2D HP Protein Folding Using Quantum Genetic Algorithm

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Summary

The paper introduces a novel approach to solving the Protein Structure Prediction (PSP) problem, specifically for 2D HP protein folding, using a Quantum Genetic Algorithm (QGA). By leveraging quantum properties, the QGA aims to find optimal solutions for PSP in a faster and more memory-efficient manner compared to traditional Genetic Algorithms (GA). The algorithm's performance is explored through simulations of various instances of the PSP problem, considering factors such as population size and algorithmic parameters.

Limitations

- **Simplified Model**: The paper focuses only on the 2D HP protein folding, so it may not be applicable to more complex, real-world 3D protein structures.

- **Parameter Sensitivity**: The performance of the QGA heavily depends on the parameter values, such as population size and the parameter μ that balances global and local search.

- **Population Size Trade-off**: Selecting a suitable population size is crucial for the QGA's effectiveness. Smaller populations might need help finding global optimal solutions, while larger populations require more computational time. Achieving the right balance is essential for achieving desired outcomes.