



Welcome to the May 2020 Virtual CCDL RNA-Seq Training Workshop!

May 4-8, 2020
Childhood Cancer Data Lab



Meet your instructors



JOSH

Joshua Shapiro

Data Scientist @ the CCDL

PhD Ecology & Evolution, *UChicago*

Postdoc Integrative Genomics, *Princeton*

Research interests:

- **Evolutionary Genomics**



jashapiro

Meet your instructors



JACLYN

Jaclyn Taroni

Principal Data Scientist @ the CCDL

PhD Genetics *Dartmouth*

Postdoc Computational Biology *UPenn*

Research interests:

- **Transcriptomics in rare, complex diseases**
- **Unsupervised pattern extraction**



jaclyn-taroni

Meet your helpers



CANDACE

Candace Savonen

Biological Data Analyst @ the CCDL

Masters Neuroscience at *Michigan State University*

Research interests:

- **Neurogenomics**
- **Single-cell transcriptomics**



cansavvy

Meet your helpers



CHANTE

Chante Bethell

Biological Data Analyst @ the CCDL

Bachelor's in Bioinformatics from *Rowan University*

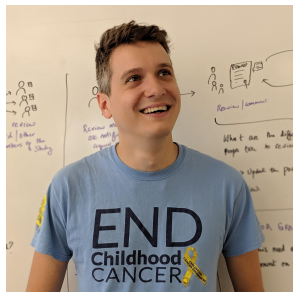
Research interests:

- **Functional motifs in the proteome**



cbethell

Other staff you may see



KURT

Kurt Wheeler

**Data Engineer
@ CCDL**

- Builds scalable systems
- Manages servers



DEEPA

Deepa Prasad

**User Experience Designer
@ CCDL**

- Talks to researchers about their needs and frustrations
- Designs usable software



TRISH

Trish Adkins

Writer @ ALSF

- Edits the ALSF blog
- Interviewer of Scientists, Translator of Science for ALSF Supporters



SHANNON

Shannon O'Connor

Writer @ ALSF

- Crafts emails, stories, you name it
- Interviews scientists, occasionally

Tell us about you!

- What's your name?
- What are you studying?
- What's one thing you are proud of?





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:
<http://bit.ly/CCDL-training-code>



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

Monday

Intro to RStudio
Server

Intro to R and the
Tidyverse

Wednesday

Bulk RNA-seq
Pre-processing
Differential expression

Friday

Consultations
Your own data
Exercise notebooks

Presentations

Tuesday

Consultations
Exercise notebooks
Your own data

Thursday

Consultations
Exercise notebooks
Your own data

Full schedule: <https://github.com/AlexsLemonade/2020-may-training/wiki/Schedule>

