

MEDS5420 Spring 2023. 8/16 students filled out the course evaluations. All responses are included.

	Question	Answer
1	The course was well organized	Agree
2	The course was an effective learning experience	Agree
3	The vignettes effectively communicated the rationale for the analyses and promoted learning	Agree
4	The vignettes provided the code in a reproducible and portable format that will make for a good reference in the future	Agree
5	The course was effectively organized on Xanadu	Agree
6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Agree
9	The course director showed interest in helping students	Strongly Agree
10	The course objectives were met	Agree
11	I am much more comfortable analyzing genomics data analysis independently	Agree
12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Agree
13	I would recommend this course to my peers	Strongly Agree
14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Agree

15	Comment box: Please provide constructive feedback for the course director	I think the vignettes/materials are high quality and would benefit us a lot in the future. I really appreciate the effort you put into designing this course.
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	strengths: detailed vignettes to follow; enough time for in-class exercise; assignments is helpful in reinforcing the concepts we covered in class.\n
17	Comment box: What topics could have been covered in more or less detail?	ATAC seq part could be covered in more detail. I think adding one assignment on this part would be also helpful.
18	Comment box: What topics that were not covered should be part of the course?	Couldn't think of much. Maybe in the RNAseq intro lecture can also include some slides regarding experimental design, t-test, two-way anova, FDR, and sc-RNAseq.\nCan also touch base on some other HTS technique such as PROseq.
19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	I think the R code like data.table or dplyr have simpler syntax for us to understand the function. Using those codes in lecture might be easier for students to follow. \nawk code is faster then those and is still a good tool to learn for large data analysis, this could be something mentioned aside.
1	The course was well organized	Strongly Agree
2	The course was an effective learning experience	Strongly Agree
3	The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
4	The vignettes provided the code in a reproducible and portable format that will make for a good reference in the future	Strongly Agree
5	The course was effectively organized on Xanadu	Strongly Agree
6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree

8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Strongly Agree
9	The course director showed interest in helping students	Strongly Agree
10	The course objectives were met	Strongly Agree
11	I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Strongly Agree
13	I would recommend this course to my peers	Strongly Agree
14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Agree
15	Comment box: Please provide constructive feedback for the course director	Great course! Everyone in biomedical sciences should take this, especially in the era of big data! Thank you for being willing to meet, almost anytime and discuss issues.
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	Strengths: important topics, thorough, and I liked how we had the ability to easily meet online (Zoom) so we could do class from where ever. Weaknesses: I found that I was getting lost in each class, but was able to catch back up just fine. I think if the code was presented in a way where we could more easily just run the scripts, that would be nice.

17	Comment box: What topics could have been covered in more or less detail?	-Awk seems super useful, but annoying. Not sure if you could do away with it without compromising its uses -I was most interested in RNA-sequecing and I wish there was more of this and we had gone though it at a slower pace. I am still confused by the who "align to genome" and "splice site match" thing -I learned that ChIP-seq is a lot harder then intially thought, and I probably don't want to do it; however, it was covered well in class. Also what happened to ATAC-seq pipeline? -I wish there was more 10x / single cell RNA-seq data processing and special features and packages used in scRNA-seq, like scRNA-scATAC, trajectory analysis, cell-cell/ligand communication, ect Please go over how to have proper data management and organize your files for ChIP and RNA seq. We learned about making directories, but knowing how to organize them may seem like an intuitive skill, but I still have lots of messy directories. -I think the best option to address these issues is to have multiple bioinformatics classes, not just this one. There should be one dedicated to scRNA-seq, one dedicated to ATAC/ChIP-seq, one dedicated that is more of a general overview (like this one), ect. This is critical in the genomics and big data era!
18	Comment box: What topics that were not covered should be part of the course?	<Unanswered>
19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	<Unanswered>
1	The course was well organized	Strongly Agree
2	The course was an effective learning experience	Strongly Agree
3	The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree

4	The vignettes provided the code in a reproducible and portable format that will make for a good reference in the future	Strongly Agree
5	The course was effectively organized on Xanadu	Strongly Agree
6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree
8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Strongly Agree
9	The course director showed interest in helping students	Strongly Agree
10	The course objectives were met	Strongly Agree
11	I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Strongly Agree
13	I would recommend this course to my peers	Strongly Agree
14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Strongly Agree

15	Comment box: Please provide constructive feedback for the course director	This class was one of my favorites, and I am so glad that I decided to take it. At the beginning of the semester, I was extremely worried that my lack of bioinformatics training would result in my inability to keep up with others in the class. Dr. G rocks! He presented the course material in an easily digestible/followable manner and he made learning what I thought would be "scary" bioinformatics fun! I never felt that I was behind and could easily keep up with each lecture. I am so proud of how far I have come with learning bioinformatics/computational techniques... Thank you so much for an amazing semester and for all of your help, Dr. G!
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	Strengths\n- Material was exceptionally organized and easy to follow\n- Dr. G was extremely patient and helpful with students, like myself, who entered the course with little-to-no bioinformatics experience\nWeaknesses\n- None
17	Comment box: What topics could have been covered in more or less detail?	I would have loved to explore more ways to make figures and learn about how to test data significance, however, I am also satisfied with the level of detail that was covered in class.
18	Comment box: What topics that were not covered should be part of the course?	I would have loved to go more in-depth in R. Perhaps Dr. G might consider making this course two parts where the second part could go into more depth with other computational languages. I would absolutely take a part two with Dr. G if offered!

19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	I enjoyed learning about awk and use it more in my everyday research than R data.table functions. Maybe at the beginning of the semester, Dr. G could survey his group of students to see which they'd prefer or find more useful for their research. Thank you, again, for a great semester Dr. G!
1	The course was well organized	Strongly Agree
2	The course was an effective learning experience	Strongly Agree
3	The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
4	The vignettes provided the code in a reproducible and portable format that will make for a good reference in the future	Strongly Agree
5	The course was effectively organized on Xanadu	Strongly Agree
6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree
8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Strongly Agree
9	The course director showed interest in helping students	Strongly Agree
10	The course objectives were met	Strongly Agree
11	I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Strongly Agree
13	I would recommend this course to my peers	Strongly Agree
14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Neither Agree nor Disagree

15	Comment box: Please provide constructive feedback for the course director	I really liked having the lectures recorded because I had to refer back to them often. It was also nice to have the flexibility to watch them at another time if we had a research/ grad school conflict during class time. This helped me not fall behind.
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	A major strength of this class was having the lecture notes and recordings posted ready to go. I also liked that it was very hands-on and I learned by doing things myself. I liked that I could watch recordings and follow along in the command line after class. I also liked that Dr. Guertin highlighted at what points an analysis could go awry and how to avoid making erroneous conclusions from data. Some of the most helpful things for me were: - seeing visual representations of pipelines - being taught the molecular biology behind the generated data - viewing the structures of different file types - appreciating differences between shell and R - learning how to breakdown code that generates error messages into smaller chunks to pinpoint the problem - being trained to make coherence checks part of a pipeline that should always be done - critically thinking about whether something is biologically meaningful regardless of the statistics (i.e. doing shrinkage on lowly expressed genes during RNAseq analysis) - feeling comfortable asking questions in class
17	Comment box: What topics could have been covered in more or less detail?	I wish the pipeline for Chip seq analysis was a little clearer and more detailed since that was the first time I was encountering the concept of a pipeline for analysis of large quantities of sequences. Specifically, figure 1 in the post-mapping processing lecture was confusing for me. I was also confused about the concept of a tee file.

