

**Dept. of Computer Science and Engineering, Graduate
National Sun Yat-sen University
Bioinformatics, Final Exam., June 27, 2007, 18:30—20:30**

Part I

- (1) Comparing the similarities and differences between prokaryotic and eukaryotic cells. (10%)
- (2) DNA replication, transcription and translation are essential processes of living cells. Choose one of the processes and describe it. (10%)
- (3) Polymerase chain reaction is a widely used experiment. What is it? What are the components included in the PCR? How to perform it? (15%)

Part II

- (4) The KMP algorithm is one of efficient algorithms for solving the string matching problem. In the algorithm, one should first calculate the prefix function f of the pattern string $P_1P_2\dots P_m$. $f(j)$ of P_j is defined as the largest $k < j$ such that $P_{1,k} = P_{j-k+1,j}$, where $P_{i,j} = P_iP_{i+1}\dots P_j$.
 - (a) Suppose the pattern string is $P=$ “ATCACACATCATCA”. Please give the value of the prefix function on each position. (6%)
 - (b) Suppose the text string is $S=$ “GATCGATCACATCATCACGA” (20 letters). Please illustrate the KMP algorithm for finding P in S by using the prefix function. (9%)
- (5) (a) The degree of each node in an unrooted evolution tree is 3. Suppose that the number of leaf nodes is n . Prove that $NE(n)=2n-3$, where $NE(n)$ denotes the number of edges in the tree.(5%)
 - (b) Suppose that there are n leaf nodes in an unrooted evolution tree. Prove that $TU(n) = (2n - 5)(2n - 7)\dots 1$, where $TU(n)$ represents the number of possible unrooted trees. (5%)
- (6) Explain the primary, secondary, tertiary structures of a protein. Explain the ab initio method and homology modeling for predicting protein structures. (10%)

Part III

- (7) What are the six goals of the human genome projects? (6%)
- (8) In pharmacogenomics, how the polymorphisms of drug metabolizing and receptor genes affect one individual's responses (14%)?
- (9) What are homologous genes? (5%)
- (10) What is a Morkov chain and hidden Morkov model (HMM), please give two examples of applications in bioinformatics. (10%)