Course Name

May 12, 2025

Table of Contents

# About

What is the essence/purpose of this course or module (2-3 sentences).



Figure 0.1: C-MOOR logo

### Audience and Prerequisites

What is the target audience?

**Prerequisites**:

* Prereq 1
* Prereq 2

Why are these needed? Provide a brief explanation that will help instructors decide whether it’s a good fit for their students.

### Format

* **Class Type:**
* **Lesson Length:**

### Learning Goals

1. Goal 1
2. Goal 2
3. Goal 3

### Core Competencies

This activity addresses the following core concepts and competencies:

**Vision and Change**

**Genetics**

**Bioinformatics**

Core concepts and competencies are taken from the following sources:

* [Vision and Change in Undergraduate Biology Education](https://visionandchange.org/) AAAS report
* [Genetics Core Competencies](https://genetics-gsa.org/education/genetics-learning-framework/) by [GSA](https://genetics-gsa.org/)
* [Bioinformatics core competencies for undergraduate life sciences education](https://doi.org/10.1371/journal.pone.0196878) by [NIBLSE](https://qubeshub.org/community/groups/niblse)

### C-MOOR Content Collection

This content is part of a collection of teaching resources developed by C-MOOR. C-MOOR works to break down barriers to scientific participation and build pathways for the next generation of data scientists through authentic research experiences. Learn more about C-MOOR by [viewing our projects](https://github.com/c-moor), or read about how C-MOOR is [integrating research experience into undergraduate biology courses](https://www.cloviscollege.edu/alumni-and-community/c-moor/c-moor.html) at Clovis Community College.

# 1 Introduction

## 1.1 Lecture: Welcome to Your Genomics Adventure!

[Slides: Welcome to Your Genomics Adventure!](https://docs.google.com/presentation/d/18hYo8xrYkyq3rG7RUy3n3-jWFK_JPs5NNW3HmM9HUeQ/edit?usp=sharing)

## 1.2 Activity: Create Accounts

### 1.2.1 Purpose

Over the course of this semester, we will use the following online platforms: - [C-MOOR Academy Discussion Forum](https://help.c-moor.org) – Join the community to get help and share your findings - [Google Docs](https://workspace.google.com/products/docs) – Collaborate on assignments and scientific posters - [Galaxy](https://usegalaxy.org) – Analyze data with >10,000 tools using a graphical user interface - [SciServer](https://sciserver.org) – Access virtual machines preinstalled with RStudio, Bioconductor, and more

### 1.2.2 Activity

*Estimated time: 30 min*

#### 1.2.2.1 Instructions

Create accounts on the following online platforms:

1. C-MOOR Academy Discussion Forum – <https://help.c-moor.org>

* Submit your username using [this form](https://docs.google.com/forms/d/e/1FAIpQLSctd0jPax7Ww9b9XGbzY0PTwmPgm6VQICmsOhVTl6OCDx18Hw/viewform)

1. Google Docs – <https://docs.google.com>

* Test by opening [tax-data-gut.tsv](https://drive.google.com/file/d/1vL6adVIrqxpONbae8rUsneK3tbdCpmR-) with Google Sheets

1. Galaxy – <https://usegalaxy.org>
2. SciServer – <https://sciserver.org>

#### 1.2.2.2 Questions

Fill out your username and insert a screenshot of that username in the boxes below.

| 1. C-MOOR Academy Discussion Forum. |
| --- |
| <Username: insert screenshot> |

| 2. Google Docs. |
| --- |
| <Username: insert screenshot> |

| 3. Galaxy. |
| --- |
| <Username: insert screenshot> |

| 4. SciServer. |
| --- |
| <Username: insert screenshot> |

#### 1.2.2.3 Grading Criteria

* Download as Microsoft Word (.docx) and upload on Canvas

#### 1.2.2.4 Footnotes

**Resources**

* Google doc

**Contributions and Affiliations**

* Frederick Tan, Johns Hopkins University

Last Revised: January 2025

## 1.3 Lecture: The Scientic Process

[Slides: The Scientic Process](https://docs.google.com/presentation/d/1VQE-rXASXIdf8rWLP5UTcrAhM_DcznARVigPTHTfw8M/edit?usp=sharing)

## 1.4 Homework: Post Introductions

### 1.4.1 Purpose

The purpose of this assignment is to learn how to post to the C-MOOR Academy Discussion Forum. This forum will be the primary place for students, their instructors, and experts to communicate about the student’s research project, professional development opportunities, and more.

### 1.4.2 Learning Objectives

1. Learn how to post to a discourse community.
2. Examine the differences between private and public discourse categories.

### 1.4.3 Introduction

Before beginning this assignment, you should have already made an account on the C-MOOR Academy Discussion Forum and been added to the course Category by your instructor. Within the C-MOOR community, you will find Categories, which can be either private or public. In this course we will use both. In our private category, students can talk to each other and their instructor and their conversations will not be publicly available. In the public category, students’ posts will be visible on the web. The value of public discourse communities is that you might get responses by experts that you do not know. In this assignment, students will post to both a public and private Category within the Community.

### 1.4.4 Activity 1 - Create a Topic in a Private Category

*Estimated time: 20 min*

#### 1.4.4.1 Instructions

1. Visit the C-MOOR Academy Discussion Forum (help.c-moor.org) and log in.
2. It is a good idea to bookmark this page so that you can easily access it throughout the course.
3. Read through the categories in the C-MOOR Academy Discussion Forum. Notice that some categories (at least one) have a lock next to them. This is a Private category, only visible to you, your classmates and your instructor. If you cannot see your course’s private category when you log in, email your instructor so that they can add you.
4. Click on the private category that belongs to your class: Spring 2025. In this private channel, we will add a “New Topic” in which you can introduce yourself to the class.
5. This first post will be an introduction to your class, including a bit about you and a photo.

