16S rRNA Microbiome Intermediate Bioinformatics Course: Int_BT

Staff Training

Day 1 Part 1 - Introduction
H3ABioNet

- Africa-wide network of bioinformatics institutions
- 28 nodes
- Nodes=bioinformatics research groups
- 17 countries
- 16 African countries
- NIH funded
- Part of H3Africa
- Develop bioinformatics capacity in Africa

http://h3abionet.org/home/consortium

16S rRNA Intermediate Bioinformatics Course: Int_BT
Verena Ras
Introduction

• Need for intermediate training
• You are among the first to take the course!

Aims:
• To equip participants with the knowledge and skills to perform analyses on 16S microbiome data.
• To allow participants to gain knowledge and practical experience through theoretical and practical sessions
Int_BT community

VIRTUAL CLASSROOM
Why staff training?

• Explain course rationale and logistics
• Provide training on online platforms
• Establish a team atmosphere within and across classrooms
• Provide training on facilitation techniques
Before we start...

• Make sure vula account activated
• Make sure you can access staff site
• Camera for team photo
Logistics for staff training

• 2 days (3 or 4 hours per day) in each local classroom with local team
• Follow day plans for each day – will instruct you exactly what to do
• Day 2 – training will be done live via zoom
• Activities
By the end of today

• Meet your classroom teammates and be familiar with your training room
• Establish your staff team and know how you might deal with certain challenges
• Understand everyone’s responsibilities
• Develop a staff timetable
• Understand the course rationale and logistics
• Be comfortable with vula and adobe connect
• Learn some facilitation techniques
Next

Watch video labeled:
Day 1 Part 2
16S rRNA Microbiome Intermediate Bioinformatics Course: Int_BT

Staff Training

Day 1 Part 2 – Meet your local team and setting ground rules
Meet your local team

Activity 1 – get to know each other (10 minutes):

1. Get into pairs (or a group of 3 if there is an odd number of people). Pair with someone that you do not know very well, if possible.
2. Have a chat to get to know each other. Make sure that you find out at least 3-5 things about your partner (5 mins).
3. After 5 minutes of chatting, organise all your chairs into a circle/semi circle so that the whole group is sitting together.
4. Introduce your partner to the rest of the group (for example ‘This is... s/he is... s/he enjoys...’). If your group is very small (only 2/3 people), then tell your partner what you remember about them from their description of themselves.

Press pause NOW
and complete Activity 1
Ground Rules

Why create ground rules?

- How we behave together
- No assumptions – ensure everyone is on the same page
- Setting expectations

‘Very often new ground rules come out of retrospectives. For example a [team] might have encountered issues with some members making decisions on their own and after a discussion about how to avoid this in the future they decide to add the ground rule “We make decisions together” to the list of rules.’

https://nomad8.com/team-ground-rules/
Ground Rules

• Examples (only suggestions)

• One person speaks at a time
• All team members are equals
• Address conflict by dealing with the issue not the person
• Notify the team in advance if you will be absent
• Be a participant, not a lurker
• Have fun, but not at the expense of someone else’s feelings
• Be present, both physically and mentally

• [Link](https://www.askteamdoc.com/setting-team-ground-rules/)
Activity 2 – steps for starting your list of ground rules (15 minutes):

1. As a group, brainstorm what is important to each member in terms of acceptable behaviour:
   1. Select a scribe
   2. Scribe to write down ALL suggestions in a place where everyone can see (suggestion: create a google document and project it on the wall/ TV screen – create this document in your IBT google folder) (5 mins)

2. As a group, decide on the top 5-7 suggestions (vote). Talk through each item to ensure each team member has a clear understanding and agrees. When you finalize your list, get confirmation from each member by having them raise their hand to physically acknowledge they agree to abide by the group behaviours. (10 mins).

3. Type up the finalised list and share with each staff member (suggestion: share via google docs).
Next

Watch video labeled:
Day 1 Part 3
16S rRNA Microbiome Intermediate Bioinformatics Course: Int_BT

Staff Training

Day 1 Part 3 – Course background
Skills-based curriculum

• Learning Objective: knowledge learned without implementation (content covered in the lecture component of contact sessions)

  vs.

