IMPLEMENTING THE SPECIFY 6 DATABASE PLATFORM IN THE INVERTEBRATE PALEONTOLOGY COLLECTION AT THE FLORIDA MUSEUM OF NATURAL HISTORY

By

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To the memory of my grandmothers, Barbara and Jean.
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A good collection management system (CMS) is critical for any museum collection. CMS are used by collections management staff to help track and update inventory, identify and locate objects, manage loans and shipping information, generate reports, print forms and labels, record donor, lender, and collector data, and also store many other pieces of information depending on the collection and object type. Museum administrators can use the CMS to keep up to date with significant collection statistics for the purposes of accountability, grant writing, and development. The CMS can be used by students, researchers, educators or members of the public to explore the collection, with most modern systems making the collection data and images available online. Using a CMS has become an integral part of managing a museum collection.

There are many options available to museums looking to choose a CMS, and each institution must select one based on the size and complexity of their collections, financial constraints, and the type of objects to be curated. In 2012 the administration of the Florida Museum of Natural History (FLMNH), the state’s official natural history museum, made the decision to begin to transition all of their neontological and paleontological collections to the
Specify 6 collections management system, with conversions beginning in early 2013. This thesis documents that transition while focusing on the FLMNH Invertebrate Paleontology (IP) Collection.

Specify, an open-source database platform, is designed to manage museum and herbarium collections and research information. Specify enables a collection staff to track specimen data, link images and documents to specimen records, publish data to online data repositories such as GBIF and iDigBio, as well as keep track of and update relevant taxonomic information. Over 300 collections worldwide currently use Specify 6 with many more in the early stages of transitioning to the database.

The FLMNH IP Collection began transitioning to the Specify 6 database platform from a custom Access Database in October, 2013. The FLMNH IP Collection is the largest FLMNH collection (based on number of specimen lots) to make the switch to the new system, with 251,000 cataloged lots at the time of migration. The collection’s size, as well as the complex nature of data associated with paleontological collections, presented unique challenges throughout the conversion to using Specify. This thesis highlights some of those challenges, the successful partnership between the FLMMH IP collection and the Specify team at the University of Kansas, and illustrates Specify’s strengths as a means to digitize, store, and disseminate data.

This project has culminated in the creation of a manual for future users of the Specify database in the FLMNH IP Collection, in order to help streamline the digitization of data. Streamlining this process will shorten the training time for new users of Specify, make it easier for visiting researchers to access the information they are seeking, and minimize the number of errors generated by staff and volunteers cataloging objects in the database on a daily basis.
CHAPTER ONE

INTRODUCTION

Collections Management Systems and Databases

Collections Management System (CMS) and its associated database are central components of any museum collection. Operating and maintaining CMS is one of the most basic duties of any museum collection staff member. Whereas “CMS” and “database” are often used interchangeably, the terms are not synonymous and should be defined, so that their importance to the museum collection is clear. A database is any collection of information about any topic or topics, and may be either digital or analog.1 In contrast, a CMS includes multiple components. As defined in the Museum Registration Methods 5th Edition, these components typically include the “hardware, software, and the network on which they are being used within the museum.”2 The database is one essential piece of the CMS, but the database can exist without the CMS.

Since documentation of objects and transactions is, along with object care, the central task of a collection management staff, a database serves as a backbone to the collection. Databases were, until relatively recently, primarily written manually, using a ledger book.3 Individual entries from a ledger could be written on catalog cards and then organized according to various categories, similar to a library card catalog system, to make searching these analog databases easier.4 Once computers became more readily available to museums in the mid-1980s,

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2 Ibid.
3 Daniel B. Reibel, Registration Methods for the Small Museum. 4th ed. (Lanham, MD: AltaMira Press, 2008), 82.
4 Ibid.
databases became digitized, and computerized CMS took the place of card catalogs to assist in the organization of data.⁵

The first computerized database system was developed as early as 1969 at the Smithsonian Institution.⁶ Smithsonian Institution Information Retrieval, or SIIR, worked by using punch cards to standardize the data input, and allowed for data entry and queries.⁷ Today, there are many choices in CMS software, including *PastPerfect*, *The Museum System*, *KE-Emu*, customized *Access* databases, and *Specify*, the focus of this thesis. Each museum needs to decide which CMS they will use based on their own collections’ needs.⁸ Considerations should include the type of objects and data being managed, the nature of personnel entering the data, anticipated users, museum mission, and budgetary constraints.⁹ The right CMS can keep a collections management staff happy and ensure an efficient workflow, while the inappropriate CMS can cause unnecessary stress.¹⁰ An art museum may not be satisfied with the same CMS as a natural history museum, and museums with very large collections may differ from smaller museums.

Once a CMS has been chosen, it can be implemented and the collection’s existing database imported. New database entries (cataloged objects, loan records, locality records, identified taxa, etc.) can be made directly to the CMS. Existing entries can be queried, viewed, and edited in the CMS. Some CMS also have the option for uploading some or part of the collection information to the internet, including allowing the storage and publication of digital

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⁷ Ibid.
⁹ Ibid.
images online, which might be done automatically or manually by a staff member.\textsuperscript{11} The most important aspects to using a CMS are staff training, data management, and the regulated and efficient workflow.

**Specify 6**

*Specify* is an open-source database platform designed to manage museum and herbarium collections and research information.\textsuperscript{12} *Specify 6* is the second generation of the software, with some users continuing to use the earlier version, *Specify 5*. *Specify* is designed with biological collections in mind, and was originally created for an ichthyology collection, at the University of Kansas.\textsuperscript{13} *Specify*’s uniquely relational database allows for easy manipulation of hierarchical data such as taxonomic information that is important to biological and paleontological collections.\textsuperscript{14} *Specify* uses Darwin Core Terms, a standardized vocabulary for biological terminology, used by many modern biological data repositories.\textsuperscript{15} \textsuperscript{16} The program is very customizable, allowing collection managers to custom-define fields included on CMS forms, type of information to be entered, label formatting and appearance, and new fields that address specific needs of a given collection.\textsuperscript{17}

*Specify 6* allows collection managers to upload collection data to the internet, using *Specify*’s “Web Portal” module.\textsuperscript{18} Using this feature, collections can publish and share data with the world online, through data repository websites such as GBIF (Global Biodiversity

\textsuperscript{11} Quigley and Sully, “Computerized Systems,” 183.
\textsuperscript{13} Roger Portell, in discussion with author, September 15, 2015.
\textsuperscript{14} “Specify 6 Desktop.”
\textsuperscript{15} Ibid.
\textsuperscript{17} “Specify 6 Desktop.”
\textsuperscript{18} Ibid.
Information Facility) and iDigBio.\textsuperscript{19} \textit{Specify} uses Globally Unique Identifiers (GUIDs) to permanently identify data records for this purpose.\textsuperscript{20}

Over 300 collections worldwide currently use \textit{Specify 6}, with many more in the process of converting to the database platform. The \textit{Specify} team now also offers \textit{Specify 7}, a web-based \textit{Specify} application that can be used alone, or together with \textit{Specify 6}.\textsuperscript{21} For all users of \textit{Specify}, the \textit{Specify} team, based at the University of Kansas, provides support, particularly through the transitional stages while a collection is migrating from their old CMS to \textit{Specify}.\textsuperscript{22}

\textbf{The Florida Museum of Natural History}

The Florida Museum of Natural History (FLMNH) was founded in 1891 as the Florida State Museum, in Lake City, Florida.\textsuperscript{23} In 1906 the collections moved to Gainesville to become a part of the newly formed University of Florida, where they continue to reside today.\textsuperscript{24} Since 1917, statutes have been in place establishing the museum as the official state museum of Florida.\textsuperscript{25} The museum changed its name to the Florida Museum of Natural History in 1988 to better reflect its mission and collections.\textsuperscript{26} The mission of the FLMNH is “Understanding, preserving and interpreting biological diversity and cultural heritage to ensure their survival for future generations,”\textsuperscript{27} and the collections are biological, paleontological, and anthropological.\textsuperscript{28}

\begin{flushleft}
\textsuperscript{19} Ibid.
\textsuperscript{20} Ibid.
\textsuperscript{22} “Specify 6 Desktop.”
\textsuperscript{24} Ibid.
\textsuperscript{25} Ibid.
\textsuperscript{26} Ibid.
\end{flushleft}
Today, the FLMNH is home to a collection of over 40 million scientific specimens. Most of the museum’s collections rank in the top ten nationally and internationally, and they are continuously expanding, with over 400,000 new specimens and artifacts cataloged in the 2013-2014 fiscal year. Collections at FLMNH focus on Florida, the Southeastern United States, and the Caribbean, but their scope is global, with research conducted in 23 countries and 19 states in fiscal year 2013-2014.

