

BIOS 10603 1 - Multiscale Modeling of Biological Systems II - Instructor(s): Esmael Jafari Haddadian

Project Title: College Course Feedback - Winter 2024

Number Enrolled: **25** Number of Responses: **14**

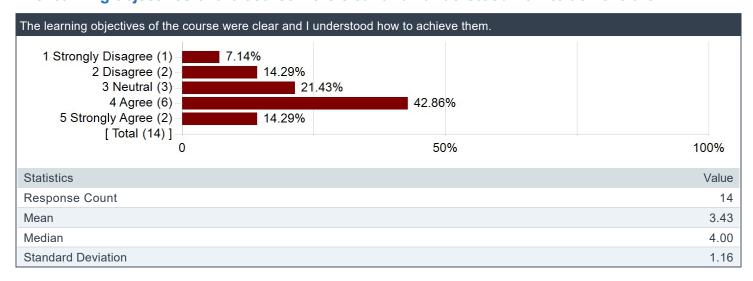
Report Comments

Opinions expressed in these evaluations are those of students enrolled in the specific course and do not represent the University.

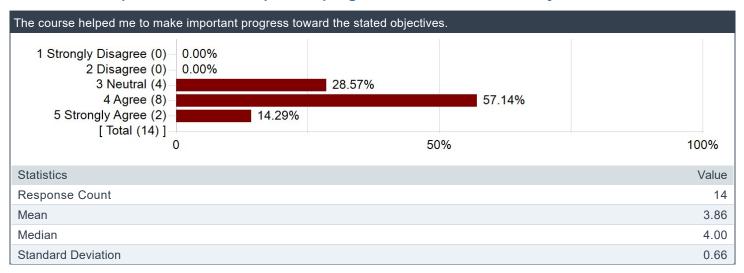
Creation Date: Thursday, March 28, 2024



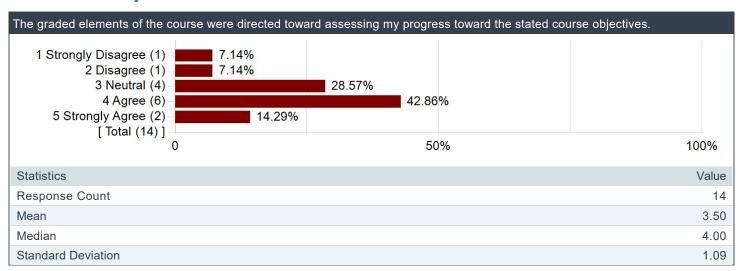
The learning objectives of the course were clear and I understood how to achieve them.



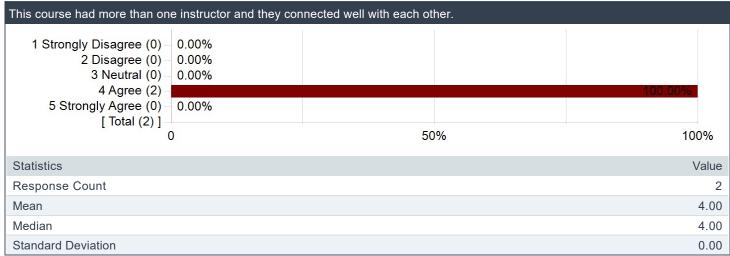
The course helped me to make important progress toward the stated objectives.

