

CaveIS: A Culture Collection Information System for Cave Microorganisms in  
CALABARZON, Philippines

A Special Problem

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CaveIS: A Culture Collection Information System for Cave Microorganisms in  
CALABARZON, Philippines

by

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In partial fulfillment of the requirements for the degree of  
Bachelor of Science in Computer Science

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## **Abstract**

CaveIS is a web application designed to manage culture collections of cave microorganisms in CALABARZON. It facilitates isolate management and employs a role-based access control mechanism to tailor operations for different user levels. Additionally, it features a Taxonomic Tree Viewer that allows users to explore taxonomic relationships and search for accessible isolates. To assess the usability of CaveIS, a System Usability Scale (SUS) questionnaire was administered to 8 respondents, including BS Biology students from the University of the Philippines Los Baños (UPLB) and members of the NICER Program: Center for Assessment of Cave Natural Resources (CAVE) in CALABARZON, affiliated with the Microbial Culture Collection, Museum of Natural History, UPLB. The results yielded an average SUS score of 83.75, indicating a well-designed system that provides a positive user experience.

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# 1 Introduction

## 1.1 Background of the Study

Caves are valuable natural resources with high levels of biodiversity, which enables these natural formations to provide essential ecosystem functions (Medellin et al., 2017). Their relative constant temperatures and large areas of mineral surfaces establish a quasi-extreme environment conducive to many organisms and microorganisms (Saiz-Jimenez, 2012).

Among the organisms caves host are bats called cave-dwelling bats (Quibod et al., 2019). Cave-dwelling bats provide various ecosystem services, including pollination, seed dispersal, and nutrient redistribution through their excrement, known as guano, making them ecologically valuable (Kunz et al., 2011). According to Richards *et al.* (Richards et al., 2014), bat guano is considered the primary source of energy from outside of cave ecosystems, as it provides nutrient support for various cave-dwelling species. In addition, they report that bat guano is also rich in phosphorus and nitrogen, making it an effective organic fertilizer (Richards et al., 2014). However, despite its benefits, De Leon *et al.* (Leon et al., 2018) found that bat guano are also reservoirs of functional and pathogenic bacteria that may pose a risk to humans and other species.

Cave microorganisms play a crucial role in shaping their habitat's distinctive ecological dynamics. They also play other roles such as nutrient cycling and becoming a food source for larger cave-dwelling organisms. However, like the pathogenic bacteria found in bat guano, they may also harbor potential risks and challenges that warrant careful consideration.

Although there are over 3,000 documented caves in the Philippines, research on cave ecosystems in the country remains limited. Insufficient knowledge about caves and the microorganisms they host has led to poor management of these valuable ecological resources, as well as an inadequate understanding of the cave-associated diseases that can be produced by pathogenic bacteria and other microorganisms. This knowledge gap hinders effective conservation efforts and emphasizes the importance of further research and awareness in the field of cave ecology and microorganism-related studies.

## **1.2 Significance of the Study**

The researchers at the Microbial Culture Collection, Museum of Natural History, University of the Philippines Los Baños (UPLB) are concerned about the country's lack of understanding of cave ecology, as well as the inadequate information on the diversity of bacteria in caves. They are isolating and identifying selected microorganisms whose samples were collected from selected caves in CALABARZON. An application focused on providing information from the cave study will help the researchers collate their findings and allow them easier access to previously collected data. Future studies involving said information may also rely on the data stored in the database.

## **1.3 Objectives**

This study sought to design and develop a culture collection information system for microorganisms in caves in CALABARZON. Specifically, this study aimed to:

1. develop a secure and responsive web-based single-page application (SPA) using the selected technology stack;
2. implement an information management system for data collected from caves; and
3. provide a dashboard view to display summary information from the cave study.

## **1.4 Scope and Limitations**

The intended users of the system are individuals with a background in biology who can understand the context behind the information presented. CaveIS operates exclusively through web browsers, as it is web-based and does not support offline services. The creation and modification of an isolate record are constrained by the existing metadata options, which only administrators can update.

## 2 Related Literature

### 2.1 Microbial Culture Collections

Tapay (Mahilum-Tapay, 2009) classifies culture collections into private, specialized, and public categories. Private culture collections are created and maintained by individuals or private institutions for exclusive use and are not made accessible to the public. Specialized collections mainly support microbial research. In contrast, public collections usually contain extensive metadata, which is openly shared with the public. UPLB'S Microbial Culture Collection researchers are utilizing a specialized culture collection for their study on cave microorganisms in CALABARZON.

According to De Leon and Siringan (Leon and m. Siringan, 2022), microbial culture collections help preserve knowledge on various fungal cultures and advance microbial research. Since 1965, the number of microbial culture collections in the Philippines has grown. The Philippine National Collection of Microorganisms (PNCM) stands as the largest general culture collection in the country, housing over 2,000 strains of bacteria and other microorganisms (Monsalud et al., 2002). However, there is still a lack of knowledge and study on cave microorganisms in the country. To effectively handle and manage data in culture collections, suitable database management systems are employed (Leon and m. Siringan, 2022). Certain databases. such as the *BacDive* prokaryotic metadatabase, are readily available online, providing convenient searchability and access to metadata (Reimer et al., 2017).

### 2.2 Web Application Architecture

Fink and Flatow (Fink and Flatow, 2014) define an SPA as a web application that operates on a single web page and utilizes JavaScript, HTML, and CSS for user interactions on the front end. They also highlighted the benefits of developing SPAs, which combine the strengths of traditional web applications and native applications. Like traditional web applications, SPAs are compatible with various operating systems. SPAs also offer the convenience of online accessibility through a web browser, eliminating the need for installation and updates required

by native applications. This flexibility benefits both users and developers, as SPAs can be updated more frequently. Additionally, SPAs provide a fast and responsive experience by utilizing client-state management where interactions are processed on the client-side, rather than waiting for the server to process requests.