18	Comment box: What topics that were not covered should be part of the course?	It would be nice to see how heat maps are generated. Those are such common figures to see in papers that it would be nice to understand how they are generated so we can interpret them more critically.\n
19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	I think this would be nice---- the awk code was super clunky for me to use and it was the source of probably 90% of the errors I encountered on the midterm, so I tried to avoid using them later in the class.
1	The course was well organized	Agree
2	The course was an effective learning experience	Strongly Agree
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6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
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9	The course director showed interest in helping students	Strongly Agree
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12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Agree
13	I would recommend this course to my peers	<Unanswered>

14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	<Unanswered>
15	Comment box: Please provide constructive feedback for the course director	<Unanswered>
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	<Unanswered>
17	Comment box: What topics could have been covered in more or less detail?	<Unanswered>
18	Comment box: What topics that were not covered should be part of the course?	<Unanswered>
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6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Strongly Agree
9	The course director showed interest in helping students	Strongly Agree
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14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Strongly Agree
15	Comment box: Please provide constructive feedback for the course director	Dr. Guertin can share the R markdown templates. So, the students can 1) learn how to use R markdown; 2) organize all codes and comments better. My girlfriend did her statistics homework in this way (in another school). \nDr. Guertin can "let it go" maybe after the midterm. He doesn't have to run the code in the class rather can talk about the principles behind the packages and softwares. \n \n
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	Strengths:\n1. Dr. Guertin spends lots of time with students for troubleshooting. This is extremely helpful for people new in the bioinformatics field. \n2. Course material is well-organized. Students can use it in future. \n3. The topic is important for students nowadays. But nobody gives such a lecture. During my undergrad, I took a bioinformatics course. It's too deep for me to learn de brujin graph in the first lesson. This course paves the way for beginners to start doing something. Unless you are super self-motivated in a wet lab, It's hard to find everything covered in this class. \n \nWeakness: \n(Maybe) focus too much on practice.
17	Comment box: What topics could have been covered in more or less detail?	I don't know.

18	Comment box: What topics that were not covered should be part of the course?	ggplot2 (I am biased)\n\nIn my humble opinion, if you can plot something by yourself, you understand the results (how to get and clean the data, transformation, what is x, what is y, etc). Maybe Dr. Guertin can teach how to replicate classic figures from other papers. It's good to know how to use genome browser generating figures.
19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	Already shared my thoughts with Dr. Guertin. \n \nAnd thank you so much for preparing this course and giving lectures.
1	The course was well organized	Agree
2	The course was an effective learning experience	Neither Agree nor Disagree
3	The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
4	The vignettes provided the code in a reproducible and portable format that will make for a good reference in the future	Agree
5	The course was effectively organized on Xanadu	Agree
6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Agree
9	The course director showed interest in helping students	Agree
10	The course objectives were met	Agree
11	I am much more comfortable analyzing genomics data analysis independently	Agree
12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Disagree
13	I would recommend this course to my peers	Agree

14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Agree
15	Comment box: Please provide constructive feedback for the course director	<Unanswered>
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	<Unanswered>
17	Comment box: What topics could have been covered in more or less detail?	<Unanswered>
18	Comment box: What topics that were not covered should be part of the course?	NA
19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	Switch to R functions and just casually mention how to utilize awk in class/for additional HW. R will be more beneficial to learn then awk for the final and independent work.
1	The course was well organized	Strongly Agree
2	The course was an effective learning experience	Strongly Agree
3	The vignettes effectively communicated the rationale for the analyses and promoted learning	Agree
4	The vignettes provided the code in a reproducible and portable format that will make for a good reference in the future	Strongly Agree
5	The course was effectively organized on Xanadu	Strongly Agree
6	The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
7	The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
8	"The homeworks, midterm, and final assignments reflected the course material appropriately"	Strongly Agree
9	The course director showed interest in helping students	Strongly Agree
10	The course objectives were met	Agree

11	I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
12	I learned more in this course than other graduate courses (Neither Agree nor Disagree = comparable; Disagree = less)	Strongly Agree
13	I would recommend this course to my peers	Strongly Agree
14	"If I generated ChIP-seq or RNA-seq data for my thesis, then I would be comfortable identifying motifs and differentially expressed genes independently."	Agree
15	Comment box: Please provide constructive feedback for the course director	<Unanswered>
16	Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	Major strengths: Dr. Guertin made and provided many resources for students to get the most out of class (detailed vignettes with in-class exercises, virtual/in-person attendance options, recorded lectures, time for questions/individual troubleshooting during class exercises, very responsive to email). This course had a steep learning curve, but Dr. Guertin was incredibly accomodating and gave every opportunity to ask questions to understand the material. I thought that the progression of vignettes/ lessons was logical and generally, the amount of time spent on a task seemed well-fit for the difficulty of the task. I also think that the course format (2 hours twice a week with expected outside-of-class time to finish in-class exercises or complete homework assignments) was appropriate. \n\nIn terms of improvement, there were audiovisual issues early in the course that made learning difficult when I couldn't attend in-person, but Dr. Guertin made sure these issues were resolved within the first couple weeks.

17	Comment box: What topics could have been covered in more or less detail?	Would have preferred more discussion of RNA-Seq data analysis than ChIP-Seq. Minor: I still don't really understand the purpose of displaying RNA-Seq data in the UCSC Genome Browser if it's not normalized to the total number of reads. More time could be spent explaining how you should go about combing through the browser to find interesting/helpful fields of view for a given type of data.
18	Comment box: What topics that were not covered should be part of the course?	I think it would be helpful to have a session/part of a session on how to identify which analytical pipelines to use from the thousands of possible options. There was one in-class exercise where you had us read through the manual for a code we didn't know yet, and that real-world troubleshooting experience was helpful (also incredibly frustrating, but I would rather learn to navigate that confusion in a classroom setting than when I actually need to analyze my own data). As another bonus homework assignment, you could have students do another sequencing analysis (like SNP calling or something) from code they source from a publication/github and learn to run themselves (as well as discuss caveats to the script they chose, etc.). Although, that would be a horribly tedious thing to grade/give feedback on, so just a suggestion. Or maybe have those final 2 classes (instead of ATAC-Seq, not sure how many people in class utilize that) be "consultation" times where students can ask questions about how to approach their specific datasets or how to design an experiment. Something very practical/applicable.
19	Comment box: Dr. Guertin is considering replacing all the awk code with data.table functions in R for 2024. Your thoughts on this would be greatly appreciated.	I think it makes sense to have awk code examples to copy/paste when needed (e.g., adding tracklines) but I agree that spending more time with R would be useful.

