



# BIOS 10602 1 - Multiscale Modeling of Biological Systems I - Instructor(s): Esmael Jafari Haddadian

Project Title: **College Course Feedback - Autumn 2023**

Number Enrolled: **24**

Number of Responses: **16**

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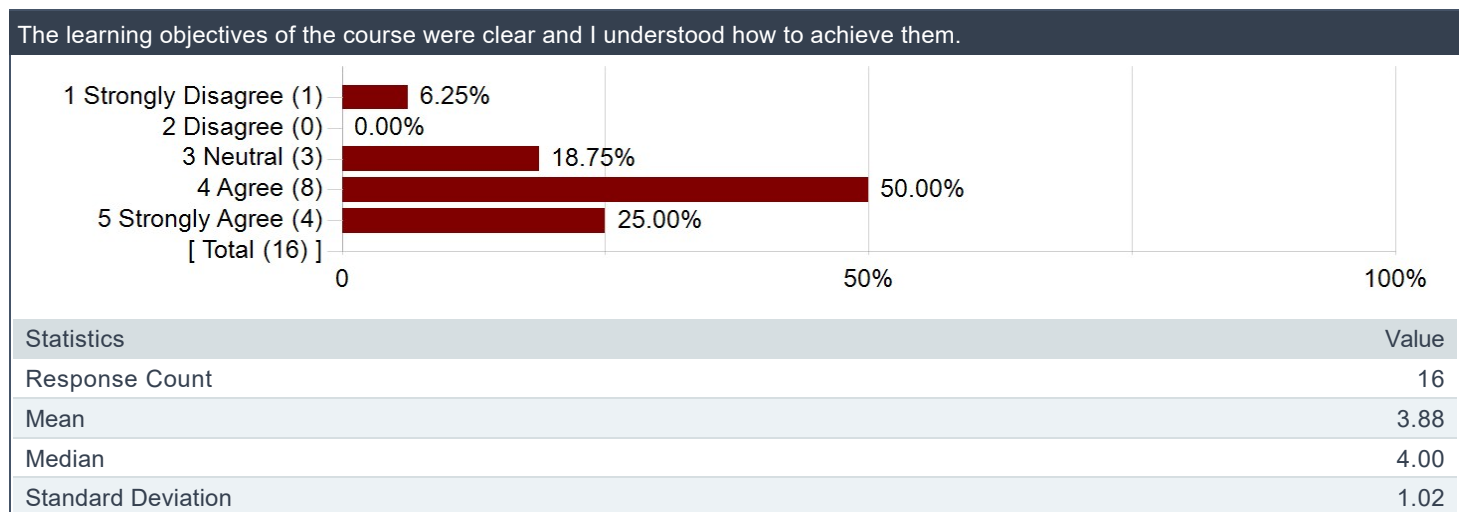
## Report Comments

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

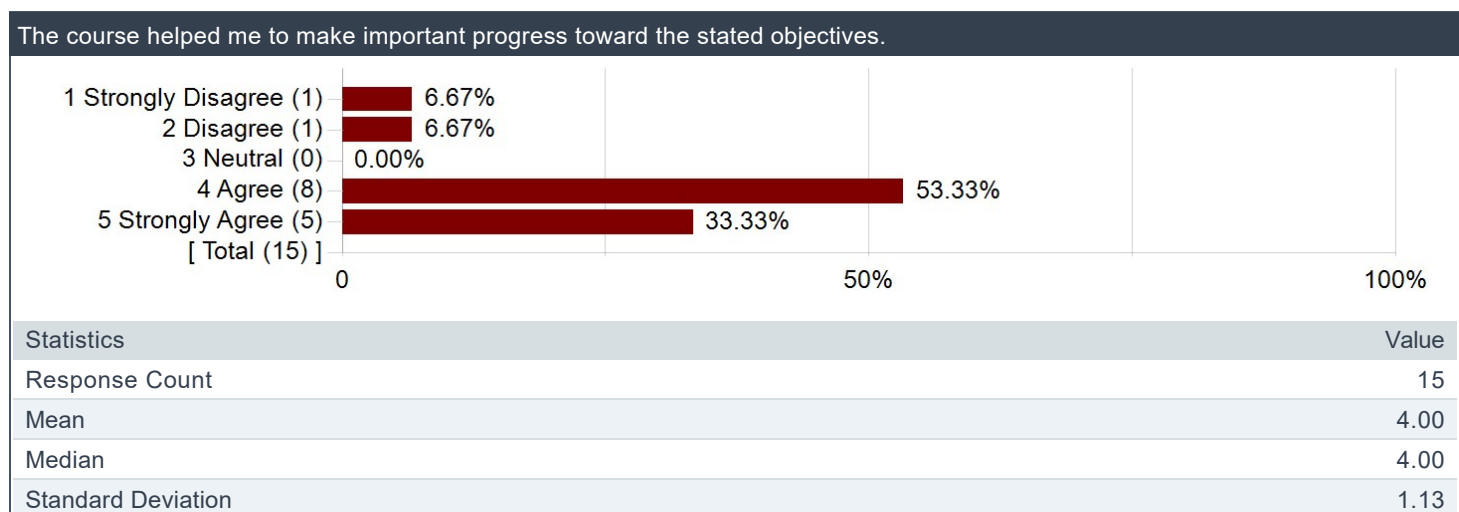
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Creation Date: **Friday, February 2, 2024**

