

BIF401-Quiz 1(Complete) Fall 21

Bioinformatics-1

by Muhammad Kashif

03064963933



BIF401 – Bioinformatics I (Quiz 1)

Question # 9 of 10 (Start time: 10:11:35 PM, 25 December 2021)

The Local & Global Alignments uses approaches.

Select the correct option

☐	None of these
☒	Dynamic programming
☐	Static programming
☐	Static & Dynamic programming

Attempted by Muhammad Kashif



BIF401 – Bioinformatics I (Quiz 1)

Question # 8 of 10 (Start time: 10:11:18 PM, 25 December 2021)

What happen when we processed so many progressive alignment in single alignment process?

Select the correct option

☐	None of these
☐	Alignment becomes fast
☐	No effect on process speed
☒	Alignment becomes slow

Attempted by Muhammad Kashif

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BIF401 – Bioinformatics I (Quiz 1)

Question # 6 of 10 (Start time: 10:09:22 PM, 25 December 2021)

..... compares protein sequence against protein databases.

Select the correct option

☒	blastp
☐	tblastx
☐	blastx
☐	blastn

Attempted by Muhammad Kashif

**Question # 5 of 10 (Start time: 10:09:08 PM, 25 December 2021)**

Which one of the following isn't a BLAST variant?

Select the correct option

☐	BLASTP
☐	BLASTX
☐	BLASTN
☒	TBLASTNX

Attempted by Muhammad Kashif



BIF401 - Bioinformatics I (Quiz 1)

Question # 4 of 10 (Start time: 10:08:41 PM, 25 December 2021)

Fasty35 compares sequence to a sequence database.

Select the correct option

☒	DNA, Protein
☐	Protein, Protein
☐	DNA, DNA
☐	Protein, DNA

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BIF401 - Bioinformatics I (Quiz 1)

Question # 3 of 10 (Start time: 10:08:04 PM, 25 December 2021)

Multiple Sequence Alignment (MSA) can extract sequences from aligned sequences.

Select the correct option

☐	Un-known
☐	Un-Aligned
☒	Consensus
☐	Aligned

Click

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**Question # 2 of 10 (Start time: 10:07:35 PM, 25 December 2021)**

tfastx35 compares sequence to a sequence database (6 - ORFs).

Select the correct option

☐	Protein, Protein
☐	DNA, Protein
☐	DNA, DNA
☒	Protein, DNA

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**Question # 1 of 10 (Start time: 10:07:21 PM, 25 December 2021)**

The the e-value, the more significant the hit.

Select the correct option

☒	lower
☐	higher
☐	superior
☐	average

Attempted by Muhammad Kashif

**Question # 10 of 10 (Start time: 10:05:44 PM, 25 December 2021)**

FASTA Algorithm can achieve alignment by using lengths of exact

Select the correct option

☐	Long, Mismatches
☐	Long, Matches
☒	Short, Matches
☐	Short, Mismatches

Attempted by Muhammad Kashif



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Question # 9 of 10 (Start time: 10:05:28 PM, 25 December 2021)

The the e-value, the more significant the hit.

Select the correct option

☐	average
☐	superior
☒	lower
☐	higher

Attempted by Muhammad Kashif



BIF401 – Bioinformatics I (Quiz 1)

Question # 8 of 10 (Start time: 10:05:10 PM, 25 December 2021)

Fastm35 compares to a protein sequence database.

Select the correct option

☐	DNA
☒	ordered peptides
☐	un-ordered peptides
☐	Proteins

Attempted by Muhammad Kashif



tfastx35 compares sequence to a sequence database (

Select the correct option

☐	Protein, Protein
☒	Protein, DNA
☐	DNA, DNA
☐	DNA, Protein

Attempted by Muhammad Kashif



Question # 7 of 10 (Start time: 10:04:33 PM, 25 December 2021)

tfastx35 compares sequence to a sequence database (6 - ORFs).

Select the correct option

☐	Protein, Protein
☒	Protein, DNA
☐	DNA, DNA
☐	DNA, Protein

Attempted by Muhammad Kashif



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BIF401 – Bioinformatics I (Quiz 1)

Question # 6 of 10 (Start time: 10:04:14 PM, 25 December 2021)

Multiple Sequence Alignment (MSA) can extract sequences from aligned sequences.