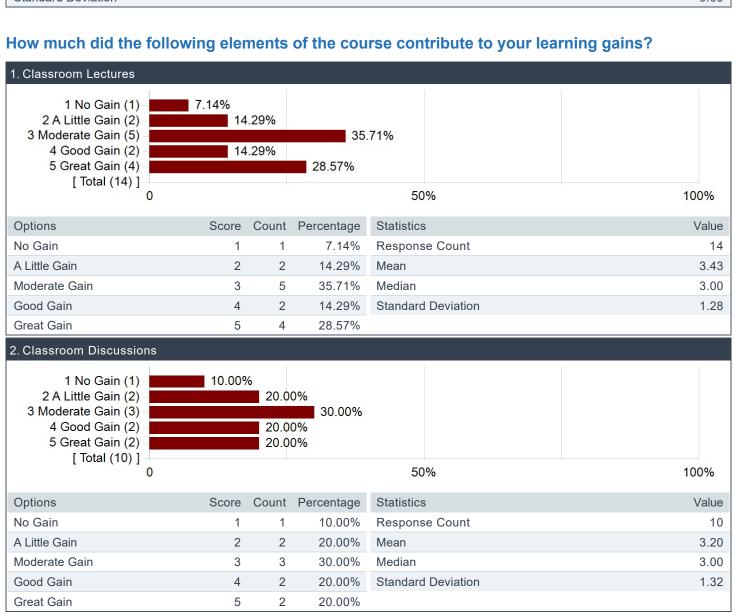


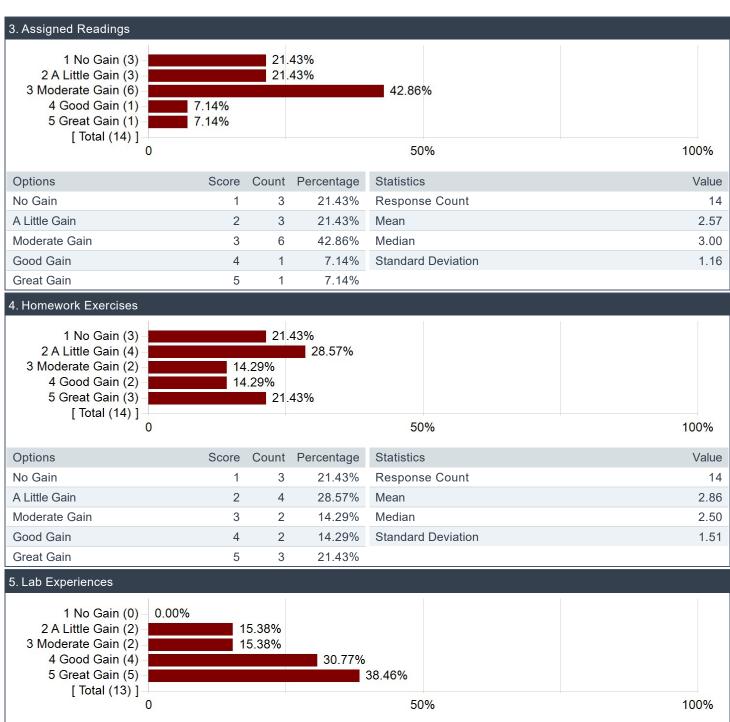
The graded elements of the course were directed toward assessing my progress toward the stated course objectives.



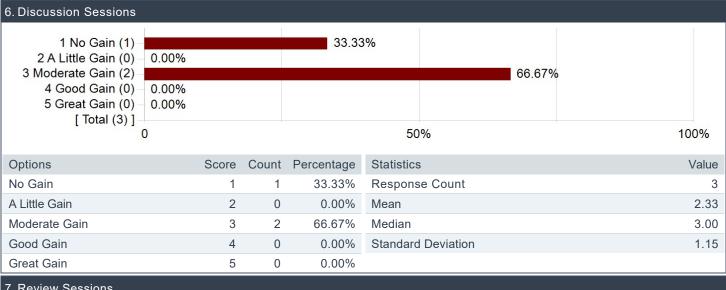
This course had more than one instructor and they connected well with each other.

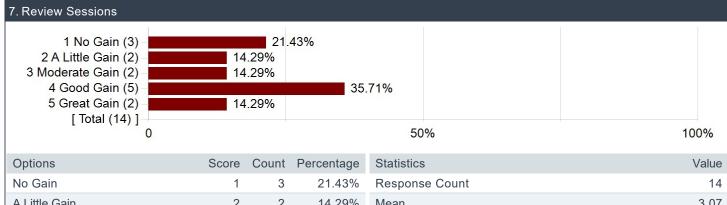




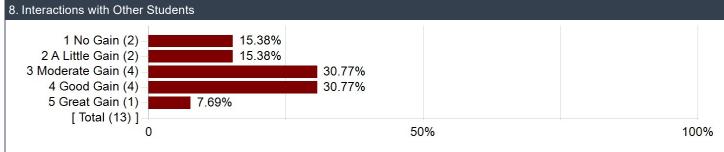


0				50%	100%
Options	Score	Count	Percentage	Statistics	Value
No Gain	1	0	0.00%	Response Count	13
A Little Gain	2	2	15.38%	Mean	3.92
Moderate Gain	3	2	15.38%	Median	4.00
Good Gain	4	4	30.77%	Standard Deviation	1.12
Great Gain	5	5	38.46%		

