Development of an Animal Microbiota Online Web-Based System Basilio: Bacterial Assemblages and Species Identity Library Online

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Abstract

Zoonotic diseases caused by infectious microorganisms transmitted from animals to humans, are becoming a greater threat to global health security. With the massive amount of data on animal microbiota and zoonosis researches that recognize the pivotal roles of microorganisms in animal physiology and human health, it is necessary to process and present the data and make them accessible to researchers, educators, and to those involved in microbiota and zoonotic infections studies. The Bacterial Assemblages and Species Identity Library Online (BASILIO) is a web-based bacterial system and database that was created to curate data from various research publications on isolated bacteria from a variety of animal species worldwide. The system focuses on the presentation of animal and bacterial taxonomy, with an emphasis on the abundance of bacterial diversity in the animals studied and the classification of bacteria according to their pathogenicity. The project gathered data on animal microbiota from published studies in reputable peer-reviewed journals. AGILE development approach was utilized to develop the information system iteratively. Unit, system, and acceptability testing were used to execute test plans. The BASILIO web-system was evaluated using ISO 9126 standards and found to be functional, usable, reliable, efficient, portable, maintainable, and usable. The BASILIO in its current state, fills in the need for a database dedicated to fast access to information on pathogenic bacteria found in animals. Future developers are proposed to adopt the BASILIO system and incorporate other data management tools and algorithms to create a more complex and robust system.

Keywords: BASILIO, bacterial database, animal microbiota, zoonosis, ISO 9126, online web-system

Introduction

Zoonotic diseases, which are caused by infectious microorganisms being transmitted from animals to humans, are becoming a greater threat to global health security (Salyer et al., 2017). In recent decades, more than two thirds of emerging infectious diseases have been zoonoses (Woolhouse & Gowtage-Sequeria, 2005; Jones et al., 2008). Such outbreaks have caused thousands of deaths and economic losses in the billions (CDC, 2016). There is a critical and unprecedented need to effectively anticipate, prevent and manage zoonotic disease threats, one of which is increasing

public awareness by developing technologies to access information about wide array of pathogenic organisms found in animals (Butala, Fyfe, & Welburn, 2021).

Animals by nature possess consortia of microorganisms that play important role in their physiology (McFall-Ngai et al., 2013). The concept of microbiota, or the diversity of microorganisms, and their influence on animal physiology is undergoing a paradigm shift, as mounting evidence demonstrates their impact on the homeostasis of intestinal development, metabolic activities, and the immune system, as well as their propensity for infection of other organisms, including humans (Esser et al., 2018; Wu & Wu, 2012).

The presence and diversity of microorganisms in animals can be influenced by variety of factors (Hasan & Yang, 2019). Animal gut, for instance, is a nutrient-rich environment resulting to a staggering number of microbes (Martinez-Guryn et al., 2019). Majority of these microbes are found in the colon and mostly are strict anaerobes (Zoetendal et al., 2012; Li et al., 2017). The immense and diverse population of microbes are highly organized, with complex interactions and sophisticated control. There is growing evidence demonstrating their active role in the physiology and health of the host, on postnatal structural and functional maturation of the gut (Jena et al., 2020), development of the immune system (Belkaid & Hand, 2014), and their influence on the nervous system (Wang et al., 2018). Moreover, microbiota also have a pivotal role in mucosal immunity and production of antimicrobial proteins (Takiishi et al., 2017).

Given the significant role of microbiota in the homeostasis of numerous physiologic processes, imbalance of microbiota has been implicated in many disease states. Among the species of microorganisms making up the microbiota of animals, many of these belong to the Kingdom Bacteria, which are also implicated in many infections in humans, or considered as pathogenic (Blumberg & Powrie, 2012). Although pathogenic bacteria are known to cause morbidity and mortality in different species of animals and humans, some of these have been found to be useful as well in treating diseases. Recently, there is a growing trend on treatment of gastrointestinal related diseases, for example *Clostridium difficile* infection (CDI) utilizing fecal microbiota, the Fecal Microbiota Transplantation (FMT) (Youngster et al., 2014). Numerous reports and clinical trials have demonstrated the impressive efficacy of FMT in the treatment of recurrent CDI (Ramai et al., 2021; Sandhu & Chopra, 2021). There are also emerging data on the potential clinical applicability of fecal microbiota transplantation in both gastrointestinal and non-gastrointestinal conditions, including inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), diabetes mellitus, obesity, multiple sclerosis (MS), Parkinsonism, autism, and depression (Kazerouni & Wein et al., 2017; Opoku-Acheampong et al., 2022).

Yet, microbiota of animals is also linked to development of diseases to humans. Zoonotic bacterial diseases are the disease that can be transmitted from animals to humans and vice-versa (Rahman et al., 2020). The infectious diseases that fall under this category are anthrax, brucellosis, bubonic plague, cat-scratch disease, erysipeloid, glanders, leptospirosis, melioidosis, pasteurellosis, pneumonic plague, rat-bite fever, salmonellosis, septicemic plague, sodoku, tularemia and vietnamese tuberculosis (Cantas & Suer, 2014).

The tremendous information microbiota must be accessible for our young and future researchers who are interested to be involved in microbiota studies and contribute to scientific endeavors in unraveling the promising world of microorganisms. Today, there is no website dedicated for quick access to information on bacterial microbiota present in animals and their role to homeostasis and disease. Most of the website on bacteria are databases limited only to access to their biochemical profiles, taxonomy, DNA sequences, genomics, proteomics, and transcriptomics (Zhulin, 2015). For this reason, it is important to develop a data portal for bacterial microbiota found in animals,

present their characteristics, not only DNA sequences but also their functional roles in animals and to give ideas on their applicability for clinical and industrial use. The data portal must present these microbiota data in simple, precise, easy-to-understand which can only be achieve by utilizing data analytics and virtual presentation application.

To fill in the need for a quick access to bacterial diversity found in animals, this project aims to design and develop a web-based system that curates, organizes, and presents data on animal microbiota. The web-system has been named the Bacterial Assemblages and Species Identity Library Online (BASILIO), a web-based system that curates data from various research publications on isolated bacteria from a variety of animal species worldwide. The system focuses on the presentation of animal and bacterial taxonomy, with an emphasis on the abundance of bacterial diversity in the animals studied and the classification of bacteria according to their pathogenicity. The project gathered data on animal microbiota from published studies in reputable peer-reviewed journals.

Materials and Methods Research Design

In developing the BASILIO web-system, the system development methodology and descriptive method were used. The iterative (AGILE) development method is an approach in developing information systems. This method creates minimal risks because of its iterative approach (Krancher, 2020). The descriptive model was used in gathering information in order to determine the system requirements. Questionnaires were also utilized to various types of respondents, such as students, professors, and IT professionals. Figure 1 shows the AGILE web-system development model for the design and development of BASILIO web-system.

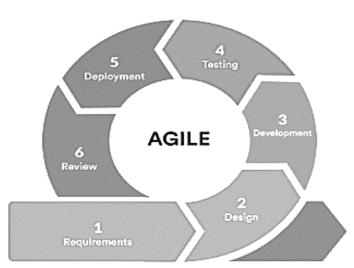


Figure 1. The AGILE approach model for the BASILIO Web-system design and development

Data Sources

The project gathered its information on animal microbiota in peer-reviewed journals following a systematic review of literature approach (Ahn & Kang, 2018). The articles were screened for the information based on the selection criteria of the study; articles published from the 2010-2021, articles that included isolation or identification of bacteria from animals by molecular methods, articles with direct object identifier (DOI), and articles from peer-reviewed journals. Articles were re-

viewed, and the information on animal and bacterial taxonomy, bacterial species identify were data mined, and were charted in a defined template. Duplicate articles were removed, and data charts were normalized and used to import files into the web-system. Table 1 summarizes the Scientific Journals included in the BASILIO Web-system and their corresponding article frequency.

