

Welcome to the May 2026 Virtual Data Lab scRNA-Seq Training Workshop!

May 11-15, 2026

Childhood Cancer Data Lab


<https://alexslemonade.github.io/2026-may-training/>

Childhood Cancer
Data  Lab

X



Tell us about you!

- What's your name?
 - What are your pronouns?
 - What lab/institution are you from?
 - What are you studying?
 - What's a recent piece of media (book, movie, TV show, etc.) you enjoyed?
- 

Meet your instructors



JOSH

Joshua Shapiro

Senior Data Scientist @ the Data Lab

PhD Ecology & Evolution, *UChicago*

Postdoc Integrative Genomics, *Princeton*

Research interests:

- **Evolutionary genomics**
- **Single cell workflows**



jashapiro

Meet your instructors



STEPHANIE

Stephanie Spielman

Data Scientist @ the Data Lab

PhD Integrative Biology *UT Austin*

Postdoc Computational Molecular Evolution *Temple*

Research interests:

- **Protein evolution and reproducible genomics**
- **Data science and bioinformatics education**



sjspielman

Meet your instructors



Ally
Ally Hawkins

Data Scientist @ the Data Lab

PhD Cancer Biology *University of Michigan*
Postdoc Computational Biology *Cornell*

Research interests:

- **Single cell data analysis**
- **Origins of pediatric solid tumors**



allyhawkins

Other staff you'll meet this week!




JEN
Jen O'Malley

Scientific Community Manager

- Helps administer Data Lab programs such as workshops
- Engages with the research community

Tell us about you!

- What's your name?
 - What are your pronouns?
 - What lab/institution are you from?
 - What are you studying?
 - What's a recent piece of media (book, movie, TV show, etc.) you enjoyed?
- 



Code of Conduct



Be kind, have fun

We value the involvement of everyone in the community. We are committed to creating a friendly and respectful place for learning, teaching, and contributing.

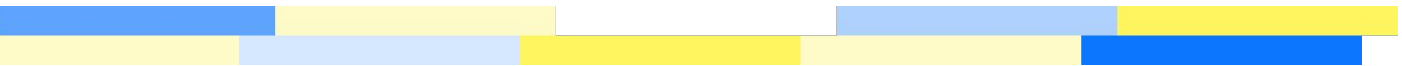
- Use welcoming and inclusive language
- Be respectful of different viewpoints and experiences
- Gracefully accept constructive criticism
- Focus on what is best for the community
- Show courtesy and respect towards other community members

Read the full Code of Conduct here:


<https://alexslimonade.github.io/2026-may-training/code-of-conduct.html>



If you at any time feel harassed or treated inappropriately, please contact ccd1@alexslimonade.org.



What you will learn (and what you won't)



What you will learn

We will introduce you to the R programming language, R Notebooks, and some reproducible research practices.

We cover pipelines for the quality control, pre-processing, and initial analysis of single-cell RNA-seq data almost entirely through hands-on exercises.

We generally elect to go *broad* and not *deep*.

Our overarching goals: To prepare you to perform “frontline” analyses of your own data, to get you more comfortable reading documentation/learning new methods on your own, and to give you tools to collaborate more effectively with analysts when needed



What you won't learn


We don't address experimental design (e.g., how many replicates you need).

We won't compare tools (e.g., Bioconductor vs. Seurat for single cell analysis).

We won't cover every feature (or assumption) of the tools we do present.

You may not be able to perform every analysis you need for your own work, particularly for complex experimental designs. For example, in the context of single-cell analysis, we do not cover integrating data from multiple samples.

We present analysis as a series of *linear steps*. In practice, it's **not**. It's important to consult analysis experts when you need to and to keep track of and report what you've done.



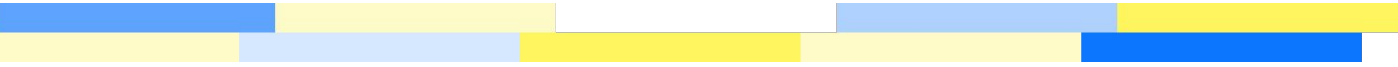
How do we pick what we teach?