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Question	Answer
The course was well organized	Strongly Agree
The course was an effective learning experience	Strongly Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
The vignettes provided the code in a reproducible and portable format	Strongly Agree
The course was effectively organized on Xanadu	Strongly Agree
The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Strongly Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	Much more than average
I would recommend this course to my peers	Strongly Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Strongly Agree
Comment box: Please provide constructive feedback for the course director	Thank so much for this wonderful and helpful class. I learn a lot in basic linux, HPC manipulation, ChIP-seq analysis and RNA-seq analysis.
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	Major strengths: \nSuper helpful class for learning basic linux, HPC manipulation, ChIP-seq analysis and RNA-seq analysis. \nSuper friendly environment for conversation and instruction between instructor and students.
Comment box: What topics could have been covered in more or less detail?	NA
Comment box: What topics that were not covered should be part of the course?	NA
The course was well organized	Agree

The course was an effective learning experience	Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Neither Agree nor Disagree
The vignettes provided the code in a reproducible and portable format	Agree
The course was effectively organized on Xanadu	Strongly Agree
The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Agree
I am much more comfortable analyzing genomics data analysis independently	Neither Agree nor Disagree
I learned more in this course than other graduate courses.	about the same
I would recommend this course to my peers	Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Strongly Agree
Comment box: Please provide constructive feedback for the course director	Overall I thought this was great for the first time running the course. Dr. Guertin spent a lot of time troubleshooting with individual students which was great but also a bit of a waste of time
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	The rationale could have been explained more in depth
Comment box: What topics could have been covered in more or less detail?	We could have spent a lot more time on R but I understand we were running out of class time
Comment box: What topics that were not covered should be part of the course?	<Unanswered>
The course was well organized	Agree
The course was an effective learning experience	Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Agree
The vignettes provided the code in a reproducible and portable format	Strongly Agree
The course was effectively organized on Xanadu	Strongly Agree

The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	Much more than average
I would recommend this course to my peers	Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Agree
Comment box: Please provide constructive feedback for the course director	I believe the course is well structured and I learned a lot.
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	I think Dr Guertin did a very good job at explaining the details so that even the people who were unfamiliar with coding could follow. Dr Guertin was very engaging and made sure everyone followed.
Comment box: What topics could have been covered in more or less detail?	I think we could have given more time to RNA seq and perhaps explored single cell RNA seq analysis as well.
Comment box: What topics that were not covered should be part of the course?	Single cell RNA seq
The course was well organized	Agree
The course was an effective learning experience	Strongly Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
The vignettes provided the code in a reproducible and portable format	Strongly Agree
The course was effectively organized on Xanadu	Agree
The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree

The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	about the same
I would recommend this course to my peers	Strongly Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Strongly Agree

Comment box: Please provide constructive feedback for the course director

Overall I thought this was a very valuable course that I feel is just going to improve over the course of time. Sometimes things were difficult to understand when they were pieces of a whole picture, but the homeworks, midterm, and final made it one clear picture that I can go back to and know exactly what was done in the course and how to apply it to real-world data. They have been some of the most useful assignments in my graduate classes thus far. One thing that would have personally helped is a timeline of events that we continually refer back to that would show us what steps in the analysis we need to take and where we are each class. Though the assignments brought all the pieces together, having a roadmap for the analysis would be a continuous way to tie the lectures together visually.

Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see

A major strength was the use of actual data and having each student work on their own separate dataset. This made it feel much more real in terms of the analysis and made me much more invested in the analysis. An improvement I would like to see is a more clear layout of the course. I know as this is the first time running the course it is difficult to judge what we could achieve in the time constraints of a semester, but for future semesters having a more clear layout of the course would be helpful.

Comment box: What topics could have been covered in more or less detail?

I felt the lecture on xanadu could have been covered in less detail. I feel that while working in the server, all the important highlights of the lecture were covered, and by shortening or removing the lecture it could have given more time for other topics that took longer for the class to understand and work through.

Comment box: What topics that were not covered should be part of the course?

Though I feel I have the tools to find out on my own, a small mention of DNA sequence analysis would have been the cherry on top of the class. This could have even been a single vignette that laid out the typical path for DNA seq analysis, especially with DNA sequencing analysis being a much more common and basic type of data all are likely to encounter.

The course was well organized

Strongly Agree

The course was an effective learning experience

Strongly Agree

The vignettes effectively communicated the rationale for the analyses and promoted learning

Strongly Agree

The vignettes provided the code in a reproducible and portable format

Strongly Agree

The course was effectively organized on Xanadu

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The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer

Strongly Agree

The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture

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The homeworks, midterm, and final assignments reflected the course material appropriately

Strongly Agree

The course director showed interest in helping students

Strongly Agree

The course objectives were met

Strongly Agree

I am much more comfortable analyzing genomics data analysis independently

Strongly Agree

I learned more in this course than other graduate courses.

Much more than average

I would recommend this course to my peers

Strongly Agree

If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.

Agree

Comment box: Please provide constructive feedback for the course director

The small size of the class allowed for the instructor to focus on each students strengths and weaknesses and the issues were effectively addressed and resolved by him during my learning process. He was friendly and encouraging which helped along with learning.

Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see

The weakness likely was the differences in the machines used for class, which increased wait time for other students to catch up. The strength was the size of the class, the course structure, the way the course was taught. All the resources like vignettes and recorded lectures provided by the instructor.

Comment box: What topics could have been covered in more or less detail?

I think ALL topics were covered really well, although more info on R programming, would have been helpful, which probably also required more time than the spring semester allowed.

Comment box: What topics that were not covered should be part of the course?

<Unanswered>

The course was well organized

Agree

The course was an effective learning experience

Agree

The vignettes effectively communicated the rationale for the analyses and promoted learning

Strongly Agree

The vignettes provided the code in a reproducible and portable format

Strongly Agree

The course was effectively organized on Xanadu

Strongly Agree

The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer

Strongly Agree

The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture

Agree

The homeworks, midterm, and final assignments reflected the course material appropriately

Strongly Agree

The course director showed interest in helping students

Strongly Agree

The course objectives were met

Neither Agree nor Disagree

I am much more comfortable analyzing genomics data analysis independently

Agree

I learned more in this course than other graduate courses.

Less than average

I would recommend this course to my peers

Neither Agree nor Disagree

If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.

Neither Agree nor Disagree

Comment box: Please provide constructive feedback for the course director

I think that the course director had every intention to help students learn. He was intelligent and approachable. I believe that in the future, he should not be quite so helpful during class time. At the start of the course, many students were getting stuck during class, and it took away so much learning time when he helped them. Either this class needs a TA to do that, or students should not be able to receive 1 on 1 help during a class session. We would have covered so much more had the students who were lost just waited to get help outside of the class. I was always very frustrated by student questions that were personal typing problems. I was able to troubleshoot on my own, and other students should do that too. Helping answer student questions is important, but I think that in this case questions were too disruptive and emphasis should be put on following along with the lecture and catching up after class if you fall behind. \nI want to mention that the midterm took a really long time. I think that this class could use more little homework assignments, and then the midterm would not have had to involve all the steps it had. I spent around 12 hours completing it. The final was a bit quicker.

Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see

Strength: At the end of the course, I am very comfortable using the terminal and I can follow vignettes easily. I really feel like I learned a lot. I was struggling to understand everything at the start, and I have come a long way. \nStrength: The instructor was always helpful and willing to meet with people to help them \nWeakness: We fell behind on content \nWeakness: We did not get to learn R and that was a major reason I took this course \nWeakness: The end of this course was just copy and pasting and I do not believe that I will be able to use that information in future data analysis. I hope that in the future, there is enough time to teach R so that this is not the case

Comment box: What topics could have been covered in more or less detail?