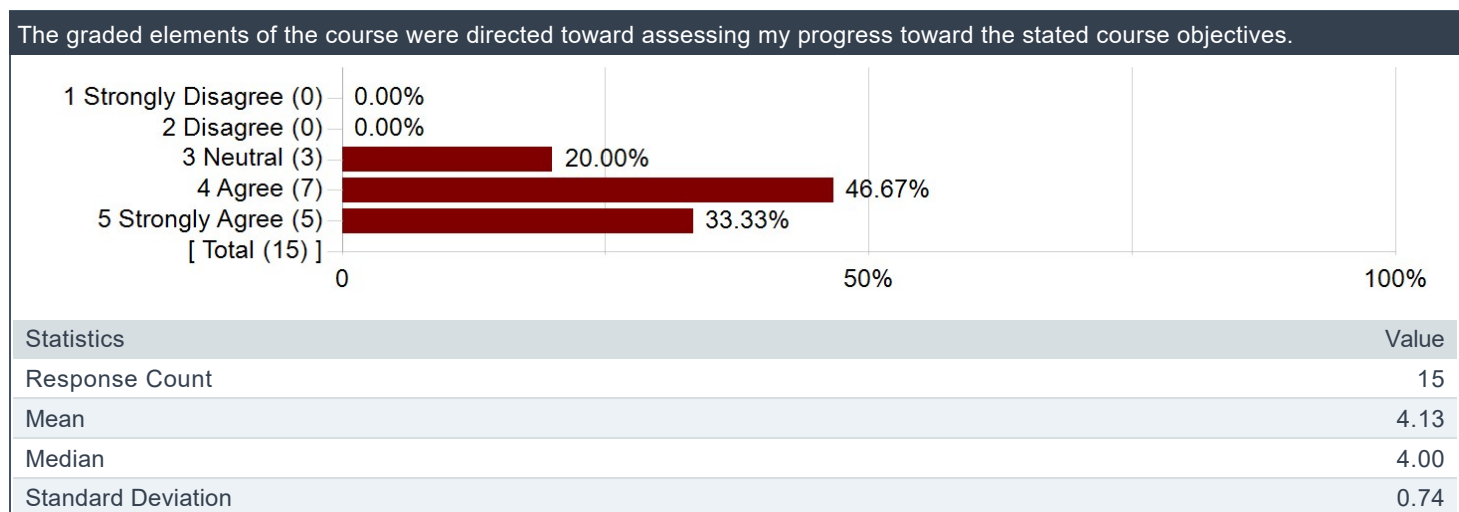
## The learning objectives of the course were clear and I understood how to achieve them.



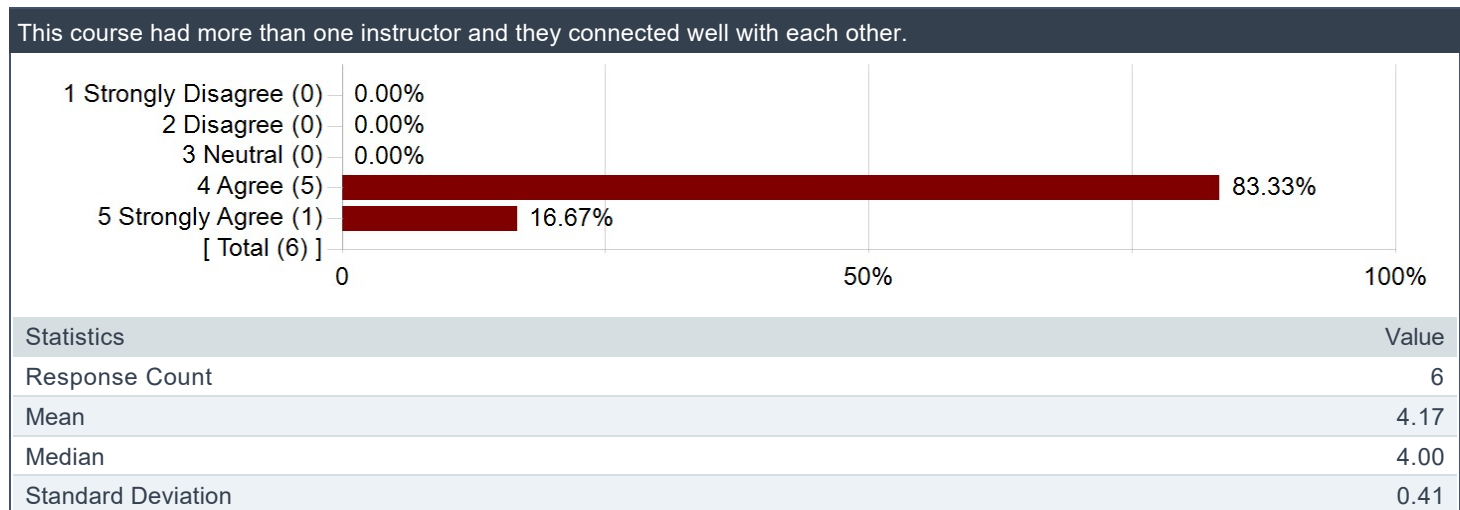
## The course helped me to make important progress toward the stated objectives.



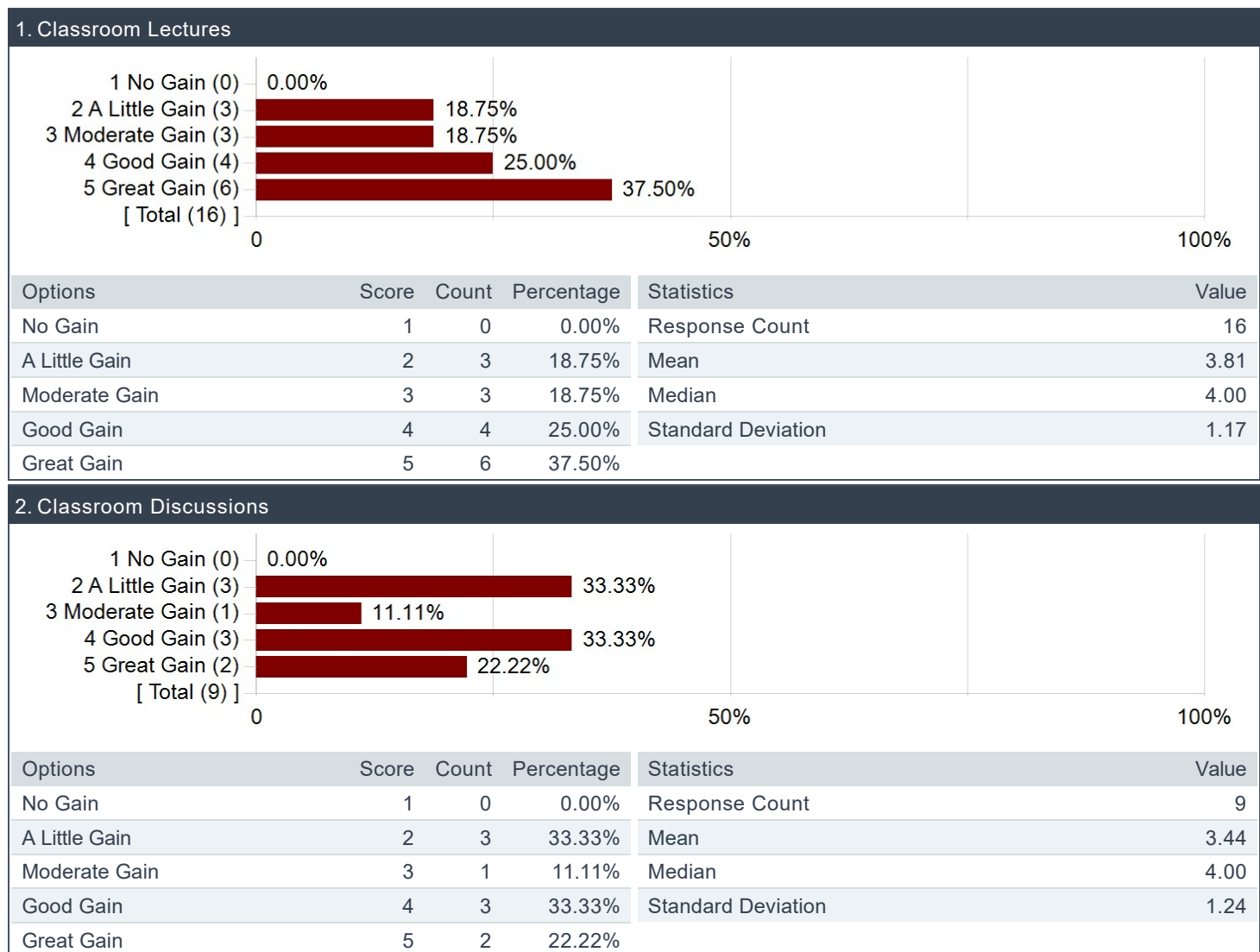
## The graded elements of the course were directed toward assessing my progress toward the stated course objectives.