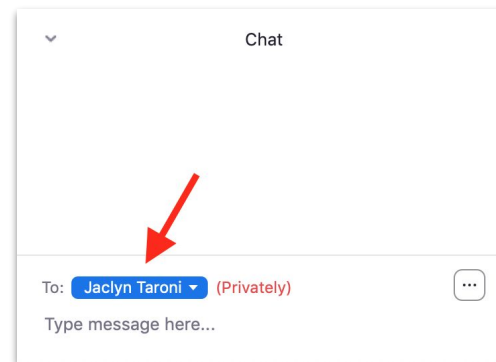


Virtual Training Procedures



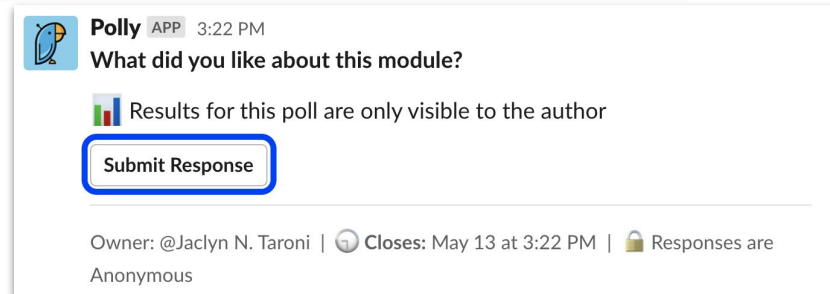
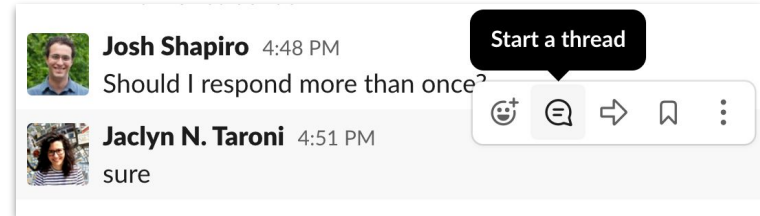
General Zoom Etiquette

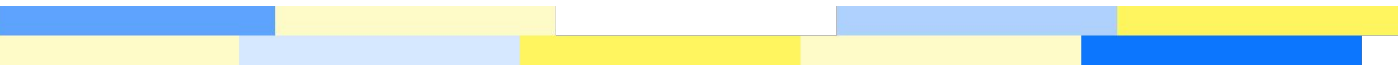
- Keep your microphone muted
- Type questions in the Chat window (directed to the host)
 - Click on the “Chat” button at the bottom of your window to open the chat.
- Use the Zoom status buttons to tell us how you are doing!
 - Click on the “Participants” button at the bottom of your zoom window to see these buttons



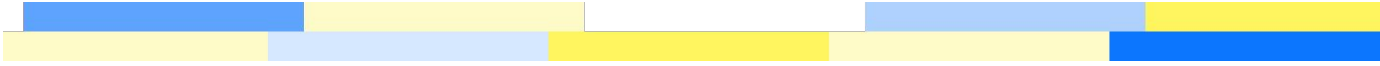
Using Slack

- Use the **#2020-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
- We will post questions at the end of each session with Polly





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, processing, and downstream analysis of bulk and 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., edgeR vs. DESeq2 for differential gene expression).

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 to perform for your own work, particularly for complex experimental designs.

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.



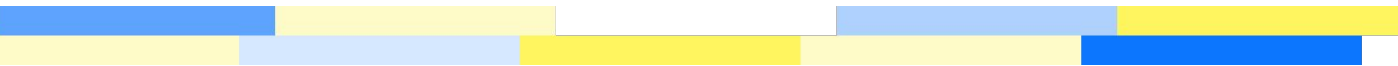
How do we pick what we teach?

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



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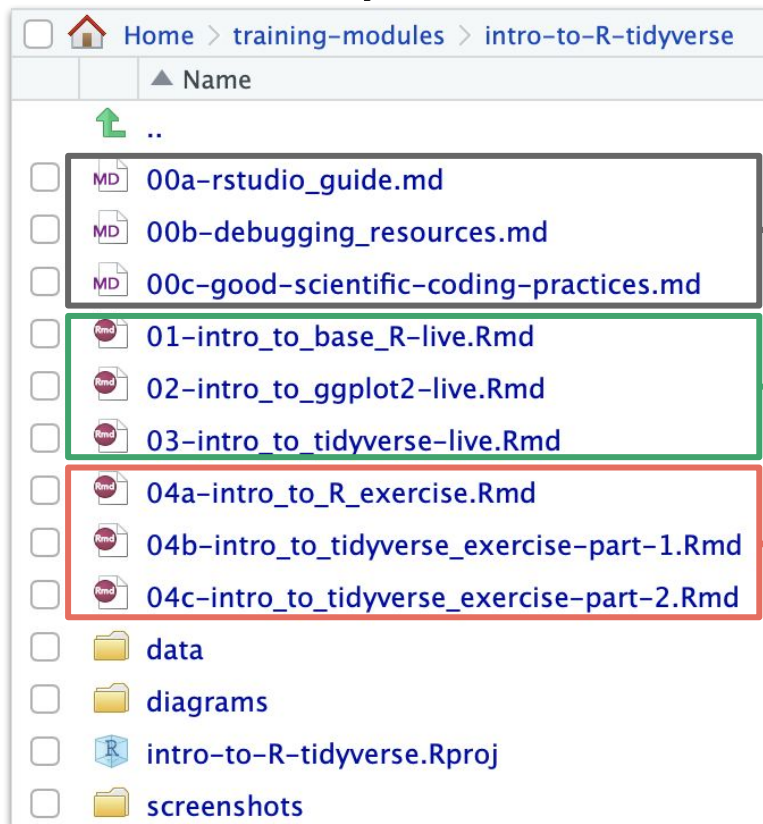
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Full schedule: <https://github.com/AlexsLemonade/2020-may-training/wiki/Schedule>