The Invertebrate Paleontology (IP) Collection at the FLMNH is the third-largest collection of invertebrate fossils in the United States, and is comprised of over six million individual specimens, with over 259,000 cataloged lots. The collection contains mollusks, arthropods, brachiopods, corals, sponges, echinoderms, annelids, foraminifera, bryozoans, and ichnofossils, with major research areas in Florida, the Southeastern United States, and the Caribbean (especially Panama). The collection is subdivided into five collection types: systematic, stratigraphic, teaching, micropaleontology, and type and figured. The systematic collection, where specimens are organized according to phylogeny, is the largest of these collections.

This thesis project details the FLMNH IP Collection’s transition to the Specify 6 database platform from a custom Access database. The chapters discuss the decision to use Specify 6, the

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32 Ibid.
33 Ibid, 12.
35 Ibid.
36 Ibid.
challenges faced by the collections staff over the course of the transition, and the successes
achieved while working together with the FLMNH Office of Museum Technology and the
Specify team in Kansas. The Appendix contains the final product of the project, a Specify 6
manual for the FLMNH IP Collection. A manual can assist in training new staff and volunteers,
and save valuable time by providing key information and preventing common errors. A manual
should be a living document, and should be updated as collection needs, technology, and
procedures change. The manual will guide FLMNH IP Collections staff and volunteers through
the use of Specify 6, and may be used as a template for other collections planning to create their
own Specify manual.

37 Quigley and Sully, “Computerized Systems,” 181.
38 Ibid.
CHAPTER TWO

WHY SPECIFY?

Prior to Specify, the FLMNH collections, including the invertebrate paleontology collection, used customized Microsoft Access databases. Such databases are common, particularly among museums and collections looking for affordable and highly customizable management system options. Each FLMNH collection operated a separate Access database with its customized design that differed across collections. While Access allowed for a high degree of customization, the rapidly growing collections at the FLMNH were quickly outgrowing the storage capacities of those custom database systems. Complaints from collections staff about limitations of the Access databases were common, and were noticed by the museum director, Dr. Doug Jones. As the museum became a leader in digitization in the new millennium, the need for a more modern, museum-wide management system became particularly critical, and the launch of the iDigBio project at the FLMNH in 2011 only made this need more urgent.

In 2007 the administrative staff at the FLMNH, led by Dr. Jones, decided that the Access databases needed to be replaced with a new, museum-wide CMS. After an initial assessment, a decision was made that the informatics team at the FLMNH could develop a new, customized, museum-wide database that would be professional-grade. The development of the CMS was

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40 Douglas S. Jones, in discussion with author, October 8, 2015.
41 Ibid.
42 Larry M. Page, email message to author, October 8, 2015.
43 Jones, in discussion with author, October 8, 2015.
44 Ibid.
pursued for almost three years. However, the project was not completed successfully. The economic recession hit the country and the state in the midst of the CMS’s development, which led to major problems in funding. Financial hardship and difficulties in communicating exactly what everyone would want in a CMS contributed to the demise of the project.

Following the termination of the CMS project, Dr. Jones and the administrative team at the FLMNH narrowed the possible solutions for the biological collections (including both paleontology and neontology) to two software choices, Specify or KE-Emu. These are the two CMS most often used by larger scale natural history collections, with KE-Emu in particular being the CMS of choice for very large collections, including the American Museum of Natural History, the National Museum of Natural History, and the Field Museum.

While the size of the collections at the FLMNH may have made it a likely candidate for KE-Emu, several factors were considered by Dr. Jones and his team that made it clear that it was not the correct choice of CMS. The significant cost of KE-Emu was perhaps the most important deciding factor. While the cost of licensing KE-Emu differs depending on the number of users, the collection type, and amount of required staff training, the cost may run as high as $17,600 per five users. Such cost was simply prohibitive for the FLMNH. Additionally, the museum was committed to using open-source software (software for which the source code is made publicly available, and can be modified by any user) whenever possible, and Specify, unlike KE-

\[\text{Ibid.}\]
\[\text{Ibid.}\]
\[\text{Ibid.}\]
\[\text{Jones, in discussion with author, October 8, 2015.}\]
**EMu**, is open-source.\(^{52}\) *Specify*’s strength in allowing collections to publish data online was also an element of the discussion.\(^{53}\) With the iDigBio project housed at the FLMNH, Dr. Jones and his administration concluded after discussions with the iDigBio team and the National Science Foundation (whose grants fund both the *Specify* project and iDigBio) that the FLMNH could set a positive example for other museums by using *Specify* and publishing data from all of the collections to iDigBio.\(^{54}\) The customization possible using *Specify 6* as well as the support offered by the *Specify* team at the University Kansas were other reasons that made this choice attractive to the FLMNH.\(^{55}\) Customization and support are both available through *KE-EMu*, but come at additional cost.\(^{56}\) Finally, looking towards the future of the museum, Dr. Jones and his team learned that should changing CMS be necessary again in the future, the conversion from *Specify* to *KE-EMu* would be an easier transition than the opposite.\(^{57}\)

*Specify 6* was officially chosen as the new CMS for the biological collections at the FLMNH in 2012, and conversions began in 2013.\(^{58} \)\(^{59}\)

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\(^{52}\) Jones, in discussion with author, October 8, 2015.

\(^{53}\) Ibid.

\(^{54}\) Ibid.

\(^{55}\) Ibid.

\(^{56}\) Ibid.

\(^{57}\) Ibid.

\(^{58}\) Ibid.

\(^{59}\) The anthropological collections at the FLMNH are also currently in the process of transitioning from *Access* databases to a new CMS, *ReDiscovery:Proficio*. (Elise V. LeCompte, email message to author, October 8, 2015.)
CHAPTER THREE
CHALLENGES IN TRANSITION

The transition from one CMS to another will never be completely smooth for any collection. Challenges faced by the FLMNH IP Collection during the conversion and ongoing transition from Access to Specify 6 have ranged from relatively small and easy to fix to substantial issues with no obvious solution. Some of these problems were inherent to Specify, while many others were due to the vast size and substantial complexity of the data associated with the FLMNH IP Collection. Specify was initially designed for an ichthyology collection, and therefore was not intended originally for paleontological data. Paleontological collections are similar in many ways to neontological collections, but there are some differences in variables, particularly as related to a localities stratigraphy and age.

Many of the issues identified earliest were small-scale problems encountered when the FLMNH IP staff started to use Specify daily to catalog specimens and localities. These problems generally were fairly easy to work around, and could be classified as minor annoyances. Having to deal with the same issue repeatedly, however, could take up valuable time that could be spent cataloging more specimens. These issues also increased the likelihood of committing errors that would be recorded in the database.

One of the earliest problems the FLMNH IP staff recognized was a quirk encountered while cataloging specimens in the Data-Collection Object tab in Specify 6. While entering information into several of the text boxes with drop-down menus, including the “Nature of Specimens” drop-down and the “Field Number” drop-down, the person cataloging needed to

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Please see Appendix A, Part II for details on cataloging specimens.
type the first word that belonged in the box, then delete the final character of that word and open the drop-down menu to find the correct option. Without deleting the final character of the word, the drop-down menu would not recognize what had been typed thus far in the text box. This was one of the earliest Specify issues addressed and resolved by the Specify team for the FLMNH IP Collection. This problem was likely due to the unique drop-down menus customized for the FLMNH IP Collections, which are populated with thousands of choices.

These very large drop-downs have caused multiple problems. The drop-down menus, populated with terms that are part of a controlled vocabulary, help to minimize cataloging errors in a collection that deals with a wide range of paleontological taxa from many collectors. The Nature of Specimens drop-down, for example, helps catalogers describe the various body parts for thousands of species from different taxonomic families. Specify 6, however, was never designed to handle such extensive picklists. Specify 6 allows users to set a limit on the maximum number of entries that can be stored in a given picklist. Once the limit is reached, the oldest entries are deleted as new entries are entered. This also causes Specify to slow down and freeze as it attempts to delete older entries. The FLMNH IP Collection has reached and exceeded the default limit for several of the drop-down lists. The limits have now been raised by the FLMNH OMT. Currently the FLMNH IP staff is looking into ways to further trim down some of these picklists by deleting unnecessary entries, such as typos or outdated terminology.