**a. Tell your group about yourself. Answer the following questions.** 1. What is your name? 2. Why did you decide to take this class? What are you excited to learn about this semester? 3. Tell us one thing you like to do outside of school and work.

**b. Include a photo:** 1. Selfie: if you would like, post a photo of yourself. 2. Unselfie: or post a photo of something else. Maybe something that you feel represents your life right now, or a picture of something you love. A pet maybe. Just make sure it tells us something about you.

1. Play around with the platform to personalize your post. As you can see in the discourse topic, you can add emojis, upload images, embed content, etc. These features appear in plain text as you’re typing, but you can see a preview of your post on the right. For your first few posts you may see a Welcome Box on the right instead, you can close this to see the preview. Once you have posted a few times, the Welcome Box will stop appearing.
2. When you are done, click “Create Topic” and it will post for the class to see.
3. If other students have posted their introductions, read them and leave a couple replies. This is a discussion platform after all!

#### 1.4.4.2 Resources

* [C-MOOR Academy Discussion Forum](https://help.c-moor.org)
* [How to add a bookmark in Chrome](https://support.google.com/chrome/answer/188842?co=GENIE.Platform%3DDesktop&hl=en)
* [Discourse New User Guide](https://meta.discourse.org/t/discourse-new-user-guide/96331)

### 1.4.5 Activity 2 - Reply to a Topic in a Public Category

*Estimated time: 10 min*

#### 1.4.5.1 Instructions

1. Navigate back to the C-MOOR Academy Discussion Forum front page.
2. Click on the “Breakroom” Category. This is an informal category where we can chat about non-science related topics.
3. Look for a topic called “Enduring a Snow Storm” Click on the topic.
4. Read the topic and then click “Reply”.
5. The same box will pop up as you used to to post a topic earlier.
6. Write a reply to the topic.
7. When you are finished click “Reply” to post.

#### 1.4.5.2 Resources

* [C-MOOR Academy Discussion Forum](https://help.c-moor.org)
* [Discourse New User Guide](https://meta.discourse.org/t/discourse-new-user-guide/96331)

#### 1.4.5.3 Grading Criteria

* Submit URL to your Private Category Topic on Canvas

#### 1.4.5.4 Footnotes

**Contributions and Affiliations**

* Katherine Cox, Johns Hopkins University
* Valeriya Gaysinskaya, Johns Hopkins University
* Frederick Tan, Johns Hopkins University
* Stephanie Coffman, Clovis Community College

Last Revised: January 2025

# 2 Scientific Literature

## 2.1 Lecture: What’s in Your XYZ?



[Slides: What’s in Your XYZ?](https://docs.google.com/presentation/d/1ph3LFw6i_mtv6ZJXssTf0-im7PhgV4FRJslDG0ICCws/edit?usp=sharing)

## 2.2 Activity: Taxonomy Profiling Spreadsheet

### 2.2.1 Purpose

First hands-on experience with real data! Compare kraken2 output for [Zymo Gut Microbiome Standard](https://www.zymoresearch.com/products/zymobiomics-gut-microbiome-standard?srsltid=AfmBOoqP_zq131c2GTidPCM0j6yA3JFcGQ0haUNu1jAJI9RQ9qsXLYSF) and [Zymo Human Fecal Reference](https://files.zymoresearch.com/protocols/d6323-zymobiomics_fecal_reference_protocol.pdf). Introduce concepts of taxa and relationships, begin forming data analysis goals like comparing how many species, most abundant species, etc. See accompanying [slides](http://docs.google.com/presentation/d/16lpgWFU6jzh-e7HuwXLHmUFpsnE8NreMzL-nTn8cJVk).

### 2.2.2 Learning Objectives

1. Explore taxonomy with Kraken 2 taxonomic assignment output.
2. Compare and contrast taxonomy between Zymo Gut Microbiome Standard and Zymo Human Fecal Reference.

### 2.2.3 Introduction

Metagenomics is the direct analysis of the genomes through genome sequencing of an environmental sample (soil, water, gut, etc). The purpose of the taxonomic classification of metagenomic sequences is to catalogue, classify and identify the species inhabiting a given environment. In the process, new species may get identified! After sampling, DNA extraction, DNA sequencing and genome assembly, genome annotation is used to assign taxonomy to the sequenced sample DNA. Here is where the Kraken 2 tool comes in; Kraken 2 is a taxonomic classification tool which assigns taxonomy to sequencing reads.

### 2.2.4 Activity 1 – Explore Zymo Gut Standard Metagenomic Diversity

*Estimated time: 25 min*

#### 2.2.4.1 Instructions

Perform the activity below and answer the embedded **questions**.

1. Access tax-data-gut.tsv and open with Google Sheets [here](http://drive.google.com/file/d/1vL6adVIrqxpONbae8rUsneK3tbdCpmR-)
2. Identify what information is provided in columns of the tax-data-gut taxonomy file.

* Col A = Counts
* Cols B-H correspond to taxonomic ranks k(Kingdom), p(Phylum), c(Class), o(Order), f(Family), g(Genus) and s(Species)
* Each row corresponds to a different taxa. There are 153 taxa that were classified for this sample.

