

# 元智大學 103 學年度研究所 碩士班 招生試題卷

系(所)別： 生物與醫學資訊 組別： 不分組  
 碩士學位學程

科目： 生物資訊概論

用紙第 1 頁共 2 頁

●不可使用電子計算機

1. Define the central dogma of biology (4%). Describe how eukaryotes and prokaryotes differ in this aspect. (12%)

2. Determine whether the following statements are true or false. (14%) *每小題 2分*

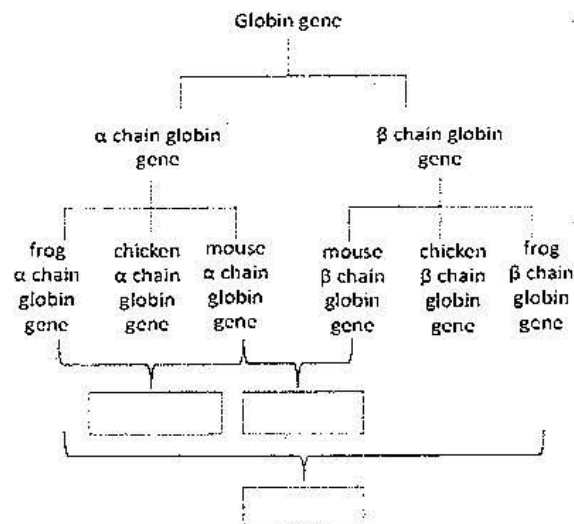
- a) DNA nucleotides consist of adenine, thymine, cytosine, and uracil.
- b) The process of making RNA by using DNA information is called transcription.
- c) The function of a protein can be regulated by chemical modifications.
- d) Transcription factors determine the amino acid sequence.
- e) There are more than one type of RNA molecules.
- f) All proteins are enzymes.
- g) A motif determines a protein's function and can exist independently.

3. Match the type of information with the correct database. (28%) *每小題 2分*

Information		Database	
a) Sequence similarity	h) Disease gene	1. BLAST	7. Ensembl
b) Phylogenetic analysis	i) Single nucleotide polymorphism	2. HapMap	8. GEO
c) Research article	j) protein sequence	3. PubMed	9. OMIM
d) Gene expression	k) microRNA	4. KEGG	10. ChustalW
e) Pathway	l) haplotype	5. dbSNP	11. miRBase
f) Gene ontology	m) protein domain	6. UniProt	12. QuickGO
g) Gene sequence	n) allele frequency		

4. Explain what a phylogenetic analysis is (4%). What kind of information do we need to perform such an analysis? (4%).

5. Given the following phylogenetic tree, identify orthologs, paralogs, and homologs by filling in the empty boxes below for each indicated relationship (3%). Then, provide the definition for each term (6%).



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用紙第 2 頁共 2 頁

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6. Explain what sequence alignment does (5%) and the purpose of doing sequence alignment (5%) in bioinformatics. Then, solve the following problem. Let  $S_1 = \underline{\text{AGGACTAATT}}$  and  $S_2 = \underline{\text{AAGAATA}}$  and let the scores of match, mismatch and gap penalty be 1, -1, and -2, respectively. Please finish the following table used in the dynamic programming algorithm for computing the **local alignment** of  $S_1$  and  $S_2$  (10%), and enumerate the best local alignment between  $S_1$  and  $S_2$  (5%).

Local	$S_1$	A	G	G	A	C	T	A	A	T	T
$S_2$	0										
A											
A											
G											
A											
A											
T											
A											

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