

BioinformHer Mini Project – Module 2

Capstone

Title:

Tracking the Evolution of the Hemoglobin Beta (HBB) Gene Across Species

Project Objective:

Use the skills learned in Module 2 to investigate the evolutionary conservation of the HBB gene across six species. This includes sequence retrieval, alignment, logo generation, and phylogenetic tree construction.

Project Tasks

1: Sequence Retrieval & BLAST Search

- Retrieve the human HBB gene (nucleotide or protein) from NCBI.
- Use BLAST to identify HBB sequences from at least 5 other species, such as chimpanzee, cow, mouse, chicken, and zebrafish.
- Download the FASTA format of these sequences.
- Create a simple table that shows:
 - Species name
 - Accession number
 - % identity with human HBB

2: Pairwise Sequence Alignment

- Choose two species from your BLAST results:
 - One closely related to humans (e.g., chimpanzee)
 - One distantly related (e.g., zebrafish)
- Perform pairwise alignments of:
 1. Human HBB vs Closely Related Species
 2. Human HBB vs Distantly Related Species
- Use a tool like EMBOSS Needle or NCBI Pairwise Alignment.

Report for each comparison:

 - % Identity
 - % Similarity
 - Number of gaps
 - A short interpretation (which one is more conserved and why)

3: Multiple Sequence Alignment (MSA)

- Perform a Multiple Sequence Alignment of all 6 sequences using: Clustal Omega or MUSCLE
- Save and include a screenshot of your alignment.
- Highlight any highly conserved regions.

4: Sequence Logo Generation

- Upload your MSA file to Skylign.
- Generate a sequence logo to visualize conserved amino acids.
- Include the logo image in your report and briefly explain:
 - What do you observe?
 - Are there highly conserved residues?
 - Why might those regions be important?

5: Phylogenetic Tree Construction

- Use your MSA to generate a phylogenetic tree using MEGA X.
- Include a screenshot of the tree.
 - Briefly explain:
 - Which species are most closely related based on HBB?
 - Does this tree match what you expect evolutionarily?