Course analysis

Course title: Applied Gene Technology and Large Scale Data Analysis	
Course code: CB2040	**Points: 7,5hp**
Course is part of program: Master's program in molecular techniques in life science	
Semester: 3	**Period: 1**
Course responsible: Patrik Ståhl	**Examiner: Patrik Ståhl**
Number of registered students: 29	**Number of passed students to date: 28**
Reply frequency to course evaluation (%): 90%	

1. Introduction and description of applied changes before this course offering

Background

The course is running its fourth year as a free-standing course in the SciLifeLab master's program in Molecular Techniques in Life Science. Patrik Ståhl is the course responsible and examiner for CB2040.

The course is composed of three main parts: the main theoretical lectures, the project work and the bioinformatics part with its own lectures and labs. This year the course has also incorporated an ethics in gene technology workshop.

For this year's course offering we set out to maintain some of the positive effects that we reached from updating the pedagogics in the bioinformatics part of the course, specifically we wanted to make sure that all students, regardless of background experience, were able to follow the course and execute the bioinformatics labs.

Course analysis 2022

The course was run in 2022 for 29 students. The course evaluation form was distributed in paper, and was answered anonymously. This year the course evaluation form was slightly updated.

Below is a summary of the course evaluation given to the students, showing their scores to the different statements, as their general comments about the course at the end. For the first two parts of the course "main lectures and project work" the "My comments" paragraphs are written by the teacher of this part of the course, Patrik Ståhl, and for the third part of the course "bioinformatics" the "Our comments" paragraphs are written by the teachers of the part of the course, Stefania Giacomello and Olof Emanuelsson, together with the course responsible, Patrik Ståhl.

At the end there is also a section titled "Final comments and conclusions, and further plans" where we summarize our analysis and reflect on the course development for future course offerings. These comments constitute our course analysis.

2. Summary of the students' course evaluations

Course Evaluation CB2040 (HT-22)

Evaluate different aspects of the course by using grade-scale 1-5, where 1 is the lowest and 5 is the highest.

My comments: We have received 26 completely filled in evaluation forms out of 29 students who attended the first exam where the forms were distributed. This is a response rate of 90%.

Presented below are the scores of the students to the different statements, at the end we have also collected the students' written general comments about the course.

Average score Q1-Q22: 4,6

Main lectures and project work (bioinformatics part follows on next page)

Average score Q1-Q13: 4,7

1. The course was interesting and I worked with interesting subjects
1 2 3 4 4 5 22 Avg = 4,9

2. The course was challenging in a stimulating way
1 2 3 3 4 11 5 12 Avg = 4,4

My comments to 1. and 2.: The students score on average 4,9 that they found the course interesting, and 4,4 that they found the course stimulating. I'm happy to see that the students liked the subjects and felt stimulated!

3. I explored parts of the subject on my own
1 2 1 3 6 4 4 5 15 Avg = 4,3

My comments to 3.: The students score on average 4,3 that they explored the subject on their own. The course is focused on teaching key concepts and technologies from the field of gene technology to the students over a limited time period, this impacts the time for the students to explore on their own. The students were however allowed to wish which project, and focused subject, they would work in. This year the project groups were also allowed to freely choose one additional article to study and present.

4. The atmosphere in the course was open and inclusive
1 2 3 4 5 26 Avg = 5,0

My comment to 4: Before the course I made a decision to try hard and make everyone feel like they were participating, creating a welcoming atmosphere that would open up for questions and a sentiment of inclusion. I also explicitly set up rules together with the students during the first lecture to how we will behave and respect each other in the class room. I'm happy to see that all the replying students' share my sentiment of an inclusive atmosphere. Mean score 5,0.

5. I understood what the teacher was talking about
1 2 3 1 4 7 5 18 Avg = 4,7

6. What do you think about the teacher's pedagogic and scientific competence?
1 2 3 4 3 5 23 Avg = 4,9 Comments: "10 ! !"

7. I could learn from concrete examples that I was able to relate to
1 2 3 2 4 9 5 15 Avg = 4,5

8. Understanding of key concepts was given high priority
1 2 3 4 2 5 24 Avg = 4,9

9. The course activities helped me to learn efficiently
1 2 3 1 4 12 5 13 Avg = 4,5

10. I understood what I was expected to learn
1 2 1 3 4 4 5 21 Avg = 4,7

11. The teacher spent time to listen to my questions, answer them properly and comment my work
1 2 3 4 2 5 24 Avg = 4,9

12. The project activity helped me to learn more effectively
1 2 3 1 4 8 5 17 Avg = 4,6

My comments to 5, 6, 7, 8, 9, 10, 11, 12: Mean scores 4,7; 4,9; 4,5; 4,9; 4,5; 4,7; 4,9; 4,6. I'm very happy to see the students' high remarks regarding the pedagogics of this part of the course. I have strived to be very clear in my explaining of theoretical concepts, while listening to the students' questions and remarks and trying to adapt to create a flexible learning environment. I have also tried to be clear on the requirements on students' regarding what they should learn.