I think one thing that can be cut is awk. We spent a long time learning that and all I ever did was copy and paste it because it was too time consuming to come up with awk lines myself. \nAt the start of the course, we spent too much time going over the basics. Yes it was really hard to learn this, but I eventually got it. I think less class time going over those things, and more easy homeworks would help. Have a homework assignment involving simply moving files from one directory to another. Ensure that when you teach a command, people show up to the next class able to execute it. \nR needed to be taught more. \nI think there needed to be more information about the biology throughout. I am not a computational scientist, so I often got lost in what the commands were doing with the biological information. Sometimes this was included, but it was too late. Try to incorporate this information at each step. For example with ChIP-seq analysis, explain what each command is doing as you show the class. I believe that it is really important that computational scientists also understand exactly what it is that they are doing. \nBy the end, it felt redundant to watch you go through all the vignettes and then just do them again myself. I'm not sure there is a

Comment box: What topics that were not covered should be part of the course?	<Unanswered>
The course was well organized	Strongly Agree
The course was an effective learning experience	Strongly Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
The vignettes provided the code in a reproducible and portable format	Strongly Agree
The course was effectively organized on Xanadu	Strongly Agree
The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Strongly Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	Much more than average
I would recommend this course to my peers	Strongly Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Strongly Agree
Comment box: Please provide constructive feedback for the course director	Dr. Guertin is an excellent teacher. He is patient, kind, and hard-working and always knows how best to help his students.
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	The course was extremely well organized, and it was obvious that Dr. Guertin put a lot of effort into the course. I had always been completely clueless about any kind of programming or genomics data analysis, but this course helped me understand it and become confident in analyzing it.
Comment box: What topics could have been covered in more or less detail?	I know we didn't have time, but I would've loved to have learned more about R!

Comment box: What topics that were not covered should be part of the course?	I can't think of any. Of course, we all want to learn the specific software that applies directly to our projects, but the ones we learned about in this class gave us enough know-how to adapt to using just about any program.
The course was well organized	Agree
The course was an effective learning experience	Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Agree
The vignettes provided the code in a reproducible and portable format	Agree
The course was effectively organized on Xanadu	Agree
The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Agree
The course director showed interest in helping students	Agree
The course objectives were met	Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	More than average
I would recommend this course to my peers	Strongly Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Agree

Comment box: Please provide constructive feedback for the course director

I would keep the course the same way for the beginning portion, since everyone is still learning the basics. Once the basics have been mastered, I might try out switching up the format such that you begin with a brief overview of the learning objectives for that day, but then give the students a problem (like one of the in class exercises) to solve. If there were any special considerations that needed to be known before running a piece of code, those could be explained briefly at the introduction. I would then give the students an hour to work alone or together to try and solve the problem, with you acting as a facilitator leading students in the right direction if they were stuck, but not giving direct answers. After students had an hour to work, I would then use the second hour to go through the code together as a group, with you leading and asking for student ideas and filling any gaps missed by the group. \nThis style may end up being a big disaster, but it's worth a shot. I think it would increase course engagement and help students to shift away from a "copy and paste" mindset.

Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see

Although they were hard, I liked the assignments. They were a good way to test if you knew what to do and to practice. \n \nThe main weakness in my opinion was that the class wasn't as engaging as it could have be been.

Comment box: What topics could have been covered in more or less detail?

I thought the course was balanced.

Comment box: What topics that were not covered should be part of the course?

I think what was covered was appropriate.

The course was well organized

Neither Agree nor Disagree

The course was an effective learning experience

Agree

The vignettes effectively communicated the rationale for the analyses and promoted learning

Neither Agree nor Disagree

The vignettes provided the code in a reproducible and portable format

Neither Agree nor Disagree

The course was effectively organized on Xanadu

Agree

The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Agree
The course director showed interest in helping students	Agree
The course objectives were met	Agree
I am much more comfortable analyzing genomics data analysis independently	Neither Agree nor Disagree
I learned more in this course than other graduate courses.	about the same
I would recommend this course to my peers	Neither Agree nor Disagree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Agree
Comment box: Please provide constructive feedback for the course director	I believe that the instruction should have been supplemented by a whiteboard. And each class lecture should have an objective outlined. The nature of problems, and why they are important should be outlined.
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	Strength was the breadth of topics. \nWeakness was the focus on code snippets and running them, instead of the nature of the problem, a computer is needed to solve.
Comment box: What topics could have been covered in more or less detail?	<Unanswered>
Comment box: What topics that were not covered should be part of the course?	<Unanswered>
The course was well organized	Strongly Agree
The course was an effective learning experience	Strongly Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Agree
The vignettes provided the code in a reproducible and portable format	Strongly Agree
The course was effectively organized on Xanadu	Strongly Agree
The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree

The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Strongly Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Strongly Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	Much more than average
I would recommend this course to my peers	Strongly Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Strongly Agree
Comment box: Please provide constructive feedback for the course director	The course was overall excellent, but I think I would have liked to have the biological background for transcription factors lecture earlier in the course, maybe right before we got into ChIP-seq, since my background in studying transcription factors is quite sparse and it would have given me more context for what we were looking at in the analyses.
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	No other comments.
Comment box: What topics could have been covered in more or less detail?	I would have liked a basic overview of how the alignment and gene ranking algorithms worked, but I also understand that this might be more detail than necessary for a class focused on the use of these tools.
Comment box: What topics that were not covered should be part of the course?	No other comments.
The course was well organized	Strongly Agree
The course was an effective learning experience	Strongly Agree
The vignettes effectively communicated the rationale for the analyses and promoted learning	Strongly Agree
The vignettes provided the code in a reproducible and portable format	Strongly Agree
The course was effectively organized on Xanadu	Strongly Agree

The course director worked with each individual to troubleshoot software and server connectivity issues on their personal computer	Strongly Agree
The lectures effectively outlined the analyses and I could reasonably follow the code execution during the lecture	Agree
The homeworks, midterm, and final assignments reflected the course material appropriately	Strongly Agree
The course director showed interest in helping students	Strongly Agree
The course objectives were met	Agree
I am much more comfortable analyzing genomics data analysis independently	Strongly Agree
I learned more in this course than other graduate courses.	Much more than average
I would recommend this course to my peers	Strongly Agree
If I were to generate ChIP-seq or RNA-seq data for my thesis, then I would be able to independently identify motifs in ChIP and differentially expressed genes in RNA-seq.	Agree
Comment box: Please provide constructive feedback for the course director	The instructor offered unparalleled support accompanied by sincere interest in and enthusiasm for students' successful learning--a rare and valuable combination that the institution certainly could use more of!
Comment box: Please comment on the major strengths and weaknesses of the course and what improvements you might like to see	The organization and detail of vignettes is a major strength of the course. The in-class exercises accompanied by real-time instructor support with troubleshooting are invaluable for practice.
Comment box: What topics could have been covered in more or less detail?	It may be beneficial to dedicate a lecture or two to R syntax to enable better understanding of some of the RNA-seq analysis.
Comment box: What topics that were not covered should be part of the course?	I think that the topics covered were adjusted well to suit an entry-level course. A course targeted at low-intermediate skill level might do well to cover ATAC-seq as well, as was originally intended for this course.