Table 1. Scientific Journals included in the BASILIO Web-system and their corresponding

article frequency data mined for inclusion in the web-system

Scientific Journals Included in the BASILIO WEB-SYSTEM	FREQUENCY
Acta Biológica Colombiana	1
African Journal of Microbiology Research	1
Anais Da Academia Brasileira de Ciências	1
Animal Microbiome	1
Animals	1
Annals of Microbiology	1
Antonie van Leeuwenhoek	2
Apidologie	1
Applied and Environmental Microbiology	13
Applied Microbiology	1
Applied Sciences	1
Applied Soil Ecology	1
Aquaculture	2
Aquaculture Research	1
Asian Pacific Journal of Cancer Prevention	1
Asian Pacific Journal of Tropical Biomedicine	1
Biocontrol Science	1
Biodiversitas Journal of Biological Diversity	1
Bioorganic & Medicinal Chemistry	1
BMC Genomics	2
BMC Microbiology	1
BMC Veterinary Research	2
Brazilian Journal of Microbiology	1
Bulletin of Entomological Researc	1
Coral Reefs	1
Current Microbiology	2
Data in Brief	1
Ecology and Evolution	2
Egyptian Journal of Aquatic Biology and Fisheries	1
Environmental Microbiology	5
FEMS Microbiology Ecology	5
FEMS Microbiology Letters	1
Folia Microbiologica	1
Freshwater mollusk biology and conservation	1
Frontiers in Cellular and Infection Microbiology	2

Scientific Journals Included in the BASILIO WEB-SYSTEM	FREQUENCY
Frontiers in Ecology and Evolution	1
Frontiers in Immunology	1
Frontiers in Marine Science	1
Frontiers in Microbiology	28
Genome Research	1
Integrative and Comparative Biology	1
International Journal of Molecular Sciences	1
International Journal of Systematic and Evolutionary Microbiology	13
International Microbiology	1
Iranian J. of Fisheries Science	1
IScience	1
Journal of Applied Microbiology	1
Journal of Basic Microbiology	1
Journal of Environmental Management	1
Journal of Insect Science	1
Journal of Invertebrate Pathology	4
Journal of Oceanology and Limnology	1
Kongunado Research Journal	1
Korean Journal of Microbiology and Biotechnology	1
Latin American Journal of Aquatic Research	1
Letters in Applied Microbiology	1
Limnology and Freshwater Biology	1
Marine Drugs	5
Marine Pollution Bulletin	2
mBio	1
Meta gene	1
Microb Biotechnol	1
Microbes and Environments	1
Microbial Ecology	5
Microbial Genomics	1
Microbiology	5
Microbiology Research	1
MicrobiologyOpen	5
Microbiome	3
Microorganisms	2
mSystems	2
Nature Communications	2
Open Biology	1
Open Journal of Ecology	1
PeerJ	8
Philosophical Transactions of the Royal Society B: Biological Sciences	1
Photochemistry and Photobiology	1
Phytoparasitica	1

Scientific Journals Included in the BASILIO WEB-SYSTEM	FREQUENCY
PLOS Biology	1
PLOS Genetics	1
PLOS Neglected Tropical Diseases	2
PLOS ONE	44
Polar Biology	3
Poultry Science	1
Proceedings of the National Academy of Sciences of the United States of America	2
Research in Microbiology	1
Saudi Journal of Biological Sciences	3
Scientific Reports	18
Systematic and Applied Microbiology	1
The Biological Bulletin	1
The European Zoological Journal	1
The FASEB Journal	1
The International Arabic Journal of Antimicrobial Agents	1
The ISME Journal	13
Toxicology and Industrial Health	1
Toxicon	1
Total	272



Figure 2. Research Articles Year of Publication and their corresponding frequency

Iterative Process Model

The process of Iterative Model is cyclic (Figure 2), unlike the more traditional models that focus on a rigorous step-by-step process of development. In this process, once the initial planning is complete, a handful of phases are repeated again and again, with the completion of each cycle incrementally improving and iterating on the software (Kitano, 2002). The biggest advantage of this

model in application to science-related system is that it is implemented during the earlier stages of software development process, which allows developers and testers to find functional or design related flaws as early as possible, which further allows them to take corrective measures, and present accurate results earlier in the development.

Iteration 1 Requirements Analysis Iteration 2 Iteration n Design Design Design Testing Testing Testing Implementation Implementation Implementation Review Review Review Deployment Maintenance

Figure 3. Iterative Process Model

Throughout the data gathering procedures, some requirements were made for the system. These requirements were: Inclusion of other members in Recording Data, providing arranged forms to consistently record data, acquiring Journals and Research from different sources, identifying pathogenic Bacteria, Animal taxonomy, disseminating the acquired information to a larger scale of audience, minimizing the repetitive recording of data, and keeping track of all the parts involved. These requirements resulted to the system on having these features: assigning journals, generating taxonomic classification, generating scientific name, and curated animal, bacteria. The system was also made to have validations, generation of reports, a collaboration feature, and having it web based.

The main case for the web-system development is "Manage BASILIO Information" (Figure 3), which is done by the admin and staff of the system. This includes the recording of all the data which will be used for including data in the database about the article source, animal taxonomy, and bacterial taxonomy including details of its pathogenicity.

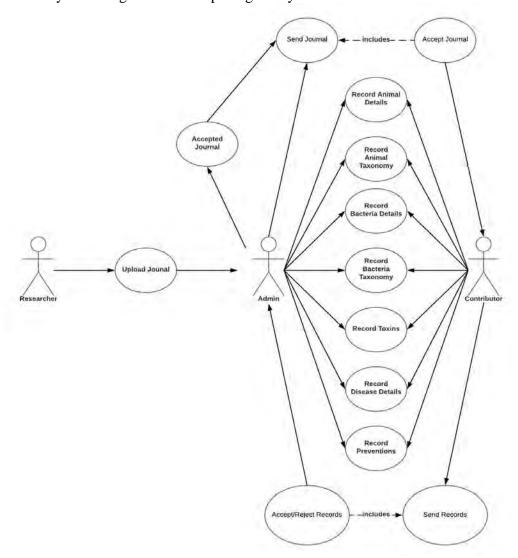


Figure 4. Use Case 1 – Manage BASILIO Information

BASILIO Web-system Graphical User Interface (GUI) Design

This section shows the graphical user interface (GUI) of the BASILIO Web-system. GUI is a system of interactive visual components for computer software. A GUI displays objects that convey information and represent actions that can be taken by the user. The objects change color, size, or visibility when the user interacts with them.

