

# Specimens as research objects: reconciliation across distributed repositories to enable metadata propagation.

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**Abstract**—Botanical specimens are shared as long-term consultable research objects in a global network of specimen repositories. Multiple specimens are generated from a shared field collection event; generated specimens are then managed individually in separate repositories and independently augmented with research and management metadata which could be propagated to their duplicate peers. Establishing a data-derived network for metadata propagation will enable the reconciliation of closely related specimens which are currently dispersed, unconnected and managed independently. Following a data mining exercise applied to an aggregated dataset of 19,827,998 specimen records from 292 separate specimen repositories, 36% or 7,102,710 specimens are assessed to participate in duplication relationships, allowing the propagation of metadata among the participants in these relationships, totalling: 93,044 type citations, 1,121,865 georeferences, 1,097,168 images and 2,191,179 scientific name determinations. The results enable the creation of networks to identify which repositories could work in collaboration. Some classes of annotation (particularly those regarding scientific name determinations) represent units of scientific work: appropriate management of this data would allow the accumulation of scholarly credit to individual researchers: potential further work in this area is discussed.

**Index Terms**—research objects, data citation, record linkage, annotation

## I. INTRODUCTION

Botanical specimens are core research objects in the science of taxonomy (the naming of biological organisms), stored for long term consultation in institutional repositories and referenced in academic works. Worldwide there are 3,001 herbaria (botanical specimen repositories), containing 387,007,790 specimens - representing collections gathered over hundreds of years [1]. Due to their physical characteristics (flattened, dried plant material is typically mounted on a large sheet of paper, stored inside a paper folder) and their management as a long term, consultable record, specimens act as vehicles for the communication of results and theories, as researchers annotate the paper sheet underlying the specimen. Annotations placed on specimen sheets are public and available for use by other researchers, this public yet potentially unpublished status is discussed in [2].

Taxonomic researchers populate institutional repositories by conducting collection events (usually field-based) which generate multiple specimens. Recommended botanical practice is for a single collection event to generate five to six specimens, which will be deliberately distributed to separate institutional repositories. Physical distribution of specimens has three main goals: to maximise access - researchers working on their local flora should be able to consult the relevant specimens in their national herbarium, to provide resilient storage - duplicate specimens insure against disastrous loss of a single repository, and to ensure efficient use of storage space within repositories [3]. Duplicate specimens are also used in genetic analyses: if the samples were collected from separate individuals, the duplicate set can be used to assess genetic diversity across the sampled population. Scientific theories regarding the recognition of species and their interrelationships are developed by researchers as they work with the specimens, which are traditionally accessed either by loan or by visits to institutions; more recently specimen digitisation initiatives have enabled online access to specimen metadata records and high quality images, this simplifies search and retrieval of specimens and associated metadata, and allows some level of specimen examination to be conducted remotely. Independent creation and management of metadata for specimen duplicates can be inefficient (metadata creation is repeated unnecessarily), and inadvertently misleading (metadata diverges between different members of a specimen duplicate group).

One particular class of research annotation is the application of a scientific name to the specimen: this may be an existing name, or the researcher may recognise that the specimen represents a new species. Species description in plants is ongoing with circa two thousand new plant species described each year [4]. When a new species is described, one specimen is chosen as a physical representation of the otherwise abstract scientific name. Specimens which formally represent a scientific name are called type specimens; the selection of these is called type citation. When a specimen is cited as a type, all peers (“duplicates”) which are generated from the same collection event - but which may be stored and managed remotely, in

separate repositories - are also considered to have type status. New scientific names are created via a formal publication process governed by the International Code of Nomenclature for algae, fungi and plants [5]. The majority of new species are discovered from historic specimens already lodged within specimen repositories, being formally described years after collection [6]. The use of duplicate specimens as vehicles for the communication of results is illustrated by the historic use of “*exsiccatae*”. These are uniform specimen sets with information displayed on printed labels distributed to multiple herbaria, and until 1953 were considered a valid publication mechanism for new scientific names [7] [5].

Taxonomists consider type specimens to be the most valuable specimens in a repository, and management reporting often includes both the total number of specimens held and the number of type specimens. The first major digitisation effort in botany (JSTOR Global Plants Initiative) focussed on the digitisation of type specimens across more than 300 institutions in over 70 countries [8]. In addition to reporting on the total numbers of specimens and types housed in an institutional repository [9], managers are also interested in the numbers of new type citations published each year as a metric of on-going research use of their specimens [10]. Some natural history institutions have experimented with bibliometrics to quantify use of their specimens in a publication context [11].