1. Create a header row and enter column information.

#### 2.2.4.2 Questions

1. Evaluate what proportion of data was taxonomically classified.
2. Insert a new column A; we will use this temporary column for calculations, so you can name this column “Calculations”.
3. In e.g. cell A2, calculate the sum of all reads observed in the gut std sample.

| **How many total counts are there?** |
| --- |
|  |

1. In e.g. cell A3, determine the percentage of unclassified reads.

| **What percentage of reads are unclassified?** |
| --- |
|  |

1. In e.g. cell A4, determine the percentage of classified reads.

| **What percentage of reads are classified?** |
| --- |
|  |

1. Identify abundant taxa (those at >1%).
2. Select columns B through I
3. In the Data menu, select “Sort range by column B (Z to A)”
4. Insert a new column C; we will use this temporary column for calculations; you can name this column “% abundance”.
5. In new column C, calculate % abundance for each row by dividing each count value by the total number of reads and multiplying by 100.
6. Quantify abundant taxa.

| **How many abundant taxa (at >1%) do you observe?** |
| --- |
|  |

1. List abundant taxa you identified in a table below.

* To consolidate the different abundant taxa, in e.g. new column D, copy the lower taxonomic rank identified for the abundant (at >1%) taxa.
* Then, enter the results into a table below.

**What abundant taxa do you observe?**

| **% abundance** | Taxonomy |
| --- | --- |
| 20.1 | s\_Faecalibacterium\_prausnitzii |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
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|  |  |

1. Compare your results with the expected taxa and abundance for [Zymo gut standard documentation](https://www.zymoresearch.com/products/zymobiomics-gut-microbiome-standard?srsltid=AfmBOor0X27Jf1gfXVmyGu5nZq3M6fx6OJXdEc0t6rqSRBPww2qeY-Yd)?

* Note, the Kraken2 output does not distinguish different *E. coli* strains, so just combine them all into a single *E. coli group*!

| **How do your results overall compare with the expected taxa and % abundance from Zymo gut standard?** |
| --- |
|  |

1. Calculate ‘Low abundance’ for < 1% abundant taxa by adding together taxa at <1%.

| **What percentage of reads are classified in a low abundance taxa?** |
| --- |
|  |

1. Create a barplot of % abundance for your 12 abundant taxa via Insert Chart.

| **Paste your barplot of % abundance for the 12 most abundant taxa** |
| --- |
|  |

### 2.2.5 Activity 2 (OPTIONAL) – Compare with Zymo Fecal Reference

*Estimated time: 20 min*

#### 2.2.5.1 Instructions

Perform the optional activity below and answer the embedded **questions**.

In this activity, repeat steps of the Activity 1 above, but now using [tax\_data\_fecal.tsv](http://drive.google.com/file/d/1CLQw9yqoqWl5caLm-ZmiHpLNtUo_Zo4s) dataset corresponding to Zymo fecal reference. The tax\_data\_fecal.tsv dataset comes from a real human fecal sample, in contrast to the tax\_data\_gut.tsv sample you explored in the Activity 1, which corresponds to cultured and pooled known species combined at specific proportions to make up a predictable standard population.

* Perform Activity 1 exercises using tax\_data\_fecal data, then, use questions below to compare the two datasets.
* See D6323 Zymo Fecal Microbiome References documentation (pg. 4) in the Resources section below.

#### 2.2.5.2 Questions

| **1. Which dataset is classified better, gut or fecal??** |
| --- |
|  |

| **2. Are there any abundant taxa (at >1%) in common between the gut standard and fecal reference?** |
| --- |
|  |

| **3. In your opinion, does the gut standard mimic the fecal reference well or not?** |
| --- |
|  |

### 2.2.6 Grading Criteria

* Download this assignment as Microsoft Word (.docx) and upload on Canvas
* Download your Google Sheet as Microsoft Excel (.xlsx) and upload on Canvas

### 2.2.7 Footnotes

**Resources**

* Google Doc
* [D6331 Zymo Gut Microbiome Standard documentation](https://www.zymoresearch.com/products/zymobiomics-gut-microbiome-standard?srsltid=AfmBOor0X27Jf1gfXVmyGu5nZq3M6fx6OJXdEc0t6rqSRBPww2qeY-Yd)
* [D6323 Zymo Fecal Microbiome References documentation](https://files.zymoresearch.com/protocols/d6323-zymobiomics_fecal_reference_protocol.pdf?_gl=1*cych1b*_gcl_au*MzEzNzgzNjc0LjE3MzQ5NTk3NzY)

**Contributions and Affiliations**

* Valeriya Gaysinskaya, Johns Hopkins University
* Gauri Paul, Clovis Community College
* Frederick Tan, Johns Hopkins University

Last Revised: January 2025

## 2.3 Activity: A short introduction to Galaxy

### 2.3.1 Introduction

Galaxy <galaxyproject.org> is a free, open-source system for analyzing data, authoring workflows, training and education, publishing tools, managing infrastructure, and more. Among the notable features:

* [Graphical user interface](https://training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-101/tutorial.html) (GUI) for interactively running tools
* [Toolshed](https://toolshed.g2.bx.psu.edu/) with 10,000 tools ready to run
* Full featured [workflow](https://training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/workflow-editor/tutorial.html) functionality
* Terabytes of the latest, curated [reference data](https://galaxyproject.org/admin/reference-data-repo)
* Extensive training [tutorials](https://training.galaxyproject.org/) and infrastructure
* Large international [community](https://galaxyproject.org/community) of users and developers

### 2.3.2 Activity

*Estimated time: 40 min*

#### 2.3.2.1 Instructions

1. Review slides for “A short introduction to Galaxy”

* <training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-short/slides.html>

1. Complete the hands-on tutorial

* <training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-short/tutorial.html>

### 2.3.3 Grading Criteria

* Submit URL to your shared Galaxy history on Canvas

### 2.3.4 Footnotes

**Resources**

* Introduction to Galaxy Analyses [topic](https://training.galaxyproject.org/training-material/topics/introduction/)

**Contributions and Affiliations**

* Frederick Tan, Johns Hopkins University

Last Revised: January 2025

## 2.4 Homework: Scientific Literature Prelab

### 2.4.1 Purpose

Obtain a high level overview of metagenomics by reading R.D. Sleator, C. Shortall, and C. Hill. Metagenomics. Letters in Applied Microbiology. 2008 Nov;47(5):361-6. [(pubmed.gov/19146522)](http://pubmed.gov/19146522)

### 2.4.2 Learning Objectives

* Read a review paper that summarizes the field of metagenomics.
* Broadly understand the scope of the review and the gaps in the field.

