



CMSC 190 SPECIAL PROBLEM, INSTITUTE OF COMPUTER SCIENCE

## BATSeq: A Web-Based System for CAVES's Nucleotide Sequences with Integrated Localized Basic Local Alignment Search Tool

Ramnick Francis P. Ramos and Arian J. Jacildo

**Abstract**— In 2021, the University of the Philippines Los Baños Museum of Natural History (UPLB-MNH), through the DOST-NICER Center for Cave Ecosystem Research (CAVES) Program, generated a comprehensive dataset containing microbial metadata and corresponding 16S rRNA sequences from cave ecosystems in CALABARZON. Despite the volume and scientific value of these outputs, no existing platform consolidated, visualized, or communicated these nucleotide findings for researchers or the general public.

This study developed *BATSeq*, a web-based database management system that centralizes the CAVES Program's nucleotide datasets and integrates core bioinformatics features, including FASTA visualization, phylogenetic tree generation, and a localized implementation of the Basic Local Alignment Search Tool (BLAST) for sequence similarity analysis. The system was evaluated through the System Usability Scale (SUS) and a task-based usability test was administered to 11 respondents with backgrounds in microbial research.

*BATSeq* obtained a SUS score of 75.45, placing it within the "Good" usability category. The task-based evaluation produced an overall mean score of 4.27 out of 5, indicating strong approval of the system's dashboard, CRUD functionalities, BLAST module, sequence visualizer, and phylogenetic tree. These results suggest that *BATSeq* is both usable and effective in supporting data curation workflows for nucleotide sequences within the CAVES Program. Future improvements may focus on enhancing navigation for novice users, expanding visualization features, and extending integration to related MNH bioinformatics systems.

bat guano, bioinformatics, BLAST, cave ecosystems, database systems, metagenomics, RNA sequences, sequence alignment

### I. INTRODUCTION

#### A. Background of the Study

In 2021, the Museum of Natural History of the University of the Philippines—Los Baños (UPLB-MNH), together with the Department of Science and Technology—Niche Centers in the Regions for R&D (DOST-NICER) Program, launched the Center for Cave Ecosystem Research (CAVES) [1]. CAVES, which is a three-year venture program, seeks to implement research-based protection of cave biodiversity within the region of CALABARZON through conservation management.

aim of biologically profiling these caves on aspects specific to the microbial culture within the bat guano isolates in there, have created datasets that provide useful insights regarding the biodiversity of the caves within the said region – aiding in the ecosystem surveillance and protection by the said research organizations.

In depthly, this program was established under the mission of conserving cave ecosystems through a thorough understanding of the ecological systems that exists therein through analyzing the various specimens from cave-dwelling species – particularly bats. Of these research-based ventures, one key output was the paper "Antibiotic-resistant Gram-negative Bacteria from the Fecal Pellets of Bats Collected from the Caving Underground River and Cave Complex, Cavinti, Laguna, Philippines" [2]. This observational biology paper provided insights, particularly on the bacterial characteristics and identity, through the 16S ribosomal ribonucleic acid (16S rRNA) of isolates. Nucleotide sequences, particularly rRNA sequences, provide a vital role in the exposition of the "changing environmental conditions" of an ecosystem where a bacteria had developed [3].

This sequence, through identification and phylogenetic analysis, will then provide an explanation on the evolutionary development of bacteria within it– which for this specific research project, the caves ecosystem in the CALABARZON Region.

To wit, the provision of the bacterial identity of bat guano samples or isolates through these rRNA sequences of the CAVES Program is crucial, for it provides an additional layer of understanding of the ecological role of cave organisms, particularly bats, in these caves. Adjunct to this bacterial identity identification, there exists current efficiency issues regarding leading bioinformatics tools that provide the bacterial identity of a given 16S rRNA sequence; this then impatively hinders the research within the NICER CAVES Program. Specifically, the National Center for Biotechnology Information (NCBI), particularly with their commonly used BLAST+ web service for identifying bacteria, had been known to have recurring unavailability tendencies (Error 505) due to web traffic [4].

Having said, this developmental study aims to provide an

# BATSeq: A Web-Based System for CAVES's RNA Sequences with Integrated Localized Basic Local Alignment Search Tool

Tailored for CAVES Program by UPLB-MNH

NAME OF PROJECT:

Bat Seq

PRESENTED BY:

Ramnick Francis P. Ramos



# Ramnick Francis Ramos

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Museum of Natural History - UPLB (UPLB-MNH)



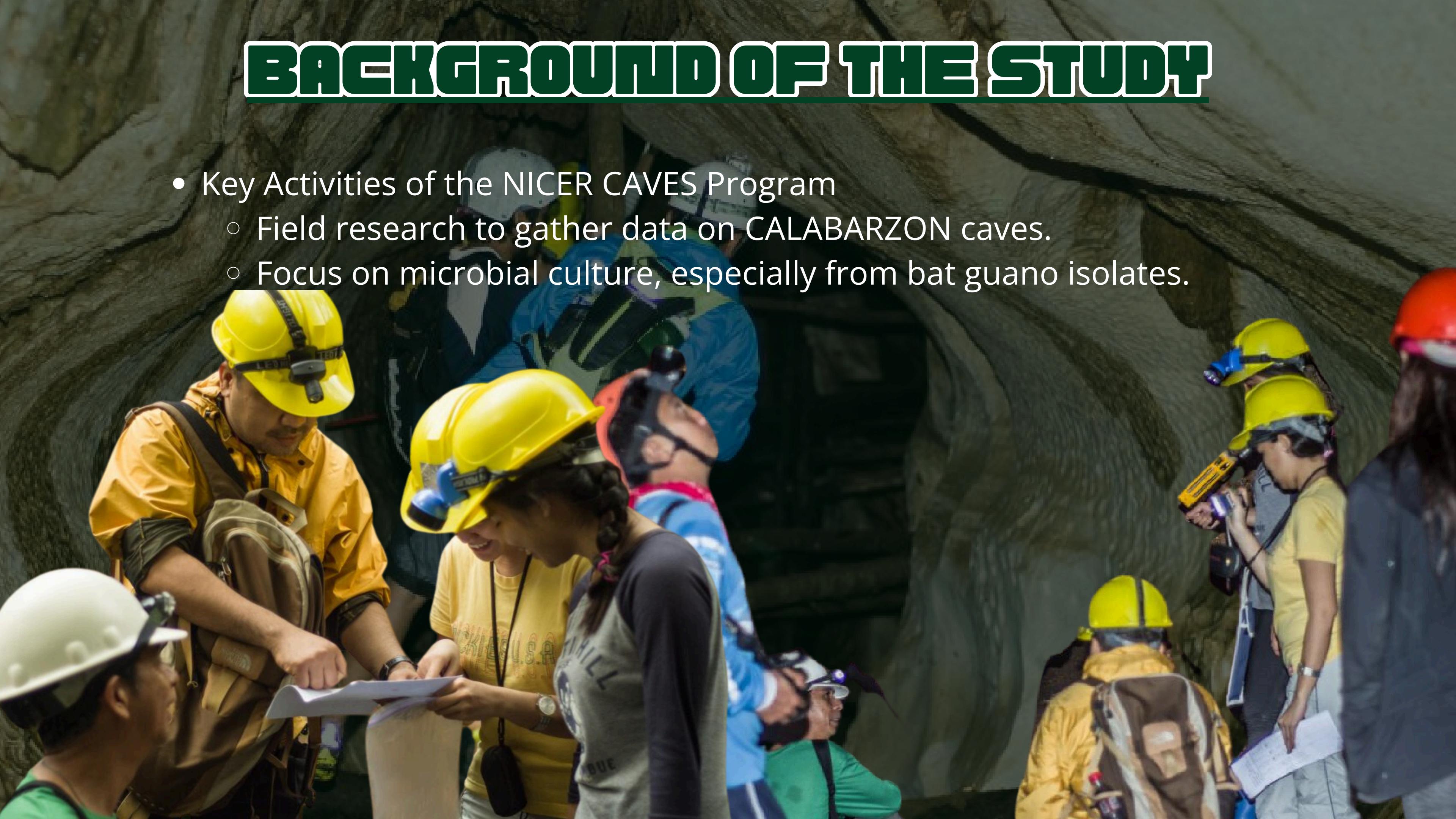
University of the Philippines  
**LOS BAÑOS**

# BACKGROUND OF THE STUDY

- The launching of the Center for Cave Ecosystem Research (CAVES) Program in 2021 [1][2]
  - it is a Collaboration between the UPLB Museum of Natural History (UPLB-MNH) and DOST-NICER Program and other research agencies.
  - Aims to promote research-based protection of cave biodiversity in CALABARZON through conservation management.



# BACKGROUND OF THE STUDY

A photograph showing a group of researchers in a dark, rocky cave. They are wearing yellow hard hats with headlamps and safety gear. One researcher in the foreground is holding a white clipboard and pointing at a large, textured rock formation. Other researchers are visible in the background, some holding cameras or equipment. The environment is dimly lit by their headlamps.

- Key Activities of the NICER CAVES Program
  - Field research to gather data on CALABARZON caves.
  - Focus on microbial culture, especially from bat guano isolates.

# BACKGROUND OF THE STUDY

- The said research program then had outputted several Observational Field Research that provided comprehensive datasets regarding cave ecosystem within CALABARZON - **particularly on bat guano isolates [2]**
- This research program had performed Biological Environmental Profiling through Metagenomics to aid in ecosystem surveillance and conservation

Sibal et al.: Antibiotic-resistant Gram-negative Bacteria from Bat Fecal Pellets

**Antibiotic-resistant Gram-negative Bacteria from the Fecal Pellets of Bats Collected from the Cavinti Underground River and Cave Complex, Cavinti, Laguna, Philippines**

Lou Gene B. Sibal<sup>1,2\*</sup>, Glaezel Angelique T. Barredo<sup>1</sup>, Noel G. Sabino<sup>1,2</sup>, and Marian P. De Leon<sup>2</sup>

<sup>1</sup>Microbiology Division, Institute of Biological Sciences, R.B. Espino Wing, L.B. Uichanco Hall, University of the Philippines Los Baños, College, Laguna 4031, Philippines

<sup>2</sup>University of the Philippines Museum of Natural History, CFNR Quadrangle, Upper Campus, University of the Philippines Los Baños, College, Laguna 4031, Philippines

Keywords: antibiotic resistance, bats, caves, enteric bacteria, pathogens

# BACKGROUND OF THE STUDY

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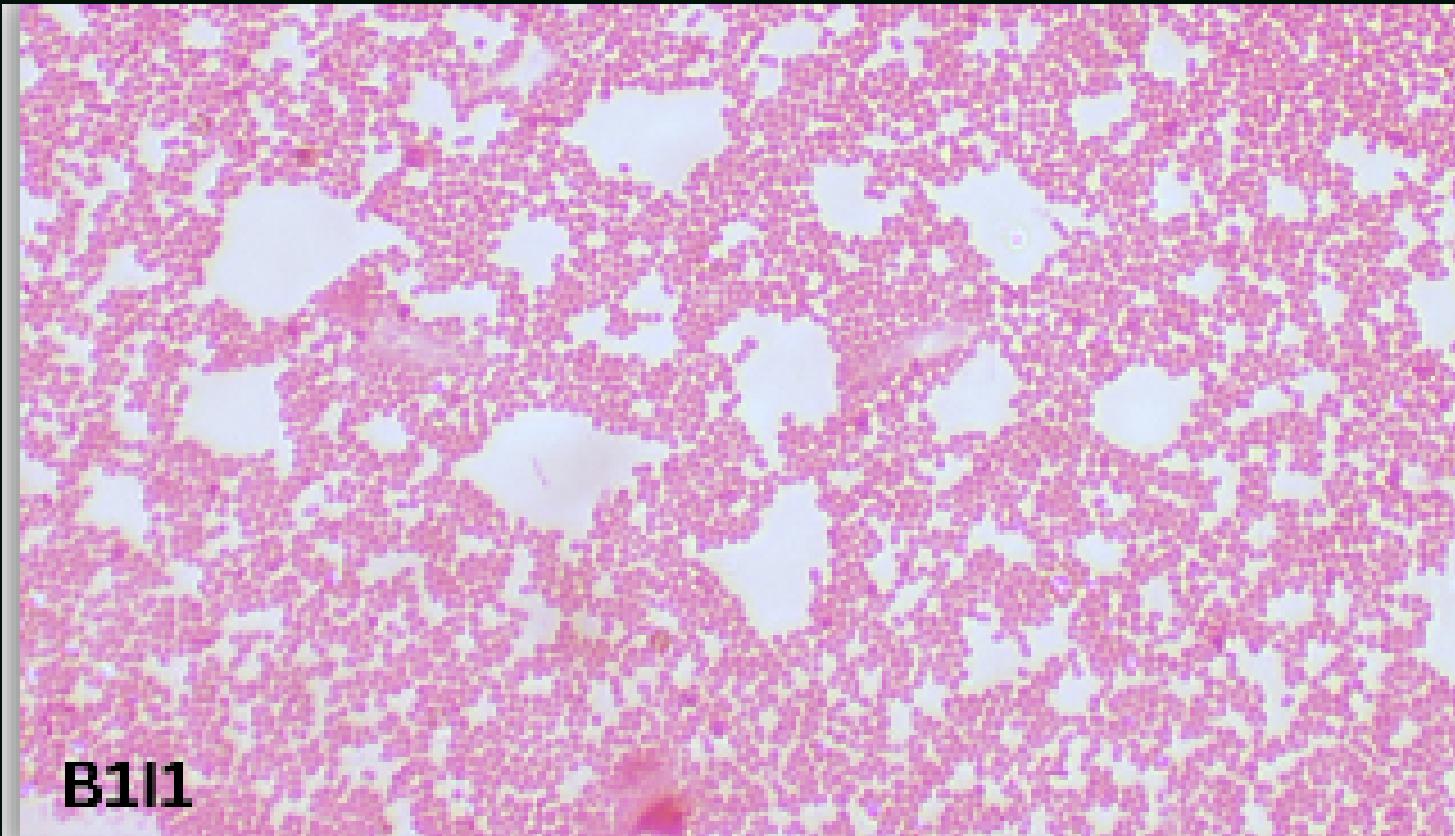
Keywords: antibiotic resistance, bats, caves, enteric bacteria, pathogens