By providing a platform for UPLB's Microbial Culture Collection researchers to consolidate their findings on microorganisms found in CALABARZON caves, CaveIS will facilitate smooth and secure progress in cave research. CaveIS will utilize the advantages of an SPA to provide users with a seamless and user-friendly metadatabase application, while ensuring convenience and efficiency.

## 3 Methodology

### 3.1 Development Tools

CaveIS was developed on a personal computer with the following specifications:

- Processor: Intel(R) Core(TM) i5-8250U CPU @ 1.60GHz 1.80 GHz
- Installed RAM: 8.00 GB
- System type: 64-bit operating system, x64-based processor
- Operating System: Windows 10

The development of the system relied on a robust technology stack to ensure optimal performance and reliability. MySQL served as the relational database management system, providing structured storage and efficient data management. Express.js, a web application framework for Node.js, facilitated the construction of the backend, while React, a JavaScript library for building user interfaces, was used for the development of dynamic and interactive frontend components. Node.js served as the JavaScript runtime environment, enabling the creation of scalable and efficient server-side applications. Visual Studio Code was selected as the primary Integrated Development Environment (IDE) for editing the project's source code, with Git ensuring effective version control throughout the development process.

To streamline deployment and enhance scalability, the web application's components were hosted across various platforms. Aiven, a renowned Database as a Service (DBaaS) platform, provided scalability and robustness for database management. Netlify, a website deployment platform, offered continuous deployment capabilities, while Render, specializing in managed infrastructure, ensured efficient deployment and scaling of web services and Application Programming Interface (API). For the efficient management of visual assets, Cloudinary, a cloud-based image and video management platform, was integrated into the system.

The integration of these tools contributed to efficient code management and reliable deployment process.

## 3.2 User Levels and Privileges

The use case diagram is shown in Fig. 1. The system employed a role-based access control mechanism, defining specific operations and management capabilities for three distinct user levels: Guest, Researcher, and Administrator. All users share certain common privileges, including the ability to view current statistics of CaveIS data, explore taxonomic relationships of accessible isolates via the Taxonomic Tree Viewer, and export isolate records to a CSV file.

Guest users are restricted to viewing publicly available isolates, authorized users (Researchers and Administrators) have broader privileges. The unique privileges of Researchers and Administrators are as follows:

### 1. Researcher

- Researchers have access to isolates with both *public* and *limited* access levels.
- Researchers have the authority to create, edit and delete isolate records.
- Researchers can update their personal account details, specifically their first name, last name, username, and password.

## 2. Administrator

- Administrators can access all isolate records, including those with *restricted* access levels.
- Administrators have the capability to create new user accounts.
- Administrators can modify user account details, including changing a user's role.
- Administrators can create, edit, and delete metadata options for isolates.

These defined user levels and privileges ensure efficient access control and management within the system.

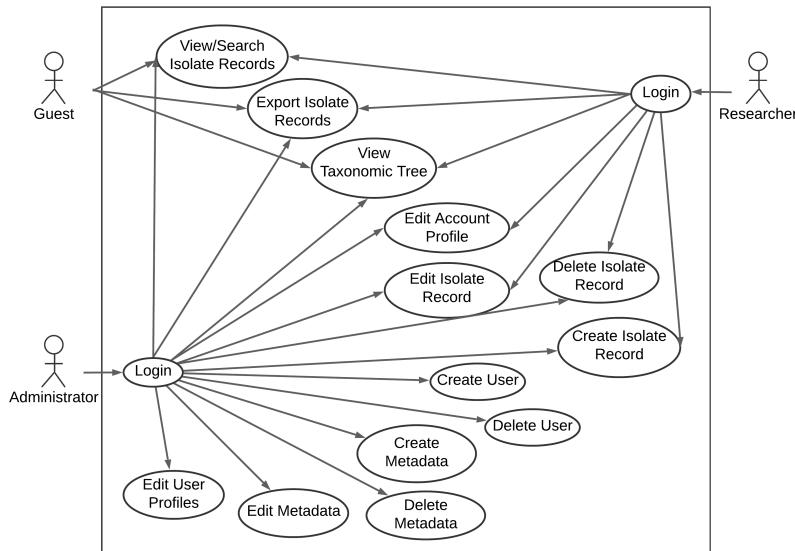


Figure 1: Use Case Diagram

## 3.3 Features

The features of the application are grouped into three parts: User Authentication and Management, Isolate Management and Exploration, and Isolate Metadata Management.

### **3.3.1 User Authentication and Management**

Registered users can log in to their accounts using their username and password, and once authenticated, they have the ability to log out and terminate their session. Administrators hold the capability to create new user accounts by providing the necessary details: user role, first name, last name, email, and username, with passwords being randomly generated and sent to the provided email address. Additionally, administrators can modify an existing user's account details, including their role, first name, last name, and username, as well as delete any existing user account if needed.

### **3.3.2 Isolate Management and Exploration**

Users can access a list of isolate records available within the system and search for specific isolates by their scientific name or accession number. They can create records of isolates by providing the necessary information: access level, organism type, taxonomic information (domain, phylum, class, order, family, genus, species), sample type, analysis method, host type, host genus, host species, cave, sampling point description, institution, and collection. Authenticated users have the ability to modify existing isolate record information, permanently remove isolate records through single or batch deletion, and upload images associated with isolate records. Users can also view and search for accessible isolates via a graphical representation of a taxonomic tree and download selected isolate records in CSV format.

### **3.3.3 Isolate Metadata Management**

Administrators can access a list of isolate metadata and the available options for each. They can create, modify, and delete options for the following isolate metadata fields: organism type, sample type, analysis method, host, cave, sampling point, location, institution, and collection.

### 3.4 Database Design

The database design consists of twelve entries: Collection, Host, Institution, IsolateInfo, Location, Method, Organism, Permission, Role, Sample, SamplingPoint, and User. It also has one association class called RolePermission that defines the relationship between Role and Permission. The unified modeling language diagram is shown in Fig. 2.