### 2.4.3 Introduction

The vast majority of all micro-organisms on Earch remain uncultured [(K.G. Lloyd et al, 2019)](https://journals.asm.org/doi/10.1128/msystems.00055-18). Additionally, in complex environments like soil and water, most micro-organisms remain unidentified [(M. Delgado-Baquerizo, 2019)](https://doi.org/10.1038/s41396-019-0405-0). The field of metagenomics is a culture-independend approach which aims to remedy these gaps in knowledge [(J. Handelsman, 2004)](https://pubmed.ncbi.nlm.nih.gov/15590779/). Metagenomics is the study of genomic (sequencing) data obtained directly from environmental (and other, e.g. clinical) samples and provides new meaningful information on the diversity and function of microorganisms.

### 2.4.4 Activity

*Estimated time: 50 min*

#### 2.4.4.1 Instructions

Read the review paper “Metagenomics” by Sleator, Shortall, and Hill, 2008 Lett Appl Microbiol and answer the following questions.

#### 2.4.4.2 Questions

1. What is one thing you learned or find interesting in the paper?
2. Define a term that is new to you (e.g. metagenome, microbiome, 16S rRNA).
3. Ask a question about the review paper.

#### 2.4.4.3 Grading Criteria

Download as Microsoft Word (.docx) and upload on Canvas

### 2.4.5 Footnotes

**Resources**

[Google Doc](https://docs.google.com/document/d/1-ruTySaAnSE-_5d6_LTdre4UmmUAx6TxMrTYBW-f3jQ/edit?usp=sharing)

**Contributions and Affiliations**

* Valeriya Gaysinskaya, Johns Hopkins University
* Frederick Tan, Johns Hopkins University

## 2.5 Discussion: Scientific Literature Prelab

### 2.5.1 Activity

*Estimated time: 25 min*

#### 2.5.1.1 Instructions

1. Form groups of four

* Add names to the “Microbial Mysteries Groups” sheet <https://docs.google.com/spreadsheets/d/11eoJgm9mehxGWWzh8IZYDCDmnCmSyshopPYHewvpC8c/edit?usp=sharing>

1. Pair up into groups (10 min)
2. Discuss – Each group member briefly describes answers to prelab assignment
3. Summarize – Identify best answer and add to slidedeck <https://docs.google.com/presentation/d/1nuA_gnL09_BPZVNJy5seL-HWejhMFLqILsmgmQztYKo/edit?usp=sharing>
4. Share group discussion (2 min each group)

## 2.6 Lecture: Scientific Literature



[Slides: Scientific Literature](https://docs.google.com/presentation/d/1zbjroITjBYmu-oxFT0qmOCx9LeEcSoaYrp_sWuy1OLM/edit?usp=sharing)

## 2.7 Homework: Scientific Literature Activity

### 2.7.1 Purpose

Examine research on metagenomic diversity by reading Xue, *et al*. Metagenome sequencing and 103 microbial genomes from ballast water and sediments. Scientific Data.2023 Aug 10;10(1):536. [(pubmed.gov/37563185)](https://pubmed.ncbi.nlm.nih.gov/37563185/)

### 2.7.2 Learning Objectives

* Understand the purpose and experimental setup of the paper
* Understand the presented evidence (Figures and Tables) of the paper

### 2.7.3 Introduction

Understanding microbial composition and diversity in different environments is critical for assessing the benefits and threats of the bacterial community in that environment. In the publication by [Xue, et al. 2023](https://pubmed.ncbi.nlm.nih.gov/37563185/), the authors study microbial diversity in the ballast-tank water from two ships, with the idea that such a unique and isolated water environment may select for specific microbes. Luckily in their research they don’t find bacterium *Vibrio cholerae*, but that is exactly what they would find in the ballast water of cargo ships if they did the analysis during the cholera pandemic(s) of the 1800s.

### 2.7.4 Activity

*Estimated time: 90 min*

#### 2.7.4.1 Instructions

Based on the study by Xue, et al.2023, answer the following questions. The main text of the paper and the supplement can be found below, in the ‘Resources’ section of this assignment.

#### 2.7.4.2 Overview of the Paper (in class)

Determine the main objectives and purpose of the paper. Read the Abstract and the introduction with your group.

1. What is the purpose of this study?
2. What is the hypothesis in this study?
3. Describe the knowledge gap. In essence, what did the scientific community not know that this study was trying to answer?

#### 2.7.4.3 Methods (in class and homework)

1. Discuss how many and what samples were used for this study? Are there any replicates?
2. Discuss some methods used in this paper.
3. Discuss steps authors used to ensure their data is available to the public.

#### 2.7.4.4 Figures (in class and Homework)

**Methods.** How did the researchers test their hypothesis? Explain in your own words the methods in each figure.

| Figure | Methods |
| --- | --- |
| Fig. 1B | in class |
| Fig. 1C | in class |
| Fig. 2 | homework |
| Fig. 3A | homework |
| Fig. 3B | homework |
| Fig. 3C | homework |

### 2.7.5 Results (in class and Homework)

**Results.** What are the main findings from each figure?

| Figure | Main Findings |
| --- | --- |
| Fig. 1B | in class |
| Fig. 1C | in class |
| Fig. 2 | homework |
| Fig. 3A | homework |
| Fig. 3B | homework |
| Fig. 3C | homework |

#### 2.7.5.1 Conclusions (Homework)

1. Read the discussion section. What were the main conclusions the authors made in this study?
2. Do the figures agree with their conclusion?

