

# MOL217 Anvendt bioinformatikk II

## Emnerapport 2014 vår

### Praktisk gjennomføring

Undervisning: Totalt 19 undervisningstimer à 2x45 minutter, som inneholdt både forelesninger og praktisk oppgaveløsning.

Undervisere: Emneansvarlig og professor Nathalie Reuter og universitetsstipendiat Sandhya Tiwari sto for undervisningen.

### Strykprosent og frafall

Kandidater	Totalt
Oppmeldt	6
Møtt	6
Bestått	6
Stryk	0
Strykprosent	0 %
Studiepoengproduksjon	60

### Karakterfordeling

A	B	C	D	E	F	Gjennomsnittskarakter
3	1	1	0	1	0	B

### Studieinformasjon og litteratur

Studieinformasjonen ble lagt ut på Min Side. Læreboka var tilgjengelig på Studia.

## Oppsummering av studentevalueringen

### Deltakelse på spørreundersøkelsen

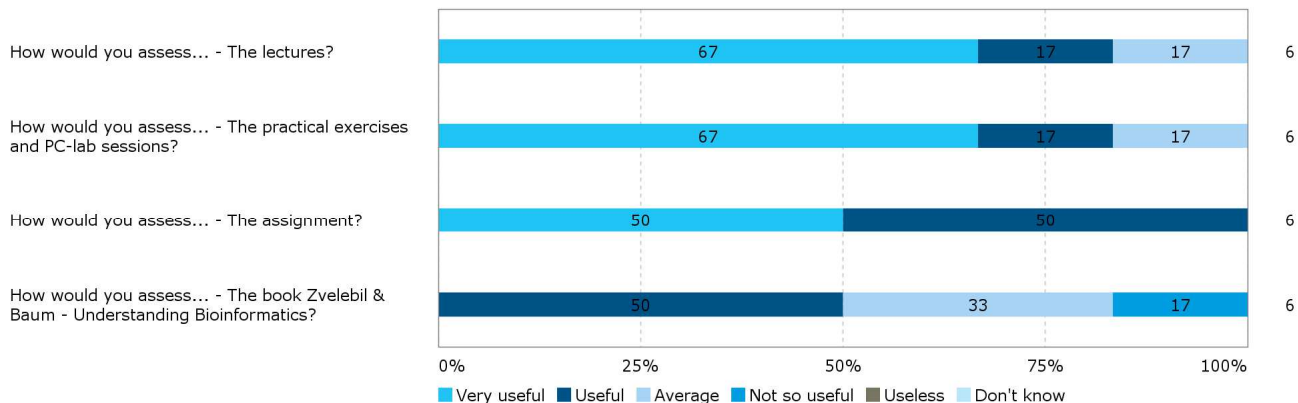
Undersøkelsen ble sendt ut på epost til seks studenter og alle deltok. Blant disse finner vi både bachelorstudenter og masterstudenter i molekylærbiologi, utvekslingsstudenter og stipendiater.

### Arbeidsmengde og forkunnskaper

Majoriteten synes arbeidsmengden er passe, mens noen synes den er litt stor og noen litt liten.

Ingen mente de manglet noen forkunnskaper. Én student mente hun/han burde fulgt bedre med i MOL204 Bioinformatikk.

## Studentenes vurdering av forelesningene, øvelsene og læreboka



### Sammendrag av kommentarer til forelesningene

- Forelesningene var inspirerende og veldig gode. Foreleseren involverte studentene ved å stille dem spørsmål, og dette trekkes frem som svært positivt.
- Timeplanen inneholdt ikke en oversikt over hvilke temaer som skulle undervises når. Dette etterlyses, slik at det er lettere å forberede seg.

### Sammendrag av kommentarer til praktiske øvelser og PC-lab

- Tidvis vanskelig å forstå instruksjonene og spørsmålene i protokollene.
- Temaene var relevante og økte forståelsen, men det kunne med fordel vært satt av mer tid til dette.
- Svært positivt at studentene fikk jobbe med bioinformatiske verktøy nesten hele tiden.
- Få studenter gjør undervisningen kvalitativ.

### Sammendrag av kommentarer til læreboka Zvelebil & Baum

- Ok, men veldig kjedelig bok. For mye informasjon og forklaringsevnen varierte veldig.
- Noen synes den er dårlig og spør om det ikke finnes bøker som fokuserer mer på proteiner og mindre på DNA/RNA.

## Innhold

Spørsmål: "A large part of MOL217 is focused on protein structural bioinformatics. Did you find this protein focus ok, or would you have liked less structural aspects stuff and more on other topics? If so, what "other topics" would you have liked to have more of?"

- No I really like structural bioinformatics, and it was the reason why I choose to take this course.
- I think having the focus on one aspect, proteins, is good as things can get confusing very quickly. Keeping everything related to one subject makes it easier to connect different aspects of the course together.
- This is the way to go. Its very consistent with what is taught in the other classes at MBI. Personally I wished that we had gone further with the homology modelling to get a even better grip on it, but I do not know if there was time.

## **Forventninger og generell vurdering av emnet**

Fem av seks oppgir at emnets mål og innhold i stor grad svarte til deres forventninger.

67 % vurderer emnet som helhet til å være «svært godt», og resten «godt»

## **Andre kommentarer til emnet**

- I would have liked to be less independent when working on my semester assignment. I feel there was in general some under-communication going on where we were largely doing it as a solo thing. Which is of course not entirely a bad thing, since we got to do a lot of cool stuff, but a more explicit specification of how we should relate the topics of the curriculum with the semester assignment would have been welcome. Other than that, I would like to take the time to say that Nathalie and Sandhya in my opinion are some of the best teachers I've encountered in my studies and I think they should both give themselves a pat on the shoulder for a job well done!
- This course was really nice. It was much more applied than I'm used too (I don't come from Bergen university). I also really like it when we have to send you report with our results. It's time consuming for you but it's a nice way to learn and be sure we understand it right. The assignment is a great idea, we have to apply what we learn in a personal project. It was exciting to do it, get the results and try to understand them. It was nice to have a feedback at mid-term in order to be sure we're going in the right direction. The learning outcomes and the important part for the assignment and the exams were clearly express, so there was no big surprise. I'm glad you gave me the possibility to take this course, thank you!
- I've learned a lot which im sure will help me in my further studies :)
- This is one of the top 3 most useful subjects that I have ever taken. Good work.

## **Kommentarer fra emneansvarlig**

It is a real pleasure to read the positive comments from MOL217 students, and also their insightful suggestions that we will take into account for the next editions of MOL217.

We have this year tried to change the teaching "style" in MOL217 to stimulate to even more active learning and increased involvement of the students compared to the previous years. This involved more frequent discussions and questions/answers sessions instead of purely lecturing.

We will definitely try to spend more time on homology modeling next time.

We will make efforts to relate the assignment to the 'pensum' and the PC labs in a better way. This is a challenging task for us as we wish to taylor MOL217 'on-the-fly' so as to adapt to (1) the current students and their background, and (2) the results and progresses on the assignment which by definition are rather unpredictable.

The book from Zvelebil and Baum has its weaknesses and we are aware of these. To our knowledge, there is no other book that covers all of the topics we would like to cover in MOL217 but we shall, in the future, try to use other sources whenever available (as we used the article from Janet Thornton and co-workers about enzyme structure-function relationships).