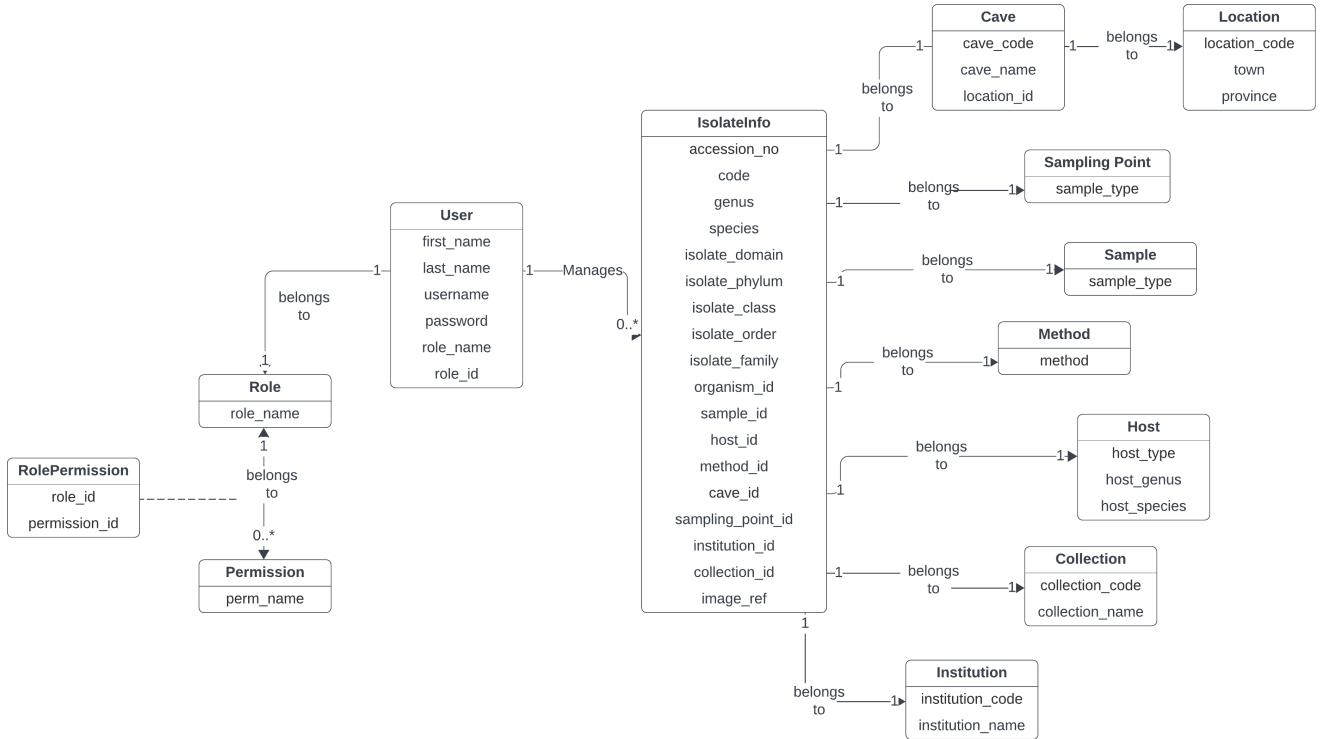


Figure 2: Unified Modeling Language (UML) diagram for CaveIS web application

## 4 Results and Discussions

The web application was created using React for the front end with Ant Design as the UI library. React's component-based architecture promoted modularity and reusability of code, which led to efficient development and maintenance. Additionally, Ant Design's extensive library of pre-built UI components accelerated the development process and ensured a consistent and user-friendly interface.

To further enhance user interaction and data exploration, a dynamic taxonomic tree, a crucial component, was implemented. This component allows users to visualize the hierarchical relationships between different taxonomic classifications of the isolates in the system and search isolates based these classifications. React D3 Tree, a React component for representing hierarchical data, was employed to create the interactive taxonomic tree element.

In the development of the web application, an existing API from the NICER Program for centralizing extensive data on microbial diversity in CALABARZON caves was utilized to streamline back-end configuration and ensure consistent data management. The API and database system provided a robust and comprehensive framework, which facilitated a seamless integration with the frontend. While the existing API provided a solid foundation, the backend functionalities were extended to better suit the application's needs. This included adding new API endpoints to support additional data operations, implementing custom data validation and transformation logic, and enhancing the database schema to accommodate new data types specific to CaveIS.

Additionally, Nodemailer was used to send credentials to new users via email, ensuring secure and efficient account management. They were informed in the email that their passwords can be changed in the account settings page of the web application. This feature streamlined the onboarding process and improved overall user experience.

## 4.1 Web Application

### 4.1.1 Homepage

On the homepage, users can search for isolates by entering their accession number or species name. Search guides are available for both options; users can view these guides by hovering over the icons located before the search options. When searching by accession number, users must follow the format [Collection Code]-[Institution Code]-[Isolate Code] (e.g., MCC-MNH-50001). To search for a species users must include the genus name (e.g., Escherichia coli). Alternatively, users can search by genus name only (e.g., Escherichia).