13. My background knowledge was sufficient to follow the course
1 2 3 4 4 5 5 17 Avg = 4,5

My comments to 14: Mean score 4,5. The SciLifeLab master's program attracts students with varying backgrounds where some are likely to have been more exposed to the subjects of the course in their previous studies than others. Yet the main lectures and project work part of the course is built so that the main lectures cover the essential topics, but with added depth compared to less advanced level courses, adding skills even for students with background knowledge in the subject area. And the project work covers state of the art technologies which most students in the master's program do not have any previous detailed knowledge about. In this way the course tries to allow for varying backgrounds without losing momentum and allowing for advanced level learning.

Bioinformatics part of the course

Average score Q14-Q22: 4,5

14. I worked with interesting subjects
1 2 3 2 4 4 5 17 Avg = 4,7

Our comments to 14: Mean score 4,7. We are happy to see that the students found the bioinformatics topics to be interesting!

15. The course was challenging in a stimulating way
1 2 3 2 4 8 5 13 Avg = 4,5

Our comments to 15: Mean score 4,5. We perceived that the background knowledge of the student group varied quite a bit. It is important to take measures to counteract this variation as it could otherwise lead to stress. This year we added a possibility for students to run R software through a cloud server. The goal is to adapt to the students' needs.

16. The atmosphere in the course was open and inclusive
1 2 3 1 4 4 5 18 Avg = 4,7

Our comments to 16: Mean score 4,7. This is a great improvement from three years ago (4,3), and consistent with the last two years (4,8). The students perceive the climate as inclusive, however it is important that all students share this sentiment. To further underline the goal of inclusiveness and openness in this course we have clarified throughout the course our core values including an open and equal discussion climate in the course, and our openness to any concerns, questions or comments. To exemplify this we have stated on the first lecture and throughout the course that we are aware of the students' varying bioinformatics backgrounds and are happy to help out.

17. I understood what the teachers were talking about
1 2 3 2 4 12 5 9 Avg = 4,3

Our comments to 17: Mean score 4,3. This is a great improvement from three years ago (3,9), and consistent with the past two years (4,5). It is of utmost importance that the key points in the course are conveyed adequately to the students. Given the varying bioinformatics backgrounds of the student group, for this year and the past two years we adjusted the information content. We need to make sure that all students are able to follow what is conveyed during and outside classes.

18. The teachers (and course assistants) spent time to listen to my questions, answer them properly and comment my work
1 2 3 1 4 7 5 15 Avg = 4,6

Our comments to 18: Mean score 4,6. This perfect score is a great improvement from three years ago (4,3), and consistent with the previous two years (4,8). To improve on the pedagogics and efficiency of communication between teachers and students we have switched to doing the computer labs in a lecture room instead of a computer room, and also on Zoom. Almost all, if not all, students use their own laptops to follow the labs, and the lecture rooms and Zoom has allowed teachers and teaching assistants to use the blackboard or slides to convey pedagogical replies to questions to the whole class instead of answering common questions from the student group to each student individually (as is often the case when in a computer room). Everyone in the teaching staff also discussed how to improve the pedagogics of the bioinformatics part of the course.

19. My background knowledge was sufficient to follow the course
1 2 2 3 3 4 7 5 11 Avg = 4,2

Our comments to 19: Mean score 4,2. This is an improvement from three years ago (3,9), and consistent with the past two years (4,4). Because of the varying background of the students, it is crucial that we adapt the bioinformatics part of the course to meet the varying demands. To do this we have cut some content to free up time to go deeper into key topics. We have also added the possibility of letting the students run R software on cloud servers. In addition, the teachers and laboratory assistants have been aware of the varying backgrounds and have tried to help out as much as needed. Other means of being better prepared for the students' background is to coordinate with earlier courses in the master's program, as well as to make sure key topics are reiterated throughout the course.

20. The teaching approach was effective
1 2 3 2 4 12 5 9 Avg = 4,3

Our comments to 20: Mean score 4,3. To improve on the pedagogics we will use slides in addition to the blackboard. The slides will serve the purpose of background information, as well as a document for the students to refresh their memory throughout the course.

21. Computer labs covered practical examples of the bioinformatics aspects treated during the course
1 2 3 1 4 5 5 17 Avg = 4,7

Our comments to 21: Mean score 4,7. We are happy to see that the students found the labs relevant in relation to the rest of the course. We will make sure that the topics treated stay relevant.

22. Computer lab instructions were clear
1 2 3 4 6 5 17 Avg = 4,7

Our comments to 22: Mean score 4,5. The students find the instructions clear. Some of the instructions were updated for this year and the past two years, as a part of the overall pedagogics overhaul of the bioinformatics part of the course. We are happy to see that this is reflected in the positive feedback from the students.

