Interactive Online Interface for Visualization and Analysis of Molecular Data

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Problem Overview

This project aims to redesign the graphical interface for DescribePROT, a tool that provides amino acid-level descriptors of protein structures and functions.

As the volume of protein sequence data continues to expand rapidly, researchers require fast, reliable, and visually appealing methods for analyzing this information.

Currently, DescribePROT's graphical output for protein-level characterization falls short in performance, often exceeding acceptable generation times, and the interface lacks the modern aesthetics and interactive elements expected by users.

Project Requirements

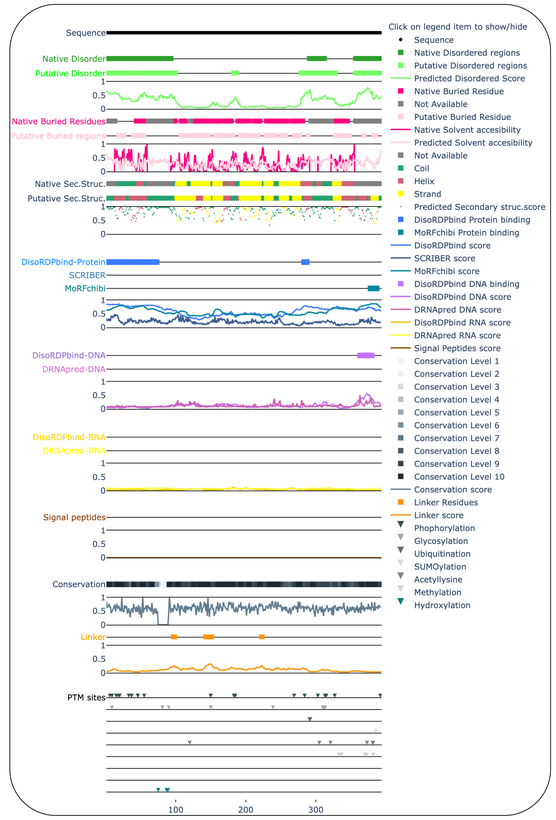
The overall goals for this project are on enhancing the Protein Level Characterization graphical interface to better serve the user's needs.

Specific Goals:

- **Assess Alternative Solutions:** Identify alternatives for building the protein graphical interface
- **Improve Performance:** Decrease the generation time of the graphical interface
- **Enhance Visual Appeal:** Improve the appearance of the visualization functions
- **Ensure Reliability:** Maintain the current level of reliability

			Current Implementation	Option 2	Option 3	Option 4	Option 5
MUST HAVE	Operational Specifications	Integration with Current System Scale: Yes/No	Yes				
		Runtime Scale: 1: Greater than or equal to current 2: 1-5 seconds 3: Subsecond	1				
		Cross-Browser Compatability Scale: Yes/No	No				
		Cost (Licensing) Scale: Open Source/Paid	Open Source				
	Interactive Elements	Zooming Scale: Yes/No	Yes				
		Panning Scale: Yes/No	Yes				
	Chart Features	Vertical Consistency Achievable Scale: Yes/No	Yes				
		Callouts Scale: Yes/No	Yes				
		Scatter/Line Plots Available Scale: Yes/No	Yes				
NICE TO HAVE	Quality of Interactive Elements	Zoom Scale: 1: Element is unintuitive, innacurate, or activation is unclear 2: Element is labeled but unspecific, activation is unreliable, or reservations exist 3: Element is clearly labeled, activation is intuitive, or has a high degree of accuracy	2				
		Panning Scale: 1: Element is unintuitive, innacurate, or activation is unclear 2: Element is labeled but unspecific, activation is unreliable, or reservations exist 3: Element is clearly labeled, activation is intuitive, or has a high degree of accuracy	2				
		Screenshot Scale: 0: Element is nonexistent 1: Element is unintuitive, innacurate, or activation is unclear 2: Element is labeled but unspecific, activation is unreliable, or reservations exist 3: Element is clearly labeled, activation is intuitive, or has a high degree of accuracy	3				
		Spike Lines Scale: 0: Element is nonexistent 1: Element is unintuitive, inaccurate, or activation is unclear 2: Element is labeled but unspecific, activation is unreliable, or reservations exist 3: Element is clearly labeled, activation is intuitive, or has a high degree of accuracy	2				
	Quality of Chart Features	Callouts Scale: 1: Fixed design 2: Layout of element is customizable	1				
	Graphical Displays	Flexible Panel Sizing Scale: Yes/No	No				
		Chart Lines Toggleable Scale: Yes/No	Yes				
	Other Considerations	Quality of Visualization Interface Scale: 1: Interface is unintuitive, data is unclear, or functionality is unclear 2: Interface is somewhat responsive, may lack some clarity in labeling, or reservations exist 3: Interface is clearly labeled, functionality is intuitive, and has a high degree of accuracy	2				
		Additional Plot Types Scale: Yes/No	No				
		Documentation Scale: Yes/No	Yes				
		Commented Code Scale: Yes/No	No				

Library Comparison Table



Current Implementation

python™ NumPy plotly scikit learn

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