

Article

How Does Sharing Data from Research Institutions on Global Biodiversity Information Facility Enhance Its Scientific Value?

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Abstract: For decades, thousands of scientific institutions worldwide have been digitizing collections documenting biodiversity. The advantages and benefits of this process are widely described. In this study, we test the hypothesis that digital data from local scientific institutions gain additional value once shared through the Global Biodiversity Information Facility (GBIF). We have closely examined the fate of over 2.2 million digital records deposited at the Faculty of Biology, Adam Mickiewicz University in Poznań, Poland (FBAMU), which have been available to the global community for over three years. The effectiveness of this effort is measured by the number of downloads (approximately 123,000), the number of records downloaded (45 billion), and most importantly, the number of scientific publications utilizing these data (an average of 3 publications per week). These publications appear both in the most prestigious scientific journals and regional sources. The thematic scope of papers utilizing FBAMU data shared through GBIF is very broad, covering 12 research areas, including fundamental biological fields (morphology, taxonomy and systematics, phylogeny and evolution, paleobiology, ecology, biogeography, biodiversity conservation, and biodiversity informatics), closely related applied research (agriculture and human health), and climate science and linguistic phylogeny. The most frequent uses of GBIF/FBAMU data have been in studies on processes and phenomena such as biodiversity loss, biological invasions, biogeographical patterns, changes in species ranges, climatic niche dynamics, interactions between organisms, and mechanisms of evolution.

Keywords: biodiversity data; digitization; open-access database; GBIF; AMUNATCOLL IT; knowledge dissemination



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1. Introduction

Natural history collections (NHCs) have long played a fundamental role in research on the variability, systematics, and evolution of organisms [1]. The scientific significance of biological specimens gathered worldwide significantly increased at the end of the 20th century due to the development of microscopic techniques and the introduction of molecular biology methods, including DNA barcoding [2–9]. NHCs have gained an entirely new dimension in the era of the computing revolution, particularly with the large-scale application of digitization, including the geotagging of spatial data [10–14].

Digital biodiversity data and analytical tools made available across multiple platforms are now widely used to address biological problems [15], including systematic [16], phylogenetic [17,18], biogeographical [19,20], ecological [20–22], phenological [23,24], and

paleobiological [25,26] issues. These problems are being tackled using new methods and research techniques developed within the field of biodiversity informatics, a relatively new scientific discipline [27,28]. The collection and analysis of biodiversity data is increasingly being driven by both local and international communities, thus advancing citizen science [29,30]. This has significant implications for education and the development of the concept of shared responsibility for nature conservation [31–33].

Global, regional, and national databases, which collect information according to established and widely used standards and are accessible to all interested users, are of fundamental importance for the development of biodiversity science and its conservation. In this regard, the Global Biodiversity Information Facility (GBIF) plays a particularly important role [34–36]. Also deserving of special mention are major projects such as Integrated Digitized Biocollections (iDigBio) [37], the Atlas of Living Australia (ALA) [38], Conabio [39], Distributed Information System for Biological Collections: Integrating Species Analyst and SinBiota (FAPESP) [40], the Distributed System of Scientific Collection (DISSCO) [41], the South African National Biodiversity Institute project [42], the unique comprehensive mega-database of georeferenced records for vascular plants in continental tropical Africa (RAINBIO) [43], and China's National Specimen Information Infrastructure [44].

The idea of transforming analog biological information into digital biodiversity data is increasingly embraced by institutions worldwide, thereby enhancing their already significant scientific, educational, cultural, and social value. Even small collections are of great importance [45]. Local and regional resources gain additional importance when integrated into global databases and made publicly accessible. Based on this premise, we have decided to track this process and evaluate its outcomes.

The primary aim of our research was to identify the effects of digitizing local NHCs and making them available through a global biodiversity platform. The subject of the analysis consisted of the collections and natural observations of the Faculty of Biology at Adam Mickiewicz University in Poznań, Poland, (FBAMU), which are available on the institutional AMUNATCOLL platform (Adam Mickiewicz University Natural Collection) as well as on the GBIF platform [33,46–49]. In this paper, we describe the process of transferring data from the local database to the global one, the method of sharing these data, and the effects of their use in scientific publications. We address the following questions:

- How frequently are the NHC data from FBAMU accessed by users of the AMUNATCOLL and GBIF platforms?
- How much data do users download from both sources?
- How often are these data cited in scientific publications?
- In which journals do publications citing FBAMU appear?
- What is the thematic scope of publications utilizing this database?
- What contributions do publications based on this type of data make to science and nature conservation?

2. Material and Methods

2.1. Natural Collections of the Faculty of Biology at Adam Mickiewicz University in the AMUNATCOLL IT System and on the GBIF Platform

The beginnings of scientific natural collections in Wielkopolska, Western Poland, date back to the 17th century. Their development was repeatedly disrupted by dramatic events, including two world wars fought in Poland in the 20th century. The rescued historical collections and specimens of algae, plants, fungi, and animals systematically collected after 1945 are stored in optimal conditions at the Faculty of Biology at Adam Mickiewicz University in Poznań (FBAMU) [46]. The current collections include approximately 2.2 million digitized objects, documenting not only the biodiversity of Wielkopolska and Poland but

also many regions of the world on all continents. The specimens held at FBAMU are widely used in taxonomic, biogeographical, phylogenetic, ecological, and genetic research. These collections also have significant educational value and contribute to the dissemination of knowledge about biodiversity [33]. Thanks to the digitization carried out mainly between 2018 and 2021, these valuable collections have been given new life [47,48]. For more than three years, they have been publicly available on the home platform AMUNATCOLL [50], from which they are systematically transferred to GBIF [49,51].

2.2. Data Transfer from AMUNATCOLL IT to GBIF

The backend layer of the AMUNATCOLL IT system enables access to the data via two interfaces: REST (REpresentational State Transfer) [52] and BioCAsE (Biological Collection Access Service) [53]. Both are foundations for architectural styles of API (application programming interface) [54] protocols that define a set of guidelines for exchanging data between applications, facilitating the segregation of the data logic layer from the presentation layer.

The first one (REST) was implemented based on HTTP technology, facilitating interaction with data collected in the AMUNATCOLL IT database. It enables both reading and writing of data via the website [50] and mobile application [55,56] based on a defined set of rules and available permissions. To ensure an appropriate level of security, most of the provided functionality is available only to logged-in users. Therefore, access to specific interface methods is secured through the use of JWT tokens [57].

The other way to access the AMUNATCOLL data is using a BioCAsE-based interface protocol. The BioCAsE serves as a global network connecting primary biodiversity repositories, integrating specimen data from natural history collections, botanical/zoological gardens, and research institutions worldwide with information from extensive observation databases. Its objective is to ensure that biodiversity data from around the world are easily accessible to everyone on the internet through data portals and web services. This mission aligns with similar initiatives like GBIF and iDigBio (Integrated Digitized Biocollections) [58]. The BioCAsE Provider Software (version 3.8.6) incorporates the BioCAsE protocol, which establishes the guidelines for interacting with a BioCAsE web service [59]. This pre-programmed protocol plays a crucial role in facilitating effective communication between the provider software and any client application, typically a network component. For due diligence, the alternative way should be mentioned to interact with GBIF, which is IPT (the Integrated Publishing Toolkit version 3.1.4) [60]. It is worth noting, however, that this method is suitable for collections containing hundreds, possibly thousands, of specimens. Above this number, it is recommended to use other solutions, such as BioCAsE.

Taking this into account, it was decided to use the BioCAsE protocol to handle data in the GBIF database, assuming that it is more convenient for a large number of records (over 2 million). This interface provides open access to selected taxonomic data collected in the database, which is widely made available to external entities. Moreover, this method also enables automatic updating of changed records with the presumed regularity (e.g., once a week). To achieve this objective, we utilized the BioCAsE provider software (BPS) [59], a middleware that is compatible with BioCAsE (Figure 1). The mapping created for BioCAsE services guarantees the coherence of the structures employed in both BioCAsE and AMUNATCOLL IT. The BioCAsE protocol is compatible with any custom-defined XML schema, making it versatile for use in various biodiversity networks. Typically, it is utilized alongside the ABCD schema (Access to Biological Collections Data) [61] in the current context. The AMUNATCOLL IT “PyWrapper Manual Query Form” is openly available at the location [62].

