## 科目：生物資訊概論　　　　　　　　　　共1頁

1. Briefly describe the central dogma of molecular biology (flow of genetic information). (10%)

2. Explain what are primary structure, secondary structure and tertiary structure of proteins. (10%)

3. A, T, G, and C are abbreviations for 4 amino acids. Write their full name and three letter codes, and briefly describe their side chain properties. (10%)

4. There are various bioinformatics databases, such as GenBank, SwissProt, PubMed, OMIM and PDB. Briefly describe the contents of these databases. (10%)

5. Homology between biological sequences is the rationale behind sequence comparison. Explain two types of homologs: orthologs and paralogs. (5%)

6. What is the longest common subsequence (LCS) problem in sequence comparison? Give an example. (10%)

7. List differences between BLAST and dynamic programming. (5%)

8. There are several variants of BLAST, such as blastn, blastp and blastx. Briefly describe their purposes. (10%)

9. A BLAST search yields several hits. Among them, subject A with 95% identity and E-value = 0.1, and subject B with 65% identity and E-value = e-32. Which one is a better hit? Why? (5%)

10. Palindromes are DNA sequences in which the reverse complement is identical to the positive strand, such as GTGCAC. Propose an algorithm to search palindromes in DNA sequences, and estimate the time complexity of your algorithm. (5%)

11. The complete genomes of various organisms are available now. Write key steps in genome sequencing. (5%)

12. What is single nucleotide polymorphism (SNP)? (5%)

13. Microarray made by Affymetrix uses photolithography to synthesize oligonucleotide probes. Briefly describe this process. (5%)

14. Write applications of microarrays. (5%)