During the course of the ongoing transition to Specify 6, several problems with the FLMNH IP loan invoice produced by Specify 6 have been identified. Some of these have been fixed while others remain unresolved. Loan invoices are essential to the operation of the FLMNH IP Collection, with over 10,000 specimens currently on loan and more requests coming in each week.
For some loans being returned to the FLMNH IP Collection, a part of the loan may be returned at one time while the remainder may be returned at a later date. When a portion of a loan is sent back, but not the entire loan (in some cases, even individual lots may be mailed back in parts), only the received portion of the loan/lot should be listed in the database as returned. In the original version of Specify 6 used by the IP Collection, only an entire loan could be returned at one time. This issue was resolved with the assistance of the FLMNH OMT.

In some cases, a loan may contain partial lots. That is, a loan recipient may receive a subset of specimens from a larger specimen lot. In this situation it is important to note the number of specimens being loaned on the loan invoice, as opposed to the number of specimens in the lot. In the initial version of Specify 6 being used by the FLMNH IP Collection, the number of specimens loaned could be noted while filling in loan information in the Interactions-Loan tab in Specify, but the number of specimens in the lot would still appear on the loan invoice. This issue was resolved with the assistance of the FLMNH OMT and the Specify team.

Large loans containing multiple lots are common in the FLMNH IP Collections. As such, many loan invoices extend to two or more printed pages. When loan invoices are more than a single page, it is important that the header and footer (including the addresses at the top of the page and page numbers at the bottom) appear on every page. This is to ensure clarity for both our records and the records of the institution receiving the loan. Page numbers in particular are helpful if a page of the invoice is lost or misplaced. While the initial versions of the loan invoices generated using Specify 6 for the FLMNH IP Collection did not carry over the header and footer to pages past the first, this issue was partially resolved with the assistance of the FLMNH OMT.

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61 Please see Appendix A, Part VII for details on returning or preparing loans.
and the Specify team. The footer, including the terms of the loan and space for signatures, and the page number, were added to the pages beyond the first. The header has yet to be added.

Loans may have more than one agent, and an agent may have more than one address. In the case where a loan agent has a primary and a secondary address (for example, a researcher normally teaches at University A, but for the next two years will be a visiting scholar at University B), Specify generates the loan form with two addresses listed but with every preparation (catalog number) appearing twice. This issue has been assessed by the Specify team and is currently being addressed by the FLMNH OMT. Currently, the FLMNH IP staff is working around this problem by never listing more than one address for a loan agent, and only listing the current or primary address for agents.

Figure 3.1. Loan invoice showing all lots appearing twice due to unsolved address issue.
Specify 6 offers a Statistics page that displays updated numbers from the collection in real time, which should include the total number of lots, specimens, and items on loan, as well as how many specimens have been cataloged each week, month, and year to date. This feature has the potential to be useful when writing grants or reporting to museum administrators, since it allows the Collection Director to know real time quantities for reports and be confident in their accuracy. However, the current statistics page does not distinguish between the total number of specimens and the total number of lots, and the meaning of some of the labels produced in the output is unclear. Currently, the FLMNH IP staff is working with the FLMNH OMT and the Specify team to change the Statistics to more accurately reflect the numbers that are important to the collections.

Figure 3.2. FLMNH IP Collection Specify 6 Statistics page.
A first attempt to change the Statistics page was unsuccessful. Changes were made to the wrong level of the OSI (Open System Interconnection), causing the custom Specify application that FLMNH IP normally uses to revert to the default Specify application. While the FLMNH IP database was intact, there was a simultaneous error that caused several catalog records to appear to have multiple determinations. To fix the error, we were able to restore to a previous version, from the previous day. This was possible because we backup Specify 6 once per day using a MySQL dump, keeping 90 days of history plus an additional annual backup. Because we restored to the previous day, we also had to re-catalog all specimens from the day for which data lost.

Specify 6 uses Google Earth to plot localities that have latitude and longitudes recorded in the database. When using GPS to record localities, there are various choices of datum that can be used, which make a difference in where precisely that latitude-longitude point will fall on a map. A datum refers to a projection of the earth used to calculate its coordinates.\(^{62}\) When entering locality data into Specify 6 for the FLMNH IP Collection, there is a custom drop-down menu with a picklist of datums commonly used by IP collectors: INTL1924, NAD27, NAD27AK, NAD27CONUS, OLDHAWAII, NAD83, NAD83CANADA, NAD27CANADA, and WGS84. However, Google Earth uses only WGS84 as its datum,\(^ {63}\) and Specify 6 does not convert any locality data entered using an alternate datum before sending the data to Google Maps to plot the locality. This is an issue because datum values are not interchangeable and will cause what is referred to as “datum shift”: localities will plot on the map shifted from their correct location by as much as several hundred meters.


For neontological collections such shifts are often not seen as problematic because living organisms, such as fish, move. If the locality plot point is some meters off, that is acceptable because the specimen would move anyway. For paleontological collections, where the specimens are static and seldom move, a few meters can mean the difference between finding a site and never seeing it again. For some sites, it may mean the difference between collecting legally and illegally, or knowing whether a site is on land or underwater. This is an issue that has not been resolved. Converting from one datum to another is not simple and Specify may not continue to use Google Earth as that product is no longer being supported or updated. Currently, the best way to work around this problem is for the Specify team to communicate to all collections using their CMS that they must collect GPS data using only WGS84 going forward. For collections such as the FLMNH IP Collection, which have locality data that may be compromised due to this issue, there are conversion tools available to manually convert all locality data collected using a non-WGS84 datum.

Locality data is essential for all natural history collections, but as previously discussed, it is particularly crucial to paleontological collections. In the FLMNH IP Collection, specific localities are assigned a code, two letters followed by three numbers. Each of these codes can only be attached to one locality in order for this system to work correctly. Specify 6 allows for a locality code to be used more than once without warning the user that the code has already been assigned a locality, a problematic feature that we learned by chance. Upon learning that this was the case, we had FLMNH OMT write a query for us using MySQL to determine how many locality codes had been used twice and what they were. We then needed to manually reassign the


65 Many tools are available free online, such as the Coordinate Conversion tool from the TAGIS office of the West Virginia DEP (http://tagis.dep.wv.gov/convert/) or the Coordinate Conversion Tool from the Geocaching Toolbox (http://www.geocachingtoolbox.com/index.php?page=coordinateConversion).
duplicates. There is no solution for this issue in Specify 6, so it is essential to check that all localities are unique before assigning them a code.

Figure 3.3. Locality duplicates found using MySQL.

A recent development in the FLMNH IP Collection has become evident since the hiring of several new part-time collections catalogers. These catalogers have limited access to Specify as part-time employees, and do not have the ability to delete most entries that they make. In most cases, this prevents the accidental deletion of cataloged objects or agents, but in the case of an accidental entry while cataloging, it can instead exacerbate an error. In this case, part-time catalogers are often adding a new “Determination” instead of a new “Catalog Object” causing a single catalog entry to have multiple determinations, and some Catalog Objects to end up
uncataloged. This can be time consuming to fix if it is not caught early, as the catalogers cannot delete the incorrect entries themselves. The repetition of this error is likely caused by the close proximity of the green plus for adding “Catalog Object” and “Determination.” A possible solution may be to move the two further apart, or to somehow make one look significantly different from the other. This is not an issue that we have addressed as of this writing with the Specify team.

Although there have been ongoing difficulties with the transition to the Specify 6, the FLMNH IP Collections staff have made significant progress with the database platform. The assistance of the FLMNH OMT and the Specify team has allowed for a number of meaningful improvements to made, an effort which will help paleontological collections transitioning to Specify in the future and perfect Specify in general moving forward. Chapter four will discuss some of these successful improvements in more detail.

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66 See Appendix A, Part II, Step 4 for further explanation of “Determination.”
CHAPTER FOUR
SUCESSES IN TRANSITION

One of the benefits to choosing Specify as a CMS is the high level of personal support that the Specify team provides during and after a collection’s transition. This support is what allows users of Specify to achieve the high level of CMS customization. At the FLMNH, we are fortunate enough to also have the support of our OMT. The Specify team and the FLMNH OMT have formed a strong partnership since the museum began its CMS transition in 2013. The FLMNH IP Collection has been able to capitalize on that partnership to achieve a high rate of success with the Specify 6.

Although, as discussed throughout the previous chapter, there have been difficulties throughout the transition to Specify 6, the majority of these issues have been resolved or are in the process of being solved. These overhauls proved feasible thanks to the fact that the FLMNH IP staff was assisted continuously by both our own museum’s OMT and the Specify team. Although the Specify team is located at the University of Kansas, they were able to meet remotely via weekly video conferences throughout this transition with the FLMNH IP and FLMNH OMT staff. During these meeting, any problems could be brought to the table, and solutions discussed. All three teams were also in constant communication via email. In particular, resolutions to daily issues have been among the most impactful successes in the FLMNH IP transition process.