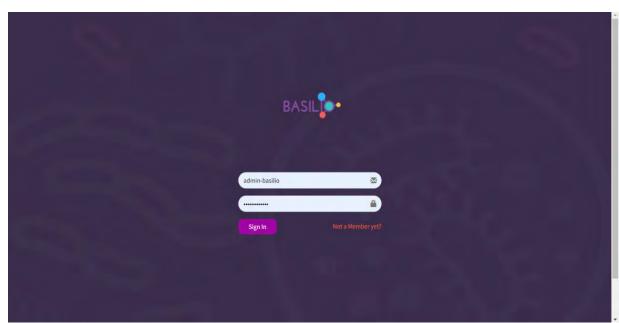


Figure 5. GUI – Log In Form

This page requires basic log in credentials such as the username and the password

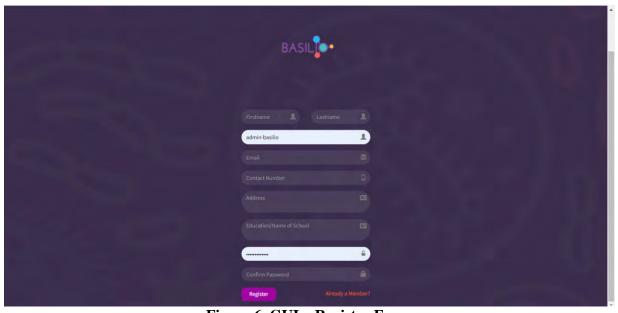


Figure 6. GUI – Register Form

This page lets you create an account when users can input the First name, Last name, Username, and Password.

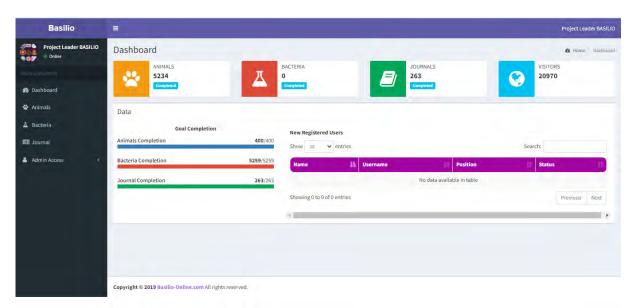


Figure 7. GUI – Administrator: Dashboard

The dashboard allows the users and administrators to visualize the Key Performance Indicators and other strategic data for the organization at a glance.

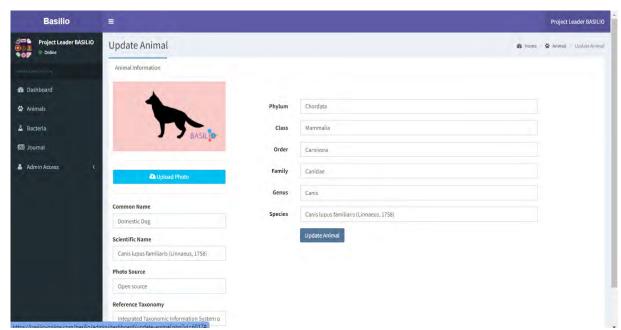


Figure 8. GUI – Administrator: Animal Form

The animal form serves as a log for animal information specified in the fields.

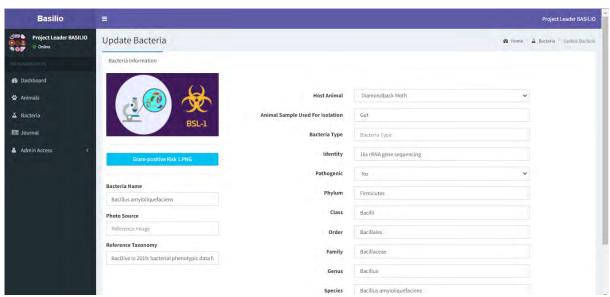


Figure 9. GUI - Administrator: Bacteria Form

The bacteria form serves as a log for bacterium information specified in the fields.

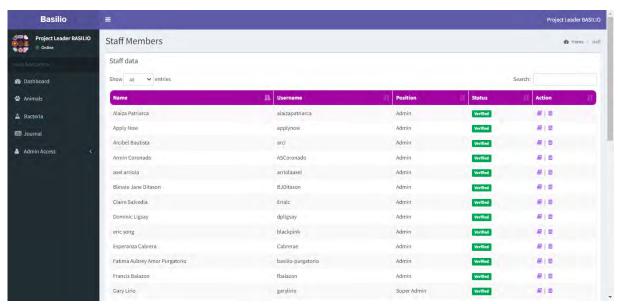


Figure 10. GUI – Administrator: Staff Members

The Staff members show the list of the registered staff members who serve as contributors of data in the BASILIO Web-system. The Staff members feature Staff editing to change their roles/function in the web-system.

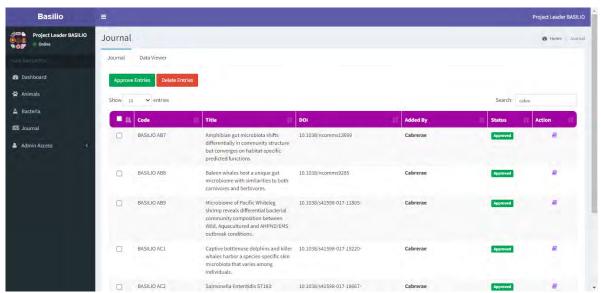


Figure 11. GUI – Administrator: Journal List

The Journal List allows the web-system Administrator to look for the contributor's articles uploaded in the web-system. This will also allow the admin to approve or delete entries particularly when duplicates have been found.

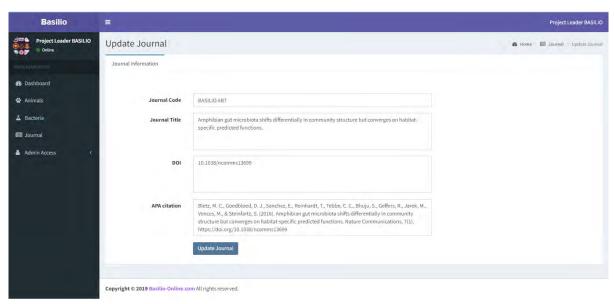


Figure 12. GUI – Administrator: Update Journal

The Update Journal allows the web-system administrator to modify information regarding the uploaded journal article. Modifications are only limited to Journal Code, Journal Title, DOI, and APA Citation.

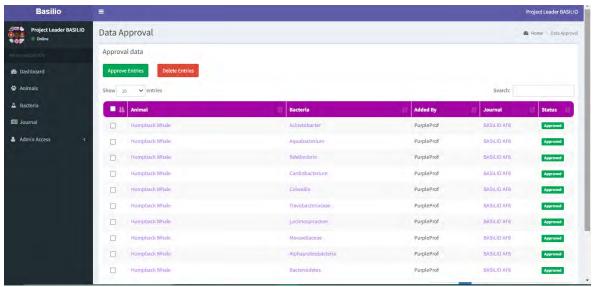


Figure 13. GUI - Administrator: Data Approval

The Data Approval allows the Administrator to check the status of data included in the database. Search bar is also included to facilitate quick access to specific Journal article code, animal species, bacterial species, and the contributor's name. Approve and Delete entries can be done in this page.

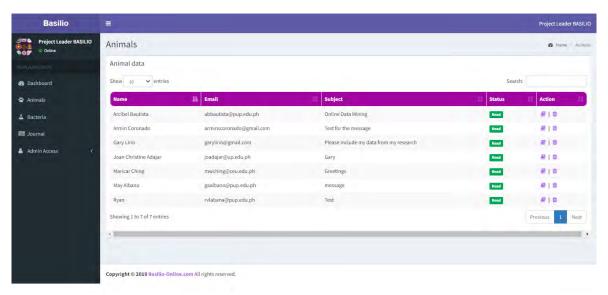


Figure 14. GUI – Administrator: Message

The Message page allows the administrator to check incoming messages from different users and a way to contact and communicate with possible contributors.

