

Protein Structure Prediction Using RL

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Outline

- 1 Protein folding problem
 - Problem Relevance
 - The Hydrophobic-Polar Model
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- The protein folding problem, which involves predicting a protein's structure from its amino acid sequence, is a major challenge in bioinformatics with significant implications for medicine and genetic engineering.
- In the following we are addressing the Bi-dimensional Protein Folding Problem (BPFB), but this model can be easily extended to the threedimensional protein folding problem.

The Hydrophobic-Polar Model

Some text about the Hydrophobic-Polar Model.

Methods

Some text about methods.