



ICEDIG.EU

Innovation and consolidation for large scale digitisation of natural heritage

Grant Agreement Number: 777483 / Acronym: ICEDIG

Call: H2020-INFRADEV-2017-1 / Type of Action: RIA

Start Date: 01 Jan 2018 / Duration: 27 months

REFERENCES:

DELIVERABLE D4.3

Work package **WP 4** / Task **4.3** / Lead: **APM**

Deadline **M19**

Updating data standards in transcription

**Authors: Quentin Groom¹, Mathias Dillen¹,
Helen Hardy², Sarah Phillips³, Luc Willemse⁴,
Zhengzhe Wu⁵**

1 – Meise Botanic Garden (Meise - Belgium)

2 – Natural History Museum (London - UK)

3 – Royal Botanic Gardens, Kew (Kew - UK)

4 – Naturalis Biodiversity Center (Leiden - the Netherlands)

5 – Finnish Museum of Natural History (Helsinki – Finland)



Summary of preprinted article

This paper is based on the findings of previous ICEDIG deliverables of work package 4 (D4.1, D4.2 and D4.4). These deliverables investigated methods of data capture from natural history specimens, both automated and manual. In this new deliverable we condense the conclusions of these previous deliverables and bring in previously published results from many other sources. We make recommendations to improve standards. We cover issues related to verbatim transcription, missing or unknown data and problems related to language and script. We also address specific aspects of the core data fields of a specimen: "what", "where", "when", "which" and "who". These recommendations are directed to standards organizations, transcribers, curators and software developers.

The ultimate goal of this paper is to improve the overall quality of transcription data and facilitate interoperability between collection management systems.

For improved visibility, we have submitted this paper for publication in a peer reviewed journal. Attached to this deliverable is the Author's Original Version of the submitted article.

D4.1: <https://doi.org/10.5281/zenodo.3364501>

D4.2: <https://doi.org/10.5281/zenodo.3364508>

D4.4: <https://doi.org/10.5281/zenodo.3361597>

Improved standardization of transcribed digital specimen data

Quentin Groom¹, Mathias Dillen¹, Helen Hardy², Sarah Phillips³, Luc Willemse⁴, Zhengzhe Wu⁵

1. Meise Botanic Garden, Meise, Belgium
2. Department of Life Sciences, Natural History Museum, London, UK
3. Royal Botanic Gardens Kew, London, United Kingdom
4. Naturalis Biodiversity Center, Leiden, The Netherlands
5. Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland

Abstract

There are more than 1.2 billion biological specimens in the world's museums and herbaria. These objects are a particularly important form of biological sample and observation. They underpin biological taxonomy, but the data they contain have many other uses in the biological and environmental sciences. Nevertheless, from their conception they are almost entirely documented on paper, either as labels attached to the specimens or in catalogues linked with catalogue numbers. In order to make the best use of these data and to improve the findability of these specimens, these data must be transcribed digitally and made to conform to standards, so that these data are also interoperable and reusable.

Through various digitization projects the authors have experimented with transcription, by volunteers, expert technicians, scientists, commercial transcription services and automated systems. We have also been consumers of specimen data for taxonomical, biogeographical and ecological research. In this paper we draw from our experiences to make specific recommendations to improve transcription data. The paper is split into two sections. We first address issues related to database implementation with relevance to data transcription, namely versioning, annotation, unknown and incomplete data and issues related to language. We then focus on particular data types that are relevant to biological collection specimens, namely nomenclature, dates, geography, collector numbers and uniquely identifying people. We make recommendations to standards organizations, software developers, data scientists and transcribers to improve these data with the specific aim of improving interoperability between collection datasets.

1. Introduction

There are an estimated 1.2 to 2.0 billion specimens in the world's herbaria and museums (1). Biological collection specimens are a distinct category of biodiversity occurrence record. They are scientifically important because, unlike field observations, specimens provide direct evidence for the occurrence that can be further studied and validated. The core data of a biological occurrence record are the identity of the taxon or taxa ("what"), the date of the occurrence ("when") and the location ("where"). Researchers use specimens for many kinds of studies, and for many such applications these data are enough. If they are not, there are many additional pieces of information that are associated with specimens, including other data related to the collection event, the collection location, the specimen's nature or preparation and the subsequent history and use of the specimen.

Collection specimens share some characteristics with those observations that are supported by photographic evidence, as they both provide evidence for the observation and the possibility of extracting additional information. However, the potential preservation of DNA and the accessibility of morphological and microscopic characters makes specimens particularly valuable from a scientific perspective. In recent years, photographically supported observations are being created in their millions, notably by online platforms such as iNaturalist (www.inaturalist.org/), Observation International (observation.org) and Biodiversidad Virtual (www.biodiversidadvirtual.org). However, an important distinction with specimens is that these platforms capture data associated with an observation digitally, directly at the point of creation, whereas the vast majority of specimens in collections are first documented on paper. Digitizing these data from paper, in a useable format, is an ongoing challenge for collection holding facilities. Harmonizing these digital data to make them semantically interoperable, is an even bigger challenge. Semantic interoperability means that data fields from different datasets have a common meaning and share compatible definitions, even if they might have different property names.

Specimens are used to support many biological studies, but perhaps their foremost use is in taxonomy and nomenclature, where they are used as type specimens to link a scientific name to a taxon. The details of such type material are published in taxonomic literature, where they are generally referenced by the institution they belong to, their collector and sometimes their collector number. As a result of this use, the identity of the person or persons who collected the specimen ("who") and the collector number ("which") are of similar importance to the what, when and where of the collection event.

Often, a collector will document additional information pertaining to the collecting event in field notebooks, scientific publications and nowadays even in mobile telephone apps. The "who" and "which" are often critical to link this additional information back to the physical specimen. At least in part as a result of this additional information, specimens have also found use in subjects as diverse as evolution, genetics, climate change impacts, history of science, morphology and ecology (2–8).

The data standards ABCD and Darwin Core were created to organize and catalogue data on biological collection specimens (9,10). The use of these standards has since been expanded to accommodate data on other types of biological observation, including those associated

with photographs (11), ecological surveys (12), species checklists (13) and geological specimens (14). Darwin Core, in particular, has received widespread use through its adoption by the Global Biodiversity Information Facility (15).

These standards have been widely adopted because the community recognises the need for data interoperability, but also because these data standards are flexible. Some recommendations exist in the standards as to the content of fields, but few terms have controlled vocabularies that are actively enforced or well-documented. This makes these standards comparatively easy to conform to, allowing for a wide degree of interpretation on how a particular field might be used (16). This flexibility is an advantage from the perspective of data publishers who both want to conform to a standard, but also must consider the local needs, priorities and resources. On the other hand, users of data, particularly of aggregated resources, find the malleability of these standards a significant hurdle to use of these data. A time consuming data “cleaning” exercise must be conducted before any data can be used (17). This often entails a large amount of manual work and, although this work results in standardised data, there is rarely a mechanism to return these corrected and standardized data to their source. Seldom has even partially automated data cleaning been achieved (18). Therefore, the dream of data interoperability has, at best, only been partially achieved, and more work is required on standards and processes to improve upon the *status quo*.