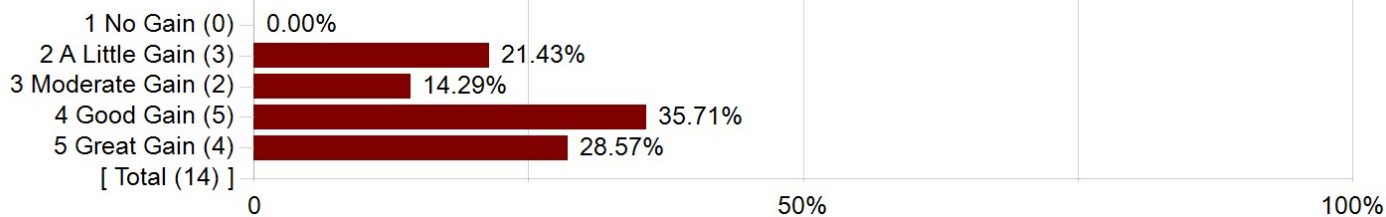
## This course had more than one instructor and they connected well with each other.



## How much did the following elements of the course contribute to your learning gains?

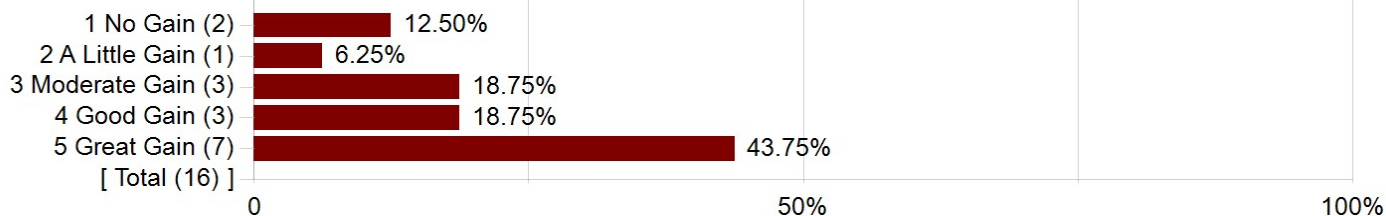


### 3. Assigned Readings



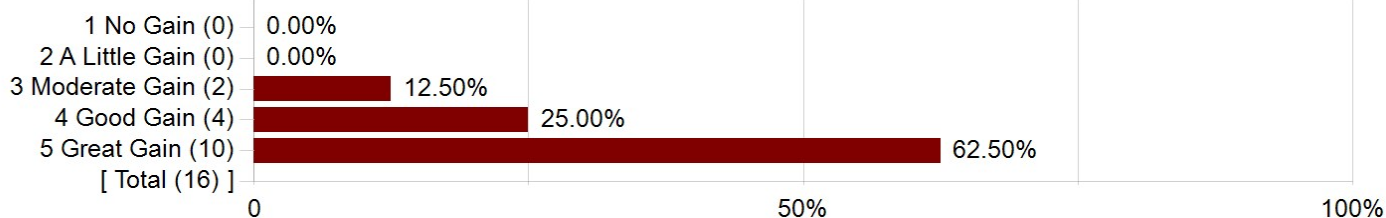
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A Little Gain	2	3	21.43%	Mean	3.71
Moderate Gain	3	2	14.29%	Median	4.00
Good Gain	4	5	35.71%	Standard Deviation	1.14
Great Gain	5	4	28.57%		

### 4. Homework Exercises



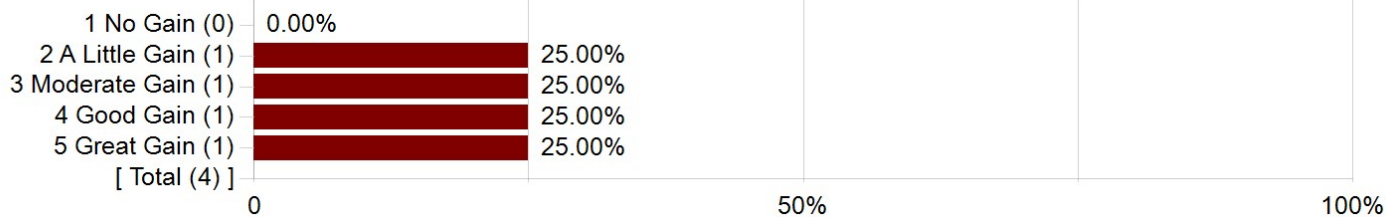
Options	Score	Count	Percentage	Statistics	Value
No Gain	1	2	12.50%	Response Count	16
A Little Gain	2	1	6.25%	Mean	3.75
Moderate Gain	3	3	18.75%	Median	4.00
Good Gain	4	3	18.75%	Standard Deviation	1.44
Great Gain	5	7	43.75%		

