

# Unit 7 - Week 5

## Course outline

How does an NPTEL online course work?

Prerequisite Assignment

Week 1

Week 2

Week 3

Week 4

Week 5

● Construction of Non-redundant datasets I

● Non-redundant datasets II

○ Protein secondary structure

● Secondary structure prediction I

● Secondary structure prediction II

● Secondary structure prediction III

○ Quiz : Assignment 5

○ Quiz : Practice Assignment 5

○ Bio-Informatics:Algorithms and Applications : Week 5 Feedback Form

Week 6

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## Assignment 5

The due date for submitting this assignment has passed.  
As per our records you have not submitted this assignment.

**Due on 2020-03-04, 23:59 IST.**

1) Which of the following conditions best represent a set of non-redundant sequences 1 point

- No two sequences have a similarity of less than 90%
- No two sequences have a similarity of greater than 90%
- No two sequences have a similarity of less than 30%
- No two sequences have a similarity of greater than 30%

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
No two sequences have a similarity of greater than 30%

2) Which of the following algorithm is used in CD-HIT? 1 point

- Smith-Waterman
- Wunsch-Needleman
- Greedy incremental
- Multicanonical monte carlo

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
Greedy incremental

3) What is the Hamming distance between the sequences, HLIKLAAILWL and HLWKLAAIWA using amino acid composition 1 point

- 0.1
- 0.2
- 0.3
- 0.4

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
0.4

4) In the command, blastclust -i infile -o outfile -p T -L .7 -b T -S 85, 0.7 stands for 1 point

- Identity of 70%
- Similarity of 70%
- Coverage of 70%
- Identify of 85%

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
Coverage of 70%

5) Protein secondary structures are formed by 1 point

- Hydrogen bonds
- Hydrophobic interactions
- Ion pairs
- van der Waals interactions

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
Hydrogen bonds

6) The  $\phi$  and  $\psi$  torsion angles are rotations along \_\_\_\_ and \_\_\_\_ bonds, respectively. 1 point

- C $\alpha$  - C and N- C $\alpha$
- N- C $\alpha$  and C $\alpha$  - C
- C. N - C $\alpha$  and C- N
- C- C $\alpha$  and C $\alpha$  - N

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
N- C $\alpha$  and C $\alpha$  - C

7) Secondary structure prediction using statistical analysis is proposed by 1 point

- GOR
- Rost and Sandor
- Barton
- Chou-Fasman

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
Chou-Fasman

8) GOR method uses the information on 1 point

- 8 residues on both sides of the central residue
- 4 states of secondary structures
- Window length of 17 residues and 4 states of secondary structures
- Window length of 17 residues and 3 states of secondary structures

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
Window length of 17 residues and 4 states of secondary structures

9) If a protein contains a total of 1800 residues and 810 of them are in helix. Considering the residue Ala, among 300 residues 210 are in helix. What is the information content of Ala in helix? 1 point

- 0.70
- 0.30
- 0.91
- 1.05

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
1.05

10) PHD in secondary structure prediction is based on 1 point

- Neural networks
- Multiple sequence alignment
- Multiple sequence alignment and neural networks
- Consensus

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
Multiple sequence alignment and neural networks