The broad scope of biodiversity occurrence data makes complete semantic interoperability of data fields extremely difficult. Indeed, for some types of data it is perhaps undesirable to enforce too strict a standard. The standard would either have to be over-complicated or overly restrictive. However, specimen data often represent a well defined subset of occurrence data, with a fairly narrow scope of potential elements and uses. For this reason, there is merit in refining the use of occurrence standards specifically for specimens.

There is a demand for some conformity not just in the fields used, but also for controlled vocabularies that restrict the allowable values for these fields. In the case of herbarium specimens, the Apple Core project has made recommendations for how Darwin Core fields should be used (applecore.biowikifarm.net/wiki/Main_Page). More generally, there are other publications that make specific recommendations for biodiversity occurrence data, including for specimens (19–21).

Here we summarize several studies we have conducted on the digital transcription of biological specimen data from their associated specimen labels. We draw on trials we have conducted on the automated and manual transcription of specimen labels (22,23). We have also investigated how specimen data are shared by institutions and how they store these data in their collection management systems (16). The goal of this paper is to make recommendations to biodiversity data scientists and standards organizations on how to make biological specimen data more interoperable and easier to use. Most of our assessments are based on experience with mounted herbarium specimens, as the digitization of these kind of specimens is at a more advanced stage than any other (24). However, most principles concerning data capture and data interoperability are similar across different types of biodiversity and geodiversity collection. The data on woody, zoological, mycological and geological specimens are also captured on labels attached to, or stored in proximity to, the physical specimen. Problems related to external sources such as notebooks and scientific articles are also similar. The what, when, where and who are

similarly the core data for these specimens. There are doubtlessly some differences for data interoperability due to the nomenclatural codes and geological classifications, yet the principles are common. We also encourage readers interested in this subject to consult other recommendations on biodiversity data management, such as (19) and (25). Furthermore, the general principles of data management are also apposite (26,27).

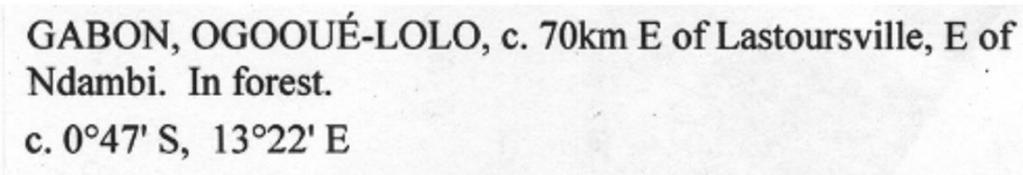
2. Transcription considerations

2.1. Verbatim transcriptions, versioning and annotations

2.1.1. Verbatim data

Verbatim data constitute the literal texts as they are written on the specimen labels, as opposed to interpreted data which are regularly available in databases. Interpreted data are generally better for the findability of specimens, aggregating data, linking related data and for scientific research. However, verbatim data are useful to understand the extent to which the standardized data have been interpreted and can support data cleaning. For instance, an unrealistic collection date can be relatively easily corrected if a correct verbatim transcription of the date is also present. Characteristic syntax, vocabulary and abbreviations in verbatim data can be a clue to the identity of the specimen's collector and the time of their life when they made the collection. Verbatim data can be searched and they are useful when a transcriber cannot interpret part of the label text, leaving a verbatim transcription for someone else to build upon later.

Increasingly, an image of the specimen label can be easily consulted or requested, and as a consequence the importance of verbatim transcriptions is diminishing. However, verbatim transcriptions may also have a new future to train machine learning algorithms that are used to automatically interpret specimen labels. Precise verbatim data are needed as ground truth data to train these algorithms in a way that interpreted text cannot be used, e.g. (28). However, one has to consider that these so called verbatim data are still, to some extent, an interpretation of the label. They can contain mistakes, but most importantly they also constitute an interpretation by the transcriber of what field a certain verbatim value should fit. For example in Fig. 1, some transcribers would list all this text (excluding the coordinates) as a verbatim value for locality, whereas others may distinguish verbatim names for country, county and/or habitat, and subsequently split these into different verbatim fields. Verbatim values distributed among different verbatim fields also provide no indication of their spatial arrangement on the original label(s), which may be relevant to improving the automated processing of the raw output in Optical Character Recognition (OCR) and Handwritten Text Recognition (HTR) algorithms.



GABON, OGOOUÉ-LOLO, c. 70km E of Lastoursville, E of Ndambi. In forest.
c. 0°47' S, 13°22' E

Fig. 1: An example of location information on a herbarium sheet label. This text can be entered into a database in several ways, even if the goal is to transcribe it in a verbatim manner. For example, should the `dwc:verbatimLocality` contain the country “Gabon”, the province “Ogooué-Lolo” and the habitat “In forest”? Transcribers may decide to distribute parts of this text into the fields `dwc:country`, `dwc:stateProvince`, `dwc:locality`, `dwc:verbatimLocality` and `dwc:habitat` or they might choose to transcribe everything literally into `dwc:verbatimLocality`. Source: <http://www.botanicalcollections.be/specimen/BR0000013860288>

The standards of Darwin Core and ABCD have verbatim terms for some data fields. In principle, there could be a verbatim alternative for any field that might be printed on a specimen label. Yet, such a proliferation of fields could be counterproductive to interoperability of data, particularly if verbatim fields were completed in preference to interpreted fields. Another problem is that these verbatim fields are also used for unstandardized data, such as dates in different formats or country names in different languages. Such data may be verbatim as they are present on the specimen, but they can also be interpretations made using obsolete or bespoke standards, such as a locally devised list of abbreviations for country names, or using external information that is not present on the actual specimen.

Table 1 summarizes use cases for verbatim transcriptions. Not all of these use cases are intercompatible: for example, the use of training data for text recognition (5) requires exact unparsed transcriptions, which is incompatible with the storage of unstandardized yet interpreted data (6).

	Use Case	Examples	Application notes
1	Facilitating data cleaning and indicating the degree of interpretation in the standardized fields.	Dates which are found to be unlikely or impossible can be easily checked for typos or erroneous transcription.	The usefulness greatly diminishes if a digital image of the label is available.
2	Discovering information hidden in the typography of how text are presented on the label.	The syntax of person names can be a clue to the writer's identity and for linking related specimens.	This is unnecessary for most specimens, but is valuable for enriching poorly documented specimens.
3	Increasing the findability of specimens.	In the absence of a fully interpreted transcription, text can still be found.	Original text can be searched in the original language.
4	Accommodating partial or uncertain transcriptions, which would otherwise clutter standardized, interpreted fields.	The use of square brackets ([]) and ellipses to indicate uncertainty or a failure to read part of the text.	Other transcribers can build on the initial attempt and it will be clear that the information is present on the label.