- **16S Ribosomal RNA Analysis of Bat Guano**
  - Critical for identifying bacterial characteristics and their environmental adaptations.
  - Provides insights into evolutionary development within cave ecosystems, providing another layer of understanding

B6I2



# **BACKGROUND OF THE STUDY**



```
>H231124-R03_C13_B1I1_27F.fasta 1207
CGCAGTGGCGGCAGCTACACATGCAG
TCGAACGGTAACAGAAAGCAGCTTGC
TGCTTGCTGACGATTGGGTTAACGTC
CCGCAACGAGCGCAACCCTTATCCTT
TGTTGCCAGCGGTCCGGCCGGAACT
CAAAGGAGACTGGCAGTGATAACTGG
AGAGAAGGGGGGGGAATAGACTCAAG
TTCTCTCTGGGGCCCTTAGAACACAGG
GGTTAACCC CGGGGA...
```

- Through understanding the RNA of these bat sample, the ecological role of bats in cave ecosystem is highlighted

# BACKGROUND OF THE STUDY

Copy of Isolates Data per Thesis Student (Project 4 - Study 2)

File Edit View Insert Format Data Tools Extensions Help

100% 5% 0.0 123 Arial 11 B I H A Y

	C	D	E	F	G	H	I	J	K	M	N
11											[Sequence]
12	Bat fecal pellet	<i>Rhinolophus rufus</i>	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... <input type="button" value="Oxidase-negative"/>	Oxidase-negative <input type="button" value="Non-endospore-forming"/>	-	-		
13	Bat fecal pellet	<i>Rhinolophus arcuatus</i>	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... <input type="button" value="Oxidase-negative"/>	Oxidase-negative <input type="button" value="Non-endospore-forming"/>	Ampicillin-resistant	portunistic human patho...	>H231124_R03_E1_B21_	
14	Bat fecal pellet	<i>Rhinolophus arcuatus</i>	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... <input type="button" value="Oxidase-negative"/>	Oxidase-negative <input type="button" value="Non-endospore-forming"/>	Ampicillin-resistant	ntially pathogenic to hu...	>H231124_R03_K02_B22_	
15	Bat fecal pellet	<i>Ptenochirus jagori</i>	Ind River and Cave Complex	Gram-negative	Rod-shaped	Obligate aer... <input type="button" value="Oxidase-positive"/>	Oxidase-positive <input type="button" value="Non-endospore-forming"/>	Multidrug-resistant	-	>H231124_R03_K11_B31_	
16	Bat fecal pellet	<i>Ptenochirus jagori</i>	Ind River and Cave Complex	Gram-negative	Rod-shaped	Obligate aer... <input type="button" value="Oxidase-positive"/>	Oxidase-positive <input type="button" value="Non-endospore-forming"/>	Multidrug-resistant	ut ( <i>Oncorhynchus mykiss</i> )	>H231124_R03_G11_B32_	
17	Bat fecal pellet	<i>Hipposideros leleupi</i>	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... <input type="button" value="Oxidase-negative"/>	Oxidase-negative <input type="button" value="Non-endospore-forming"/>	-	-	>H231124_R03_A11_B61_	

BAT SEQ Dashboard About BLAST View Phylogenetic Tree

B111 B112 B211

Isolate Code B111 Isolate Code B112 Isolate Code B211

Type of Sample Bat fecal pellet Type of Sample Bat fecal pellet Type of Sample Bat fecal pellet

Source *Rhinolophus rufus* Source *Rhinolophus rufus* Source *Rhinolophus rufus*

Cavinti Underground River and Cave Complex, Cavinti, Laguna Cavinti Underground River and Cave Complex, Cavinti, Laguna Cavinti Underground River and Cave Complex, Cavinti, Laguna

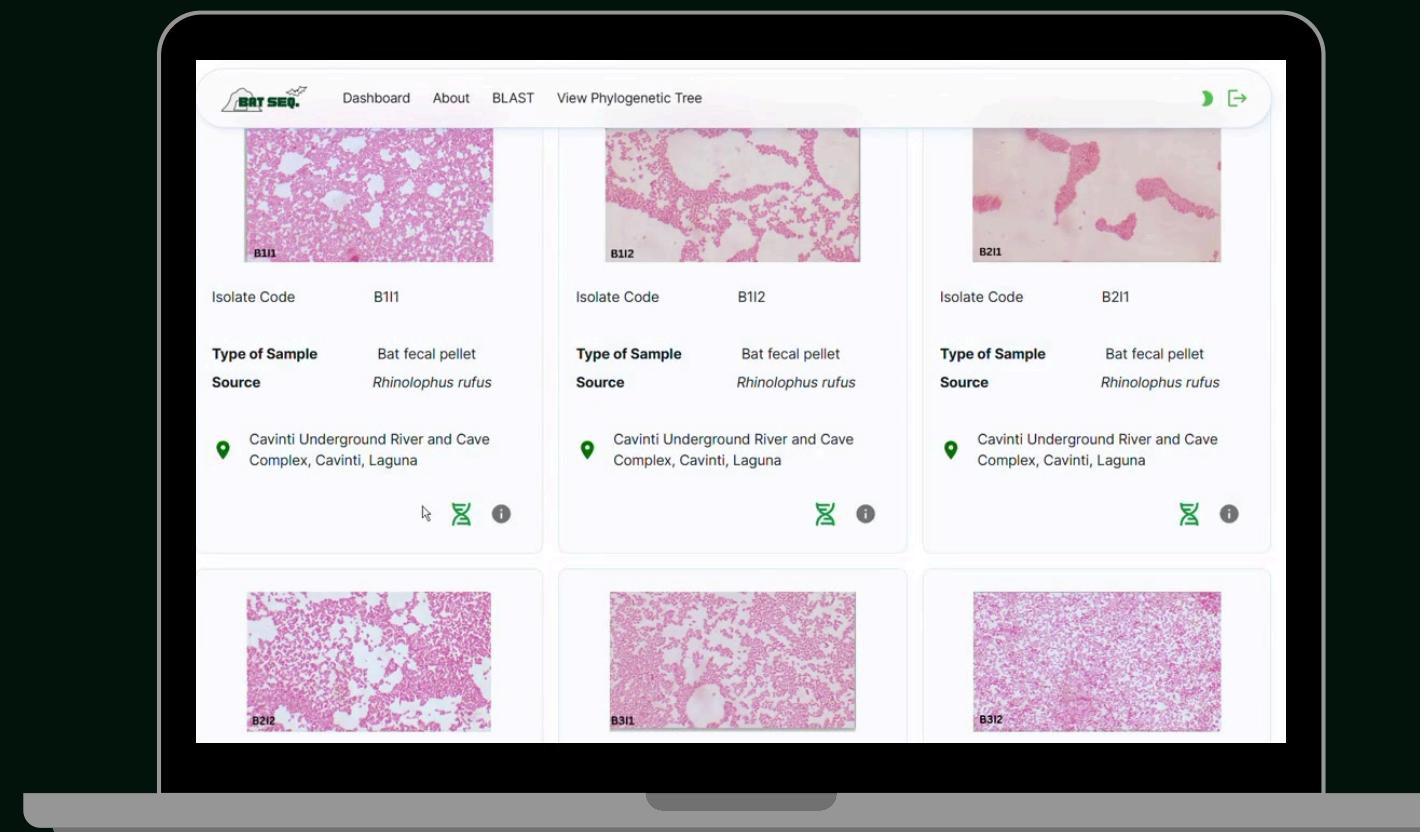
B112 B311 B312

# BACKGROUND OF THE STUDY

There then exists a need for an interface that communicates the current findings of nucleotide-information-bearing research within the NICER-CAVES program.

With the need for resource-intensive expansive genomic mapping, localizing a **basic alignment search tool** through a customization for the needs of the NICER-CAVES would be beneficial for the optimal bioinformatics-tool needs of their researchers.

Copy of Isolates Data per Thesis Student (Project 4 - Study 2)												
Oxidase-negative												
	C	D	E	F	G	H	I	J	K	M	N	
												ITCTGATACGGCAAGCCTT TAGCGTGAATGGTAG CCCTGTGACGAAGACTG GATTAGATACCTGGTAG GTCAGTGAACTGGCTGG GGGAGTACGGCCCAAAG CAAGCGGTGAGCATGTT TGGGCTTACATCCACGG ACCGTGAACAGCGTCTG TTGGAAATGTCGCCGAA TCCGGCCGAGACTGAA GGGGGATAAGACTGAGTT CCGGGGAA
12	Bat fecal pellet	Rhinolophus rufus	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... Oxidase-negative	Non-endospore-forming	-	-	-	>H231124_R03_E11_B21_1 AGATGTGGCGCAGCC TTGGCTTGGTGACCG AAGATGTTGGCGGCG >H231124_R03_K09_B21_2 GCCCTTGCGGGAGCTAI CTCTCGTGACGGCTG AAGATGTTGGCGGCG >H231124_R03_K11_B31_1 AGATGGCGCAGCTTCAAT CGGGGGGGGGGGGGGG AAGATGTTGGCGGCG >H231124_R03_G11_B31_2 GCAGGGGGGGCAGCTAC CTCTTGAAAGCGCGGAA TGSGGGGAAACCTTGGAG AAGATGTTGGCGGCG >H231124_R03_A11_B51_1 CGGGGGGGGGGGGGGG GCTGGGGGGGGGGGGGG CGATGAGGGGGGATAAC GCAAGACCAAGAGGGG GATGGGTTAGCTTGTAG TAGCTGTTCTGAGAGGAT GACTCTACGGGAGGGCA TGATGGCGCGCATGGCGG	
13	Bat fecal pellet	Rhinolophus arcuatus	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... Oxidase-negative	Non-endospore-forming	Ampicillin-resistant	portunistic human pathogen			
14	Bat fecal pellet	Rhinolophus arcuatus	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... Oxidase-negative	Non-endospore-forming	Ampicillin-resistant	initially pathogenic to humans			
15	Bat fecal pellet	Ptenochirus jagori	Ind River and Cave Complex	Gram-negative	Rod-shaped	Obligate aer... Oxidase-positive	Non-endospore-forming	Multidrug-resistant	-			
16	Bat fecal pellet	Ptenochirus jagori	Ind River and Cave Complex	Gram-negative	Rod-shaped	Obligate aer... Oxidase-positive	Non-endospore-forming	Multidrug-resistant	ut ( <i>Oncorhynchus mykiss</i> )			
17	Bat fecal pellet	Hipposideros lekaguli	Ind River and Cave Complex	Gram-negative	Rod-shaped	Facultative a... Oxidase-negative	Non-endospore-forming	-	-	-	>H231124_R03_A11_B51_2 CGGGGGGGGGGGGGGG GCTGGGGGGGGGGGGGG CGATGAGGGGGGATAAC GCAAGACCAAGAGGGG GATGGGTTAGCTTGTAG TAGCTGTTCTGAGAGGAT GACTCTACGGGAGGGCA TGATGGCGCGCATGGCGG	





