RNA-seq miniCURE

January, 2023

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# About this Course

This miniCURE allows students to develop a project using RNA-seq datasets to introduce how model organisms, high-throughput sequencing, and the scientific process are used in both basic and clinical research.



Skills Level

*Genetics*  
**Novice**: Introduction to [central dogma of molecular biology](https://en.wikipedia.org/wiki/Central_dogma_of_molecular_biology)

*Programming skills*  
**Novice**: No programming experience needed

Learning Objectives

* Learn about model organisms
* Explore high-throughput sequencing datasets
* Practice the [scientific process](https://www.biointeractive.org/classroom-resources/how-science-works)

C-MOOR Collection

More coming soon!

# 1 Join SciServer

# 2 First LearnR

# 3 Scientific Literature

# 4 Model Organisms and Databases

## 4.1 Pre-lab: Model Organisms



Image credit: [Max Westby](http://cubocube.com/dashboard.php?a=1179&b=1228&c=10). Some of the most important genetic model organisms in use today. Clockwise from top left: yeast, fruit fly, arabidopsis, mouse, roundworm, zebrafish. License: [CC ANS 2.5](https://creativecommons.org/licenses/by-nc-sa/2.5/)

### 4.1.1 Purpose

The two tutorials in this pre-lab will familiarize you with the concepts of model organisms, with an emphasis on Drosophila. In Lab 8, this information will help you look up information about Drosophila genes.

### 4.1.2 Learning Objectives

1. Explain the importance of model organisms and identify some of their desirable characteristics.
2. Describe the usefulness of Drosophila as a model system.

### 4.1.3 Introduction

Scientists frequently use a few specific organisms, called “model organisms” for their experiments. This tutorial will introduce you to a few of the most popular model organisms and will discuss why these organisms were chosen and what they are useful for.

The fruit fly (Drosophila melanogaster) is a popular model organism used to study a wide range of biological questions. The second tutorial will introduce you to some of the types of research being conducted with fruit flies, give a brief overview of Drosophila biology, and show you what it’s like to work with Drosophila in the lab.

### 4.1.4 Activity 1 - Model Organisms

Estimated time: 15 min

#### 4.1.4.1 Instructions

1. [Click here to open the Model Organisms Tutorial.](https://clovis.shinyapps.io/BIOL11A_Model_Organisms)
2. To move through the activities click “Continue” at the bottom of the screen. When you are done with a topic, click “Next Topic” to move on.
3. As you complete the tutorial, answer the questions below.

#### 4.1.4.2 Questions

| 1A. Explain what a “model organism” is and why they are useful. |
| --- |
|  |

| 1B. Define ortholog and explain how model organisms can be used to understand human genes. |
| --- |
|  |

| 1C. Name 4 commonly used model organisms |
| --- |
|  |

### 4.1.5 Activity 2 - Drosophila melanogaster

Estimated time: 15 min

#### 4.1.5.1 Instructions

1. [Click here to open the Drosophila melanogaster Tutorial.](https://clovis.shinyapps.io/BIOL11A_Drosophila/)
2. To move through the activities click “Continue” at the bottom of the screen. When you are done with a topic, click “Next Topic” to move on.
3. As you complete the tutorial, answer the questions below.

#### 4.1.5.2 Questions

| 2A. Provide 3 reasons why fruit flies are useful for scientific research. |
| --- |
|  |

| 2B. List 3 ways in which fruit flies are similar to humans. |
| --- |
|  |

| 2C. Compare and contrast the fruit fly genome to the human genome. |
| --- |
|  |