5	Providing training and validation source data for automated text capture methods.	Automated reading of 19 th century handwriting and recognition of symbols used on labels.	Finding gold standard training data for algorithms is a common problem.
6	Accommodating data that are not sufficiently standardized for the interpreted field or that fail to comply with the restrictions of the interpreted field.	Dates that lack a year or data awaiting interpretation.	It is common to find verbatim fields containing data in non-standard formats, even though they are not transcribed data.
7	Accommodating data following obsolete or bespoke standards.	Grid system location codes.	When a database is migrated from one system to another then verbatim field are used to store old formats.
8	Preserving the original language when interpretation has included translation.	Habitats can have some very specific meanings in different languages and they are difficult to translate, because there may not be a direct equivalent.	This also improves the finability of specimens written in a different language.

Table 1: A list of use cases for verbatim data, with examples and notes on applications.

2.1.2. Versions as an alternative

An alternative to using verbatim data fields is the use of record versioning. One can imagine many different versions of a specimen record derived from different sources and methodologies. The different sources might be directly from the physical specimen, from literature about the specimen, from a different transcriber, from a field notebook or from duplicate specimens (29). The different methodologies would include verbatim transcription, interpretive transcription, OCR or some other form of artificial intelligence. However versions are created they should be associated with metadata to make their origin clear. It must also be clear to the user which version of a record is suited to their requirements. This implies a standardization of version metadata.

A common approach is to always have a best or recommended version as the default. A similar approach is used in Wikimedia projects and research data repositories, such as Zenodo (zenodo.org), where the latest version is generally the most accurate, up-to-date and complete. However, this may not be the case for specimen record versions, as newer 'versions' might be the product of OCR or external sources such as duplicate specimens. These newer versions may be complementary or superior in content to the previous version, but they may also be worse or different in scope (e.g. verbatim transcription for algorithm training vs standardized data for biological research).

2.1.3. Annotation as an alternative

Written annotations have a long tradition with specimens, particularly on herbarium sheets, where there is ample space. These annotations can be written on separate labels, on the original label, pinned to specimens or stamped on the mounting sheet. These annotations record identifications, typifications, ownership and other history of the specimen. Specimen annotation also has a digital equivalent (30,31). Digital annotations could potentially take many other forms, varying from comments concerning individual data fields (e.g. this scientific name is incorrect) to those concerning the whole record. Much like different versions, structured metadata are necessary to understand the context of an annotation, such as when it occurred, who made it and which field or fields it refers to.

There is considerable overlap between the data that could be maintained as a digital annotation; a version or a verbatim transcription. There is also a danger that digital annotations, versions and verbatim fields could be used inappropriately to add any data to a specimen in an unstructured manner, where structured alternatives exist.

Recommendations for standards and software development: Versions, annotations and verbatim transcriptions all overlap in function to express different information about a specimen and its transcribed label data. They are needed because data do change, for example when a new determination is made or new transcription methodologies are employed. Digital annotations should not be used as a dustbin for any kind of information that cannot be easily updated on a record, due to lack of support for those data in standards and lack of support for versioning in software. We feel that time-stamped and signed versions of digital specimen records is what we should aim for and annotations should only be used for notes that are intended to be temporary or contain exceptional information. The origins of these data should also be made explicit in metadata so that the methods used to derive the data are clear.

Recommendations for transcription: Verbatim transcription should be exactly that: a literal digital rendition of the text as it is present on the physical specimen. The only exception is the use of square brackets to indicate omissions and uncertainty as described in section 2.2. However, verbatim sentences containing different types of data must be parsed into core data fields to make them more easily interpretable. When requesting verbatim transcription, consider their downstreams uses.

2.2. Unknown and incomplete data

Data concerning a specimen may not be available for different reasons. The data may have never been recorded on the labels, nor in registers and notebooks and hence may not be immediately, or ever, knowable. For reasons of speed and cost, label data may have only been partially transcribed, in which case some data might only be available if one has access to either the specimen or an image of the specimen. When prioritizing transcription work, it would be useful to know beforehand what data are available on the labels to be transcribed, but often it is not known what is there, only that it might be. Still, there is a critical difference between data that are known to be unavailable and data which might be. Collection managers and funders want to track the progress and costs of digitization, so they need to know which data

are yet to be transcribed. Furthermore, research services, such as digitization on demand, can only be offered efficiently if the degree of digitization is known (32).

In addition to missing data, sometimes data are actively withheld by a data provider. Withheld data are currently identified in Darwin Core and ABCD using an information withheld field (`dwc:informationWithheld`, `abcd:InformationWithheld`). A downside of this approach is that it is not apparent from a data field itself that information has been withheld. Currently, the information withheld fields in Darwin Core and ABCD are not machine readable, because they have neither a controlled vocabulary nor a standard format.

These esoteric distinctions between different sorts of missing data do not impact many users. If data are missing, it is disappointing for a scientist, but the reasons are moot. Still, some best practices are needed, particularly for monitoring the state of digitization. In a numeric field such as `dwc:sampleSizeValue`, it is poor practice to use text, zeros, negative numbers or large numbers as indicators of an empty field or withheld information (21). In these cases machine readable metadata are essential to provide information on what blank entries mean and what data are withheld. In text fields, distinct values should be used for data that are known to be unavailable. For example, if no collection date is available for a specimen, a standard value indicating this can be written in the `dwc:verbatimEventDate` field. A traditional method of indicating this has been the use of “S.D.”, an abbreviation for the Latin *sine dato*. Various versions of this can be found, including “sd” and “s.d.”. Another complication are partial dates where the year or century is unknown. Such cases are not covered by the ISO standard for dates (8601), but standardized information on the time of year may yet be relevant.

Recommendations for standards: Machine readable metadata should be available for a standard. This should define the data types and permitted values for each field. All text fields should allow the values “unknown:missing”, “unknown:undigitized”, “indecipherable” and “withheld”. For certain fields, such as collector and location, allowable synonyms for “unknown:missing” could be “s.c.” and “s.l.”, respectively. ABCD is currently defined by an XML Schema, but this is lacking for Darwin Core and both standards could be more explicit about the allowable values for their fields.

Recommendations for transcription: It is preferable to create a distinction between incomplete and uncertain transcriptions. Square brackets and ellipsis are a widespread and commonly used format to add explanations to text and indicate omissions of text and we recommend their use in verbatim transcription (33). The characters “[...]” can be used to indicate incompleteness, whereas any other characters between square brackets identify uncertainty of the transcriber. Do not use question marks or other characters outside square brackets unless they are actually present on the label. These proofreading symbols should never be used with interpreted fields.