# SIGNIFICANCE OF THE STUDY

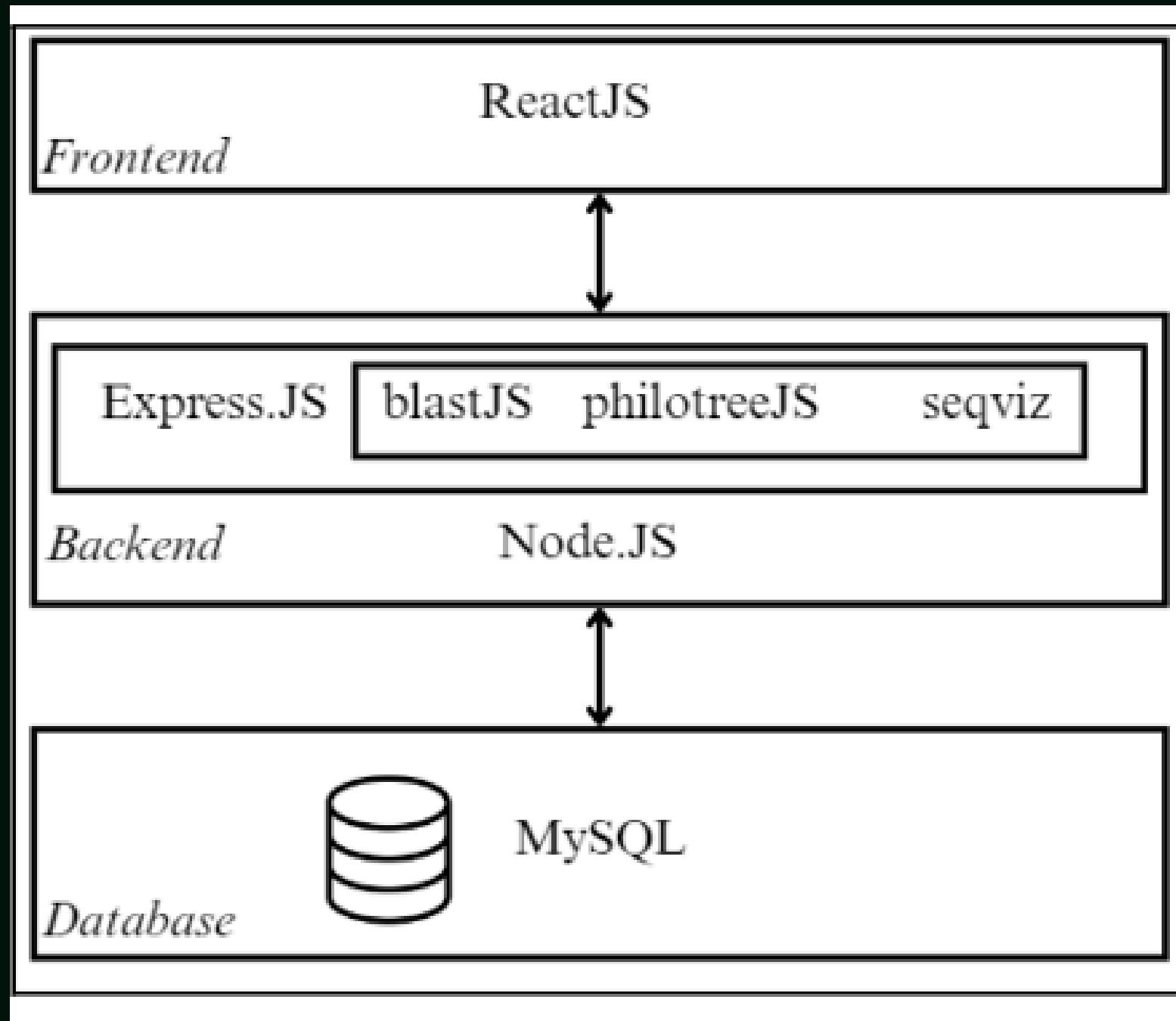


- **BAT Sequences , A Nucleotide Bank**
  - addresses the communication gap of the research findings on nucleotides to the public that the outputs within this program face
  - through localizing and hosting the basic local alignment search tool in a dedicated server space, the integrated BLAST within the system will then be able to optimally manage the specific needs of researchers within the CAVES Program
    - expansive genomic mapping needs will be addressed as the localization of the BLAST-ing will ensure a more robust and realibale tool for CAVES's researchers

# **OBJECTIVES OF THE STUDY**

- 1) To develop a web-based ribonucleic acid sequence database system tailored to addressing the functional needs of researchers of the Center for Cave Ecosystems Research (CAVES) of the University of the Philippines Los Banos Museum of Natural History (UPLB MNH);
- 2) To streamline the data curation process of researchers under the CAVES Program by developing an interface that will enable them to view a report dashboard, perform basic creation, reading, updating, and deletion operations on deoxy- and ribonucleic acid sequence, to view the phylogenetic tree of the current dataset, and to perform Basic Local Alignment Search Tool (BLAST) searching within the database; and
- 3) To assess the effective performance of said web-based database management system vis-a-vis its unit-specific functions.

# PROPOSED SOLUTION

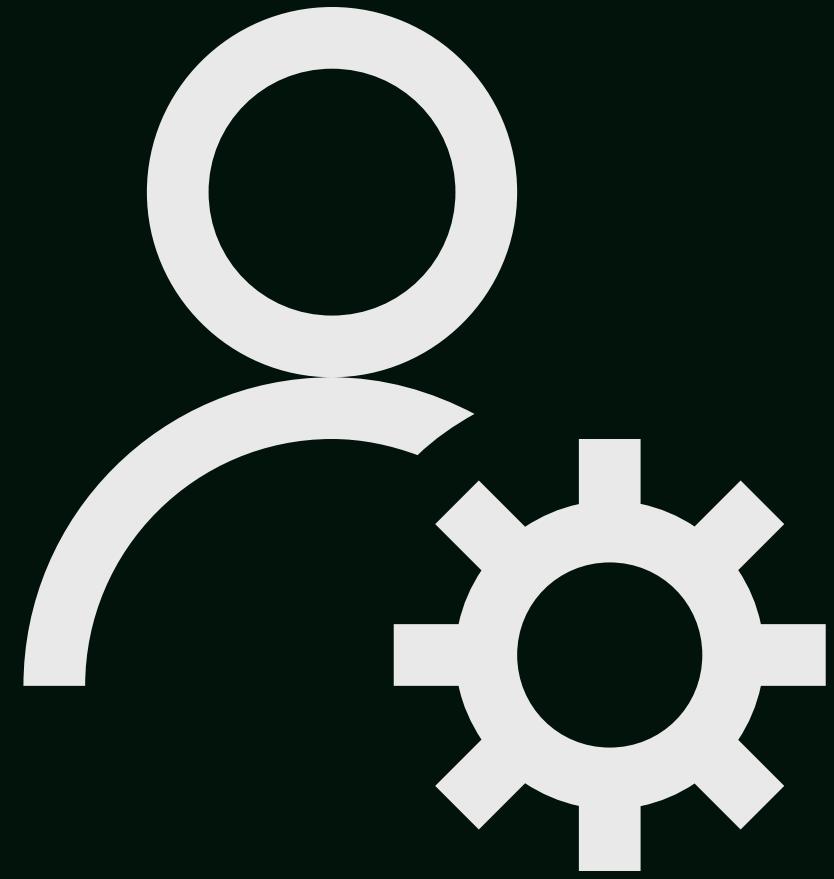


Development of a MySQL, ExpressJS, ReactJS, NodeJS (MERN) Application for a Management Database System that incorporates Bioinformatics Module for BLAST, Phylogenetic Tree Creation, and Sequence Visualizing

Fig. 1. System Architecture Diagram of the MERN Stack Environment with the bioinformatics/visualization libraries