Module Layout




This is a reference document.
We will not go through this.

We'll walk through these notebooks
together, step-by-step

You will practice what you have
learned. We're here to help!

Module cheatsheets cover key functions

<https://github.com/AlexsLemonade/training-modules>



RNA-seq
docker-install
intro-to-R-tidyverse
machine-learning
module-cheatsheets
scRNA-seq
.gitignore
LICENSE.md
README.md
cdl-training-waiver.DOCX
ready.png
ready_script.R
structure_course.png

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
dplyr	<code>%>%</code>	Pipe operator	Funnels a <code>data.frame</code> through tidyverse operations
dplyr	<code>filter()</code>	Filter	Returns a subset of rows matching the conditions of the specified logical argument
dplyr	<code>arrange()</code>	Arrange	Reorders rows in ascending order. <code>arrange(desc())</code> would reorder rows in descending order.
dplyr	<code>select()</code>	Select	Selects columns that match the specified argument
dplyr	<code>mutate()</code>	Mutate	Adds a new column that is a function of existing columns
dplyr	<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.
dplyr	<code>rename()</code>	Rename	Renames designated columns while keeping all variables of the <code>data.frame</code>
dplyr	<code>group_by()</code>	Group By	Groups data into rows that contain the same specified value(s)
dplyr	<code>inner_join()</code>	Inner Join	Joins data from two data frames, retaining only the rows that are in both datasets.


We want your feedback!

At the end of each module,
we will post a few questions
in the Slack channel.

- The most difficult or confusing point of the module ("muddiest point")
Responses to this question will be anonymously posted in the channel
- What did you like about the module?
- How we can improve the module?
These responses will be collected anonymously (and not posted).

 **Polly** APP 3:22 PM

What did you like about this module?

 Results for this poll are only visible to the author

[Submit Response](#)

Owner: @Jaclyn N. Taroni | ⌚ Closes: May 13 at 3:22 PM | 🔒 Responses are Anonymous

Consultation Days

- We will post additional material at the start of each consultation day, responding to your **muddiest point** questions.
- Spend your time as you like, reviewing previous day presentations, working through exercise notebooks, or analyzing your own data.
 - We will ask the day before (using Polly in Slack) what you want to work on so we can be ready to assist you with your plans.
 - Work in groups, if you like! We can assist setting up groups with similar types of data or interests.
- CCDL staff are available in the Slack channel with Zoom meetings as needed.

Friday

Own data/Exercise
notebooks

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

Presentations

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

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 CCDL staff member



- I have an **general question** that does not need an answer right away.
 - **Post** in #2020-may-training
- I'm having trouble **logging in** to RStudio Server
 - **Direct Message** a CCDL staff member (not the current host or instructor)

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

Communication at other times (consultation days)



- I have questions about **yesterday's instruction** or **exercise notebooks**
 - **Post** in #2020-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 #2020-may-training; we will set you up in a Zoom breakout room
- I have a question that is **highly specific to my data**
 - **Direct Message** a CCDL staff member
- I'm having trouble **logging in** to RStudio Server
 - **Direct Message** a CCDL staff member

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