For data that are not digitized a blank field can be used (21). If a whole data type has not been transcribed, then exported data should not contain a blank column for this field. This helps avoid the situation where a blank column is converted to a series of “NULL”, “NA” or

some other indication of missing data. Such representations of data could be construed as data that are not available on the specimen.

2.3. Languages and scripts

Labels, particularly in large international collections, are written in different languages and scripts with accented and non-Latin characters such as the German ß and the Scandinavian Å. A sample of 1800 specimens from nine European herbaria revealed labels written in at least twelve languages (34). These languages may have characters not found on local keyboards and optical character recognition might not be configured to recognize them. Certain symbols, particularly those peculiar to biology, may not be easily recognized or transcribed correctly, such as the characters ±, ♂, ♀, ♂, ×, ⊙ and ⊖.

This problem will be exacerbated for languages which do not make use of Latin script and for handwritten labels. However, such labels are unlikely to be digitized effectively, or at all, by people unfamiliar with the script (and language). The impact of the language that transcribers are familiar with on their transcriptive behavior is not clear. Transcribers may be expected to provide more correct transcriptions, as they will be more capable of recognizing the vocabulary and certain grammatical patterns. Transcribers who do not understand the label language will be more likely to transcribe on a verbatim basis, possibly misinterpreting certain terms into the wrong fields or transcribing non-existent words. They may also be more likely to use indicators of uncertainty or incompleteness (see section 2.2).

Recommendations for software development

Use an implementation of Unicode encoding, such as UTF-8 to facilitate the introduction of non-Latin characters to a verbatim field. For characters that are relatively common on labels but not on keyboards, introduce a tool or widget that facilitates their insertion into the different transcription fields. Where the choice of field entries can be restricted a dropdown menu this is an option for adding entries with non-keyboard characters. Another useful approach could be to allow transcribers to signal the label language. This would serve as an indication of uncertainty due to unfamiliarity with that language and as an invitation for a native speaker to validate the transcription.

Recommendations for transcription

If a verbatim data field is going to be used, then the actual language and script of the text should be used. While it is appreciated transcribers may be unfamiliar with some scripts, a translation or transliteration is an interpretation of a field.

3. Recommendations for core data

As described in the introduction, many different sorts of data can be associated with a biological specimen, but the core data are what, when, where, which and who. In this section, we will discuss these core data types in more detail.

3.1. What: Taxonomic names

Specimen labels may have mistakes in their scientific names and other legitimate spelling variants, such as abbreviations. Also, many taxon names mentioned on labels are no longer the currently accepted name. Nevertheless, these names must be documented to understand the identity and determination history of the specimen. Although there is no central names registry for all published taxonomic names, there are some excellent and extensive repositories for names. For example, there are the International Plant Names Index (IPNI), MycoBank, Index Fungorum, Zoobank, Index Nominum Algarum, AlgaeBase, Index Nominum Genericorum (ING), The International Fossil Plants Names Index and the Plant Fossil Names Registry. Neither Darwin Core nor ABCD have a verbatim field for taxon names, so there is no way to record the words on the specimen label unless different versions of the record can be created. Without the option of a verbatim field, there is little point recording the verbatim data as this will reduce the utility and findability of the data. The scientific name on the label should be interpreted so it can be linked to one of the repositories of taxonomic names. This is not recognition that this name is the accepted name of the taxon, but a quality control on the existence of the name on the label.

For author names in taxon names the ICZN (Art. 51) and ICN (Art. 46) do make recommendation on formats, but give such leeway that there is, in effect, little consistency. The ICN (Rec. 46A) does note the use of standard abbreviations of authors that are based upon (35) and maintained by the International Plant Names Index (<http://www.ipni.org>) and Index Fungorum (<http://www.indexfungorum.org>). However, use of these abbreviations is only a recommendation and no such system exists for zoological names.

Diacritical signs and ligatures are not permitted in scientific names by the ICN (Art. 60.7) and ICZN (Art. 27), so if these do occur on labels they must be removed. However, this only concerns the Latin portion of the name, not the authorship. In the ICN it is recommended that the author name is romanized without diacritical signs, but this is only a recommendation and the author's preference is followed (Rec. 46B).

Recommendations for transcription: All scientific names on a specimen should be linked to the stable identifier of that name in a nomenclatural repository. In Darwin Core, this can be done by linking the name to the stable identifier for that name in `dwc:scientificNameID`. All published names not found in the taxonomically relevant repository should be reported to a repository, preferably with details of its publication.

In rare cases, label names will not be found in names repositories. All names repositories welcome submission of new names and much of the source material is available online in places such as the Biodiversity Heritage Library. Though this might seem like additional work, it can turn a largely useless specimen into the source of scientific information and it may even be an unrecognised nomenclatural type specimen. In the rare cases where a published name cannot be found in a repository the name can be linked to its publication in Darwin Core using `dwc:namePublishedIn` and `dwc:namePublishedInID`.

Occasionally, there are also names on specimens that have never been published. It is better that such names are restricted to a notes field, rather than these names gaining authority by being distributed more widely through data aggregators.

Recommendations for software development: In transcription systems, an auto-suggest functionality for taxonomic names based on repositories such as the ones listed above is the quickest route to consistency. This can be complementary to a verbatim field.

Recommendations to taxonomists, nomenclaturists and nomenclatural repositories: Where not already available, seek to completely document all published scientific names; support registration of new names and provide stable persistent identifiers for all names. Use standard abbreviations for name authors where they are available and begin the process of standardizing author names for zoology.

3.2. What: Nomenclatural Types

Nomenclatural type specimens are fundamentally important to biological nomenclature and taxonomy. Type specimens link a published name to a taxon concept. Yet there is no requirement from the international codes of nomenclature to register types and there is no central repository for typification information. Moreover, there are few examples of collections that know all the types they hold. Even in cases where types are identified and curated in a collection, it is even rarer that the category of type (e.g. isotype, lectotype...) is known. These data and this information deficit are a serious impediment to the smooth and efficient working of the codes of biological nomenclature. Names can be accidentally typified multiple times, specimens can be considered lost and, description of new taxa can be delayed or made in error.

Nomenclatural types are inseparable from the literature that declared them to be a type. In documenting types, it is essential to include the bibliographical reference of typification. The international codes for nomenclature make recommendations for publications to ensure that type material can be found from the starting point of literature, such as articles 9C and 40A of the ICN (36). However, it is considerably harder from the starting point of a specimen to discover what sort of type it is, where it was typified and whether it is even a type. Only a few years ago this was largely irrelevant, because the main route to specimen data was through the literature. However, now that digitization is making specimen data more widely accessible than typification literature, taxonomists are more likely to find type specimens first and ask the question, as to where it was typified.