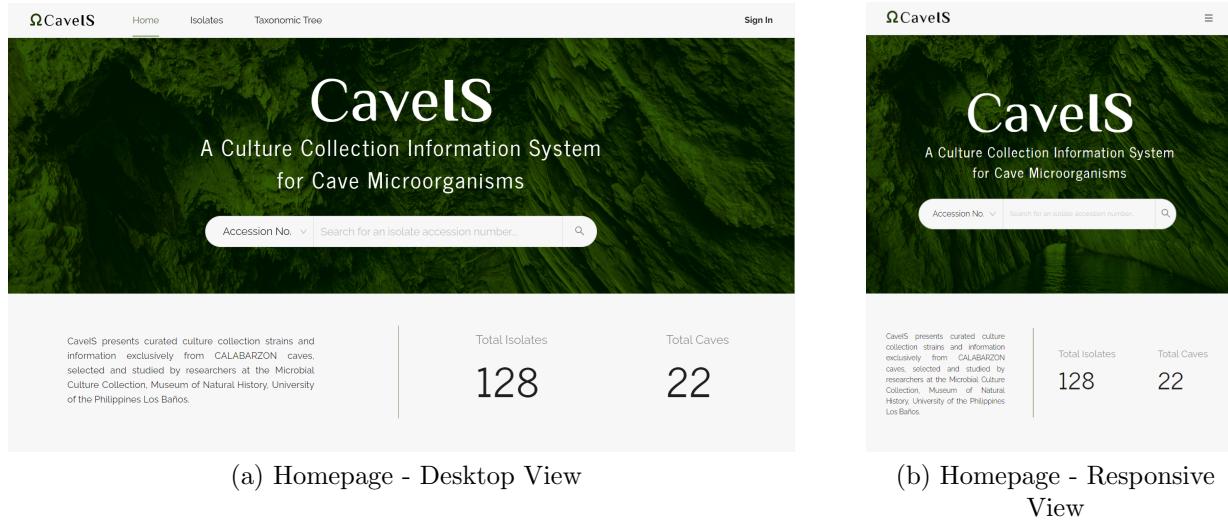


Figure 3: Homepage Displayed in Desktop and Responsive Views

Users can also view CaveIS Statistics on the homepage, where they will find key insights into cave microorganisms presented through concise data visualizations. These visualizations consist of graphs showing isolate distribution across various locations, caves, organism types, and sample types. Users can explore these visualizations to uncover trends, patterns, and summaries of the data, providing valuable insights into the diversity and distribution of cave microorganisms within the system.

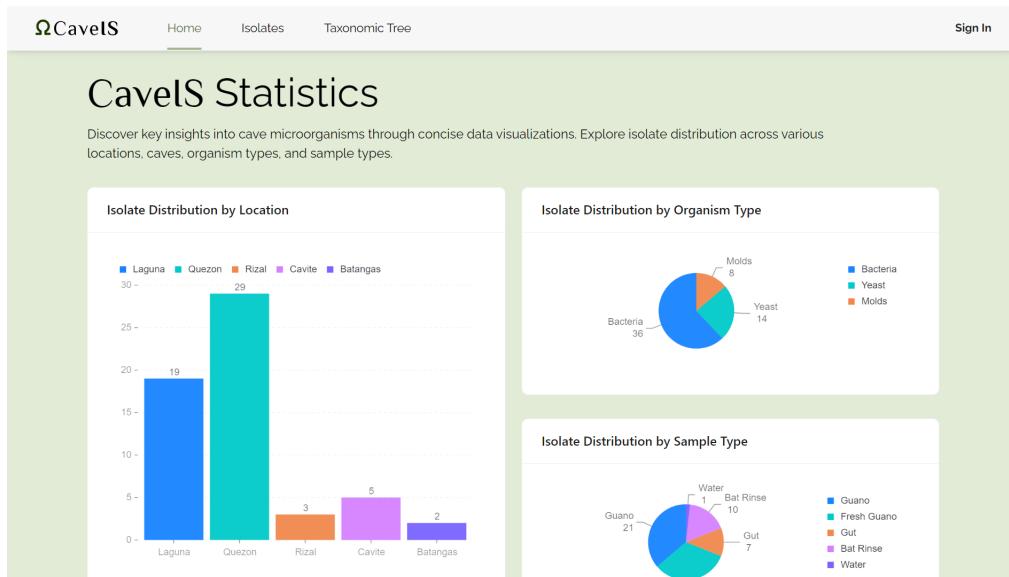


Figure 4: Home Page: Statistics Section

#### 4.1.2 Isolates Page

Users can view a table listing the isolates available to them based on their user level in the Isolates Page. The data in the table can be sorted by isolate code or by genus and species combined. Users can search the table by entering the full genus and species name in the search bar. Additionally, the list of isolate's can be filtered by location, organism type, and sample type. Authenticated users have the added ability to filter isolates by their access level.

When isolates are selected using the checkboxes in the leftmost column of the table, users have the option to either export the selected isolates to a CSV file or delete them. Clicking on a isolate's genus and species name will navigate users to the detailed page for that specific isolate record.

(a) Isolates Page - Desktop View

Code	Isolates (58)	Genus-Species	Accession No.	Location	Organism Type	Sample Type
50001	<i>Escherichia coli</i> >	<i>Escherichia coli</i>	MCC-MNH-50001	Cavinti, Laguna	Bacteria	Guano
50002	<i>Enterobacter aerogenes</i> >	<i>Enterobacter aerogenes</i>	MCC-MNH-50002	Cavinti, Laguna	Bacteria	Guano
50003	<i>Staphylococcus aureus</i> >	<i>Staphylococcus aureus</i>	MCC-MNH-50003	Cavinti, Laguna	Bacteria	Fresh Guano
50004	<i>Bacillus subtilis</i> >	<i>Bacillus subtilis</i>	MCC-MNH-50004	Cavinti, Laguna	Bacteria	Guano
50006	<i>Salmonella enterica</i> >	<i>Salmonella enterica</i>	MCC-MNH-50006		Bacteria	Fresh Guano

(b) Isolates Page - Responsive View

Figure 5: Isolates Page Displayed in Desktop and Responsive Views

#### 4.1.3 Taxonomic Tree Page

Users can explore taxonomic relationships visually with the interactive Taxonomic Tree Viewer on the Taxonomic Tree Page. Users can scroll to zoom in and out of the taxonomic tree, click and drag to move around, and click on nodes to expand or collapse them. Additionally, there are "Expand All" and "Collapse All" buttons for easier exploration.

