

# INF281 Exercise 01 solutions

## 1. Eukaryotic and prokaryotic cells

Cells are the most basic building blocks of all living organisms. Several aspects differ between prokaryotic and eukaryotic cells.

- (a) Which one of the two cell types, prokaryotes or eukaryotes, lacks a distinct nucleus?

**Solution:** Prokaryotes

- (b) Can eukaryotes be unicellular?

**Solution:** Yes

## 2. Cell organelles

A cell consists of a number of specialized subunits called organelles. Answer the most suitable organelle that matches the explanation.

- (a) The key role of this organelle is to produce energy rich molecules for the cell.

**Solution:** Mitochondria

- (b) It is a membrane-enclosed organelle. It contains genetic material called chromosomes.

**Solution:** Nucleus

## 3. DNA

Deoxyribonucleic acid (DNA) is an important molecule that stores genetic information. DNA consists of four different nucleotides - Adenine (A), Cytosine (C), Guanine (G), and Thymine (T).

- (a) What is the DNA sequence when its opposite strand is ACCGT?

**Solution:** TGGCA

## 4. Central dogma of molecular biology

The central dogma of molecular biology describes the flow of genetic information by three processes - Replication, Transcription, and Translation.

- (a) What are the two main molecules involved in transcription?

**Solution:** DNA and RNA

- (b) What are the two main molecules involved in translation?

**Solution:** RNA and protein

## 5. RNA

Ribonucleic acid (RNA) conveys genetic information from its corresponding DNA to ribosome where proteins are synthesized. Similar to DNA, RNA has four different forms - Adenine (A), Cytosine (C), Guanine (G), and Uracil (U).

- (a) What is the transcribed RNA sequence when the corresponding DNA sequence is TATAGC?

**Solution:** UAUAGC

## 6. Genetic code

The genetic code defines how three RNA nucleotides, called codon, should be translated into an amino-acid.

<i>First position</i>	<i>Second position</i>				<i>Third position</i>
	T	C	A	G	
T	F	S	Y	C	T
	F	S	Y	C	C
	L	S	Stop	Stop	A
	L	S	Stop	W	G
C	L	P	H	R	T
	L	P	H	R	C
	L	P	Q	R	A
	L	P	Q	R	G
A	I	T	N	S	T
	I	T	N	S	C
	I	T	K	R	A
	M	T	K	R	G
G	V	A	D	G	T
	V	A	D	G	C
	V	A	E	G	A
	V	A	E	G	G

A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic acid
E	Glu	Glutamic acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

- (a) Stop codons are special codons that terminate the protein synthesis. Specify all three stop codons.

**Solution:** UAA, UGA, UAG

- (b) Both one-letter and three-letter abbreviations are often used instead of the full names. What is the three-letter abbreviation of Tyrosine?

**Solution:** Tyr

- (c) What is the one-letter abbreviation of the amino acid that is synthesized from the codon AGA?

**Solution:** R (Arginine)

## 7. Pairwise alignments

Pairwise alignments are two aligned sequences of DNA, RNA, or protein. DNA and RNA sequences consist of four different nucleotides, whereas protein sequences consist of 20 different amino acids. The “-” sign is used to represent a blank or a gap, which indicates an insertion or a deletion from one sequence to the other.

Use the simple scoring scheme and calculate the score of the following alignments.

### Scoring scheme:

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

$$g = 1$$

#### (a) Alignment 1

q: ATGCT

d: CA--T

**Solution: -1**

#### (b) Alignment 2

q: CAGCT

d: C-A-T

**Solution: 0**

## 8. Table representation

An alignment can be represented as a table with arrows. Vertical and horizontal arrows indicate gaps, while diagonal arrows indicate matches and mismatches.

Identify the alignment that corresponds to the arrows in the following tables.

#### (a) Table 1

q\d		C	A	T	
S					
C					
A					
G					
C					
T					

**Solution:**

q: CAGCT

d: CA--T

(b) Table 2

q\d		C	A	T
S				
C				
A				
G				
C				
T				

**Solution:**

q: -CAGCT-  
d: C----AT

## 9. Brute force approach

A brute force approach can be used to find the optimal alignment. Use the sequences  $q$  and  $d$  below and answer the questions.

Sequences:

q: CG, d: AC

Scoring scheme:

$$R_{ab} = 1 \text{ for } a = b$$

$$R_{ab} = 0 \text{ for } a \neq b$$

$$g = 1$$

(a) Identify all possible alignments.

**Solution:**

1 = 4 CG-- C-G- C--G -CG- -C-G --CG  
--AC -A-C -AC- A--C A-C- AC--

1 = 3 CG- CG- C-G C-G -CG -CG  
A-C -AC AC- -AC A-C AC-

1 = 2 CG  
AC

(b) Identify the optimal alignment with its score.

**Solution:**

CG  
AC Score: 0