BASILIO Website GUI Design

This section presents the GUI of the BASILIO website. The BASILIO website is an open-access website accessible at https://basilio-online.com/basilio/index.php. The BASILIO website has nine (9) tabs which include Home, Animal, Bacteria, About, Contact, Downloads, References, Lo-

gin, and Register. The BASILIO website serves as login portal as well for the administrators, staff, and contributors to access the BASILIO web-system.

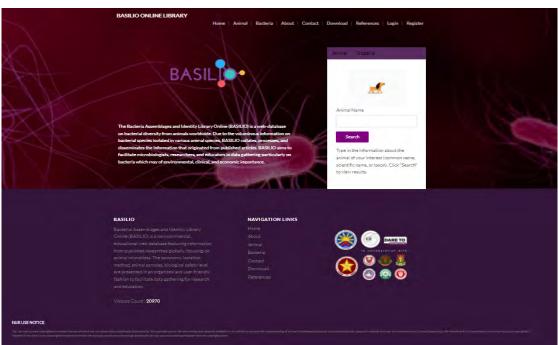


Figure 15: **GUI – BASILIO website: Home Page**

The Home Page presents an overview of what the BASILIO website is all about. Also, the Homepage contains the quick search for Animals or Bacteria of interest.

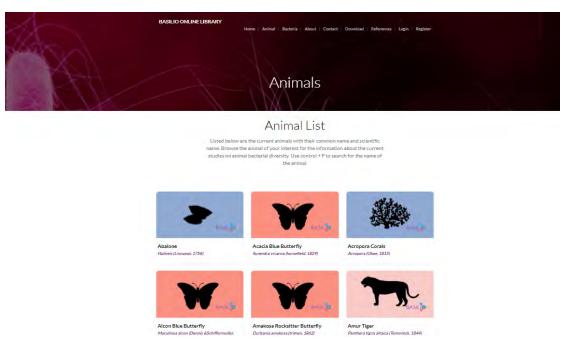


Figure 16: GUI – BASILIO website: Animal List

The Animal List in BASILIO website presents all the animal species included in the system. An instruction on how to search and navigate the search for animals is presented in the page.

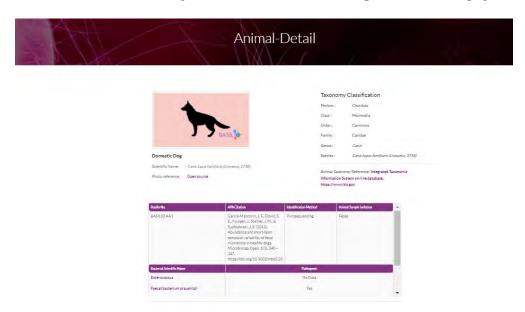


Figure 17. GUI – BASILIO website: Animal Detail

The Animal Detail page in BASILIO website shows the details of specific Animal searched from the website. Information on animals includes Taxonomic classification, related literature that studied the animal, and the corresponding bacterial species found in that animal. Preview of the pathogenicity of the bacteria found in the animal is shown in the page.

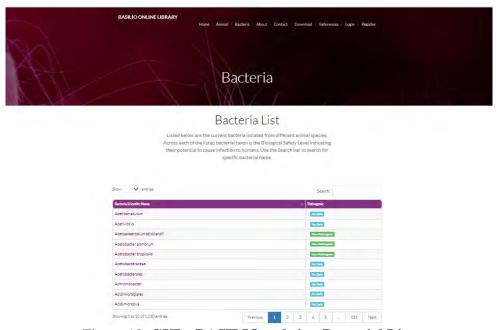


Figure 18. GUI – BASILIO website: Bacterial List

The Bacterial List in BASILIO website contains the list of all the bacterial species found in the database. The search bar allows quick search for the bacterial species of interest. Preview of their Biorisk classification is also presented in this page.



Figure 19. GUI – BASILIO website: Bacterial Detail

The Bacterial Detail in the BASILIO website previews the specific bacterial species searched by the user. The page contains the taxonomic classification of the bacteria, related studies that isolated the bacterial species, the methods for identification, animal sample used, and the animal species of the study. Details on the pathogenicity of the organisms in humans are presented; Red for Pathogenic, Green for Non-pathogenic, Blue for No Data.

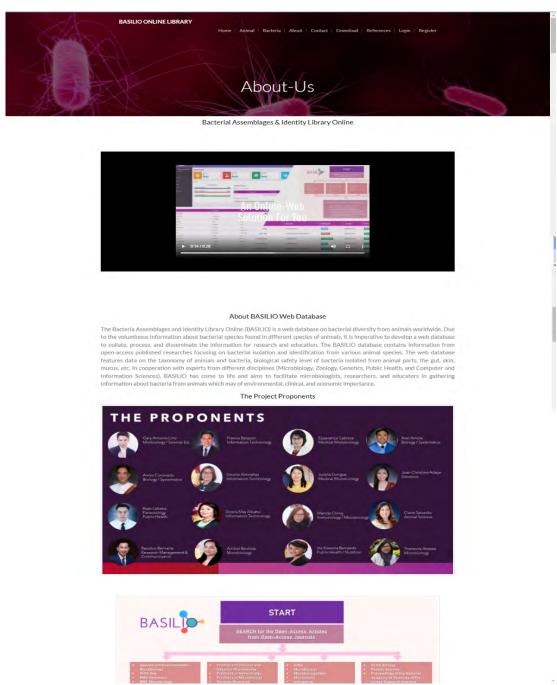


Figure 20. GUI – BASILIO website: About Us

The About Us of the BASILIO website presents the proponents of the web-system and the process flow for the processing of data to be included in the BASILIO web-system. The BASILIO project is a collaborative project of researchers from different State Universities and Colleges in the Philippines.

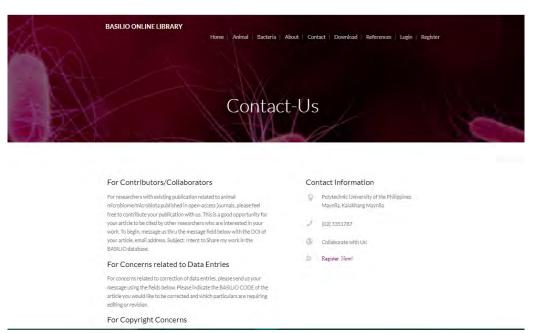


Figure 21. GUI – BASILIO website: Contact Us

The Contact us presents information about how users and future contributors can contact the BASILIO Administrator for collaboration and possible inclusion of new articles in the database.

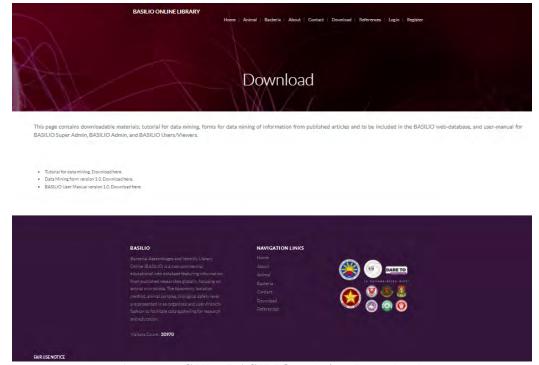


Figure 22. GUI – BASILIO website: Downloads

The Download page presents the important files that can be downloaded for users to contribute their articles in the web-system. Forms such as Data Mining form which is required for importation of data to the web-system can be accessed in this page.