• Learning Outcome: measurable - skills gained (covered in the practical assignment component of contact sessions)

• Important for participants to be able to go out and perform the analyses on their own after the course

• Mapped to specific ISCB competencies alongside trainers
Competencies

- Competencies are bundles of the essential knowledge, skills, and abilities (KSAs) required to achieve an acceptable level of performance, while learning objectives are specific to a course of instruction. A learning objective is a very specific statement that describes exactly what a participant will be able to do in a measurable way after completion of the course. By accomplishing the objectives, the individual develops the necessary competencies.
Leon (bioinformatics user)

Leon is on his second postdoctoral fellowship, working on quorum sensing in bacteria. "I'm using a combination of transcriptomics, proteomics and metabolomics to understand these pathogenic changes better," he explains. "I end up with big spreadsheets of protein or gene IDs and I'm trying to piece together what signaling pathways are involved in flipping to the pathogenic state." He has been on an introductory Unix course but is much more comfortable with GUIs than with the command line. "I just have a visual brain," he says.

Career timeline

<table>
<thead>
<tr>
<th>Age</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>25</td>
<td>BSc, Biochemistry, Leeds, UK</td>
</tr>
<tr>
<td>30</td>
<td>PhD, NHLI, UK</td>
</tr>
<tr>
<td>32</td>
<td>1st postdoc, U Penn, USA</td>
</tr>
<tr>
<td>40</td>
<td>2nd postdoc, MUnchen, DE</td>
</tr>
</tbody>
</table>

Typical activities

- Obtaining ethical approval
- Prepping samples
- QA and data analysis
- Interpretation of results

% of typical working week

Distribution of time between bench-work and computational work

- Bench-work: 40% effort
- Computational work: 60% effort

Preference for using GUI vs command line

- GUI: 90% effort
- Command line: 10% effort

https://doi.org/10.1371/journal.pcbi.1003496
# Martha (bioinformatics scientist)

Martha is a senior bioinformatician in an international structural genomics consortium. Her biggest project is on predicting the functions of proteins whose structures have just been solved; she’s building a structure-to-function prediction pipeline for the project. This is funded partly by the NIH and partly through industrial funding. She also has a fascination for predicting structure and usually has a student or two working on structural prediction projects.

## Career timeline

<table>
<thead>
<tr>
<th>Age</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>20</td>
<td>Math major, Cornell, USA</td>
</tr>
<tr>
<td>25</td>
<td>PhD, physics, Princeton, USA</td>
</tr>
<tr>
<td>30</td>
<td>1st postdoc, University of Saskatchewan, Canada</td>
</tr>
<tr>
<td>35</td>
<td>Tenure Track position, U. Toronto, Canada</td>
</tr>
<tr>
<td>40</td>
<td>2nd postdoc, LMB, Cambridge, UK</td>
</tr>
</tbody>
</table>

## Typical activities

<table>
<thead>
<tr>
<th>Activity</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Obtaining test data sets from public resources</td>
<td>30%</td>
</tr>
<tr>
<td>Writing and testing algorithms</td>
<td>20%</td>
</tr>
<tr>
<td>Building and testing pipelines</td>
<td>15%</td>
</tr>
<tr>
<td>Writing papers, giving talks, supervision</td>
<td>10%</td>
</tr>
</tbody>
</table>

## Distribution of time between bench work and computational work

<table>
<thead>
<tr>
<th>Bench-work</th>
<th>Computational work</th>
</tr>
</thead>
<tbody>
<tr>
<td>0%</td>
<td>100%</td>
</tr>
<tr>
<td>% effort</td>
<td>% effort</td>
</tr>
</tbody>
</table>

## Preference using for GUI vs command line

<table>
<thead>
<tr>
<th>GUI</th>
<th>Command line</th>
</tr>
</thead>
<tbody>
<tr>
<td>30%</td>
<td>70%</td>
</tr>
</tbody>
</table>