Recommendations to curators and taxonomists

If a specimen or illustration becomes a nomenclatural type, it should be clearly labelled as such upon publication of the typification and the collection catalogue should be updated with the publication details, particularly the identifiers for the publication, such as a Digital Object Identifier, or an ISSN. If primary and secondary type material are not in the institution where the taxonomist works, they have a responsibility to inform the responsible collection holding institute. This is also a recommendation of the ICZN in articles 72D and 72F (International Commission on Zoological Nomenclature 1999). However this is not yet a recommendation of the ICN (36).

Recommendations to standards organizations, developers and data scientists

Darwin Core has a `Types and Specimen` extension and ABCD has a “`NomenclaturalTypeDesignations`” container element for typification information.

Nevertheless, typification data are poorly supported in specimen catalogues and standards lack clear vocabularies for typification data. These data need improvement. Of course, these data also need to be shared openly because types are dispersed across collections, particularly iso-, para- and syntypes.

Recommendations to data aggregators

Creators of scientific name aggregations should put more emphasis on typification information, making the links between names, publications and specimens. In aggregated data the rules of nomenclature and particularly typification can be tested and errors can be identified. In this way, errors in data or typification can be corrected. For example, for any scientific name there should be only one holotype, lectotype or neotype; syntypes should not exist if there is a neotype, isotypes should share the same collecting details and allotypes should not be the same sex as the holotype (36,37).

3.3. When: Dates

On the face of it, dates are one of the simplest data types to be documented and validated. They are also one of the most important data elements for use in conservation assessments, climate change research and historical studies. Nevertheless, for many reasons, they are often the source of confusion and errors (Fig. 2). Dates on labels can come in a wide range of formats and a wide range of errors or ambiguities can be present. The century is frequently omitted from a handwritten date and numbers can be particularly difficult to distinguish in handwriting, as there are no contextual clues that aid word recognition. Dates may also simply be non-existent (Fig. 2d) or ambiguous (Fig. 2e).

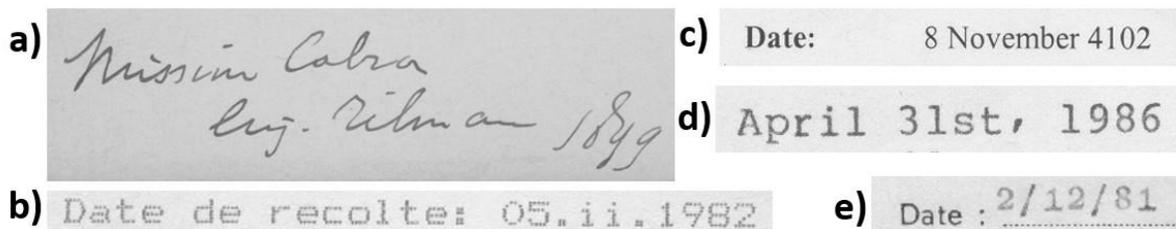


Fig.2: Examples of potential problems encountered while transcribing dates from specimen labels. **a)** Handwriting difficult to interpret (1849 or 1899). **b)** Symbolism used can be interpreted differently (5th of February or 5th of November). **c)** Impossible but partially true date (correct year was 2002). **d)** Impossible but likely mostly true date. **e)** Uncertainty of order of day and month and missing century digits (2nd of December or 12th of February, of 1981 or 1881). All examples from specimens in the Meise Botanic Garden herbarium.

Today, the ISO Standard 1806 is recommended for dates (19). This format can accommodate single dates and ranges, but also times and imprecise dates. However, there are still many local date formats which have changed with time (cf. Fig. 2). The popular spreadsheet program Microsoft Excel has several date-related issues in its basic programming, which can be the cause of corruption of date data. It fails to parse dates before 1900 in its own date format, as it stores dates internally as days since 1900-01-01 (<http://www.exceluser.com/formulas/earlydates.htm>). It also erroneously sees 1900 as a leap year, causing dates between 1900-01-01 and 1900-02-28 to be stored incorrectly

(<https://support.microsoft.com/en-us/help/214326/>). Finally, if during import or processing a certain column is formatted with the “Date” data type, partial dates with only a value for year may become corrupted as Excel will interpret them as the number of days since 1900-01-01. For example, the year 1989 will become 1905-06-11.

Another common cause of date corruption has been the frequent use of work-arounds to indicate an imprecise date, such as using the first or mid point of the year or month. Locally, these work-arounds are known by data managers, but they frequently find their way to aggregated data where they can be misunderstood (Fig. 3). For dates where the year is not known (e.g. the label indicates “October” or “summer”), various ad hoc solutions exist, such as a placeholder of “3000” on the DoeDat transcription platform. These partial dates still have some utility, such as phenology, but they are not compatible with ISO 1806.

From the perspective of database integrity and computational efficiency it would be ideal for dates to be stored as single dates in a single database column, but this is incompatible with date ranges and partial dates.

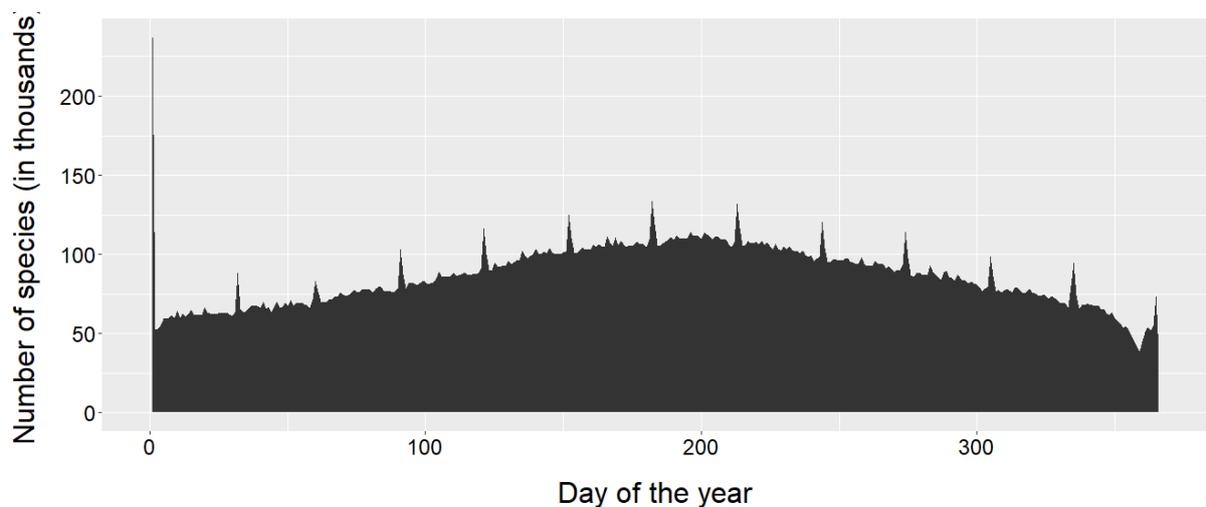


Fig. 3: Change in dates of observation for occurrence records on GBIF. Note the 12 spikes corresponding to the first day of each month, with a disproportionately large spike for the first of January. This is more than likely caused by many systems, including GBIF itself, storing partial dates as the first day of the month and only using the start date of a date range. Created from a snapshot of GBIF taken on 2019-04-06.

