity knowledge graph defined by Roderick D.M. Page (2013, 2016). Genomics data comprise one facet of the biodiversity knowledge graph, where questions and approaches in biodiversity research traverse the paths in this graph, and where all parts of the graph are constantly 'evolving' and growing. Wikimedia Commons CC-BY-4.0.

In addition to the above examples of biodiversity projects and infrastructures that make up the global network of ongoing efforts in the domain, and in the context of ELIXIR's participation and contribution to the network, the following two examples highlight ongoing activities in the field of biodiversity and in the context of the European research sphere.

Example: Biodiversity Community Integrated Knowledge Library (BiCIKL)

Several ELIXIR Nodes are involved in European projects with a focus on biodiversity. The BiCIKL project is building the Biodiversity Knowledge Hub (BKH) - a single knowledge portal to interlinked machine-readable FAIR data - using unique stable identifiers on specimens, sequences, taxonomy and publications (Penev *et al.*, 2021, 2022). A set of core global biodiversity databases (GBIF, ENA, PlutoF, Plazi, DiSSCo, OpenBioDiv, ToL, *etc.*) are contributing with the aim to develop services to augment the interlinking of biodiversity contents, starting with biotic interactions. The project is also financing competitive implementation studies to develop transnational resources.

Example: European Open Science Cloud (EOSC)

The European Open Science Cloud initiative (2023) intends to offer a federated and open multi-disciplinary environment where tools, data and services can be published, sought, and re-used. Via enabling seamless access and FAIR management EOSC aims to develop a Web of FAIR Data and services for science, innovation and education in Europe through which value-added services can be offered. The EOSC-Life initiative connects 13 life science 'ESFRI' research infrastructures to create an open, digital and collaborative space for biological and medical research. Among the EOSC-Life "FAIR" published data and catalogued services (by participating RIs), ones related to biodiversity are included. The workflow for marine Genomic Observatories data analysis is such an example (EBI, 2021).

Conclusions: A roadmap for the ELIXIR Biodiversity Community

Considering the context discussed above in terms of the complex landscape of ongoing initiatives working to meet the most pressing needs supporting biodiversity research and services, the ELIXIR Biodiversity Community aims to contribute towards the global aim of tackling the biodiversity crisis by helping to make possible a future where:

- Large-scale sustainable data production services are meeting the routine needs of hundreds of laboratories and thousands of citizen scientists for sequence-based biodiversity research and biomonitoring;

- ELIXIR is part of a network of well-connected, stable, and long-term infrastructures that is supporting a growing portfolio of stakeholders in biodiversity research by improving their access to, and integration of well-curated, high-quality, richly annotated, and connected molecular data.

- State-of-the-art computational tools and services are available for large-scale projects related to biodiversity, including data standardisation initiatives, allowing for the enhanced exploitation of the collected and connected data within the biodiversity knowledge graph.

To define a roadmap for the ELIXIR Biodiversity Community to help drive progress towards advances in these three overarching priority areas – data production, data integration, and data exploitation – a set of five guiding goals has been established:

1. To enhance ELIXIR's network of networks in helping to deliver connected data for biodiversity research by: exposing and augmenting relevant ELIXIR services and infrastructures contributing to efforts to catalogue, protect, and restore biodiversity and ecosystem services; supporting ELIXIR Nodes in expanding their activities related to biodiversity data and research and relevant for the new programme priority areas; and communicating ELIXIR activities and services relevant to the biodiversity domain to broader audiences including scientists, policy makers, and the general public.

2. To support the development of standards and promote best practices in biodiversity research by: supporting and promoting the development and use of global standards, formats, guidelines, and ontologies across the domain; supporting the development of best practices in Research Data Management for biodiversity research, with a focus on molecular data but not excluding other areas; and collecting, exposing, and maintaining, a dedicated RDMkit domain for biodiversity collating relevant documentation and tools that support good practices in research data management.

3. To promote tools and workflows that facilitate reliable and reproducible biodiversity data analyses by: identifying, curating, and promoting high-quality biodiversity-related analysis tools and services to the wider community of users; connecting developers with data-generation initiatives and data users to fuel synergies that deliver tools and workflows serving their needs; and maintaining curated catalogues of FAIR biodiversity-focused tools and workflows in Bio.tools and WorkflowHub.

4. To enhance biodiversity database/infrastructure usability and interoperability by: identifying and acting on opportunities to develop technical solutions that improve connectivity amongst heterogenous biodiversity data infrastructures and resources; fostering collaborative exchanges between users and providers of biodiversity-related databases/infrastructures to improve usability and functionality; and promoting the usage of persistent identifiers across the domain, including taxonomies as the backbone of biodiversity knowledge.

5. To foster knowledge transfer in biodiversity data management and analysis by: supporting community-driven skills sharing focused on understanding how to benefit from the use of available standards and best practices; connecting developers of tools/workflows/databases with user communities through training that responds to changing technologies and associated services; and exposing collections of training materials, for example through TeSS, the Galaxy Training Network, and RDMkit.

To complement these guiding goals, the ELIXIR Biodiversity Community proposes a roadmap towards achieving our long-term objectives. Table 3 shows five long-term objectives for the ELIXIR Biodiversity Community to address,

Table 3. The ELIXIR Biodiversity Community long-term objectives.

Objectives	Example approaches
Identify and support key stakeholders in the biodiversity domain	• Support efforts to harmonise data management activities within large-scale projects and transcending initiatives to result in high-quality, interoperable data and metadata • Build routes for user communities to access and add to the knowledge graph (curation) of growing resources *e.g.*, trait measurements, observations beyond geolocations *etc.* • Include primary production sectors (industry *etc.*) affecting biodiversity in the collaborative processes aiming to identify data-informed win-win solutions

Table 3. *Continued*

Objectives	Example approaches
Connect and align biodiversity infrastructures	• Foster interactions and promote the alignment of key infrastructures contributing to worldwide efforts to sequence and catalogue Earth's biodiversity • Increase interoperability in biodiversity infrastructures through alignment of taxonomies and data/metadata standards • Work towards the inclusion of relevant citizen science initiatives (*e.g.*, Atlas of Living Australia, iNaturalist, eBird) in the biodiversity infrastructure landscape
Contribute to data-informed policy decision making	• Facilitate high-level alignment of strategy and policy in the biodiversity data domain • Support reconciliation of the interests of primary producers in biodiversity-rich environments
Deliver production services for sequence-based biodiversity monitoring	• Identify and address gaps in the platforms/frameworks that exist to support the biodiversity data life cycle • Coordinate and integrate services that support workflows through all stages of the process: from sampling, taxonomic identification and vouchering, sequence generation, annotation, cataloguing and further application of the data • Reinforce the network of services that meet the route needed by hundreds of labs and thousands of citizen scientists
Connect to and leverage the full potential of ELIXIR	• Establish the network of Nodes through integrated bioinformatics resources, tools, and services delivery • Leverage and invest in training expertise and networks to connect user communities with developers of data science solutions • Focus on community integration and re-use (rather than disjointed efforts) to exploit ELIXIR tools and services that can support the biodiversity data ecosystem • Connect with other ongoing ELIXIR efforts in data production and management, standards and best practices development, as well as in analysis and exploitation

centred on engaging with stakeholders, aligning infrastructures, contributing to policy, supporting production, and enhancing ELIXIR's portfolio in the biodiversity domain. The current focus is on the informatics, databases, and tools more than on the biological questions, so as the Community grows, it will be important to widen the diversity of its membership to ensure that the technical developments will serve the needs of biodiversity researchers. Beyond the ELIXIR Biodiversity Community itself, it is also vital to engage with other communities in the domain, including with stakeholders such as practitioners and citizen science initiatives in order to contribute towards bridging the gaps between research and implementation (Dubois *et al.*, 2020; Fraisl *et al.*, 2022).

Data availability

Underlying data

No data are associated with this article.

Extended data

Figshare: Extended Data 1: Biodiversity RIs & Projects. https://doi.org/10.6084/m9.figshare.22723432 (Waterhouse, 2023).

This project contains the following extended data:

- Extended_Data_1_Biodiversity_RIs_Projects.xlsx (A non-exhaustive list of biodiversity research infrastructures, collected as part of the development of the ELIXIR Biodiversity Community white paper 2022-2023.)

Data are available under the terms of the Creative Commons Zero "No rights reserved" data waiver (CC0 1.0 Public domain dedication).

Acknowledgements

The authors thank all members of the ELIXIR Biodiversity Community, the ELIXIR Hub, and the ELIXIR Heads of Nodes, for useful feedback during the development of this Community White Paper, and the reviewers for their invaluable input.