In addition to their core use in the science of taxonomy, specimens provide physical “what, where, when” evidence and are used for a wide range of scientific applications such as species distribution modelling [12]. Specimen exchange networks have also been used for historical social network analysis [13]. These applications are generally dependent on aggregations of specimen metadata mapped to a common data standard and sourced from many different institutional repositories.

**Problem statement** Despite the widespread recognition that botanical specimens form a global collection, there is currently no flow of data from the point of creation (via the field collection event) to the generated specimens wherever they may be located for long term storage. Despite advances in the mobilisation and standardized representation of specimen metadata across the different specimen repositories, duplicate specimens have so far gone undetected, with metadata records for duplicates appearing unlinked in aggregated datasets. The main data elements needed to assess specimens as potentially arising from a shared collection event - collector name, along with the collector’s recordnumber and eventdate - are not formally managed. These missing links mean that valuable research annotations and type citations are not easily shared between repositories, and impacts all downstream users of specimen data: taxonomic researchers working with individual specimens are unable to benefit from knowledge added elsewhere, leading to misinterpretation due to inaccurate and/or out of date naming, and users working with large aggregations of specimen data can find that specimen number estimates are overstated, as their datasets contain hidden duplicates.

The research described in this paper applies machine learn-

ing to a set of aggregated specimen metadata to identify and reconcile the collectors responsible for the creation of specimens, enabling the detection and linkage of specimen duplicates generated from the field work of the identified collectors. In contrast to existing work on annotation propagation - which has focussed on potential changes in working practices and tools and techniques to enable and incentivize this [14] [15] - this work applies these techniques to a dataset of existing digitally available specimen data in order to calculate the numbers of existing metadata elements and annotations which may be propagated between separate institutional repositories.

The remainder of this paper is structured as follows: a background section further introduces the problem domain with an explanation of the specimen life cycle and the kinds of annotations applied at each stage, and worked examples of distributed specimen sets whose members are independently managed at different institutions. Materials and methods describes the application of a machine learning process to a dataset of specimen data from the Global Biodiversity Information Facility to identify specimen duplicates. Criteria for the identification and assessment of duplicate sets are proposed. The resulting specimen duplicate analysis is used to answer the following questions:

1. How many distributed, independently managed specimens can be reconciled across separate institutional repositories and linked as generated products of a common collection event?
2. How many metadata elements and research annotations can be propagated between institutional specimen repositories?
3. Can specimen duplicate linkages be used to infer network relationships between institutional repositories, which institutions are most frequently linked and do sub-communities or cliques exist in the inferred network?

Preliminary results are presented and ideas for expansion and future work are proposed.

## II. BACKGROUND

This section outlines the stages in the specimen life cycle, and indicates relevant projects at each stage.

**Collection and storage:** these activities represent standard practice across the specimen repositories

- **Collection:** material is gathered from the field and details of the collection locality (associated species, geology, habitat etc) are recorded in the collectors field notebook. The collectors recordnumber provides the cross-reference between the data recorded in the field notebook and the physical material collected, this is usually a sequential number managed individually by the collector.
- **Accessioning:** material is received by a specimen repository and prepared for long term storage, including mounting on a sheet of paper (for dried specimens).

**Digitisation:** due to the number of specimens held in the global collection, digitisation is incomplete, and is progressing through a variety of cross-cutting institutional, regional,

international and thematic projects. The JSTOR Global Plants Initiative selected a particular class of specimens for digitisation (type specimens) across 300 institutions [8], other projects have been set up to digitise all specimens gathered from a particular country to enable data repatriation, as in the Brazilian REFLORE programme [16] and to digitise specimens held within a particular country as in the US National Science Foundation funded Advancing Digitisation of Biocollections programme [17]. These latter projects show a trend of government funding for digitisation, recognising that these are part of the national scientific infrastructure [9] [18].