### 5. Lab Experiences



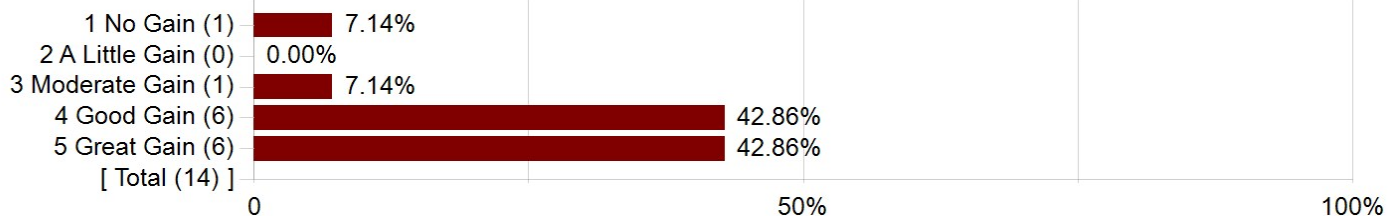
Options	Score	Count	Percentage	Statistics	Value
No Gain	1	0	0.00%	Response Count	16
A Little Gain	2	0	0.00%	Mean	4.50
Moderate Gain	3	2	12.50%	Median	5.00
Good Gain	4	4	25.00%	Standard Deviation	0.73
Great Gain	5	10	62.50%		

## 6. Discussion Sessions



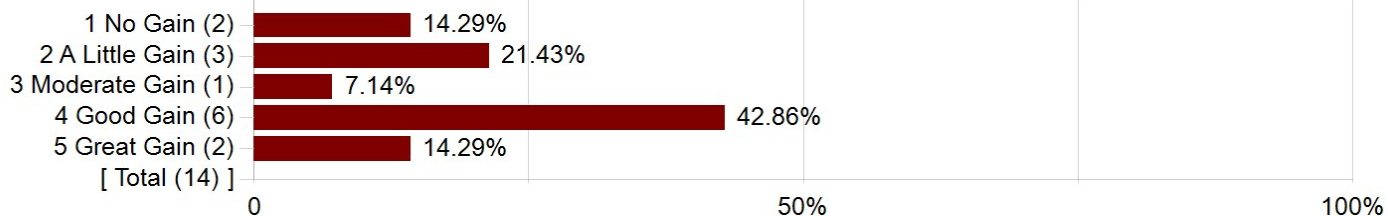
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No Gain	1	0	0.00%	Response Count	4
A Little Gain	2	1	25.00%	Mean	3.50
Moderate Gain	3	1	25.00%	Median	3.50
Good Gain	4	1	25.00%	Standard Deviation	1.29
Great Gain	5	1	25.00%		

## 7. Review Sessions



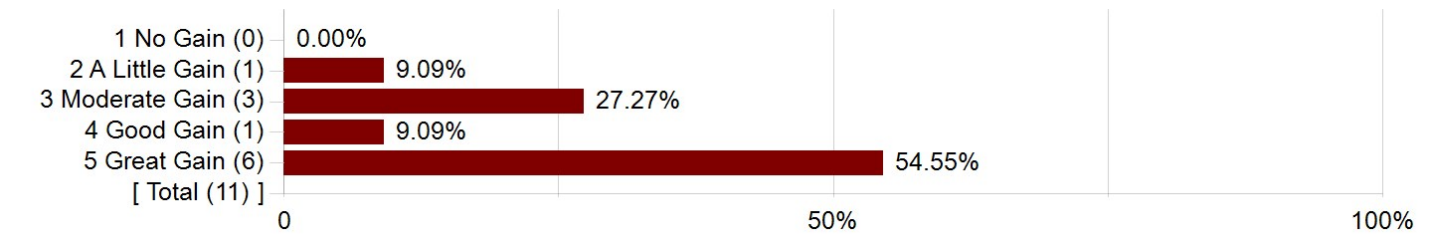
Options	Score	Count	Percentage	Statistics	Value
No Gain	1	1	7.14%	Response Count	14
A Little Gain	2	0	0.00%	Mean	4.14
Moderate Gain	3	1	7.14%	Median	4.00
Good Gain	4	6	42.86%	Standard Deviation	1.10
Great Gain	5	6	42.86%		

## 8. Interactions with Other Students



Options	Score	Count	Percentage	Statistics	Value
No Gain	1	2	14.29%	Response Count	14
A Little Gain	2	3	21.43%	Mean	3.21
Moderate Gain	3	1	7.14%	Median	4.00
Good Gain	4	6	42.86%	Standard Deviation	1.37
Great Gain	5	2	14.29%		

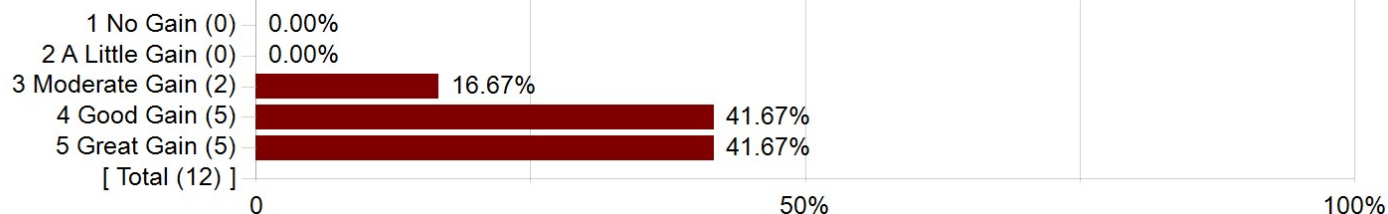
9. Faculty Office Hours



Options	Score	Count	Percentage	Statistics	Value
No Gain	1	0	0.00%	Response Count	11
A Little Gain	2	1	9.09%	Mean	4.09
Moderate Gain	3	3	27.27%	Median	5.00
Good Gain	4	1	9.09%	Standard Deviation	1.14
Great Gain	5	6	54.55%		

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

### 10. Teaching Assistant Office Hours



Options	Score	Count	Percentage	Statistics	Value
No Gain	1	0	0.00%	Response Count	12
A Little Gain	2	0	0.00%	Mean	4.25
Moderate Gain	3	2	16.67%	Median	4.00
Good Gain	4	5	41.67%	Standard Deviation	0.75
Great Gain	5	5	41.67%		

## 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

Most important thing: Unix commands.

Still Unclear: Point Accepted Mutations

DNA structure and replication. How some major algorithms work and how they are implemented are unclear.

I learned a lot about the algorithms used in bioinformatics. A lot of the "bio" part of that is still unclear to me but I understand the computational side quite well.

coding in R

We started by covering the necessary biology and chemistry you need to know for bioinformatics, which mimicked a crash-course in the first semester of AP Chem or AP Bio. The most important were probably the processes of DNA replication, expression of DNA as proteins, what makes up proteins and DNA, and the structure of genes (exonic and intronic regions).