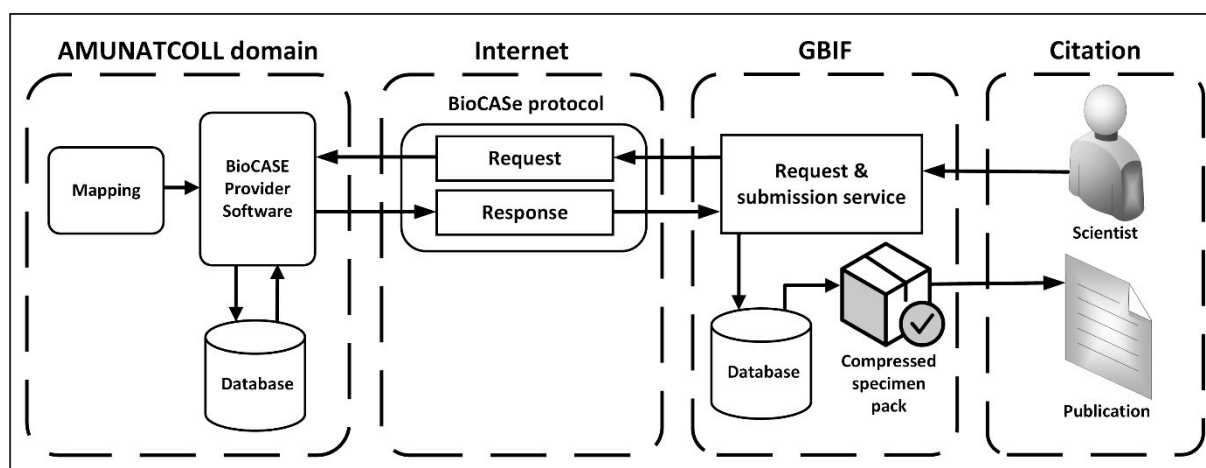


Figure 1. The flow of biodiversity data from a research institution through GBIF to scientific publications.

2.3. Data Sources, Scope, and Analysis Methods

In search of answers to the questions posed in the introduction, data and analytical tools from both the AMUNATCOLL database [50] and the GBIF database [63] were used.

For the data from the Faculty of Biology at Adam Mickiewicz University in Poznań (FBAMU) deposited in AMUNATCOLL [50], the following parameters were taken into account: (1) the number of users, (2) the number of visitors, (3) the number of visits, (4) the number of records downloaded, and (5) the number of taxa (species) for which data were downloaded. These data can be accessed by authorized users directly from the AMUNATCOLL system.

For the FBAMU data transferred to the global database (GBIF/FBAMU), a number of parameters were retrieved from the “Adam Mickiewicz University in Poznań” page created on the GBIF platform [63]. This is possible because the GBIF Secretariat runs a continuous literature-tracking program that identifies research applications and citations of biodiversity information available through the global GBIF infrastructure (Figure 1). This program includes the process of searching, reviewing, and adding newly published articles to the index [64].

By using search strings that combine frequently cited phrases (e.g., GBIF, Global Biodiversity Information Facility, etc.), DOI prefixes (e.g., 10.15468), IPT installation URLs, and names of GBIF nodes and local databases (e.g., Atlas of Living Australia, Natural History Collections of the Faculty of Biology AMU, etc.), the results of daily searches are automatically entered into a spreadsheet, which serves as a raw database of potential GBIF usage cases. Articles are retrieved using alerts and XML-based feeds from the following sources: Google Scholar, Scopus, Wiley Online Library, SpringerLink, NCBI PubMed, and bioRxiv. New search results delivered by e-mail are piped through mailparser.io with customized rules set up for each source, ensuring a uniform and consistent output. The services use webhooks to add an entry to a Google Sheet for each new paper containing a timestamp, the source, a title, and a URL. RSS feeds are added to the same sheet using an IFTTT applet. At the data-cleaning stage, the GBIF Secretariat applies several semi-automated techniques to remove duplicates and false positive results. These preliminary steps typically remove about half of the raw input data, as approximately 30 percent are duplicates and 20 percent are false positive results. After cleaning, the documents are classified and categorized according to a set of criteria. Additional metadata are retrieved (mainly via the CrossRef API) and stored in the literature database (currently Mendeley), which is regularly indexed by GBIF.org and displayed in the literature resources section. If the article contains a DOI representing data mediated by GBIF used in the study, the link is

directly included in the index, so that datasets and publishers display links (if they exist) to articles that have used their data. Links between research articles and data in GBIF are displayed in several ways on GBIF.org, including on the dataset, publisher, and download pages (Figure 2).

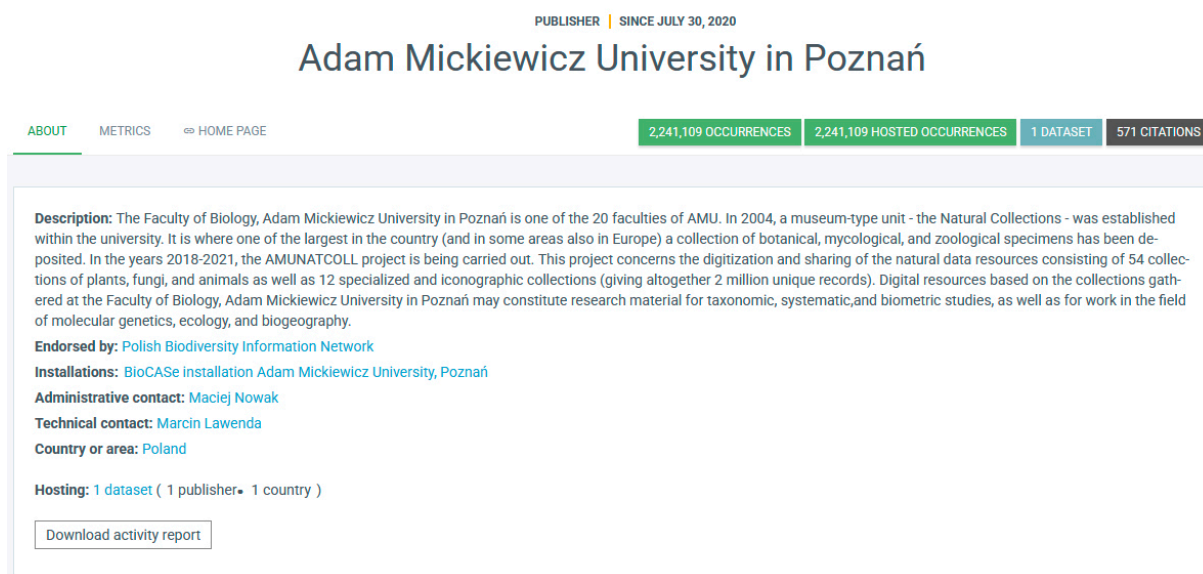


Figure 2. The dataset page of Adam Mickiewicz University in Poznań with information on the number of citations and a link to the collection of publications citing data from the NHCs of the Faculty of Biology AMU “[63] accessed on 25 February 2025”.

Using publicly available tools provided by GBIF, a study was conducted on the FBAMU dataset hosted on this global biodiversity information platform. The following aspects were initially determined: (1) the total number of FBAMU records transferred to the GBIF database, (2) the number of records taxonomically classified into the main kingdoms of organisms, (3) the number of records located in individual countries, (4) the number of records downloaded by users, and (5) the number of publications citing FBAMU records. The central stage of the research involved a formal and substantive analysis of the collection of publications that cite FBAMU data. At this stage, the following elements were determined: (1) the thematic areas associated with the publications citing FBAMU, according to the classification adopted by GBIF; (2) the journals and other scientific sources where these publications appeared, along with their ranking based on Web of Science categorization [65]; (3) the geographical origin of the authors of these publications; and (4) the thematic areas of the journals in which the publications citing FBAMU were published, according to Web of Science classification [65]. (5) Additionally, we classified the publications based on our own in-depth substantive analysis, in which we took into account the subject area as well as the process and phenomenon analyzed in the paper. In the substantive analysis, only publications published in peer-reviewed journals, and less frequently in other scientific works, were considered. Citations in other sources, primarily in preprints, were excluded. Based on a thorough analysis of the publication content, the main issue, phenomenon, or process (taxonomic status, species invasion) addressed in the paper was identified and classified into a specific research area (e.g., systematics, biogeography). The results of this analysis are presented in numerical form, accompanied by concise commentary on publications representative of each research area.