- **Databasing:** details of the specimen (metadata) are added to an institutional data repository.
- **Aggregation:** databased records can be mapped to a data standard (e.g. Darwin Core [19]) and shared with aggregation projects. The Global Biodiversity Information Facility is an intergovernmental organisation that aggregates specimen-derived species occurrence records (alongside records from observations) to facilitate scientific research, iDigBio is a US based aggregator which focusses only on specimen derived data.
- **Georeferencing:** the metadata record in the institutional repository can have latitude and longitude added (this may be a costly step for historic records where the original collection locality is only a textual description of the place). Economies of scale are possible if records can be ordered so that similar places are georeferenced together [20] [21].
- **Imaging:** the specimen is imaged and a reference to the image is added to the metadata. If the specimen metadata is shared with an aggregator the digital image may also be mobilised.

Depending on their range of holdings, some institutions are involved in multiple digitisation projects, others not at all. With technical advances in digitisation and the setup of high-throughput imaging facilities, some of these steps may be performed out of sequence - if the digitisation project is of a sufficient scale, it may be cost effective to rapidly image the specimens first and perform the metadata capture later, from a high quality digital image [22] [23] [24].

**Use as a research object:** these steps outline the use of the specimen as a taxonomic research object. The use of specimens as a data source for computational applications such as species modelling is covered in the digitisation steps above, digitisation steps also facilitate discovery and access of specimens for taxonomic research. Annotation mobilisation work has focussed on tooling for the collection and propagation of newly generated annotations, including the projects AnnoSys [14] and Filtered Push [15]. There has also been an effort to standardise the citation of specimens so that different repositories use a common HTTP URI based naming convention by which their digital metadata records can be accessed [25]. By convention, the citation of specimen records irrespective of digitisation status is made by stating the collector name, number and date, along with the herbarium

code [1] in which the physical specimen may be found. These kinds of references can be found throughout the botanical literature, and examples are shown in the worked examples in the next section.

- **Determination:** the specimen is labelled with a scientific name, the date and the name of the researcher who made the determination are also added.
- **Citation:** the specimen is cited in a published academic work (e.g. to evidence the presence of a species in a geographic region).
- **Type citation:** the specimen is referenced as a type specimen in a published academic work to create a new species name.

The long term creation of a global network of specimen repositories, the more recent efforts to enable virtual access to specimens and their metadata, and the practice of sharing research annotations all fit well with the FAIR principles for scientific data management [26]: ensuring that the metadata and specimens on which scientific analyses are based are Findable, Accessible, Interoperable and Retrievable.

#### A. Worked examples

This section is intended to illustrate the problem statement - that specimen duplicates are (1) widely present in distributed specimen repositories, (2) unidentified in data aggregations built by combining specimen datasets and (3) that specimen metadata attached to derived specimens generated from a single source can diverge due to separate and independent data curation practices. Two examples have been selected, representing the two extremes of species description citing botanical specimens: species discovery in-field formalised by rapid publication just one year after collection, and species discovery in-repository with formalised description decades after field collection. A considerable proportion of new species are described from material already collected and stored in specimen repositories [6]. The second example shows a species description occurring 46 years after the field collection of the plant material on which it is based.

For each example we will assemble a dataset of potential specimens, which is constructed as the superset of the specimens referenced in the literature (which may or may not be digitised) and the relevant specimen records found in digital form in a data aggregator. We then examine the metadata attached to the specimens, showing where this has diverged due to independent management. These are shown in table I.

1) *Example 1: Rapid publication of species discovered in-field:* See table I, example 1. (Table data source: gbif.org)

The publication data (displayed below) shows that there are at least 9 specimen duplicates, stored in different institutional repositories, indicated by the capitalised alphabetic herbarium codes (WTU, BH etc [1]). The exclamation mark (!) after a code is a convention to indicate that the author has actually seen the specimen. In this case the author is also the collector of the specimen, so all are listed as having been seen.

*Sedum citrinum* Zika, *sp. nov.* **Type:**—UNITED STATES. California: Del Norte County, ridge 1.4 air