My teaching material prior to coming to UConn Health

Excellence in Teaching Nomination Form

Name of nominee: Dr. Michael Guertin

Department: Biochemistry and Molecular Genetics

Name of primary Nominator: Arun Brendan Dutta

Primary nominator's phone number: 434-962-2369

Primary nominator's e-mail address: ABD3X@hscmail.mcc.virginia.edu

Type of student: MD/PhD student

References (name/phone/e-mail):

1. Anna Cetnarowska

Master student, Fulbright scholar, BioLAB program

434-227-3632

ac6hj@virginia.edu

2. Piotr Przanowski

Research Associate

434-227-0307

pp9z@virginia.edu

3. Roza Kamila Przanowska

Biomedical Sciences (BIMS) PhD candidate

434-227-0307

rkw4f@virginia.edu

Dear Committee for the Dean's Excellence in Teaching Award,

It is my pleasure to write this letter nominating Dr. Michael Guertin's for the Dean's Excellence in Teaching Award. I began my graduate training in the Guertin lab in April 2018. Thanks to Dr. Guertin's guidance I have vastly expanded my scientific skill set, improved my technical writing, and refined my approach to biological problems. He distinguishes himself with his availability and willingness to entertain ideas for new experiments and projects. Dr. Guertin is an incredibly patient and knowledgeable teacher and I appreciate his mentorship every day.

Dr. Guertin extensive experience with both experimental and computational approaches to molecular biology makes him a versatile teacher. The first stage of my project required me to perform a variety of experimental assays. Dr. Guertin consistently provided valuable insight and suggestions as I optimized these assays. In one case, he joined me at the bench as I carried out my first ATAC-seq experiment. As my project progressed I spent more time at the computer analyzing data generated by our group and others. I had virtually no bioinformatics experience before starting my graduate work. Under Dr. Guertin's tutelage I am now comfortable working with a variety of genomics data types. My current project is entirely computational, something that would have seemed unfathomable just two years ago. Most advisors would only be able to help with either the data generation or the computational analysis. Dr. Guertin is the rare teacher who can assist with both.

Dr. Guertin's mentoring style produces confident and independent trainees. Soon after joining the lab Dr. Guertin encouraged me to apply for an immersive three week course at Cold Spring Harbor Laboratories on Chromatin, Transcription, and Gene Expression. He personally wrote to the organizers of the course and recommended they accept my application despite being a new graduate student. His confidence in me convinced the organizers and I benefited enormously from attending the course. I appreciated this early show of support and have seen it reflected in his actions on behalf of other trainees. Thanks to his sustained confidence in my scientific abilities, I feel comfortable proposing new analyses and projects to Dr. Guertin. He is always willing to engage in long discussions on the pros and cons of theoretical experiments. I am a much more confident scientist thanks to Dr. Guertin's support.

While Dr. Guertin encourages my growth as an independent scientist, he provides a high level of guidance when needed. He demonstrates a willingness to fully engage with the challenges faced by his trainees. His office door is almost always open. For example, I submitted my first fellowship application last year. This was the greatest technical writing challenge I had faced in my career so far. Dr. Guertin and I sat in his office for almost twelve hours on a Sunday going through every word of my six page research strategy. Dr. Guertin takes the same approach with his teaching engagements. He invests significant time in responding to students' individual queries and tailors his responses to match their specific research problems. Most of my peers do not enjoy this level of involvement and attention from their mentors and teachers.

I believe Dr. Guertin is an exceptional teacher and research mentor. He is committed to enriching the scientific community by training and encouraging the next generation of researchers. The trainees he interacts with in his lab, in the department, in classes, and on committees all benefit from his commitment to teaching and passion for science. He is an excellent candidate for this award.

Sincerely,

Arun Brendan Dutta
MD/PhD Student, University of Virginia School of Medicine

June 27, 2020

Dear Dean's Excellence in Teaching Award Committee Members,

It is my pleasure to nominate Dr. Michael (Mike) Guertin, an Assistant Professor in the Department of Biochemistry and Molecular Genetics (BMG) and Center for Public Health Genomics, for the Dean's Excellence in Teaching Award. Mike's research is focused on characterizing the role that transcription factors play in regulating gene expression in normal cells as well as how these factors are dysregulated in diseases including cancer. He uses functional genomics approaches extensively to address relevant research questions. Importantly, this includes both generating and analyzing functional genomics data.

First and foremost, Mike is an extremely passionate and earnest person/investigator. With regard to his moral convictions, research interests, etc., he gives it his all! This includes mentoring people in his lab. I have had conversations with Mike over lunch and in the hallway, and I know he is very passionate about mentoring his students rigorously and ensuring that they have everything in order to succeed. I believe his students' letters will clearly demonstrate this.

Second, Mike approached me in the middle of Fall of 2019 to see if I would start teaching my Spring Bioinformatics Module BIOC 8145, Bioinformatics and Functional Analysis of Genomes. I told him that I would on the condition that we could team teach it. I was able to get four other (along with Mike) instructors to teach the class. Because the shutdown of labs at UVA in response to the COVID-19 pandemic coincided with the start of the Spring II module, and many graduate students, postdocs and even faculty want/need to learn these analysis approaches; enrollment for our module shot up to 30 along with 40 auditing the course. I gave all the instructors the goal of arriving at teaching material that was a mix of theoretical lectures and practical hands-on assignments and in-class demonstrations. I started the course off covering use of the UNIX operating system and programming in R. Mike was among the few co-instructors who attended every one of my lectures to get a feeling for the approach that I was taking in teaching the course. He did a great job executing his portion of the course, which was to teach RNA-seq analysis. He in particular highlighted rigor and reproducibility, which he is passionate about. He generated a 34-page vignette for students to follow as well as all the scripts/programs to execute the analysis if students were having difficulty at any stage. He also started office hours 30min before the start of each lecture (which subsequent instructors did as well). He also sincerely sought out questions and would address them relatively quickly if any students had them. This is a hands-on course, so this can be rather time-consuming.

For these reasons, it is my pleasure to nominate/recommend Dr. Michael (Mike) Guertin for the Dean's Excellence in Teaching Award.

Sincerely,

Stefan Bekiranov

Stefan Bekiranov, PhD
Associate Professor
Department of Biochemistry and Molecular Genetics

26 June 2020

Dear Evaluation Committee,

It is my pleasure to write this nomination letter of Dr. Michael Guertin for Dean's Excellence in Teaching Award. I am Visiting Graduate Student in BioLab program, supported by Fulbright Commission and Dr. Guertin is my mentor for the past year.

I entered the Guertin lab with a molecular and cellular biology background, but I had driven motivation to learn how to analyze genomic data. Dr. Guertin was supportive in taking steps into computational analysis and getting comfortable with R and shell scripting. During my traineeship as a computational part, I learnt how to analyze Precision run-on sequencing (PRO-seq) and RNA-seq data. In the course of the learning process, Dr. Guertin is always present and provides sources, but he also expects to take ownership of the project, being always eager to discuss and ready to help with obstacles. He allows for big independence in planning and conducting experiments, always giving thoughtful comments and critical feedback. I extremely enjoy this way of teaching and after a year of Dr. Guertin mentoring I gained computational skills as well as practice in molecular biology such as using CRISPR-Cas9 and developing system which allows rapid degradation of protein (ARF-AID system).