# **PROPOSED SOLUTION**

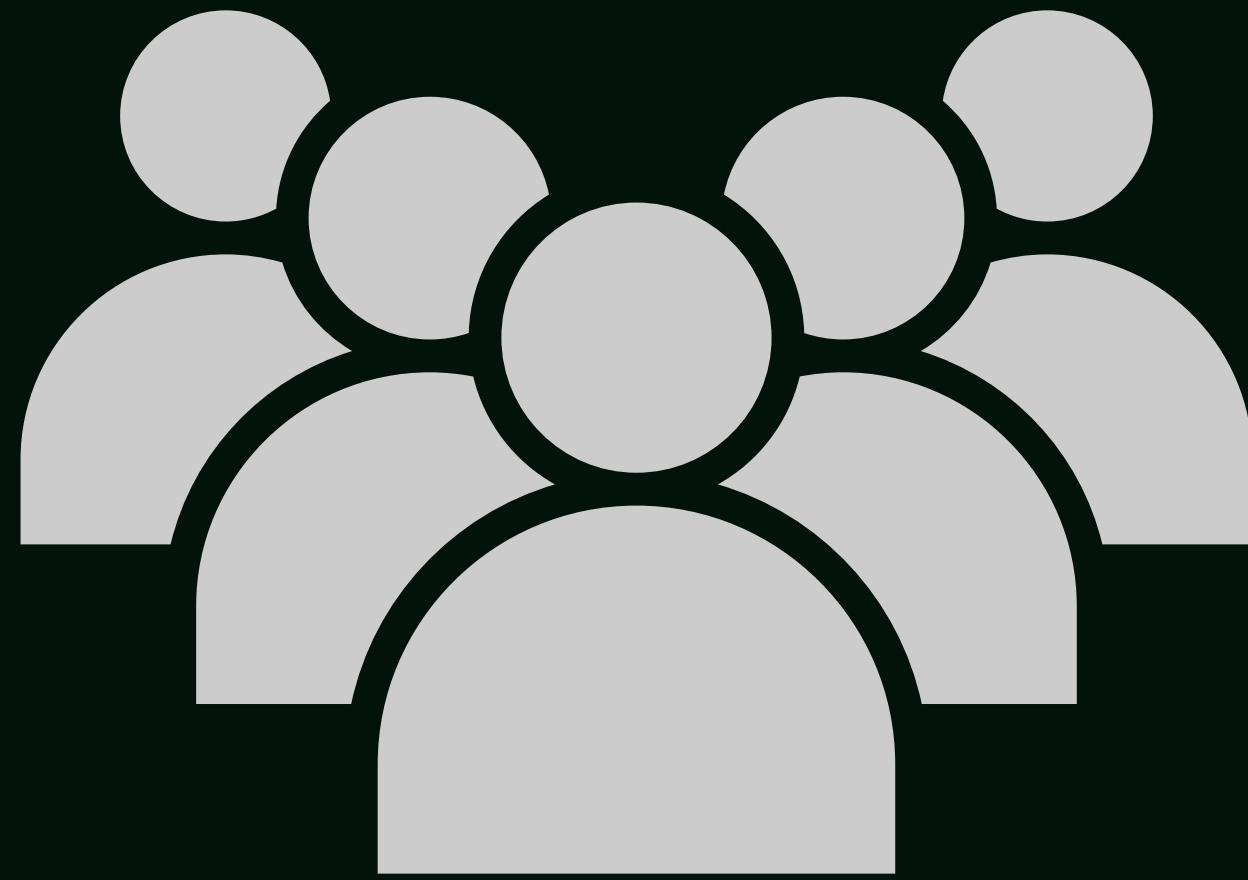
## **TYPES OF USERS**



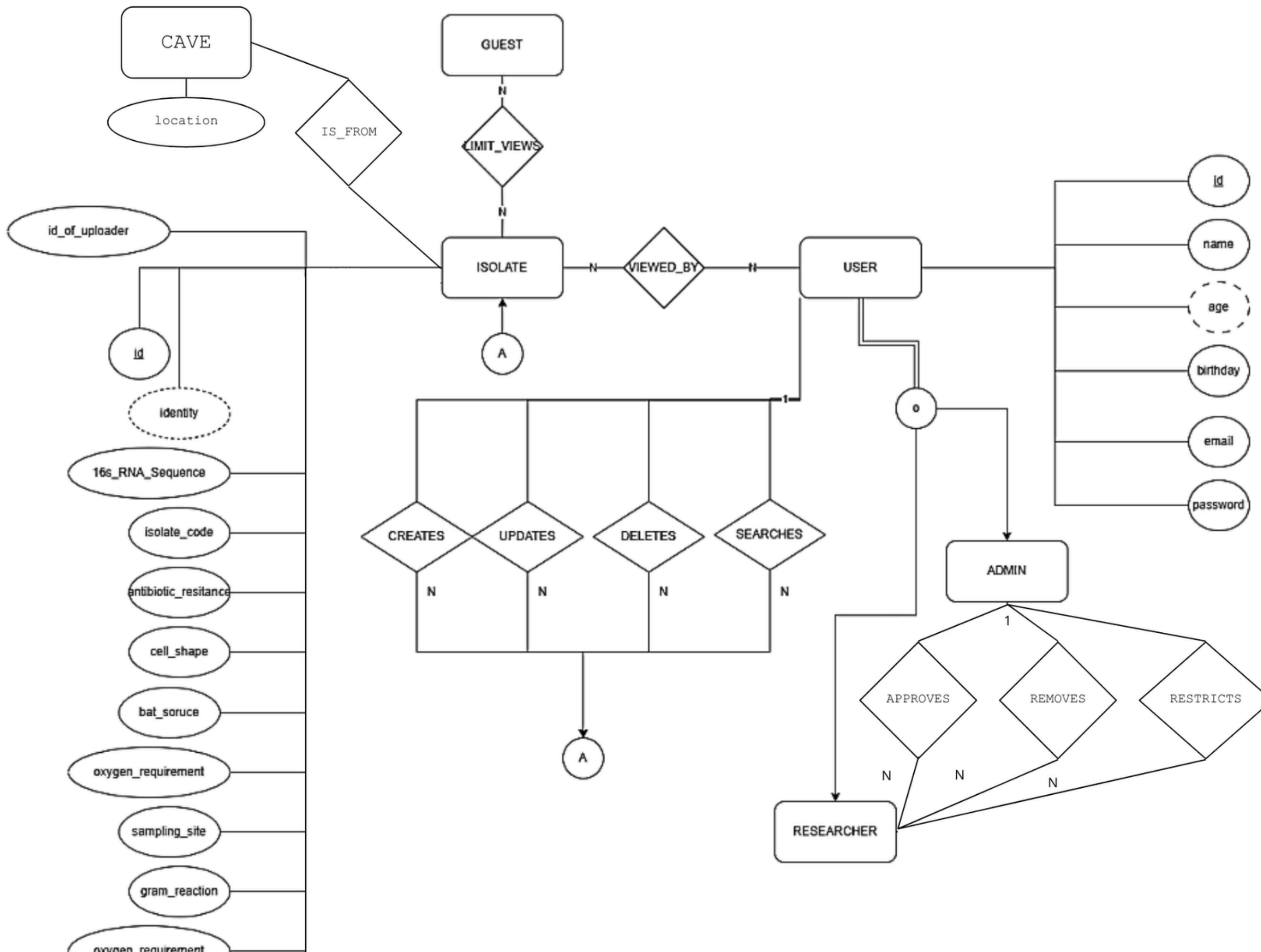
Admin

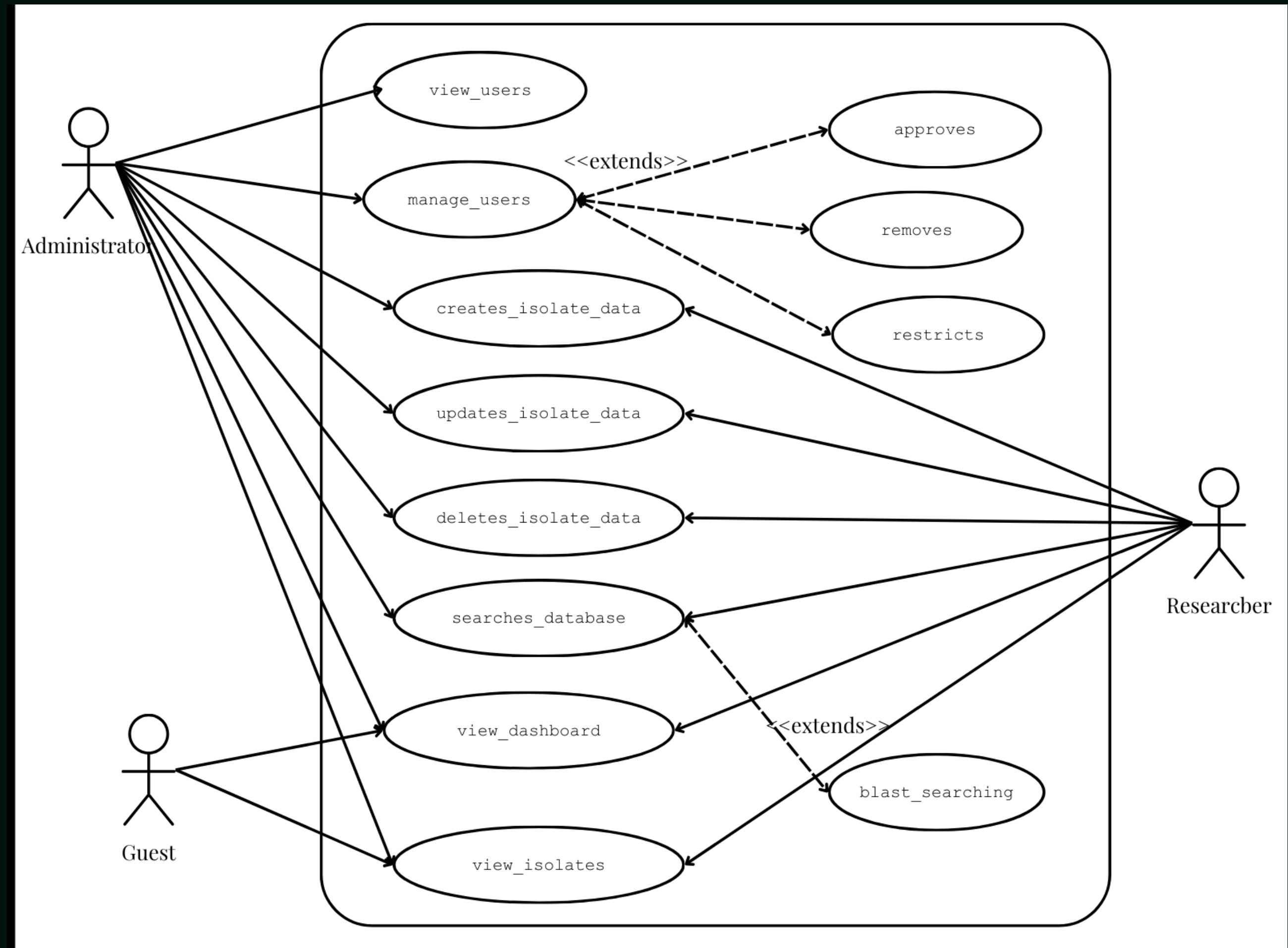


Researchers

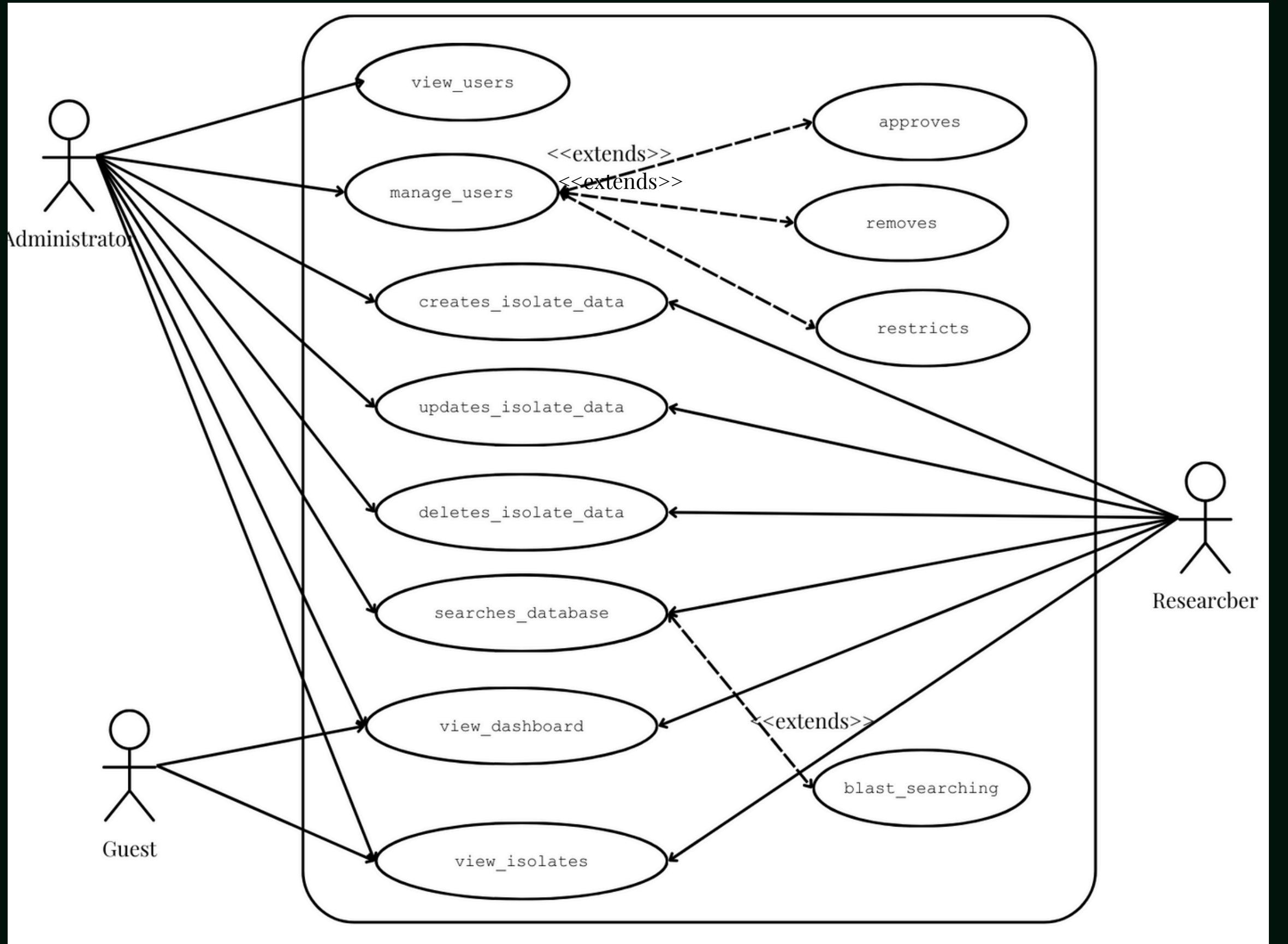


Public (Guest)