[https://doi.org/10.1371/journal.pcbi.1003496](https://doi.org/10.1371/journal.pcbi.1003496)
## Competencies

### Persona: Bioinformatics Scientist

<table>
<thead>
<tr>
<th>16S rRNA Microbiome Intermediate Bioinformatics Training_Mapping</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Competency/ies</strong></td>
<td><strong>Bloom's Taxonomy</strong></td>
<td><strong>Knowledge</strong></td>
<td><strong>Skills</strong></td>
</tr>
<tr>
<td>General biology</td>
<td>Comprehension</td>
<td>K1, K2, K3</td>
<td>S2, S3</td>
</tr>
<tr>
<td>Depth in at least one area of biology (e.g., evolutionary biology, genetics, molecular biology, biochemistry, anatomy, physiology)</td>
<td>Comprehension</td>
<td>K1, K2, K3</td>
<td>S1, S2, S3</td>
</tr>
<tr>
<td>Details of the scientific discovery process and of the role of bioinformatics in it</td>
<td>Comprehension</td>
<td>K1, K2, K3, K4, K5</td>
<td>S3, S4, S5</td>
</tr>
<tr>
<td>Biological data generation technologies</td>
<td>Comprehension</td>
<td>K1, K2, K3, K4</td>
<td>S1, S2, S3, S4</td>
</tr>
<tr>
<td>Statistical, machine learning and data science research methods in the context of molecular biology, genomics, medical, and population genetics research.</td>
<td>Analysis</td>
<td>K1, K2, K3, K4, K5</td>
<td>S1, S2, S3, S4, S5, S6</td>
</tr>
<tr>
<td>Data management</td>
<td>Application</td>
<td>K1, K20</td>
<td>S1, S2, S3, S4, S5, S6</td>
</tr>
<tr>
<td>Bioinformatics tools and resources and their usage.</td>
<td>Analysis</td>
<td>K1, K4, K5</td>
<td>S1, S2, S3, S4, S5, S6, S7, S8</td>
</tr>
<tr>
<td>Fundamentals of computer science theory</td>
<td>Application</td>
<td>K1, K2, K3, K4, K5, K6, K7, K8, K9</td>
<td>S1, S2, S3, S4, S5</td>
</tr>
<tr>
<td>Human–computer interaction (HCI)</td>
<td>Analysis</td>
<td>K3, K6</td>
<td>S2</td>
</tr>
<tr>
<td>Scripting and programming appropriate to the discipline</td>
<td>Analysis</td>
<td>K1, K2, K4, K5, K6, K8, K9, K10, K11</td>
<td>S37, S1, S38, S39, S40</td>
</tr>
</tbody>
</table>
Modules

Introduction to the command line and R

Gerrit Botha, H3ABioNet, University of Cape Town

Introduction to the microbiome and study design – why 16S

Katie Lennard, H3ABioNet, University of Cape Town

Downstream analysis in R

Shantel Claassen-Weitz, University of Cape Town

Bioinformatics pipeline - The theory

Samson Kilaza, Dar es Salaam Institute of Technology

Sample collection, extraction and library prep for 16S NGS analyses

Imane Allali, H3ABioNet, University of Cape Town

16S analysis pipeline

16S rRNA Intermediate Bioinformatics Course: Int_BT
Verena Ras
Next

For more information on course logistics, watch video labelled:
Day 1 Part 4
Staff Training
Day 1 Part 4 – Logistics; how will the course run
Course design

Prerecorded lectures by experts - distance learning

- Videos to become available on the course website at least a few days before each contact session
- Head TA/sys admin to ensure that the videos have been downloaded ahead of each contact session
- TAs to familiarize themselves with content before the contact session

Local Classrooms - face to face

- Bi weekly contact sessions
- Local administrative and academic support
- TAs and sys admin needed at every session

Virtual classroom

- Practical assignments
- Module assessments
- Question and discussion forums
- Feedback forms
## Contact session layout