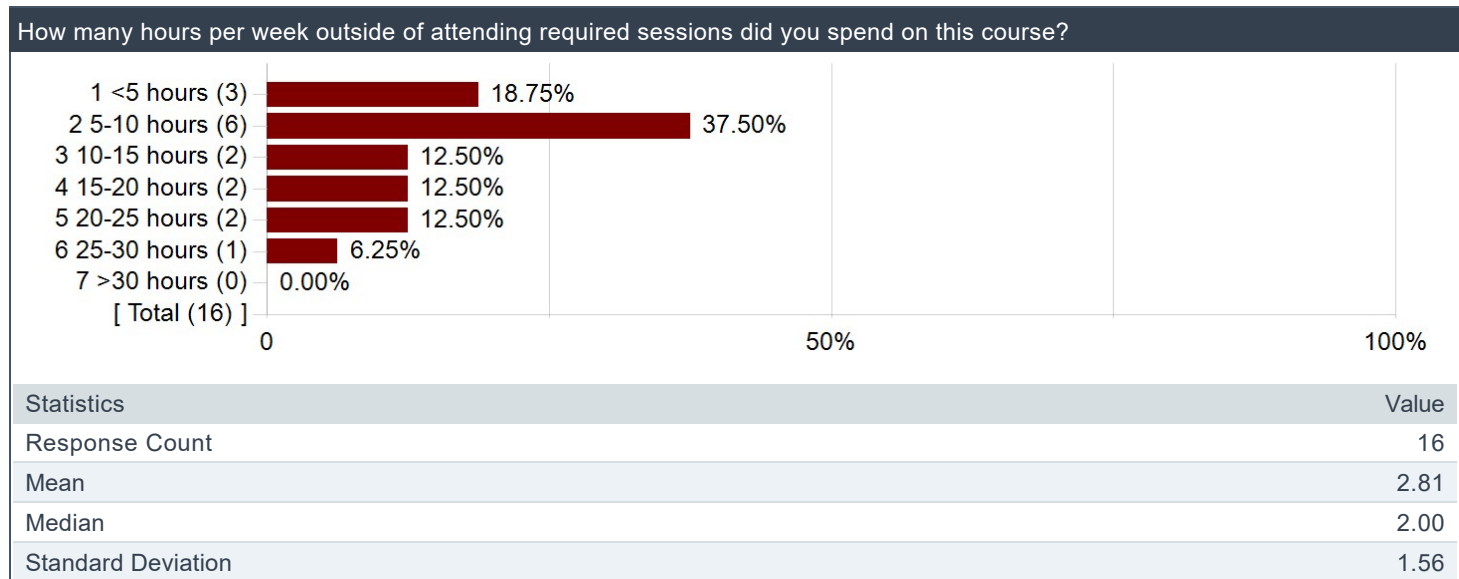
We then covered the many bioinformatics topics: carbon dating of organic matter, local, global, and multi sequence alignment and their algorithms (Needleman–Wunsch, Smith–Watermann, and Center–Star Alignment), construction of scoring matrices, substitution matrices, and alignment matrices (PAM1–250, BLOSUM), DNA sequencing methods (Sanger and Next–Gen), and sequence analysis via BLAST algorithm. It's tough to say which was most important, because they're all connected and are all very important to succeeding in this course.

A significant portion of the course content was in labs, with the R programming language and working with biological data. Towards the end, basic scripting and Linux terminal fluency was taught so we could use the Midway supercomputer.

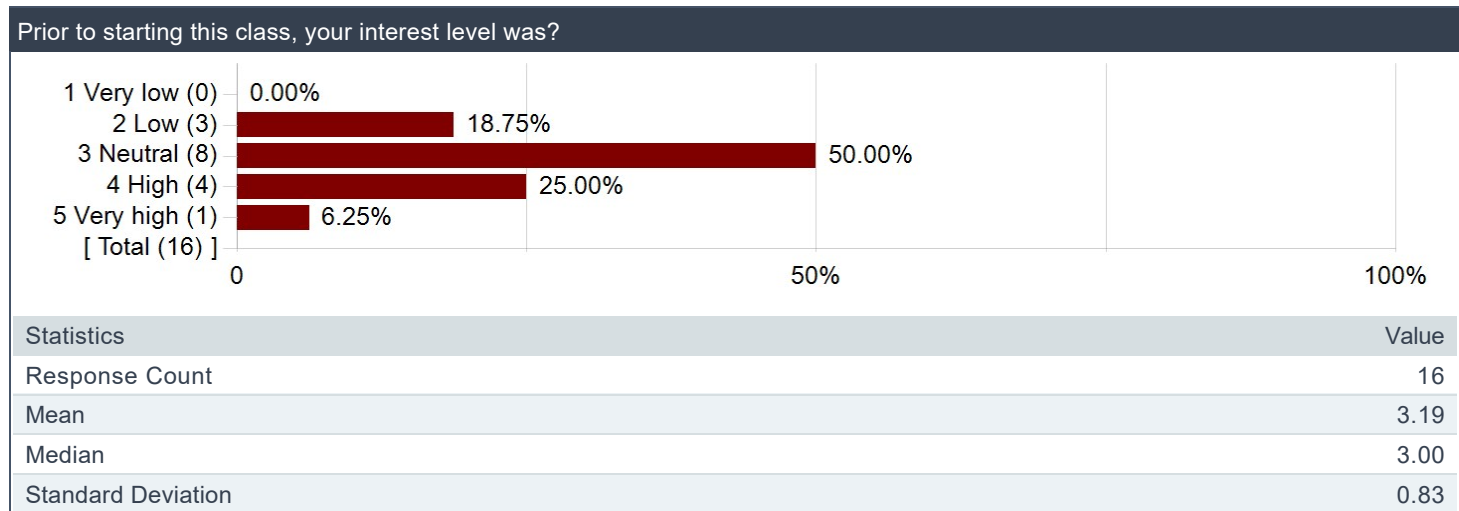
The most important thing I learned in this course was how amino acids mutate at different rates depending on their physical and chemical properties which either preserve or damage the function of the protein. One thing that I could have learned better is the statistics behind how the probabilities for these mutations were calculated.

DNA and amino acid sequencing and analysis.