References

Abarenkov K, *et al.*: **PlutoF—a Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences.** *Evol. Bioinforma.* 2010; **6**: EBO.S6271.
Publisher Full Text

Balech B, Sandionigi A, Marzano M, *et al.*: **MetaCOXI: an integrated collection of metazoan mitochondrial cytochrome oxidase subunit-I DNA sequences. Database. 2022:baab084.** 2022.
Publisher Full Text

BGE: **BGE - Biodiversity Genomics Europe.** 2023. (Accessed April 7, 2023).
Reference Source

Bispo A, Willenz P, Hajdu E: **Diving into the unknown: fourteen new species of haplosclerid sponges (Demospongiae: Haplosclerida) revealed along the Peruvian coast (Southeastern Pacific).** *Zootaxa.* 2022; **5087**: 201–252.
Publisher Full Text

Black M, *et al.* **EDAM: the bioscientific data analysis ontology (update 2021).** 2022.
Publisher Full Text

Blaxter M, Floyd R: **Molecular taxonomics for biodiversity surveys: already a reality.** *Trends Ecol. Evol.* 2003; **18**: 268–269.
Publisher Full Text

Blicharska M, *et al.*: **Biodiversity's contributions to sustainable development.** *Nat. Sustain.* 2019; **2**: 1083–1093.
Publisher Full Text

Boekhout T, *et al.*: **Trends in yeast diversity discovery.** *Fungal Divers.* 2022; **114**: 491–537.
Publisher Full Text

Breed MF, *et al.*: **The potential of genomics for restoring ecosystems and biodiversity.** *Nat. Rev. Genet.* 2019; **20**: 615–628.
Publisher Full Text

Capella-Gutierrez S, *et al.*: **Lessons Learned: Recommendations for Establishing Critical Periodic Scientific Benchmarking.** *Bioinformatics.* 2017.
Publisher Full Text

Chimeno C, *et al.*: **Peering into the Darkness: DNA Barcoding Reveals Surprisingly High Diversity of Unknown Species of Diptera (Insecta) in Germany.** *Insects.* 2022; **13**: 82.
PubMed Abstract | Publisher Full Text | Free Full Text

Costello MJ, May RM, Stork NE: **Can We Name Earth's Species Before They Go Extinct?** *Science.* 2013; **339**: 413–416.
PubMed Abstract | Publisher Full Text

Dubois NS, Gomez A, Carlson S, *et al.*: **Bridging the research-implementation gap requires engagement from practitioners.** *Conserv. Sci. Pract.* 2020; **2**: e134.
Publisher Full Text

EBI: **A workflow for marine genomic data analysis.** 2021. (Accessed April 7, 2023).
Reference Source

ELIXIR: **ELIXIR|ESFRI Roadmap 2021.** 2021. (Accessed April 7, 2023).
Reference Source

EOSC Portal: **EOSC Portal.** 2023. (Accessed April 7, 2023).
Reference Source

ERGA: **The European Reference Genome Atlas (ERGA) initiative. erga.** 2023. (Accessed April 7, 2023).
Reference Source

ESFRI: **ESFRI Strategy Report and Roadmap 2018.** 2018. (Accessed April 7, 2023).
Reference Source

ESFRI: **ESFRI Strategy Report on Research Infrastructures.** 2021. (Accessed April 7, 2023).
Reference Source

FAO: *The state of the world's biodiversity for food and agriculture.* Rome: FAO Commission on Genetic Resources for Food and Agriculture; 2019.

Finn C, Grattarola F, Pincheira-Donoso D: **More losers than winners: investigating Anthropocene defaunation through the diversity of population trends.** *Biol. Rev.* 2023; **98**: 1732–1748.
PubMed Abstract | Publisher Full Text

Formenti G, *et al.*: **The era of reference genomes in conservation genomics.** *Trends Ecol. Evol.* 2022; **37**: 197–202.
Publisher Full Text

Fraisl D, Hager G, Bedessem B, *et al.*: **Citizen science in environmental and ecological sciences.** *Nat. Rev. Methods Primer.* 2022; **2**: 64.
Publisher Full Text

Frumkin H, Haines A: **Global Environmental Change and Noncommunicable Disease Risks.** *Annu. Rev. Public Health.* 2019; **40**: 261–282.
Publisher Full Text

Gadelha LMR, *et al.*: **A survey of biodiversity informatics: Concepts, practices, and challenges.** *WIREs Data Min. Knowl. Discov.* 2021; **11**.
Publisher Full Text

GBF: **Kunming-Montreal Global Biodiversity Framework.** 2023. (Accessed April 7, 2023).
Reference Source

Goble C, *et al.*: **Implementing FAIR Digital Objects in the EOSC-Life Workflow Collaboratory.** 2021.
Publisher Full Text

Harrow J, *et al.*: **ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future.** *EMBO J.* 2021; **40**: e107409.
PubMed Abstract | Publisher Full Text | Free Full Text

Heil KF, Garrard C: *ELIXIR Communities Handbook 2024.* 2024;
Publisher Full Text

Hermoso V, *et al.*: **The EU Biodiversity Strategy for 2030: Opportunities and challenges on the path towards biodiversity recovery.** *Environ. Sci. Policy.* 2022; **127**: 263–271.
Publisher Full Text

Hoban S, *et al.*: **Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved.** *Biol. Conserv.* 2020; **248**: 108654.
Publisher Full Text

Hoban S, *et al.*: **Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible.** *Bioscience.* 2021; **71**: 964–976.
PubMed Abstract | Publisher Full Text | Free Full Text

Hobern D: **BIOSCAN: DNA barcoding to accelerate taxonomy and biogeography for conservation and sustainability Adamowicz, S, editor.** *Genome.* 2021; **64**: 161–164.
PubMed Abstract | Publisher Full Text

Huang X, *et al.*: **Willing or unwilling to share primary biodiversity data: results and implications of an international survey.** *Conserv. Lett.* 2012; **5**: 399–406.
Publisher Full Text

IPBES: **Global assessment report on biodiversity and ecosystem services of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services.** *Zenodo.* 2019.
Publisher Full Text

IPCC: *Climate Change 2022: Impacts, Adaptation, and Vulnerability. Contribution of Working Group II to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change.* Cambridge, UK and New York, NY, USA: Cambridge University Press; 2022.
Reference Source

Ison J, *et al.*: **The bio.tools registry of software tools and data resources for the life sciences.** *Genome Biol.* 2019; **20**: 164.
PubMed Abstract | Publisher Full Text | Free Full Text

Jetz W, *et al.*: **Essential biodiversity variables for mapping and monitoring species populations.** *Nat. Ecol. Evol.* 2019; **3**: 539–551.
PubMed Abstract | Publisher Full Text

Jiménez RC, *et al.*: **Four simple recommendations to encourage best practices in research software.** *F1000Res.* 2017; **6**: 876.
PubMed Abstract | Publisher Full Text | Free Full Text

Johnson CN, *et al.*: **Biodiversity losses and conservation responses in the Anthropocene.** *Science.* 2017; **356**: 270–275.
PubMed Abstract | Publisher Full Text

Karp A, *et al.*: **Molecular technologies for biodiversity evaluation: Opportunities and challenges.** *Nat. Biotechnol.* 1997; **15**: 625–628.
PubMed Abstract | Publisher Full Text

Kissling WD, *et al.*: **Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale.** *Biol. Rev.* 2018; **93**: 600–625.
Publisher Full Text

König C, Weigelt P, Schrader J, *et al.*: **Biodiversity data integration—the significance of data resolution and domain Mace, GM, editor.** *PLOS Biol.* 2019; **17**: e3000183.
PubMed Abstract | Publisher Full Text | Free Full Text

Lannom L, Koureas D, Hardisty AR: **FAIR Data and Services in Biodiversity Science and Geoscience.** *Data Intell.* 2020; **2**: 122–130.
Publisher Full Text

Levin N, *et al.*: **Biodiversity data requirements for systematic conservation planning in the Mediterranean Sea.** *Mar. Ecol. Prog. Ser.* 2014; **508**: 261–281.
Publisher Full Text

Lewin HA, *et al.*: **Earth BioGenome Project: Sequencing life for the future of life.** *Proc. Natl. Acad. Sci.* 2018; **115**: 4325–4333.
PubMed Abstract | Publisher Full Text | Free Full Text

Lewin HA, *et al.*: **The Earth BioGenome Project 2020: Starting the clock.** *Proc. Natl. Acad. Sci.* 2022; **119**: e2115635118.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Marselle MR, *et al.*: **Pathways linking biodiversity to human health: A conceptual framework.** *Environ. Int.* 2021; **150**: 106420.
Publisher Full Text

Mazzoni CJ, Ciofi C, Waterhouse RM: **Biodiversity: an atlas of European reference genomes.** *Nature.* 2023; **619**: 252.
PubMed Abstract | **Publisher Full Text**

McGee KM, Robinson CV, Hajibabaei M: **Gaps in DNA-Based Biomonitoring Across the Globe.** *Front. Ecol. Evol.* 2019; **7**: 337.
Publisher Full Text