### Typical day plan

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:20 CAT</td>
<td>Sign in to Adobe Connect</td>
</tr>
<tr>
<td>10:30 CAT</td>
<td>Introduction (in Adobe Connect) webcams activated!</td>
</tr>
<tr>
<td></td>
<td>• Meet the featured classroom</td>
</tr>
<tr>
<td>10:40 CAT</td>
<td>Watch lecture recordings (in classroom)</td>
</tr>
<tr>
<td>12:30 CAT</td>
<td>Break</td>
</tr>
<tr>
<td>13:00 CAT</td>
<td>Work through practical assignment (trainer will be available during this time to answer questions via Adobe Connect chat or Vula forums)</td>
</tr>
<tr>
<td>14:00 CAT</td>
<td>Ask the trainer</td>
</tr>
<tr>
<td></td>
<td>• Meet the trainer</td>
</tr>
<tr>
<td></td>
<td>• Practical session wrap up</td>
</tr>
<tr>
<td></td>
<td>• Q&amp;A</td>
</tr>
</tbody>
</table>

**TA responsibilities during contact sessions:**
- Answer queries about the lecture recordings and practical assignments (tips and tricks for facilitating will be covered in tomorrow’s session)
- Encourage participants to ask questions via Adobe Connect or via Vula forums
- Record attendance
- Engage and make yourself available

**Sys admin responsibilities during contact sessions:**
- Ensure that projector is set up
- Log into Adobe Connect room
- Ensure that all the computers are working
- Troubleshoot any tech issues – slack group
Adobe Connect -> Zoom

The url for the IBT meeting room in Zoom will be displayed to you once you register on the circulated link.

- One login per classroom (use classroom acronym e.g. UCT-type in the chat room to name your institution)
- Wait moderator approval - not necessary

Please note: the Int_BT meeting room will only be available during contact session time or by prior arrangement with the Int_BT core team.
Int_BT 2019

Staff ONLY

This site is for the trainers, teaching assistants (TA), system administrators and coordinators of the H3ABioNet Int_BT_2019 course. Restricted access material (such as practical assignment memos) will be available via the 'Resources' tab on this site.

The 'Questions and Discussion' tab may be used as a space for staff to engage and discuss academic and logistic topics or queries.

Lecture recordings can be viewed on our Youtube Channel: https://www.youtube.com/watch?v=AVuWENpsGyG&list=PLcQ0XMykNhCQXNw6gTeoBw0DMIT7XeS

We also upload videos on Vula.
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We also upload videos on Vula.

Welcome to the staff site
(Verena Ras - 08-Aug-2019 16:32)
For participants to pass the course...
In order to pass the course, participants are required to:

• Attend all contact sessions.
• Submit 90% of practical assignments by the relevant hand-in date.
• Submit assessments by the relevant hand-in date and obtain a minimum grade of 60% overall for the assessments.
Consolidation Sessions

• Every few weeks
• A mental ’breather’
• Explore real world relevance of a topic
• Group exercise
• Submit response via Vula forums

What can you bring and what can you learn?

Activity 3 (10 minutes):

1. Take 5 minutes to write down:
   1. 3 things that you are good at/ have experience in and that you can help others with.
   2. 3 things that you would like help/ support with.

2. After 5 minutes, if not already in a circle, move your chairs so that everyone is sitting in one circle.

3. Give each person in the circle an opportunity to share what they wrote down. (Remember your ground rules when listening to others 😊)

4. Suggestion: write down what each person is willing to help others with and share this document with the staff team to use as a reference for who to ask for help.
Now watch the video labelled: Day 1 Part 5
Staff Training
Day 1 Part 5 - Commitments and Responsibilities: It’s a two way street
Core team commitments

Commits to provide

• Support for Adobe Connect
• Support for Vula usage
• Provide lecture material, practical assignments and other course material
• Support for challenges that classrooms encounter
• Some support for technical issues
• Updates on course modules, trainers and logistics
• Grading of assessments
• Guidance on creating a community atmosphere across classrooms
Class registers and general “housekeeping”