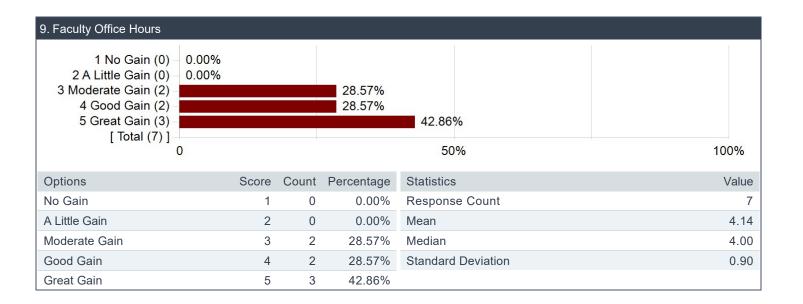




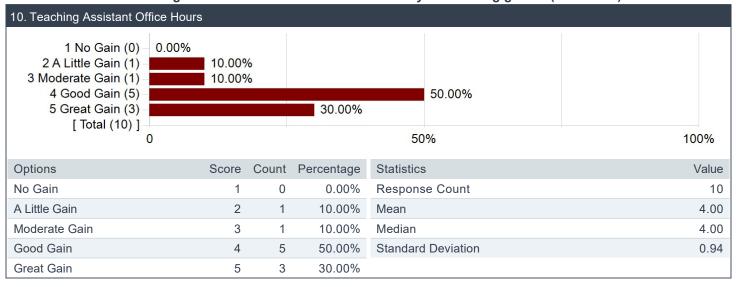
Great Gain	5	2	14.29%		
Good Gain	4	5	35.71%	Standard Deviation	1.44
Moderate Gain	3	2	14.29%	Median	3.50
A Little Gain	2	2	14.29%	Mean	3.07
No Gain	1	3	21.43%	Response Count	14
Options	Score	Count	Percentage	Statistics	Value



Options	Score	Count	Percentage	Statistics	Value
No Gain	1	2	15.38%	Response Count	13
A Little Gain	2	2	15.38%	Mean	3.00
Moderate Gain	3	4	30.77%	Median	3.00
Good Gain	4	4	30.77%	Standard Deviation	1.22
Great Gain	5	1	7.69%		



How much did the following elements of the course contribute to your learning gains? (continued)



What was the most important thing (to you) that you learned in this course? What aspect of the material is still unclear for you, that you wish you could have learned better?

Comments

Molecular Dynamics simulations. Most of protein structure etc are still unclear

R coding

Understanding molecular dynamic simulations is pretty cool, despite the amount of work it took to get there. Sometimes the physics explained in this class felt a little skimmed over, although I enjoyed it.

I learned a little of how to script in Tcl. What is unclear to me in general is how much of the simulations work, or how entropy works, or what ATP actually does in the cell.

Most important thing is the biology. Even more than the MD simulations and the DNA sequence coding that we did, I think the biology was extremely fun to learn. I honestly wish we could have just studied that all two quarters and then taken a third course with the simulations as like one of those "lab research classes." It was all great, but I wish we could have dived even deeper into the biology.

Basics of proteins. They're crazy

I learned a lot about coding and data analysis.

MD simulation of protein systems using NAMD and VMD on the Midway supercomputer was the major topic of this course. It was a pretty nice shift from BIOS 10602, where we were working a lot with R code on data that felt pre—setup to deduce some result. Here, we simulated our own individual proteins of our choice and did actual science on them. It's really cool seeing your protein system in—action once you fetch the computed data from Midway.

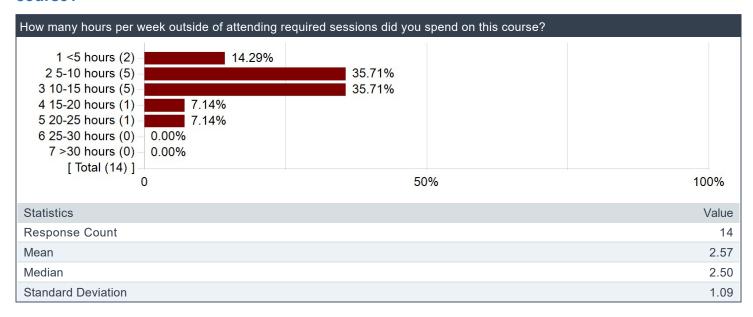
What's unclear to me still is how the miscellaneous biological topics we learned ties into MD. After we were done learning how MD simulation is done, we started talking about various biological subjects like basic thermodynamics, free energy, and basic overview of enzymes. These topics never came up in lab, unlike the MD topics, which makes sense since MD is what we were focused on in lab, but it made those extra topics feel disjointed from everything.