Some of the transition challenges identified by the FLMNH IP staff resulted in improvements that benefited many users of Specify, including collections at other institutions.
For example, because Specify was initially designed for an ichthyology collection, it was not fully adequate for paleontological data.\(^67\) As case in point, paleontological collections require some special considerations, particularly as related to locality data. Early on in the FLMNH IP transition, Collection Director Roger Portell noted that the Specify field for “Paleo Context,” which includes all the paleontological information about specimen collection site (such as the geologic time period and the lithostratigraphic unit),\(^68\) was associated with the “Collection Object” rather than the “Locality”. Portell’s opinion was that it would be more beneficial for paleontology collections to have the Paleo Context associated with the Locality. The Specify team surveyed managers of other paleontological collections that use Specify as their CMS. A majority of those collections agreed that the Paleo Context should link to the Locality.\(^69\) In the next version of Specify 6 that was released, collections now had the ability to attach the Paleo Context data table to their choice of either Locality, Collection Object, or Collecting Event.\(^70\)

The wider Specify community has also been able to benefit from some add-ons designed by the FLMNH OMT team to accommodate the FLMNH IP Collection’s conversion and customizations. The very large drop-down menus needed for the FLMNH IP Collection in the Data-Collection Object tab were not easily accommodated by the picklist editor that is built into the Specify 6 software. The original Specify picklist editor was designed for short picklists, and only allowed one item in the picklist to be viewed at a time. The items in the picklist had to be navigated through by using a set of forward and back arrows.

\(^{67}\) Portell, in discussion with author, September 15, 2015.
\(^{69}\) Warren Brown, in discussion with author, October 8, 2015.
Figure 4.1. Original picklist editor, built into Specify 6.

This would work well for very short picklists, but for the FLMNH IP Collection’s picklists containing several thousand items, this design was unworkable. The FLMNH OMT designed an add-on feature that allows the user to upload a picklist and then edit it using a data grid instead of seeing only one item at a time. This add-on feature is available for any Specify user to download through the FLMNH website.\(^{71}\)

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Figure 4.2. Picklist editor add-on for Specify 6 designed by FLMNH OMT.
FLMNH already considered itself a leader in museum digitization before the decision was made to transition to Specify.72 As a part of that effort, the FLMNH IP Collection had spent several years taking images of thousands of specimens and adding those to the digital catalog available through the FLMNH website.73 During the conversion to Specify, these images created a need for a new tool to assist in the conversion because an unknown number of the over 3,000 images had already been attached in Specify 6, but an unknown number had not been successfully attached. Using the built-in Specify attachment wizard would have duplicated all of the images which were already attached without recognizing them as duplicates. The FLMNH OMT created a Specify Attachment Parser which is able to compare a file system directory to attachments in Specify and identify those files not already present in Specify. It also has the ability to copy those files to a chosen target directory. This add-on tool is available to any Specify user through the FLMNH website.74

One of the goals in transitioning all FLMNH biological collections to a single CMS was the integration of all collection data into a single data space accessible to researchers. An important part of meeting that goal is the ability to search across all of the collections. The FLMNH OMT was able to design an aggregated collection web portal for Specify, which allows for searches across all collections instead of a single search portal per collection.75 This tool will allow for a more broad range of research to be conducted by ecologists, biologists, paleontologists and others interested in studying more than a single group of organisms.76

72 Jones, in discussion with author, October 8, 2015.
74 Brown, “Specify Picklist Tool.”
76 Ibid.
The successes of this transition reflect the effective partnership between the FLMNH IP Collection staff, the FLMNH OMT, and the Specify team. This partnership made it possible to identify changes needed to improve the functionality of Specify and create the add-ons and customizations that addressed those needs. Only the collection’s users can identify the changes that need to be made on the front-end of the system, so those who use the CMS daily can perform their tasks efficiently and effectively. By discussing these needs with the OMT and the Specify team, the changes that need to be made on the back-end of the system, such as writing new lines of code, can be made and implemented correctly. When making changes to the back-end, the OMT and the Specify team primarily work with MySQL, an open-source management system for relational databases. 

![MySQL Workbench](image)

Figure 4.3. Making changes using MySQL.

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CHAPTER FIVE
CONCLUSIONS

**Ongoing Projects**

The transition to *Specify 6* is still an ongoing process for the FLMNH IP Collection at the time of this writing, and for the FLMNH biological collections as a whole. The IP Collection staff is currently focusing on several ongoing projects. Some of the challenges, already identified but not yet solved, are at the top of the priority list. In particular, with the help of the *Specify* team and the FLMNH OMT, we are hoping to perfect the Statistics screen as well as the Loan Invoice forms in the near future.

The FLMNH IP Collection has a parsing project that we will work on in the near future, to fix some of the errors made during the data conversion. This project would involve the clean-up of “Agent” data, which contain terms appropriate for the old *Access* database, but not for the *Specify* database. This project will also include the elimination of unsuitable terms in the “Nature of Specimens” picklist by deleting outdated terms and typographical errors. This project will be time consuming and require a degree of expertise in the collection and its history, which are limiting factors.

The FLMNH IP research staff is also looking forward to future projects using *Specify*. Curator Michal Kowalewski would like to see the inclusion of further customized fields that may be included in the “Collection Object” form for research purposes. Such customized fields would allow the Collection to capture valuable paleoecological data not generally included in catalog records, and enable researchers to query for specific terms.
One of the currently pursued projects is to improve the way that FLMNH IP data is being published to the GBIF website. When searching through our data on GBIF, the taxa we have uploaded to the repository show up as Genus followed by Author, instead of Genus followed by Species. The OMT has checked the IPT to ensure that the data is being sent correctly from Specify and our end, which it is. Therefore there is a parsing error happening on GBIF’s end which needs to be resolved.

As the transition continues, small problems keep arising. Fortunately, the strong partnership between the FLMNH IP Collection, the FLMNH OMT, and the Specify team will make any issues easier to handle.

**Conclusion**

Choosing a CMS is one of the most important decisions that a museum or collection will make, whether it is to choose a new CMS or to transition from one CMS to another. The CMS will be used every day for almost every aspect of collections management, so it is important that all possible factors are considered in making the choice, from usability to cost. The committee making the final decision should consider the short term and the long term impact of their choice, as the new CMS should be able to serve the museum or collection for the foreseeable future.

The high degree of customization offered by Specify can be a double-edged sword for collections staff. FLMNH is very lucky to have an OMT to assist through the transitional period. The onsite OMT staff can make smaller changes without the help of the Specify team and are able to assist the Specify team with larger issues. Museums and collections without a designated Information Technology staff should be cautioned. Specify is open source and assumes that it
will be customized for each individual collection. While the Specify team is available to assist, their team is small and with several hundred collections to oversee, they may only be able to give a limited amount of individual attention to every issue that arises. Consequently, collections or museums that consider transition to Specify should strongly consider the above issues when making their decisions.

The FLMNH has found that Specify meets the needs of the biological collections of this museum. In fact, thanks to onsite resources available to a large museum, we have been able to make positive changes to the Specify software project. These changes are expected to benefit hundreds of other collections currently using the program. Not every CMS will meet the needs of every museum and Specify may not be right for every collection.

The transition to Specify has been and continues to be a significant effort. While the transition has been frustrating at times, the ultimate reward cannot be understated. A unified CMS can make museum collections run much more smoothly. As importantly, a unified CMS facilitates global data sharing, which is the central goal of modern collections. Any museum transitioning to Specify or any other new CMS will experience challenges, but the challenges can be outweighed by the successes.
APPENDIX A
FLORIDA MUSEUM OF NATURAL HISTORY INVERTEBRATE PALEONTOLOGY
SPECIFY 6 DATABASE MANUAL

Florida Museum of Natural History
Invertebrate Paleontology Collection
Specify 6 Database Manual

By Katy Estes-Smargiassi
Collections Assistant
**Introduction**

Welcome to the *Specify 6* database. *Specify* is the platform the Florida Museum of Natural History (FLMNH) uses as a collections management system across all of its biological and paleontological collections. In the Invertebrate Paleontology (IP) Collection, you may use *Specify* to catalog new specimens, search the collection, manage loans, and add new taxa to the database. This manual will teach you how to begin using *Specify*, demonstrate daily tasks you will execute using the program, the steps you will need to learn to perform each of these tasks, and highlight some of the most common mistakes to avoid.