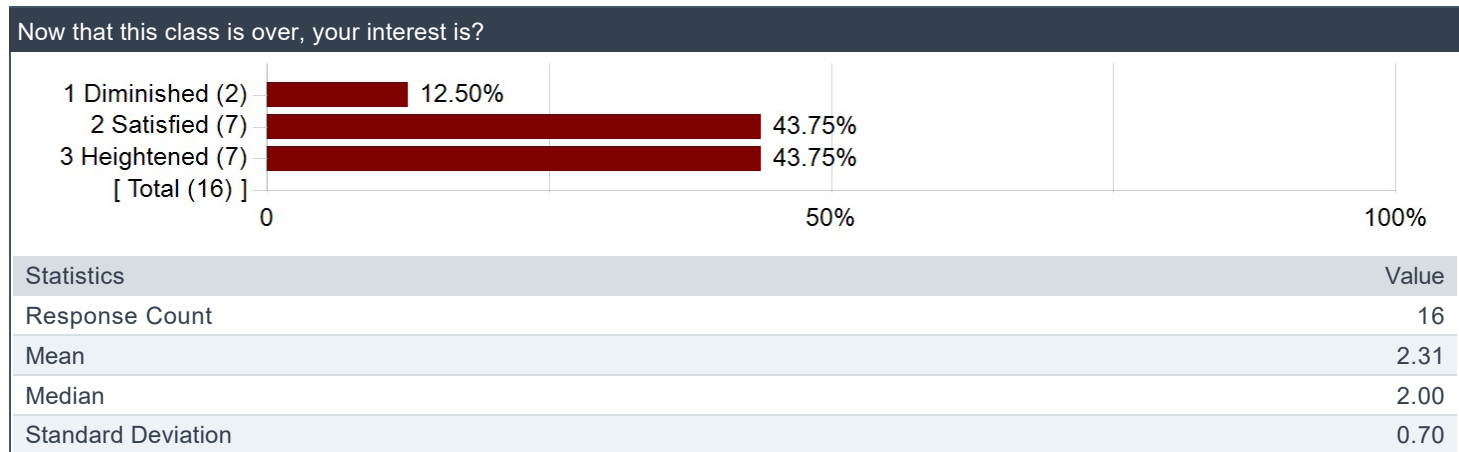
## How many hours per week outside of attending required sessions did you spend on this course?



## Prior to starting this class, your interest level was?

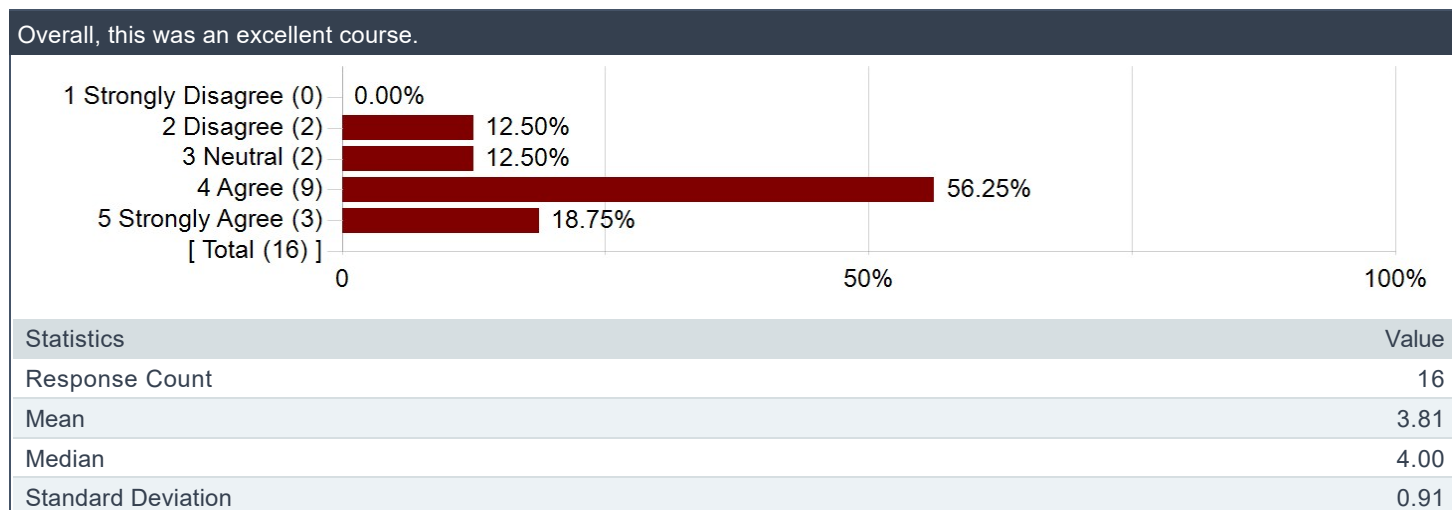


## Now that this class is over, your interest is?





## Overall, this was an excellent course.



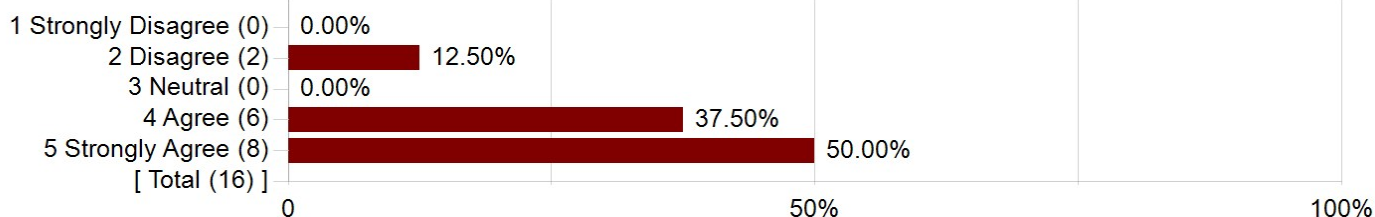
## Please share any advice you have for students who are considering taking the course.

Comments
This course consists of two (largely separate) halves. The bio half (lectures + readings) is a fairly standard and traditional bio course, and the coding half (labs + final project) dives into R and bioinformatics. Make sure to spend time studying both.
Do not take this course unless you are a really good programmer. Or else you will just end up dropping.
Be prepared to do a lot of work and reading on your own. If you're a grinder with free time or you have a strong interest in bioinformatics this course is good for you, otherwise take an easier course.
It is memorization heavy. I was led to assume that it would be mostly coding.
If you're a CS Major, PLEASE PLEASE take this course for your core bio, I cannot recommend it enough. You wouldn't think it for a core bio course, but BIOS 10602 incorporates many components that are soooo fascinating if you've also studied CS and have completed the intro sequence. Learning R was very interesting coming from CMSC 14200, where you worked with Python and Python Pandas, you can really see the differences in design choices between R and Pandas. The intro sequence already teaches you how to SSH into the CSIL machines, so SSH-ing into and using the Midway supercomputer came naturally and was awesome to use. It felt quite powerful to get a hands-on chance to do some high-performance computation with raw experimental data.
Finally, for a CS major, I believe the absolute highlight of the course is the tour-visit to Midway. We got to have the director of the data center where Midway is hosted show us around the facility and explain how it all works and its ins-and-outs. Coming from 14400 and seeing those giant compute-nodes and the innards of a decommissioned motherboard with its gigantic CPU with 70+ cores and dozens of multi-terabyte drives... it was all just too cool man.
If you're NOT a CS Major or have zero programming experience, I warn that you may struggle greatly with the labs in this course. Lab 1 is essentially a crash-course in programming, and after that, you're dropped into the deep-end of R and have to either sink or swim. Having prior programming experience was an invaluable asset to completing the labs, because they take a VERY LONG time to do, even as an experienced programmer. It wasn't uncommon for my entire day to be taken up by lab, you need to plan around them.
I think it's very telling that, after Week 3, anyone who wasn't a CS major dropped this course. Beware!
The course is challenging (especially for those without prior programming experience), but it's highly rewarding for those genuinely interested in the subject matter.
Go to all the labs and lectures and don't be afraid to ask questions when you don't understand something. Prof. Haddadian is more than happy to help you understand something you are confused about.
Not a good class for your GPA; you will be competing against some very smart math and CS double majors. However, I feel like I learned more than I would have in a traditional BIOS core class.
If the content seems really interesting to you and you have coding background I would take the course but if not, it's not worth it.
Think again. If you're not committed, this class may be HARD.