Dates of many events can be documented with a specimen. The collection date is the most obvious, but also the typification date, dates of expeditions, accession dates, determination dates and the date of transcription and digitization. Furthermore, there are other related dates, such as the birth and death dates of people, such as the collector and determiner, that can be used to validate these dates.

Some dates associated with specimens have no term in current standards. These include curatorial activities, such as received or communicated, as well as citation dates. By fully documenting the history of a specimen, the data becomes useful for more types of investigation and through cross-validation of the data the confidence in the data becomes stronger. The existence of dates and the length of date ranges are also useful metrics indicating the degree of transcription completeness.

Incidentally, the `dwc:eventDate` is one of a limited number of fields in Darwin Core that has a verbatim equivalent, `dwc:verbatimEventDate`. These verbatim fields are intended to be an exact transcription of what is written on the specimen to indicate to users how an interpreted standardized event date was derived (38). They can also be used to validate automatically generated data such as through OCR (Optical Character Recognition) or to store data which could not immediately be converted to a standard such as ISO 1806, which may be two different use cases (see Table 1).

Recommendations to standards organizations, developers and data scientists: All IT systems should support date ranges. Locally, they can be stored in a way that is easy to query, but for data exchange only ISO 1806 should be supported. Specimens without an explicit documented date of collection should be dated by other means, such as from itineraries of the collector. This step can be done automatically before the actual transcription takes place. However, interpretations of dates like this need to be documented. No digitised specimen record should lack some sort of date as, at the very least, the digitisation date is available. Even a broad date range, such as knowing the century (e.g. in the shape of 1901-01-01/2000-12-31), is useful for validation, and is sufficient for some use cases. Someone might be interested in all specimens in a certain collection from the 18th century, for instance. Many databases support generated columns, and this would be a way to maintain a single authoritative date field in a database, but also provide efficient indexing for date-based searches and sorting. On the other hand, dates which lack a year are not compatible with ISO 1806 and should never be present in a standardized date field. Though it can be added to the verbatim field.

All dates associated with a specimen can be cross-validated and should be consistent. For example, a specimen cannot be determined or used as a nomenclatural type before it is collected. A specimen cannot be collected before its collector is born. Furthermore, if dates are missing, then their possible range can be determined from all the other dates. If dates are inferred, this should be indicated in a human and machine readable manner to avoid creating a self-assuring cycle of validation.

A simple, machine readable controlled vocabulary is required to indicate the origin of an event date. Such a vocabulary might include the following elements.

- Verbatim transcription from the specimen label
- Interpretation from the specimen label
- Interpreted from date of expedition
- Date of a duplicate specimen
- Interpreted from the sequence of collector numbers
- Interpreted from biographical details
- Interpreted from literature

Dates are one of the most useful types of data associated with a specimen and also one of the easiest data elements to validate and cross-validate. Nevertheless, we have inherited a jumble of differently formatted dates in different implementations. This is one area where meticulous conformity to standards could make a significant contribution to interoperability.

3.4. Where: Geography

Geographic location is one of the three core elements of a natural history observation and it is critical to associate a specimen with other information, such as climate, soil and land cover. The vast majority of specimens were collected before the advent of global positioning systems and the data written on these specimens are susceptible to large errors in comparison to what we are now used to. In many countries, particularly in the second half of the 20th century, biological recording has been based on national standard grid systems. These grid systems are based on a particular geographic projection and coordinate system and have a specific notation (e.g. Ordnance Survey National Grid, Belgian IFBL grid system). For example, the Ordnance Survey National Grid of Great Britain uses a grid laid on Airy 1830 ellipsoid that uses the Universal Transverse Mercator coordinate system with an origin to the south-west of Great Britain. The grid cells are then identifiable by letters denoting the 100 × 100 km grid cells and numbers for the cells within these. For example, NZ2085 identifies a 1 × 1 km grid cell with easting and northings of its south-western corner of 420000,585000 to the nearest meter.

Grid coordinates are generally converted to a grid centroid coordinate and error radius before they are shared on GBIF. This is misleading and degrades the value of this geographic information. Unfortunately, it has not been appreciated that all coordinate systems refer to an isosceles trapezoid on the Earth's surface and not a true point. The conversion of grids to points is particularly regrettable because all points must be regridded to use them in species distribution models, but at that point the details of the survey have been lost as observations made in a grid will have been mixed with observations collected as points and radii. However, centroid-radius notation is so embedded in data collection that both systems must be accommodated.

Some geographic entities are clearly delimited and identifiable so can be specified with stable identifiers. These include political entities such as countries and counties, but also entities of physical geography, such as mountains, islands, rivers and other landmarks. The boundaries of these entities vary in how fixed they are and political boundaries tend to change with time. However, identifiers for geographic entities could play a much greater role in disambiguating places than is currently the case.

Location information is useful in validation of other specimen information, constructing collector itineraries and for ecological research. Coordinates are in principle a good identifier, but only if the coordinate system and datum are known. Coordinate precision is also critical, which if not given may be estimated based on the method of georeferencing used.

Georeferencing of specimens is a time consuming form of data enrichment. It can take considerable research into other specimens, databases, maps and literature to estimate the collection location of a specimen and the margin of error that is given to it. Yet, if this research is not documented and the provenance not recorded, it is possible that this work can be undone by someone not informed about the source of the georeferencing or an automated coordinate validation tool.

Recommendations to standards organizations and developers

Collection management systems and data standards should anticipate the use of local and national grid systems and have a means to validate them. Georeferencing tools should be available in the transcription system to ease and improve the transcription of geographic locations.

Recommendations to transcribers and data scientists

Local grid references should be documented in a verbatim coordinates field. National mapping agencies do change their coordinate systems, so clarity is also needed on which system is used. Users of Darwin Core should complete the `dwc:verbatimCoordinateSystem` and `dwc:verbatimSRS` fields.

Within institutional gazetteers stable identifiers should be linked to geographic entities. Sources of such identifiers are Geonames (<https://www.geonames.org/>), Getty Thesaurus of Geographic Names[®] (<https://www.getty.edu/research/tools/vocabularies/tgn/about.html>) and Wikidata (<https://www.wikidata.org/>). Use these identifiers to cross reference locations and to validate coordinates. Share these data openly so that they can be used by others to validate their locations and build upon your work. Where georeferencing decisions are potentially controversial explain your reasoning in georeference remarks.

