

Peer Review

Review of: "Protein Structure Prediction in the 3D HP Model Using Deep Reinforcement Learning"

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Predicting Protein Structures in the 3D HP Model via Deep Reinforcement Learning

This study introduces a Deep Reinforcement Learning (DRL) framework to address the protein folding problem, modeling it as a Self-Avoiding Walk (SAW) on a 3D cubic lattice. The key contributions of this research include:

- Formulating protein folding as a Markov Decision Process (MDP).
- Applying Deep Q-Learning with stabilization techniques to manage the high-dimensional complexity.
- Designing an optimized reward function based on protein folding energy.

While I have not yet explored deep learning methods in depth, the strategies outlined in this paper appear highly promising.

Limitations: Implementing such methods necessitates extensive testing and large datasets for model training. Additionally, the data must enable the identification of the desired outcome—the optimal protein conformation. However, a significant challenge in this domain is the limited availability of proteins with well-determined optimal conformations.

Declarations

Potential competing interests: No potential competing interests to declare.