Mora C, Tittensor DP, Adl S, *et al.*: **How Many Species Are There on Earth and in the Ocean? Mace, GM, editor.** *PLoS Biol.* 2011; **9**: e1001127.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Moura MR, Jetz W: **Shortfalls and opportunities in terrestrial vertebrate species discovery.** *Nat. Ecol. Evol.* 2021; **5**: 631–639.
PubMed Abstract | **Publisher Full Text**

Nature.: **Biodiversity faces its make-or-break year, and research will be key.** *Nature.* 2022; **601**: 298–298.
PubMed Abstract | **Publisher Full Text**

Nic Lughadha E, *et al.*: **Extinction risk and threats to plants and fungi.** *PLANTS PEOPLE PLANET.* 2020; **2**: 389–408.
Publisher Full Text

van Ommen KE, *et al.*: **ARISE: Building an infrastructure for species recognition and biodiversity monitoring in the Netherlands.** *Biodivers. Inf. Sci. Stand.* 2022; **6**: e93613.
Publisher Full Text

Page R: **Towards a biodiversity knowledge graph.** *Res. Ideas Outcomes.* 2016; **2**: e8767.
Publisher Full Text

Page RDM: **BioNames: linking taxonomy, texts, and trees.** *PeerJ.* 2013; **1**: e190.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Pearman PB, *et al.*: **Monitoring of species' genetic diversity in Europe varies greatly and overlooks potential climate change impacts.** *Nat. Ecol. Evol.* 2024; **8**: 267–281.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Penev L, *et al.*: **Towards Interlinked FAIR Biodiversity Knowledge: The BiCIKL perspective.** *Biodivers. Inf. Sci. Stand.* 2021; **5**: e74233.
Publisher Full Text

Penev L, *et al.*: **Biodiversity Community Integrated Knowledge Library (BiCIKL).** *Res. Ideas Outcomes.* 2022; **8**: e81136.
Publisher Full Text

Pereira HM, Navarro LM, Martins IS: **Global Biodiversity Change: The Bad, the Good, and the Unknown.** *Annu. Rev. Environ. Resour.* 2012; **37**: 25–50.
Publisher Full Text

Porter TM, Hajibabaei M: **Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis.** *Mol. Ecol.* 2018; **27**: 313–338.
PubMed Abstract | **Publisher Full Text**

Rahman MM, Burian A, Creedy TJ, *et al.*: **DNA -based assessment of environmental degradation in an unknown fauna: The freshwater macroinvertebrates of the Indo-Burmese hotspot.** *J. Appl. Ecol.* 2022; **59**: 1644–1658.
Publisher Full Text

Robinson WD, Peres CA: **Editorial: Benchmarking Biodiversity in an Era of Rapid Change.** *Front. Ecol. Evol.* 2021; **9**: 810287.
Publisher Full Text

Segelbacher G, *et al.*: **New developments in the field of genomic technologies and their relevance to conservation management.** *Conserv. Genet.* 2022; **23**: 217–242.
Publisher Full Text

Smith V, *et al.*: **Research Infrastructure Contact Zones: a framework and dataset to characterise the activities of major biodiversity informatics initiatives.** *Biodiversity Data Journal.* 2022; **10**.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Soulé ME, Wilcox BA, editors: *Conservation biology: an evolutionary-ecological perspective.* Sunderland, Mass: Sinauer Associates; 1980.

Theissinger K, *et al.*: **How genomics can help biodiversity conservation.** *Trends Genet.* 2023. S0168952523000203.
PubMed Abstract | **Publisher Full Text**

Turvey ST, Crees JJ: **Extinction in the Anthropocene.** *Curr. Biol.* 2019; **29**: R982–R986.
PubMed Abstract | **Publisher Full Text**

UN: **THE 17 GOALS|Sustainable Development.** 2015. (Accessed April 7, 2023).
Reference Source

da Veiga Leprevost F, *et al.*: **BioContainers: an open-source and community-driven framework for software standardization Valencia, A, editor.** *Bioinformatics.* 2017; **33**: 2580–2582.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Waterhouse RM, *et al.*: **Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR.** *F1000Res.* 2022; **10**: 1238.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

Waterhouse RM: Extended Data 1: Biodiversity RIs & Projects. [Dataset]. *figshare.* 2023.
Publisher Full Text

Waterhouse R, Burgin J, Gabaldón T, *et al.*: *The ELIXIR biodiversity community: Actions, goals, & implementation study.* 2023.
Publisher Full Text

Wetzel FT, *et al.*: **Unlocking biodiversity data: Prioritization and filling the gaps in biodiversity observation data in Europe.** *Biol. Conserv.* 2018; **221**: 78–85.
Publisher Full Text

Wezel A, *et al.*: **Agroecological principles and elements and their implications for transitioning to sustainable food systems. A review.** *Agron. Sustain. Dev.* 2020; **40**: 40.
Publisher Full Text

Wilkinson MD, *et al.*: **The FAIR Guiding Principles for scientific data management and stewardship.** *Sci. Data.* 2016; **3**: 160018.
PubMed Abstract | **Publisher Full Text** | **Free Full Text**

WWF: *The Living Planet Report 2022 – Building a nature-positive society.* Almond REA, Grooten M, Juffe Bignoli D, *et al.*, editors. WWF; **Reference Source** 2022.

Open Peer Review

Current Peer Review Status: ✓ ✓ ✓

Version 2

Reviewer Report 29 June 2024

https://doi.org/10.5256/f1000research.166159.r281457

✓ **Abigail Benson**

US Geological Survey, Colorado, USA

The author revisions sufficiently addressed the concerned raised.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: biodiversity informatics, open science, data standards

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 14 June 2024

https://doi.org/10.5256/f1000research.166159.r281455

✓ **Cher FY Chow**

Centre for Biological Diversity, University of St Andrews, St Andrews, Scotland, UK

The authors have sufficiently addressed my concerns and this article can be approved.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: macroecology, biodiversity data, ecoinformatics, marine ecology

I confirm that I have read this submission and believe that I have an appropriate level of

expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 28 May 2024

https://doi.org/10.5256/f1000research.166159.r281456

✓ **Patrick Comer**
NatureServe, Arlington, Virginia, USA

I think the paper is fine in its revised form.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Biodiversity Conservation, Landscape Ecology, Biodiversity status assessment, Climate change vulnerability and adaptation

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 05 March 2024

https://doi.org/10.5256/f1000research.146735.r232449

✗ **Cher FY Chow**
Centre for Biological Diversity, University of St Andrews, St Andrews, Scotland, UK

Waterhouse et al. present here an opinion article presenting ELIXIR as a solution that can help standardise biodiversity monitoring at scale for the European region and globally. This paper first describes the current landscape of challenges and responses to biodiversity monitoring, and later presents the efforts undertaken by the ELIXIR consortium that can address this. There is a demonstrated need to detect biodiversity change in a coordinated manner at a large spatial scale as emphasised by priorities set by IPBES, Global Biodiversity Framework, and the UN Sustainable Goals. The authors outline the current needs in biodiversity research and policy efforts and highlight the utility of incorporating more “omics” and molecular techniques. They discuss a complex landscape of biodiversity informatics, where challenges exist from data collection to data management and linkages across sources. They present the ELIXIR consortium infrastructure and network of projects/initiatives which help address these challenges.

I first would like to commend the authors for their effort in tackling a complex set of challenges. I appreciate the practical nature of this article, and I can envision it targeted as a relevant reference for European governmental bodies and researchers. However, the article currently needs further development in order to demonstrate to readers 1) the authors' concept of biodiversity informatics, 2) where in this network there are gaps or challenges, and finally 3) how its breadth of initiatives, tools, and platforms can be used by scientists or environmental managers. I outline below my general concerns and questions I would like the authors to respond to.

Article aim: I understand this article is currently presented as an opinion article. The authors state their aim the in the abstract as "[to present] a set of plans, both technical and community-oriented, that should both enhance how ELIXIR Services are applied in the biodiversity field and how ELIXIR builds connections across the many other infrastructures active in this area." However, from my reading, it is unclear to me what questions or knowledge gaps the authors are tackling, or presented opinions, and secondly, what the authors want me to take away from the article. Are they presenting the results from the ELIXIR consortium? If the aim is to provide some roadmap of resources within biodiversity informatics, I find the latter half of the article difficult to interpret and apply from a user perspective. It is unclear to me how some projects listed in Table 1, e.g. a barcoding project based in the Norfolk Broads on page 6, meets informatics or infrastructure challenges outlined previously. This needs to be made clearer and more explicit to the reader. Furthermore, I find the title a mismatch from the article contents and would suggest the authors adjust it to better reflect the aims.

Introduction of ELIXIR: Please include a section that introduces ELIXIR and its structure. As it is presented, the consortium is mentioned and introduced in parts interspersed throughout the first five pages but not completely.