Probably just general biological knowledge about amino acid and processes was the most helpful. I don't think I'm unclear on any aspect of the course.

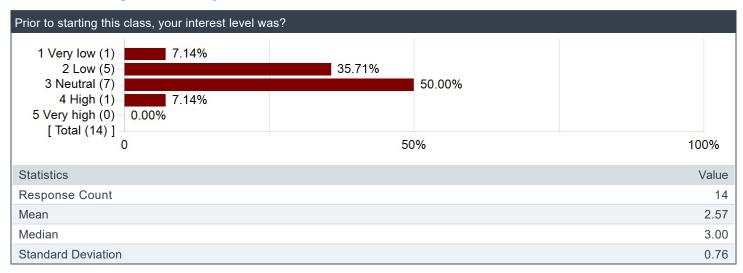
learned about MD simulations, proteins, and amino acids.

Better book material, would be better if there were less information.

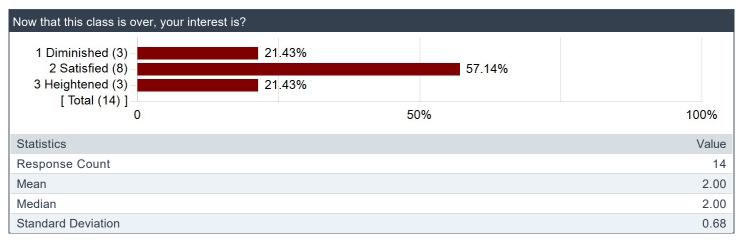
How many hours per week outside of attending required sessions did you spend on this course?



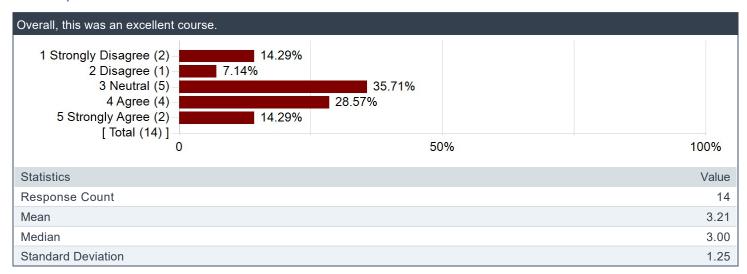
Prior to starting this class, your interest level was?



Now that this class is over, your interest is?



Overall, this was an excellent course.



Please share any advice you have for students who are considering taking the course.

Comments

It is much harder then the regular bio core even if you are good at coding.

Do not take this course unless you have a genuine, strong interest in knowing more about biological simulations. It is very cool if you really really want to have a deeper under standing of that subject, but the workload was far too much for someone with a passing interest, like me, to keep up with

You should only take this if you are someone with basically no other work to do and a heavy chemistry background. Otherwise, the time investment is not worth it.

If you don't have any past bio experience and want to learn more about DNA and molecular biology, I can't think of a better course. Just make sure to balance the other classes. Don't take this if you want to just finish the bio requirement. I just don't see why that would be a good idea. Don't take it if you are like, "yeah I am good at coding." The coding in this class is way too easy, it's the bio part that makes it hard. I don't think its hard to get an A, but I just don't see what's the point in taking this class if you it's for the grade. There is just way too much work. However, it's probably the most interesting biology core fulfilling class that this school offers.

N/A

Be careful before you choose to take this course: it is true that you will need to memorize less, but the workload is larger than necessary and much is mundane. The course has interesting content, but it is buried in a mountain of busywork.

If you are good at coding and don't mind a lot of work, it is probably pretty rewarding. Otherwise, I would say it is doable, but not without some trials. Not sure how it compares to other core bio. It may be more fun and we do produce some cool output.

This course is so much work. This course is so. Much. Work. I, like many other students who took this course, am a math + CS major, yet despite taking 3 courses for my majors alongside this one, this course took up significantly more time during the week than any of my other math/CS classes.