Dr. Michael Guertin has a passion for science and exhibits enthusiasm which is infectious and energizing. His expertise of the field is enormous and foremost he can easily share the knowledge and simply explains concepts, what I find crucial in the teaching process. He is very direct and tries to guide students to be the best versions of their scientific selves. Dr. Guertin is student-oriented. Thanks to skills and experiences which I learnt during my traineeship as well as Dr. Guertin dedication, continuous support and help with polishing my public speaking and transparent communication skills I got into my dream PhD program. I will have the opportunity to develop my scientific interests and I will try, in future, to become such a thoughtful mentor as Dr. Guertin.

As a master's as well as an international student I was taking part in several scientific projects, traineeships in Poland and Europe. From all of my experiences, Dr. Guertin stands out as a mentor who is willing to share expertise and truly inspires. I wish every student to meet such a teacher on its scientific way.

Sincerely,

Anna Cetnarowska

June 26th, 2020

Dear Selection Committee for the Dean's Excellence in Teaching Award,

I am writing this letter to strongly and unconditionally support Dr. Michael Guertin's nomination for the Dean's Excellence in Teaching Award. For the last four years I have worked at University of Virginia as a Research Associate and I joined Dr. Guertin's laboratory in November 2019.

During my scientific carrier, I had many great mentors and teachers. I was introduced to science by great teachers at University of Warsaw (Poland). They put a lot of effort both in teaching theoretical knowledge as well as ensuring that students have enough practical skills to be able to work in molecular biology laboratory. Next I started International PhD program, where I worked in three independent teams in Warsaw, Poland (Nencki Institute of Experimental Biology), Berlin, Germany (Max Delbrück Center for Molecular Medicine) and Uppsala, Sweden (Uppsala University). During that time I was familiarized with many different teaching techniques and mentoring styles. I was lucky - most of teachers and mentors that I had was extraordinary in their job. This let me to not only advance my carrier and publish many scientific papers, but also encourage me to be a mentor myself. During my postdoctoral training at UVA I helped to mentor many undergraduate and graduate students (recipients of multiple awards, i.e. The Double Hoo Research Grant and The Harrison Undergraduate Research Award). In 2019 my students nominated me to international "Best Postdoc Mentor Award" where I was the finalist. That being said Dr. Guertin is with certainty the best mentor and teacher that I have ever met. In his work, he is able to combine two very different and distinct skills: uncompromising attitude in pursuit of science excellence and truth, and extraordinary care for wellbeing of his trainees (both in their work and in personal life). Joining these two so different sides of teaching is a rare skill and Dr. Guertin is the first person I know that is doing it so well.

His teaching and mentoring are not only limited to members of his laboratory. He also teaches many classes at the Department of Biochemistry and Molecular Genetics and School of Medicine levels; BIOC8150, BIOC8145, BIOC8450 to name a few. Even during COVID-19 pandemic he taught an online course on RNA-seq analysis that allowed peoples not trained earlier in bioinformatics (as myself) to understand and perform high-throughput sequencing data analysis. He is also a mentor and thesis committee member for graduate students in our department.

Dr. Guertin is a unique PI, who doesn't stick to only his own research directions, but also supports other people, lab members and trainees' ideas. He clearly knows how to adjust the level of mentoring to each trainee's experience. I am very grateful to Dr. Guertin that he allows me for high independence during last stage of my postdoctoral training, what will make me a better PI and mentor in the future. In summary I think that Dr. Michael Guertin is the best candidate for Dean's Excellence in Teaching Award. I enthusiastically and strongly recommend him.

Sincerely,

Piotr Przanowski
Research Associate
Guertin Lab
Department of Biochemistry and Molecular Genetics
School of Medicine
University of Virginia

June 26th, 2020

Dear Selection Committee for the Dean's Excellence in Teaching Award,

It is a pleasure to write this letter in full support of Dr. Michael Guertin nomination for the Dean's Excellence in Teaching Award. I have no doubts that Dr. Guertin is one of the three best mentors and teachers which I meet in biomedical sciences during last 10 years in Poland, Germany and USA.

I began my PhD work at the University of Virginia in July of 2016 and I rotated in Dr. Michael Guertin group for six weeks. My goal for rotation was to analyze the RNA-seq data which I have previously obtained during my Fulbright scholarship in Dr. Anindya Dutta's laboratory. The main difficulty in achieving this goal was the fact I had zero experience with bioinformatics analyses. For whole my training during B.Sc. and M.Sc. studies I worked only in wet-lab and had zero knowledge about programs and languages used for data analysis. When I told Dr. Guertin I know nothing, but I would like to learn at least how to analyze my own data, he was more than happy to help. He guided me step-by-step, created useful vignettes, checked all my progress and helped with any problems which I encountered. His teaching skills and high fluency in translating the bioinformatics specialized language into easy to understand information was extremely impressive. After only 6 weeks long rotation I finished not only with analyzed RNA-seq data, but also completed the first step in developing independence in analyzing high throughput sequencing data. Recently, I also took an additional class (BIOC 8145) during which I learned how to analyze different functional genomics data sets. Dr. Guertin was one of the course director. This was very special class for me and all the students – because of COVID19 global pandemic it was led through Zoom. I am grateful we have such amazing and devoted teachers, who support our learning process independent of the conditions.

During my rotation in Dr. Guertin laboratory I learned also about different projects researched by his group. I was involved in their group lab meeting during which I had opportunity to polish my presentation and discussion skills. As a foreigner student my English is far from perfect (and believe me, it was much worse 4 years ago). Dr. Guertin not only encouraged me to take scientific writing class, but also gifted me *The Elements of Style* to refine more nuanced writing skills. To deeply immerse me in the scientific English he shared with me his R01 proposal and most recent publication from his laboratory. Thanks to his teaching and support my writing and oral communication skills improved a lot, allowing me to (successfully) apply for numerous grants and fellowships. Dr. Guertin provides letters of support for all my applications and always is eager to review my scientific proposals.

Once all the rotations completed I had to choose my future lab for PhD thesis. I decided to continue my work on noncoding RNAs in skeletal muscle differentiation in Dr. Anindya Dutta's laboratory. At the same time I really wanted to continue my collaboration with Dr. Michael Guertin. I asked him if he would agree to be my secondary mentor and train me specifically on the bioinformatics and computational aspects of my thesis work. He said he will be honored by this. Dr. Guertin is also a member of my thesis committee. We meet at least once a month to discuss my scientific progress and well-being. Dr. Guertin takes care not only about the data, but also (if not even more) about the mental and physical health of his trainees.

Dr. Guertin is an exquisite example of great teacher and scientist - fully devoted to science and always looking for best for his students and postdocs. I am glad I can support his nomination for the Dean's Excellence in Teaching Award, as he is an excellent candidate for this award.

