**Deep Learning-Based Advances in Protein Structure Prediction**

**Abstract:**

Accurate prediction of protein structure is critical for advancing our understanding of biological mechanisms. While traditional machine learning algorithms like K-Nearest Neighbors (KNN) offer simplicity and interpretability, achieving reasonable accuracy (81% in our project), they often fall short when dealing with the complex relationships inherent in protein sequences. In contrast, Deep Learning (DL)-based methods have revolutionized the field of protein structure prediction, as seen in advancements like AlphaFold2, which leverages state-of-the-art architectures such as Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), and Transformer Networks. These approaches are particularly effective for handling intricate tasks like protein contact map prediction, distogram prediction, and real-valued distance prediction. While KNN can capture local sequence similarities, DL-based methods excel at modeling long-range dependencies and structural properties in a more nuanced way. Additionally, DL algorithms like Graph Neural Networks (GNNs) and 3D CNNs have demonstrated superior performance in analyzing 3D protein structures from Cryo-Electron Microscopy (Cryo-EM) data. The gap between traditional methods like KNN and DL-based approaches highlights the latter's potential in providing more accurate and scalable solutions for protein structure prediction.

**Keywords:**

Accuracy, AlphaFold2, Convolutional neural network, Deep Learning, K-nearest Neighbors, Protein Structure Prediction.