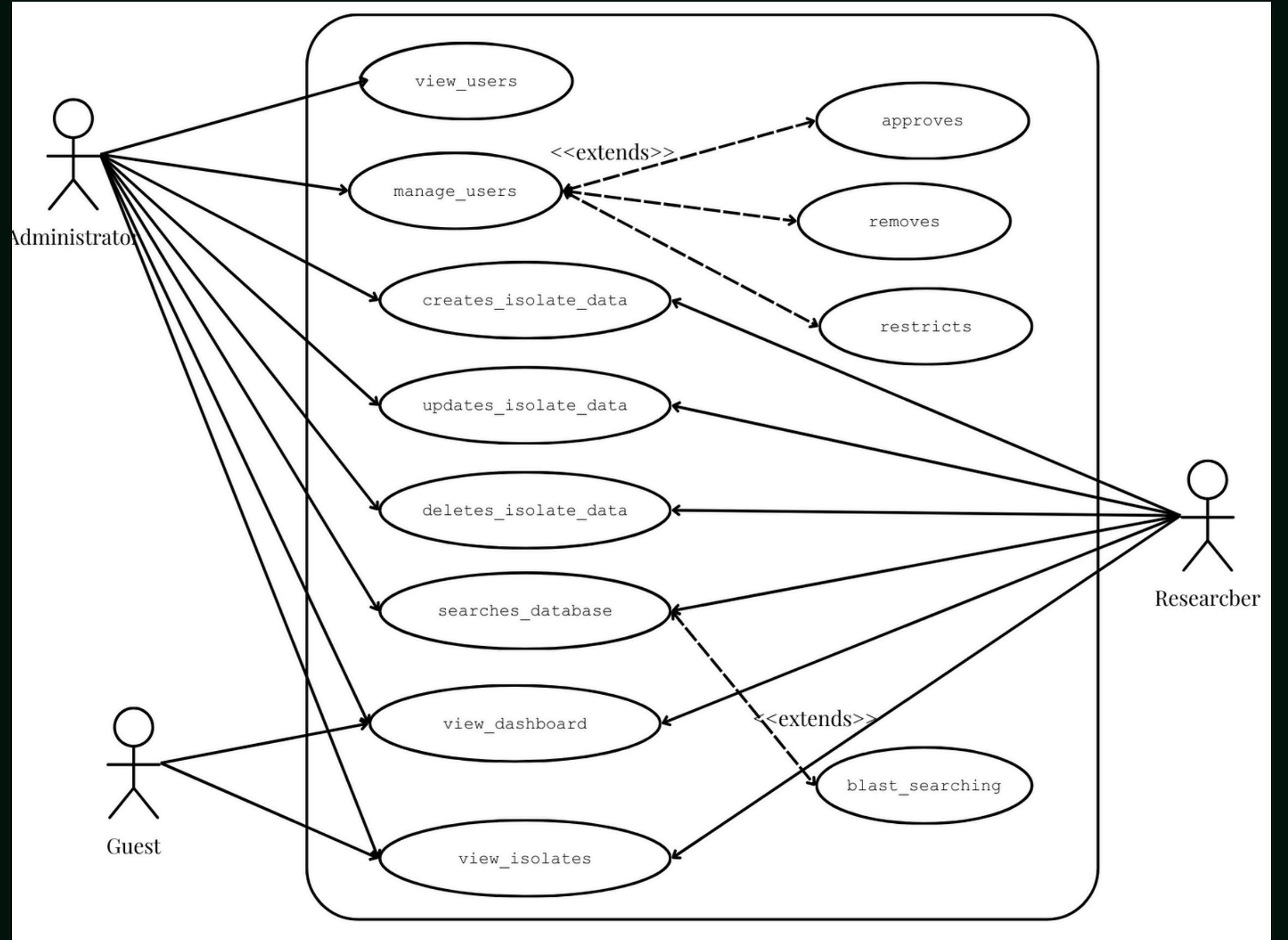




# Administrator

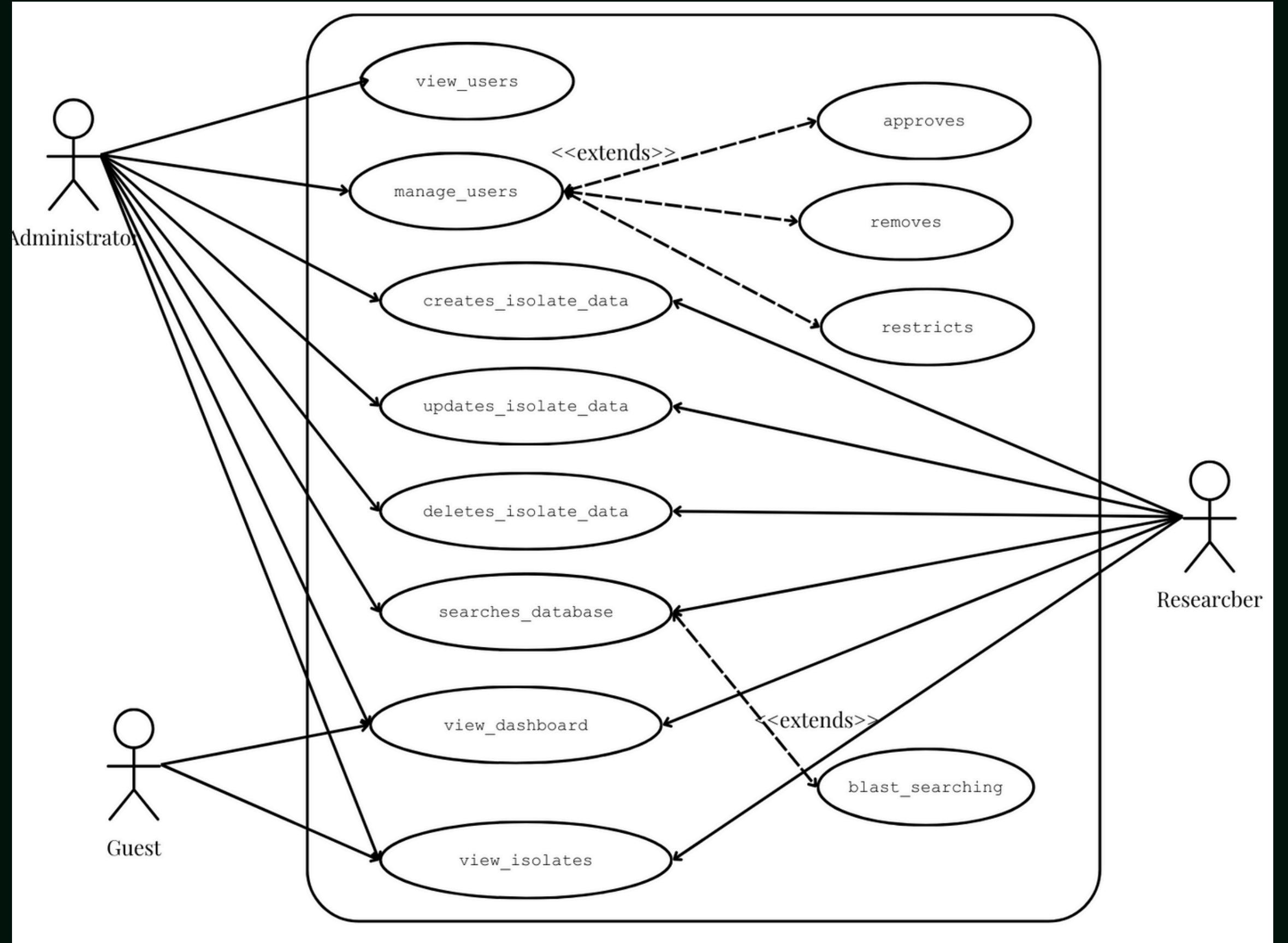


- (PREREQUISITE) **Log in**, Administrators will be required to log in to the application via their respective account
- View Researcher-Users Details**, the Administrator is capable of viewing the tables and the entirety of its values on the researcher-users
- Manage Researcher-Users**, the administrator is allowed to create, update, and delete researchers within the database system
- Manage Isolates**, the administrator is allowed to create, update, and delete all Isolate data within the database system
- View Dashboard**, the Administrator is capable of viewing the dashboard containing the phylogenetic tree of all the Isolates, including a breakdown snapshot of the database
- View Isolates**, through sequence visualizers, the administrator can view the details of the Isolates together with their 16S rRNA sequence



## Researchers

- CRUD their own Isolates**, once within the system, the researcher-users are allowed to add, remove, update, and delete their own respective isolates
- View Dashboard**, just like the Administrator, the researchers are capable of viewing the dashboard...
- View Isolates**, similarly with the Administrator, through sequence visualizers...



## General Users

- a. **Read Function**, the general users (unlogged-in users), may continue to visit the website and view the dashboard containing a snapshot of the database
- b. **View Isolates**, similarly to the Administrator and Researchers, through sequence visualizers, the guest users can view the details of the Isolates together with their 16S rRNA sequence

## **EVALUATING THE PERFORMANCE**

**System Usability  
Scale (SUS)**

**Usability Testing**

# EVALUATING THE PERFORMANCE

## System Usability Scale (SUS)

The System Usability Scale (SUS) will be used to determine the general usability of the web application

Responsive to Objective #1: To develop a web-based and ribonucleic acid sequence database system tailored to addressing the functional needs of researchers of the Center for Cave Ecosystems Research (CAVES) of the University of the Philippines Los Baños Museum of Natural History (UPLB MNH);

No.	Questions
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.

# EVALUATING THE PERFORMANCE

## User Testing

Adjuncts and complements the findings of SUS, User testing will be used to give specific insights into the usefulness of the system.

Responsive to Objective #2: To streamline the data curation process of researchers under the CAVES Program by developing an interface that will enable them to view a report dashboard, perform basic creation, reading, updating, and deletion operations on deoxy- and ribonucleic acid sequence, to view the phylogenetic tree of the current dataset, and to perform Basic Local Alignment Search

# EVALUATING THE PERFORMANCE

## User Testing

To evaluate how effectively BATSeq supports researchers in curating RNA sequence data, assessing its usability, clarity of workflow, and performance when used by actual domain-knowledgeable users.

Answered mostly in Likert Scale.

**BATSEQ**

**BATSeq: A Web-Based System for CAVES's RNA Sequences with  
Integrated Localized Basic Local Alignment  
Search Tool**

**Usability and User Testing Questionnaire**

# EVALUATING THE PERFORMANCE

## User Testing

### GENERAL USABILITY

- **Ease of Use:** The dashboard and the interface can be easily navigated.
- **Effectiveness of the Dashboard:** The dashboard reports contain the necessary information and visualizations for providing insights on the data of the NICER CAVES Program.
- **Intuitiveness:** It was easy to understand how to perform the creation, deletion, and updating of RNA sequences and their metadata in the web application.
- **User Interface Design:** The visual layout of the website was appealing.

### BIOINFORMATICS

- **Basic CRUD Operations:** I was able to add, edit, and delete metadata and RNA sequences without any difficulty.
- **Search Functionality:** The nucleotide sequence search features made it easy to explore the database.
- **Integration of BLAST:** The BLAST tool was integrated seamlessly with the website.
- **BLAST Hits Result Presentation:** The BLAST results, particularly the user interface, were easy to understand.
- **Sequence Visualizer:** The sequence visualizer was helpful in understanding the data.
- **Phylogenetic Tree:** The phylogenetic tree was helpful in adding insights to the system.

### OVERALL EXPERIENCE

- Speed: The web application responded quickly to my queries and interactions.
- Satisfaction: Overall, I am satisfied with the system's capabilities in curating metadata and RNA sequence data for the NICER CAVES Program.

# OUTPUT





ERUDI

# ADD ISOLATES

The screenshot shows a web application titled "Bat Guano Isolates Information System" with a dark theme. The main title is "Add New Isolate". The form includes the following fields:

- Location: Cavinti Underground River and Cave Complex, Cavinti, Laguna
- Gram Reaction: Gram-Negative
- Cell Shape: Rod-shaped
- Oxygen Requirement: Facultative anaerobe
- Possession of Cytochrome c Oxidase: Oxidase Negative
- Endospore-Forming Capability: Non-endospore-forming
- Antibiotic Resistance Profile (partially visible)
- Identity: Escherichia coli
- Pathogenicity: Potentially pathogenic to humans

At the bottom, there are two buttons: "Upload 16S rRNA (FASTA)" and "Upload Image". Below the form, there are two small images labeled B1I1 and B2I1, which appear to be microscopic images of the isolates. At the very bottom, there are buttons for "Isolate Code", "B1I1", "Isolate Code", "B1I2", "Cancel", "Add Isolate", and "Isolate Code", "B2I1".