We want methods to be or to have:

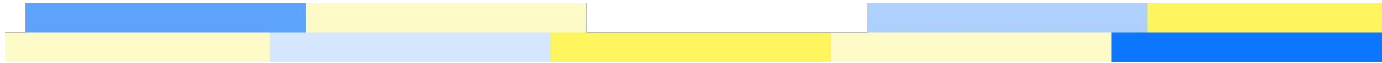
- Useful for a wide range of experimental designs, sample sizes
- Easy to use, well-documented, and consistently updated
- Solid tutorials, a sizeable user base, and responsive authors/maintainers

We have a preference for methods that integrate easily into a single workflow that can be run on a laptop (and our own personal biases as scientists).





Schedule



Monday

Workshop Intro

Intro to R

RStudio Server
Base R
ggplot2 & tidyverse

Consultations

Exercise notebooks

Wednesday

Single-cell RNA-seq

Dimensionality reduction
Clustering
Marker identification

Consultations

Exercise notebooks
Your own data

Friday

Consultations

Your own data
Exercise notebooks

Presentations

Tuesday

Single-cell RNA-seq

Quantification & QC
Filtering & Normalization

Consultations

Exercise notebooks
Your own data

Thursday

Single-cell RNA-seq

Cell-type annotation
Working with CITE-Seq
data

Consultations

Exercise notebooks
Your own data

Daily Schedule Outline

Instruction

Full group
Lectures

- Introduce concepts and background
- Demonstrate usage
- Answer general questions

Breakout

Small groups
Start exercise notebooks











- Split up into Zoom breakout rooms
- Ask questions of instructors and other participants

Consultation Period

Exercise notebooks
Your own data

- Practice what you have learned
- Work on exercises individually or in groups
- Work with your own data

Module Layout

 00a-rstudio_guide.Rmd
 00b-debugging_resources.Rmd
 00c-good_scientific_coding_practices.Rmd
 01-intro_to_base_R-live.Rmd
 02-intro_to_ggplot2-live.Rmd
 03-intro_to_tidyverse-live.Rmd
 exercise_01-intro_to_base_R.Rmd
 exercise_02-intro_to_R.Rmd
 exercise_03a-intro_to_tidyverse.Rmd
 exercise-03b-intro_to_tidyverse.Rmd

These are **reference** documents.
Go through these on your own.

These are **Instruction** notebooks.
We'll walk through these together,
step-by-step, during the workshop.

These are **Exercise** notebooks.
Use these to practice what you've
learned. We're here to help!

Module cheatsheets cover key functions

<https://github.com/AlexsLemonade/training-modules/tree/2026-may/module-cheatsheets>

dplyr

Read the `dplyr` package documentation [here](#).

A vignette on the usage of the `dplyr` package can be found [here](#).

Library/Package	Piece of code	What it's called	What it does
<code>dplyr</code>	<code>%>%</code>	Pipe operator	Funnels a <code>data.frame</code> through tidyverse operations
<code>dplyr</code>	<code>filter()</code>	Filter	Returns a subset of rows matching the conditions of the specified logical argument
<code>dplyr</code>	<code>arrange()</code>	Arrange	Reorders rows in ascending order. <code>arrange(desc())</code> would reorder rows in descending order.
<code>dplyr</code>	<code>select()</code>	Select	Selects columns that match the specified argument
<code>dplyr</code>	<code>mutate()</code>	Mutate	Adds a new column that is a function of existing columns
<code>dplyr</code>	<code>summarise()</code>	Summarise	Summarises multiple values in an object into a single value. This function can be used with other functions to retrieve a single output value for the grouped values. <code>summarize</code> and <code>summarise</code> are synonyms in this package.
<code>dplyr</code>	<code>rename()</code>	Rename	Renames designated columns while keeping all variables of the <code>data.frame</code>
<code>dplyr</code>	<code>group_by()</code>	Group By	Groups data into rows that contain the same specified value(s)
<code>dplyr</code>	<code>inner_join()</code>	Inner Join	Joins data from two <code>data.frames</code> , retaining only the rows that are in both datasets.

Feedback: Training Sessions

We'll collect feedback before we split into breakout rooms at the end of each module. You will *anonymously* submit your responses to the following questions through a Zoom poll. (We'll also send a link to the poll questions after the workshop incase you miss it!)

- The most difficult or confusing point of the module ("muddiest point")
We will post additional material answering your questions the next day
- What did you like about the module?
- How we can improve the module?