*Specify* allows collections to customize their databases to match their needs, so even if you have used *Specify* in the past elsewhere, your screen may look slightly unfamiliar to you. Refer to this manual to ensure that you are following the proper protocol for the FLMNH IP Collection when entering data, or simply searching the database.
Appendix A, Part I: Welcome to Specify

Before you begin using Specify regularly, you will need to work with the Collection Director and the FLMNH Office of Museum Technology to log on for the first time. You will need to be able to log onto an FLMNH computer using your GatorLink username and password, and you will need to receive a unique password and key that will allow you to log into Specify. Do not lose this key. You will need it any time you log into Specify for the first time on a different computer, or if your computer system updates.

Once you have received your Specify login information, and have logged in at least once on the computer you will regularly be using, you will be able to log onto the database using just your username and password (except in the situations discussed above). Click on the Specify 6 icon on your desktop. It will bring up the Specify login screen. Log onto the database.

Once logged in, you will be viewing the welcome screen. From here, you can choose any of Specify’s functions, using the icons at the top of the page.
Before you get started, there is some essential *Specify* vocabulary that you should know.

- **Collection Object**: This refers to any specimen or specimen lot that is cataloged and has received a catalog number.

- **Agent**: Any person whose name has been entered into the database as a collector, identifier, donor, etc. is an agent.

- **Accession**: While in museums generally, accession can refer to a system of numbering donated objects as they are received by the museum. However, in the FLMNH IP Collection, historically accession was used to refer to each collecting event. After the *Specify* conversion, the FLMNH IP Collection additionally uses accession to refer to the donor(s) (who may be an agent, another museum, or a university) who we received the object from. This helps us to keep track of the chain of custody for the object, since we will be able to record the original collector as well as any donors who had the object(s) after the collector but before it was received by us.
Now you are ready to begin using *Specify*. Turn to Section II to begin cataloging objects.
Appendix A, Part II: Cataloging

Cataloging will likely be the task you perform most often in the Specify 6 database. When specimens have been either collected or donated to the FLMNH IP Collection, they must be organized and identified, then finally cataloged to become an official part of the formed collection. When you catalog them into the IP Specify database, they will be added to our taxonomic tree, become searchable as a part of the collection, and receive a catalog number. Specimens may be cataloged individually in some cases, or in lots. Lots may be as small as one or two specimens or as large as several hundred or several thousand. This section will guide you through the steps of cataloging specimens using the FLMNH IP Specify database.

Note: Before beginning, check whether any of the specimens you are about to catalog needs to be painted, and paint them before beginning so that they will have sufficient time to dry. See Appendix A, Part III for details on painting specimens for labeling.
Step 1:

In the icon bar at the top of your Specify page, click on Data.

Step 2:

Once you have opened up the sidebar for Data, click on Collection Object in the sidebar.

Step 3:

Select specimen or lot, and the associated header box for specimen information. This is the information you will enter into the Collection Object page. Most often, you will be cataloging lots from a large tray. The header box will be located in the top left-hand corner of the tray and you will catalog the lot directly below it first. Work your way down through the columns (top to bottom) and left to right through the tray.

Step 4:

Click on the green plus sign next to the “Determination” box. This will allow you to begin your catalog record. In this box, enter your taxon information, which will usually be found on a slip of paper in each box of specimens. This will usually be a genus and species, or a genus
followed by “sp.”, or a family name. In the FLMNH IP Collection, we enter all of our data into the database in ALL CAPITAL LETTERS to avoid confusion. Once you have typed your taxon name into the determination box, you need to click on the down arrow to open the drop-down menu and choose the correct taxon name. If you do not use the drop-down menu, anything you type will not be saved in this box.

If your taxon is a genus followed by “sp.”, you will need to use the “Addendum” drop-down menu to choose that option (this is also true of “spp.”, “isp.”, and a few other options). If your taxon contains “cf.” or “?”, you will need to choose that from the “Qualifier” drop-down menu.

**Step 5:**

The Identifier may be found on either the header information or on the taxon identifying sheet, found in each specimen box. Enter the last name of the Identifier, if there is one, in the “Identifier” box. Use the down arrow to open up the drop-down menu and choose the correct full name, which should be formatted LAST NAME, FIRST NAME, MI. If the correct name is not yet available in the drop-down, you can click the green plus next to the “Identifier” box, which will open up a pop-out box and allow you to enter the correct full name, and save it.
If there is also a Date Identified, enter that date in the Date Identified box. This may be formatted as a full date, a month and year, or a just a year. You can choose one of these options from the drop-down menu, either “Full Date,” “Mon/Year” or “Year.” Do not confuse the Date Identified with the Collection Date, which will be entered later.

**Step 6:**

If your header information contains an accession, enter that information next. Accession is located above the determination and to the right of catalog number. Enter the first word or words of the accession and then use the down arrow to open the drop-down menu and choose the correct option.

If the correct option is not available, you will need to add it to the database. To do this, choose the green plus sign next to Accession. Place the accession name into the “Accession Number” box. This name may need to be shortened if the Specify field length will not allow it to fit. Use your best judgment. Under accession type, choose “gift” and under status, choose “complete.” Do not fill in any other boxes. Click “save.”
Step 7:
Click on the green plus button next to “Preparations” to open the Preparations box. For Prep Type, choose “Prep” using the drop-down menu. Count the number of specimens in your lot, and enter that number into the “Number of Specimens” field.

Nature of Specimens will usually be specified on the same sheet of paper that told you what the taxon was. This could be TEST(S), BURROW(S), CORRALUM, or any of thousands of choices available in the drop-down menu. Information for Nature of Specimens is not always provided. For example, for most gastropod specimens, this field will be left blank. In that case, the blank field is synonymous with “shell”, although “shell” is not written.

For all bivalve specimens, this field will be VALVE(S), unless there is at least one pair of valves in the lot. If the lot contains only a single pair of valves, the Nature of Specimens will be VALVES (PAIR). If the lot contains many valves, but 2 of the valves are a pair, the Nature of Specimens will be VALVES (1 PAIR). If there is more than one pair in a lot, the Nature of Specimens will be VALVES (2 PAIR), VALVES (3 PAIR), etc. If a pair of valves is still attached to one another, they should be counted as 2 specimens and as a pair (see photo below).
When entering Nature of Specimens, begin typing the Nature of Specimens, then use the down arrow to open up the drop-down menu and choose the correct option. If the correct option is not yet available in the drop-down, you can simply type it into the box and press enter (ensure that you are still typing in ALL CAPITAL LETTERS). This will save it to the IP Specify database, and make it available in the future.

**Step 8:**

At the top of your header information, you will find a locality code, formatted 2 letters followed by 3 numbers or just 5 numbers. Enter this code into the “Locality” box under “Collecting Information.” Once you have entered the code, use the down arrow to open up the drop-down menu and choose the correct locality option.

There is often, but not always, a collection date associated with the specimens, which you will also find on the header information. The date may be a complete date, a month and year, just a year, or sometimes a range of dates if we are unsure of the exact date of collection. These dates
are entered right below the Locality, also under “Collecting Information.” You may choose the date format using the dropdown menu, either “Full Date,” “Mon/Year” or “Year.” If there is only one date, place the date in the “Start Date” box. If there is a date range, use both the “Start Date” and “End Date” boxes.

**Step 9:**

The Collector or Collectors of the specimens can also be found on your header information. To open the “Collectors” box, click the green plus \( + \) next to “Collectors.” Once the pop-out box has opened, enter the Collector’s last name in the “Agent” box. Once you have typed in the last name, use the down arrow to open up the drop-down box and choose the correct full name. The correct format should be LAST NAME, FIRST NAME, MI. If the correct name is not yet available in the drop-down, you can click the green plus \( + \) next to the “Agent” box, which will open up another pop-out box and allow you to enter the correct full name, and save it. Once you have chosen the correct name from the drop-down menu, hit the “Accept” button to close the pop-out box. If there is more than one Collector, you will need to hit the green plus again to open the pop-out box again and repeat the process. Repeat for as many Collectors as necessary.
Step 10:
If the header information contains a “Strat” or “Position,” this information will go in the “Position” box. This could be “SPOIL,” “UNIT 1,” or any one of thousands of options that describe a stratigraphic position. Type the position into the box then use the down arrow to open up the drop-down menu and choose the correct option. If the correct option is not yet available in the drop-down, you can simply type it into the box and press enter. This will save it to the IP Specify database, and make it available in the future.