# DELETE ISOLATES

BATGIS Dashboard About

Cavinti Underground River and Cave Complex, Cavinti, Laguna

Cavinti Underground River and Cave Complex, Cavinti, Laguna

Cavinti Underground River and Cave Complex, Cavinti, Laguna

Isolate Code B4I1

Type of Sample Bat fecal pellet

Source *Hipposideros lekaguli*

Cavinti Underground River and Cave Complex, Cavinti, Laguna

Isolate Code B5I1

Type of Sample Bat fecal pellet

Source *Eonycteris spelaea*

Cavinti Underground River and Cave Complex, Cavinti, Laguna

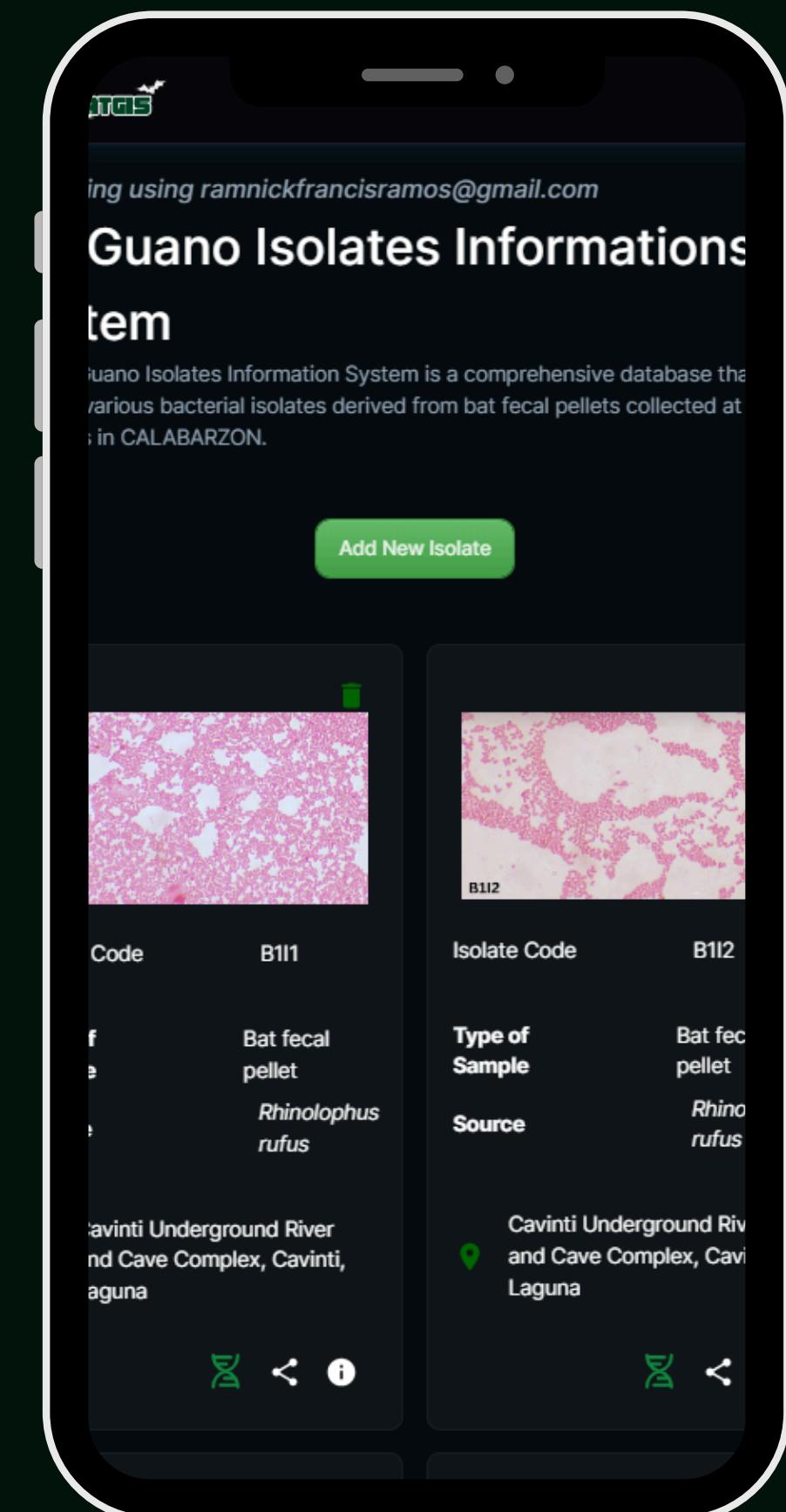
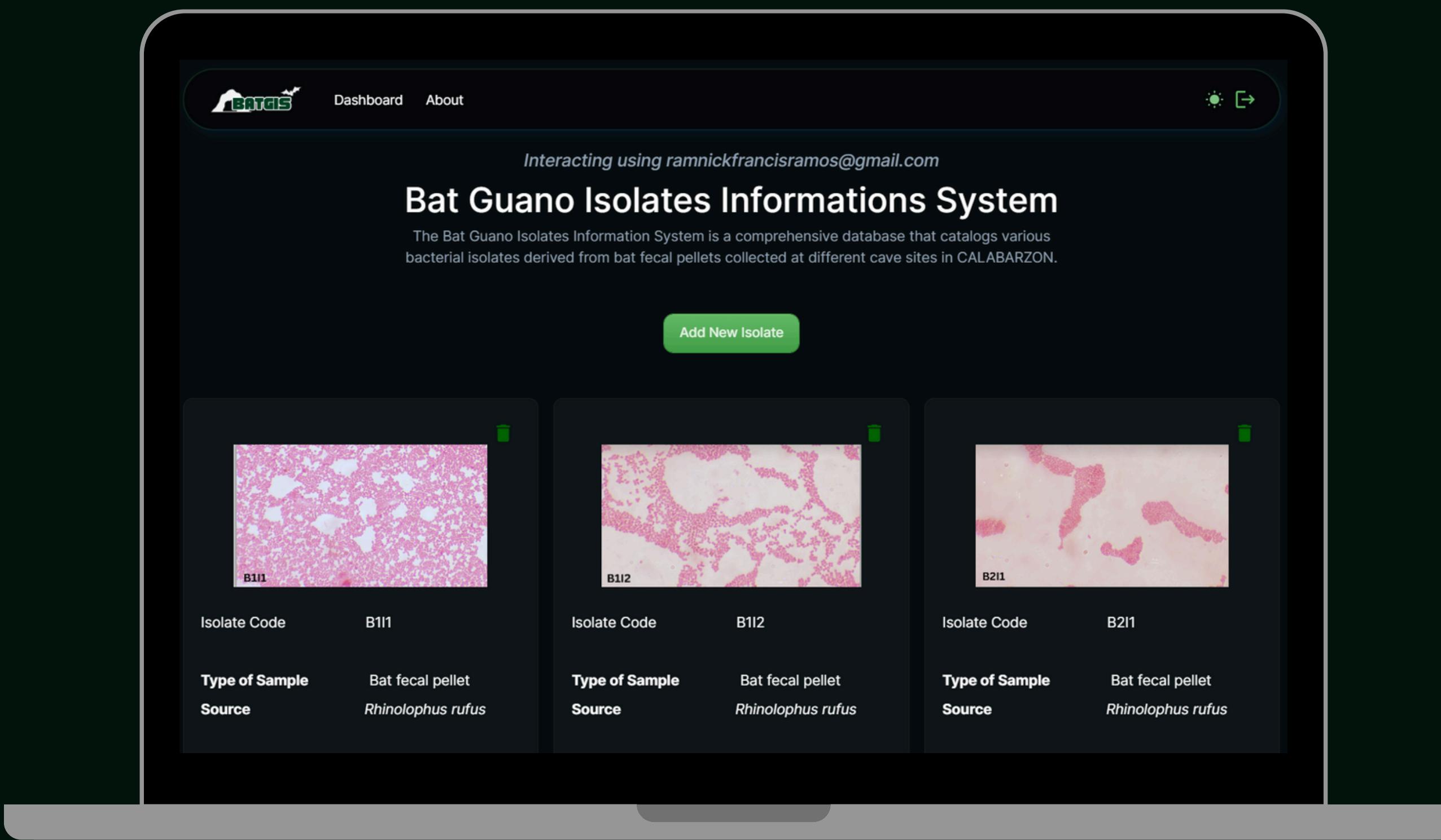
Isolate Code B5I2

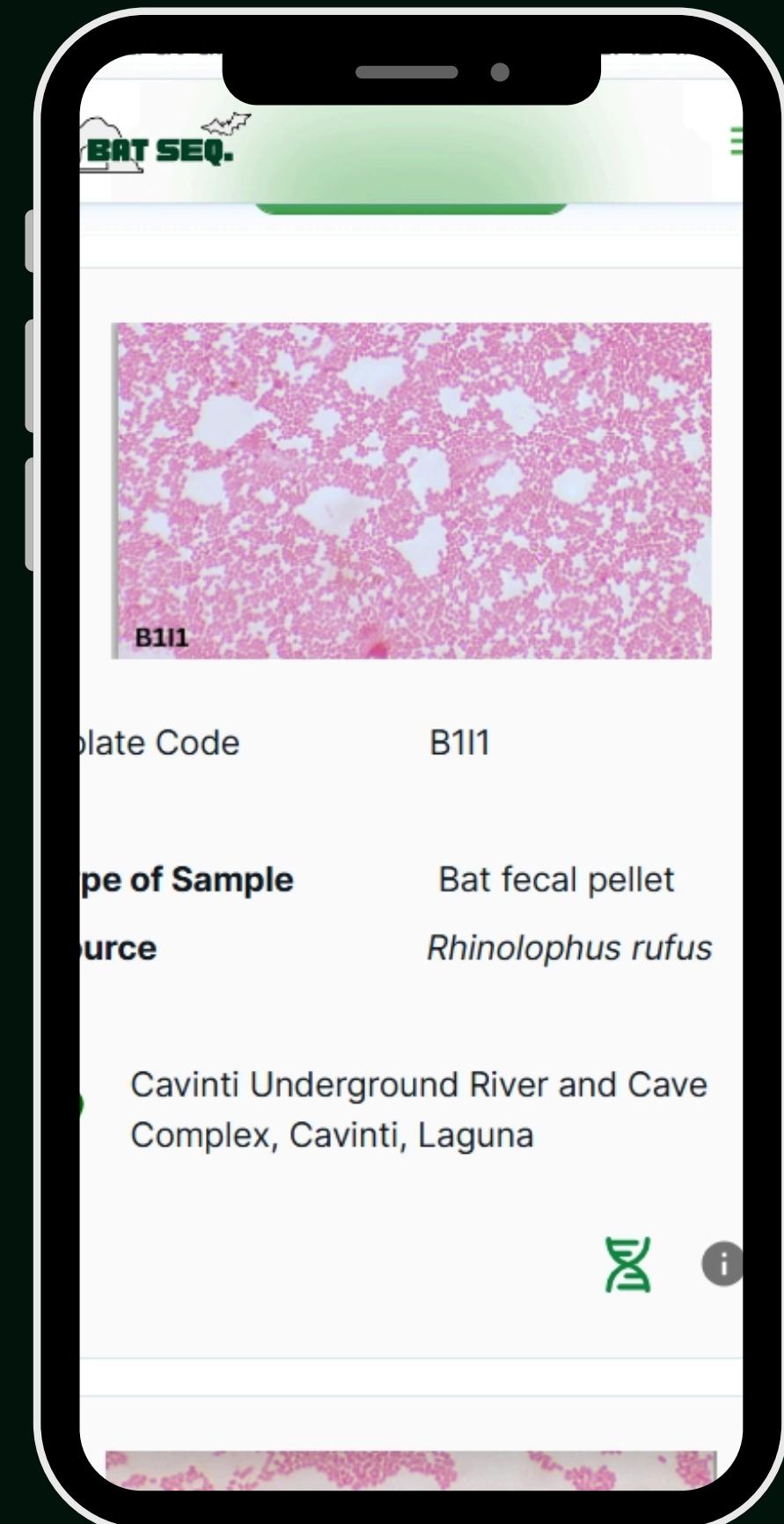
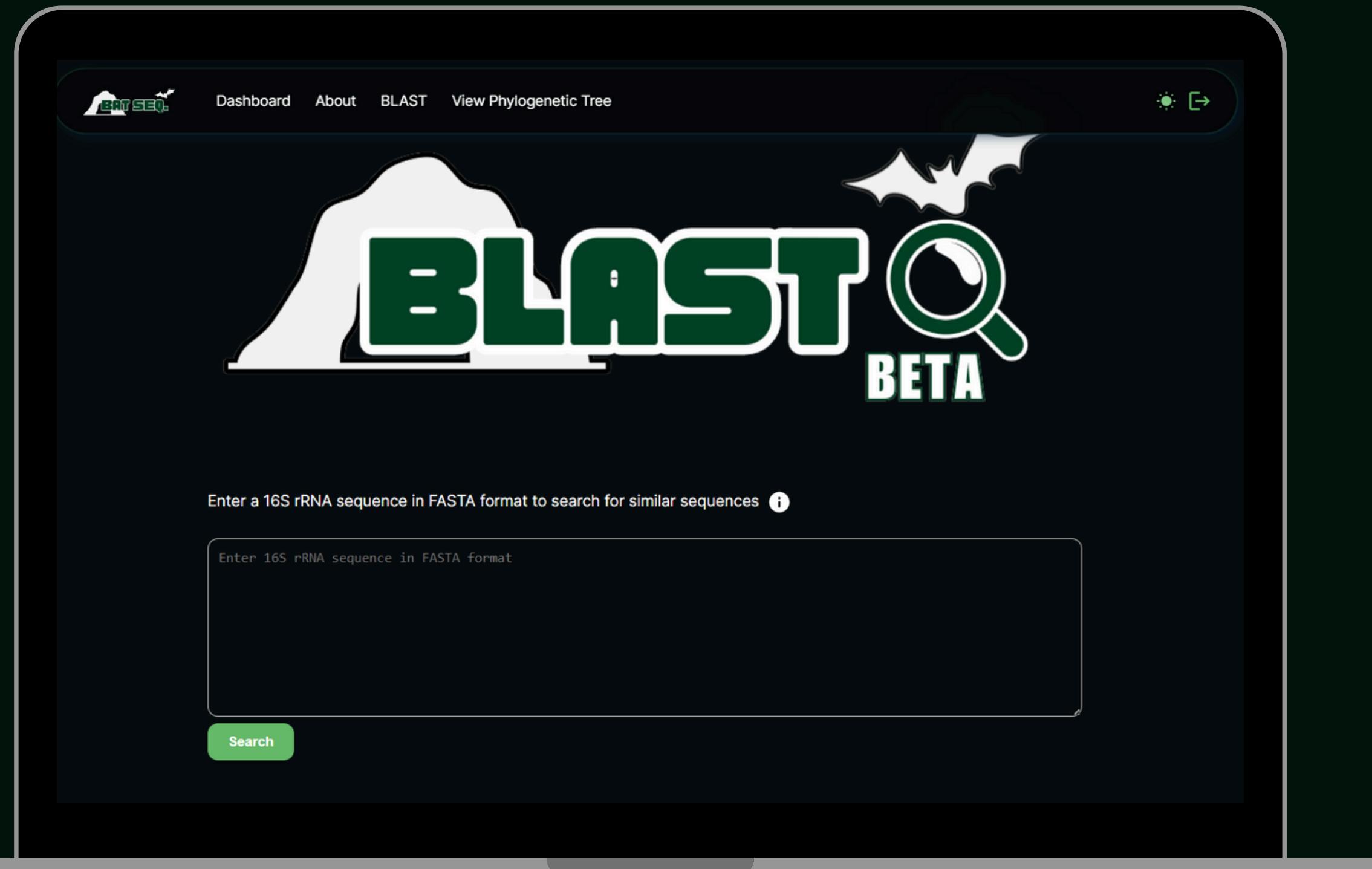
Type of Sample Bat fecal pellet

Source *Eonycteris spelaea*

Cavinti Underground River and Cave Complex, Cavinti, Laguna

# VIEW ISOLATES





Interacting using ramnickfrancisramos@gmail.com

**Bat Guano Isolates Information System**

The Bat Guano Isolates Information System is a comprehensive database that catalogs various bacterial isolates derived from bat fecal pellets collected at different cave sites in CALABARZON.

Add New Isolate

Isolate Code	Type of Sample	Source
B1I1	Bat fecal pellet	Rhinolophus rufus
B1I2	Bat fecal pellet	Rhinolophus rufus
B2I1	Bat fecal pellet	Rhinolophus rufus

# DARK MODE

# LIGHT MODE

Interacting using ramnickfrancisramos@gmail.com

**Genome Sequence**

The Bat Guano Isolates Information System is a comprehensive database that catalogs various bacterial isolates derived from bat fecal pellets collected at different cave sites in CALABARZON.