Sincerely,



Roza K Przanowska

BIMS PhD student

Dutta Lab

Department of Biochemistry and Molecular Genetics

School of Medicine

University of Virginia

Q1 - Expectations for this module were clearly communicated at the beginning of the module.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	5%	1
Agree	21%	4
Strongly agree	74%	14
Not applicable	0%	0
Total	100%	19

Q2 - The overall mode of teaching for this module was effective.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	26%	5
Agree	37%	7
Strongly agree	37%	7
Not applicable	0%	0
Total	100%	19

Q3 - This module was well organized.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	11%	2
Agree	32%	6
Strongly agree	58%	11
Not applicable	0%	0
Total	100%	19

Q4 - Topics covered were appropriate for this module.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	5%	1
Agree	16%	3
Strongly agree	79%	15
Not applicable	0%	0
Total	100%	19

Q5 - The amount of time spent on each topic was appropriate.

Answer	%	Count
Strongly disagree	0%	0
Disagree	5%	1
Neutral	5%	1
Agree	58%	11
Strongly agree	32%	6
Not applicable	0%	0
Total	100%	19

Q6 - The amount of work required outside of class was appropriate for each lecture.

Answer	%	Count
Strongly disagree	0%	0
Disagree	5%	1
Neutral	26%	5
Agree	47%	9
Strongly agree	21%	4
Not applicable	0%	0
Total	100%	19

Q7 - The assigned reading was helpful and supplemented the lectures.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	21%	4
Agree	37%	7
Strongly agree	42%	8
Not applicable	0%	0
Total	100%	19

Q8 - Please indicate your overall satisfaction with this module.

Answer	%	Count
Very dissatisfied	0%	0
Dissatisfied	5%	1
Neutral	5%	1
Satisfied	32%	6
Very satisfied	58%	11
Not applicable	0%	0
Total	100%	19

Q9 - Please provide constructive comments regarding the effectiveness of this module overall.

The existence of this class is very much appreciated for any students getting starting at bioinformatics/computational biology research. I could only wish this class happened sooner (when I was in my first year)!

My only major criticism of this course was regarding homeworks for the early lectures. I could see it being really useful for someone without much experience, and I would agree that they are necessary fundamentals for the course. However, multiple 45-minute tutorials on basic functionality of terminal & R was a bit much for me. That being said, I did want to provide positive feedback to all of the lecturers. Everyone was helpful and accessible. Additionally, the vignettes for the course were immensely useful and really easy to follow. I've bookmarked the site and expect to return to them as I am doing some of my own analyses.

This course was way too hard for someone with no programming/general background in these areas, even if it was a guaranteed A

This module was effective as an introduction to functional genomics analysis.

This module is definitely effective, especially for students without a bioinformatics background. But I would expect more background introduction at the beginning of each week.

Issues with storage space on Rivanna were consistent. Would have been useful to have instruction provided for PC/Mac to do assignments on our own machine

This module was great. I went from not knowing how to do any coding at all to being able to work with my own RNA sequencing data, generate graphs on R studio, and troubleshoot alignment issues. I found this to be really rewarding, and now I know enough of the basics so that googling to try to find answers can actually really help. Additionally, the vignettes that were provided by the instructors were incredibly useful and I will save them and use them whenever I will need to analyze that kind of data. I appreciate all the time that went into creating them. Probably one of the best classes I have ever taken at UVA.

I believe that the course would have been more effective if it was longer and more time was given for each section. Two weeks per section would be more appropriate and provide for a better background on the options that are present for each type of analysis. The course was designed for beginners, but with the short course time proper background was hard to come by. More comprehensive "best practices" would have been better than just "follow these steps". However, overall the course was successful in providing some background on how to perform a number of bioinformatics analyses. While this course was initially intended to be taught in a classroom, the virtual classroom made the course material difficult to learn. If possible, in classroom instruction would be ideal.

Q10 - Instructor teaching style was effective.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0%	0	0%	0	26%	5	32%	6	42%	8	0%	0	19

Q11 - Instructor stimulated my interest in the subject.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0%	0	0%	0	5%	1	32%	6	58%	11	5%	1	19

Q12 - Instructor communicated ideas and concepts clearly.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0%	0	0%	0	16%	3	42%	8	42%	8	0%	0	19

Q13 - Instructor was receptive to and answered questions effectively.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0%	0	0%	0	5%	1	37%	7	58%	11	0%	0	19

Q17 - Instructor's assignments were clear and useful

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0%	0	0%	0	32%	6	21%	4	47%	9	0%	0	19

Q14 - Please provide constructive comments regarding the effectiveness of individual instructors:

<u>Michael Guertin</u>
This instructor put together a useful vignette to explain the process and work through an example of an RNAseq analysis. I also liked that he gave us an opportunity to ask questions in the assignment.
Dataset assigned led to storage issues and long runtimes, would probably be easier to use a smaller dataset
Dr. Guertin was great. His vignette was very thorough which I appreciated. He was very helpful with questions and even helped me work through some issues with my own data. This was one of my favorite weeks of the class other than the beginning two weeks.
The UNIX code provided in the assignment was unclear for Windows users and the overall "vibe" was that Windows users were on their own to figure out what they needed to download and what they did not.

Q1 - Expectations for this module were clearly communicated at the beginning of the module.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	0%	0
Agree	25%	4
Strongly agree	75%	12
Not applicable	0%	0
Total	100%	16

Q2 - The overall mode of teaching for this module was effective.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	0%	0
Agree	31%	5
Strongly agree	69%	11
Not applicable	0%	0
Total	100%	16

Q3 - This module was well organized.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	0%	0
Agree	13%	2
Strongly agree	88%	14
Not applicable	0%	0
Total	100%	16

Q4 - Topics covered were appropriate for this module.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	0%	0
Agree	31%	5
Strongly agree	69%	11
Not applicable	0%	0
Total	100%	16

Q5 - The amount of time spent on each topic was appropriate.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	6%	1
Agree	50%	8
Strongly agree	38%	6
Not applicable	6%	1
Total	100%	16

Q6 - The amount of work required outside of class was appropriate for each lecture.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	19%	3
Agree	25%	4
Strongly agree	31%	5
Not applicable	25%	4
Total	100%	16

Q7 - The assigned reading was helpful and supplemented the lectures.

Answer	%	Count
Strongly disagree	0%	0
Disagree	0%	0
Neutral	13%	2
Agree	13%	2
Strongly agree	56%	9
Not applicable	19%	3
Total	100%	16

Q8 - Please indicate your overall satisfaction with this module.

Answer	%	Count
Very dissatisfied	0%	0
Dissatisfied	0%	0
Neutral	0%	0
Satisfied	31%	5
Very satisfied	69%	11
Not applicable	0%	0
Total	100%	16

Q9 - Please provide constructive comments regarding the effectiveness of this module overall.

I would love to hear less about technical protocols, more on-hands pipeline usage. Really liked the proportions in Dr. Guertin classes. The statistic class could be longer - it was really interesting and useful! It is also nice to get slides before the class (some of them were only available through website). Overall, it was really amazing class.

The GitHub site was incredibly organized and made it easy to find relevant information

Great workshop, and Stephan made a terrific effort recruiting scientists with the relevant expertise for teaching the relevant material

I am a beginner in the field and started learning from this workshop. Week1 and 2 lectures were very clear to me. From Week3 coding wise it got a bit heavier. I think if instructors could spent some more time on basic coding (UNIX) before going into advanced coding analyses, it would be more productive.

Great course! This course adapted well to an online format and made effective use of the time allotted. I appreciated being exposed to a wide variety of data types to analyze. The only shortcoming I found is that the modules could have gone into more depth about the analysis techniques. However, this could only really be done if the course was longer.

