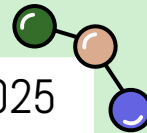


2024/2025

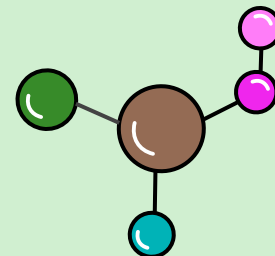
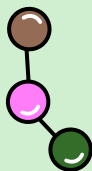


Short project : Assignment and detection of protein transmembrane regions

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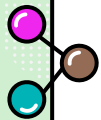


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You can describe the topic of the section here

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THE STRUCTURE OF THE ATOM

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PERIODIC TABLE HISTORY

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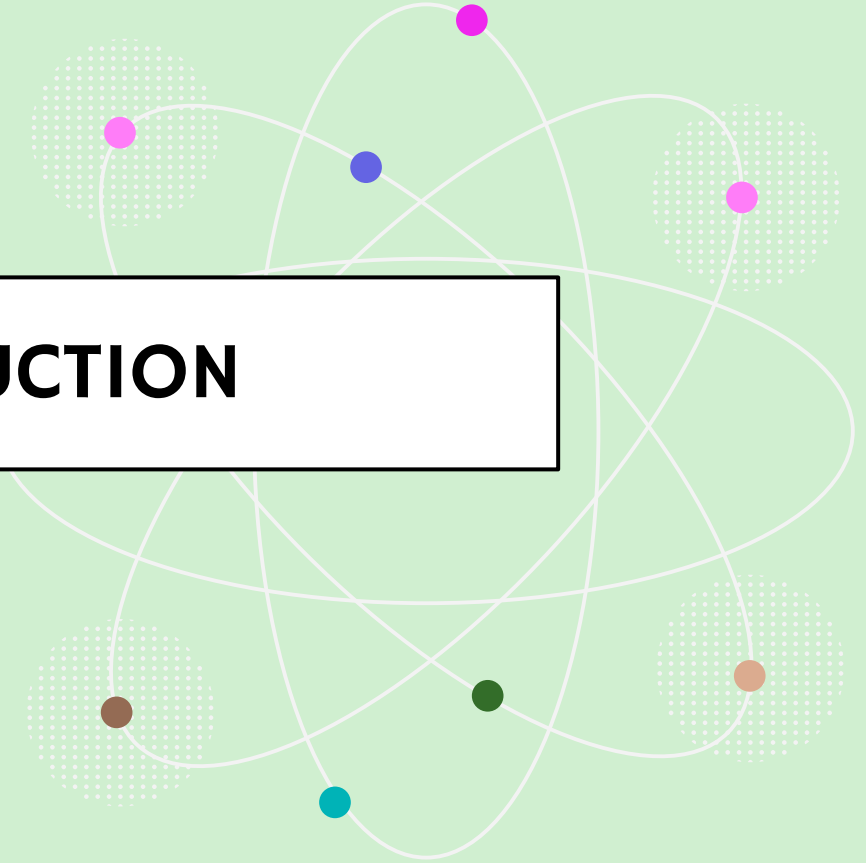
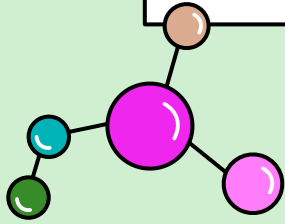
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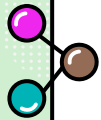
PERIODIC TRENDS

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Q1

INTRODUCTION





INTRODUCTION

Overview of Transmembrane Proteins:

- Play essential roles in molecular transport and signal transduction.
- Structural analysis is complex due to challenges in crystallizing without lipid bilayers.
- Underrepresented in databases such as the Protein Data Bank.

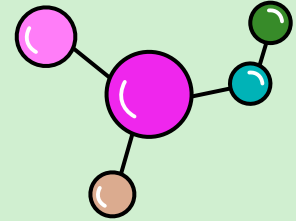
Project Objective:

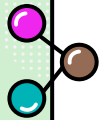
- Develop a computational tool to detect and assign transmembrane regions based on atomic coordinates.
- Utilize structural data like hydrophobicity and solvent-accessible surface areas to identify membrane boundaries and differentiate membrane proteins from globular proteins.

The background is a light green color. It features several white, overlapping elliptical lines that resemble atomic orbits. Scattered along these lines are small, solid-colored dots in teal, brown, green, orange, blue, and pink. There are also four larger, semi-transparent circles with a white dot pattern, positioned at the corners of the frame.

METHODOLOGY

02





METHODOLOGY - Input and Preprocessing

Input:

- Takes a Protein Data Bank (PDB) file with the 3D protein structure.

Preprocessing:

- DSSP Algorithm: Used to calculate solvent accessibility of each residue.
- Filter to retain only surface-exposed residues.
- Data stored in a dictionary, including residue names and 3D coordinates.