3.5. Which: Collection number

Collection numbers or field numbers are identifiers for specimens or collecting events that are widely used in botany, and to a lesser extent in zoology. They are indicated on the physical specimen and often refer to an entry in a field notebook with more detailed information concerning the collection event. They may refer to a single specimen's collecting event or multiple specimens collected at the same time, in the same place and by the same people, for instance when duplicates are sent to multiple herbaria, also known as a gathering (36). In their simplest form, they may simply constitute numbers starting from 1 for the first specimen(s) collected. This means that there is no guarantee that these numbers are unique. Other information, such as who, where and/or when are required to uniquely identify a specimen and possibly its duplicates. Most collectors use their own format for their specimen numbers and there are no guarantees that these formats are utilized consistently. For instance, they may implement deviations of their standard approach as they encounter unusual situations.

Nevertheless, these numbers have more potential for analysis than simply a locally unique identifier (39). Often, specimen numbers are ordered by their time of collection, so that the order of collecting can be inferred and an itinerary approximated for the whole collecting trip. Missing data for certain specimens, such as when or where, can be inferred based on their position in the sequence of specimen numbers. However, this requires these numbers to be processed as numbers, whereas they often include additional non-numeric characters in various ways. These characters may be some sort of identifier for the collector or the collecting trip's location, but also part of the numbering protocol. Example collection numbers from the collection of Meise Botanic Garden include: 25, SP07L26, 4674_BIS, 262A, 699*, 1874/12 and DDV/77/108.

Previously, the recommendation was made to separate non-numeric prefixes and suffixes from the actual (numeric) numbers (23). This occurs in other systems as well, such as BG-BASE™, a collection management system designed for use by botanic gardens. The standards of Dwc and ABCD have only a single term for it: `dwc:recordNumber` and `abcd:CollectorsFieldNumber`. The problem with the split approach is that identifying the correct prefix and suffix is not always possible. It's also not clear within this approach how to deal with characters that are neither numbers nor letters. These may be used as delimiters (e.g. 1874/12), but also add another layer of uniqueness: e.g. 699* for a distinct (but possibly similar) specimen to the one with 699 as a number. Some numbers will also have a combination of characters that cannot easily be separated into prefix, number and suffix (e.g. SP07L26).

Recommendations for transcribers and standards organizations

Collection numbers today are mostly transcribed in a verbatim manner and, if they are interpreted in some way, there is no standard as to how they are supposed to be interpreted. This is partially a consequence of how poorly they can be standardized. We would suggest differentiating between a verbatim and an interpreted data field for this property. The interpreted field should include no characters other than alphanumeric ones. This approach was taken in a previous report (23) to improve finding matches between different transcriptions of the same specimen and should do the same for finding matches between identical numbers on different specimens and related numbers on similar specimens. This would facilitate matchmaking more than splitting up the data, as it reduces the interpretation made by the transcriber in how the split has to be made.

3.6. Who: People

Many people can be associated with a specimen: the collector, curator, determiner, annotator, mounter, transcriber, digitizer etc. For many reasons, these people are important to science. Knowing the person gives a degree of credibility to the specimen and its identity. The biographical data of the people can help validate data, but also credit the people for the work they have done. People often work as teams and this should be documented as well. Indeed, the order in which people's names are written is important and needs to be maintained. The whole name of a person is relevant, including titles, prefixes and suffixes. These can be used to determine the gender, qualifications, relationships, organizational membership and profession and so are invaluable for disambiguation. For a specimen's collector, ABCD has a "GatheringAgentsText" field, where full name details could be written, but Darwin Core lacks a verbatim field for the collector or any other person associated with the specimen. In general, people are identified more completely and unambiguously on other academic and creative works, such as publications.

Recommendations for transcribers and standards organizations

Teams should always be broken down into individuals and their sequence preserved explicitly. Where available, the full verbatim name and the interpreted name should be recorded. Also, where available, people should be disambiguated with unique identifiers that link to their biographies.

Recommendations to software developers

Data entry systems should cross validate data at the point of entry, such as cross referencing collector biographies with collection date. Transcription systems should provide supplementary information to the transcribers to make informed decisions when trying to disambiguate people.

4. Discussion

There are several reasons why it is important to improve the quality of transcribed label data and standardize it across institutions. Firstly, there is a large amount of time and money invested in transcription, whether through creation of citizen science crowdsourcing platforms or commercial transcription. Secondly, to fulfil the aims of digitization we need to provide the data that users need in a format suitable for their analysis. This inevitably means ensuring interoperability with other systems. Thirdly, once transcribed, these data are intended to last a long time and they will hopefully be curated and improved. Lastly, perhaps the most dynamic post-transcriptional addition to a specimen record will be linking it to other information on taxa, people, other specimens, geography etc. The ability to link data such as these is directly related to our ability to identify these entities clearly on labels.

A globally linked infrastructure of specimens is foreseeable in the near future (40). We already have the Global Biodiversity Information Facility where much of these data are available. However, the numerous papers on data cleaning and data quality attest to the need for further standardization and improvement. The responsibility for such improvements is shared by many institutions, professions and individuals, but in all cases there must be a collaborative effort to work with standards and improve them.

5. Funding

This work was supported by the ICEDIG project (*Innovation and Consolidation for large scale digitisation of natural heritage*), funded by the Horizon 2020 Framework Programme of the European Union, grant agreement number 777483.

6. Acknowledgements

The authors thank Tim Robertson of the Global Biodiversity Information Facility for his help in the production of a figure and the staff and volunteers of Digivol, DoeDat, Die Herbonauten, Les Herbonautes and Notes from Nature.

7. References

1. Ariño, A. H. (2010) Approaches to estimating the universe of natural history collections data. *Biodivers. Informatics*, **7**, 81–92.
2. Lavoie, C. (2013) Biological collections in an ever changing world: Herbaria as tools for biogeographical and environmental studies. *Perspect. Plant Ecol. Evol. Syst.*, **15**, 68–76.
3. Vellend, M., Brown, C., Kharouba, H., et al. (2013) Historical ecology: Using