| 2D. Briefly describe the fruit fly life cycle. |
| --- |
|  |

### 4.1.6 Footnotes

#### 4.1.6.1 Resources

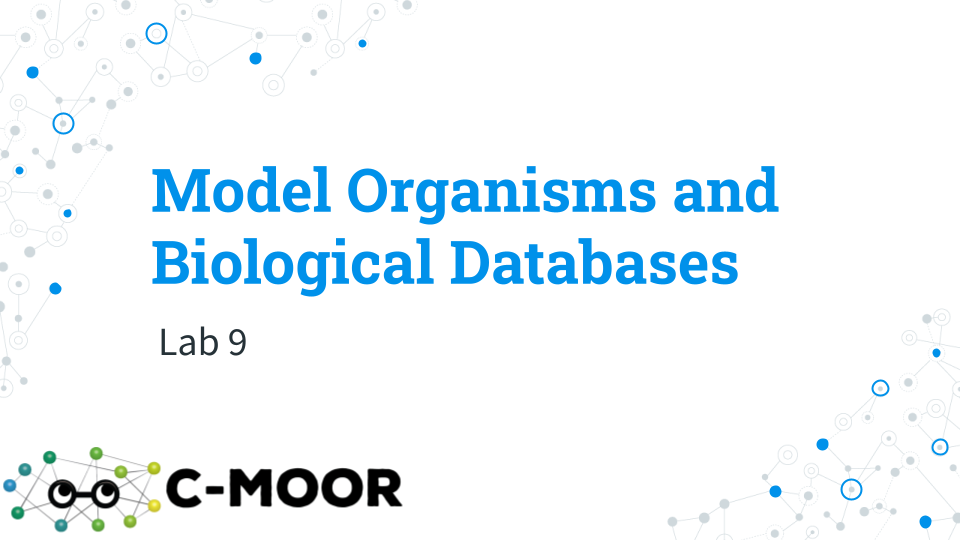
* [Google Doc](https://docs.google.com/document/d/1vFhm2XLMO9vjMDNT6CxZJ4VJuinw0BEo)

#### 4.1.6.2 Contributions and Affiliations

* Stephanie R. Coffman, Ph.D.

Last Revised: February 2022

## 4.2 Lab Slides



[[slides](https://docs.google.com/presentation/d/1kt0lW4D8AWqQm1j6FMo0rRDGM_G3zkLmPy3EZNDg3s0)]

## 4.3 Lab Activities: Biological Databases

### 4.3.1 Purpose

In this activity, students will learn to search the same online databases used by scientists to collect information about a set of genes and present them to your group. This will give you an opportunity to engage in inquiry-based learning and apply the concepts in molecular biology and genetics from this course.

### 4.3.2 Learning Objectives

1. Use online databases to look up information about a gene.

### 4.3.3 Activity 1 - Databases

Estimated time: 15 min

#### 4.3.3.1 Instructions

1. Follow [these directions](https://docs.google.com/document/d/1nQ-wd4hX0Xtd4mfloXcpbbtK_CqDzY874oqmBYql1M8) to launch your first LearnR tutorial: Biological Databases Tutorial.
2. To move through the activities click “Continue” at the bottom of the screen. When you are done with a topic, click “Next Topic” to move on.
3. As you complete the tutorial, fill in the table below. This will help you know which database to go back to later on.

#### 4.3.3.2 Questions

Table 1. Databases

| Database | Description |
| --- | --- |
| GenBank |  |
| OMIM |  |
| Human Protein Atlas |  |
| PDB |  |

### 4.3.4 Activity 2 - FlyBase

Estimated time: 15 min

#### 4.3.4.1 Instructions

1. Work through the FlyBase Tutorial in SciServer.
2. To move through the activities click “Continue” at the bottom of the screen. When you are done with a topic, click “Next Topic” to move on.

#### 4.3.4.2 Questions

| 2A. What is one question you have about using FlyBase? |
| --- |
|  |

| 2B. What is something that surprised you or that you found interesting about using FlyBase? |
| --- |
|  |

### 4.3.5 Activity 3 - Human Protein Atlas

Estimated time: 15 min

#### 4.3.5.1 Instructions

1. Work through the Human Protein Atlas in SciServer.
2. To move through the activities click “Continue” at the bottom of the screen. When you are done with a topic, click “Next Topic” to move on.

#### 4.3.5.2 Questions

| 3A. What is one question you have about using HPA? |
| --- |
|  |

| 3B. What is something that surprised you or that you found interesting about using HPA? |
| --- |
|  |

### 4.3.6 Activity 4 - Research a Gene!

Estimated time: 45 min

#### 4.3.6.1 Instructions

1. Before getting started on this activity, your instructor will assign your group a letter that corresponds to a group of 4 genes.

| Group Assigned Letter |
| --- |
|  |

1. [Look up your letter here](https://docs.google.com/spreadsheets/d/1GZtHz2GU3B4KMOd9yuKrcQLJJLn7qlnZgPN5c6SNqGg) and write the names of the four genes your group is assigned at the top of each column in the table below.
2. In your group, assign each student one of the four genes to research.

| Individual Assigned Gene |
| --- |
|  |

1. Use FlyBase to look up the information in Table 2 below.
2. Use HPA to look up the information in Table 3 below.

Table 2. FlyBase Information

| Category | Information |
| --- | --- |
| **General Information** |  |
| Full Gene Name |  |
| FlyBase ID |  |
| Sequence Location |  |
| **Function** |  |
| Biological Process |  |
| Cellular Component |  |
| **Expression Data** |  |
| Anatomical Expression |  |
| Developmental Stage |  |
| **Orthologs** |  |
| Orthologs in other species |  |
| Human Orthologs |  |