Step 11:
If the header information contains a “Field Number,” this information will go in the “Field Number” box located directly below “Position.” A Field Number is generally formatted as a combination of letters and numbers, or a name followed by numbers. Begin typing the field number into the box, then use the down arrow to open up the drop-down menu and choose the correct option. Make sure you have chosen the correct numbers and not just the correct letters. If
the correct option is not yet available in the drop-down, you can simply type it into the box and press enter. This will save it to the IP Specify database, and make it available in the future.

**Step 12:**

You will always need to choose a Collection Type. This will usually be located in the top right corner of the header information in parentheses. Most often you will see (TX), indicating that these specimens belong in the Taxonomic collection. The other collections are: Stratigraphic (ST), Teaching (TE), Type and Figured (TP), and Microseries (MS).

**Step 13:**

You will always need to choose a Specimen Status from the “Specimen Status” drop-down menu. You will always choose “In Collection” from this drop-down.

**Step 14:**

Before saving this first catalog record, you may open the “Data” drop-down menu from the top bar of your Specify screen (located next to “File” and “Edit”), and choose “Configure Carry Forward.” This will open a pop-out menu. Choose “Select All” to check all of the boxes, and hit the save button. This ensures that all the information you just entered will be copied to the next new entry after you save and create a new record, thus speeding up the cataloging process. The only reason not to use this feature is if you know that there is no overlap of information between the specimen you are cataloging and the next specimen you will catalog.

**Step 15:**

Ensure that you have entered all of the header information and that your taxon and specimen counts are correct. If everything is correct, hit the save button at the bottom right of the page. Once it has saved, a catalog number will be generated automatically at the top of the page, under “Collection Object.”
Step 16:
At this point, you may label your specimens. Please see Appendix A, Part III, for more instruction on labeling specimens. Once the specimens are labeled, return them back to the tray.

Step 17:
To begin the next catalog record, click on the green plus next to “Collection Object.” If you followed Step 17 correctly, all the data you just entered should have copied and pasted to this new record. Retrieve the next box from the tray, and begin the process again. You should only need to change the details such as taxon and specimen count.

If you come to a new header box in your tray, or you begin a new tray with new header information, you will need to change those details as well.
Appendix A, Part III: Labeling Specimens

Now that you have finished cataloging a specimen lot, you will need to label it before you can move on to cataloging the next lot. Although this is done by hand, not using Specify, it is an essential step in the cataloging process. If the catalog numbers in the database do not match the numbers labeled on the actual specimens, we will not be able to find objects in the collection.

There are a few tools you will need for labeling specimens in the FLMNH IP Collection:

- Rapidograph ink pen
- White, archival quality paint (Gesso)
- Fine paintbrush
- Gelatin (gel) caps in various sizes

Once you have all of these materials, you can begin. It is best to check that all of your labeling tools are ready before you begin cataloging.

Painting specimens:

If your specimens need to be painted before labeling, you will need to do this first. In fact, it is easiest to check for specimens that will need to be painted before you begin cataloging, and paint them all before you start the cataloging process. This way the specimens have time to dry while you are entering information into the database.

Specimens that have a rough, uneven, or porous surface will need to be painted before they can be labeled. Specimens that will almost always need to be painted include corals, echinoid tests, and external molds. You may also need to paint specimens that have a smooth surface, but unexpectedly cause the pen ink to run.
To paint a specimen, use the fine paint brush and the Gesso to make a small, white rectangle on the specimen. This strip of paint should be small and out of the way, just large enough for you to write the catalog number on it. On specimens with more uneven or rougher surfaces, you may need more paint layers in order to create a more even surface to write on. Wait for the paint to dry completely before writing on the specimen.

Labeling specimens:

For specimens that do not require painting, you will write directly on the specimen surface with the Rapidograph pen. **ALL SPECIMENS** in each lot need to be labeled individually, in the format UFXXXXXX (UF followed by the catalog number). You should write this number as small and as neatly as possibly. This number should also be written on **ALL** slips of paper in the specimen lot box, including the identifying sheet and any papers included from the original collector. When writing the catalog number on these historical papers, which are often very small, try to place the number in a top or bottom corner. If it will not fit on the front, it can be written on the back of the paper.

For specimens that are too small to write on individually, you have several sizes of gel cap to choose from. One or more specimens may be fit into a gel cap, but do not overfill a gel cap. It should be able to close comfortably. Each gel cap can be labeled with the catalog number. The catalog number should be written only on the top half of the gel cap.
Figures: Examples of various labeled specimens (gastropods, a gel cap, an echinoid test, and a single bivalve.)
Labeling valve pairs:

If your lot contains one or more pairs of valves, they will need to be labeled as pairs. We use a lettering system to match the pairs. The first pair will be labeled as UFXXXXXXXXA and UFXXXXXXXXA, the second will be labeled as UFXXXXXXXXB and UFXXXXXXXXB, and so on. This will ensure that if any valves are lost or misplaced, it is clear which should have a second half, and makes it easier for future users of the collection to pair them off. This is true for valve pairs that are unattached and attached. See examples below.
Appendix A, Part IV: Generating and Printing Labels

Once you have completed cataloging a tray, you will need to generate labels for all the lots in that tray, print them, then cut them and place them in each lot.

Step 1:
Before you begin generating labels, check your work. Look for common mistakes. One of the most common errors made while cataloging in the FLMNH IP Specify 6 database is forgetting to remove the “sp.” addendum for taxa that do not call for it. Also check that you have chosen a Collection Type and a Specimen Status for every object cataloged.

Step 2:
Once you are satisfied that you have thoroughly checked for errors, you can close the “Collection Object” tab at the bottom of your Specify screen. This will close your cataloging session.

Step 3:
You will now need to generate the labels for the lots you have just finished cataloging. To begin, find the “Query” icon at the top of your Specify screen and click on it to open. On the side panel that is now open, choose “Collection Object.” From the menu that opens, choose “Catalog Number” by double-clicking. This will open a Catalog Number search bar.
Step 4:

To the left of the search box, there is a drop-down menu. It will automatically have “=” chosen for you. Open up the drop-down and choose “>=” meaning greater than or equal to. Find the first object you cataloged in your tray, and enter that number into the search box. Press enter to generate a list of all the catalog numbers from this tray.
Step 5:

Now you will create a “Record Set.” This is a way to save a list of catalog numbers. There are several icons to the left side of the green bar near the top of this page in your Specify window. The first of those icons is a small circle with a hole in the middle. Click this icon. It will pull up a pop-out window that will prompt you to “Enter a Record Set Name.” You may enter anything for this name. Your initials are a good way to start. Press the OK button to save the record set. Please refer to Appendix A, Part V for further details on Record Sets.

Step 6:

Once you have saved your record set, find and click the “Reports” icon at the top of your Specify screen. On the left side of your screen, you will be able to see your record set in the sidebar,
indicated by the name you gave it. Above the saved record set, you will see several choices, including “IVP Label.” Click and drag your record set, and drop it into “IVP Label.” This will take a few moments to load, and then the labels for every object in your record set will appear on screen. If they take up more than one page, you can navigate the document using the arrows near the top of the page (located under the large icons).

**Step 7:**
Scroll through the labels to make a final check for obvious errors. Once you are satisfied, click on the printer icon. Make sure that you are printing labels using the archival quality, acid-free paper. This paper is located in Tray 2 of the printer in the IP range. Print the labels.

**Step 8:**
Using the paper cutter located in the IP range, cut out the individual labels. Make sure you are cutting straight lines. Leave as little white margin space as possible without cutting off any of the information on the label. Once the labels are cut, place them in their boxes with the correct lots.
Congratulations! You have finished the cataloging process! If you are ready to move onto learning some of Specify’s other uses, please move onto the next section.
Appendix A, Part V: Querying the Database

You have already had a short introduction to queries in Specify 6 while learning how to generate and print labels (Appendix A, Part IV). This section will elaborate on ways to query (or search) the database for various types of data.

Querying a single object:

If you only want to search the database for a single object, for instance, you may need to find the catalog record of a particular specimen lot for a researcher, you can use the search bar that is always located at the top of your Specify window. Type the object’s catalog number into the search bar and press enter. A new tab will be generated in Specify showing the records your search turned up in the database.

Select the correct object from the results by either double clicking or by clicking on the third icon (from the left) on the green bar in your window above the results.