Feedback: AI Usage

At the beginning and end of the workshop, we'll also include a brief *anonymous* poll about AI use in coding. Your feedback will help us understand how researchers are currently using AI tools, which may inform decisions about future Data Lab products and services!

- Are you currently using AI tools to assist with writing code?
- If so, how successful have AI tools been for your coding tasks?



Friday

Your own projects
Exercise notebooks

Spend Friday working with your own data, getting assistance as needed from Data Lab staff and each other.

Presentations

Present what you worked on during the consultation times to the group!

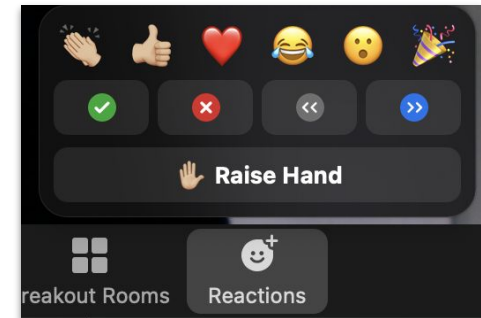
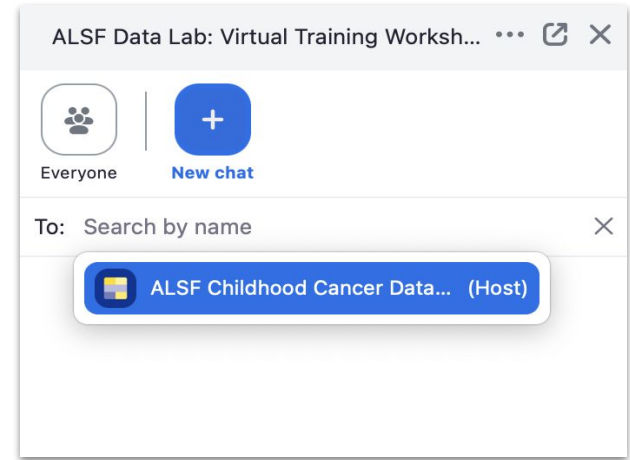


Virtual Training Procedures



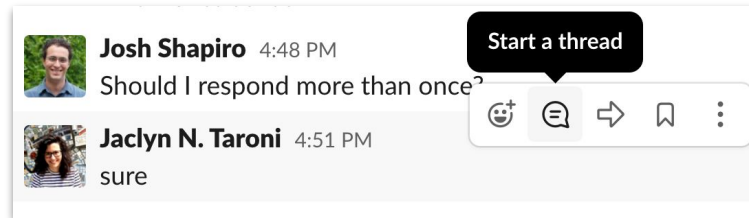
General Zoom Etiquette

- Keep your microphone muted
- Type questions in the Chat window (directed to the host!)
 - Click on the “Chat” button at the bottom of your window to open the chat.
 - The ability to message everyone in the “Main Chat” will be unavailable.
 - Instead, click “New Chat” and send a direct message to “ALSF Childhood Cancer Data Lab.”
- We encourage you to use zoom reactions!



Using Slack

- Use the **#2026-may-training** Slack channel
- Post public questions, get help with errors and debugging, make comments, and help your fellow participants!
 - Use threads to keep related content together



Communication during instruction



- I have an **urgent question** that needs an answer before moving on:
 - **Raise Hand** or **Chat** with the meeting host
- I'm **stuck with an error** and can't proceed with the hands-on exercise
 - **Chat** with meeting host: Request 1:1 and you will be placed in a breakout room with a Data Lab staff member



- I have an **general question** that does not need an answer right away.
 - **Post** in #2026-may-training
- I'm **having trouble logging in** to RStudio Server
 - **Direct Message** a Data Lab staff member (not the current host or instructor)

Trouble logging into Zoom and Slack? **Email** training@ccdatalab.org

Communication at other times (consultation periods)



- I have questions about **previous instruction or exercise notebooks**
 - **Post** in #2026-may-training
 - If you need to share your screen, we will set up a 1:1 or group Zoom call
- I would like to be paired up with other participants
 - **Post** in #2026-may-training; we can set you up in a Zoom breakout room
- I have a question that is **highly specific to my data**
 - **Direct Message** a Data Lab staff member
- I'm having trouble **logging in** to RStudio Server
 - **Direct Message** a Data Lab staff member

Trouble logging into Zoom and Slack? **Email** training@ccdatalab.org