The use of GBIF/FBAMU data is presented quantitatively, in the form of simple numerical indicators and as a review of publications representative of specific research areas.

3. Results

3.1. Use of FBAMU Data Made Available on the AMUNATCOLL Platform

The AMUNATCOLL IT system has accumulated 2,239,574 records describing specimens (68.7%) and human observations (31.3%) deposited at the Faculty of Biology at Adam Mickiewicz University in Poznań. Animals are the most represented group (75.9%), followed by plants (22.7%) and fungi (1.4%). The biodiversity data originate from all continents, with the largest portion coming from Europe, primarily from Poland (87.6%) (Figure 3).

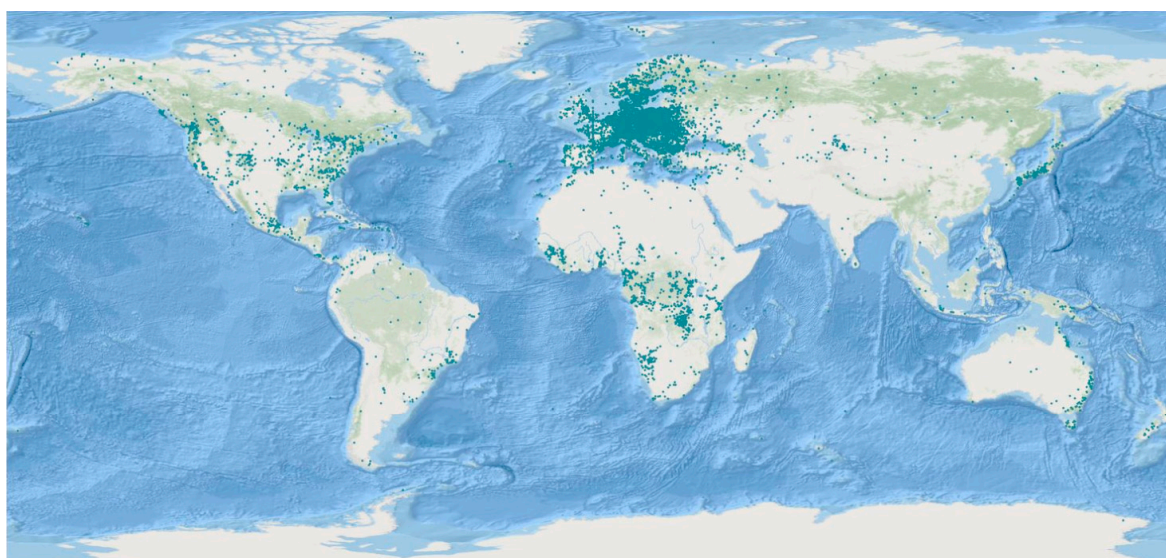


Figure 3. Distribution of specimens and human observations collected in the AMUNATCOLL IT system “[50] accessed on 25 October 2024”.

During the first 24 months of AMUNATCOLL IT’s open functioning, the portal was visited by 58,611 users, including 1232 who logged into the system. During this period, they downloaded 111,149 records from the database, containing information about 56,037 species. On a monthly basis, the number of users was quite variable: from 16 in the first month of the portal’s activity to 171 in the 21st month. On average, 51.3 logged-in users accessed the database per month (Figure 4). More than 92% of users were from Poland (230), while the remaining users represented 45 countries, including 28 from Europe, 6 from Asia, 5 from Africa, 3 from South America, 2 from North America, and 1 from Australia.

The number of records downloaded showed less variability than the number of users (an average of 4631.2), although a noticeable peak can be observed in the 23rd month of the portal’s functioning, as well as a significantly higher number of records downloaded in the 14th month compared to the average value (Figure 5).

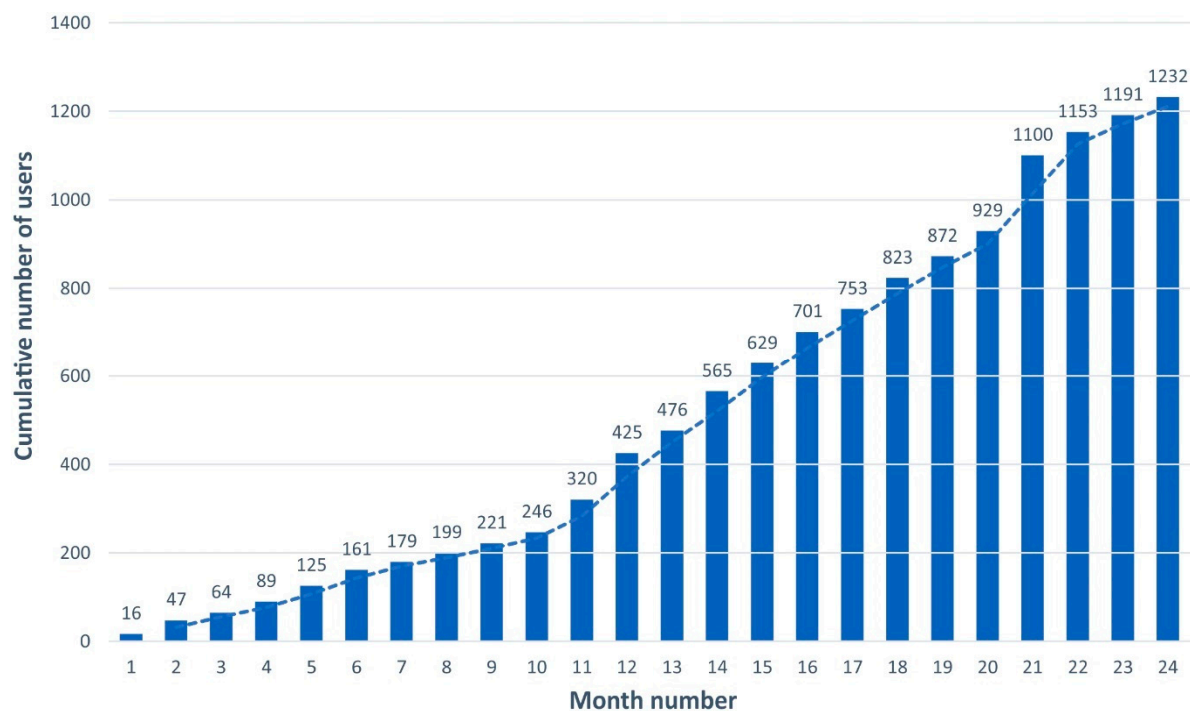


Figure 4. The cumulative increase in the number of users of AMUNATCOLL IT from 1 November 2022 to 31 October 2024.

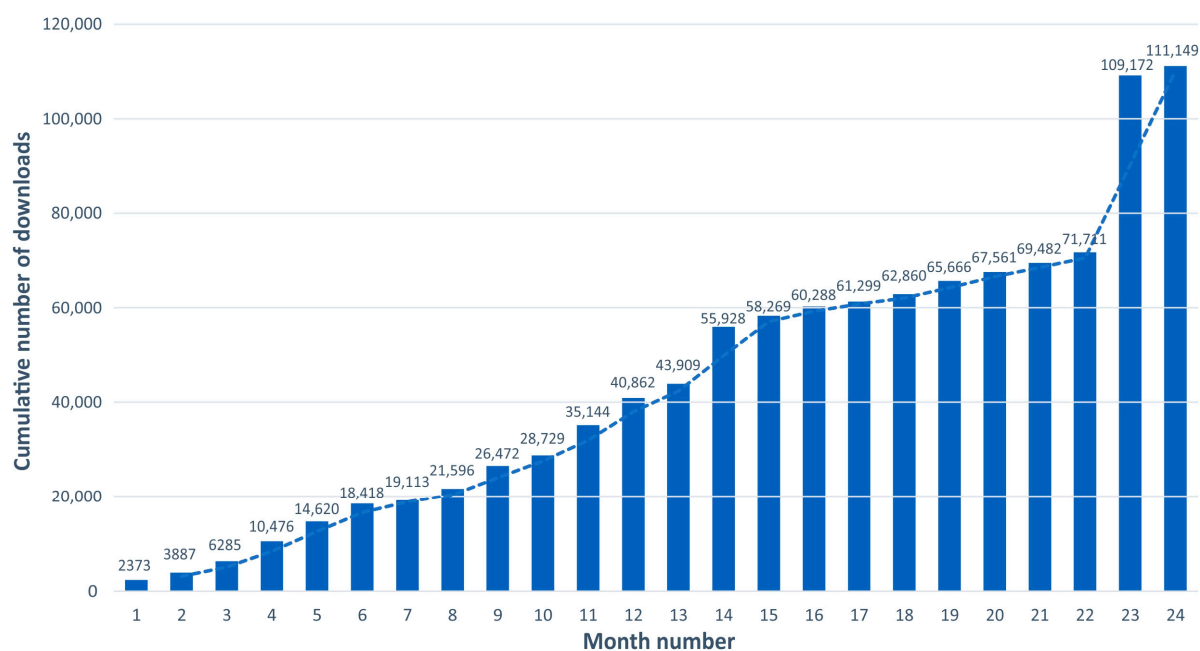


Figure 5. Cumulative increase in the number of records downloaded from AMUNATCOLL IT from 1 November 2022 to 31 October 2024.