This will open the object’s catalog record so that it can be viewed or edited.
Querying more than one object:

At the top of your Specify screen, find the “Query” icon and click on it to open the query panel. On the side panel that is now open, choose “Collection Object.” From the menu that opens, choose “Catalog Number” by double-clicking. This will open a Catalog Number search bar. To the left of the search box, there is a drop-down menu. It will automatically have “=” chosen for you, but by opening the drop-down menu, you can choose from several options.

Depending whether the objects you need to query are sequential in the database or not, you will choose a different option from this dropdown. If you are searching for a list of objects with sequential catalog numbers, you should choose “Between” from this dropdown. Enter the first catalog number of the sequence in the first box and the final catalog number of the sequence in the second box. Press enter to generate the list of results (up to 20,000 records only).
If the objects you need to query are not sequential, you should choose “In” from this dropdown. In the resulting search box, type the catalog numbers, each separated by space. Press enter to generate a list of results.
Now that you have a list of results, you can either view them immediately, or you can create a record set. To view the results immediately, you can click on the third icon in the green bar in your window above the results. This will open the catalog records of all the objects you queried, which you can scroll through using the arrows at the bottom of the page.

To create a record set, choose the first icon in the green bar in your window above the results. This will pull up a pop-out window that will prompt you to “Enter a Record Set Name.” You may enter anything for this name. Your initials are a good way to start. Press the OK button to save the record set.

If you create a record set, you can use the record set to open and view or edit the catalog records of all objects in the record set. Find the “Data” icon at the top of the screen. Click on the icon to open the “Data” side bar. You will see your saved record set in the side bar, indicated by the name you gave it. Above the saved record set, you will see several choices, including “Collection Object.” Click and drag your record set, and drop it into “Collection Object.” This will open the catalog records of all the objects you queried, which you can scroll through using the arrows at the bottom of the page.

**Other query types:**

Specify’s Query function also allows you to query other types of information stored in the database. After choosing the “Query” icon from the top of your screen, there are several options
to choose from in the side bar that opens up. You may choose “Agent,” “Collecting Information,” “Collection Object,” “Loan,” “Locality,” or “Taxon.” There are several means of searching through each of these categories, which will appear in your window once you have selected an option.

For example, if you need to search for a specific loan, in order to find out what objects are associated with that loan, you should select “Loan” from the side bar. Next you will need to select how you want to search for the loan. If you know the Loan Number, you can choose that option. You may also search by Loan Agent or Loan Date. Type the Loan Number (or agent name, date, etc.) in the search bar, and press enter. This will generate a list of results. Choose the correct result to view it.

![Image of a computer interface with search options highlighted]

**Querying using multiple search terms:**

For more complicated queries, you may want to use more than one search term. For example, if you want to search for all the loans with a specific loan agent in a specific year, you can choose
the arrow next to “Loan Agent” to expand it and include more search terms. From the expanded terms, you can choose “Loan Date (Year).” Only search terms with an arrow next to them can be expanded to include more search terms.

Once you have added two or more search terms, you can use the check boxes next to the search boxes to either use those terms or not, or use the “x” to remove a search term you do not need anymore.

After creating a query with multiple search terms, you may want to save the query. Saving a query will allow you to reuse the same query quickly and easily without having to go through the process of adding all search terms every time. To save a query, use the save button at the bottom right of the screen.
Appendix A, Part VI: Editing Catalog Records

Editing catalog records in Specify is an essential skill when managing the database. From time to time mistakes will be made while cataloging that need to be corrected. Also, the identifications of specimens may change and require update, specimens may be lost or destroyed while on loan and need to be recounted, or updated information will need to be added to a given record. Depending on your permission level within Specify, you may or may not be able to edit some or all records.

Step 1:
Query the database for the catalog numbers you need to edit, using what you learned in Appendix A, Part V.

Step 2:
Once you have found and opened the record, you will notice that you cannot make any changes at first. By default, they will be in “View” mode. At the bottom right corner of your screen, find the “View” button, and use the arrow to change the mode to “Edit.” Now you can begin to edit your Catalog Objects.

Step 3:
Make all the edits needed. Make sure to hit save before you move on to the next record. Use the arrows at the bottom center of your screen to navigate to the next record.
Editing other information:

Do you have permission to make additional changes or edits to the database? If not, you can read this section to familiarize yourself with editing, but do not try to make any additional edits in Specify until you have permission from your supervisor.

Sometimes, you may need to make changes to information that has already been saved in the database, such as an Agent’s data, or an Accession. If this is the case, click on the pencil icon located next to the box. This will open a pop-out menu that will allow you to make required edits. Make sure to save your changes once they are completed.
Appendix A, Part VII: Loans

While working in the FLMNH IP Collection, you may help create or return loans that we send to researchers around the world. The paperwork for these loaned specimens is stored in Specify. This section will guide you through how to create a new loan, and then return a loan that has come back to the museum.

STOP Have you been authorized by the Collection Director to work on loans? Do not attempt to try to do anything in this section without first asking permission from your supervisor. You may read through this section to familiarize yourself with the loan functions, but do not try it in Specify unless you are sure you are working with a real loan and you have the authority to do so.

Create a loan

To begin the process of creating a loan, find the “Interactions” icon at the top of your Specify screen and click on it. From the new side panel that is now open, choose “Loan.” This will open a pop-out window, asking you to choose a source of collection objects. You may choose to fill your loan using either a record set that you have already created, or you can enter the catalog numbers manually.
If you choose to enter the catalog numbers manually, choose the “Enter Catalog Numbers” button. This will open another pop-out box, in which you can enter all of the catalog numbers that will be used in this loan, each separated by a space. When you have finished typing the catalog numbers, press “OK."

![Enter a List of Catalog Numbers](image)

This will open a new Loan tab in Specify. You will now need to enter all of the information for the loan. The “Current Due Date” is generally 6 months from the date the loan is created, or the date the loan is shipped to the borrower. There may be one or more loan agents. The first is the borrower. If the borrower is not the person who the loan will be shipped to, then that person will also need to be added as an agent. Add a second agent by clicking on the green plus sign next to “Loan Agents.” Be sure to specify the “Role” of each agent using the drop-down menu. Check to make sure that the Agents’ address, email, and phone number are entered into their Agent information by clicking on the pencil next to their name. If there is more than one Agent, the Agent who the loan will be shipped to should be checked as “Is Primary.”

Enter the shipping information under “Shipments.” Fill in the date the package will be shipped in the “Shipment Date” box. Fill in the last name of the correct agent in the “Shipped To” box, and use the down arrow to open the drop-down and choose the correct name. Fill in the Collection Director’s last name (unless otherwise specified) in the “Shipped By” box, and use the down arrow to open the drop-down and choose the correct name. Record the number of packages that will be shipped for this loan in the “Num Of Packages” box, and choose the correct method of shipping from the “Method” drop-down.
Under “Loan Preparations” you will see that the catalog numbers you entered or imported from your record set have filled in automatically, including the number of specimens in each lot. If you are sending all the specimens in each lot in the loan, you are ready to hit the “Save” button. If you will only be sending partial lots for some or all of these catalog numbers, you will need to edit the number of specimens by double clicking on each catalog number. This will open a pop-out menu, in which you can edit the number of specimens.

Once you have edited the Loan Preparations to reflect the correct number of specimens being loaned, you can hit the “Save” button in the bottom right corner of your screen.

To generate the loan invoice, you can check the “Generate Invoice on Save” box and then hit the save button. A pop-out window will appear, prompting you to choose an Invoice. Choose “IVP Loan Invoice” and hit “OK.” The loan invoice will appear on your screen, ready to be checked and printed.
Loans without preps

You also have the choice to create a “Loan w/o Preps” when choosing from the “Interactions” side panel. This option is used rarely. A Loan without Preps refers to a loan of objects that do not have catalog numbers. Occasionally the FLMNH IP Collection loans bulk sediment, specimens collected by graduate students or other non-cataloged objects. These would fall under “Loans w/o Preps.” When creating a Loan without preps, you will need to be descriptive in your remarks, because there are no catalog numbers and specimen counts. If the loan has specimens, make sure to count them (if possible) and include the count in your remarks. If the specimens are numbered in any way, include that in your remarks as well. If the loan is a bulk sediment sample for which you will not be including a specimen count, include any information about the sediment sample you have in remarks.
Return a loan

There are two ways to return a loan. The first and simplest way, is used when a loan has been returned to the FLMNH IP Collection in its entirety. To make sure this is the case you must unpack the entire loan and count every specimen in every lot, to make sure it matches the record of the original loan. Once you have determined that the entire loan has been returned, find the “Interactions” icon at the top of your Specify screen and click on it. From the new side panel that is now open, choose “Return Loan.” This will open a pop-out window, prompting you to “Enter Loan Numbers.” Type the loan number of the returned loan in this box and press “OK.” The loan will be returned automatically, and this will be registered in the database.
If the loan is returned incomplete, you will need to open the loan first by querying it (please see Appendix A, Part V for more information on Queries). Once the loan is open on your Specify screen, you can return individual lots or parts of lots by double clicking on the catalog number to open the pop-out menu.