Select the correct option

☐	Un-known
☒	Consensus
☐	Aligned
☐	Un-Aligned

Cli

Attempted by Muhammad Kashif

**Question # 5 of 10 (Start time: 10:03:48 PM, 25 December 2021)**

The expansion of BLAST is,

Select the correct option

☐	Bioinformatics Logical Alignment Search Tool
☐	Basic Logical Alignment Search Tool
☐	Beginners Local Alignment Search Tool
☒	Basic Local Alignment Search Tool

Attempted by Muhammad Kashif

**Question # 4 of 10 (Start time: 10:03:18 PM, 25 December 2021)**

Fasty35 compares sequence to a sequence database.

Select the correct option

☐	Protein, DNA
☒	DNA, Protein
☐	DNA, DNA
☐	Protein, Protein

Attempted by Muhammad Kashif



..... compares protein sequence against protein databases.

Select the correct option

☐	blastx
☐	tblastx
☐	blastn
☒	blastp

Attempted by Muhammad Kashif



BIF401 - Bioinformatics I (Quiz 1)

Question # 3 of 10 (Start time: 10:02:53 PM, 25 December 2021)

..... compares protein sequence against protein databases.

Select the correct option

☐	blastx
☐	tblastx
☐	blastn
☒	blastp

Attempted by Muhammad Kashif



BIF401 – Bioinformatics I (Quiz 1)

Question # 2 of 10 (Start time: 10:02:39 PM, 25 December 2021)

Which one of the following isn't a BLAST variant?

Select the correct option

☐	BLASTP
☐	BLASTN
☐	BLASTX
☒	TBLASTNX

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BIF401 - Bioinformatics I (Quiz 1)

Question # 1 of 10 (Start time: 10:02:18 PM, 25 December 2021)

What happen when we processed so many progressive alignment in single alignment process?

Select the correct option

- | | |
|----------------------------------|----------------------------|
| ☒ | Alignment becomes slow |
| ☐ | Alignment becomes fast |
| ☐ | No effect on process speed |
| ☐ | None of these |

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BIF401 - Bioinformatics I (Quiz 1)

Question # 10 of 10 (Start time: 09:35:57 PM, 25 December 2021)

FASTA Algorithm can achieve alignment by using lengths of exact

Select the correct option

☒	Short, Matches
☐	Long, Mismatches
☐	Long, Matches
☐	Short, Mismatches

Attempted by Muhammad Kashif



BIF401 – Bioinformatics I (Quiz 1)

Question # 9 of 10 (Start time: 09:35:00 PM, 25 December 2021)

The Local & Global Alignments uses approaches.

Select the correct option

☐	None of these
☐	Static programming
☒	Dynamic programming
☐	Static & Dynamic programming

Attempted by Muhammad Kashif



Question # 8 of 10 (Start time: 09:34:17 PM, 25 December 2021)

The expansion of BLAST is,

Select the correct option

☐	Basic Logical Alignment Search Tool
☒	Basic Local Alignment Search Tool
☐	Bioinformatics Logical Alignment Search Tool
☐	Beginners Local Alignment Search Tool

Attempted by Muhammad Kashif



Question # 7 of 10 (Start time: 09:33:02 PM, 25 December 2021)

What happen when we processed so many progressive alignment in single alignment process?

Select the correct option

☒	Alignment becomes slow
☐	Alignment becomes fast
☐	None of these
☐	No effect on process speed

Click

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**Question # 6 of 10 (Start time: 09:32:35 PM, 25 December 2021)**

Fastm35 compares to a protein sequence database.

Select the correct option

☒	ordered peptides
☐	DNA
☐	Proteins
☐	un-ordered peptides

Attempted by Muhammad Kashif



BIF401 - Bioinformatics I (Quiz 1)

Question # 7 of 10 (Start time: 10:09:37 PM, 25 December 2021)

Which one of the following statements does not apply to BLAST Algorithm?

Select the correct option

☐	Even if no word/base are similar, there is an alignment to be considered
☐	It stands for Basic Local Alignment Search Tool
☒	It uses word matching like FASTA algorithm
☐	It is one of the tools of NCBI

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BIF401 – Bioinformatics I (Quiz 1)

Question # 5 of 10 (Start time: 09:32:18 PM, 25 December 2021)

The the e-value, the more significant the hit.