3.2. Use of FBAMU Data Made Available on the GBIF Platform

3.2.1. FBAMU Biodiversity Data in GBIF

A total of 2,239,555 records transferred from the FBAMU database have been made available on the GBIF platform [63], including 64.7% specimens, 31.3% human observations, and 4.0% living specimens. The oldest collections date back to 1734. The distribution of 2,189,539 records with georeferences confirms their origin from all continents (Figures 6 and 7).

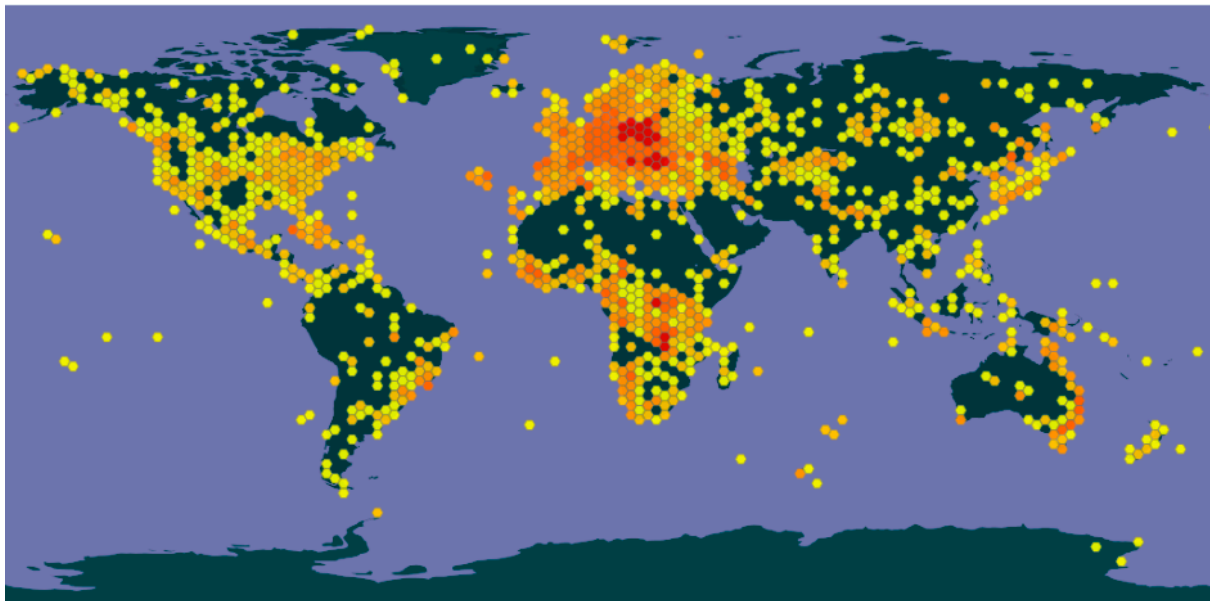


Figure 6. Distribution of specimens and human observations from GBIF/FBAMU worldwide “[63] accessed on 25 February 2025”.

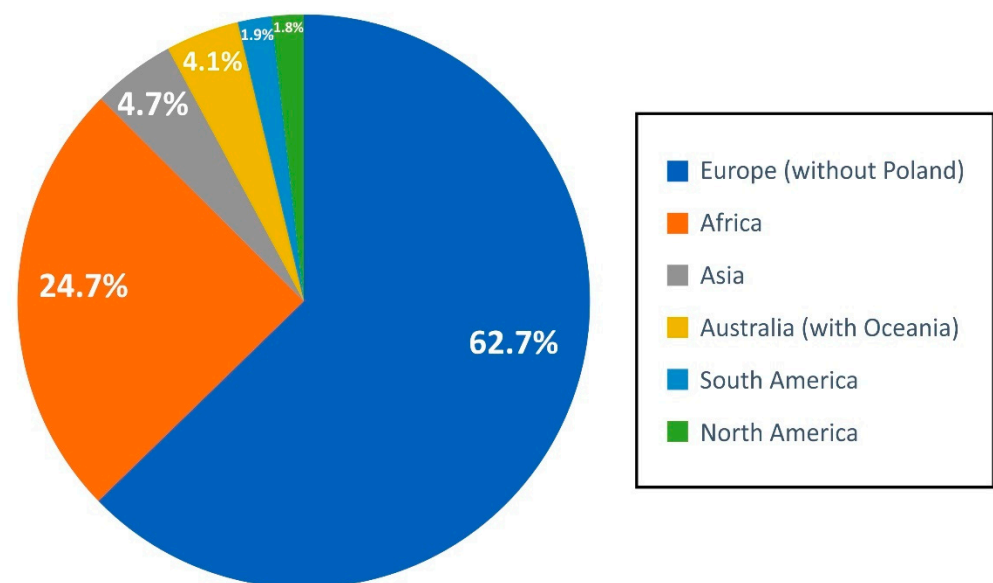


Figure 7. Distribution of GBIF/FBAMU specimens across continents. The share of 260 samples from Antarctica, not depicted in the chart, is 0.01%.

The records predominantly document specimens and observations from Poland, which account for 89.3%. The remaining specimens and observations were collected in 51 countries in Europe, 50 in Africa, 39 in Asia, 19 countries and administrative units in North America, 19 in South America, and 10 in Australia and Oceania. The highest number of specimens and observations come from the following countries: Democratic Republic of the Congo, Bulgaria, Ukraine, and Germany.

The GBIF/FBAMU dataset represents taxa from six kingdoms, with the vast majority belonging to Animalia (1,384,723 records; 61.8%). Over 21.1% (474,012 records) pertain to the kingdom Plantae, while fewer records are from the kingdom Fungi (30,239, 1.4%). The remaining kingdoms, namely Chromista, Protozoa, and Bacteria, together account for 1052 records, or approximately 0.05%, which is significantly lower. It should be noted

that a large group of specimens remains classified as *incertae sedis* (351,083), awaiting further classification.

3.2.2. GBIF/FBAMU Data Download Statistics

During the first 36 months of functioning of the GBIF/FBAMU dataset, the data were downloaded 216,317 times, averaging 6008.81 downloads per month. The range of downloads is very wide, from several dozen in the first month to around 16 thousand in the 27th month of GBIF/FBAMU data exposure. Regardless of the variations between months, it is evident that the number of downloads has steadily increased from the beginning (Figure 8).

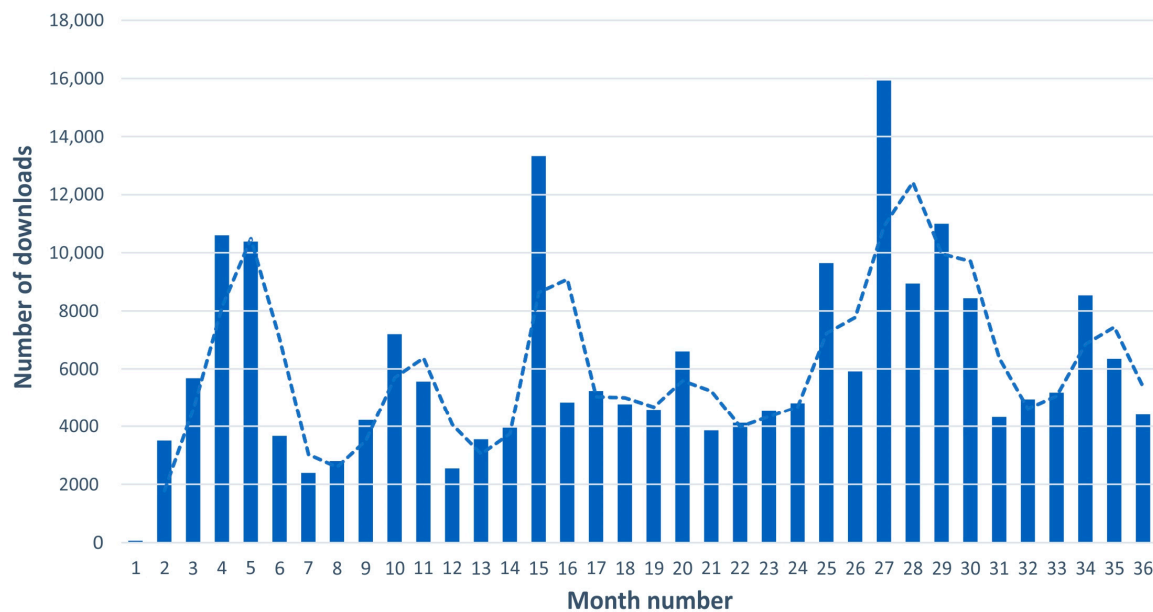


Figure 8. Number of downloads from the GBIF/FBAMU dataset over the 36 months of database availability (from 1 January 2022 to 31 December 2024).