Biodiversity change and molecular approaches: The authors introduce biodiversity change, global policy responses, and the need for incorporating molecular techniques. However, the authors have not demonstrated a clear conceptual link between molecular approaches and the crisis of biodiversity loss and extinction. There are several facets to biodiversity and change is occurring in a myriad of patterns and scales (e.g. [1]; [2] ; [3]; [4]; [5]. Genetic diversity assessments, enhancing species detections through eDNA, and resolved taxonomy are examples of critical components to understanding biodiversity change. The authors hint at these but not in a clear, demonstrated manner. How is a lack of high-throughput and -omics approaches failing our understanding of biodiversity? How can genetic diversity data be linked with the research examples listed under "Scientific opportunities in biodiversity research"? Are there examples where this potential is demonstrated?

The network of biodiversity knowledge: I like Figure 1 as a conceptual figure to ground the idea of how biodiversity monitoring or research requires a network of components. From my knowledge of biodiversity informatics, this concept forms the basis of the first five pages. However, the authors should clearly state this conceptual landscape in the introduction before presenting challenges. This can then demonstrate to the reader how molecular approaches fit into that framework.

Citations needed:
Page 5 can be improved by engaging and contextualising its ideas with existing literature on biodiversity informatics and data management. The ELIXIR consortium is not alone in researching how to improve infrastructure for biodiversity data. The ideas presented in this article build upon previous work. This should be recognised. For example:

- Page 4 under “Biodiversity research and infrastructures increasingly rely on molecular data”: [12];[13]; [7]
- Page 5: “FAIRification of digital research objects... is increasingly recognised as essential in biodiversity research”: [8]; [9]
- Page 5: “This heterogeneity, however, gives rise to many challenges, both technical in terms of data analysis (due to inadequacies of existing methodologies), data integration and data interaction, and at the level of the scientific community, which faces a heterogeneous landscape of infrastructures and resources that can be difficult to navigate.”: [11]; [12]; [10]

Minor comments
I appreciate that ELIXIR is an extensive research infrastructure project and have been well-represented in other published works. This paper should stand alone without relying on previously published works for introduction. There are several instances of unintroduced abbreviations which assumes that the reader is already familiar with the organisations involved. Please include clearer introductions of ELIXIR as a consortium and mentioned nodes.

References

1. Pereira H, Navarro L, Martins I: Global Biodiversity Change: The Bad, the Good, and the Unknown. *Annual Review of Environment and Resources*. 2012; **37** (1): 25-50 Publisher Full Text
2. Vellend M, Dornelas M, Baeten L, Beauséjour R, et al.: Estimates of local biodiversity change over time stand up to scrutiny.*Ecology*. 2017; **98** (2): 583-590 PubMed Abstract | Publisher Full Text
3. Leung B, Hargreaves AL, Greenberg DA, McGill B, et al.: Clustered versus catastrophic global vertebrate declines.*Nature*. 2020; **588** (7837): 267-271 PubMed Abstract | Publisher Full Text
4. Martins IS, Dornelas M, Vellend M, Thomas CD: A millennium of increasing diversity of ecosystems until the mid-20th century.*Glob Chang Biol*. 2022; **28** (20): 5945-5955 PubMed Abstract | Publisher Full Text
5. Finn C, Grattarola F, Pincheira-Donoso D: More losers than winners: investigating Anthropocene defaunation through the diversity of population trends.*Biol Rev Camb Philos Soc*. 2023; **98** (5): 1732-1748 PubMed Abstract | Publisher Full Text
6. Porter TM, Hajibabaei M: Scaling up: A guide to high-throughput genomic approaches for biodiversity analysis.*Mol Ecol*. 2018; **27** (2): 313-338 PubMed Abstract | Publisher Full Text
7. Wilkinson MD, Dumontier M, Aalbersberg IJ, Appleton G, et al.: The FAIR Guiding Principles for scientific data management and stewardship.*Sci Data*. 2016; **3**: 160018 PubMed Abstract | Publisher Full Text
8. Lannom L, Koureas D, Hardisty A: FAIR Data and Services in Biodiversity Science and Geoscience. *Data Intelligence*. 2020; **2** (1-2): 122-130 Publisher Full Text
9. Wetzel F, Bingham H, Groom Q, Haase P, et al.: Unlocking biodiversity data: Prioritization and filling the gaps in biodiversity observation data in Europe. *Biological Conservation*. 2018; **221**: 78-85 Publisher Full Text
10. Huang X, Hawkins B, Lei F, Miller G, et al.: Willing or unwilling to share primary biodiversity data: results and implications of an international survey. *Conservation Letters*. 2012; **5** (5): 399-406 Publisher Full Text

11. Levin N, Coll M, Fraschetti S, Gal G, et al.: Biodiversity data requirements for systematic conservation planning in the Mediterranean Sea. *Marine Ecology Progress Series*. 2014; **508**: 261-281 Publisher Full Text
12. Blaxter M, Floyd R: Molecular taxonomics for biodiversity surveys: already a reality. *Trends in Ecology & Evolution*. 2003; **18** (6): 268-269 Publisher Full Text
13. Karp A, Edwards KJ, Bruford M, Funk S, et al.: Molecular technologies for biodiversity evaluation: opportunities and challenges.*Nat Biotechnol*. 1997; **15** (7): 625-8 PubMed Abstract | Publisher Full Text

Is the topic of the opinion article discussed accurately in the context of the current literature?
Yes

Are all factual statements correct and adequately supported by citations?
No

Are arguments sufficiently supported by evidence from the published literature?
Partly

Are the conclusions drawn balanced and justified on the basis of the presented arguments?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: macroecology, biodiversity data, ecoinformatics, marine ecology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Author Response 07 May 2024

Robert Waterhouse

Waterhouse et al. present here an opinion article presenting ELIXIR as a solution that can help standardise biodiversity monitoring at scale for the European region and globally. This paper first describes the current landscape of challenges and responses to biodiversity monitoring, and later presents the efforts undertaken by the ELIXIR consortium that can address this. There is a demonstrated need to detect biodiversity change in a coordinated manner at a large spatial scale as emphasised by priorities set by IPBES, Global Biodiversity Framework, and the UN Sustainable Goals. The authors outline the current needs in biodiversity research and policy efforts and highlight the utility of incorporating more “omics” and molecular techniques. They discuss a complex landscape of biodiversity informatics, where challenges exist from data collection to data management and linkages across sources. They present the ELIXIR consortium infrastructure and network of projects/initiatives which help address these challenges.

RESPONSE ⇒ We thank the reviewer for their positive summary.

I first would like to commend the authors for their effort in tackling a complex set of challenges. I appreciate the practical nature of this article, and I can envision it targeted as a relevant reference for European governmental bodies and researchers. However, the article currently needs further development in order to demonstrate to readers 1) the authors' concept of biodiversity informatics, 2) where in this network there are gaps or challenges, and finally 3) how its breadth of initiatives, tools, and platforms can be used by scientists or environmental managers. I outline below my general concerns and questions I would like the authors to respond to.

RESPONSE ⇒ We thank the reviewer for their appreciation of our efforts to describe the goals of the Community and how they fit in the broader landscape. The section in the introduction "Informatics challenges facing biodiversity infrastructures and resources" was intended to briefly summarise the current landscape of biodiversity informatics, pointing to a previous output of the ELIXIR Biodiversity Community - "Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR" (Waterhouse et al, 2022) - where we covered this topic in much more detail, including outlining the gaps and challenges. We have now summarised these primary "needs" as emerging themes from our prior survey (included in the much extended section 'The ELIXIR Biodiversity Community: An "ecosystem" of projects'. We also summarised the activities of the Community Implementation Study, which exemplifies how ELIXIR tools and services are being developed and connected for use by researchers.

ADDED ⇒ ELIXIR Communities are groups of experts across ELIXIR Nodes and beyond that represent a scientific or technological theme which drives the development of standards, services, and/or training in and across services offered by ELIXIR, thereby connecting the infrastructure services to research domains (Heil & Garrard, 2024). The ELIXIR Biodiversity Community was first launched in 2019 as a Focus Group to develop and coordinate ELIXIR Nodes' tools, resources, and research work connected to the biodiversity domain. As part of the process of maturing from a Focus Group to a Community, members initiated activities including: (1) cataloguing ELIXIR Services that support biodiversity research; (2) developing and publishing their "Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR" (Waterhouse et al., 2022); (3) coordinating ELIXIR Node participation in Horizon Europe project proposals - The Biodiversity Community Integrated Knowledge Library (BiCIKL) and Biodiversity Genomics Europe (BGE); and (4) beginning to establish connections with key external partners/projects in the biodiversity domain (such as those listed in Table 1); leading to the formal recognition in 2022 as an ELIXIR Community (Waterhouse et al., 2023).