TABLE I  
WORKED EXAMPLES

recordedBy	recordNumber	eventDate	scientificName	institutionCode	referenced in publication	digitised	typestatus	georeferenced	imaged
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	BH	✓	-	-	-	-
Zika, Peter F.	26185	2013-06-09	Sedum citrinum Zika	CAS	✓	✓	✓	✓	-
Peter F. Zika	26185	2013-06-09	Sedum citrinum Zika	CAS-BOT-BC	-	✓	-	-	-
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	CHSC	-	✓	-	✓	-
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	GH	✓	-	-	-	-
Zika, P.F.	26185	2013-06-09	Sedum citrinum Zika	K	-	✓	✓	-	✓
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	MO	✓	-	-	-	-
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	NY	-	✓	✓	✓	✓
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	OSC	✓	-	-	-	-
Peter F. Zika	26185	2013-06-09	Sedum citrinum Zika	RSA	✓	✓	-	✓	-
Peter F. Zika	26185	2013-06-09	Sedum citrinum Zika	UC	✓	✓	-	✓	-
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	US	✓	✓	✓	-	✓
P. F. Zika	26185	2013-06-09	Sedum citrinum Zika	WTU	✓	-	✓	-	-
P. C. Hutchison & J. K. Wright	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	F	✓	✓	✓	-	✓
P. C. Hutchison & J. K. Wright	5738	1964-06-19	Solanum aligerum Schltdl.	F	-	✓	-	-	-
Hutchison, P.C.	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	K	✓	✓	✓	✓	✓
Paul C. Hutchison—J. Kenneth Wright	Hutchison 5738	1964-06-19	Solanum cutervanum Zahlbr.	MO	-	✓	-	-	-
P. C. Hutchison	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	NY	-	✓	✓	✓	✓
P. C. Hutchison	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	NY	-	✓	✓	✓	✓
P.C. Hutchison & J.K. Wright	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	P	✓	-	-	-	-
P. C. Hutchison & J. K. Wright	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	US	✓	-	✓	-	✓
P.C. Hutchison & J.K. Wright	5738	1964-06-19	Solanum sanchez-vegae S.Knapp	USM	✓	-	-	-	-

km north of South Red Mountain, 1050 m, 9 June 2013, *P. F. Zika* 26185 (holotype: WTU!; isotypes: BH!, CAS!, GH!, MO!, OSC!, RSA!, UC!, US!). [27]

There are 8 digitally available records for this set of specimens, drawn from 8 separate institutional specimen repositories. These are independently managed and not interlinked. Despite being generated from the same collection event, the specimen metadata show variation due to isolated management in separate repositories: 5 of the 8 are georeferenced, 4 of the 8 specify a type status and 3 of the 8 have an associated image. We can therefore calculate that the group contains propagable annotations for georeferences, typestatus and image (i.e. that for each annotation class, the group contains records with and without the annotation set, meaning that the annotation could be propagated from the specimens with the annotation to their peers without it). Of the digitised specimens in the group: 3 could receive a georeference, 4 could receive a type status annotation and 5 could be linked to an associated image. The creation of a specimen group could also make the initial creation of the specimen records for the currently undigitised members more efficient, by using existing data as a starting point rather than independently re-creating it.

2) *Example 2: Species discovery in-repository:* See table I, example 2. (Table data source: gbif.org)

The publication data (displayed below) shows that there are at least 6 specimen duplicates, stored in 5 different institutional repositories. The author has supplied a numeric identifier for some of the specimens (shown in square brackets), to help the reader locate the relevant records in specimen repository and / or its associated metadata catalogue(s).

*Solanum sanchez-vegae* S.Knapp, *sp. nov.* [urn:lsid:ipni.org:names:77103635-1] **Type:** Peru. Amazonas: Prov. Chachapoyas, W side of Cerros Calla-Calla, 45 km above Balsas, mid-way on road to Leimebamba, 3100 m, 19 Jun 1964, *P.C. Hutchison & J.K. Wright* 5738 (holotype,

USM; isotypes, F [F-163831], K [K000545365], P [P00549320], US [US-246605], USM). [28]

There are 7 digitally available records for this set of specimens, from 5 separate institutional specimen repositories. These are independently managed and not interlinked. As per the first example, despite being generated from the same collection event, the specimen metadata show variation due to isolated management in separate repositories, with all annotation categories holding inconsistent information: 3 of the 7 are georeferenced, 5 of the 7 specify a type status, 5 of the 7 have an associated image and 2 of the 7 have an outdated scientific name. We can therefore calculate that of the 7 digitised specimens in the group: 4 could receive a georeference, 2 could receive a type status annotation and 2 could be linked to an associated image.