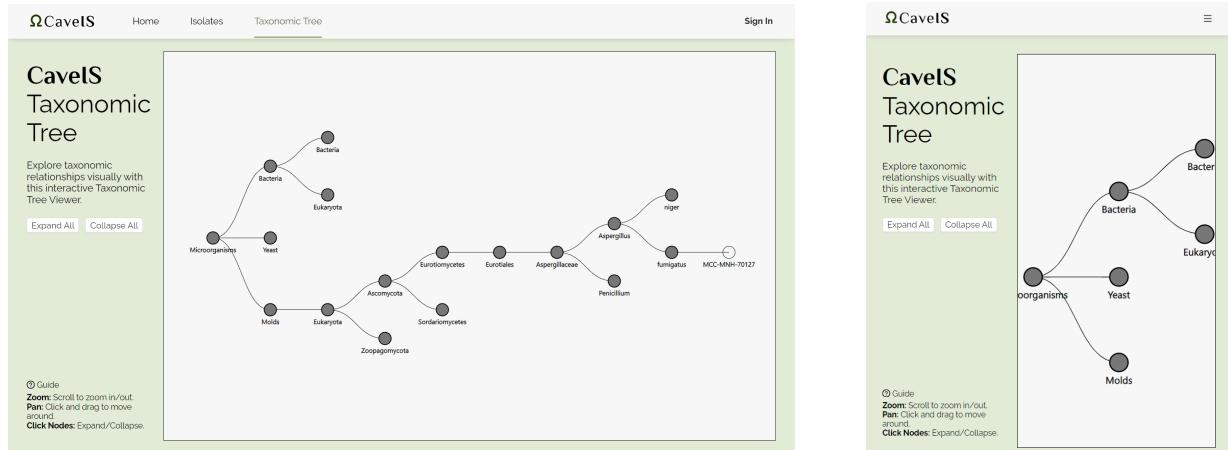


Figure 6: Taxonomic Tree Page Displayed in Desktop and Responsive Views

#### 4.1.4 Login

Registered users can log in to their accounts by entering their username and password. Upon submission, the system verifies the credentials against the stored information in the database. If authentication is successful, the sign-in modal closes, providing users with access to their accounts. If an error occurs, such as an incorrect username or password, the modal remains open and displays an appropriate error message.

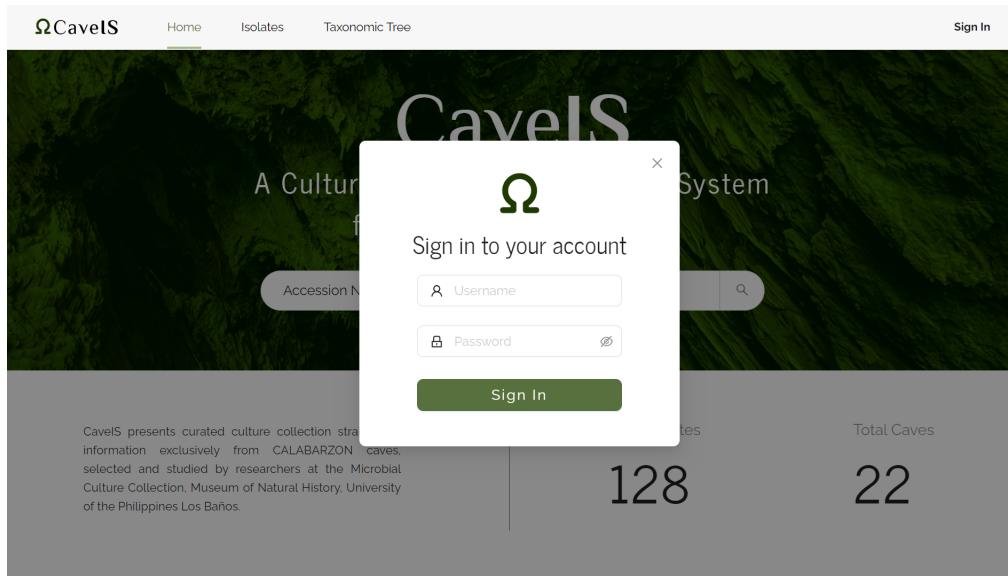


Figure 7: Log In Modal

#### 4.1.5 Create Isolate Page

To create an isolate, users must provide the **Name and Taxonomic Classification** of the isolate, which includes Organism Type, Domain, Phylum, Class, Order, and Family. They must also provide **Isolation, Sampling, and Environmental Information**, which includes Sample Type, Analysis Method, Host Type, Host Genus and Species, Cave, Sampling Point Description, Institution, and Collection. Users must also select the access level of the isolate: Restricted for Administrator access only, Limited for both Administrator and Researcher access, or Public for Guest users. Additionally, users have the option to upload an image associated with the isolate. Before the isolate is created, a modal summarizing all the input will be shown for confirmation. Screenshot of the isolate confirmation modal is shown on Fig. 16.

The screenshot shows the 'Create Isolate' page of the CavesS application. At the top, there is a navigation bar with links for Home, Isolates, and Taxonomic Tree. On the right side of the header is a user profile icon. Below the header, there is a breadcrumb trail showing the current location: Isolates. A prominent green 'Create Isolate' button is located in the top right corner of the main form area. The form itself has several sections:

- Access Level:** A dropdown menu set to "Limited". To its right is a "Upload Image" button and a preview area showing a small thumbnail of an image file named "z.jpg".
- Name and Taxonomic Classification:** This section contains dropdown menus for the following taxonomic ranks:
  - Organism Type: Bacteria
  - Domain: Bacteria
  - Phylum: Proteobacteria
  - Class: Gammaproteobacteria
  - Order: Enterobacteriales
  - Family: Enterobacteriaceae
  - Cave: (This field is partially visible at the bottom)

Figure 8: Create Isolate Page

#### 4.1.6 Isolate Record Page

The isolate record page shows all the information of an isolate. A Researcher or Administrator can edit or delete the isolate in this page.

**(a) Isolate Record Page - Desktop View**

**(b) Isolate Record Page - Responsive View**

Figure 9: Isolate Record Page Displayed in Desktop and Responsive Views

#### 4.1.7 Account Settings Page

Users can view and update their profile details and password settings in this page. They have the option to modify their first name, last name, and username. Additionally, users can change their password by specifying their new password and entering their current password for confirmation.