The BASILIO Team would like to extend our deepest gratitude to the original owner of the data presented in this database.

References

Coming Soon

Online Resources/Website/Databases

- Integrated Taxonomic Information System on-line database, http://www.itis.gov.
- BacDive in 2019: bacterial phenotypic data for High-throughput biodiversity analysisZReimer, L. C., Vetcininova, A., Sardà Carbasse, J., Söhngen, C., Gleim, D., Ebeling, C., Overmann, J.Z.Nucleic Acids Research; database issue 2019. https://bacdive.dsmz.de/
- Parte, A.C., Sardà Carbasse, J., Meier-Kolthoff, J.P., Reimer, L.C. and Göker, M. List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. International Journal of Systematic and Evolutionary Microbiology, accepted for publication; DOI: 10.1099/ijsem.0.004332. https://lpsn.dsmz.de
- DOI Citation Formatter, https://citation.crosscite.org/

Figure 23. **GUI – BASILIO website: References**

The References presents the list of third-party sources that were used to complete the data for the system.

Database Schema

The BASILIO web-database system's schema was created to deliver the most precise results possible. This was accomplished by providing the elements with relationships that would enable them to produce an accurate outcome. Further, the entity-relationship diagram was constructed using the following business rules: at least one animal or bacterium record must be entered by the administrator.

Development Tools

Visual Studio Code

Microsoft developed Visual Studio Code, a source code editor for Windows, Linux, and macOS. It has debugging, integrated Git control, syntax highlighting, intelligent code completion, code snippets, and code refactoring. Visual Studio Code is built on top of Electron, a platform for deploying Node.js apps (Microsoft, 2021).

Git Hub

Git is a version control system for recording changes to computer files and coordinating several people's work on those files. It is primarily used in software development for source code management, although it may be used to track changes to any set of files. It is a distributed revision control system that prioritizes performance, data quality, and support for distributed, non-linear processes.

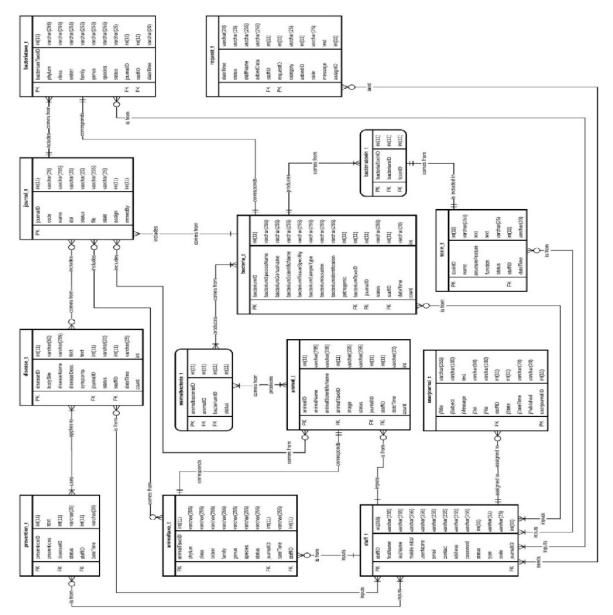


Figure 24. Entity-Relationship Diagram

Platform: Node.js

Node.js is an open-source, cross-platform JavaScript runtime environment for executing JavaScript code in a non-browser context. Historically, JavaScript was largely used for client-side scripting, in which JavaScript scripts were embedded in the HTML of a webpage and executed client-side by a JavaScript engine installed in the user's web browser. Node.js enables developers to construct Command Line tools and server-side scripting—the process of running scripts server-side to generate dynamic web page content prior to sending the page to the user's web browser. As a result, Node.js offers a "JavaScript everywhere" paradigm, unifying web application development around a single programming language rather than requiring separate languages for server-side and client-side scripts.

Framework: Express.js

Express.js, or simply Express, is a Node.js web application framework released under the MIT License as free and open-source software. It is intended for use in the development of web applications and APIs. It has been dubbed the de facto standard Node.js server framework.

Database: MySQL

MySQL is a free and open-source database management system for relational databases (RDBMS). The term "SQL" stands for Structured Query Language. There are various paid editions available for commercial use that add additional functionality. MySQL is written in the C and C++ programming languages. MySQL is compatible with a wide variety of operating systems, including Linux, macOS, and Microsoft Windows.

HTML

The Hypertext Markup Language (HTML) is the industry-standard markup language for web pages and web applications. Together with Cascading Style Sheets and JavaScript, it comprises a trinity of Web-related technologies.

CSS

Cascading Style Sheets (CSS) is a style sheet language that is used to describe the appearance of a document produced in a markup language such as HTML. CSS, along with HTML and JavaScript, is a foundational technology of the World Wide Web.

Bootstrap

Bootstrap is a free and open-source front-end framework for web design. It includes design templates for typography, forms, buttons, navigation, and other user interface components written in HTML and CSS, as well as optional JavaScript extensions.

JQuery

jQuery is a cross-platform JavaScript framework that simplifies the scripting of HTML on the client side. It is completely free and open-source software distributed under the permissive MIT License. According to web research, it is by far the most extensively deployed JavaScript library.

JavaScript

JavaScript (JS) is a fast, interpreted or JIT-compiled scripting language that supports first-class functions. Although JavaScript is best known as a scripting language for Web pages, it is also used in a variety of non-browser settings, including node is and Apache CouchDB.

XAMPP

XAMPP is a free and open-source cross-platform web server solution stack built by Apache Friends. It includes the Apache HTTP Server, the MariaDB database, and interpreters for PHP and Perl scripts.

ĒJS

EJS (Embedded JavaScript) is a straightforward template language that enables the generation of HTML markup using standard JavaScript.

System Requirements

A well-designed requirement for a project can save the developer much time and effort. System requirements are the most efficient method of addressing user needs and minimizing implementation costs. This section outlines the system requirements for the BASILIO web-system development

Hardware

Table 2. Hardware Requirements

Hardware Component	Recommended Specification	Minimum Specification	
Processor	Quad-core, 4GHz	Single-core, 1 GHz	
Installed Memory (RAM)	64GB RAM	2GB RAM	

Hardware Component	Recommended Specification	Minimum Specification	
Hard Disk Drive	1TB	500 GB	
Network Speed	10Mbps	5Mbps	

Software Requirements

Table 3. Software Requirements

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Software Component	Recommended Specification	Minimum Specification				
Operating System	Windows 10 (64-bit)	Windows 8 (32-bit)				
Database Management System	phpMyAdmin v4.6.5.2	phpMyAdmin v4.0				
Web Browser	Google Chrome, Opera	Google Chrome, Opera, Mi-				
		crosoft Edge, Mozilla Firefox				
Apache Web Server	XAMPP v3.2.2	XAMPP v3.0				

Test Methodology and Procedure

Unit Testing.

During unit testing, each component of the system was tested independently. Each module's functionality was verified using the White Box approach, which requires testers to understand the system's internal workings.

System Testing

During system testing, the entire system was examined from the user's perspective. The Black Box method (also known as Behavioral Testing) was employed, which does not need testers to dive into the system's inner workings. The system was inspected for erroneous or missing functionalities, interface issues, data structure errors, performance errors, and startup and shutdown errors.

