

DNA sequence alignment on a quantum computer

Motivation:

Sequence alignment is one of the major challenges in computational biology. To find evolutionary, structural or functional relationships within a set of DNA or proteins, we search a large database to find similar sequences. Because of the huge database, it requires intensive computation resource and takes days to run on a supercomputer. Apart from biological applications, sequence alignment can also be used for financial data and natural language analyzing.

Using superposition and entanglement, quantum computers run parallel and can be exponentially faster than classical computers on certain tasks. Quantum computers will be a game changer, but few work [1,2] is connected to sequence alignment. We will explore potential ways to harness quantum power to speedup bioinformatics.

Project description:

Collaborating with the postdoctoral researcher, in this project we will explore

- Existing algorithms for (multiple) sequence alignment
- Quantum search algorithms for pattern matching
- How to tailor quantum power to accelerate sequence alignment
- Test a small scale quantum algorithms on the quantum cloud (IBM quantum experience or Rigetti quantum cloud)

Supervisors:

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Reference

- [1] Hollenberg, L. C. L. (2000). Fast quantum search algorithms in protein sequence comparisons: Quantum bioinformatics. *Phys. Rev. E*, 62(5), 7532–7535.
- [2] Meshoul, S., Layeb, A., & Batouche, M. (2005). A Quantum Evolutionary Algorithm for Effective Multiple Sequence Alignment. In C. Bento, A. Cardoso, & G. Dias (Eds.), *Progress in Artificial Intelligence* (pp. 260–271).