**(a) Account Settings Page - Desktop View**

**(b) Account Settings Page - Responsive View**

Figure 10: Account Settings Page Displayed in Desktop and Responsive Views

#### 4.1.8 Manage Users Page

In the Manage Users Page, administrators have access to a table listing all users of the web application. This table displays each user's name, username, email, and role. Administrators can create a new user accounts by providing a first name, last name, email, and username. Additionally, administrators must designate a role for the new user. Upon successful creation of the account, the username and a randomly generated password that will serve as the user's login credentials will be sent to the email address of the new user. Furthermore, administrators can edit existing user accounts. They can modify a user's role, first name, last name, and username as needed. Lastly, administrators have the ability to delete an existing user account.

	Name	Username	Email	Role	Actions
	Test Admin	testadmin	testadmin@admin.com	Admin	
	Test Researcher	testresearcher	testresearcher@researcher.com	Researcher	
	Keith Martin	kcmartin	kcmartin@up.edu.ph	Admin	

Figure 11: Manage Users Page

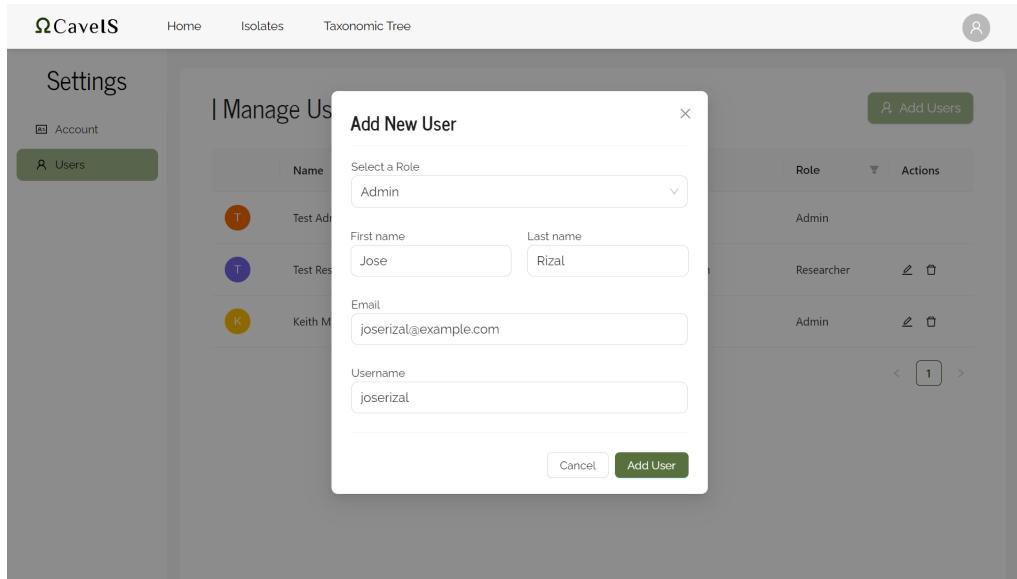


Figure 12: Add User Modal

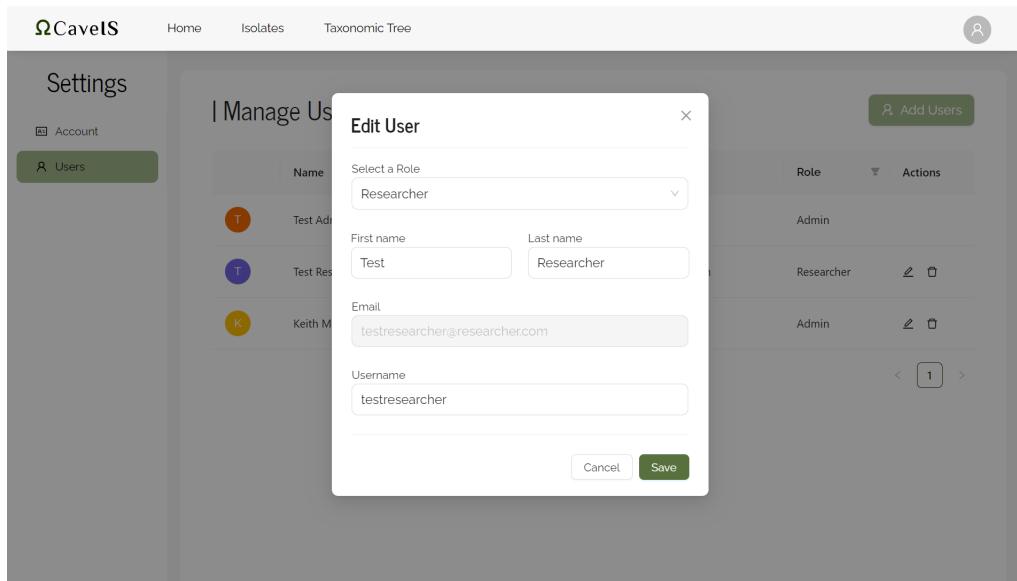


Figure 13: Edit User Modal

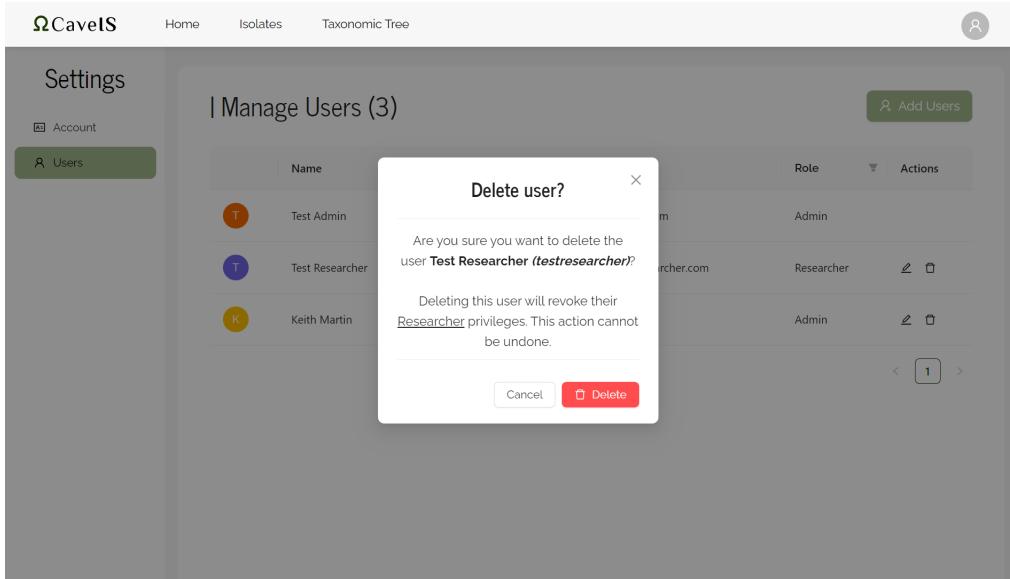


Figure 14: Delete User Modal

#### 4.1.9 Manage Metadata Page

In the Manage Metadata Page, administrators have access to tables of the the metadata fields within the system, which are Organism Type, Sample Type, Analysis Method, Host, and Cave. Each table displays the options specific to the corresponding metadata field, along with their associated properties. Administrators can create and introduce new options, providing flexibility for expanding or customizing the available choices for creating and modifying isolate information. Existing options can be modified or updated to accommodate any necessary changes or updates. Additionally, administrators can remove options from the metadata field, ensuring the maintenance of a concise and relevant set of choices.

Welcome Admin! This page provides you with extensive control over CaveIS isolate metadata, enabling effortless configuration and updates.

Institution Code	Institution Name	Actions
MNH	Museum of Natural History	

Collection Code	Collection Name	Actions
MCC	Microbial Culture Collection	

Organism Type	Actions
Bacteria	
Proteobacteria	
Gammaproteobacteria	
Enterobacteriales	
Enterobacteriaceae	
Escherichia	
coli	

Figure 15: Manage Metadata Page

You are about to create a new isolate with the following details:

- **Domain:** Bacteria
- **Phylum:** Proteobacteria