Select the correct option

☐	higher
☒	lower
☐	average
☐	superior

Attempted by Muhammad Kashif



BIF401 - Bioinformatics I (Quiz 1)

Question # 4 of 10 (Start time: 09:32:01 PM, 25 December 2021)

Which one of the following isn't a BLAST variant?

Select the correct option

☐	BLASTN
☒	TBLASTNX
☐	BLASTP
☐	BLASTX

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BIF401 - Bioinformatics I (Quiz 1)

Question # 2 of 10 (Start time: 09:29:14 PM, 25 December 2021)

Multiple Sequence Alignment (MSA) can extract sequences from aligned sequence

Select the correct option

☐	Un-Aligned
☐	Aligned
☒	Consensus
☐	Un-known

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**Question # 1 of 10 (Start time: 09:28:45 PM, 25 December 2021)**

Fasty35 compares sequence to a sequence database.

Select the correct option

☐	DNA, DNA
☒	DNA, Protein
☐	Protein, DNA
☐	Protein, Protein

Attempted by Muhammad Kashif

**BIF401 – Bioinformatics I (Quiz 1)****Question # 10 of 10 (Start time: 09:26:53 PM, 25 December 2021)**

tfastx35 compares sequence to a sequence database (6 - ORFs).

Select the correct option

☐	Protein, Protein
☐	DNA, DNA
☐	DNA, Protein
☒	Protein, DNA

Attempted by Muhammad Kashif



Question # 9 of 10 (Start time: 09:25:24 PM, 25 December 2021)

The Local & Global Alignments uses approaches.

Select the correct option

- | | |
|----------------------------------|------------------------------|
| ☒ | Dynamic programming |
| ☐ | Static programming |
| ☐ | Static & Dynamic programming |
| ☐ | None of these |

Attempted by Muhammad Kashif



BIF401 – Bioinformatics I (Quiz 1)

Question # 8 of 10 (Start time: 09:25:07 PM, 25 December 2021)

..... compares protein sequence against protein databases.

Select the correct option

☐	blastn
☐	blastx
☒	blastp
☐	tblastx

Attempted by Muhammad Kashif

**Question # 7 of 10 (Start time: 09:23:19 PM, 25 December 2021)**

Multiple Sequence Alignment (MSA) can extract sequences from aligned sequences.

Select the correct option

☐	Un-known
☐	Aligned
☐	Un-Aligned
☒	Consensus



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**Question # 6 of 10 (Start time: 09:23:04 PM, 25 December 2021)**

Which one of the following isn't a BLAST variant?

Select the correct option

☐	BLASTP
☒	TBLASTNX
☐	BLASTX
☐	BLASTN

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BIF401 - Bioinformatics I (Quiz 1)

Question # 5 of 10 (Start time: 09:22:20 PM, 25 December 2021)

Fastm35 compares to a protein sequence database.

Select the correct option

☒	ordered peptides
☐	DNA
☐	un-ordered peptides
☐	Proteins

Attempted by Muhammad Kashif

**Question # 4 of 10 (Start time: 09:21:43 PM, 25 December 2021)**

Fasty35 compares sequence to a sequence database.

Select the correct option

☐	DNA, DNA
☒	DNA, Protein
☐	Protein, Protein
☐	Protein, DNA

Attempted by Muhammad Kashif



BIF401 - Bioinformatics I (Quiz 1)

Question # 3 of 10 (Start time: 09:21:29 PM, 25 December 2021)

The the e-value, the more significant the hit.

Select the correct option

☐	average
☐	higher
☒	lower
☐	superior

Attempted by Muhammad Kashif

**BIF401 – Bioinformatics I (Quiz 1)****Question # 2 of 10 (Start time: 09:20:34 PM, 25 December 2021)**

FASTA Algorithm can achieve alignment by using lengths of exact ...

Select the correct option

☐	Short, Mismatches
☒	Short, Matches
☐	Long, Matches
☐	Long, Mismatches

Attempted by Muhammad Kashif



BIF401 – Bioinformatics I (Quiz 1)

Question # 1 of 10 (Start time: 09:18:58 PM, 25 December 2021)

The expansion of BLAST is,

Select the correct option

☐	Beginners Local Alignment Search Tool
☒	Basic Logical Alignment Search Tool
☐	Basic Local Alignment Search Tool
☐	Bioinformatics Logical Alignment Search Tool

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