A total of 7,713,734,343 records were downloaded during all sessions. On average, 214,270,398 records were downloaded per month. The fewest records (40,091) were downloaded in the first month of GBIF/FBAMU functioning, while the most (over 353 million) were downloaded in the 22nd month of database availability (Figure 9).

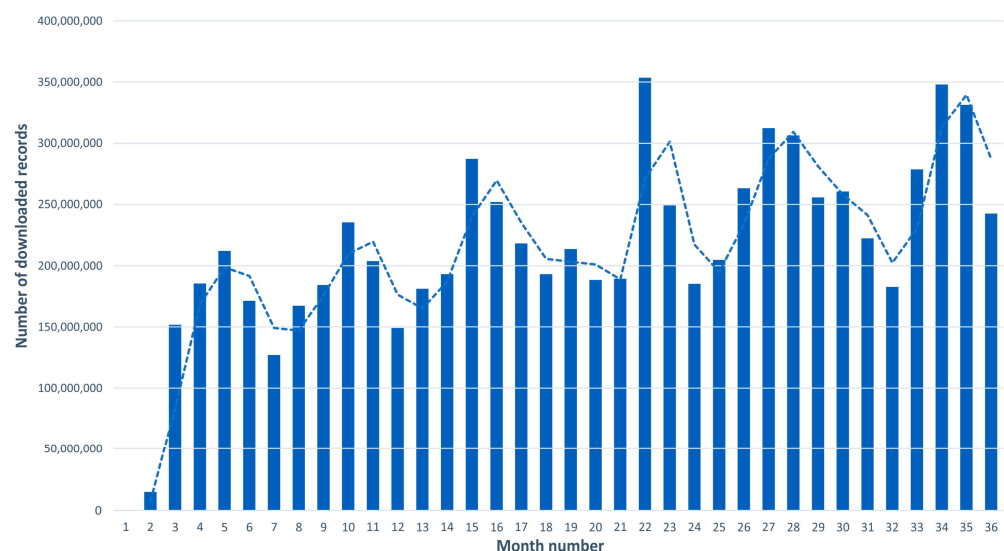


Figure 9. Number of records downloaded from the GBIF/FBAMU dataset over the 36 months of database availability (from 1 January 2022 to 31 December 2024).

3.2.3. GBIF/FBAMU Data in Scientific Publications

By the end of October 2024, 426 sources citing the GBIF/FBAMU data had been identified, including 42 in 2022, 192 in 2023, and 192 over the first 10 months of 2024. The vast majority of citations (324) refer to papers published in peer-reviewed scientific journals or book chapters. The remaining references primarily appear in works published in open online repositories such as *Authorea*, *bioRxiv*, *BioHackrXiv.org*, *EcoEvoRxiv*, *EGUsphere*, *ESS Open Archive*, *JMIR Preprints*, *Research Square*, and *Zenodo*. For a small portion of the works, information about their place of publication is missing, or they exist in the form of manuscripts.

According to the classification adopted by GBIF, articles and other peer-reviewed publications represent 17 thematic areas, with some being assigned to more than one area (Figure 10). The largest proportion of papers falls within the broadly defined field of ecology (19.1%). Two particularly prominent thematic areas in the last 30 years are climate change and biological invasions (14.0% and 12.5%, respectively). Slightly fewer articles are classified under biodiversity science (8.5%) and conservation biology (7.9%). The proportion of publications in the next three thematic areas is relatively consistent: evolution (6.2%), biogeography (6.2%), and phylogenetics (5.9%). Taxonomy is represented to a lesser extent (4.2%). This may be due to the lack of important diagnostic features in the digitized specimens and a lower level of trust from specialists in digital data. It is also worth noting the presence of publications addressing applied topics such as human health (3.8%) and agriculture (3.6%). Around 2.6% of publications focus on species distribution. Digitized biodiversity data from GBIF/FBAMU are also used in publications focused on data analysis and data management, categorized under the data paper and data management thematic areas, as well as articles concerning vanishing aquatic ecosystems (marine and freshwater) and those dedicated to citizen science.

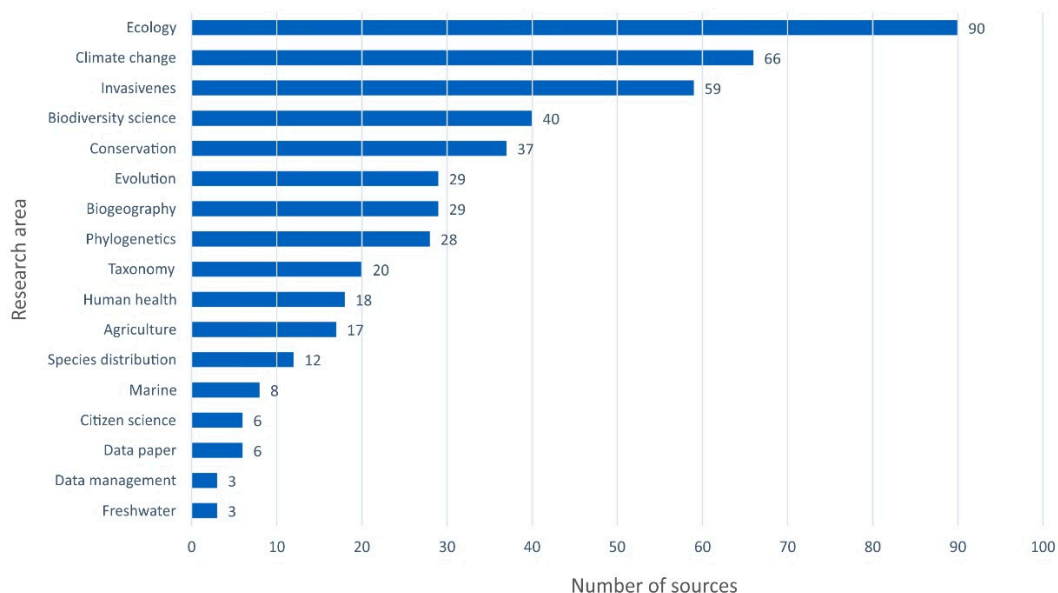


Figure 10. Distribution of publications citing GBIF/FBAMU data across 17 research areas (471 sources).

The vast majority (291) of the 325 papers citing data from the GBIF/FBAMU dataset were published in journals indexed in the Web of Science database. The share of other journals is smaller because not all of them are searched by GBIF. It cannot be ruled out that GBIF/FBAMU data are also cited in those journals. More than half of the 149 journals

publishing research results that include biodiversity data from the GBIF/FBAMU dataset are ranked in the first quartile by Web of Science (Figure 11).