BIOS 10602 was already a lot, but 10603 is next—level amounts of time commitment. Be prepared for labs that involve a lot of shuffling of files in Midway, and wrangling with the programs VMD/NAMD for working with your protein project, because it will take up so much more of your time compared to any of the labs in BIOS 10602.

I am not kidding when I say that some of the labs took me 10+ hours to complete, when they were allotted just 3.5 hours of time in the registrar.

If you also include the waiting time it takes for NAMD to finish and the simulation check–ins that happened on the weekend, the completion time per lab can easily surpass 13+ hours a week, not including lectures or readings or exams or homework.

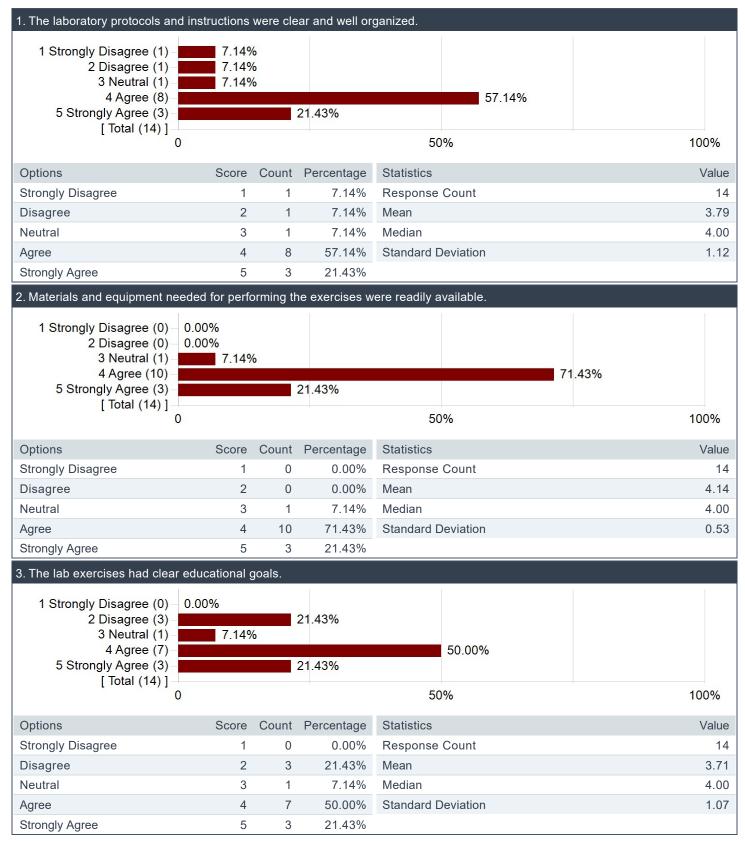
Don't take this course unless you have a fair bit of CA experience

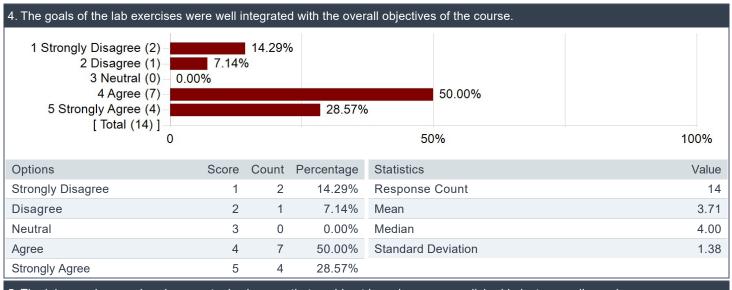
Don't take this course unless the content is very interesting to you prior to starting AND you want a hard core bio. I took this course because I thought it sounded interesting and wanted to challenge myself for bio but regret it. The lecture content was extremely boring. Although it did end up challenging me, it did so without much benefit of an interesting course.