These two different examples both show that the separate specimen records held in different specimen repositories hold divergent metadata, and that there is the potential for metadata propagation between members of a specimen group. Specimen groups can be identified by grouping on the collector, their field-assigned record number and the eventdate, but this is non-trivial due to the variation in the recording style of the collecting team (shown in the recordedBy column), as duplicate records have been independently digitised to different data standards in different institutions and projects.

### III. MATERIALS AND METHODS

#### A. Data

A dataset of specimen data relating to vascular plants (those with specialised tissues for the transport of water, encompassing ferns and allied groups, and all seed plants) was downloaded from GBIF [29] in Darwin Core [19] archive format. This was input into a data mining process based on the clustering technique DBSCAN in order to detect collector entities [30]. Specimen records are eligible for data mining if they have a numeric component in their *recordnumber* (the sequential number managed by an individual collector and assigned to field collection events), a precise date recorded to

the level of day (*eventdate*), and a collector name (*recordedby*). The data mining process augments the specimen dataset with a numeric identifier for the primary collector of the specimen represented in the metadata record. This allows data to be grouped as the product of the work of a particular collector, irrespective of the lexical variation in the transcription of the collectors names.

#### B. Detection of duplicate groups

A group of specimens are asserted to be generated from a single collection event if they share the same collector identifier (the results of the collector data mining exercise), *eventdate* (when the field collection event was carried out) and collector-assigned record number. The record number has any alphabetic prefixes stripped from the value - this normalises values which are sometimes presented with the surname of the collector in the *recordnumber* field (see the worked example in I).

See procedure listing `detectDuplicateGroups`. The input into this algorithm is a tabular data structure where each row represents a specimen, with fields for *collector\_id*, *eventdate* and *recordnumber*.

#### C. Establishing a confidence measure

A confidence measure is applied to candidate duplicate groups by examining the range of variation in fields within the duplicate group. Three assessments are made, a spatial assessment using the *countrycode* field (duplicate specimen records originating from the same collection event should logically be located in the same country) and two taxonomic assessments using the *order* and *family* fields. Biological taxonomy uses a hierarchical system, where species are arranged into families, and families into orders. Although a specimen may be re-determined (have different scientific names applied to it) during its lifetime in a specimen repository, it is less likely to be re-determined across higher taxonomic boundaries. These flags detect variation in these higher-level categories within a duplicate group.

Three Boolean flags were created (one for each assessment field), these were set to True if all members of the candidate duplicate group share the same value of the assessment field. All possible combinations of these three flags were used to assess the duplicate groups. Only duplicate groups meeting the most conservative assessment criteria (where all of the assessment flags are True, indicating no variation in these fields within the duplicate group) were carried forward for use in subsequent analyses.

See procedure listing `assessDuplicateGroups`. The input into this algorithm is a tabular data structure where each row represents a specimen, with fields for *duplicate\_group\_id*, *countrycode*, *order* and *family*. This is the labelled output from the preceding algorithm `detectDuplicateGroups`.

#### D. Assessing annotation status per specimen and detecting groups with uneven annotation statuses

Boolean flags were created to indicate if the specimen is georeferenced, if the specimen has an associated image, and

if the specimen is recorded as having type status. *Typestatus* values were used as described in [31].

For each annotation examined, two new Boolean fields were created on the aggregated dataset - these are set to True if *all* specimens in the duplicate group have the annotation set and if *any* specimens in the duplicate group have the annotation set. A group is said to have propagable annotations if it has any and not all annotations set for the specimens within the group. Two count fields were also created for each annotation, these were set to hold the number of specimens within the group with and without the annotation set. The number of specimens which could receive propagable annotations was determined by totalling the number of specimens within groups with propagable annotations which did not themselves have the annotation set.

See procedure listing `findPropagableAnnotations`. The input into this algorithm is a tabular data structure where each row represents a specimen, with a field for *duplicate\_group\_id* and a set of Boolean fields to indicate the presence of annotations on the specimen (*georeference*, *typestatus*, *image*). This is the assessed, labelled output from the preceding algorithm `assessDuplicateGroups`.

#### E. Repository relationship analysis

The sharing of specimens in a duplicate group implies a relationship between the two (or more) institutional repositories participating in the group. In this analysis, the data are reshaped to build a graph data structure where nodes are institutional repositories and links are created between a pair of nodes if the corresponding repositories share specimens in a duplicate group. The links are weighted by the number of groups shared. The resulting data structure is a weighted, undirected graph. This inferred network data structure is visualised in Gephi [32], using an OpenOrd [33] layout following modularity analysis [34] for community detection.