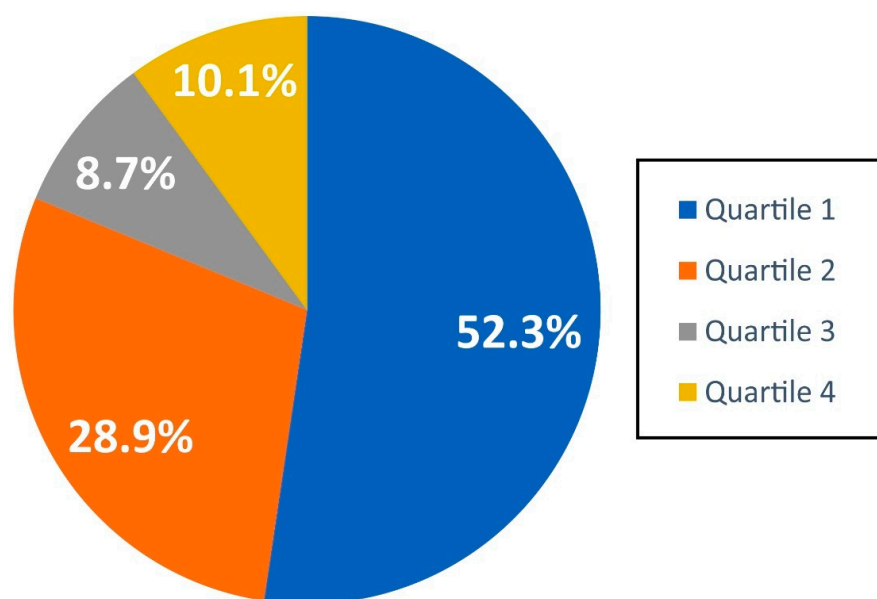


Figure 11. Category rank of journals publishing research that utilizes GBIF/FBAMU data (149 journals).

Among these are journals widely recognized as some of the most prestigious in the world (Table 1). It is worth emphasizing that, in addition to journals within the field of biological sciences, the JCR category of multidisciplinary sciences is also well represented. It can also be noted that in this group of journals, the most relevant articles for our purposes were published in *New Phytologist*, *Science of The Total Environment*, *Nature Communications*, and *Global Change Biology*.

Table 1. Top 20 journals publishing research utilizing GBIF/FBAMU data.

Journal Name	JCR Category	JIF 5-Year	No. of Papers
New Phytologist	Plant sciences	10.5	9
Science of The Total Environment	Environmental sciences	9.6	8
Global Change Biology	Biodiversity conservation	12.3	7
Nature Communications	Multidisciplinary sciences	17.0	7
Scientific Data	Multidisciplinary sciences	10.8	5
Ecology Letters	Ecology	9.8	3
Nature Plants	Plant sciences	18.6	3
Nature Ecology & Evolution	Ecology	16.9	2
PNAS	Multidisciplinary sciences	12.0	2
Biological Reviews	Biology	12.8	1
BioScience	Biology	9.7	1
Ecological Monographs	Ecology	9.0	1
Journal of Integrative Plant Biology	Biochemistry & molecular biology	9.3	1
International Journal of Extreme Manufacturing	Engineering, manufacturing	13.3	1
Nature Climate Change	Environmental sciences	31.4	1
Nature Sustainability	Environmental sciences	29.2	1
Systematic Biology	Evolutionary biology	11.0	1
Water Research	Engineering, environmental	12.2	1

3.2.4. Phenomena and Processes Investigated Using GBIF/FBAMU Data

Studies utilizing, among others, GBIF/FBAMU data have led to the resolution of many fundamental issues within the broadly defined field of biodiversity knowledge, and even in several areas beyond this scientific domain (Table 2). Among the 12 research areas highlighted in this compilation, publications in the fields of ecology and biogeography are by far the most represented. The second group, with a similar quantitative share, includes biodiversity informatics, phylogeny and evolution, and biodiversity conservation. Among research areas that inherently rely on biological specimens, the representation of publications in morphology, taxonomy and systematics, and paleobiology is somewhat smaller. It is also noteworthy to mention research areas beyond the biological sciences, such as agriculture and human health, as well as the presence of a few publications in climate science and linguistic phylogeny. The quantitative analysis of phenomena, processes, and top issues shows that researchers utilizing GBIF/FBAMU data have shown particular interest in biodiversity loss, biological invasions, biogeographical patterns, changes in species ranges, climatic niche dynamics, interactions between organisms, and mechanisms of evolution.

Table 2. Classification of publications citing GBIF/FBAMU data based on the subject of research and analyzed phenomena and processes.

Subject Areas	No. of Papers	Phenomena and Processes *
Agriculture	11	Agriculture's environmental footprint · Changes in species ranges (2) · Climate change adaptation · Climate change · Climatic niche dynamics · Epidemic spread · Open-access database · Plant hardiness zones · Regulated pests · Temperature sensitivity
Biodiversity conservation	22	Biodiversity loss (13) · Biological invasions · Conservation prioritization · Data density · Ecoregions · In situ conservation · Protected areas · Restoration · Spatial conservation (2) ·
Biodiversity informatics	37	Big data · Biodiversity hotspot · Biodiversity loss (2) · Changes in species ranges · Climate change · Completeness and geographical biases · Data analysis (9) · Data cleaning · Database (4) · Fungal diversity · Geospatial suitability model · Global collection · Imperfect data · Knowledge gaps (4) · Plant diversity · Potential of the data (2) · Species distribution modeling (5)
Biogeography	81	Animal diversity · Biodiversity data (2) · Biodiversity hotspot (3) · Biodiversity loss (2) · Biogeographical patterns (13) · Biological invasions (8) · Biome evolution (2) · Changes in species ranges (17) · Changes in flora and vegetation · Checklists · Climate change adaptation · Climatic niche dynamics (4) · Cultural evolution · Database (2) · Disjunct distribution (2) · Geographical names · Interactions between organisms · Mechanisms of evolution · New record (6) · Plant diversity · Regionalization (2) · Relicts · Species distribution modeling (7) · Vicariance
Climate science	1	Greenhouse–icehouse transition
Ecology	100	Biodiversity loss (3) · Bioindication (3) · Biological invasions (15) · Carbon accumulation (2) · Changes in species ranges (3) · Changes in flora and Vegetation (6) · Climate change adaptation (8) · Climatic niche dynamics (22) · Community changes (6) · Data analysis · Diet · Dietary or habitat needs · Environmental changes (2) · Flora diversity · Forest management · Interactions between organisms (12) · Mechanisms of evolution · Organisms and habitat (5) · Remediation · Restoration of degraded sites · Spatial patterns · Toxicity · Transplantation · Tree mortality · Weed biocontrol
Human health	16	Bioactivities (7) · Biological invasions (2) · Bioprospecting · Database · Epidemic modeling · Metabolic syndrome · Schistosomatozoa · Specialized metabolism · Toxicity
Linguistic phylogeny	1	Changes in species ranges

Table 2. Cont.

Subject Areas	No. of Papers	Phenomena and Processes *
Morphology	2	Leaf characteristics · Shape modeling
Paleobiology	8	Environmental changes (2) · Fossil fruits · Fossil plants · Interactions between organisms · New record · Refugia · Vegetation reconstruction
Phylogeny and evolution	34	Biogeographical patterns · Climatic niche dynamics · Conservation prioritization · Convergent evolution · Evolutionary radiations · Genetic variability (3) · Hybridization (2) · Interactions between organisms (3) · Mechanisms of evolution (8) · Monophyly · Mutation pressure · Origin and speciation (6) · Peripheral populations · Polyploidy (2) · Reticulate evolution · Species distribution model
Taxonomy and systematics	11	Cryptic species (2) · New taxon · Nomenclatural issue · Taxon identification (4) · Taxonomical status · Typification · Variability

* The numbers in parentheses represent the number of publications. If no number of papers is provided in parentheses following the term process or phenomenon, it means that they appeared in a single paper.

The following review includes papers that are representative of the respective research areas.

Morphology, Taxonomy, and Systematics

Research on morphology, taxonomy, and systematics had predominantly relied on specimens housed at NHCs until recently. Currently, digitalized specimens are gaining increasing importance. Digital data from GBIF/FBAMU have been cited, among other instances, in publications regarding the micromorphology and anatomy of the leaves of the grass species *Andropogon gayanus* Kunth [66]. They have also been used in the description of *Hohenbuehelia filicina* sp. nov. from Southwestern Siberia (Russia) [67], to resolve controversies surrounding cryptic taxa within the genus *Acorus* L. in Eurasia and America [68], and to estimate global insect taxonomic diversity, including cryptic species [69].