#### 2.7.5.2 Future Directions (Homework)

1. Scientific work builds on previous studies. What do you believe could be the next step to further the work these researchers did?

* What follow-up question(s) do you have for the authors?

1. What is the impact of this research area in general (or this study in particular?)

* Do you believe further research in this area may benefit society? Can we build on what this study found?
* Do you think there are risks associated with such studies?

### 2.7.6 Grading Criteria

* Download as Microsoft Word (.docx) and upload on Canvas.

### 2.7.7 Footnotes

**Resources**

[Google Doc](https://docs.google.com/document/d/1kKnvMGq8jBfwKzC7W5YEJ7CtTgFNahAaDfV3LNknznM/edit?usp=sharing)

**Contributions and Affiliations**

* Valeriya Gaysinskaya, Johns Hopkins University
* Frederick Tan, Johns Hopkins University

## 2.8 Presentation: Scientific Literature Activity

### 2.8.1 Activity

*Estimated time: 25 min*

#### 2.8.1.1 Instructions

1. Open the “Scientific Literature Presentation” slidedeck [here](https://docs.google.com/presentation/d/1wwfiTSgm0ialrYlBFnA21zdZsw7mVA58YPMiTnDGCrc/edit?usp=sharing)
2. For your assigned figure from Xue, et al., 2023, create two slides to present methods and results
3. Add bullet points on key details you understand (Notice) and questions you have (Wonder)
4. Search for and insert at least one additional image that relates to your figure
5. Update slide title to summarize your main takeaway
6. Present at next class (5 min each group)

### 2.8.2 Footnotes

**Contributions and Affiliations**

* Valeriya Gaysinskaya, Johns Hopkins University
* Frederick Tan, Johns Hopkins University

Last Revised: January 2025

# 3 Microbial Genomes

## 3.1 Lecture: Microbial Genome



[Slides: Microbial Genomes](https://docs.google.com/presentation/d/1bnFhIIu6ZXSCjlrz5qWc7BZNz-7VfYWkKgbz3kL-ZNU/edit?usp=sharing)

## 3.2 Homework: Microbial Genomes Prelab

### 3.2.1 Purpose

Impress all the information that is freely available about well studied (and not so well studied) bacterial species. Start with E. coli as one of the best and longest studied before going into recently discovered bacteria (with less information).

### 3.2.2 Learning Objectives

1. GenBank – Explore sequence database of all publicly available DNA sequences
2. Sequence Browser – Observe genome organization using graphical representation
3. Bacterial database BV-BRC - Explore bacterial genes and their function
4. Taxonomy Browser – Identify relationships between taxa
5. Lifemap - Tree of Live viewer to visualize relationships between taxa

### 3.2.3 Activity 1 – GenBank



### 3.2.4 Activity 1 - Part I

*Estimated time: 5 min*

#### 3.2.4.1 Instructions

Navigate to **GenBank** <https://www.ncbi.nlm.nih.gov/genbank> and enter ‘E. coli strain K-12’ in the search bar (which should default to **Nucleotide**). This will give you a list of almost 300,000 E. coli sequences. Go down the list and click on the entry that corresponds to the complete genome of the substrain MG1655, which should be on page 1! Click on the selection and answer the following questions.

#### 3.2.4.2 Questions

| **1. What is the size of this *E. coli* genome in bp and Kbp**? |
| --- |
|  |

| **2. Is the *E. coli* genome linear or circular**? |
| --- |
|  |

| **3. What is the ACCESSION number?** |
| --- |
|  |

### 3.2.5 Activity 1 - Part II

*Estimated time: 5 min*

#### 3.2.5.1 Instructions

Back in GenBank <https://www.ncbi.nlm.nih.gov/genbank>, under the **Nucleotide** search tab, instead of typing ‘E. coli strain K-12’, type in the ACCESSION number you found (NZ\_CP169634).

#### 3.2.5.2 Questions

| **1. How many records do you observe after an ACCESSION number entry?** |
| --- |
|  |

| **2. What can you conclude about what is the ACCESSION number?** |
| --- |
|  |

### 3.2.6 Activity 2 – Genomes, genes, and other databases (BV-BRC)

### 3.2.7 Activity 2 - Part I

*Estimated time: 5 min*

#### 3.2.7.1 Instructions

After entering your accession number, the on the right of the page, under **Related Information**, click on Assembly link to explore genome assembly information.

| **1. How many chromosomes does E. coli have?** |
| --- |
|  |

| **2. What is the genome coverage of this sequenced genome?** |
| --- |
|  |

| **3. How many genes were annotated for this genome?** |
| --- |
|  |

### 3.2.8 Activity 2 - Part II

*Estimated time: 10 min*

#### 3.2.8.1 Instructions

Go back and on the top of the page and click on **Graphics** to explore genome browser.

1. Hover along one of many green vertical sticks.

* You can also zoom into a smaller and smaller genomic region for higher resolution.

1. Hover along one of many red vertical sticks.

* You can also zoom into a smaller and smaller genomic region for higher resolution.

| **1. What do the ‘green sticks’ represent?** |
| --- |
|  |

| **2. What do the ‘red sticks’ represent?** |
| --- |
|  |

| **3. Record 5 genes you found present in E. coli**. |
| --- |
| Gene 1 |
| Gene 2 |
| Gene 3 |
| Gene 4 |
| Gene 5 |
|  |

### 3.2.9 Activity 2 - Part III

*Estimated time: 10 min*

#### 3.2.9.1 Instructions

To learn more about the genes of interest and their function scientists often use specialized databases. One such bacterial database is BV-BRC <https://www.bv-brc.org>. Use BV-BRC to find information about some of the E. coli genes. If there are 0 results then indicate No results found.