- **Class:** Gammaproteobacteria
- **Order:** Enterobacteriales
- **Family:** Enterobacteriaceae
- **Genus:** *Escherichia*
- **Species:** *coli*
- **Access Level:** Limited
- **Organism Type:** Bacteria
- **Sample Type:** Guano
- **Analysis Method:** Cultivation Method
- **Host Type:** Bat
- **Host Genus/Species:** *Acerodon jubatus*

Figure 16: Confirm Isolate Creation Modal

The screenshot shows the QCAvEIS application interface. The top navigation bar includes links for Home, Isolates, Taxonomic Tree, and a user profile icon. On the left, a sidebar titled 'Manage Metadata' lists categories: Institutions, Collections, Organism Types, Sample Types, Hosts, Analysis Methods, Sampling Points, Locations, and Caves. 'Locations' is currently selected. The main content area displays a table titled 'Caves (28)' with columns for Location Code and Actions. A modal window titled 'Create Cave' is open in the center, containing fields for 'Cave Code' (with placeholder 'Cave'), 'Name' (with placeholder 'Cave'), and 'Location Code' (with dropdown menu). Below the modal is a table showing two rows: 'BATC' and 'Bat Cave' in the first column, and 'BONIC' and 'Bonifacio Cave' in the second column. At the bottom right of the modal are 'Cancel' and 'Create' buttons.

Figure 17: Example of Create Modal for Metadata Field (Cave)

This screenshot is similar to Figure 17, showing the 'Edit Cave' modal instead of the 'Create' one. The modal displays the same three input fields: 'Cave Code' (ANACC), 'Name' (Anacleta Cave), and 'Location Code' (MQ). The background table 'Caves (28)' is identical to Figure 17, showing the same two rows of data. The 'Save' button is visible at the bottom right of the modal.

Figure 18: Example of Edit Modal for Metadata Field (Cave)

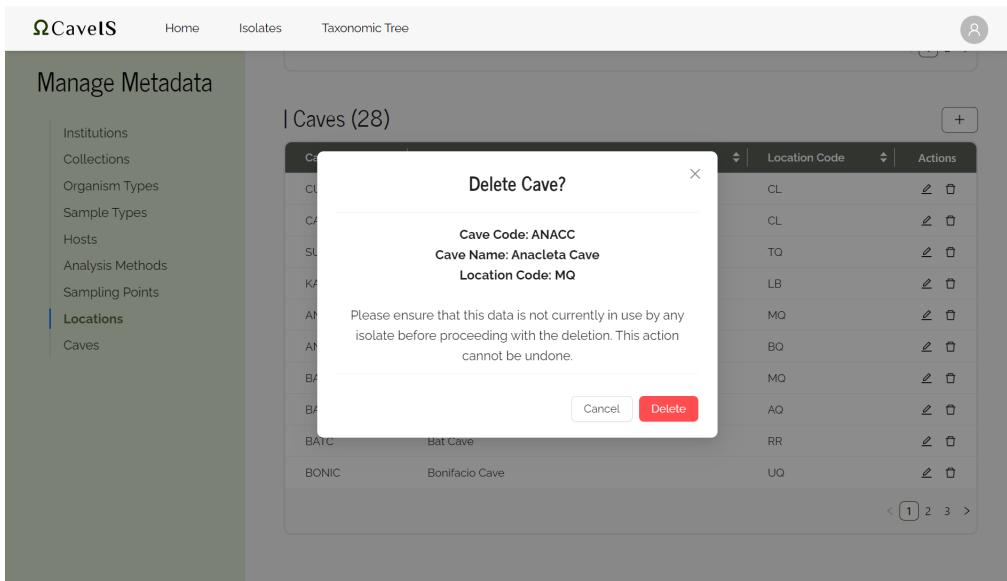


Figure 19: Example of Delete Confirmation Modal for Metadata Field (Cave)

## 4.2 Testing

The usability and effectiveness of the CaveIS web application was evaluated by conducting remote usability testing sessions with a diverse group of participants. This approach allowed participants to test the application at their own convenience and in their own environment to reflect real-world usage scenarios. The testing pool consisted of 8 individuals, including BS Biology students from UPLB and members of the NICER Program: Center for Assessment of Cave Natural Resources (CAVE) in CALABARZON, affiliated with the Microbial Culture Collection, Museum of Natural History, UPLB. Each participant was provided with detailed instructions on how to access the web application. They were also tasked with completing scenarios where they can evaluate its navigation, layout, and overall user interface.