Data from the GBIF/FBAMU dataset have been cited in a study reporting the rediscovery of *Tagetes dombeyi* Schiavinato, D.G.Gut. & Adr. Bartoli, a yearly species described in the 18th century based on herbarium specimens and photographs of the plant in its natural habitat in the central Andes [70]. These data have also been referenced in a paper highlighting local variation of *Campanula ramosissima* Sm. in the Balkan Peninsula [71], as well as in publications containing identification keys for species of the genus *Erica* L. [72] and carnivorous species from the *Drosera microphylla* Endl. complex in southwestern Western Australia [73]. Subsequent studies have presented the classification and distribution of species from the genus *Bacopa* Aublet [74], the results of a revision of *Tulostoma* Pers. specimens collected in Ukraine [75], the species status of *Philonthus sideropterus* (Kolenati, 1846) [76], and a nomenclatural discussion concerning the genus *Sticherus* C. Presl [77].

Biogeography

Digital data from GBIF/FBAMU have been utilized in numerous biogeographical publications. A significant group of these studies consists of discoveries of first or particularly valuable species locations across various systematic groups and regions worldwide, such as *Gloeotrichia natans* Rabh. in Yakutia, Russia [78]; *Pisolithus arhizus* (Scop.) Rauschert in Central Asia [79]; *Clathrus columnatus* Bosc on the Galápagos Islands in Ecuador [80]; species from the genus *Chlorophanus* C.R. Sahlberg, 1823, in Turkey [81]; the African grass stem wasp (*Tetramesa*; Eurytomidae) on the invasive grass *Eragrostis curvula* (Schrud.) Nees in Australia [82]; and noteworthy records of mammals (Mammalia, Theria) from Nicaragua [83]. A wide range of digital GBIF/FBAMU data has also been used by the

authors of the taxonomically verified and vouchered checklist of the vascular plants of the Republic of Guinea [84].

The GBIF/FBAMU data have proven particularly useful in analyses of species range dynamics and the search for biogeographical patterns. These studies are currently very intensive, particularly in the context of climate change. Among the publications concerning plants, studies can be highlighted that focus on predicting the ranges of species such as *Ostrya carpinifolia* Scop. in Europe [85], *Trapa natans* L. at the eastern range boundary of this species in Central Europe [86], *Castanea sativa* Mill. in Anatolia [87], and *Impatiens glandulifera* Royle in North America [88], as well as *Cordyla pinnata* (Lepr. ex A.Rich.) Milne-Redh., *Faidherbia albida* (Delile) A.Chev., and *Balanites aegyptiaca* (L.) Delile, which are key agroforestry species in Senegal [89]. Predictive studies have also focused on animals, such as *Cochlodina laminata* (Montagu, 1803), a native snail in Eastern Europe [90]; non-native land snail species in the western Palaearctic region [91]; and the invasive starlings *Acridotheres tristis* (Linnaeus, 1766) and *Sturnus vulgaris* (Linnaeus, 1758) in New Zealand [92]. In the context of climate change, the current and future range of *Trilocha varians* (Walker, 1855), a major pest of plants from the genus *Ficus* L. in China, has also been analyzed [93].

In some publications, predictive studies on geographic range changes have considered potential shifts in ecological niches. This approach has shown that niche shifts weaken the effectiveness of distribution models for *Myriophyllum aquaticum* (Vell.) Verdc. on a global scale [94], and has also demonstrated the significant role of environmental and topographical variables in modeling the current and future potential habitats of three *Juniperus* species (*J. jaliscana* Martinez, *J. monticola* Martinez, and *J. pinchotii* Sudw.) in Mexico [95].

Chorological studies utilizing digital data from GBIF/FBAMU have also focused on disjunct, relict, and vicariant species. Notably, research has shown that niche filling is a dominant phenomenon in the naturalization process of disjunct plant species from genera that are geographically separated across continents [96]. By utilizing georeferenced specimen databases and considering Canadian species ranges, the historical biogeography of the disjunct distribution of vascular plants occurring between western North America and the Great Lakes region has been better understood [97]. Studies conducted in Poland have revealed the relict nature of the *Carpinus betulus* L. (hornbeam) population in a specific climatic–terrestrial niche in the northern part of the Carpathian Basin [98]. In another study on historical biogeography, it was found that vicariance was the main process responsible for the current distribution of *Ledebouria* A.W. Roth in Eurasia [99].

Digital data are also highly valuable in biogeographical regionalization, assessing areas of exceptional biodiversity, and in discussions on biomes. This is demonstrated, among other things, by studies on the status of the Revillagigedo archipelago in Mexico [100] and the regionalization of marine biota in the western Atlantic [101]. Occurrence records from GBIF/FBAMU were used to assess the taxonomic richness of marine snails and identify global hotspots for species in this group [102]. Additionally, an analysis of 6.1 million fungal fruiting bodies revealed that major terrestrial biomes exhibit both similarities and differences in fruiting events [103].

Ecology

At the forefront of ecological issues addressed in studies using FBAMU/GBIF digital data is the dynamics of ecological niches. This phenomenon was already highlighted when discussing biogeographical issues, as it has both geographical and ecological dimensions. In this context, examples will be provided where the primary focus was placed on the ecology of plant, fungal, and animal species.

For example, the authors of a publication concerning two Australian cities (Sydney and Melbourne) attempted to answer the question of whether the climatic niche of species can predict tree crown growth, functional traits, and phenotypic plasticity in urban trees [104]. In another project, ecological niche differentiation between *Myrothamnus flabellifolius* Welw. and *M. moschatus* (Baill.) Baill., shrubs belonging to the African endemic family Myrothamnaceae Nied., was studied, along with their ability to respond to future climate changes [105]. In the context of future climate change, habitat data for *Melia azedarach* L., an important economic tree widely distributed in the tropical and subtropical regions of China and some other countries, were also explored [106]. Identifying ecological descriptors of native forage grass species was the focus of research conducted in the dry and semi-dry regions of Mexico [107]. Hawaiian dry ferns were used as a model for studying the interaction between land use change and competition from naturalized species in occupying habitats [108]. Environmental predictors were applied to model the ecological niche of the industrially significant fungus *Ganoderma lucidum* (Leys.) Karsten on a global scale [109], as well as *Paederus fuscipes* (Curtis, 1826) in China [110].

Ecological niches of invasive alien species are increasingly the subject of modeling. Using climate and hydroclimatic models, environmental factors driving the global invasion of marsh snails were identified [111]. Meanwhile, applying ecophysiological mechanistic models that quantify fundamental thermal niches, the area threatened by the invasion of birds introduced to Europe was precisely determined [112].

GBIF/FBAMU digital data are also used beyond the currently dominant research trend in invasion biology based on ecological niches. Among other applications, they were used to assess the history of introduction, distribution, and naturalization of tree and shrub species from the genus *Myoporum* G.Forster in South Africa [113], were applied to recognize the impact of introduction pathways on the success of invasive plant species along environmental gradients in Catalonia [114], and proved useful in developing an invasion risk atlas for alien aquatic plant species on the Iberian Peninsula [115]. Furthermore, using *Robinia pseudoacacia* L. and the herbivores associated with this invasive tree, it was demonstrated that insect invasions track a tree invasion [116]. Digitized herbarium data are increasingly being used in phenological analyses, including in the context of global climate change [117,118].

A significant place in the discussed group of publications is occupied by studies on the ecology of interactions between representatives of different organism groups. One such study demonstrated the low specificity of native truffles (*Tuber P.Micheli* ex F.H.Wigg.) in Central Europe towards their ectomycorrhizal tree partners [119]. Research conducted in Patagonia revealed that floating populations of macroalgae *Ulva* L. and *Undaria pinnatifida* (Harvey) Suringar provide good habitats for invertebrates but not for fish [120]. Another study focused on interactions between vascular plants and animals, testing Cruden's hypothesis, in which patterns of pollinator rotation (insects and birds) in relation to elevation in tropical and temperate zones of both Americas were extensively described and discussed [121]. The thematic scope of interaction ecology can also be broadened by applied research on the climatic suitability of *Engytatus passionarius* (Minghetti, Maestro & Dellapé, 2021) as a biological control agent for the invasive, foul-smelling passionflower *Passiflora foetida* L. in Australia [122].

GBIF/FBAMU data are also employed to showcase studies on organism–environment interactions, with a stronger emphasis on plants compared to animals. Studies conducted in the northeastern part of Spain revealed that the growth of trees (*Pinus sylvestris* L.) and shrubs (*Amelanchier ovalis* Medik.) is limited by drought, with shrubs being more sensitive in dry areas [123]. Other studies have shown that moderately woody angiosperm species acquire tolerance to water stress during the growing season [124]. In research on

Microchloa caffra Nees, conducted along an environmental gradient from mesic to xeric conditions in South Africa, it was observed that higher-order polyploids exhibited greater drought tolerance compared to lower-order polyploids [125]. Additionally, in parallel laboratory and field studies, the effects of severe and prolonged moisture treatments on thermal tolerance and sensitivity to climate change were tested in click beetles (Coleoptera: Elateridae) living at high latitudes [126].