**For the 3 genes below, and one gene of your choice from activity above**, in the BV-BRC **Search** space,

**a)** from a dropdown menu select **“Pathways”** ,

**b)** type in the gene name and **click enter**. This will result in a lot of entries for different organisms.

**c)** To retrieve information specifically for *E. coli (Escherichia coli)*, in the **Keyword** space type “Escherichia”.

**d)** Check one of the boxes corresponding to *E. coli* strains and enter below which E. coli strain **(Genome Name)** you selected. If no E. coli entry is present, select and record another bacterial Genome Name to learn about your gene’s function.

#### 3.2.9.2 Questions

| **1. Record Genome Name associated with the following genes**. |  |
| --- | --- |
| **Gene ID** | **Genome Name** |
| Gene 1: ampC | Escherichia coli 07798 |
| Gene 2: mgtA |  |
| Gene 3: cdd |  |
| Gene 4: Your gene |  |
|  |  |

| **2. For the 3 genes from the activity above, record gene Product**. |  |
| --- | --- |
| **Gene ID** | **Gene Product** |
| Gene 1: ampC | Beta-lactamase |
| Gene 2: |  |
| Gene 3: |  |
|  |  |

| **3. For the 3 genes from the activity above, record Pathway Name (relates to function)**. |  |
| --- | --- |
| **Gene ID** | **Pathway Name** |
| Gene 1: ampC | beta-Lactam resistance |
| Gene 2: |  |
| Gene 3: |  |
|  |  |

**Note**, For some well characterized genes you can additionally obtain more detailed information about the gene/protein function.

* To do so, from the ‘green’ menu on the right, select **FEATURE** option, to learn from the Special Properties section about a special property of your gene.

### 3.2.10 Activity 3 - Taxonomy and tree of life

*Estimated time: 30 min*

### 3.2.11 Activity 3 - Part I

#### 3.2.11.1 Instructions

1. Back in NCBI enter the *E. coli* accession number again. Under **Related Information** on the right, click on **Taxonomy** and then on the provided link for the *E. coli*.
2. Find Lineage information. Full Lineage information contains 7 core taxonomy ranks: Kingdom, Phylum, Class, Order, Family, Genus and Species, plus any additional classification ranks. To just get the 7 core lineage names, click on Lineage link for the abbreviated Lineage, or, simply hover over lineage names.

#### 3.2.11.2 Questions

| 1. **Record 7 core taxonomy ranks below**. |  |
| --- | --- |
| Kingdom: |  |
| Phylum: |  |
| Class: |  |
| Order: |  |
| Family: |  |
| Genus: |  |
| Species: |  |
|  |  |

### 3.2.12 Activity 3 - Part II

#### 3.2.12.1 Instructions

1. As with the BV-BRC database above, we can use another database called **Lifemap** to visually explore the *E. coli* in the context of the tree of life. Go to <https://lifemap-ncbi.univ-lyon1.fr>, type E. coli and click species tab.
2. On the tree map, the yellow tag will indicate *E. coli*. Use plus and minus tabs to zoom in and out and visualize E. coli relative to other organisms on the map.

| **1. How many Domains of life are there?**. |
| --- |
|  |

| **2. Zoom into and find nodes for the E. coli Genus, Family, Order, Class and Phylum. Do they match what you found in the NCBI Taxonomy Browser for Lineage?**. |
| --- |
|  |

| **3. What are some other members of the Genus (Escherichia) to which E. coli belongs?**. |
| --- |
|  |

| **4. What are some other members of the Family (Enterobacteriaceae) to which E. coli belongs?**. |
| --- |
|  |

| **5. What are some other members of the Order (Enterobacterales) to which E. coli belongs?**. |
| --- |
|  |

| **6. What are some other members of the Class (Gammaproteobacteria) to which E. coli belongs?**. |
| --- |
|  |

| **7. What are some other members of the Phylum (Pseudomonadota) to which E. coli belongs?**. |
| --- |
|  |

### 3.2.13 Grading Criteria

* Download as Microsoft Word (.docx) and upload on Canvas.

### 3.2.14 Footnotes

**Resources**

* Google Doc

**Contributions and Affiliations**

* Valeriya Gaysinskaya, Johns Hopkins University
* Frederick Tan, Johns Hopkins University

Last Revised: February 2025

## 3.3 Homework: QC and Galaxy Workflows

### 3.3.1 Introduction

In the “A short introduction to Galaxy” activity you learned how to upload a file, use a tool, view results, view histories, extract and run a workflow, and share a history. You will now practice using these skills to do one of the first things when encountering a new sequencing dataset – quality control (QC). After assessing the quality of both short and long reads, gain more practice with workflows by creating and editing a new workflow.

### 3.3.2 Activity 1 – Quality Control (QC)

*Estimated time: 90 min*

#### 3.3.2.1 Instructions

1. Complete the “Quality Control” hands-on tutorial: [training.galaxyproject.org/training-material/topics/sequence-analysis/tutorials/quality-control/tutorial](https://training.galaxyproject.org/training-material/topics/sequence-analysis/tutorials/quality-control/tutorial.html)

* **NOTE**: Do all hands-on steps in a single Galaxy history

### 3.3.3 Activity 2 – Creating, Editing and Importing Galaxy Workflows

*Estimated time: 30 min*

#### 3.3.3.1 Instructions

1. Complete the “Creating, Editing and Importing Galaxy Workflows” hands-on tutorial: [training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/workflow-editor/tutorial](https://training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/workflow-editor/tutorial.html)

### 3.3.4 Grading Criteria

* Submit URL to your shared Galaxy “Quality Control” history on Canvas

### 3.3.5 Footnotes

**Resources**

* Using Galaxy and Managing your Data [topic](https://training.galaxyproject.org/training-material/topics/galaxy-interface/)
* Introduction to Galaxy and Sequence analysis [pathway](https://training.galaxyproject.org/training-material/learning-pathways/intro-to-galaxy-and-genomics.html)