Once participants finished exploring the app with guided instructions, they were asked to fill out a System Usability Scale (SUS) questionnaire in Google Forms. The SUS is a widely used questionnaire for assessing the perceived usability of a system. It consists of a set of ten standardized questions, and respondents are required to rate their agreement or disagreement with statements related to the usability of the system on a five-point Likert scale. On this scale, a rating of 1 indicates "Strongly Disagree", and a rating of 5 indicates "Strongly Agree".

1	I think that I would like to use this system frequently.
2	I found the system unnecessarily complex.
3	I thought the system was easy to use.
4	I think that I would need the support of a technical person to be able to use this system.
5	I found the various functions in this system were well integrated.
6	I thought there was too much inconsistency in this system.
7	I would imagine that most people would learn to use this system very quickly.
8	I found the system very awkward to use.
9	I felt very confident using the system.
10	I needed to learn a lot of things before I could get going with this system.

Table 1: List of Questions in the SUS

Overall, the application received a mean SUS score of 83.75 across all 8 participants. This indicates that the system is well-designed and provides a positive user experience, though they may still be specific areas where improvements could be made to enhance the usability further. Table 1 shows the individual scores from the survey.

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	Individual Score
R1	4	2	5	1	5	1	5	1	4	1	92.5
R2	4	1	5	1	4	1	5	1	5	1	95
R3	3	1	5	2	5	2	5	1	5	3	85
R4	5	1	5	1	4	1	4	1	4	1	90
R5	4	1	5	2	5	1	4	1	4	2	87.5
R6	4	3	4	2	3	2	3	2	4	3	62.5
R7	4	1	5	1	5	1	4	1	5	1	90
R8	5	5	5	3	5	3	5	1	4	5	67.5
Mean											83.75

Table 2: Individual SUS Scores for Participants

In addition to completing the SUS survey, participants were invited to share any additional comments, feedback, or suggestions they had regarding the web application. The following

excerpts highlight key themes and insights from their feedback.

- **Value for Wildlife Scientists and Microbiologists**

Participants noted the significant value the application provides to wildlife scientists and microbiologists. One participant mentioned, "It is nice to have a software like this because I have never heard of databases for microorganisms. This would truly help wildlife scientists and microbiologists identify the organisms present in caves as this location is not that well studied. This would help not only identify but also serve as a good starting point to be well informed and prevent possible zoonotic diseases that might cause harmful effects to human, animal, and environmental health."

- **User Interface Design**

The user interface received positive feedback for its simplicity and aesthetic appeal. A participant remarked, "The user interface is pleasing to the eyes, simple and not overwhelming."

- **Account Management and Data Update**

The ability to manage different types of accounts and update data was seen as a beneficial feature. One participant stated, "Having different types of account depending on the user is a plus, allowing researchers and admin to update data."

- **Data Tracking and Attribution**

Suggestions for improvement in data tracking and attribution were provided. One user suggested, "It would be great if the name of the last one to edit the data and the date could be seen at the bottom of the page." Another added, "Also, it is important to cite the source where the information was retrieved, to assure the user that the information can be trusted." Additionally, a participant recommended, "It might be more helpful to put the specific article published by researchers from Microbial Culture Collection, Museum of Natural History, UPLB to help future researchers gain more knowledge about the isolated cave microorganisms."

- **Overall Usability and Educational Value**

The overall usability and educational value of the application were highly praised. One participant commented, "Overall, the website is easy to navigate, which is good for educational presentations. It serves its purpose and such a system that covers local data is very helpful for researchers." Another participant noted, "It is a really nice, user-friendly web app that will help researchers, even students, to collect information about a certain isolate."

The diverse feedback provided by participants shows the value of the CaveIS web application. These insights serve as guidance for refining the application's functionality and ensuring its effectiveness as a valuable tool.

## 5 Conclusion

The study successfully developed a web application that serves as a culture collection information system for cave microorganisms, offering researchers and microbiologists a way to collate their findings on cave microorganism research. It also allows users easier access to previously collected data. The web application was able to achieve its objectives of developing a secure and responsive web-based SPA. It was able to provide a way for authenticated users to manage isolate records and metadata options. Lastly, it was able to provide users graphical representations of summary information of isolates within the system. Successful results from the SUS survey and positive feedback from the testers indicate that CaveIS will prove to be useful for both researchers and students in the field of microbiology, facilitating more efficient data management and potentially aiding in the discovery and study of new cave-dwelling microorganisms locally.

## 6 Recommendations

Future work can broaden the scope of the web application by incorporating project management features within the system. This would allow isolates and researchers to be assigned to

specific projects, thereby aiding in the management and control of access to particular isolate records. Additionally, the database structure can be improved to provide more comprehensive information about cave microorganisms and isolates. Enhancements to the database would support more detailed and accurate data analysis and reporting.

Since this study was only able to gather a small sample size for testing, future research should consider increasing the sample size to enhance the validity and generalizability of the findings. A larger sample would provide a more comprehensive understanding of the system's usability. Several participants from the testing suggested adding links to references or articles where the information was sourced to ensure the reliability of the data. This addition would also improve transparency and trust in the information provided by the system.

Implementing these recommendations would significantly enhance the functionality, reliability, and usability of the web application, ultimately benefitting researchers and the broader scientific community.

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