Acceptance Testing

Acceptance testing verifies the system's acceptability. It is formal testing of the system's compliance with user needs, requirements, and business procedures.

Evaluation of BASILIO Web-System

The BASILIO web system was evaluated in accordance with ISO 9126 standards (SO/IEC IS 9126-1., 2001). ISO 9126 is an international standard for software evaluation (Software Quality Assurance). The standard is organized into four sections, each of which addresses a different subject: the quality model; external metrics; internal metrics; and quality in use metrics. ISO 9126 Part 1, abbreviated ISO 9126-1, is a continuation of past efforts to define a set of software quality standards.

The ISO 9126-1 software quality model identifies six primary quality characteristics: functionality, dependability, usability, efficiency, maintainability, and portability.

Table 4. ISO 9126 Standards

Quality	Description		
Functionality	Business rules, scopes, and limitations were kept in mind to en-		
	sure the system's objective functionality.		
Reliability	The system limited the original usage of API's. This is to ensure		
	that the data presented in the system will be reliable for long pe-		
	riods of time.		
Usability	The system is capable of providing users with alert messages to		

Quality	Description			
	give them the optimal usage of the system. This also includes an			
	informative User's Guide along with the system.			
Efficiency	Under system requirements are the minimum and recommended			
	specifications to efficiently run the system. The system is also			
	equipped with multiple algorithms that can produce outputs			
	more efficiently.			
Maintainability	The system was developed to be adaptive. The original use			
	API's were limited to its original use to ensure a more concrete			
	form of maintaining the system and its data.			
Portability	The system can be very adaptive in multiple devices because it is			
	a web-based system, which maintains its portability.			

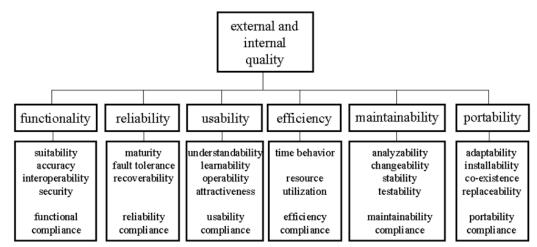


Figure 25. ISO 9126

User Acceptance Test

The user acceptability test was tailored to the system's clients and potential users in accordance with ISO 9126 standards. The system's evaluation approach was broken into two stages. The system was assessed by the various categories of users. The evaluation mostly was based on the ISO 9126 standards. User acceptability testing was also done to verify whether the system is capable of performing the needed activities and serving its intended purpose.

Table 5. User Categories for the Evaluation of the BASILIO Web-system

User	Role
Administrator	The administrator's feedback on the evaluation aids in the system's development.
Contributors	The Contributors are course instructors and researchers different colleges and universities. Contributor evaluation is critical in the system's development
Students	Students of Information Technology and Microbiology from several colleges and universities were invited to participate in the evaluation to determine the website's usefulness.

User	Role		
Practitioners	Practitioners from various computer companies and institutions invited		
	to participate in the system's overall evaluation. Six academics from var-		
	ious universities and three IT specialists from various computer organi-		
	zations comprised the Practitioners.		

Statistical Treatment

Throughout its development, the BASILIO web-system was evaluated. There is a discussion of the results of several testing and evaluations. The system's objective is to create and implement the BASILIO web-based system. It intended to specifically address the evaluation of the system's various users in terms of the criteria defined by the ISO 9126 standards. A five-point Likert Scale was used to interpret and translate the results of the tabulations.

Table 6. Likert Scale for the Evaluation of the BASILIO Web-system utilizing ISO 9126 instrument

Sca	Rang	Likert		Descriptive Interpretation					
le	e	Scale In- terpreta- tion	Functio- nality	Relia- bility	Usa- bility	Effi- ciency	Maintai- nability	Porta- bility	Satisfac- tion
5	4.20 - 5.00	Strongly Agree	Func- tional	Relia- ble	Usa- ble	Effi- cient	Maintain- able	Porta- ble	Very sa- tisfactory
4	3.40 - 4.19	Agree	Func- tional	Relia- ble	Usa- ble	Effi- cient	Maintain- able	Porta- ble	Satisfac- tory
3	2.60 - 3.39	Mod- erately Agree	Func- tional	Relia- ble	Usa- ble	Effi- cient	Maintain- able	Porta- ble	Neutral
2	1.80 - 2.29	Disagree	Not function-	Not reliable	Unus- able	Not Effi- cient	Not main- tainable	Not Porta- ble	Unsatis- factory
1	1.00 - 1.79	Strongly Disagree	Not function- al	Not reliable	Unus- able	Not Effi- cient	Not main- tainable	Not Porta- ble	Very un- satisfacto- ry

The mean was computed to know the verbal interpretation for each criterion. **Mean:**

$$\bar{X} = \frac{\Sigma X}{N}$$

Where:

 $\bar{X} = \text{mean}$

 Σ = symbol for summation

X = score

Results and Discussion

Users' Evaluation Results

By getting the mean of each category, the Likert Scale was used to interpret the results of the evaluation questionnaires below:

Table 7. UAT – FUNCTIONALITY

Functionality	Mean	Interpretation
The system does what is appropriate.	4.53	Functional
(Adequacy)		
The system has all the functions required	4.10	Functional
for its execution. (Adequacy)		
The system does what was specified	4.50	Functional
correctly. (Accuracy)		
The system is precise in executing the	4.40	Functional
functions. (Accuracy)		
The system is precise in its results. (Accu-	4.40	Functional
racy)		
The system interacts with the specified	4.40	Functional
modules. (Interoperability)		
The system has secure access through	4.53	Functional
passwords. (Secure Access)		
Average Mean	4.41	Functional

Concentrating on the system's functionality as a whole, the result was a mean of 4.41, interpreted as Functional, indicating that respondents were satisfied with the system's adequacy, accuracy, interoperability, and secure access.

Table 8. UAT – RELIABILITY

Reliability	Mean	Interpretation
The Information system has no frequent	4.10	Reliable
failures. (Maturity)		
The Information system reacts appropriate-	4.13	Reliable
ly when failure occurs. (Fault Tolerance)		
The Information system informs users	4.33	Reliable
concerning invalid data entry. (Fault Toler-		
ance)		
The Information system can provide correct	4.23	Reliable
output all the time in all requested informa-		
tion without service interrupts. (Maturity)		
Average Mean	4.20	Reliable

On the reliability of the system, the result came up with a mean of 4.20 translates as Reliable as per its Maturity and Fault Tolerance.

Table 9. UAT – USABILITY

Usability	Mean	Interpretation
The Information system is easy to understand the concept and application (Intelligibility)	4.53	Usable
The Information system is easy to perform its functions. (Intelligibility)	4.67	Usable
The Information system is easy to learn how to use. (Learnability)	4.40	Usable
The Information system facilitates the users' data entry. (Learnability)	4.50	Usable
The Information system is easy to operate and control. (Operability)	4.50	Usable
The Information system provides help in a clear manner. (Operability)	4.40	Usable
Average Mean	4.50	Usable

Based on the system's usability study, a mean of 4.50 was determined, indicating that the system is Usable in terms of Intelligibility, Learnability, and Operability.

Table 10. UAT – EFFICIENCY

Tuble 100 citi		
Efficiency	Mean	Interpretation
The Information system's response time is	4.36	Efficient
appropriate. (Time)		
The Information system's execution time is	4.20	Efficient
appropriate. (Time)		
The resources used by the Information	4.43	Efficient
system are appropriate. (Time)		
Average Mean	4.33	Efficient

Emphasis on the system's overall efficiency yielded a mean of 4.33, which translates to Efficient in terms of response time, execution time, and resources.