**Contributions and Affiliations**

* Frederick Tan, Johns Hopkins University

Last Revised: February 2025

## 3.4 Discussion: Microbial Genomes Prelab

### 3.4.1 Activity

*Estimated time: 25 min*

#### 3.4.1.1 Instructions

1. Form new groups of four [here](https://docs.google.com/spreadsheets/d/11eoJgm9mehxGWWzh8IZYDCDmnCmSyshopPYHewvpC8c/edit?usp=sharing).
2. Pair up into groups (10 min).
3. Discuss – Each group member briefly describes answers to prelab assignment.
4. Summarize – Identify best answer and add to slidedeck [here](https://docs.google.com/presentation/d/1PxqLt-MDFCTSBWm0-j-mY268b3YUiPMRqYMtcJ5JDL4/edit?usp=sharing)
5. Share group discussion (2 min each group)

### 3.4.2 Footnotes

**Contributions and Affiliations**

* Valeriya Gaysinskaya, Johns Hopkins University
* Frederick Tan, Johns Hopkins University

Last Revised: February 2025

## 3.5 Homework: Microbial Genomes Project

### 3.5.1 Purpose

Explore information about new bacterial MAGs from Zue Z et al, Nature Scientific Data 2023 <https://pubmed.ncbi.nlm.nih.gov/37563185/>.

### 3.5.2 Learning Objectives

1. Explore and better understand MAGs and contigs by following up one MAG and one contig in NCBI.
2. Utilize knowledge learned by navigating MAG information using previously learned tools such as GenBank, Sequence Browser, BV-BRC, Taxonomy Browser and Lifemap.
3. Go deeper and see what you can find on the organism from your MAG of choice and a gene from a MAG of choice (in 15 minutes each!) using any tools available to you (Pubmed, Google, BV-BRC, other databases).

### 3.5.3 Activity 1 – MAGs and Taxonomy

*Estimated time: [40] min*

### 3.5.4 Activity 1 - Part I: Pick a MAG

#### 3.5.4.1 Instructions

In the research study by Zue Z et al, Nature Scientific Data 2023 <https://pubmed.ncbi.nlm.nih.gov/37563185/>, 17 of 103 uncovered MAGs from ballast water or sediment are of very high quality and completeness. Choose one of these 17 MAGs (see 17 GenBank IDs below) to follow up in this activity.

| 17 MAGs |
| --- |
| 1. GCF\_030147545.1 |
| 2. GCF\_030148435.1 |
| 3. GCF\_030149225.1 |
| 4. GCF\_030148195.1 |
| 5. GCF\_030148855.1 |
| 6. GCF\_030148245.1 |
| 7. GCF\_030149045.1 |
| 8. GCF\_030148385.1 |
| 9. GCF\_030147715.1 |
| 10. GCF\_030149085.1 |
| 11. GCF\_030149145.1 |
| 12. GCF\_030148125.1 |
| 13. GCF\_030149425.1 |
| 14. GCF\_030149235.1 |
| 15. GCF\_030148515.1 |
| 16. GCF\_030147875.1 |
| 17. GCF\_030149465.1 |

| **1. Record the GenBank ID number below for one of 17 high quality MAGs you will follow up below?**. |
| --- |
|  |

### 3.5.5 Activity 1 - Part II: Explore your MAG

#### 3.5.5.1 Instructions

In GenBank <https://www.ncbi.nlm.nih.gov/nucleotide/>, under the Nucleotide search tab type in the GenBank number from activity above.

#### 3.5.5.2 Questions

| **1. Record below the genome name for the MAG assembly associated with the GenBank ID you entered.** |
| --- |
|  |

* Click on the Genome name of your MAG to explore genome assembly summary information

| **2. What is the taxon of your MAG?** |
| --- |
|  |

| **3. What is the genome size of your MAG?** |
| --- |
|  |

| **4. How many genes were annotated?** |
| --- |
|  |

| **5. How comparable is your MAG genome to the E. coli genome from the microbial-genomes-pre-lab, in terms of genome size and number of genes?** |
| --- |
|  |

### 3.5.6 Activity 1 - Part III: Obtain Contig Info

#### 3.5.6.1 Instructions

Locate the Assembly statistics section and scroll down slightly to find ‘view RefSeq sequences’ which will provide you with the information on all of the Contigs that made up your MAG.

#### 3.5.6.2 Questions

| **1. How many contigs contributed to your MAG assembly?** |
| --- |
|  |

| **2. MAGs are made up of Contigs. Based on your lecture material, and your experience with MAGs and contigs from Zue Z et al, Nature Scientific Data 2023 and this exercise, in your own words define MAGs and Contigs below.** |
| --- |
| MAGs: |
| Contigs: |
|  |

| \*\*3. Choose a contig of reasonably large size (> 75 kb) and record below this Contig’s ID (Accession number) for further examination. |
| --- |
| Tip: You can sort the entries by length via’ Sort by Sequence Length’ on top! |
|  |

### 3.5.7 Activity 1 - Part IV: Find Contig Lineage

#### 3.5.7.1 Instructions

For the contig you chose in activity above, under **Related Information** on the right, click on **Taxonomy** and then on the provided link.