Example classroom register

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td></td>
<td>Date</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>first name</td>
<td>last name</td>
<td>email</td>
<td>9.05.17</td>
<td>11.05.17</td>
<td>16.05.17</td>
</tr>
<tr>
<td>3</td>
<td>participant 1</td>
<td></td>
<td></td>
<td></td>
<td>absent</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>participant 2</td>
<td></td>
<td></td>
<td></td>
<td>present</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>participant 3</td>
<td></td>
<td></td>
<td></td>
<td>present</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>etc</td>
<td></td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>7</td>
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<td>8</td>
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<td>10</td>
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</tbody>
</table>
Staff registers and scheduling

Each classroom should determine a schedule for the TAs for each contact session

• Ensure that the participant to TA ratio is reasonable (i.e. 1 TA:10 participants)
• We have provided a Google spreadsheet template for doing this in your classroom Google drive folder
• Each classroom should fill out this Google spreadsheet together with the TAs
• The head TA and Sys Admin should be present or contactable during every contact session
Communicating with the core team

- Queries from participants should be attempted to be resolved locally
- Use Vula forum if appropriate
- If you cannot resolve the issue locally, contact the Int_BT core team via Vula or email
- Tackle some approaches on how to do this
Activity to deal with challenges

• As a group brainstorm potential challenges that might arise
• Make use of the “ground rules” brainstorming session outlined in day 1 –part 2
• Go through the list of challenges and brainstorm how as a group you can find solutions to the challenge
• If the Int_BT core team can provide support in any way explicitly state how
• Select your top 5 challenges and solutions and enter this into the template document found here: Int_BT_2020 STAFF site -> Resources -> Staff Training -> Int_BT_2020 staff training Day 1 part 5 template.docx
• Also cut and paste your top 5 challenges and solutions to: Int_BT_2020 STAFF site -> Question and Discussion Forums -> Staff Training -> Challenges and Solutions

If your classroom encounters a challenge, have a look at the Challenges and Solutions thread

Other classrooms may have anticipated similar challenges and may have suggested a feasible solution for your classroom
Vula Questions and Discussion Forum

**Bootstrap values**

(06 Oct 2016 11:52 AM) - Read by: 16

What are the bootstrap values to report for academic work? I am currently inferring phylogenies using maximum likelihood methods (PHYML and RAxML programs) but I am unsure of the values to report. Phylogeny experts are not unanimous on a specific bootstrap threshold, with some saying that bootstrap values above 50% are good while others sticking to 70% and above. Kindly assist. Thanks

**Re: Bootstrap values**

(06 Oct 2016 12:41 PM) - Read by: 14

Hello, that's a good question. So far nobody has undertaken the work to associate meaningful p-values with standard bootstrap proportions (BP), so there are only rules-of-thumb out there to decide whether a branch is "well supported" or not. The threshold I have been hearing of is rather 80% than 50% or 70%, though, but the threshold you want to take into account depends on many factors, primarily the type of data (is there lots of phylogenetic divergence in the dataset or not?) and the distance between sequences (if sequences are far apart from each other you will tend to be content with lower BP than if you are dealing with a clean alignment with reduced variability). The depth in the tree is also a factor to take into consideration; you will be more demanding in terms of bootstrap support for branches relatively close to leaves (outer branches) than for inner branches: a BP of 70% only on a branch leading to a cherry (two taxa distant of two edges) is an indication of a poor phylogenetic signal, whereas if you get 70% on a deep branch of the tree, I would say it is significant enough to consider that branch as relatively well supported.

So the short answer is: rule of thumb and comparison to other papers dealing with the same type of data. Talk to a biologist who is a specialist of phylogenies similar to the one you are battling with.
What the video labelled
Day 1 Part 6
16S rRNA Microbiome Intermediate Bioinformatics Course: Int_BT

Staff Training

Day 1 Part 6 – Team Biographies
Forming a community

• The success of the course is based on developing a sense of community between classrooms
• Leverage on the fact that you are part of a larger community from diverse backgrounds all with a common interest in teaching and learning bioinformatics
• Easier to do this when you can put faces and a bit of context to your colleagues across the continent
Team Biography

- We have provided instructions and a template for generating the biography here:
- Int_BT_2020 STAFF site -> Resources -> Staff Training -
- > Int_BT_2020 staff training day 1 part 6 template.docx
- A single biography should be uploaded for each team – elect a person to upload the biography and photograph to Vula on behalf of the classroom
Have fun and I will see you next time!
16S rRNA Microbiome Intermediate Bioinformatics Course: Int_BT_2019

Staff Training

Day 2 Part 1
By the end of today...