## Laboratory Meetings

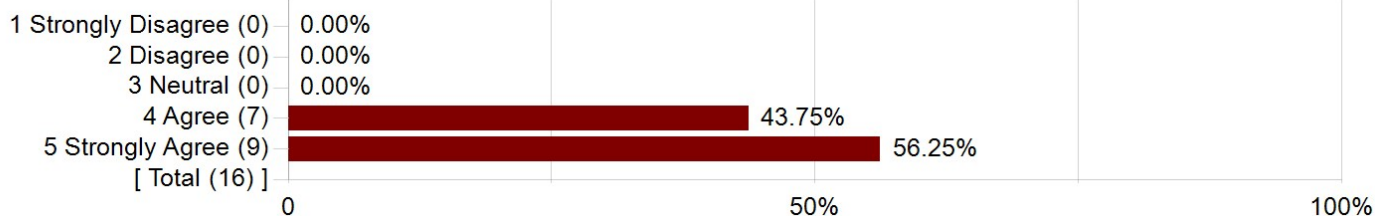
For each of the following statements, please indicate your level of agreement.

### 1. The laboratory protocols and instructions were clear and well organized.



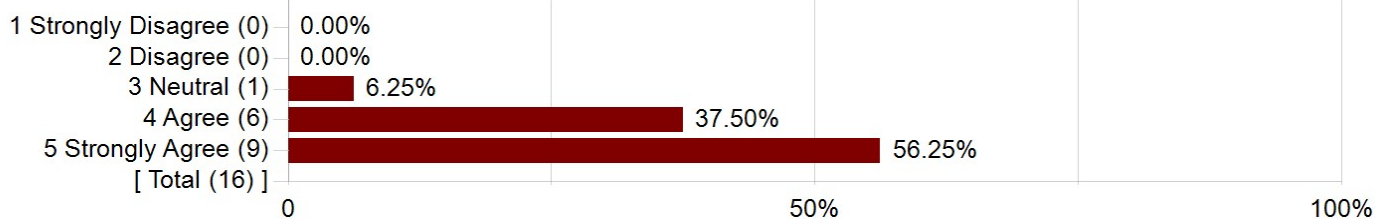
Options	Score	Count	Percentage	Statistics	Value
Strongly Disagree	1	0	0.00%	Response Count	16
Disagree	2	2	12.50%	Mean	4.25
Neutral	3	0	0.00%	Median	4.50
Agree	4	6	37.50%	Standard Deviation	1.00
Strongly Agree	5	8	50.00%		

### 2. Materials and equipment needed for performing the exercises were readily available.



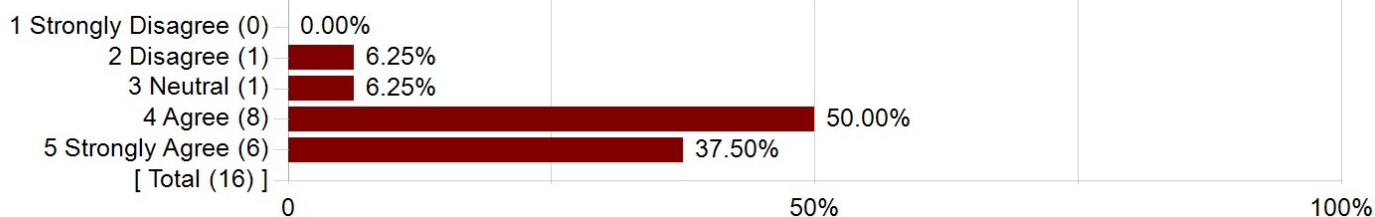
Options	Score	Count	Percentage	Statistics	Value
Strongly Disagree	1	0	0.00%	Response Count	16
Disagree	2	0	0.00%	Mean	4.56
Neutral	3	0	0.00%	Median	5.00
Agree	4	7	43.75%	Standard Deviation	0.51
Strongly Agree	5	9	56.25%		

### 3. The lab exercises had clear educational goals.



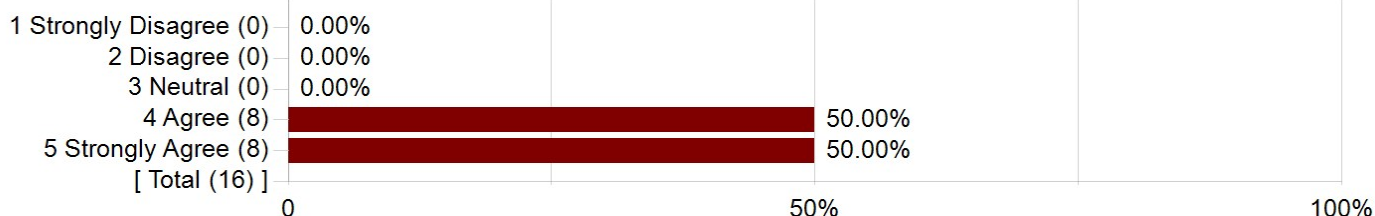
Options	Score	Count	Percentage	Statistics	Value
Strongly Disagree	1	0	0.00%	Response Count	16
Disagree	2	0	0.00%	Mean	4.50
Neutral	3	1	6.25%	Median	5.00
Agree	4	6	37.50%	Standard Deviation	0.63
Strongly Agree	5	9	56.25%		

