

Ankara University
Computer Engineering Department
Special Topics Midterm

Duration: 80mins.

Notes: 1. Write your answers in the blanks below the questions.

2. Questions will be answered by only using the techniques explained in the classes.

QUESTIONS

1. (10 points) Describe the role of DNA in protein synthesis.

DNA acts as the information storage, proteins are manufactured using the information encoded in DNA, and this process is called as central dogma of molecular biology, DNA → RNA using transcription then the information is translated into proteins

2. (10 points) Find the template DNA sequence and the coding strand for the given t-RNA sequence.

t-RNA	A	U	G	C	U	U	A	G	C	U
Template DNA strand	A	T	G	C	T	T	A	G	C	T
Coding DNA strand	T	A	C	G	A	A	T	C	G	A

3. (10 points) Explain codon structure and describe the relationship between codon and amino acids.

amino acid is encoded by a set of three consecutive bases. The three-base sets in RNA are called codons also each 1 amino acid can have more than 1 corresponding codon but each codon has only 1 matching amino acid

4. (10 points) Explain the 4 levels proteins are examined.

1	Primary Structure is the protein sequence, the types and order of the amino acids in the protein chain
2	Secondary Structure is the first level of protein folding, in which parts of the chain fold to form generic structures that are found in all proteins
3	Tertiary Structure is formed by the further folding and packing together of these elements to give the final three-dimensional conformation unique to the protein
4	Quaternary Conformation, the subunit (protein chain) composition and arrangement in such multisubunit proteins

5. (10 points) Describe, compare and contrast homology and similarity concepts.

Similarity is simply a descriptive term telling you that the sequences in question show some degree of match.

Homology, in contrast, has distinct evolutionary and biological implications. In the molecular biological context, it is generally defined as referring specifically to similarity in sequence or structure due to descent from a common ancestor.

6. (10 points) Create the dot-plot for the given sequences.

	G	C	T	A	G	T	C	A	G	A
G	<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>	
A				<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>
T			<input checked="" type="checkbox"/>			<input checked="" type="checkbox"/>				
G	<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>	
G	<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>	
T			<input checked="" type="checkbox"/>			<input checked="" type="checkbox"/>				
C		<input checked="" type="checkbox"/>					<input checked="" type="checkbox"/>			
A				<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>		
C		<input checked="" type="checkbox"/>					<input checked="" type="checkbox"/>			
A				<input checked="" type="checkbox"/>				<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>

7. (10 points) Describe the method used for removing the background noise in dot-plots by elaborating the parameters used in the method.

we use a filtering method which uses a sliding window, which uses 2 parameters window size and minimum identity score (stringency) over the window size to consider this window.

insertion of gaps?

Answer: 1 256 465 alternative alignments

Use the following scoring scheme: match: 3, mismatch: -1 gap penalty: -2

Optimal Global alignment:

G _ _ T G A B C
G B C T _ T A C