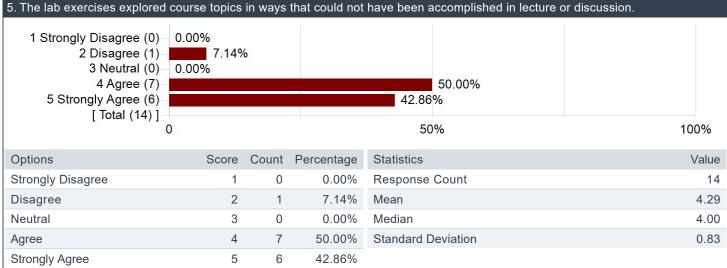
Participate in Labs actively

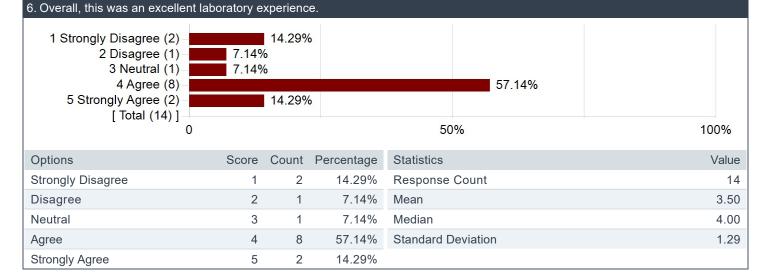
Laboratory Meetings

For each of the following statements, please indicate your level of agreement.

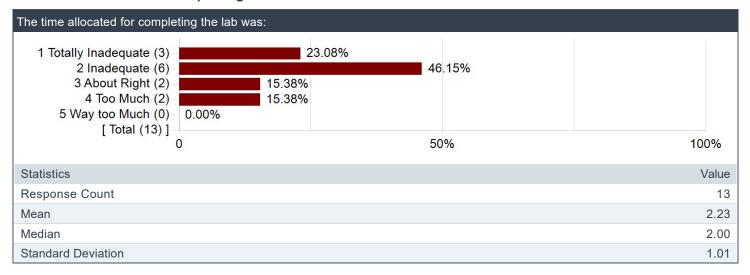








The time allocated for completing the lab was:



What observational, analytical, or technical skills did you gain during the laboratory exercises that enhanced your understanding of how biologists answer questions in this particular field?

Comments

Running Molecular Dynamic Simulations

Using unix.

Data analysis was key in this course. I also got a good understanding of the limitations that biologists face when doing molecular simulations

I learned that biologists use a combination of extinct scripting languages, old simulational suites, and uncommented code to run protein simulations.

We learned a lot about MD simulations which is an amazing skill to have. The labs honestly taught them to the highest possible level in this time frame.

Molecular Dynamics simulations

Labs taught us how to actually use tools to do analysis.

We worked on protein modeling. It was cool.

Unlike 10603 which dealt with R code, here we conducted MD simulations and analysis in labs. The skill gained of using VMD and NAMD is really specific to computational biology, but because we used them so much, you're also forced to gain a lot of general computer fluency and hyper efficient work–ethic to not be in the labs for hours and hours.

A lot of experience with tools that real biologists use.

VMD techniques, data analysis and other molecular dynamics skills.

Please share any recommendations to improve the laboratory learning experience.

Comments

Decrease the length of the labs

No more pre lab quiz

Make them shorter. The length of the labs are ridiculous, especially when so much of it is busy work that did not seem to contribute to a clear learning outcome.

The labs are far too long for the allotted time (four hours), and contain unclear instructions. Especially frustrating are the "fill in the script" portions of the lab as the code is poorly—organized.

Nothing.

Less busywork/more focus

The labs are largely disjoint from the course, which creates effectively two parallel classes (one in lectures, one in labs) which is frankly unacceptable. Content from one of these needs to get cut: for instance, if the labs (and final project) were shortened, that would help.

Some of the lab questions were not particularly relevant, and made the labs longer than they needed to be. The TA introduction videos, Professor's pre–lab lectures, and the lab manual were often redundant.

The labs desperately need to be shortened to not always extend past their time allocation. Except for the first two, I never completed a lab within the 3 and a half hour time slot.

One way to do this could be to lessen the busy work of the labs that are unrelated to the work of conducting MD simulations. For example, after learning about the phi/psi dihedral angles in textbook and lecture, it's really unnecessary to have a whole part of the lab deal with slowly charting the phi–psi angles of several peptide planes across ubiquitin.

On another note, it'd be a lot nicer if the labs were self–contained. When a lab question advises me to use Google to find the answer, it makes me feel really uneasy about the correctness of my response. Less "hint: use Google" and more "find the answer in this curated resource" would've been appreciated.

Please less plotting things in R, we were very experienced at this by midway through the quarter.

less busy work. just give us the stuff that is important