Please, reflect your thoughts on positive/negative parts of the course. What can be done to improve the quality of the course?

Statements compiled from all evaluation forms (copied as is, including spelling etc.)

My favorite course in this program so far. Learnt a lot from the lectures as well as computer labs and project presentation.

Positive parts: Interesting, cutting edge topics. Negative parts: My background knowledge wasn't sufficient.

Positive part: 1. The teachers are expert in the techniques and provides very good insight into these applications and commercialization. 2. The bioinfo analysis is very very very great. Negative part: We have been studying these sequencing technologies from the 1st day of the master program and still have not done the related experiments but memorizing the theoretical parts (and often forget them after the exam : ( ). I hope the courses can be more coherent and more practicals.

A very very nice course! Enjoy these fancy technologies and the lectures! The only advice is to perhaps place the final exam before the clinical application of biotechnology's exam, which is text-heavy and difficult for recap.

+focus on understanding, no need to learn things by heart, +state-of-the-art, not learning old techniques, -a bit overlap in bioinfo parts about spatial transcriptomics that is covered enough in the course by Patrik, also Olof does not need to talk about sequencing methods, -statistics for R labs and bioinformatics were hard to grasp (eg. PCA, UMAP, transformation, etc) and could have gotten more attention. Overall feeling: very good! I learned a lot!

Honestly , this has been my favorite course at MTLS. I really appreciate the attention given to critical thinking and thorough understanding over memorization. I have learned a lot. The R labs were also very nicely designed and a great resource. Thank you.

Comment to question 20: I found majority of diagrams hard to follow -> personally needed more text learning first. Comment to question 21: very helpful 10/10. More comments: Labs very helpful. I find it hard personally to learn through diagrams the majority of the time.

A bigger project on R at the end, I would like to be able to do one type of analysis from A to Z. More applied part (lab).

The bioinformatics part: the lab material is well structured and clearly explained although sometimes it is a bit hard to follow without R or statistic background. It may be helpful to include some optional pre-lab materials such as some online resources explaining some concepts (eg PCA, transformation, basic R logics) so we can read and learn before coming to lab.

For main lectures: I like the teaching style of drawing diagrams to explain principles. Very helpful for me to remember and understand. A final "roadmap" summarizing and comparing the technologies we learnt so far would be helpful.

Maybe worth to have it as flipped-classroom? With teacher's lectures recorded previously for key concepts Sanger/Illumina/Pacbio… It was hard for me to follow some discussions in class because I need to spend some time visualizing the methods by myself before understanding each dependency. Slides could use more words for later referencing, and the papers the images are taken from (eg SBE, SBE tag…). Otherwise, as report reflect, I was happy with the course.

Comment to question 6: 10 ! !

I really enjoyed the projects. I also liked the ethics portion since it was not mandatory, many people did not prepare. I think the beginning of the course was too slow and could be compacted a bit more (especially since the later parts with the projects were challenging). The R labs were useful, although felt a bit "cut and paste". It could've been interesting to have a question like "pick and interesting part of the data then graph it and make a comment". I felt the analysis related questions did you encourage much critical thinking. Overall I thought Patrik was a great instructor with helpful diagrams and clearly interested in students' success.

Our comments:

The main themes of the general comments for the whole course are:

Pros:
+The students seem to like the course, two student say it's the best course on the master's program so far,
+Several students say they find the teaching very good
+Overall very good, really enjoyed the course
+R labs overall appreciated

Cons:
-Some overlap in the teaching
-Some practical labs would be nice
-Some students found R labs difficult, some students found them easy

3. Reflections on the course execution and results and 4. Suggestions of changes for upcoming course offerings

Please see reflections related to the different questions in the course evaluation above, and our related actions in the summary below.

Final comments and conclusions, and further plans

We are of course very happy that many students express strongly that they like the course.

For this year's and the previous years' course offerings we set out to improve the pedagogics in the bioinformatics part of the course, specifically we wanted to make sure that all students, regardless of background experience, were able to follow the course and execute the bioinformatics labs. Three years ago some students found this part stressful.

Based on the student's comments this year and last year we seem to have achieved a lot of what we set out to do. The average score for the questions on the bioinformatics part of the course was improved from 4,1 three years ago to 4,5 this year. This is a great improvement due to a clearly directed effort involving all teachers and teaching assistants.

Specifically for the bioinformatics part we will continue to work on the pedagogics, and make sure the study material adheres well to the lecture and lab content. This year we implemented a cloud server where the students could access R software without having to do a local installation. This saved a lot of effort compared to previous years.

Generally for the course we will continue to work especially hard on the inclusiveness and openness experience of the students in the course. This is key to having a positive learning experience. The varying background knowledge of the students, primarily in bioinformatics, needs to continuously be paid attention to in order to create a positive learning experience. We will also continue developing the ethics in gene technology part of the course. We will also consider making sustainability questions more explicitly visible throughout the course.