Add New Isolate

Isolate Code	Type of Sample	Source
B1I1	Bat fecal pellet	Rhinolophus rufus
B1I2	Bat fecal pellet	Rhinolophus rufus
B2I1	Bat fecal pellet	Rhinolophus rufus

Cavinti Underground River and Cave Complex, Cavinti, Laguna

Interacting using rannickfrancisramos@gmail.com



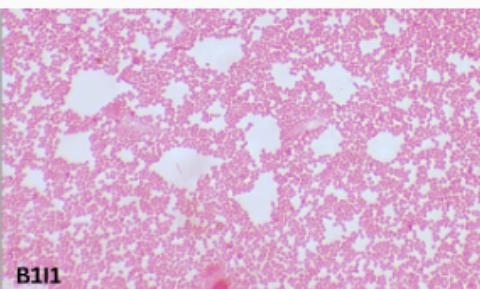
Dashboard About



## Genome Sequence

The Bat Guano Isolates Information System is a comprehensive database that catalogs various bacterial isolates derived from bat fecal pellets collected at different cave sites in CALABARZON.

Add New Isolate



Isolate Code

B1I1

Type of Sample

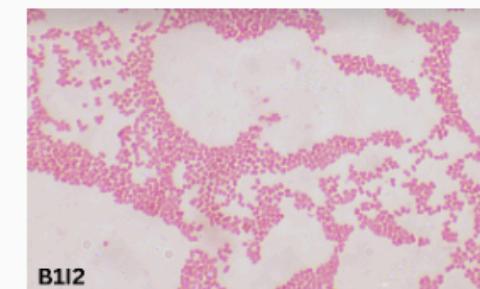
Bat fecal pellet

Source

*Rhinolophus rufus*



Cavinti Underground River and Cave Complex, Cavinti, Laguna



Isolate Code

B1I2

Type of Sample

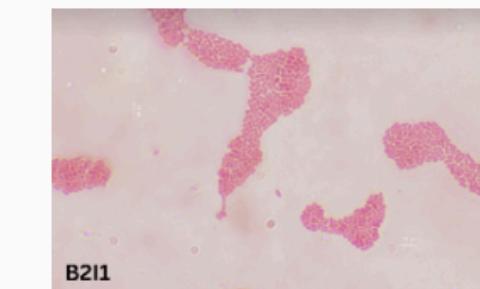
Bat fecal pellet

Source

*Rhinolophus rufus*



Cavinti Underground River and Cave Complex, Cavinti, Laguna



Isolate Code

B2I1

Type of Sample

Bat fecal pellet

Source

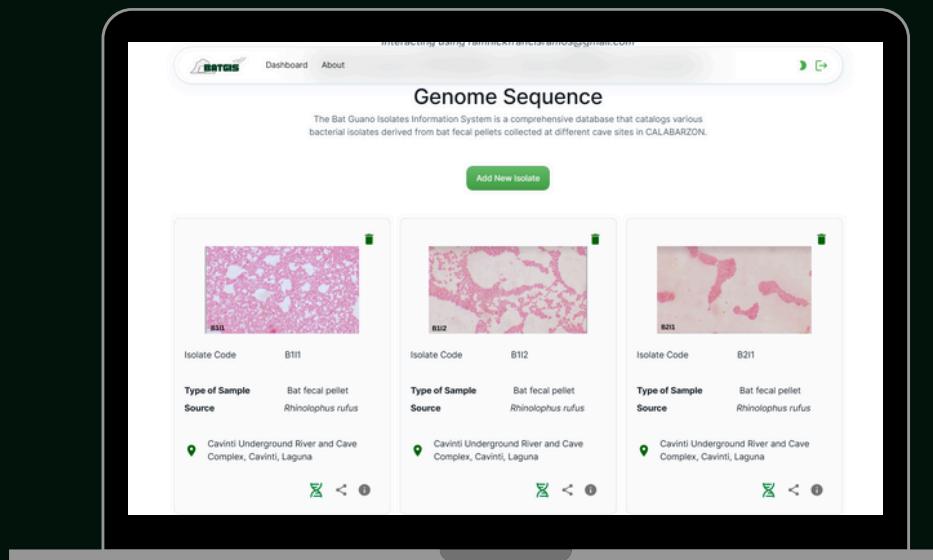
*Rhinolophus rufus*



Cavinti Underground River and Cave Complex, Cavinti, Laguna



# VIEW DETAILS



A detailed view of Isolate B1I1 is shown in a modal window. The window has a title 'Details of B1I1' and a green 'Edit' button in the top right corner. Below the title is a large thumbnail image of a pinkish-red tissue sample labeled 'B1I1'. The main content area contains a table of biological characteristics:

Isolate Code	B1I1
Type of Sample	Bat fecal pellet
Bat Source	Rhinolophus rufus
Sampling Site	Cavinti Underground River and Cave Complex, Cavinti, Laguna
Gram reaction	Gram-Negative
Cell shape	Rod-shaped
Oxygen requirement	Facultative anaerobe
Presence of cytochrome c oxidase	Oxidase-Negative
Endospore-forming capability	Non-endospore-forming
Antibiotic resistance profile	(This row is partially visible)

At the bottom right of the modal window is a green 'Close' button.



**BIOINFORMATICS**  
**MODULE**

# BASIC LOCAL ALIGNMENT SEARCH TOOL

The screenshot shows the BLAST Beta search interface. At the top, there is a navigation bar with links for 'Dashboard', 'About', 'BLAST', and 'View Phylogenetic Tree'. On the right side of the navigation bar are icons for a sun, a battery, and a user profile. Below the navigation bar is the main search area. The word 'BLAST' is prominently displayed in large green letters, with a magnifying glass icon integrated into the letter 'A'. Below 'BLAST' is the word 'BETA' in white. A large, semi-transparent watermark of a bat is positioned behind the text. Below the main title, there is a text input field with placeholder text 'Enter a 16S rRNA sequence in FASTA format to search for similar sequences'. To the right of the placeholder text is an information icon (a small circle with a question mark). Below the input field is a green button labeled 'Search'.

Enter a 16S rRNA sequence in FASTA format to search for similar sequences ⓘ

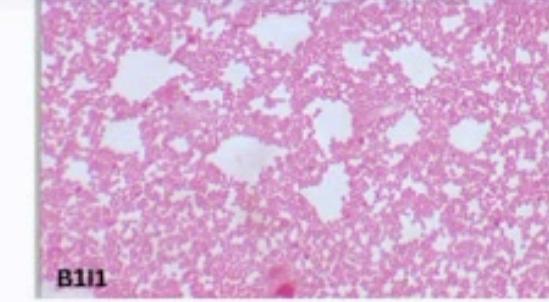
Enter 16S rRNA sequence in FASTA format

Search

# SEQUENCE VISUALIZER

BAT SEQ.

Dashboard   About   BLAST   View Phylogenetic Tree

 B1I1

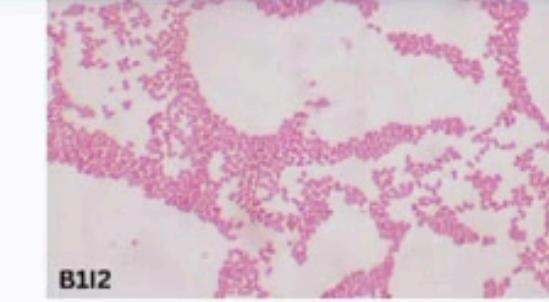
Isolate Code: B1I1

Type of Sample: Bat fecal pellet

Source: *Rhinolophus rufus*

 Cavinti Underground River and Cave Complex, Cavinti, Laguna

 B1I2

Isolate Code: B1I2

Type of Sample: Bat fecal pellet

Source: *Rhinolophus rufus*

 Cavinti Underground River and Cave Complex, Cavinti, Laguna



 B2I1

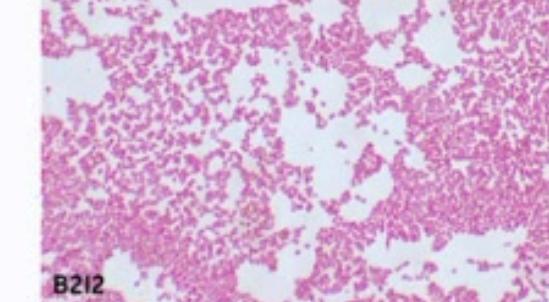
Isolate Code: B2I1

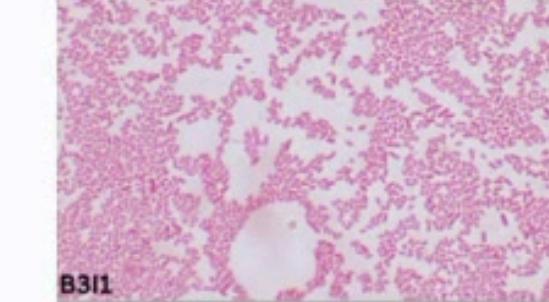
Type of Sample: Bat fecal pellet

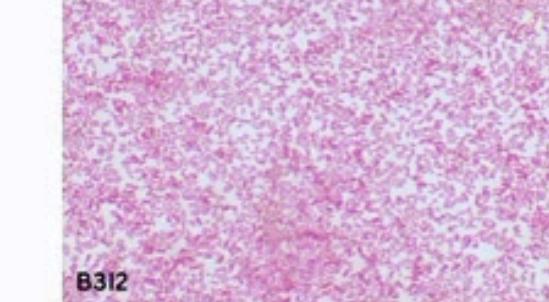
Source: *Rhinolophus rufus*

 Cavinti Underground River and Cave Complex, Cavinti, Laguna



 B2I2

 B3I1

 B3I2

# PHYLOGENETIC TREE

The screenshot shows the homepage of the BLAST Q BETA search interface. At the top, there is a navigation bar with links for 'Dashboard', 'About', 'BLAST', and 'View Phylogenetic Tree'. On the right side of the header is a user profile icon with a green dot and a gear icon. Below the header, the word 'BLAST' is prominently displayed in large green letters, with a magnifying glass icon and the word 'BETA' underneath it. To the left of 'BLAST' is a large, stylized white cloud-like shape. A cursor arrow is visible above the 'BLAST' text. Below the main title area, there is a text input field with placeholder text: 'Enter a 16S rRNA sequence in FASTA format to search for similar sequences'. A small information icon is located next to the placeholder text. At the bottom of the page, there is a large block of DNA sequence text in a monospaced font, starting with 'CGCAGTGGCGGCAGCTACACATGCAGTCGAACGGTAACAGAAAAGCAGCTT' and continuing for several lines.

Enter a 16S rRNA sequence in FASTA format to search for similar sequences ⓘ

```
CGCAGTGGCGGCAGCTACACATGCAGTCGAACGGTAACAGAAAAGCAGCTT  
GCTGCTTGCTGACGAGTGGCGACGGGTGAGTAATGTCTGGGAAACTGC  
CTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGT  
CGCAAGACCAAAGAGGGGGACCTTCGGGCCCTTGCCTAGGGACGATGCC  
AGATGGGATTAGCTAGTAGGTGGGTAAGGCTCACCTAGGGACGATCC  
CTAGCTGGTCTGAGAGGATGACCAGCCACTGGAACTGAGACACGGTCC  
AGACTCCTACGGGAGGGCAGCTGGGAATATTGCACAATGGGCGCAAGC  
CTGATGCAGCCATGCCCGGTGTATGAAGAAGGCTTCGGGTTGTAAAGTA  
CTTCAGCGGGAGGAAGGGAGTAAAGTTAACCTTGCTCATTGACGT  
TACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGGTAATA
```

## OVERVIEW OF THE TESTER

- USERNAME: TESTER ACCOUNT
- EMAIL: TESTER@UP.EDU.PH
- PASSWORD: TESTPASS
- ROLE: USER
- APPROVED STATUS: 1 (APPROVED)
- CREATED AT: 2025-11-20 12:05 PM
- UPDATED AT: 2025-11-20 12:05 PM



## OVERVIEW OF THE TASKS (5 MINS)

- ADD ISOLATE - UPLOAD AND REGISTER NEW RNA SEQUENCES INTO THE SYSTEM.
- DELETE SEQUENCE - REMOVE EXISTING RNA ENTRIES FROM THE DATABASE.
- VIEW SEQUENCE - DISPLAY STORED RNA SEQUENCES WITH METADATA.
- VIEW PHYLOGENETIC TREE - GENERATE AND VISUALIZE EVOLUTIONARY RELATIONSHIPS FROM STORED SEQUENCES.
- RUN BLAST - COMPARE SEQUENCES AGAINST PUBLIC DATABASES FOR SIMILARITY SEARCH.