- Feel a part of the wider Int_BT staff body
- Understand how classrooms might support each other
- List at least 3 good facilitation practices
- Describe at least 3 facilitation techniques and will know how to implement them
- Have an idea of how you might stimulate engagement (with and across classrooms and with the local bioinformatics community)
- Navigate and use Int_BT online platforms, namely: Vula, the Int_BT website site, Youtube, and Adobe Connect
Sign onto vula and read some of the biographies of the other classrooms

Take 10 mins to do this

Then sign onto adobe connect to meet some of the other classrooms!

Pause the video at this point and come back to it after the adobe session!
Sharing Solutions

**Activity (10-15 minutes):**

1. Use the projector system in your classroom to project the Vula interface (log in using any staff member’s account)
2. Navigate to Int_BT STAFF -> Question and Discussion Forums -> Staff Training -> Challenges and Solutions
3. As a group, read through the challenges and corresponding solutions for each classroom.
4. As a group, respond to 3 posts with a solution to a challenge raised in that post - for some of the classrooms, their might be challenges with no solution. For other challenges, your staff team might have a different solution to the one proposed in that post.
5. Consider responding to posts that do
   - not yet have any comments
   - In order to respond to the post...
Responding to a Vula Forum post
Responding to a Vula Forum post
Responding to a Vula Forum post
Next

Watch the video labelled

Day 2: Part 2
16S rRNA Microbiome Intermediate Bioinformatics Course: Int_BT_2019

Staff Training

Day 2 Part 2 – Tips and Tricks
Teacher vs. facilitator

**Activity**

- List 3 good facilitation practices and why you think they are effective. Post it onto vula forums under “good facilitation practices”
Tips and Tricks

Tips and tricks for facilitating active learning

Facilitating: a way of interacting, asking questions, valuing opinions, information flowing in all directions

Active learning: learning by doing

“I hear and I forget. I see and I remember. I do and I understand.” – Confucius

http://www.crlt.umich.edu/tstrategies/tsal
Tips and Tricks

1. Green and Red sticky notes
   http://swcarpentry.github.io/instructor-training/15-practices/

Tips and Tricks

2. Take it slow and explain step-by-step

• The way you speak to people and answer questions matters!
• A bit of kindness and sensitivity goes a long way (remember back to when you just started out in bioinformatics...)

Motivation vs. Demotivation: http://swcarpentry.github.io/instructor-training/16-motivation/
Tips and Tricks

3. Gamification (for recap)

• “Make a list of concepts/keywords and write it on the whiteboard (or a flipchart). You may also have cards stuck on the wall of the classroom with terms written on them.
• Throw a light and soft object to a participant, who will have catch the object, stand up, pick a term from the list and explain its meaning (or usage) in a few sentences (not more than 20-30 seconds).
• After the explanation, the participant will throw the object to another participant. Continue until the end of the list.”

#GTPB – The Gulbenkian Training Programme in Bioinformatics #ELIXIR
– EXCELERATE Train-the Trainer subtask
https://github.com/Pfern/TtT-in-Portugal-2016/blob/master/TtT_session_2.md#games

16S rRNA Intermediate Bioinformatics Course: Int_BT
Verena Ras
4. Encourage more advanced participants to help people next to them.
Tips and Tricks

5. Don’t ‘munch in a bunch’
Tips and Tricks

For more tips and tricks:

http://swcarpentry.github.io/instructor-training/
https://software-carpentry.org/blog/2016/04/tips-tricks-live-coding.html
https://swcarpentry.github.io/instructor-training/15-practices/
15-20 minute BREAK

Next session: Live session in Adobe – Software installations and setup

Please make sure you are signed on to adobe