ADDED ⇒ Operationally, monthly online meetings coordinated by the Community co-leads with support from the ELIXIR Hub serve as the primary forum for interactions, complemented by discussions and notifications on the ELIXIR Slack Workspace's Biodiversity Community channel. These include sharing information on members' participation in ongoing or planned biodiversity-related projects and initiatives, including the Community-led Implementation Study "Biodiversity Networks for ELIXIR". The online meetings also feature presentations on tools and services developed by ELIXIR Nodes as well as hosting invited speakers representing key external partners/projects. The Community's Implementation Study encompasses four key areas of work to drive Community activities: (1) to survey and catalogue Research Data Management (RDM) elements relevant to the biodiversity domain, with a focus on molecular data; (2) to catalogue, review, and categorise tools, services, and analytical workflows currently in use by ELIXIR Nodes and the wider community, that process and analyse biodiversity-related data; (3) to describe the landscape of stakeholders ELIXIR is working with or needs to better engage with to establish a "network of networks" for biodiversity research and services; and (4) to leverage the strengths of ELIXIR's training experience to help support the growth of the Biodiversity Community through network-driven sharing of training experiences and knowledge transfer and materials. Together, these actions are serving to enhance ELIXIR's network of networks in helping to deliver connected data to advance biodiversity research.

ADDED ⇒ In terms of informatics solutions connected to such projects, the ELIXIR Biodiversity Community is guided by themes emerging from surveying approaches by which molecular technologies are helping to inform understanding of biodiversity (Waterhouse et al., 2022): biodiversity-related and informatics infrastructures need to develop close and strategic collaborations; work on taxonomy needs to be better aligned and standardised across different infrastructures and fields of study; metadata urgently needs harmonisation and common approaches to research data management must be widely adopted; current data science solutions need to be scaled up to address the rapidly accumulating amounts of molecular data; bioinformatics support for biodiversity research needs to be made widely available and properly maintained; user training on biodiversity research tools, services, and infrastructures needs to be prioritised; and community initiatives need to be collaborative, proactive, and solution-driven.

Article aim: I understand this article is currently presented as an opinion article. The authors state their aim the in the abstract as "[to present] a set of plans, both technical and community-oriented, that should both enhance how ELIXIR Services are applied in the biodiversity field and how ELIXIR builds connections across the many other infrastructures active in this area." However, from my reading, it is unclear to me what questions or knowledge gaps the authors are tackling, or presented opinions, and secondly, what the authors want me to take away from the article. Are they presenting the results from the ELIXIR consortium? If the aim is to provide some roadmap of resources within biodiversity informatics, I find the latter half of the article difficult to interpret and apply from a user perspective. It is unclear to me how some projects listed in Table 1, e.g. a barcoding project based in the Norfolk Broads on page 6, meets informatics or infrastructure challenges outlined previously. This needs to be made clearer and more explicit to the reader. Furthermore, I find the title a mismatch from the article contents and would suggest the authors adjust it to better reflect the aims.

RESPONSE ⇒ We thank the reviewer for their frank assessment, and apologise for some lack of clarity with respect to the purpose of the White Paper publication, which would be particularly unclear to readers who are new to ELIXIR. Much of the parts dedicated to outlining other initiatives, projects, tools, services, and connections with ELIXIR Platforms and other Communities are primarily for the benefit of ELIXIR members who review the Community's White Paper as part of the formal process of becoming an ELIXIR Community.

The aim is not to present results of ELIXIR actions but rather to outline where ELIXIR might be well-placed to contribute and how as a Community we can begin to develop initiatives in the domain of biodiversity research and services by connecting and growing ELIXIR Node activities in data science that can support the field. The substantially revised roadmap section at the end of the paper is designed to articulate the goals and practical aspects of what the Community aims to tackle and how. We hope these changes now provide a clearer picture, especially to readers who are new to ELIXIR.

ADDED ⇒ The revisions to this final section are rather extensive, please see the new content of "Conclusions: A roadmap for the ELIXIR Biodiversity Community" for all the details.

Introduction of ELIXIR: Please include a section that introduces ELIXIR and its structure. As it is presented, the consortium is mentioned and introduced in parts interspersed throughout the first five pages but not completely.

RESPONSE ⇒ We have now included a brief introduction of ELIXIR and its structure.
ADDED (Introduction) ⇒ As a European life sciences infrastructure, ELIXIR strives to coordinate bioinformatics resources from across Europe to enable researchers to access and analyse life science data, to improve the value and impact of life science research on public health, the environment, and the economy.

Biodiversity change and molecular approaches: The authors introduce biodiversity change, global policy responses, and the need for incorporating molecular techniques. However, the authors have not demonstrated a clear conceptual link between molecular approaches and the crisis of biodiversity loss and extinction. There are several facets to biodiversity and change is occurring in a myriad of patterns and scales (e.g. [1]; [2] ; [3]; [4]; [5]. Genetic diversity assessments, enhancing species detections through eDNA, and resolved taxonomy are examples of critical components to understanding biodiversity change. The authors hint at these but not in a clear, demonstrated manner. How is a lack of high-throughput and -omics approaches failing our understanding of biodiversity? How can genetic diversity data be linked with the research examples listed under "Scientific opportunities in biodiversity research"? Are there examples where this potential is demonstrated?

RESPONSE ⇒ The background in the introduction was designed to be concise and general, so we avoided detailed explanations of the different facets and how they might come together to address our understanding of biodiversity change. Instead, these more technical points are presented in an earlier output of the community, emerging from surveying approaches by which molecular technologies are helping to inform understanding of biodiversity (Waterhouse et al., 2022). We have now included a summary of these themes in the much extended section describing the ELIXIR Biodiversity Community. For the examples listed in this section without references we have now added supporting references where appropriate.

The network of biodiversity knowledge: I like Figure 1 as a conceptual figure to ground the idea of how biodiversity monitoring or research requires a network of components. From my knowledge of biodiversity informatics, this concept forms the basis of the first five pages. However, the authors should clearly state this conceptual landscape in the introduction before presenting challenges. This can then demonstrate to the reader how molecular approaches fit into that framework.

RESPONSE ⇒ The use of Rod Page's Biodiversity Knowledge graph as figure 1 was intended as a highly recognisable way to emphasise how data connectivity is important and that the ELIXIR Community's current focus on molecular data does not imply that other facets are less important. The introduction sets the scene, while the main focus is on the establishment, operations, and goals of the ELIXIR Biodiversity Community in the context of that scene. Now that we have added the operational description of the Community to more clearly describe the community structure and how it interfaces with other research infrastructures and key projects/initiatives in the biodiversity domain, and greatly elaborated the Community goals we hope it is much clearer why this figure is used here rather than in the general introduction.

Citations needed:
Page 5 can be improved by engaging and contextualising its ideas with existing literature on biodiversity informatics and data management. The ELIXIR consortium is not alone in researching how to improve infrastructure for biodiversity data. The ideas presented in this article build upon previous work. This should be recognised. For example:
Page 4 under "Biodiversity research and infrastructures increasingly rely on molecular data": [12];[13]; [7]
Page 5: "FAIRification of digital research objects… is increasingly recognised as essential in biodiversity research": [8]; [9]
Page 5: "This heterogeneity, however, gives rise to many challenges, both technical in terms of data analysis (due to inadequacies of existing methodologies), data integration and data interaction, and at the level of the scientific community, which faces a heterogeneous landscape of infrastructures and resources that can be difficult to navigate.": [11]; [12]; [10]

RESPONSE ⇒ We thank the reviewer to pointing us to these key references that we now use to support the statements being made.

Minor comments
I appreciate that ELIXIR is an extensive research infrastructure project and have been well-represented in other published works. This paper should stand alone without relying on previously published works for introduction. There are several instances of unintroduced abbreviations which assumes that the reader is already familiar with the organisations involved. Please include clearer introductions of ELIXIR as a consortium and mentioned nodes.

RESPONSE ⇒ We thank the reviewer for this observation that we need to bring more clarity especially for readers less familiar with ELIXIR, so we have taken measures to remedy this throughout, including a brief definition presented early in the introduction.
ADDED (Introduction) ⇒ As a European life sciences infrastructure, ELIXIR strives to coordinate bioinformatics resources from across Europe to enable researchers to access and analyse life science data, to improve the value and impact of life science research on public health, the environment, and the economy.

Competing Interests: No competing interests were disclosed.

Reviewer Report 22 February 2024

https://doi.org/10.5256/f1000research.146735.r223867

Abigail Benson
US Geological Survey, Colorado, USA
Stephen Formel
U.S. Geological Survey, Colorado, USA

The ELIXIR Biodiversity Community: Understanding short- and long-term changes in biodiversity highlights the need for biodiversity informatics to address challenges facing our world and provides lists of projects and entities working to contribute biodiversity informatics solutions.

We were really interested in this work and excited to read it. However, we struggled with finding the conceptual thread that tied the disparate sections together. The introduction provided an important summary about biodiversity but was missing the summarization of the current landscape of biodiversity informatics that would provide the foundation for where ELIXIR fits into the puzzle. The lists of tools are valuable but too extensive and missing the connective text that was needed to understand why these projects were being listed. One challenge we had as readers is that we are new to ELIXIR and it's not spelled out or described in the text. We were confused about the connection between ELIXIR and the threats and challenges that were described. We were left wondering which ones ELIXIR addresses and how? We had expected based on the title to learn about the ELIXIR community, how it's organized, how it interacts, and what makes it a community but we didn't find that information in the paper so we were left wondering what the ELIXIR community is?