Find Lineage information. Full Lineage information contains 7 core taxonomy ranks: Kingdom, Phylum, Class, Order, Family, Genus and Species, plus any additional classification ranks. To just get the 7 core lineage names, click on Lineage link for the abbreviated Lineage, or, simply hover over lineage names.

| \*\*1. Record 7 core taxonomy ranks for your Contig. |  |
| --- | --- |
| Kingdom: |  |
| Phylum: |  |
| Class: |  |
| Order: |  |
| Family: |  |
| Genus: |  |
| Species: |  |
|  |  |

### 3.5.8 Activity 1 - Part V: Visualize your Contig in a tree of life.

#### 3.5.8.1 Introduction

1. Use Lifemap to visually explore the contig taxonomy in the context of the tree of life. Go to <https://lifemap-ncbi.univ-lyon1.fr> and **enter the lowest taxonomy rank observed for your contig** (most likely the species or genus level, but can also correspond to order or family).
2. On the tree map, use plus and minus tabs to zoom in and out and visualize your Contig entry relative to other organisms on the map. Zoom in and find nodes corresponding to the higher taxonomic ranks. For example, if your contig corresponds to genus level classification, you will not be able to identify species level information, but you will be able to identify the corresponding Family, Order, Class and Phylum.

| \*\*1. Record 7 core taxonomy ranks for your Contig. |  |
| --- | --- |
| Kingdom: |  |
| Phylum: |  |
| Class: |  |
| Order: |  |
| Family: |  |
| Genus: |  |
| Species: |  |
|  |  |

| **2. What are some other members of the Genus to which your Contig belongs?** |
| --- |
|  |

| **3. What are some other members of the Family to which your Contig belongs?** |
| --- |
|  |

| **4. What are some other members of the Order to which your Contig belongs?** |
| --- |
|  |

| **5. What are some other members of the Class to which your Contig belongs?** |
| --- |
|  |

| **6. What are some other members of the Phylum to which your Contig belongs?** |
| --- |
|  |

### 3.5.9 Activity 2 - – Genomes, Genes, and Databases

*Estimated time: [20] min*

#### 3.5.9.1 Instructions

## 3.6 Activity: test-driveR

## 3.7 Presentation: Microbial Genomes Project

# 4 Taxonomy Profiling

# About the Authors

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| Figure Artist(s) | Created figures/plots for course |
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## ─ Session info ───────────────────────────────────────────────────────────────  
## setting value  
## version R version 4.3.2 (2023-10-31)  
## os Ubuntu 22.04.4 LTS  
## system x86\_64, linux-gnu  
## ui X11  
## language (EN)  
## collate en\_US.UTF-8  
## ctype en\_US.UTF-8  
## tz Etc/UTC  
## date 2025-05-12  
## pandoc 3.1.1 @ /usr/local/bin/ (via rmarkdown)  
##   
## ─ Packages ───────────────────────────────────────────────────────────────────  
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## cachem 1.0.8 2023-05-01 [1] RSPM (R 4.3.0)  
## cli 3.6.2 2023-12-11 [1] RSPM (R 4.3.0)  
## devtools 2.4.5 2022-10-11 [1] RSPM (R 4.3.0)  
## digest 0.6.34 2024-01-11 [1] RSPM (R 4.3.0)  
## ellipsis 0.3.2 2021-04-29 [1] RSPM (R 4.3.0)  
## evaluate 0.23 2023-11-01 [1] RSPM (R 4.3.0)  
## fastmap 1.1.1 2023-02-24 [1] RSPM (R 4.3.0)  
## fs 1.6.3 2023-07-20 [1] RSPM (R 4.3.0)  
## glue 1.7.0 2024-01-09 [1] RSPM (R 4.3.0)  
## htmltools 0.5.7 2023-11-03 [1] RSPM (R 4.3.0)  
## htmlwidgets 1.6.4 2023-12-06 [1] RSPM (R 4.3.0)  
## httpuv 1.6.14 2024-01-26 [1] RSPM (R 4.3.0)  
## knitr 1.48 2024-07-07 [1] CRAN (R 4.3.2)  
## later 1.3.2 2023-12-06 [1] RSPM (R 4.3.0)  
## lifecycle 1.0.4 2023-11-07 [1] RSPM (R 4.3.0)  
## magrittr 2.0.3 2022-03-30 [1] RSPM (R 4.3.0)  
## memoise 2.0.1 2021-11-26 [1] RSPM (R 4.3.0)  
## mime 0.12 2021-09-28 [1] RSPM (R 4.3.0)  
## miniUI 0.1.1.1 2018-05-18 [1] RSPM (R 4.3.0)  
## pkgbuild 1.4.3 2023-12-10 [1] RSPM (R 4.3.0)  
## pkgload 1.3.4 2024-01-16 [1] RSPM (R 4.3.0)  
## profvis 0.3.8 2023-05-02 [1] RSPM (R 4.3.0)  
## promises 1.2.1 2023-08-10 [1] RSPM (R 4.3.0)  
## purrr 1.0.2 2023-08-10 [1] RSPM (R 4.3.0)  
## R6 2.5.1 2021-08-19 [1] RSPM (R 4.3.0)  
## Rcpp 1.0.12 2024-01-09 [1] RSPM (R 4.3.0)  
## remotes 2.4.2.1 2023-07-18 [1] RSPM (R 4.3.0)  
## rlang 1.1.4 2024-06-04 [1] CRAN (R 4.3.2)  
## rmarkdown 2.25 2023-09-18 [1] RSPM (R 4.3.0)  
## sessioninfo 1.2.2 2021-12-06 [1] RSPM (R 4.3.0)  
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## stringi 1.8.3 2023-12-11 [1] RSPM (R 4.3.0)  
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## xfun 0.48 2024-10-03 [1] CRAN (R 4.3.2)  
## xtable 1.8-4 2019-04-21 [1] RSPM (R 4.3.0)  
## yaml 2.3.8 2023-12-11 [1] RSPM (R 4.3.0)  
##   
## [1] /usr/local/lib/R/site-library  
## [2] /usr/local/lib/R/library  
##   
## ──────────────────────────────────────────────────────────────────────────────

# References