Summary of course evaluation for KEMM25 Structural Biochemistry HT 2020

Course responsible: Derek Logan

Other teachers: Ingemar André, Susanna Horsefield, Salam al-Karadaghi, Kristofer Modig, Esko Oksanen (ESS), Ipsita Banerjee, Niels Meijer (kursassistent), Maria Gourdon (LP3), Oskar Berntsson, Ana Gonzalez (MAX IV), Julian Conrad (SciLifeLab, Stockholm University)

Number of students: 15, of whom 4 were PhD students.

Grades: 1 student U, 6 students G, 8 students VG. Average grade: 69%.

Utvärdering
   I.   **Summary of the course evaluation**
        Total no. of responses: 8 (53%)

        Brief summary of the evaluation: The students who responded were in general very happy with the course. Some of the comments were among the most positive we have received. Suggestions for improvement were very constructive. The students appreciated our accessibility and engagement under unusual circumstances. It could of course that some of the more negative opinions were not expressed by the respondents.

        The students thought that the balance of course elements was good. They particularly appreciated the fact that all lectures were recorded this year. They were also very positive about how we had dealt with the coronavirus situation. The special videos that we made on data collection at the BioMAX beamline and crystallisation at Lund Protein Production Platform were very well appreciated, which is gratifying in view of the length of time it took to make them. Nevertheless the actual site visits to MAX IV and LP3 were missed.

        Only one student commented on the lack of a course book, which demonstrates that the lecture material is in general enough on its own and that it was a correct move to eliminate the course book that we were using.

   II. **Comments of the teaching team**
        We found the students this year to be enthusiastic and easy to maintain a dialogue with. They generally performed well in the exam and in the practical exercises.

III.   Evaluation of changes since the last course
The course was run through Canvas, which went very smoothly and was a vast improvement over LiveatLund.

Our first attempt to introduce cryoEM to the course was only partially successful. The lectures were seen as "too much, too late" as they were pitched at too high a level and came too close to the exam.

Our computer exercises were all run using software installed on the students' own computers. We know that some students found that troubleshooting the software installation took too much time from the exercises and that they had to spend several hours more completing the exercises.

IV.   Suggestions for changes to the next course
Encourage all teachers to make their lecture notes as self-sufficient as possible (in the style of the crystallography lectures) so that the students can use them as study aids without having to seek out a lot of extra material. In general, work on consolidating our lecture styles, so that we e.g. all include summaries of the intended learning outcomes at the beginning or end of the lectures.

Extend the amount of time devoted to cryoEM by at least one lecture. The cryoEM lectures should be reduced in complexity. Make use of new external web sites such as www.cryoem101.org. Include a practical exercise for cryoEM, as requested by several students. However, the form of this exercise still has to be decided and coordinated with local EM resources.

Expansion of the cryoEM module will require shortening or removal of other modules. How this can be achieved will be discussed in the coming months.

Consider an alternative solution to the computer exercises, e.g remote login to one or more Linux computers at Kemicentrum. We considered this for the 2020 course but decided in the end that it would be too impractical. However it may be possible if undertaken sufficiently far in advance. In particular, this requires a higher level of IT support than what we have experienced is available for the computers in the Bioinformatics Dungeon.

2021-03-19, summary made by Derek Logan, course responsible.