

Unit 5 - Week 3

Course outline

How does an NPTEL online course work?

Prerequisite Assignment

Week 1

Week 2

Week 3

Sequence alignment

Sequence alignment II

Sequence alignment: Online resources

Sequence alignment: Online resources II

Conservation score

Conservation score II

Blast Demo

Quiz : Assignment 3

Quiz : Practice Assignment 3

Bio-Informatics:Algorithms and Applications : Week 3 Feedback Form

Week 4

Week 5

Week 6

Week 7

Week 8

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Week 11

Week 12

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Assignment 3

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

Due on 2020-02-19, 23:59 IST.

1) PAM-1 is appropriate to compare

1 point

- Closely related sequences
- Distantly related sequences
- Both closely and distantly related sequences
- None of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
Closely related sequences

2) In PAM 250 matrix, which of the following mutation is the most acceptable one?

1 point

- Glu to Asp
- Glu to Cys
- Glu to Arg
- Glu to Val

No, the answer is incorrect.
Score: 0

Accepted Answers:
Glu to Asp

3) BLAST is the expansion for

1 point

- Basic local alignment similarity tool
- Binary local alignment search tool
- Basic local alignment sensitive tool
- Basic local alignment search tool

No, the answer is incorrect.
Score: 0

Accepted Answers:
Basic local alignment search tool

4) Which algorithm is used for global alignment

1 point

- Smith Waterman
- Wunsch Needleman
- Smith Needleman
- Smith Wunsch

No, the answer is incorrect.
Score: 0

Accepted Answers:
Wunsch Needleman

5) The score obtained in local alignment is

1 point

- 0
- Positive
- Negative
- Negative and positive

No, the answer is incorrect.
Score: 0

Accepted Answers:
Positive

6) Local alignment is used for identifying

1 point

- Similar sub-sequences
- Overall alignment efficiency
- Number of gaps
- Number of mismatches

No, the answer is incorrect.
Score: 0

Accepted Answers:
Similar sub-sequences

7) The quality and time for database searching depend on

1 point

- Size of the query sequence
- Number of sequences in the database
- Both A and B
- None of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
Both A and B

8) How far human and chicken hemoglobins (b chain) are similar

1 point

- 69%
- 82%
- 95%
- 10%

No, the answer is incorrect.
Score: 0

Accepted Answers:
82%

9) In a multiple sequence alignment, if a particular position is occupied with the same amino acid residue, the conservation score obtained by entropy based measure is

1 point

- 1
- 0
- 1
- 0.5

No, the answer is incorrect.
Score: 0

Accepted Answers:
0

10) Which of the following software is used for calculating the conservation score?

1 point

- Clustal
- MAFFT
- AL2CO
- BLAST

No, the answer is incorrect.
Score: 0

Accepted Answers:
AL2CO