Precision in Mutation

Enhancing Drug Design with Advanced Protein Stability Prediction Tools

Team 4 | AlgoRxplorers

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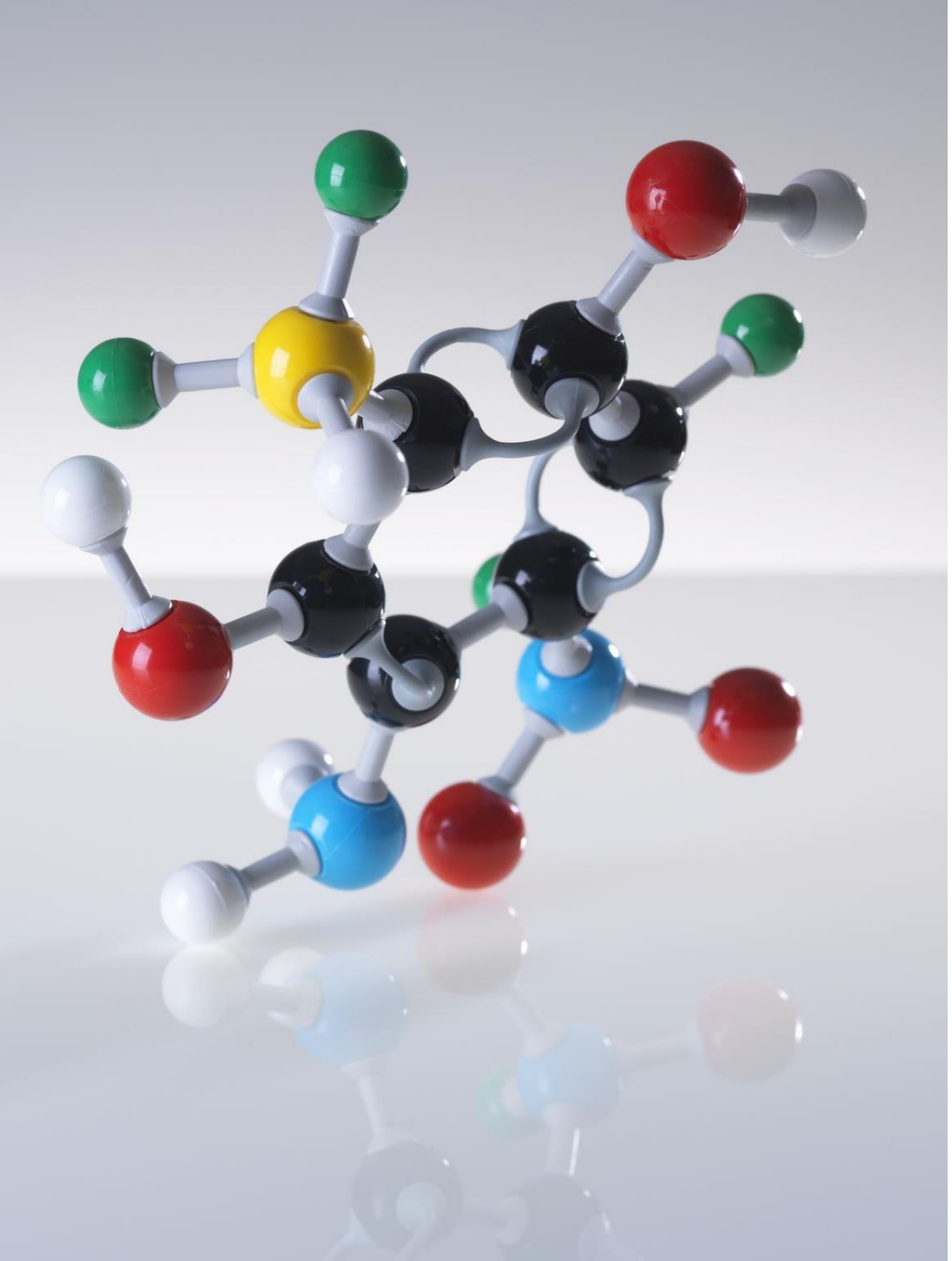
Agenda

- Background & Objectives
- Our Approach
- Current Practices
- Importance & Potential Impact



Background & Objectives

- Predict protein stability changes from mutations using advanced deep learning, streamlining drug design
- Enhance research and pharmaceutical development with predictive, interactive, and user-friendly visualizations

Our Approach

- Latent transfusion of ThermoMPNN with Meta's Evolutionary Scale Modeling(ESM) for precise mutation impact prediction.
- Utilizing data from FireProtDB and RCSB Protein Data Bank (PDB)

Current Practices

- Utilization of AlphaFold models for drug discovery: Feasibility and challenges. Histone deacetylase 11 as a case study [1]
- Graph Multiset Transformer: Use an attention mechanism focusing on molecular graphs and atomic distance to predict molecular properties [2]
- DeepDDG: Process various features related to the proteins' structure and amino acid properties using a deep neural network to estimate ΔΔG [3]
- Biological Structure and Function: Meta's pretrained protein transformer model introduced, Evolutionary Scale Modeling (ESM) [4]
- ThermoNet and MPNN: Neural Network architecture to help predict thermo-dynamic properties including ΔΔG [5]

Thank You

References

[1] Fady Baselious, Dina Robaa, and Wolfgang Sippl. Utilization of alphafold models for drug discovery: Feasibility and challenges. Histone deacetylase 11 as a case study. Computers in Biology and Medicine, 167:107700, 2023.

[2] Jinheon Baek, Minki Kang, and Sung Ju Hwang. Accurate learning of graph representations with graph multiset pooling. 2021.

[3] Huali Cao, Jingxue Wang, Liping He, Yifei Qi, and John Z Zhang. Deepddg: predicting the stability change of protein point mutations using neural networks. Journal of chemical information and modeling, 59(4):1508–1514, 2019.

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