Study questions for Week 2

These study questions are derived from lecture notes in the course IN4030. The answers are usually found inside the lectures notes. The questions are given to students as a way to learn important concepts in the course. Students can for example quiz each other using these questions before the final exam.

1. What does one mean by "similarity"?
2. What does one mean by "homology"?
3. What does a high degree of similarity imply?
4. What is the "safe zone" in protein sequence alignment? Twilight zone? Midnight zone?
5. What is a scoring matrix?
6. What is a substitution score matrix?
7. What is a gap penalty, and gap function?
8. What are the different penalty functions?
9. What is a concave gap penalty?
10. Why are concave gap penalties biologically meaningful?
11. What is the definition of global alignment?
12. What is the definition of a local alignment?
13. What is the difference between pairwise and multiple alignment?
14. Can 2 blank symbols (gaps) be aligned?
15. What is the definition of optimal global alignment?
16. What is a brute force algorithm?
17. What is dynamic programming?