We also felt that the text could use more supporting references. There are times when strong statements are provided but are not backed up with needed citations.

We would suggest the authors narrow the focus in the challenges section to the ones the ELIXIR community is best poised to address and make those connections explicit in the text. We also would find it beneficial for ELIXIR to be described and more thoroughly contextualized. We also found it confusing when the paper mentions another project or RI as an official collaborator with ELIXIR, and when they merely serve as example. Perhaps replacing Figure 1 with some visual explanation of the community structure would help.

We are hopeful that the paper can be revised.

Is the topic of the opinion article discussed accurately in the context of the current literature?
Partly

Are all factual statements correct and adequately supported by citations?
Partly

Are arguments sufficiently supported by evidence from the published literature?
Partly

Are the conclusions drawn balanced and justified on the basis of the presented arguments?
Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: biodiversity informatics, open science, data standards

We confirm that we have read this submission and believe that we have an appropriate level of expertise to state that we do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Author Response 07 May 2024

Robert Waterhouse

The ELIXIR Biodiversity Community: Understanding short- and long-term changes in biodiversity highlights the need for biodiversity informatics to address challenges facing our world and provides lists of projects and entities working to contribute biodiversity informatics solutions. We were really interested in this work and excited to read it. However, we struggled with finding the conceptual thread that tied the disparate sections together. The introduction provided an important summary about biodiversity but was missing the summarization of the current landscape of biodiversity informatics that would provide the foundation for where ELIXIR fits into the puzzle. The lists of tools are valuable but too extensive and missing the connective text that was needed to understand why these projects were being listed. One challenge we had as readers is that we are new to ELIXIR and it’s not spelled out or described in the text. We were confused about the connection between ELIXIR and the threats and challenges that were described. We were left wondering which ones ELIXIR addresses and how? We had expected based on the title to learn about the ELIXIR community, how it’s organized, how it interacts, and what makes it a community but we didn’t find that information in the paper so we were left wondering what the ELIXIR community is?

RESPONSE ⇒ We thank the reviewers for their interest and apologise that some aspects were not covered in enough detail to provide complete answers, especially to readers who are new to ELIXIR. The section in the introduction “Informatics challenges facing biodiversity infrastructures and resources” was intended to briefly summarise the current landscape of biodiversity informatics, pointing to a previous output of the ELIXIR Biodiversity Community

(Waterhouse et al, 2022) where we covered this topic in much more detail. In the introduction we outlined global challenges and potential solutions, and only later in the text we describe how ELIXIR might fit into these landscapes - with a focus on molecular data and their integration into the broader biodiversity knowledge graph. To clarify ELIXIR's operational standing and Community model, we have added a detailed description to the section immediately following the introduction: 'The ELIXIR Biodiversity Community: An "ecosystem" of projects'. The substantially revised roadmap section at the end of the paper is also designed to clarify the goals and practical aspects of what the Community aims to tackle and how. Regarding the named/listed tools, projects, platforms, and other communities - this is primarily for the benefit of ELIXIR members who review the Community's White Paper as part of the formal process of becoming an ELIXIR Community. We hope these changes now provide a clearer picture, especially to readers who are new to ELIXIR.

ADDED ⇒ ELIXIR Communities are groups of experts across ELIXIR Nodes and beyond that represent a scientific or technological theme which drives the development of standards, services, and/or training in and across services offered by ELIXIR, thereby connecting the infrastructure services to research domains (Heil & Garrard, 2024). The ELIXIR Biodiversity Community was first launched in 2019 as a Focus Group to develop and coordinate ELIXIR Nodes' tools, resources, and research work connected to the biodiversity domain. As part of the process of maturing from a Focus Group to a Community, members initiated activities including: (1) cataloguing ELIXIR Services that support biodiversity research; (2) developing and publishing their "Recommendations for connecting molecular sequence and biodiversity research infrastructures through ELIXIR" (Waterhouse et al., 2022); (3) coordinating ELIXIR Node participation in Horizon Europe project proposals - The Biodiversity Community Integrated Knowledge Library (BiCIKL) and Biodiversity Genomics Europe (BGE); and (4) beginning to establish connections with key external partners/projects in the biodiversity domain (such as those listed in Table 1); leading to the formal recognition in 2022 as an ELIXIR Community (Waterhouse et al., 2023).

ADDED ⇒ Operationally, monthly online meetings coordinated by the Community co-leads with support from the ELIXIR Hub serve as the primary forum for interactions, complemented by discussions and notifications on the ELIXIR Slack Workspace's Biodiversity Community channel. These include sharing information on members' participation in ongoing or planned biodiversity-related projects and initiatives, including the Community-led Implementation Study "Biodiversity Networks for ELIXIR". The online meetings also feature presentations on tools and services developed by ELIXIR Nodes as well as hosting invited speakers representing key external partners/projects. The Community's Implementation Study encompasses four key areas of work to drive Community activities: (1) to survey and catalogue Research Data Management (RDM) elements relevant to the biodiversity domain, with a focus on molecular data; (2) to catalogue, review, and categorise tools, services, and analytical workflows currently in use by ELIXIR Nodes and the wider community, that process and analyse biodiversity-related data; (3) to describe the landscape of stakeholders ELIXIR is working with or needs to better engage with to establish a "network of networks" for biodiversity research and services; and (4) to leverage the strengths of ELIXIR's training experience to help support the growth of the Biodiversity Community through network-driven sharing of training experiences and knowledge transfer and materials. Together, these actions are serving to enhance ELIXIR’s network of networks in helping to deliver connected data to advance biodiversity research.

ADDED ⇒ In terms of informatics solutions connected to such projects, the ELIXIR Biodiversity Community is guided by themes emerging from surveying approaches by which molecular technologies are helping to inform understanding of biodiversity (Waterhouse et al., 2022): biodiversity-related and informatics infrastructures need to develop close and strategic collaborations; work on taxonomy needs to be better aligned and standardised across different infrastructures and fields of study; metadata urgently needs harmonisation and common approaches to research data management must be widely adopted; current data science solutions need to be scaled up to address the rapidly accumulating amounts of molecular data; bioinformatics support for biodiversity research needs to be made widely available and properly maintained; user training on biodiversity research tools, services, and infrastructures needs to be prioritised; and community initiatives need to be collaborative, proactive, and solution-driven.

We also felt that the text could use more supporting references. There are times when strong statements are provided but are not backed up with needed citations.
RESPONSE ⇒ We have included a number of additional references in the revised manuscript. If there are additional specific recommendations we would be happy to incorporate them into the text as needed.

We would suggest the authors narrow the focus in the challenges section to the ones the ELIXIR community is best poised to address and make those connections explicit in the text. We also would find it beneficial for ELIXIR to be described and more thoroughly contextualized. We also found it confusing when the paper mentions another project or RI as an official collaborator with ELIXIR, and when they merely serve as example. Perhaps replacing Figure 1 with some visual explanation of the community structure would help.

RESPONSE ⇒ We designed the introduction to first encompass the broader perspectives on key challenges in biodiversity research, including highlighting what is needed to advance the status quo, and then follow that up with “ELIXIR’s roles”, i.e. where ELIXIR activities could contribute to meeting these challenges. We have revised the text in parts to clarify the motivation to contribute to the wider landscape of efforts, bringing expertise in data management solutions, particularly with respect to molecular data. We added some context on ELIXIR as a whole (introduction), and we now describe the Community operations and key themes that guide Community activities connected to biodiversity-related projects and initiatives. The considerable re-working of the concluding roadmap section is aimed at narrowing the focus on where the ELIXIR Biodiversity Community is best poised to contribute. The use of Rod Page’s Biodiversity Knowledge graph as figure 1 emphasises why data connectivity is important and that the ELIXIR Community’s current focus on molecular data does not imply that other facets are less important. We hope that the added operational description of the Community now addresses the community structure and how it interfaces with other research infrastructures and key projects/initiatives in the biodiversity domain.

ADDED (Introduction) ⇒ As a European life sciences infrastructure, ELIXIR strives to coordinate bioinformatics resources from across Europe to enable researchers to access and analyse life science data, to improve the value and impact of life science research on public health, the environment, and the economy.

ADDED ('The ELIXIR Biodiversity Community: An "ecosystem" of projects'.) ⇒ See the added text in the response above.

We are hopeful that the paper can be revised.

RESPONSE ⇒ We thank the reviewers for their helpful comments and suggestions, particularly from the perspective of researchers not already familiar with ELIXIR and its operations. We hope that the resultant additions and revisions address your concerns.

Competing Interests: No competing interests were disclosed.

Reviewer Report 13 February 2024

https://doi.org/10.5256/f1000research.146735.r218316

?