RESULTS

# RESPONDENTS



Fig. 9: Familiarity with RNA Sequences

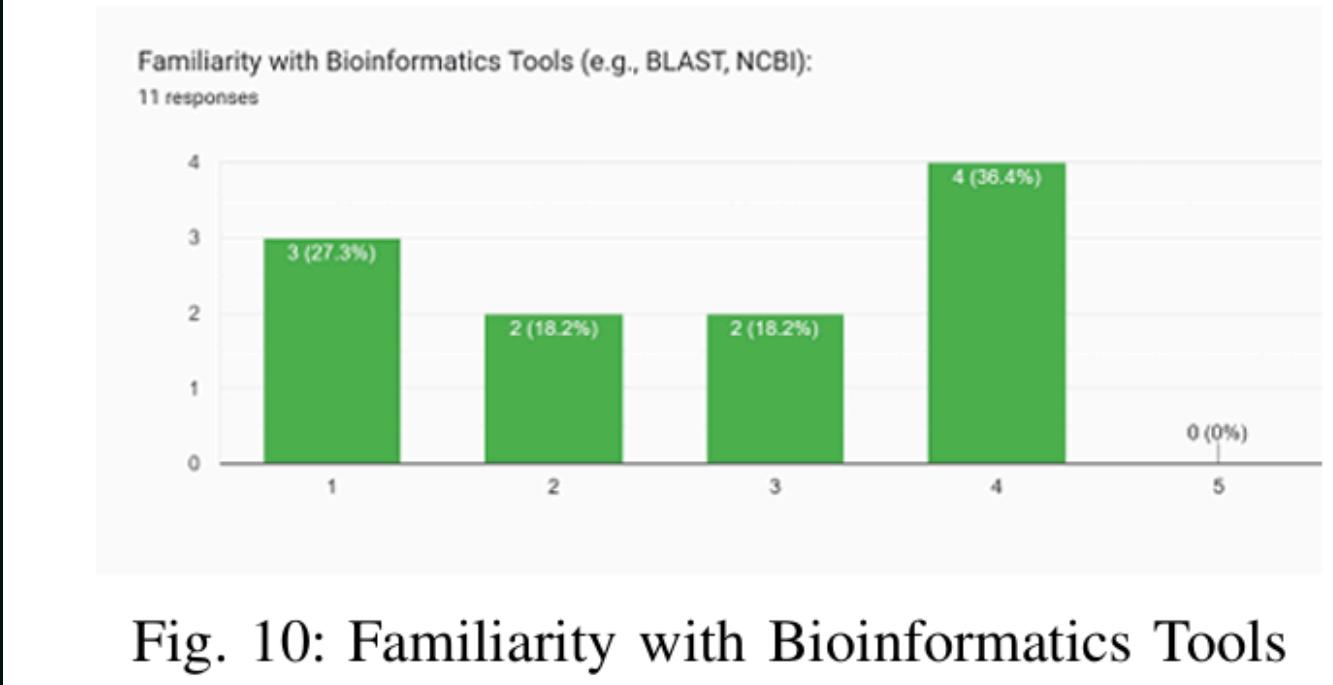


Fig. 10: Familiarity with Bioinformatics Tools

## Respondent Profile Summary

- Total Respondents: 11
- Testing Date: November 20, 2025
- Participants were selected via **purposive sampling**
- Ensuring they had prior knowledge of RNA sequencing or microbial research

## Affiliations

- Majority from the Institute of Biological Sciences (IBS)
- Others from:
  - College of Arts and Sciences (CAS)
  - UPLB Museum of Natural History (MNH)
  - Institute of Computer Science (ICS)
- Represents a mix of biology, microbiology, MST, and computer science backgrounds

## Demographics

- Age Range: 19–48
- Sex Distribution: Male and Female respondents
- Participants included both students and research staff

# RESULTS

## System Usability Scale (SUS): 74.1 MISPRINT IN PAPER

(SUS:  $M = 74.1$ ,  $Mdn = 77.5$ ,  $Min = 47.5$ ,  $Max = 100$ ,  $SD = 16.2$ )

- Classified as “Good” usability, within the 80th percentile
- Indicates BATSeq is intuitive, consistent, and confidence-building for users

## Task-Based Usability Performance

TABLE III: Summary of the Results of Usability Testing

Area	Question Focus	Mean
General Usability & Interface	Ease of Use	3.18
	Effectiveness of Dashboard	4.36
	Intuitiveness	4.18
	User Interface Design	4.27
Data Curation Functionalities	CRUD Operations	4.18
	Search Functionality	4.27
Bioinformatics Module	Integration of BLAST	4.36
	BLAST Hits Result Presentation	4.18
	Sequence Visualizer	4.45
	Phylogenetic Tree	4.36
Overall Performance	Speed	4.18
	Satisfaction	4.36

# RESULTS

## User Insights

- Users appreciated the visualization tools, especially for sequence comprehension
- Sequence-based search was considered powerful and convenient
- Majority found the UI appealing and logical

## Areas for Improvement

- Ease of Use scored 3.18, indicating onboarding adjustments needed for beginners
- Some users requested:
  - Clearer labels
  - More visual elements
  - Additional isolate samples
  - Expanded phylogenetic information

# CONCLUSION

- BATSeq successfully achieved its goal of providing a web-based database system for managing NICER CAVES' RNA sequence data.
- The platform effectively integrates **BLAST, sequence visualization, and a phylogenetic tree generator**, supporting scientific analysis workflows.
- User evaluations show strong usability:
  - SUS Score: Good usability category
  - Task-Based Evaluation: High performance (mean = 4.27/5)
- The system streamlined key research tasks:
  - CRUD operations for isolate metadata
  - Sequence identification and visualization
  - Data-driven insights via dashboard and phylogenetic analysis
- Respondents found the system intuitive, functional, and research-supportive, especially for bioinformatics workflows.

# FUTURE WORKS

## Enhancement Opportunities

- Improve Instruction and Navigation
  - Add clearer labels, tooltips, and beginner-friendly explanations
  - Provide guided walkthroughs for users unfamiliar with RNA analysis
- Expand Visualization Features
  - Enhance dashboard aesthetics
  - Add richer phylogenetic annotations
  - Allow customizable visualizations
- Editable FASTA Handling
  - Allow in-system editing of FASTA sequences
  - Validate and clean uploaded sequences automatically
- **Integrate with Other MNH / NICER Systems**
  - Connect BATSeq with existing databases and web apps as an imported component
  - Enable cross-platform data sharing and routing

# FUTURE WORKS

```
MariaDB [cinterlabs]> desc gene_seq_integ;
+-----+-----+-----+-----+-----+
| Field | Type   | Null | Key  | Default | Extra |
+-----+-----+-----+-----+-----+
| isolate_code | varchar(100) | NO   | PRI  | NULL    |        |
| sequence      | text            | NO   |       | NULL    |        |
| created_at    | timestamp       | YES  |       | current_timestamp() |        |
+-----+-----+-----+-----+-----+
3 rows in set (0.018 sec)
```

```
MariaDB [cinterlabs]>
```

## components

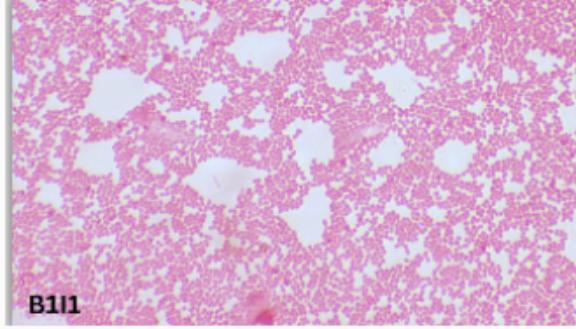
- JS Accounts.js
- JS AppAppBar.js
- TSX AppAppBar.tsx
- JS BlastSearch.js

```
tsx Pricing.tsx  
JS seqviz.js  
TSX Testimonials.tsx
```

*New Table gene\_seq\_integ  
Components Exports  
Importation to iCAVES*

# FUTURE WORKS

 Dashboard   About   BLAST   View Phylogenetic Tree   



**B1I1**

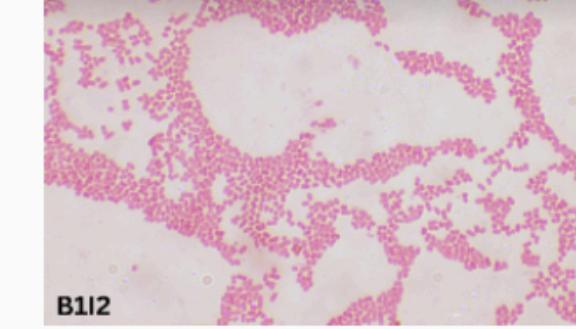
Isolate Code      B1I1

Type of Sample    Bat fecal pellet

Source            *Rhinolophus rufus*

 Cavinti Underground River and Cave Complex, Cavinti, Laguna



**B1I2**

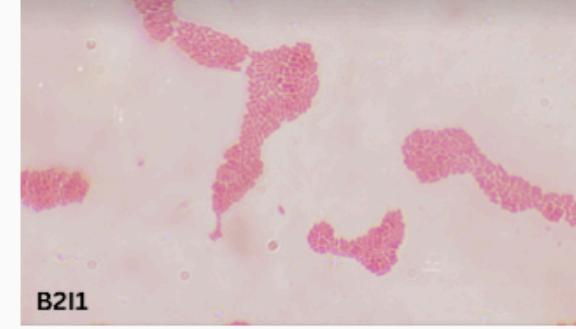
Isolate Code      B1I2

Type of Sample    Bat fecal pellet

Source            *Rhinolophus rufus*

 Cavinti Underground River and Cave Complex, Cavinti, Laguna



**B2I1**

Isolate Code      B2I1

Type of Sample    Bat fecal pellet

Source            *Rhinolophus rufus*

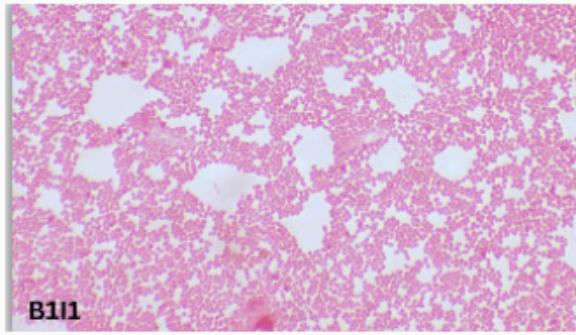
 Cavinti Underground River and Cave Complex, Cavinti, Laguna

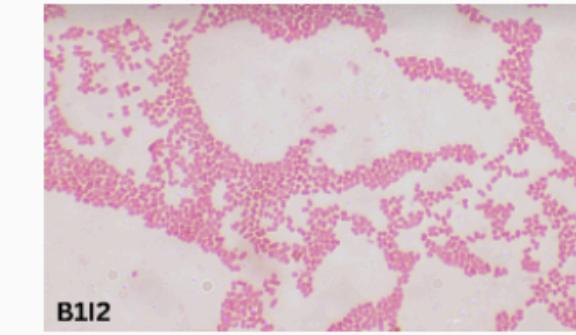
# FUTURE WORKS

BAT SEQ.

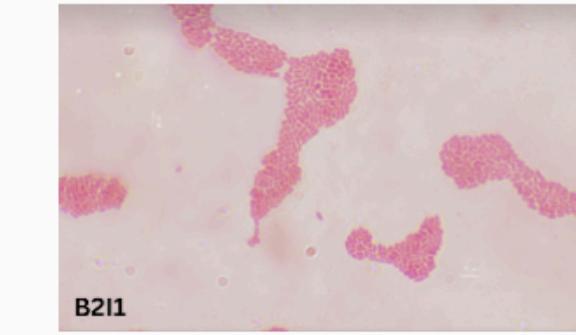
Dashboard   About   BLAST   View Phylogenetic Tree   



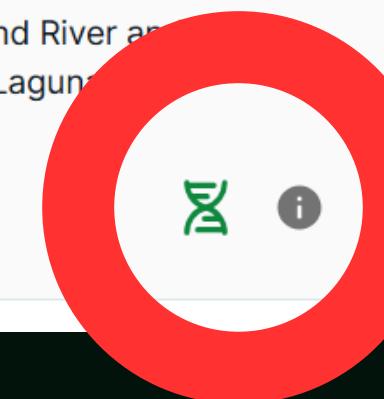
Isolate Code      B1I1  
**Type of Sample**   Bat fecal pellet  
**Source**           *Rhinolophus rufus*  
📍 Cavinti Underground River and Cave Complex, Cavinti, Laguna



Isolate Code      B1I2  
**Type of Sample**   Bat fecal pellet  
**Source**           *Rhinolophus rufus*  
📍 Cavinti Underground River and Cave Complex, Cavinti, Laguna



Isolate Code      B2I1  
**Type of Sample**   Bat fecal pellet  
**Source**           *Rhinolophus rufus*  
📍 Cavinti Underground River and Cave Complex, Cavinti, Laguna



*Import to iCAVES*

**THANK YOU!**

**RAMNICK FRANCIS P. RAMOS**

**PRESENTER**

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