## IV. RESULTS

#### A. Data mining

The initial dataset downloaded from GBIF contained 63,492,620 records, of these 19,827,998 records were eligible to be input into the data mining process to detect the collector. The data mining process resulted in 19,489,798 specimen records being labelled with an identifier for the collector.

#### B. Duplicate identification and assessment

Of the 19,489,798 data mined records, 7,347,705 records participate in a duplicate relationship, forming 2,914,181 duplicate groups. All combinations of assessment flags with associated group and record counts are depicted in figure 1.

Only the subset of duplicate groups meeting the most conservative assessment criteria were used in subsequent analyses: 7,102,710 specimens in 2,823,651 groups. The sizes of the conservatively assessed duplicate groups are shown in figure 2.

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**Procedure** detectDuplicateGroups(Specimens)

---

**Input:** Specimens**Output:** LabelledSpecimenslet  $S$  be Specimens, the set of specimens to be groupedlet  $DuplicateGroups$  be  $S$  grouped by  $s.collector\_id$ ,  $s.eventdate$ ,  $s.recordnumber$ 

Apply an identifier to each group

```
for  $i \leftarrow 1$  to  $|DG|$  do
   $dg \leftarrow DG[i]$ 
  for  $s$  in  $dg$  do
     $s.duplicate\_group\_id \leftarrow i$ 
    LabelledSpecimens.append( $s$ )
  end
end
```

---

---

**Procedure** assessDuplicateGroups(LabelledSpecimens)

---

**Input:** LabelledSpecimens**Output:** AssessedLabelledSpecimenslet  $DuplicateGroups$  be LabelledSpecimens grouped by  $duplicate\_group\_id$ 

```
for  $dg$  in  $DuplicateGroups$  do
  for  $assessment\_field$  in {countrycode, order, family} do
    Create a new boolean field [assessment]_conservative, which is set to True
    if all members of the duplicate group share a single value for this field
     $assessment\_values \leftarrow []$ 
    for  $s$  in  $dg$  do
      |  $assessment\_values.append(s[assessment\_field])$ 
    end
     $dg[assessment\_conservative] \leftarrow |assessment\_values| == 1$ 
    Copy the assessment flag down to specimen level
    for  $s$  in  $dg$  do
      |  $s.assessment\_conservative \leftarrow dg.assessment\_conservative$ 
      | AssessedLabelledSpecimens.append( $s$ )
    end
  end
end
```

---

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**Procedure** findPropagableAnnotations(assessedLabelledSpecimens)

---

**Input:** AssessedLabelledSpecimens**Output:** AssessedLabelledCountedSpecimenslet  $DuplicateGroups$  be AssessedLabelledSpecimens grouped by  $duplicate\_group\_id$ 

```
for  $dg$  in  $DuplicateGroups$  do
  let  $s$  be the set of specimens included in  $dg$ 
  Annotation fields are Boolean flags indicating if the specimen has this annotation set
  for  $annotation\_field$  in {georef, tpestatus, image} do
     $dg[annotation\_propagable] \leftarrow any(s.annotation\_field)$  and not  $all(s.annotation\_field)$ 
    Copy the propagable flag down to specimen level
    for  $s$  in  $dg$  do
      |  $s.annotation\_propagable \leftarrow dg.annotation\_propagable$ 
      | AssessedLabelledCountedSpecimens.append( $s$ )
    end
  end
end
```

