**🧬 28 Interactive Bioinformatics Classroom Tasks**

Unit 1: Introduction to Bioinformatics & Central Dogma (DNA → RNA → Protein)

🧠 DNA→RNA→Protein Simulation:

Use an online central dogma simulator (e.g., Learn.Genetics Utah) to visualize transcription & translation.

✍🏽 Manual Transcription & Translation Exercise:

Given a short DNA sequence, students transcribe it into mRNA and then translate it into a protein using the codon table.

🔠 Base Pair Matching Game:

Create DNA base-pair flashcards (A–T, G–C) for quick matching competitions.

🔍 Explore Gene Structure:

Identify exons, introns, start/stop codons using an example gene (e.g., TP53 human from NCBI).

Unit 2: Genomic Sequences & Sequence Representation

5. 💻 Download a Real Gene Sequence:

From NCBI → Search “TP53 human” → view in FASTA & GenBank formats.

📂 Format Identification Activity:

Provide mixed-format files (FASTA, GenBank, EMBL) and have students label which is which.

📈 Genome Comparison Task:

Compare genome sizes of human, E. coli, and yeast using NCBI Genome database.

Unit 3: Sequence Alignment Basics (Pairwise Alignment, Scoring Matrices)

8. ✏️ Manual Alignment Practice:

Align two short sequences (e.g., ATGCT vs ATTT) manually using scoring rules.

💡 Global vs Local Alignment Experiment:

Perform both alignments using EMBOSS Needle (global) and EMBOSS Water (local).

📊 Scoring Matrix Demo:

Compare PAM and BLOSUM scoring results for the same protein pair.

🧩 Alignment Visualization:

Use Jalview or Clustal Omega to visualize sequence alignments and color-code similarities.

Unit 4: Online Databases (BLAST, Advanced BLAST)

12. 🔍 Basic BLAST Search:

Paste a known DNA sequence into NCBI BLAST → Identify the closest matching species.

🧠 Advanced BLAST Filters:

Use filters for organism, E-value threshold, or sequence identity cutoff.

🌎 BLAST Result Interpretation:

Interpret alignment score, E-value, and identity % from output.

Unit 5: Molecular Phylogeny & Alignment Methods

15. 🔬 Dot Matrix Plot Creation:

Use a dot plot tool (e.g., EMBOSS Dotmatcher) to visualize similarities between two sequences.

⚙️ Dynamic Programming Walkthrough:

Manually fill in a small scoring matrix to understand optimal alignment logic.

💻 Nucleic Acid Analysis:

Use NCBI or UGENE to identify GC content and motif regions.

🧬 Multiple Sequence Alignment:

Align three related gene sequences using Clustal Omega or MUSCLE.

Unit 6: Protein Structure & Hierarchy

19. 🔍 Explore Protein Databank (PDB):

Search a protein (e.g., hemoglobin) and view 3D structure in RCSB PDB.

🧩 Protein Structure Levels Matching:

Match examples to structure types — Primary, Secondary (α-helix, β-sheet), Tertiary, Quaternary.

🔄 Secondary Structure Prediction:

Use tools like PSIPRED or SOPMA for protein secondary structure prediction.

🧬 Tertiary Structure Modeling:

Use SWISS-MODEL or AlphaFold DB to visualize predicted 3D protein structure.

Unit 7: Phylogenetics & Tree Construction

23. 🌳 Tree Diagram Drawing:

Draw a simple evolutionary tree by hand using example species data.

💻 Build a Phylogenetic Tree:

Use MEGA or Phylogeny.fr to construct a tree from aligned sequences.

🧠 Tree Method Comparison:

Compare trees built using Stepwise Clustering, Maximum Parsimony, and Maximum Likelihood.

🔎 Ancestral Studies Using Phylogeny:

Trace back a specific gene (e.g., cytochrome c) to find its ancestral origin across species.

Unit 8: DNA Replication, Multiple Sequence Alignment & Digital DNA Storage

27. ⚙️ DNA Replication Simulation:

Use a virtual simulation to visualize replication fork, transcription, and translation processes.

💾 DNA Data Storage Demo:

Encode a short text (“HELLO”) into a DNA sequence using an online DNA digital encoding tool, showing how information can be archived in DNA.