Table 11. UAT - MAINATINABILITY

Maintainability	Mean	Interpretation
Changes are easy to test. (Testability)	4.13	Maintainable
The Information system is easy to find a failure when it occurs. (Analyzability)	4.17	Maintainable
The Information system is easy to modify and adapt. (Modifiability)	4.30	Maintainable
Average Mean	4.20	Maintainable

On the maintainability of the system, a mean of 4.20 was obtained, which corresponds to Maintainable on the system's testability, analyzability, and modifiability.

Table 12. UAT – PORTABILITY

Portability	Mean	Verbal Interpretation
The Information system is easy to adapt to	4.30	Portable
other environments. (Adaptability)		
The Information system is in agreement	4.27	Portable
with portability standards. (Conformity)		
The Information system is easy to use to	4.13	Portable
replace another program. (Capacity to re-		
place)		
Average Mean	4.23	Portable

Based on the system's portability evaluation, a mean of 4.23 was determined, which corresponds to respondents strongly agreeing that the system is Portable attributing to its adaptability, conformity, and capacity to replace.

Table 13. UAT – USEFULNESS

Usefulness	Mean	Interpretation
The Information system helps me be more	4.53	Useful
effective.		
The Information system helps me be more	4.37	Useful
productive.		
The Information system gives me more	4.33	Useful
control over the activities in my life.		
The Information system makes the things I	4.33	Useful
want to accomplish to get done.		
The Information system does everything I	4.17	Useful
would expect it to do.		
The Information system meets my needs.	4.33	Useful
The Information system saves me time	4.43	Useful
when I use it.		
Average Mean	4.36	Useful

On the system's overall usefulness, the result was a mean of 4.36, indicating that respondents are strongly agreeing that the system is Useful.

Table 14. UAT – SATISFACTION

Satisfaction	Mean	Interpretation
I am satisfied with the system.	4.43	Very satisfactory
I would recommend the Information system.	4.63	Very satisfactory
The Information system is fun to use.	4.63	Very satisfactory
The Information system works the way I	4.27	Very satisfactory
want it.		
I feel I need to have the Information system.	4.30	Very satisfactory
The Information system is wonderful.	4.47	Very satisfactory
The Information system is pleasant to use.	4.63	Very satisfactory
Average Mean	4.48	Very satisfactory

Based on the satisfaction rating of the system, a mean of 4.48 was determined, indicating that respondents strongly agreeing that the system is very satisfactory on its many aspects and features of a web-system.

Table 15. Summary of UAT Evaluation

ISO 9126 Standards	Mean	Verbal Interpretation
Functionality	4.41	Functional
Reliability	4.20	Reliable
Usability	4.50	Usable
Efficiency	4.33	Efficient
Maintainability	4.20	Maintainable
Portability	4.23	Portable
Usefulness	4.36	Useful
Satisfaction	4.48	Very Satisfactory

Conclusions

With a better understanding of the medical significance of zoonotic diseases, which continue to pose a threat to global health security, and the concept of microbiota diversity, which demonstrates their impact on organisms' homeostasis, and the massive amounts of data available from various research studies, curating this information is necessary. Thus, the BASILIO web-system was developed with the goal of curating, organizing, and presenting data on animal microbiota. The BA-SILIO web-system presents animal and bacterial taxonomy, with an emphasis on the quantity of bacterial variety in the animals investigated and the classification of bacteria by their pathogenicity. BASILIO's web-system was successfully designed and developed using an AGILE development methodology and iterative process model. From its inception, the BASILIO web-system curated a total of 272 research articles for data mining, spanning the years 2010–2021. The evaluation of the BASILIO Web-system provided an opportunity to discover problems and enhance the web-current system's functionality. Following a review of the ISO 9126 system by designated users, the BASI-LIO web-system considered to be quite relevant based on its current characteristics for presenting data in an ordered and user-friendly manner. The BASILIO web-based system satisfies the need for a database dedicated to providing rapid access to information about harmful bacteria discovered in animals and has been certified ISO 9126 compliant.

Even before development starts, the BASILIO web-system design and development team identified difficulties. These flaws and disadvantages were identified and rectified when they were discovered. When researchers are looking for bacteria of medical significance isolated from animals, they frequently consult a variety of sources. The BASILIO web-system recognizes this issue, and the utilization of organized data culled from published journals and research conducted throughout the world enables academics to meet their demands. BASILIO was built as a web-based method to effectively communicate the obtained data. Thus, a greater number of people can profit from its goal; to efficiently manage such large amounts of data, the binary search algorithm was applied. This results in a speedier response time while accessing the system's data. Algorithms were utilized to manipulate and present these data in ways that maximized its utility.

There are potential for improvement in system development, most likely in terms of acceptable research conduct. The developers make the following recommendation based on the evaluation results. To ensure that the system is implemented and used optimally, so that all types of researchers

can benefit from its features. Investigate ways to continue developing a more useful source of information so that the system can do more than its initial aim. Investigate more precise approaches to describe the extent of the system posing significant hazards in order to avoid information misuse. With the potential for the BASILIO web-system to gain popularity due to its features for presenting data on animal microbiota and the growing amount of data associated with microbiota research, it is recommended that future developers adopt the BASILIO system and incorporate additional data management tools and algorithms to create a more complex and robust system.

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References

- Ahn, E., & Kang, H. (2018). Introduction to systematic review and meta-analysis. *Korean journal of anesthesiology*, 71(2), 103–112. https://doi.org/10.4097/kjae.2018.71.2.103
- Belkaid, Y., & Hand, T. W. (2014). Role of the Microbiota in Immunity and Inflammation. In Cell (Vol. 157, Issue 1, pp. 121–141). Elsevier BV. https://doi.org/10.1016/j.cell.2014.03.011
- Blumberg, R., & Powrie, F. (2012). Microbiota, disease, and back to health: a metastable journey. Science translational medicine, 4(137), 137rv7. https://doi.org/10.1126/scitranslmed.3004184
- Butala, C., Fyfe, J., & Welburn, S. C. (2021). The Contribution of Community Health Education to Sustainable Control of the Neglected Zoonotic Diseases. In *Frontiers in Public Health* (9). Frontiers Media SA. https://doi.org/10.3389/fpubh.2021.729973
- Cantas, L., & Suer, K. (2014). Review: The Important Bacterial Zoonoses in â€eOne Health†Concept. In *Frontiers in Public Health*, 2. Frontiers Media SA. https://doi.org/10.3389/fpubh.2014.00144
- Centers for Disease Control and Prevention. Cost of the Ebola epidemic. 2016. Aug 8 [cited 2017 Feb 12]. https://www.cdc.gov/vhf/ebola/outbreaks/2014-west-africa/cost-of-ebola.html
- Esser, D., Lange, J., Marinos, G., Sieber, M., Best, L., Prasse, D., Bathia, J., Rühlemann, M. C., Boersch, K., Jaspers, C., & Sommer, F. (2018). Functions of the Microbiota for the Physiology of Animal Metaorganisms. In *Journal of Innate Immunity*, 11(5), 393–404). S. Karger AG. https://doi.org/10.1159/000495115
- Hasan, N., & Yang, H. (2019). Factors affecting the composition of the gut microbiota, and its modulation. In PeerJ (Vol. 7, p. e7502). PeerJ. https://doi.org/10.7717/peerj.7502
- Jena, A., Montoya, C. A., Mullaney, J. A., Dilger, R. N., Young, W., McNabb, W. C., & Roy, N. C. (2020). Gut-Brain Axis in the Early Postnatal Years of Life: A Developmental Perspective. In *Frontiers in Integrative Neuroscience*, 14. Frontiers Media SA. https://doi.org/10.3389/fnint.2020.00044
- Jones, K. E., Patel, N. G., Levy, M. A., Storeygard, A., Balk, D., Gittleman, J. L., & Daszak, P. (2008). Global trends in emerging infectious diseases. *Nature*, 451(7181), 990–993. https://doi.org/10.1038/nature06536
- Openly accessible at http://www.european-science.com