---

Fig. 1. Assessment flag combination counts

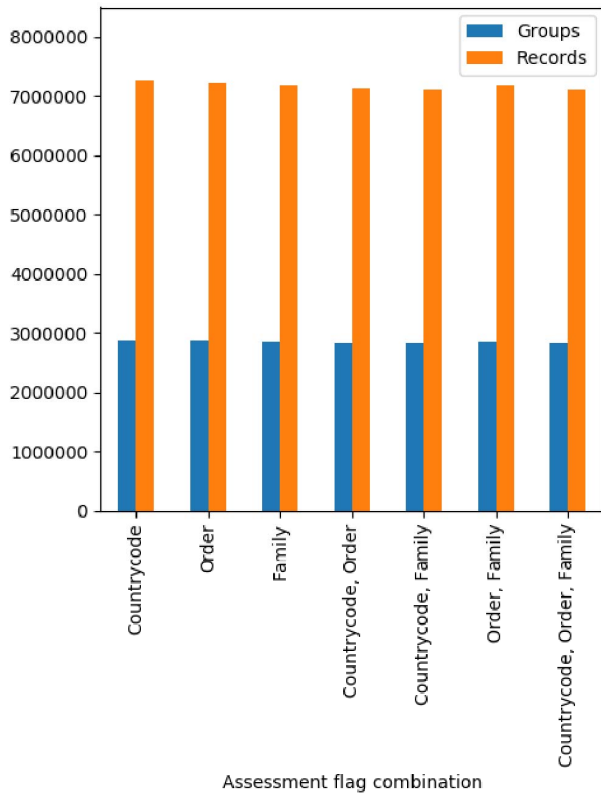
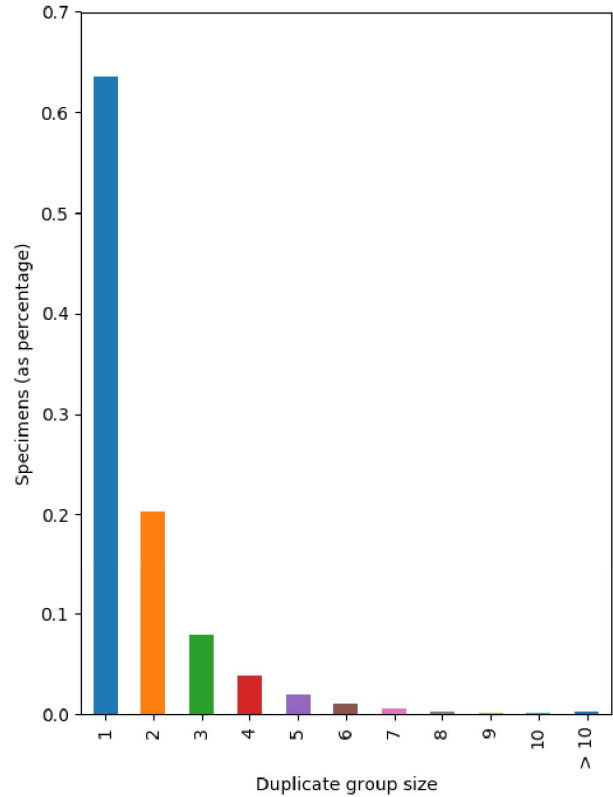


Fig. 2. Duplicate group sizes



### C. Propagation of annotations

Members of duplicate sets are located at different institutional repositories and therefore may have been curated differently. Reconciliation of duplicate sets allows the propagation of several classes of annotations - georeferences, type citations, specimen images and determinations - between holders. Of the conservatively assessed duplicate sets:

- 93,044 specimens in 54,435 groups could receive a type citation from a peer in their duplicate group
- 1,121,865 specimens in 782,655 groups could receive a georeference from a peer in their duplicate group
- 1,097,168 specimens in 758,416 groups could be linked to an associated specimen image from a peer in their duplicate group
- 2,191,179 specimens are in 792,274 groups which have multiple scientific names within the group (indicating uneven scientific name determination amongst the members of the specimen duplicate group)

### D. Repository relationship analysis

The relationship graph derived from duplication links at institutional level (see figure 3) comprises 260 nodes (institutions) and 6,588 weighted edges (relationships between institutions, based on co-participation in a specimen duplicate group, weighted by the number of co-occurrences). The graph

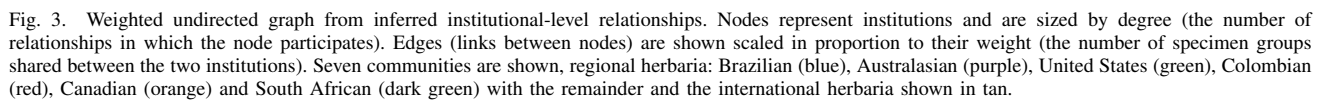
was found to contain seven communities: Brazilian herbaria, Australasian herbaria, the regional herbaria in the United States, Colombian herbaria, Canadian herbaria, South African herbaria, and the internationally focussed herbaria found in North America and Europe.