Table 3. Human Protein Atlas

| Category | Information |
| --- | --- |
| Function |  |
| Is the gene tissue specific? Which tissue? |  |
| Where is it localized in cells? |  |

### 4.3.7 Activity 5 - Present to your Group

Estimated time: 15 min

#### 4.3.7.1 Instructions

1. Present your gene to your group.
2. Take turns presenting your genes among your group and decide on one gene that you think is the most interesting.

### 4.3.8 Activity 6 - Class Presentation

Estimated time: 30 min

#### 4.3.8.1 Instructions

1. With your group, create a short presentation to present your chosen gene to the class.
2. Your presentation should have about four slides and be thorough:
   1. Slide 1: The GENE you picked to share with your group, your name and date
   2. Slide 2 - 4: Present the information you collected about the gene. For full credit, include relevant images/ diagrams on your slides.
3. One student in the group should post your slides on Canvas to the discussion board. Make sure you mention everyone in your group by name so they also get credit for the presentation.

### 4.3.9 Footnotes

#### 4.3.9.1 Resources

* [Google Doc](https://docs.google.com/document/d/1M7rtDzyGVUxO2GVBp09bTBu4fMDxocTs)

#### 4.3.9.2 Contributions and Affiliations

* Rosa Alcazar, Ph.D., Clovis Community College
* Katherine Cox, Ph.D., John Hopkins
* Stephanie R. Coffman, Ph.D., Clovis Community College

Last Revised: September 2021

# 5 RNA-seq Analysis

# 6 Differential Gene Expression

# 7 Project Work

# 8 Scientific Communication

# 9 Example miniCURE Projects

Read more about what these students did and how you can help

Zellweger Spectrum Disorder

[Drosophila Melanogaster a Good Model System of Zellweger Spectrum Disorder BIO11A SP2022](https://help.c-moor.org/t/326)



Look at This!

Explore other miniCURE and CURE projects in our [Look at This!](https://help.c-moor.org/c/look-at-this/8) category

# 10 C-MOOR Scholars

Meet the C-MOOR Scholars and learn how you can support them

* <https://www.cloviscollege.edu/alumni-and-community/c-moor/c-moor-scholars.html>

# 11 Online Community

Join the discussion at <https://help.c-moor.org>

# About the Authors

These credits are based on our [course contributors table guidelines](https://github.com/jhudsl/OTTR_Template/wiki/How-to-give-credits).

| Credits | Names |
| --- | --- |
| **Pedagogy** |  |
| Lead Content Instructor(s) | [FirstName LastName](link%20to%20personal%20website) |
| Lecturer(s) (include chapter name/link in parentheses if only for specific chapters) - make new line if more than one chapter involved | Delivered the course in some way - video or audio |
| Content Author(s) (include chapter name/link in parentheses if only for specific chapters) - make new line if more than one chapter involved | If any other authors besides lead instructor |
| Content Contributor(s) (include section name/link in parentheses) - make new line if more than one section involved | Wrote less than a chapter |
| Content Editor(s)/Reviewer(s) | Checked your content |
| Content Director(s) | Helped guide the content direction |
| Content Consultants (include chapter name/link in parentheses or word “General”) - make new line if more than one chapter involved | Gave high level advice on content |
| Acknowledgments | Gave small assistance to content but not to the level of consulting |
| **Production** |  |
| Content Publisher(s) | Helped with publishing platform |
| Content Publishing Reviewer(s) | Reviewed overall content and aesthetics on publishing platform |
| **Technical** |  |
| Course Publishing Engineer(s) | Helped with the code for the technical aspects related to the specific course generation |
| Template Publishing Engineers | [Candace Savonen](https://www.cansavvy.com/), [Carrie Wright](https://carriewright11.github.io/) |
| Publishing Maintenance Engineer | [Candace Savonen](https://www.cansavvy.com/) |
| Technical Publishing Stylists | [Carrie Wright](https://carriewright11.github.io/), [Candace Savonen](https://www.cansavvy.com/) |
| Package Developers ([ottrpal](https://github.com/jhudsl/ottrpal)) [Candace Savonen](https://www.cansavvy.com/), [John Muschelli](https://johnmuschelli.com/), [Carrie Wright](https://carriewright11.github.io/) |  |
| **Art and Design** |  |
| Illustrator(s) | Created graphics for the course |
| Figure Artist(s) | Created figures/plots for course |
| Videographer(s) | Filmed videos |
| Videography Editor(s) | Edited film |
| Audiographer(s) | Recorded audio |
| Audiography Editor(s) | Edited audio recordings |
| **Funding** |  |
| Funder(s) | Institution/individual who funded course including grant number |
| Funding Staff | Staff members who help with funding |

