

Bioinformatics Task
Irbo 26
Mordad 1402



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1. Recap of Yesterday's Alignment Lesson (45 Min)

You have given a set of 5 DNA sequences (Seq 1 to Seq 5). These 5 sequences belong to an original sequence and have overlap with each other. Find the original sequence using alignment of these sequences.

Answer the following questions:

1. Was the original DNA sequence linear or circular?
2. What was the original order of sequences (e.g. 4->1->2->5->3)



Relaxed Circular
DNA

VS



Linear
DNA

2. Introduction to Genomic Databases - Uniprot (45 Min)

In this section we will use the UniProt Database to get information about a specific protein called Melittin, which is the toxin in the bee venom.

Answer the following questions:

1. What is the Uniprot ID of this protein?
2. What is the location of this protein in this organism?
3. What is the full sequence of this protein?
4. What different parts does this protein have?
5. What known variants have been found for this protein?



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3. Introduction to Structural Bioinformatics (90 Min)

In this section we start with some introduction on how Artificial Intelligence helped with solving the protein folding problem then will use AlphaFold2 (an AI model) to predict the Melittin protein structure vs its mutated form.

Website: [AlphaFold2.ipynb - Colaboratory \(google.com\)](https://colab.research.google.com/github/alphafold/alphafold2.ipynb)

Answer the following questions:

1. What is the difference between normal and mutated protein sequence?
2. What was the result of this mutation on the structure? Describe the before and after structure.