METHODOLOGY - Membrane Interaction Analysis

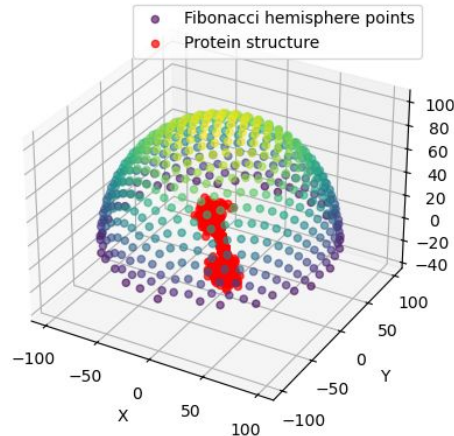
Spherical Sampling:

- Protein is sliced along axes generated using Fibonacci lattice methods to analyze membrane interaction.
- Each axis is defined by vectors extending from the protein's center of mass.

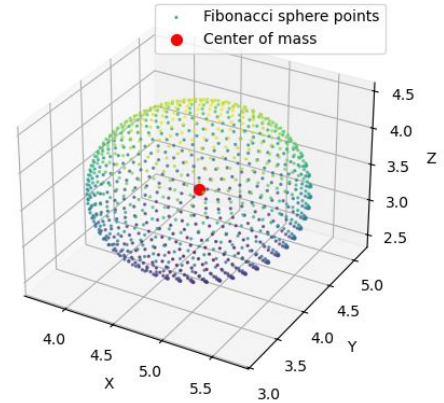
Hydrophobicity Profiling:

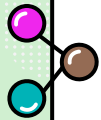
- For each axis, the protein is sliced into 1 Å thick sections.
- Residue hydrophobicity is evaluated using predefined scales.
- The ratio of hydrophobic residues near the membrane surface is analyzed to identify transmembrane regions..

Fibonacci Hemisphere with Protein Structure



Fibonacci Sphere with Center of Mass





METHODOLOGY - Membrane Plane Construction

Membrane Planes:

- After determining the optimal axis, two membrane planes are generated perpendicular to this axis.
- Membrane planes positioned 15 Å above and below the center of mass (30 Å total thickness).

Recalculation:

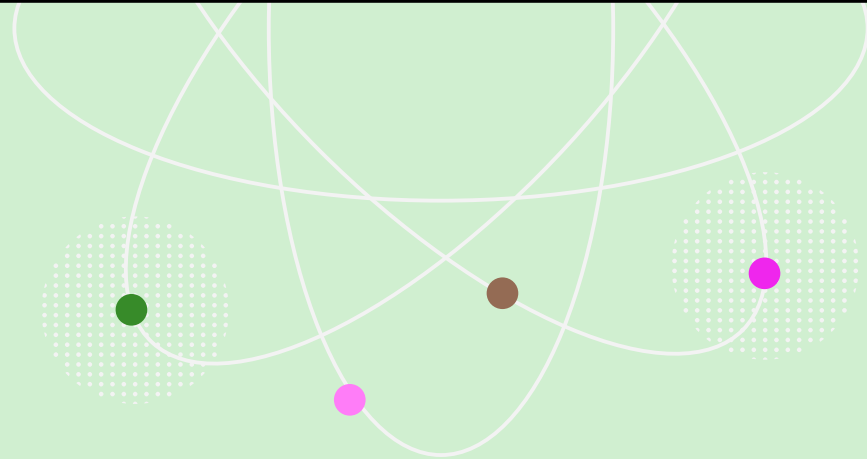
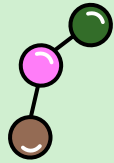
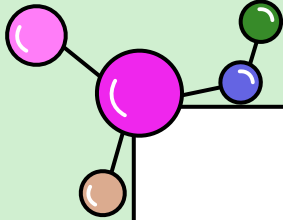
- Hydrophobicity ratio recalculated for different membrane thicknesses to find optimal boundaries.

Visualization:

- Outputs a modified PDB file with dummy atoms representing membrane planes and a PyMOL script to visualize the protein and membranes.

03

RESULTS



RESULTS - Test Protein (2MOZ)

Efficiency:

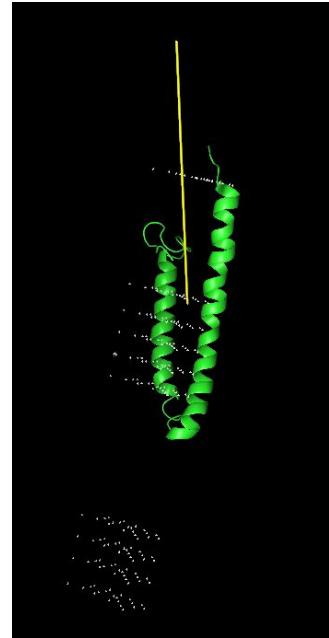
- Successfully generated points on a hemisphere and calculated the hydrophobicity ratio.
- Membrane Plane Accuracy: The tool positioned the two membrane planes at a 32 Å distance instead of the expected 30 Å.