Q10 - Instructor teaching style was effective.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Did not attend class		Total
Michael Guertin	0%	0	0%	0	0%	0	27%	4	53%	8	20%	3	15

Q11 - Instructor stimulated my interest in the subject.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Did not attend class		Total
Michael Guertin	0%	0	0%	0	6%	1	31%	5	44%	7	19%	3	16

Q12 - Instructor communicated ideas and concepts clearly.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Did not attend class		Total
Michael Guertin	0%	0	0%	0	6%	1	25%	4	50%	8	19%	3	16

Q13 - Instructor was receptive to and answered questions effectively.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Did not attend class		Total
Michael Guertin	0%	0	7%	1	0%	0	27%	4	47%	7	20%	3	15

Q17 - Instructor's assignments were clear and useful

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Did not attend class		Total
Michael Guertin	0%	0	0%	0	7%	1	27%	4	47%	7	20%	3	15

Q14 - Please provide constructive comments regarding the effectiveness of individual instructors:

<u>Michael Guertin</u>
It was the best class! Just perfect. Thank you! Maybe it's worth to add some intro for Windows user as well.
Very effective

F19: CELL 8450 - Effective Science Writing for Grants and Fellowships

February 5th 2020, 11:16 am MST

Q1 - Expectations for this module were clearly communicated at the beginning of the module.

#	Answer	%	Count
1	Strongly disagree	0.00%	0
2	Disagree	10.53%	2
3	Neutral	5.26%	1
4	Agree	36.84%	7
5	Strongly agree	47.37%	9
6	Not applicable	0.00%	0
	Total	100%	19

Q2 - The overall mode of teaching for this module was effective.

#	Answer	%	Count
4	Strongly disagree	0.00%	0
5	Disagree	0.00%	0
6	Neutral	5.26%	1
7	Agree	68.42%	13
8	Strongly agree	26.32%	5
9	Not applicable	0.00%	0
	Total	100%	19

Q3 - This module was well organized.

#	Answer	%	Count
10	Strongly disagree	0.00%	0
11	Disagree	10.53%	2
12	Neutral	10.53%	2
13	Agree	52.63%	10
14	Strongly agree	26.32%	5
15	Not applicable	0.00%	0
	Total	100%	19

Q4 - Topics covered were appropriate for this module.

#	Answer	%	Count
4	Strongly disagree	0.00%	0
5	Disagree	0.00%	0
6	Neutral	0.00%	0
7	Agree	36.84%	7
8	Strongly agree	57.89%	11
9	Not applicable	5.26%	1
	Total	100%	19

Q5 - The amount of time spent on each topic was appropriate.

#	Answer	%	Count
4	Strongly disagree	0.00%	0
5	Disagree	5.26%	1
6	Neutral	15.79%	3
7	Agree	36.84%	7
8	Strongly agree	42.11%	8
9	Not applicable	0.00%	0
	Total	100%	19

Q6 - The amount of work required outside of class was appropriate for each lecture.

#	Answer	%	Count
10	Strongly disagree	0.00%	0
11	Disagree	0.00%	0
12	Neutral	5.26%	1
13	Agree	63.16%	12
14	Strongly agree	31.58%	6
15	Not applicable	0.00%	0
	Total	100%	19

Q7 - The assigned reading was helpful and supplemented the lectures.

#	Answer	%	Count
4	Strongly disagree	0.00%	0
5	Disagree	0.00%	0
6	Neutral	15.79%	3
7	Agree	15.79%	3
8	Strongly agree	5.26%	1
9	Not applicable	63.16%	12
	Total	100%	19

Q8 - Please indicate your overall satisfaction with this module.

#	Answer	%	Count
301	Very dissatisfied	0.00%	0
302	Dissatisfied	0.00%	0
303	Neutral	0.00%	0
304	Satisfied	66.67%	12
305	Very satisfied	33.33%	6
306	Not applicable	0.00%	0
	Total	100%	18

Q9 - Please provide constructive comments regarding the effectiveness of this module overall.

Please provide constructive comments regarding the effectiveness of this module overall.

I really think just making the syllabus/schedule more clear would make things run smoothly.

Especially near the end, group feedback seemed lacking. I am not sure if there is a way to make sure people are really reading and thinking about each group member's assignments critically, but that was the one thing I found frustrating.

The fast turn around and transition times from week 2 of one module to week 1 of the next made it difficult to complete all suggested edits from week 2. Adding in a week or two throughout to catch up on these comments would be useful to strengthen all proposals. Also, it may be worth considering doing mock study sections without the original grant authors present for the review. I feel like this would encourage more discussion within the study section.

Going over the logistics (ie how many times to edit/comment peer's grants, how we are graded) on the first day would be very helpful. Great course!

More organization and effective communication is needed. Students often confused what the actual assignment was

Overall I found the class to be very helpful in improving my scientific writing. Deadlines for edits on the weeks that there were no class were not very well defined, however, and led to group members submitting at random times. Because of this it was hard to get secondary edits submitted. Moreover, it was not clear from the beginning that secondary edits were necessary for every assignment. Lastly, the weeks leading up to the mock study section felt a little haphazard and rushed and the expectations for our reviews, particularly our secondary reviews, were unclear.

It was very difficult to get feedback on an engineering centered project with no other engineers in my peer group. By the end of the semester, my peer group had stopped giving me helpful feedback. However, the faculty reviewer for my group was still very helpful despite not being in my field. I think it would be beneficial to put any engineering students in a single peer group.

Overall I really enjoyed this class. My only suggestion is to make the class a bit longer to allow for more time to work on each section of the grant since the Saturday at 5pm deadlines were challenging to make.

I found this module helpful for communicating complex immunological concepts to scientists outside the field of immunology. I appreciated working in groups and receiving regular feedback from both my peers and my group's mentor.

I thought this class was very helpful for me to better understand my project and to think critically about how I write about it. I do think the deadlines of Saturday/Sunday night for written assignments and Monday/Tuesday afternoon at 12:00 pm for peer edits (depending on the section) felt monotonous at times, especially the Saturday evening deadline. It would have helped for assignments to be due on Sunday/Monday at 5:00 pm and the peer edits due by 9:00 am the day of class just to give more time to write, especially during weekend travels. Most students I talked to, myself included, didn't even look at the peer edits until the classes in which we discussed them because we knew we were going to go through them with one another anyway. Overall though, I am glad that I took this course and definitely think it strengthened my scientific writing.

Q10 - Instructor teaching style was effective.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0.00%	0	0.00%	0	0.00%	0	27.78%	5	5.56%	1	66.67%	12	18

Q11 - Instructor stimulated my interest in the subject.

#	Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
	Michael Guertin	0.00%	0	0.00%	0	11.11%	2	16.67%	3	5.56%	1	66.67%	12	18

Q12 - Instructor communicated ideas and concepts clearly.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0.00%	0	0.00%	0	0.00%	0	11.11%	2	11.11%	2	77.78%	14	18

Q13 - Instructor was receptive to and answered questions effectively.

Question	Strongly disagree		Disagree		Neutral		Agree		Strongly agree		Not applicable		Total
Michael Guertin	0.00%	0	0.00%	0	0.00%	0	16.67%	3	11.11%	2	72.22%	13	18