- unconventional data sources to test for effects of global environmental change. *Am. J. Bot.*, **100**, 1294–1305.
4. Groom, Q. J., O'Reilly, C. and Humphrey, T. (2014) Herbarium specimens reveal the exchange network of British and Irish botanists , 1856 – 1932. *New J. Bot.*, **4**, 95–103.
 5. Groom, Q. J. (2015) Piecing together the biogeographic history of *Chenopodium vulvaria* L . using botanical literature and collections. *PeerJ*, **3**.
 6. Rawal, D., Kasel, S., Keatley, M., et al. (2014) Herbarium records identify sensitivity of flowering phenology of eucalypts to climate: Implications for species response to climate change. *Austral Ecol.*, **40**, 117–125.
 7. MacLean, H., Nielsen, M., Kingsolver, J., et al. (2018) Using museum specimens to track morphological shifts through climate change. *Philos. Trans. R. Soc. B*, **374**.
 8. Schmitt, J., Cook, J., Zamudio, K., et al. (2018) Museum specimens of terrestrial vertebrates are sensitive indicators of environmental change in the Anthropocene. *Philos. Trans. R. Soc. B*, **374**.
 9. ABCD task group (2007) Access to Biological Collection Data (ABCD), Version 2.06. Biodiversity Information Standards (TDWG). <http://www.tdwg.org/standards/115>.
 10. Wieczorek, J., Bloom, D., Guralnick, R., et al. (2012) Darwin core: An evolving community-developed biodiversity data standard. *PLoS One*, **7**.
 11. iNaturalist.org (2018) iNaturalist Research-grade Observations. Occurrence dataset <https://doi.org/10.15468/ab3s5x> accessed via GBIF.org on 2018-07-20. .
 12. Wieczorek, J., Bánki, O., Blum, S., et al. (2013) Meeting Report : GBIF hackathon-workshop on Darwin Core and sample data (22-24 May 2013). *Standards*, **9**, 585–598.
 13. Remsen, D., Knapp, S., Georgiev, T., et al. (2012) From text to structured data : Converting a word- processed floristic checklist into Darwin Core Archive format. *PhytoKeys*, **9**, 1–13.
 14. Petersen, M., Glöckler, F., Kiessling, W., et al. (2018) History and development of ABCDEFG : a data standard for geosciences. *Foss. Rec.*, **21**, 47–53.
 15. Robertson, T., Döring, M., Guralnick, R., et al. (2014) The GBIF integrated publishing toolkit: Facilitating the efficient publishing of biodiversity data on the internet. *PLoS One*, **9**.
 16. Dillen, M., Groom, Q. and Hardisty, A. (2019) ICEDIG Deliverable 4.4: Interoperability of Collection Management Systems. *ICEDIG Deliverable 4.4: Interoperability of Collection Management Systems*; (2019) .
 17. Gueta, T. and Carmel, Y. (2016) Quantifying the value of user-level data cleaning for big data: A case study using mammal distribution models. *Ecol. Inform.*, **34**, 139–145.
 18. Mathew, C., Güntsch, A., Obst, M., et al. (2014) A semi-automated workflow for biodiversity data retrieval , cleaning, and quality control. *Biodivers. Data J.*, **2**.
 19. Costello, M. J. and Wieczorek, J. (2014) Best practice for biodiversity data management and publication. *Biol. Conserv.*, **173**, 68–73.
 20. Faith, D. P., Collen, B., Ariño, A., et al. (2013) Bridging biodiversity data gaps : Recommendations to meet users ' data needs. *Biodivers. Informatics*, **8**, 41–58.
 21. White, E. P., Baldrige, E., Brym, Z. T., et al. (2013) Nine simple ways to make it easier to (re) use your data. *Ideas Ecol. Evol.*, **6**, 1–10.
 22. Owen, D., Groom, Q., Hardisty, A., et al. (2019) Methods for Automated Text Digitisation. ICEDIG Deliverable 4.1. *Methods for Automated Text Digitisation. ICEDIG Deliverable 4.1.*; (2019) .
 23. Phillips, S., Dillen, M., Groom, Q., et al. (2019) Report on New Methods for Data Quality Assurance, Verification and Enrichment. ICEDIG Deliverable 4.2. *Report on New Methods for Data Quality Assurance, Verification and Enrichment. ICEDIG Deliverable 4.2.*; (2019) .
 24. Sweeney, P. W., Starly, B., Morris, P. J., et al. (2018) Large-scale digitization of herbarium specimens : Development and usage of an automated , high-throughput

- conveyor system. *Taxon*, **67**, 165–178.
25. Veiga, A. K., Saraiva, A. M., Chapman, A. D., et al. (2017) A conceptual framework for quality assessment and management of biodiversity data. *PLoS One*, **12**, 1–21.
 26. Wickham, H. (2014) Tidy Data. *J. Stat. Softw.*, **59**.
 27. Penev, L., Mietchen, D., Chavan, V. S., et al. (2017) Strategies and guidelines for scholarly publishing of biodiversity data. *Res. Ideas Outcomes*, **3**, 1–12.
 28. Springmann, U., Reul, C., Dipper, S., et al. Ground Truth for training OCR engines on historical documents in German Fraktur and Early Modern Latin. *arXiv Prepr.*
 29. Groom, Q. J. (2015) Using legacy botanical literature as a source of phytogeographical data. *Plant Ecol. Evol.*, **148**, 256–266.
 30. Abarenkov, K., Tedersoo, L., Nilsson, R. H., et al. (2010) PlutoF — a Web Based Workbench for Ecological and Taxonomic Research , with an Online Implementation for Fungal ITS Sequences. *Evol. Bioinforma.*, **6**, 189–196.
 31. Suhrbier, L., Kusber, W.-H., Schöpe, O., et al. (2017) AnnoSys — implementation of a generic annotation system for schema-based data using the example of biodiversity collection data. *Database*, 1–20.
 32. Knapp, S., Vincent, S., Arvanitidis, C., et al. (2019) Access to Natural History Collections – from SYNTHESYS to DiSSCo. *Biodivers. Inf. Sci. Stand.*, **3**.
 33. Chicago Manual of Style (2017) The Chicago Manual of Style, 17th ed. *The Chicago Manual of Style, 17th ed.*; Chicago: University of Chicago Press, (2017) .
 34. Dillen, M., Groom, Q., Chagnoux, S., et al. (2019) A benchmark dataset of herbarium specimen images with label data. *Biodivers. Data J.*, **7**.
 35. Brummitt, R. K. and Powell, C. E. (1992) Authors of plant names. *Authors of plant names*; Royal Botanic Gardens KEW., (1992) .
 36. Turland, N., Wiersema, J., Barrie, F., et al. (2018) International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code) adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017. *International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code) adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017.*; Regnum Veg.; Glashütten: Koeltz Botanical Books, (2018) .
 37. ICZN (1999) International Code of Zoological Nomenclature. <https://www.iczn.org/the-code/the-international-code-of-zoological-nomenclature/the-code-online/>.
 38. Tegelberg, R., Haapala, J., Mononen, T., et al. (2012) The development of a digitising service centre for natural history collections. *Zookeys*, **209**, 75–86.
 39. Nicolson, N., Paton, A., Phillips, S., et al. (2018) Specimens as research objects : reconciliation across distributed repositories to enable metadata propagation. *2018 IEEE 14th International Conference on e-Science (e-Science)*, pp. 125–135.
 40. Hobern, D., Baptiste, B., Copas, K., et al. (2019) Connecting data and expertise : a new alliance for biodiversity knowledge. *Biodivers. Data J.*, **7**.