GBIF/FBAMU digital data are utilized in studies on changes in flora, fauna, vegetation, and the environment, as well as in assessing biodiversity loss. Among the publications addressing this issue, one example includes research evaluating the vulnerability of western Mediterranean forests to climate change on the Iberian Peninsula [127]. Other studies have presented forecasts of shifts in the distribution and grazing value of grassland communities dominated by *Stipa* L. species on the Eurasian steppes [128], as well as shown that ferns play a role in facilitating community recovery after biotic disturbances [129]. Data from GBIF/FBAMU have also been used to describe community reorganizations in response to climate change for nine taxonomic groups of animals (ants, bats, bees, birds, butterflies, earthworms, frogs, rodents, salamanders). It is worth emphasizing that most of these groups had never been studied in this context before [130]. Additionally, using globally collected data, researchers have gained insight into the impact of averaged fire regimes over time on the spatial diversity of wild bird species [131].

One of the most significant causes of environmental changes today is urban development. In this context, it is worth noting studies that have shown increasing biodiversity losses of insects along an urbanization gradient in a subtropical city [132].

Biodiversity Conservation

Digital data from GBIF/FBAMU are proving useful in studies related to biodiversity loss, as well as various aspects of species and ecosystem conservation. For example, in China, they were used to assess the extinction risk of the endemic coniferous tree *Cupressus funebris* Endl. [133]. In other studies, based on machine learning analysis, it was concluded that more than half of the 7699 species classified as DD (data deficient) in the IUCN classification are indeed at risk of extinction [134]. Digital data were also used to assess the conservation status of vascular epiphytes in the neotropical zone for families that represent over 80% of the global diversity of epiphytes (Araceae Juss., Bromeliaceae Juss., Orchidaceae Juss., Piperaceae C. Agardh, and Polypodiaceae Bercht. & J. Presl) [135].

The success of biodiversity conservation largely depends on recognizing areas of concentration for particularly valuable species, habitats, and ecosystems. In this regard, GBIF/FBAMU data are of significant importance. This is exemplified by the determination of priority areas for the establishment of genetic reserves to actively protect key wild species related to cultivated plants in Italy [136], the pinpointing of priority protection areas for protected saproxylic beetles in Romania [137], and the designation of important plant areas for beneficial plant species in Colombia [138].

Paleobiology

Although paleobiological research primarily relies on historical material, contemporary collections are also highly useful in this field. GBIF/FBAMU digital data have been used, for example, to reconstruct paleoenvironmental conditions that led to the formation of Eocene subbituminous coal deposits in the Hungarian Paleogene basin [139]. They were also employed to explore the history of plants from the Icacinaceae family in western Gondwana [140] and to explain historical changes in the relationship between the flowers of *Ludwigia* L. species and their primary pollinators [141]. Contemporary records are also cited in studies aimed at testing the hypothesis of long-term floral continuity in the Carpathian

Basin [142] and have been used to reconstruct the vegetation structure of the late Oligocene around Enspel, Germany [143].

Phylogeny and Evolution

In all the thematic areas discussed above, phylogenetic and evolutionary issues have already appeared to some extent, either directly or indirectly. In a large number of studies supported by GBIF/FBAMU digital data, these issues take center stage. Therefore, it is worth illustrating them with representative examples. In the studies analyzed from this perspective, mechanisms of evolution, speciation, hybridization, polyploidy, evolutionary radiation, and genetic diversity were examined.

This thematic area includes, among other things, studies that have shown that temperature, particularly the highest temperature of the warmest month, is the most consistent climatic factor influencing the evolution of annual strategies in flowering plants [144]. Other studies, focusing on phylogenomics and historical biogeography of Hydrangeaceae (Hydrangeaceae Dumort.), shed light on evolutionary radiation and floral concentration in East Asia, as well as the disjunction between East Asia and North America [145]. Two additional papers address hybridization. The first demonstrates that hybridization facilitated the expansion of range and resistance to climate change in two key boreal forest tree species, *Picea abies* (L.) H.Karst and *Picea obovata* Ledeb [146]. The second describes the discovery of natural triploid hybrids of *Paspalum* L. (Poaceae) near sympatric populations of *Paspalum urvillei* Steud. and species from the Paniculata group in northeastern Argentina [147]. Finally, it is worth noting research on genetic diversity, such as a study on genetic diversity in predatory soil arthropods (Myriapoda: Chilopoda), which—as shown—varies according to species characteristics and geographic latitude [148].

Biodiversity Informatics

The review of biological sources utilizing GBIF/FBAMU digital data concludes with a brief analysis of studies focused on discovering new or improving previously known methods of processing biodiversity information, as well as of papers evaluating the quality of open databases or highlighting their limitations.

Many positive opinions about digital data and databases have been expressed in a paper highlighting the importance of integrated global natural history collections for decision-makers [149], as well as in a publication emphasizing the undeniable role of herbarium collections in the context of complementary observations in social science [150]. On the other hand, it is emphasized that the mass production of unverified documents does not fully reflect global biodiversity patterns [151], and there is a suggestion to carefully consider the emerging biases when using biodiversity data from various sources [152]. It is emphasized that despite many efforts, the still inconsistent way of sharing biodiversity information hinders its use in conservation, and therefore, further integrative actions are urgently needed [153]. These issues are addressed by new analytical tools, such as occTest, which enable an integrated approach to quality control of species occurrence data [154]; a new R package for analyzing plant species occurrence records and transforming them into unique collection events, effectively reducing data redundancy [155]; and solutions aimed at reducing the dimensionality of environmental variables, which significantly impacts the effectiveness of species distribution models [156].

Applied Sciences and Other Research

The use of digital data from GBIF/FBAMU extends beyond basic biological sciences. They are also applied in agriculture and human health, climate science, and even in linguistic phylogeny.

For example, studies in the field of agriculture have focused on the temperature sensitivity of marine macroalgae in aquaculture in China [157], quarantine pests in the European Union [158], the suitability of the main 23 food crops in agriculture across Africa [159], and the verification of plant hardiness zones in the United States [160].

Publications related to human health have primarily focused on the bioactivity of plants, such as *Thymus algeriensis* Boiss. et Reut [161], *Seseli* L. [162], and *Rhodiola* L. [163]. Among the numerous studies on biodiversity in the context of climate change, as previously mentioned, one notable publication represents the field of climate science and addresses the West Antarctic, which was devoid of an ice cover during the peak of the early Oligocene glaciation [164].

Due to its distinctiveness, special attention to a publication in the field of linguistic phylogeny is deserved, which focused on the time and place of origin of the South Caucasian languages [165].

4. Conclusions

The digitization of natural history collections is a global phenomenon encompassing major, medium, and smaller scientific institutions, particularly those that have been gathering specimens documenting scientific discoveries for centuries. The ongoing standardization of data and the harmonization of the digitization process are contributing to the development of a global biodiversity information system, in which each component holds significant importance.

In our research, we positively verified the hypothesis that the scientific value of biological data digitized in a medium-sized institution significantly increases after being made available on the GBIF platform. During the same period, the number of records downloaded directly from the regional AMUNATCOLL database constitutes a negligible fraction (0.002%) of the records downloaded from the GBIF/FBAMU database. This is reflected in the number of publications citing GBIF/FBAMU data, which have been published frequently in dozens of international journals (an average of three publications per week). Studies based on this data cover a wide thematic range (12 areas) and clearly extend beyond taxonomy and paleobiology, which dominate traditional studies relying on queries and reviews of regional natural history collections. These fields even make use of the most concise descriptions of specimens, referring to the date and location of the collected sample.

The scientific value of locally collected biodiversity data significantly increases once made available on the GBIF platform, due to several key factors, such as enhanced accessibility and increased reliability, the ability for global comparisons, and its use in new analyses and applications.

The tangible benefits of data sharing by local scientific institutions on the GBIF platform serve as a motivating factor for continuing and improving this type of activity. Thus, a kind of feedback mechanism is created, which greatly contributes to the development of knowledge about biodiversity and its conservation.

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