You will notice that in this pop-out window there is a “Return Preparations” button. Hit this button to open a second pop-out. In this pop-out, hit the green plus (+) to allow changes to be made. Fill in the appropriate information. In “Received By” you will write the Collections Director’s name, unless otherwise specified. If the entire lot was returned, put the total number of specimens in the “Quantity Returned” box. If only part of the lot was returned, count the specimens and put the number returned in the “Quantity Returned” box. When you have finished, click the “Done” button and move onto the next catalog number. When you have finished with all returned lots, make sure to click the save button, found at the bottom right corner of your screen.
Appendix A, Part VIII: Taxon Tree

The taxon tree in Specify stores all of the data about every taxon that we have cataloged in the database. You can use it to search for a taxon name, add a taxon name to the database, or edit any taxon name that already exists in the database. The taxon tree is useful for checking higher-level taxonomic assignment of a given taxon (e.g., if you want to find out a family assignment for a given genus). The taxon tree is also useful for checking whether a taxon is already stored in the database.

STOP

Do you have permission from the Collection Director to work on the Taxon Tree?

Before you view or edit the tree, or try anything in this section, make sure you have permission from your supervisor. You can read through this section to familiarize yourself with the tree, but do not try anything in Specify until you are sure you have the authority to do so.

Viewing the Taxon Tree

At the top of your Specify screen, find the “Trees” icon and click on it. From the new side panel that is now open, choose “Taxon” under “View Tree.” This will open the Taxon Tree. You will see the headings at the top, “Life,” “Kingdom,” “Phylum,” “Class,” “Order,” “Family,” “Genus,” and “Species” with taxon names underneath. You can expand these taxa to see what other taxa fall under them in the tree by clicking on the small arrows to the left of each name. In parentheses next to each name there are numbers, these numbers tell you how many records of that taxon are stored in the database.

You can search the Taxon Tree by typing a search term, such as a genus name, into the search bar located at the bottom left of your screen. Check or uncheck the “Exact” box.
depending on whether you plan to type in the entire taxon name and find only records that match what you typed exactly, or you plan to type in only a partial name and find all names that contain the string of letter that you entered.

Once you have found the taxon you are searching for, you can view the catalog records associated with that taxon by right clicking on the name (make sure that the name is highlighted) and choosing the “Associated Collection Objects” option. This action will open all of the associated catalog records in a “Collection Object” tab.

**Editing the Taxon Tree**

Do you have permission to make edits to the Taxon Tree? Even if you have permission to view the Taxon Tree, be sure that you also have permission to make edits to the tree before proceeding. You can read this section to familiarize yourself with the editing process, but do not
make any edits in the Taxon Tree until you have been cleared to do so by your supervisor. Edits will affect all FLMNH IP *Specify* users and are difficult to change or delete.

At the top of your *Specify* screen, find the “Trees” icon and click on it. From the new side panel that is now open, choose “Taxon” under “Edit Tree.”

The most common reason to make an edit to the Taxon Tree is to add a new genus or species to the database. While cataloging, you may find an identification that has never been cataloged in our database; therefore it will need to be added. This is done by editing the Taxon Tree. If it is a species that needs to be added, you will need to know what the author and publication date for that species is, and whether or not the author and date is in parentheses. Begin by finding the parent taxon. If you are adding a species, find the genus, if you are adding a genus, find the family. Make sure that you have correctly identified the parent taxon before proceeding further (many names are VERY similar in spelling). Use the search bar located at the bottom left of your screen in the Taxon Tree window to find the parent taxon. Once you have found the parent taxon in the tree, right click on it (make sure that the name is highlighted). From the right click menu options, choose “Add Child.” This will open a pop-out menu.
Once the pop-out window is open, type the name of the taxon you want to add in the “Name” box. The “Parent taxon” box should already be filled out for you. If it is a species you are adding, you will also need to fill out the “Author” box, with both the author name and the date, and in parentheses if appropriate. Once you have filled out this information, you can hit the “Save” button. This taxon will be saved to the database and can now be used while cataloging.
In some situations, you will need to move a taxon to a new parent taxon. This happens when identifications are updated, for instance, when a species is moved from one genus into another.

You can do this in the Taxon Tree by first selecting the taxon that you need to move (make sure that the taxon you want to move is highlighted). Click and drag the taxon to its new parent taxon, and drop it there. A pop-out window titled “Tree Action Options” will automatically open. Click the “Move” button in this pop-out window. The taxon will now be moved to its new parent taxon in the Taxon Tree and will be updated in the database.

In some situations, you may need to either merge or synonymize taxa as identifications are updated. This will occur, for instance, when a species name is changed to reflect that it is actually the same as another species. To either merge or synonymize two taxa, first select the taxon that you want to change (make sure the taxon you want to drag is highlighted), click and
drag it to the taxon that it will be changed to, and drop it there. A pop-up box will appear and ask whether you would like to “Merge” or “Synonymize.” Choose the correct option. A synonymy is appropriate if you would still like Specify to recognize the old identification. Once a synonymy has occurred, Specify will still show the original taxon name under the original parent taxon, but as a link that leads to the new, correct parent taxon and taxon name. The new name will become the “Preferred Taxon” but the old name will still be searchable in the database. Merging is appropriate if no record of the original taxon name is needed.
Appendix A, Part IX: User Permissions

Specify 6 allows an administrator to customize access of all users to Specify features.

Administrators have permission to use all features for their collection freely, while other users have more restricted access. Setting these restrictions can be time consuming, with many options to sort through. The purpose of this section is to provide a reference for the FLMNH IP Specify administrator on what permissions should be given at each level of Specify user.

Are you a Specify administrator for the FLMNH IP Collection? Do you have permission from the Collection Director to make changes to the User Permissions? You can read through this section to familiarize yourself with the procedure for changing user permissions, but unless you have administrator permissions in Specify and permission from the Collection Director, you cannot and should not perform any of the operations described below.

Administrative Permissions

Administrators have the highest level of access to the FLMMH IP Specify CMS and have full access to all available features on Specify 6 as well as the ability to make administrative changes, including changing the permission levels of other users. Currently, the Office of Museum Technology Administrator, the IP Collection Director, and the IP Museum Operations Specialist have Administrative permissions.

Manager Permissions

Managers also have full access to the available features of Specify, but they cannot make administrative changes unless they are also an Administrator. All of the Administrators are also
Managers. Other current managers include the Curatorial Assistant and the author (a collections assistant).

Limited Access Users

*Specify 6* allows for a very high degree of customization of permissions. Groups of limited access users can be set up with different limited permissions as needed. Currently, IP has one group of limited access users, which includes all IP cataloging staff, the IP intern, and the IP curator. These users have the ability to view, modify, and add to most categories. The delete function is not available to limited access users for most categories. Recently, we added the delete function for limited access users for the “Collectors” portion of the Data-Collection Object tab. To add or remove permissions for limited access users, choose the correct user group while viewing the IP collections as an administrator on *Specify 6*. There will be a series of checkboxes next to a list of every available feature of *Specify 6*. The checkboxes can be checked...
or unchecked for each feature based on whether that user or user group should be able to View, Add, Modify, or Delete when using that feature.
BIBLIOGRAPHY


BIOGRAPHICAL SKETCH

Katy Estes-Smargiassi was born in Boston, Massachusetts, where she had the great fortune to grow up going to the Boston Children’s Museum, the Museum of Science, the Isabella Stewart Gardener Museum, the Harvard Museum of Natural History and so many more. In 2008 she moved to St. Petersburg, Florida to attend Eckerd College, where she earned a B.S. in Geosciences, with a minor in Physics. After college, Katy joined AmeriCorps VISTA and worked at a very large homeless shelter administered by the Pinellas County Sheriff’s Office in Tampa Bay, Florida. She began the Museum Studies graduate program at the University of Florida immediately following her time in AmeriCorps, concentrating in Paleontology and Collections Management. Throughout her time at UF, Katy interned in the Invertebrate Paleontology Collection at the Florida Museum of Natural History, and was a Graduate Assistant at the University Gallery. Currently, Katy works as a Collections Assistant at the Florida Museum of Natural History and an Archivist at the Cade Museum for Creativity and Invention.