Visualization:

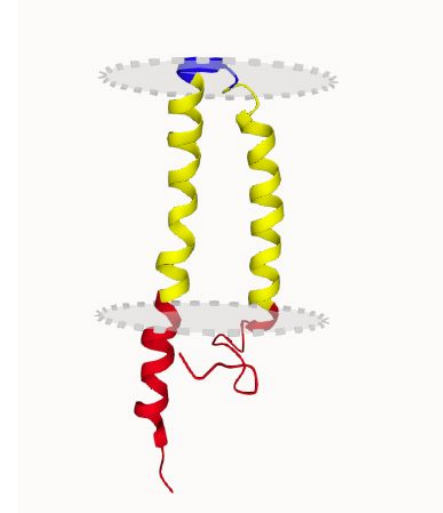
- Created PyMOL (.pml) file, but the membrane planes were not perfectly aligned.

Program Performance:

- Best axis identified with a hydrophobicity factor of 0.6805.
- Runtime: 2.18 seconds



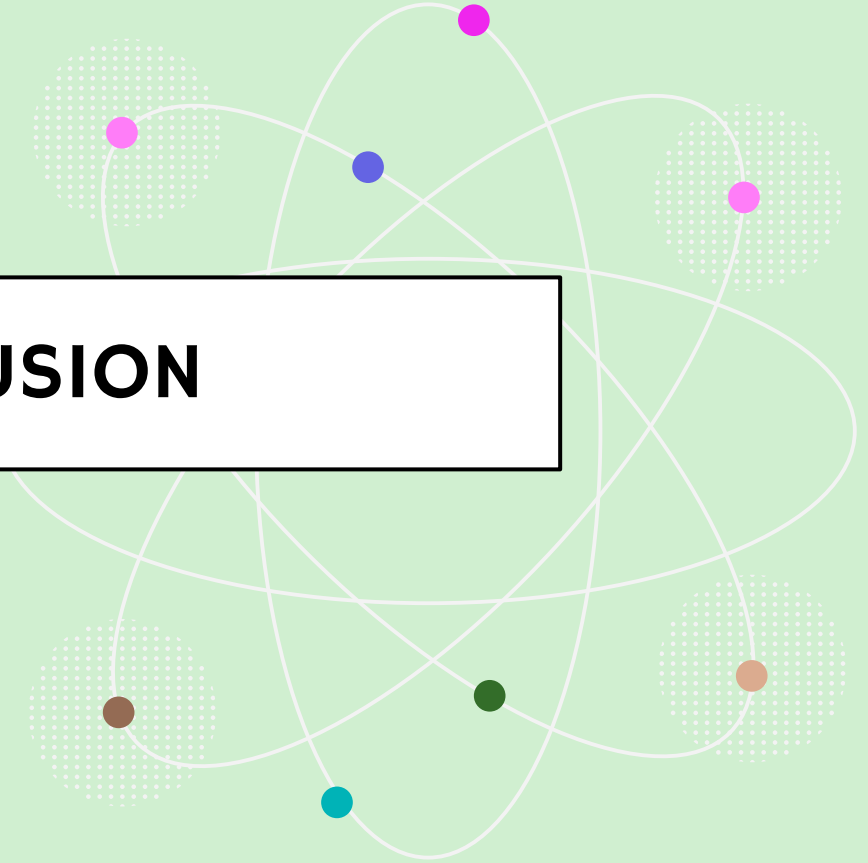
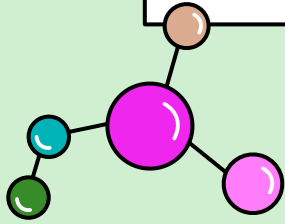
PyMol visualization

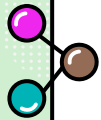


PDB_TM representation

04

CONCLUSION





CONCLUSION

Successes:

- Efficient identification of membrane axes using multiprocessing.
- Hydrophobicity analysis successfully detects transmembrane regions.

Limitations:

- Membrane plane positioning was not possible.
- Need for a more robust membrane plane generation method.

Future Work:

- Implement a mechanism to adjust membrane thickness.
- Further optimize the placement and orientation of membrane planes.

The background is a light green color. It features several stylized molecular structures in the corners: top-left (a central pink sphere with three smaller spheres: green, blue, and orange), top-right (a chain of three spheres: green, orange, and blue), bottom-left (a chain of three spheres: brown, pink, and green), and bottom-right (a central brown sphere with three smaller spheres: green, pink, and cyan). In the center, there are white elliptical lines representing orbits, with small colored spheres (pink, blue, green, brown) placed at various points along these paths. Some of these spheres are surrounded by a dotted circular pattern.

**THANK YOU FOR
LISTENING !**