Patrick Comer
NatureServe, Arlington, Virginia, USA

Peer Review: The ELIXIR Biodiversity Community: Understanding short- and long-term changes in biodiversity – RM Waterhouse et al

This article provides a concise overview of the ELIXIR Biodiversity Community which can serve as a hub for the molecular sciences and bioinformatics as it applies to biodiversity science. ELIXIR's overarching mission has been stated to "support the management of public research data, integrate and coordinate life science resources, and foster the development of innovative services and technical solutions in Europe" (Harrow *et al.,* 2021[1]). Given unprecedented and escalating loss in biodiversity, there is increasing urgency for new scientific discovery, data processing, and data sharing of biodiversity information among scientists, conservation practitioners, and policy makers. This opinion piece summarizes biodiversity threats, societal challenges and global responses, and scientific opportunities in biodiversity research. It then discusses informatics challenges facing biodiversity infrastructures and resources, organizational opportunities for ELIXIR partners, and connections with ELIXIR platforms and communities. The piece concludes with a roadmap listing key goals and long-term objectives for the ELIXIR Biodiversity Community.

The article might best be viewed in the context of the large and growing field of scientists, practitioners, and policy analysts, in government, academic, and non-government (NGO) sectors responding to the emerging crisis of biodiversity loss. Starting in the mid-20th century with many academic researchers who initially documented biodiversity declines, biodiversity science - and biodiversity conservation - has been steadily mainstreamed worldwide (Locke *et al.,*2019[2]). One of the founders of "conservation biology" the late Michael Soulé described this science as a "discipline with a deadline" working against accelerating extinctions to sustain the wellbeing of society and the environment (Soulé and Wilcox,1980[3]). While encompassing the full spectrum from basic to applied, biodiversity conservation science has often emphasized practical ways to identify key information suitable for action on the ground. One good example coming from the North American NGO NatureServe network is the practical methods for systematic field inventories for natural communities and species to characterize their location, health, and status (Stein *et al.,* 2000[4]). In full disclosure, I have spent most of my working life in this network, first established by The Nature Conservancy in the 1970s.

With much biodiversity conservation initially focused on identifying local areas for nature preserves, the maturing disciplines of landscape ecology, meta-population dynamics, and now climate change research, forced consideration of increasing broader scales of conservation action (Lindenmayer and Franklin, 2013[5]). With rapidly advancing technology and data, and emphasis on remote sensing and modeling with spatial data have become routine (Wiens *et al.,* 2009[6]). And increasingly (one could say belatedly), the value of social science been acknowledged as it has deepened our understanding of complex interactions of people and nature that underlay nearly all conservation strategies (Sandbrook *et al.,* 2013[7]).

Therefore, while I found this piece to be factual, accurate, and well supported by the current literature, it would benefit from a broader interpretation of biodiversity science and more directed treatment of ELIXIR's potential contributions to the "broader ecosystem" of biodiversity conservation. For example, the rapid advances in genomic science and its application to biodiversity conservation has many parallels to several allied fields previously mentioned, such as in remote sensing and several variants of the social sciences. The ELIXIR Biodiversity Community could gain by considering this prior experience. Thus, avoiding prior mistakes and replicating prior successes. Among the many ways expanding genomic science could affect biodiversity conservation include ecosystem characterization and monitoring, support to biodiversity status assessment, and evaluating progress of conservation actions.

The article states that "A long-term vision sees a future where sequence-based biodiversity monitoring at scale becomes the default and provides the means for ecosystem biodiversity characterisation in space and time." One area where we may see near-term progress here is in the links between genomic data and remote sensing; where our current forms of ecosystem characterization centered on measures of species composition, ecosystem structure, and environmental setting may be enhanced by remotely-sensed data (hyperspectral and others) indicating patterns within and among readily observed communities and species (Yamasaki *et al.,* 2017[8]). Relationships between measurable genetic diversity and detectable light spectra will always be complex and challenging, but with increasing frequency of remote data collection one can now envision substantial opportunities to identify leading indicators of ecosystem change through their combination.

Current standards to assess and document endangerment status of species and ecosystems – such as those of red listing under IUCN - require documented knowledge of changing health of populations and communities (IUCN 2012[9]; Bland *et al.,* 2017[10]). These standards attempt to simplify complex ecological phenomena into standard categories to provide a reliable status assessment for use by policy makers and engaged stakeholders. Once clear health markers are identified with genomic data, this could contribute substantially to the rigor, efficiency, and impact of biodiversity status assessment.

This naturally follows on to the potential benefit of genomic data to contribute to evaluating success (or failure) of conservation actions. As noted in the article, that these data should contribute to understanding "population-level adaptation and migration processes, in the context of anthropogenic activities (*e.g.*, climate change and urbanisation consequences), and understand[ing] key aspects necessary to restore ecosystem functions." It is in planning and implementation of conservation actions where one can surely recognize biodiversity conservation as inherently a human-driven process, so once again, the information used must be clear and compelling to all involved, regardless of their interests and biases.

Prior experience in related fields suggest at least several considerations for the ELIXIR Biodiversity Community. As noted in the article, "ELIXIR can serve a critical function here, as a fundamental aspect of its mission is to make connections and coordinate across complex activities." And "the biodiversity community needs to proactively seek common solutions (without unnecessary duplication of effort) that enable molecular technologies to advance biodiversity research. I would underscore the importance of limiting duplication of effort. Much of the history of biodiversity conservation in marked by unnecessary competition, stove-piping, and duplicated effort among those involved.

And while ELIXIR's "current focus is on the informatics, databases, and tools more than on the biological questions, . . . as the Community grows, it will be important to widen the diversity of its membership to ensure that the technical developments will serve the needs of biodiversity researchers," I would encourage this community to begin early to seek out and identify feedback loops from the full spectrum of user communities. As noted above, the users of genomic data for biodiversity conservation will be diverse and demanding, so deeper consideration of user needs (Dubois *et al.,* 2020[11]), and participatory biodiversity science (Zoellick *et al.,* 2012[12]) could have substantial payoffs into the future.

Biodiversity conservation is based on both ecological and social science that is both urgent and time sensitive. It is that applied side of the spectrum that requires urgent support from the ELIXIR Biodiversity Community.

References

1. Harrow J, Hancock J, ELIXIR-EXCELERATE Community, Blomberg N: ELIXIR-EXCELERATE: establishing Europe's data infrastructure for the life science research of the future.*EMBO J*. 2021; **40** (6): e107409 PubMed Abstract | Publisher Full Text
2. Locke H, Ellis EC, Venter O, Schuster R, et al.: Three global conditions for biodiversity conservation and sustainable use: an implementation framework.*Natl Sci Rev*. 2019; **6** (6): 1080-1082 PubMed Abstract | Publisher Full Text
3. Soulé ME, Wilcox BA: Conservation Biology: An Evolutionary-Ecological Perspective. *Sinauer*. 1980.
4. Stein BA, Kutner LS, Adams JS: Precious heritage: the status of biodiversity in the United States. *Oxford University Press*. 2000.
5. Lindenmayer DB, Franklin JF: Conserving forest biodiversity: a comprehensive multiscaled approach. *Island press*. 2013.
6. Wiens J, Sutter R, Anderson M, Blanchard J, et al.: Selecting and conserving lands for biodiversity:

The role of remote sensing. *Remote Sensing of Environment*. 2009; **113** (7): 1370-1381 Publisher Full Text
7. Sandbrook C, Adams WM, Büscher B, Vira B: Social research and biodiversity conservation. *Conserv Biol*. 2013; **27** (6): 1487-90 PubMed Abstract | Publisher Full Text
8. Yamasaki E, Altermatt F, Cavender-Bares J, Schuman M, et al.: Genomics meets remote sensing in global change studies: monitoring and predicting phenology, evolution and biodiversity. *Current Opinion in Environmental Sustainability*. 2017; **29**: 177-186 Publisher Full Text
9. IUCN: IUCN Red List Categories and Criteria: Version 3.1. *Gland, Switzerland and Cambridge, UK*. 2012.
10. Guidelines for the application of IUCN Red List of Ecosystems Categories and Criteria. Version 1.1. 2017. Publisher Full Text
11. Dubois N, Gomez A, Carlson S, Russell D: Bridging the research-implementation gap requires engagement from practitioners. *Conservation Science and Practice*. 2020; **2** (1). Publisher Full Text
12. Jones A, Whitesell C, Tadikonda A, Perry MF, et al.: "I feel like it gives me what I need to know": A qualitative study on adolescent perceptions of two contraceptive decision aids.*Contraception*. 2023; **128**: 110277 PubMed Abstract | Publisher Full Text

Is the topic of the opinion article discussed accurately in the context of the current literature?

Yes

Are all factual statements correct and adequately supported by citations?

Yes

Are arguments sufficiently supported by evidence from the published literature?

Yes

Are the conclusions drawn balanced and justified on the basis of the presented arguments?

Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Biodiversity Conservation, Landscape Ecology, Biodiversity status assessment, Climate change vulnerability and adaptation

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 07 May 2024

Robert Waterhouse

This article provides a concise overview of the ELIXIR Biodiversity Community which can serve as a hub for the molecular sciences and bioinformatics as it applies to biodiversity science. ELIXIR’s overarching mission has been stated to “support the management of public research data, integrate and coordinate life science resources, and foster the development of innovative services and technical solutions in Europe" (Harrow et al., 20211). Given unprecedented and escalating loss in biodiversity, there is increasing urgency for new scientific discovery, data processing, and data sharing of biodiversity information among scientists, conservation practitioners, and policy makers. This opinion piece summarizes biodiversity threats, societal challenges and global responses, and scientific opportunities in biodiversity research. It then discusses informatics challenges facing biodiversity infrastructures and resources, organizational opportunities for ELIXIR partners, and connections with ELIXIR platforms and communities. The piece concludes with a roadmap listing key goals and long-term objectives for the ELIXIR Biodiversity Community.

RESPONSE ⇒ We thank the reviewer for their positive summary.

The article might best be viewed in the context of the large and growing field of scientists, practitioners, and policy analysts, in government, academic, and non-government (NGO) sectors responding to the emerging crisis of biodiversity loss. Starting in the mid-20th century with many academic researchers who initially documented biodiversity declines, biodiversity science - and biodiversity conservation - has been steadily mainstreamed worldwide (Locke et al.,20192). One of the founders of "conservation biology" the late Michael Soulé described this science as a "discipline with a deadline" working against accelerating extinctions to sustain the wellbeing of society and the environment (Soulé and Wilcox,19803). While encompassing the full spectrum from basic to applied, biodiversity conservation science has often emphasized practical ways to identify key information suitable for action on the ground. One good example coming from the North American NGO NatureServe network is the practical methods for systematic field inventories for natural communities and species to characterize their location, health, and status (Stein et al., 20004). In full disclosure, I have spent most of my working life in this network, first established by The Nature Conservancy in the 1970s. With much biodiversity conservation initially focused on identifying local areas for nature preserves, the maturing disciplines of landscape ecology, meta-population dynamics, and now climate change research, forced consideration of increasing broader scales of conservation action (Lindenmayer and Franklin, 20135). With rapidly advancing technology and data, and emphasis on remote sensing and modeling with spatial data have become routine (Wiens et al., 20096). And increasingly (one could say belatedly), the value of social science been acknowledged as it has deepened our understanding of complex interactions of people and nature that underlay nearly all conservation strategies (Sandbrook et al., 20137).

RESPONSE ⇒ We thank the reviewer for the additional background, and have taken the opportunity to mention the ideas of Soulé and the field of conservation biology in the introduction.
ADDED: "The urgency to act is recognised particularly in the field of conservation biology, which has been described as a "discipline with a deadline" (Soulé & Wilcox 1980)."

Therefore, while I found this piece to be factual, accurate, and well supported by the current literature, it would benefit from a broader interpretation of biodiversity science and more directed treatment of ELIXIR's potential contributions to the "broader ecosystem" of biodiversity conservation. For example, the rapid advances in genomic science and its application to biodiversity conservation has many parallels to several allied fields previously mentioned, such as in remote sensing and several variants of the social sciences. The ELIXIR Biodiversity Community could gain by considering this prior experience. Thus, avoiding prior mistakes and replicating prior successes. Among the many ways expanding genomic science could affect biodiversity conservation include ecosystem characterization and monitoring, support to biodiversity status assessment, and evaluating progress of conservation actions.

RESPONSE ⇒ While, we agree with the reviewer's ideas to highlight better the "broader ecosystem" of biodiversity conservation,the role of the ELIXIR Biodiversity Community has been clearly defined in the section "Organisational opportunities and ELIXIR's roles" as we recognise that there is a plethora of initiatives already tackling exactly these kinds of issues. Rather, the Community is focused on the data management aspects, in particular with regards to molecular data, that are needed to effectively support and grow the many existing activities in the domain of biomonitoring and ecosystem health. We have made changes to the text to ensure that there is clarity to the role that the ELIXIR Biodiversity Community plays (data science support versus frontline conservation actions).

The article states that "A long-term vision sees a future where sequence-based biodiversity monitoring at scale becomes the default and provides the means for ecosystem biodiversity characterisation in space and time." One area where we may see near-term progress here is in the links between genomic data and remote sensing; where our current forms of ecosystem characterization centered on measures of species composition, ecosystem structure, and environmental setting may be enhanced by remotely-sensed data (hyperspectral and others) indicating patterns within and among readily observed communities and species (Yamasaki et al., 20178). Relationships between measurable genetic diversity and detectable light spectra will always be complex and challenging, but with increasing frequency of remote data collection one can now envision substantial opportunities to identify leading indicators of ecosystem change through their combination.

RESPONSE ⇒ This example is an excellent case study of how different data types - if made available and interoperable - can be co-interrogated to improve how we measure and monitor biodiversity. We have revised the text to more clearly indicate the complementarity of different types of data and their applications.
EDITED ⇒ A long-term vision sees a future where sequence-based biodiversity monitoring at scale becomes a default and provides the means for ecosystem biodiversity characterisation in space and time, complemented and enhanced by other biomonitoring technologies.

Current standards to assess and document endangerment status of species and ecosystems – such as those of red listing under IUCN - require documented knowledge of changing health of populations and communities (IUCN 20129; Bland et al., 201710). These standards attempt to simplify complex ecological phenomena into standard categories to provide a reliable status assessment for use by policy makers and engaged stakeholders. Once clear health markers are identified with genomic data, this could contribute substantially to the rigor, efficiency, and impact of biodiversity status assessment. This naturally follows on to the potential benefit of genomic data to contribute to evaluating success (or failure) of conservation actions. As noted in the article, that these data should contribute to understanding "population-level adaptation and migration processes, in the context of anthropogenic activities (e.g., climate change and urbanisation consequences), and understand[ing] key aspects necessary to restore ecosystem functions." It is in planning and implementation of conservation actions where one can surely recognize biodiversity conservation as inherently a human-driven process, so once again, the information used must be clear and compelling to all involved, regardless of their interests and biases.

RESPONSE ⇒ We agree that this is a key goal in biodiversity genomics, being able to get the most out of the data to improve the way assessments are made and how to interpret the results for policy makers and engaged stakeholders. We see the role of ELIXIR here as focused on helping to build systems that will ensure access to data and tools and services that enable experts to perform assessments and make decisions based on the best available data and methods. We have made changes to ensure clarity to this distinction (data science support versus frontline conservation actions).

Prior experience in related fields suggest at least several considerations for the ELIXIR Biodiversity Community. As noted in the article, "ELIXIR can serve a critical function here, as a fundamental aspect of its mission is to make connections and coordinate across complex activities." And "the biodiversity community needs to proactively seek common solutions (without unnecessary duplication of effort) that enable molecular technologies to advance biodiversity research. I would underscore the importance of limiting duplication of effort. Much of the history of biodiversity conservation in marked by unnecessary competition, stove-piping, and duplicated effort among those involved.

RESPONSE ⇒ We thank the reviewer for highlighting this important point. One of the strengths of ELIXIR's operations and activities in other domains like human health has been to contribute to better coordinated efforts across Europe. It is a cornerstone of the principle of distributed infrastructure for life-science data and we have incorporated your suggestions.
ADDED ⇒ A key part of this is the building of distributed infrastructures for life-science data that avoid or minimise unnecessary duplication of effort to be able to advance efficiently towards common goals.

And while ELIXIR's "current focus is on the informatics, databases, and tools more than on the biological questions, . . . as the Community grows, it will be important to widen the diversity of its membership to ensure that the technical developments will serve the needs of biodiversity researchers," I would encourage this community to begin early to seek out and identify feedback loops from the full spectrum of user communities. As noted above, the users of genomic data for biodiversity conservation will be diverse and demanding, so deeper consideration of user needs (Dubois et al., 202011), and participatory biodiversity science (Zoellick et al., 201212) could have substantial payoffs into the future. Biodiversity conservation is based on both ecological and social science that is both urgent and time sensitive. It is that applied side of the spectrum that requires urgent support from the ELIXIR Biodiversity Community.

RESPONSE ⇒ Since this manuscript was first published the Community has embarked on its first Implementation Study, within which there is a dedicated effort to describe the landscape of stakeholders ELIXIR is working with or needs to better engage with and to

establish a functional “network of networks” for biodiversity research. Following your suggestions, we have revised the last section of the manuscript, highlighting the needs to engage beyond ELIXIR members and interact with other communities of practice in the domain.
ADDED ⇒ Beyond the ELIXIR Biodiversity Community itself, it is also vital to engage with other communities in the domain, including with stakeholders such as practitioners and citizen science initiatives in order to contribute towards bridging the gaps between research and implementation (Dubois et al., 2020; Fraisl et al. 2022).

Competing Interests: No competing interests were disclosed.