- Kazerouni, A., & Wein, L. M. (2017). Exploring the Efficacy of Pooled Stools in Fecal Microbiota Transplantation for Microbiota-Associated Chronic Diseases. In F. Cominelli (Ed.), *PLOS ONE*, 12(1), e0163956. Public Library of Science (PLoS). https://doi.org/10.1371/journal.pone.0163956
- Kitano, H. (2002). Computational systems biology, *Nature*, 420(6912), 206–210. Springer Science and Business Media LLC. https://doi.org/10.1038/nature01254
- Krancher O. (2020). Agile Software Development Practices and Success in Outsourced Projects: The Moderating Role of Requirements Risk. *Agile Processes in Software Engineering and Extreme Programming: 21st International Conference on Agile Software Development, XP 2020*, Copenhagen, Denmark, June 8–12, 2020, Proceedings, 383, 56–72. https://doi.org/10.1007/978-3-030-49392-9_4
- Li, D., Chen, H., Mao, B., Yang, Q., Zhao, J., Gu, Z., Zhang, H., Chen, Y. Q., & Chen, W. (2017). Microbial Biogeography and Core Microbiota of the Rat Digestive Tract. In *Scientific Reports*, 7(1). Springer Science and Business Media LLC. https://doi.org/10.1038/srep45840
- Martinez-Guryn, K., Leone, V., & Chang, E. B. (2019). Regional Diversity of the Gastrointestinal Microbiome. *Cell Host & Microbe*, 26(3), 314–324. Elsevier BV. https://doi.org/10.1016/j.chom.2019.08.011
- McFall-Ngai, M., Hadfield, M. G., Bosch, T. C. G., Carey, H. V., Domazet-Lošo, T., Douglas, A. E., Dubilier, N., Eberl, G., Fukami, T., Gilbert, S. F., Hentschel, U., King, N., Kjelleberg, S., Knoll, A. H., Kremer, N., Mazmanian, S. K., Metcalf, J. L., Nealson, K., Pierce, N. E., ... Wernegreen, J. J. (2013). Animals in a bacterial world, a new imperative for the life sciences, *Proceedings of the National Academy of Sciences*, 110(9), 3229–3236. https://doi.org/10.1073/pnas.1218525110
- Microsoft. (2021, November 3). Visual Studio Code. Visualstudio.com; Microsoft. https://code.visualstudio.com/docs
- Opoku-Acheampong, I., McLaud, T., & Anderson, O. S. (2022). Fecal Microbiota Transplantation to Prevent and Treat Chronic Disease: Implications for Dietetics Practice. *Journal of the Academy of Nutrition and Dietetics*, 122(1), 33–37. https://doi.org/10.1016/j.jand.2021.08.112
- Rahman, M. T., Sobur, M. A., Islam, M. S., Ievy, S., Hossain, M. J., El Zowalaty, M. E., Rahman, A. T., & Ashour, H. M. (2020). Zoonotic Diseases: Etiology, Impact, and Control. *Microorganisms*, 8(9), 1405. https://doi.org/10.3390/microorganisms8091405
- Ramai, D., Zakhia, K., Fields, P. J., Ofosu, A., Patel, G., Shahnazarian, V., Lai, J. K., Dhaliwal, A., Reddy, M., & Chang, S. (2021). Fecal Microbiota Transplantation (FMT) with Colonoscopy Is Superior to Enema and Nasogastric Tube While Comparable to Capsule for the Treatment of Recurrent Clostridioides difficile Infection: A Systematic Review and Meta-Analysis. *Digestive diseases and sciences*, 66(2), 369–380. https://doi.org/10.1007/s10620-020-06185-7
- Salyer, S. J., Silver, R., Simone, K., & Barton Behravesh, C. (2017). Prioritizing Zoonoses for Global Health Capacity Building-Themes from One Health Zoonotic Disease Workshops in 7 Countries, 2014-2016. *Emerging infectious diseases*, 23(13), S55–S64. https://doi.org/10.3201/eid2313.170418
- Sandhu, A., & Chopra, T. (2021). Fecal microbiota transplantation for recurrent Clostridioides difficile, safety, and pitfalls. *Therapeutic advances in gastroenterology*, 14, 17562848211053105. https://doi.org/10.1177/17562848211053105
- SO/IEC IS 9126-1. (2001). *Software Engineering Product Quality Part 1: Quality Model*. International Organization for Standarization, Geneva, Switzerland.

- Takiishi, T., Fenero, C., & Câmara, N. (2017). Intestinal barrier and gut microbiota: Shaping our immune responses throughout life. *Tissue barriers*, 5(4), e1373208. https://doi.org/10.1080/21688370.2017.1373208
- Wang, Y., Wang, Z., Wang, Y., Li, F., Jia, J., Song, X., Qin, S., Wang, R., Jin, F., Kitazato, K., & Wang, Y. (2018). The Gut-Microglia Connection: Implications for Central Nervous System Diseases, *Frontiers in Immunology*, 9. Frontiers Media SA. https://doi.org/10.3389/fimmu.2018.02325
- Woolhouse, M. E., & Gowtage-Sequeria, S. (2005). Host range and emerging and reemerging pathogens. *Emerging infectious diseases*, 11(12), 1842–1847. https://doi.org/10.3201/eid1112.050997
- Wu, H.-J., & Wu, E. (2012). The role of gut microbiota in immune homeostasis and autoimmunity. Gut Microbes, 3(1), 4–14. Informa UK Limited. https://doi.org/10.4161/gmic.19320
- Youngster, I., Sauk, J., Pindar, C., Wilson, R. G., Kaplan, J. L., Smith, M. B., Alm, E. J., Gevers, D., Russell, G. H., & Hohmann, E. L. (2014). Fecal microbiota transplant for relapsing Clostridium difficile infection using a frozen inoculum from unrelated donors: a randomized, openlabel, controlled pilot study. *Clinical infectious diseases: an official publication of the Infectious Diseases Society of America*, 58(11), 1515–1522. https://doi.org/10.1093/cid/ciu135
- Zhulin, I. B. (2015). Databases for Microbiologists. In W. W. Margolin (Ed.), *Journal of Bacteriology*, 197(15), 2458–2467. American Society for Microbiology. https://doi.org/10.1128/jb.00330-15
- Zoetendal, E. G., Raes, J., van den Bogert, B., Arumugam, M., Booijink, C. C., Troost, F. J., Bork, P., Wels, M., de Vos, W. M., & Kleerebezem, M. (2012). The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. In *The ISME Journal*, 6(7), 1415–1426. Springer Science and Business Media LLC. https://doi.org/10.1038/ismej.2011.212