#### 4. The goals of the lab exercises were well integrated with the overall objectives of the course.



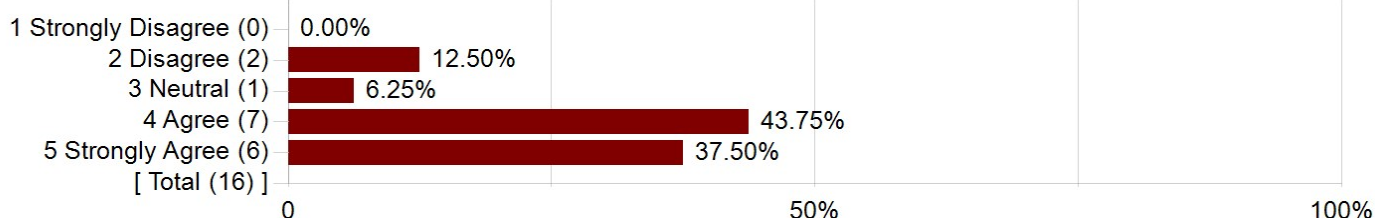
Options	Score	Count	Percentage	Statistics	Value
Strongly Disagree	1	0	0.00%	Response Count	16
Disagree	2	1	6.25%	Mean	4.19
Neutral	3	1	6.25%	Median	4.00
Agree	4	8	50.00%	Standard Deviation	0.83
Strongly Agree	5	6	37.50%		

#### 5. The lab exercises explored course topics in ways that could not have been accomplished in lecture or discussion.



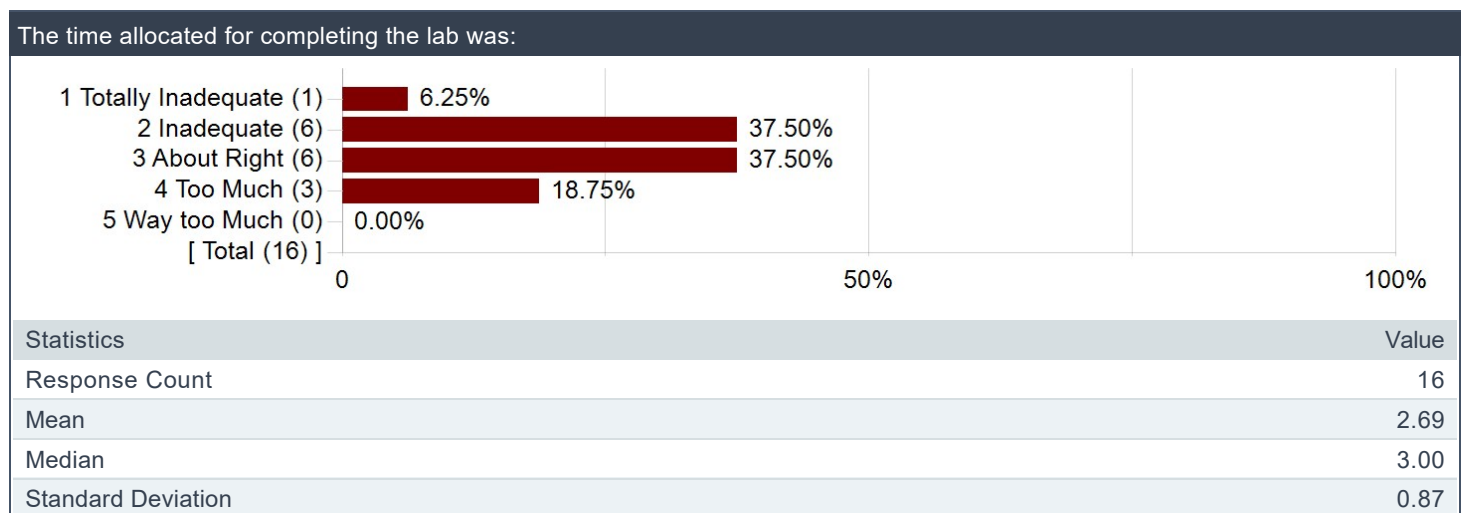
Options	Score	Count	Percentage	Statistics	Value
Strongly Disagree	1	0	0.00%	Response Count	16
Disagree	2	0	0.00%	Mean	4.50
Neutral	3	0	0.00%	Median	4.50
Agree	4	8	50.00%	Standard Deviation	0.52
Strongly Agree	5	8	50.00%		

#### 6. Overall, this was an excellent laboratory experience.



Options	Score	Count	Percentage	Statistics	Value
Strongly Disagree	1	0	0.00%	Response Count	16
Disagree	2	2	12.50%	Mean	4.06
Neutral	3	1	6.25%	Median	4.00
Agree	4	7	43.75%	Standard Deviation	1.00
Strongly Agree	5	6	37.50%		

## 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
We learned and implemented algorithms that biologists use to study DNA
R algorithms
Running the algorithms in R. However, most of this included simply running a function given to you, which did not need any understanding
Knowledge of the algorithms we use in this field. Learned about the heuristics used and the way biologists view data emergence. Used more R than I ever have before. Learned Linux terminal for remote access.
I learned how to code in R for sequencing
In labs, we used R to either implement or use the algorithms that bioinformaticians use to perform the tasks of sequence alignment, high performance computation, presenting graphs of data and light statistical analysis.
What was nice was that the labs almost always aligned directly with what we were learning in lecture. Labs often dealt with the gritty details of algorithms used, which was helpful to better understand why we use these algorithms and how they work.
You wouldn't expect graph theory, 2 pointers, and dynamic programming to appear in a bio course, but it did, and it was pretty cool.
R, shell commands, & sequence alignment algorithms
We learned about quantitative and computational methods used by biologists to analyze DNA and amino acid sequences.
Exposure to tools
Learned R and using the terminal to do sequence analysis and alignment.
R programming, linux/shell commands, how to submit jobs to Midway
Basically everything.

**Please share any recommendations to improve the laboratory learning experience.**

Comments
The lab documents had mistakes sometimes and often they were just took a very very long time to complete
Replace R with Python. 100%.
Harder labs.
shorter videos. Or video summery in text form
Prof. Haddadian often gave lectures right at the beginning of lab that further cemented what we needed to know and what biological information could help us answer the lab analysis questions. Super super helpful, I'd keep doing these.
Making us do the Needle–Wunsch algorithm by hand on paper for Lab 5 was AGONY. I spent like an hour writing up the resulting matrix, when implementing the actual code for it took like 15 minutes! Please remove this aspect of that lab.
Streamline
Sometimes the labs were really good but other times there was a lot of extra work that really just seemed like busy work that didn't contribute to anything, it just made the labs take much longer than necessary. There were also biology focused questions that I'm not really sure how we were supposed to answer without prior knowledge or asking the TA for the answer, which was pretty annoying.