## ─ Session info ───────────────────────────────────────────────────────────────  
## setting value   
## version R version 4.0.2 (2020-06-22)  
## os Ubuntu 20.04.3 LTS   
## system x86\_64, linux-gnu   
## ui X11   
## language (EN)   
## collate en\_US.UTF-8   
## ctype en\_US.UTF-8   
## tz Etc/UTC   
## date 2023-01-19   
##   
## ─ Packages ───────────────────────────────────────────────────────────────────  
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## assertthat 0.2.1 2019-03-21 [1] RSPM (R 4.0.3)   
## bookdown 0.24 2022-02-15 [1] Github (rstudio/bookdown@88bc4ea)   
## callr 3.4.4 2020-09-07 [1] RSPM (R 4.0.2)   
## cli 2.0.2 2020-02-28 [1] RSPM (R 4.0.0)   
## crayon 1.3.4 2017-09-16 [1] RSPM (R 4.0.0)   
## desc 1.2.0 2018-05-01 [1] RSPM (R 4.0.3)   
## devtools 2.3.2 2020-09-18 [1] RSPM (R 4.0.3)   
## digest 0.6.25 2020-02-23 [1] RSPM (R 4.0.0)   
## ellipsis 0.3.1 2020-05-15 [1] RSPM (R 4.0.3)   
## evaluate 0.14 2019-05-28 [1] RSPM (R 4.0.3)   
## fansi 0.4.1 2020-01-08 [1] RSPM (R 4.0.0)   
## fs 1.5.0 2020-07-31 [1] RSPM (R 4.0.3)   
## glue 1.6.1 2022-01-22 [1] CRAN (R 4.0.2)   
## htmltools 0.5.0 2020-06-16 [1] RSPM (R 4.0.1)   
## knitr 1.33 2022-02-15 [1] Github (yihui/knitr@a1052d1)   
## lifecycle 1.0.0 2021-02-15 [1] CRAN (R 4.0.2)   
## magrittr 2.0.2 2022-01-26 [1] CRAN (R 4.0.2)   
## memoise 1.1.0 2017-04-21 [1] RSPM (R 4.0.0)   
## pkgbuild 1.1.0 2020-07-13 [1] RSPM (R 4.0.2)   
## pkgload 1.1.0 2020-05-29 [1] RSPM (R 4.0.3)   
## prettyunits 1.1.1 2020-01-24 [1] RSPM (R 4.0.3)   
## processx 3.4.4 2020-09-03 [1] RSPM (R 4.0.2)   
## ps 1.3.4 2020-08-11 [1] RSPM (R 4.0.2)   
## purrr 0.3.4 2020-04-17 [1] RSPM (R 4.0.3)   
## R6 2.4.1 2019-11-12 [1] RSPM (R 4.0.0)   
## remotes 2.2.0 2020-07-21 [1] RSPM (R 4.0.3)   
## rlang 0.4.10 2022-02-15 [1] Github (r-lib/rlang@f0c9be5)   
## rmarkdown 2.10 2022-02-15 [1] Github (rstudio/rmarkdown@02d3c25)  
## rprojroot 2.0.2 2020-11-15 [1] CRAN (R 4.0.2)   
## sessioninfo 1.1.1 2018-11-05 [1] RSPM (R 4.0.3)   
## stringi 1.5.3 2020-09-09 [1] RSPM (R 4.0.3)   
## stringr 1.4.0 2019-02-10 [1] RSPM (R 4.0.3)   
## testthat 3.0.1 2022-02-15 [1] Github (R-lib/testthat@e99155a)   
## usethis 2.1.5.9000 2022-02-15 [1] Github (r-lib/usethis@57b109a)   
## withr 2.3.0 2020-09-22 [1] RSPM (R 4.0.2)   
## xfun 0.26 2022-02-15 [1] Github (yihui/xfun@74c2a66)   
## yaml 2.2.1 2020-02-01 [1] RSPM (R 4.0.3)   
##   
## [1] /usr/local/lib/R/site-library  
## [2] /usr/local/lib/R/library