## V. DISCUSSION

### A. Duplicate identification and assessment

A considerable number of duplicate groups were found in the datamined dataset, and these appear relatively stable across the different assessment flag combinations (see 1), permitting the reconciliation of many specimen duplicates between different specimen repositories. The reconciliation of specimen duplicate groups show that many metadata annotations could be propagated between specimen repositories. As these annotations represent both the most expensive parts of the digitisation process (georeferencing) and the most valuable kind of usage citation (type citation), mobilising these between partners would reduce data management costs, improve the utility of the digitised specimen data and improve institution level data usage reporting. It is only possible to supply an estimate range for the cost saving of mobilising such a large number of georeferences. Standard procedures tend to batch work by locality, which improves georeferencing speed by focussing on a particular area. A software description paper







reports a project georeferencing at a rate of 16.6 ( 8.3) georeferences per hour and a further separate project achieving a doubling of this rate [20]. A herbarium type specimen focussed project reported “whole process of georeferencing the ca. 3400 Type specimens took eight months (appx. 100 specimens per week)” [21]. It seems that there are significant savings that could be made using the results of this research, given that the number of propagable georeferences is counted at around a million.

### B. Repository relationship analysis

The different repositories represented in the dataset are well connected. Viewed at an institutional level, the low incidence of isolated cliques shows healthy inter-institutional working relationships in botany. There are strong links among regionally focussed herbaria in the United States and Australasia. The interconnections between the Brazilian herbaria and their international counterparts show the volume of work that has been focussed on the world’s most mega-diverse country [35] and also suggest that the data repatriation projects which aim to mobilise data held out of country [16] have been successful. Quantifying the links between specimen repositories enables evidence drawn from specimen duplicate sharing to be used when building project collaborations. Sets of institutions could be selected to maximise overlap or to maximise complementarity. Better sharing of specimen data between institutions facilitates community curation and helps to reduce data management costs.

## VI. FURTHER WORK

There are several areas in which future work could develop this analysis including further refinement of the analytical approach to cover more data sources, community assessment of interlinked repositories and quality control of annotations by comparison between duplicates. It may be useful to separate future work into two streams: a stream regarding data management and refinement of the data pipeline, and a more conceptual stream regarding implications of the results. An example from each area is outlined here: investigation of the reasons why specimens are not currently identified as duplicates - singleton analysis - and further work on the research recognition of determination annotations made on specimen objects.

Singleton specimens may be due to uneven digitisation and / or lack of participation in data mining process, rather than true singletons, further data analysis work is required to investigate this. It should be possible to use the results from the data mining process to calculate for each collector the likely number of specimens gathered at each collecting event. These numbers would give us a potential view on the number of currently un-digitised specimens, and among these, the likely location of duplicates (in which institutional repositories will they be found).

Traditional taxonomic activity can be separated into three phases - collection of specimens, labelling specimen with names and formal publication of results. The first two phases

are absent from traditional publication focussed career credit, yet generate long-term research-grade outputs which may be consulted and referenced by others. As these outputs are now mobilised and used much more widely (due to data mobilisation via the internet) there have been calls for these to be included in the career assessment system for taxonomists [36]. If we recognise that specimens are persistent research objects, which can be uniformly accessed [25], then the labelling of specimens with scientific names could each be considered to meet the minimum criteria for a nanopublication - the smallest unit of research work [37] and credited to individual researchers.

## VII. CONCLUSION

Specimens are research objects which are managed for long term consultation, facilitate scientific discovery and act as vehicles for the dissemination of results. This paper demonstrates that specimens form a shared global resource, and that fragmented information management can be overcome by the reconciliation of specimen duplicates across institutional boundaries. Specimen digitisation efforts and work to define standard representations of digitised metadata have built a critical mass of computable information, which can be used as the input into this process. Identification of specimen duplicates allows quantification of potential specimen metadata exchange between institutional specimen repositories. The result of implementing this data exchange would be to develop and strengthen ties between institutional repositories, improve efficiency of data curation (by eliminating repeated work such as specimen georeferencing) and to improve the metadata holdings and reporting figures for institutional repositories. Conceptually, specimens should be recognised as a unit of research work more granular than the scientific paper, but fulfilling the same functions - communication of results and establishment of a long term record. This recognition of the specimen as a research object would eventually allow the annotation of specimens to be regarded as research work and credited to individual researchers. This may start to address some concerns recently voiced with regard to the many phases of research work conducted by taxonomists which remain absent from publication-focussed career metrics [36].

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