

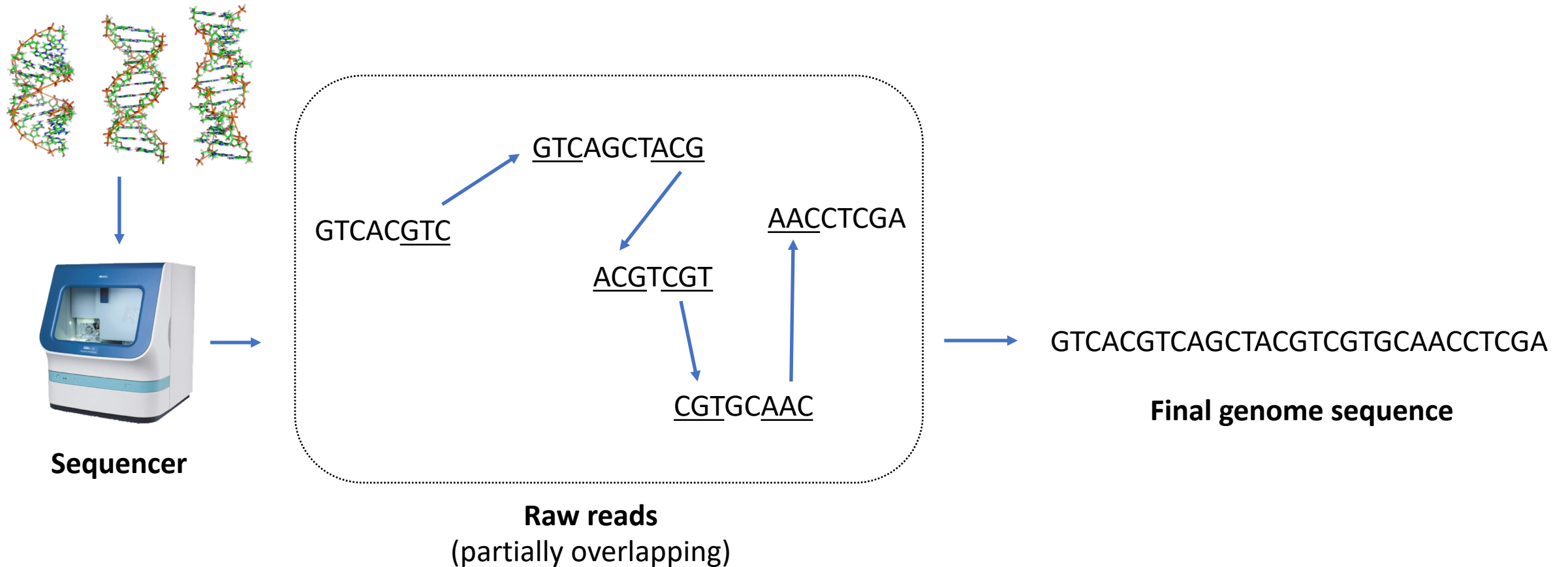


DeNovo Genome Assembly Using Adiabatic Quantum Computing

RQC_Team

Overview

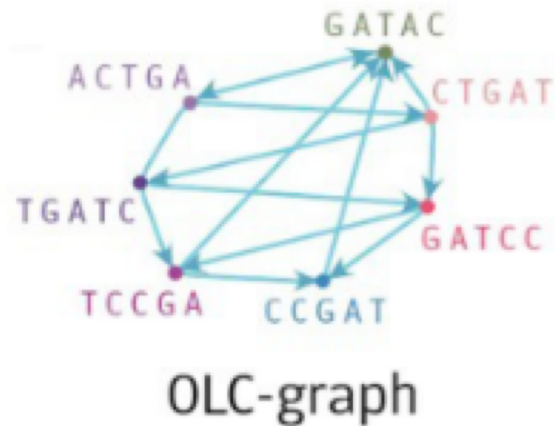
- . DeNovo Genome Assembly is one of the most computationally expensive problems in bioinformatics
- . Modern sequencing devices produce pieces of DNA called reads, which represent 4-alphabet strings (A,C,G,T)
- . The goal of DeNovo Genome Assembly is to assemble reads into a single longest sequence



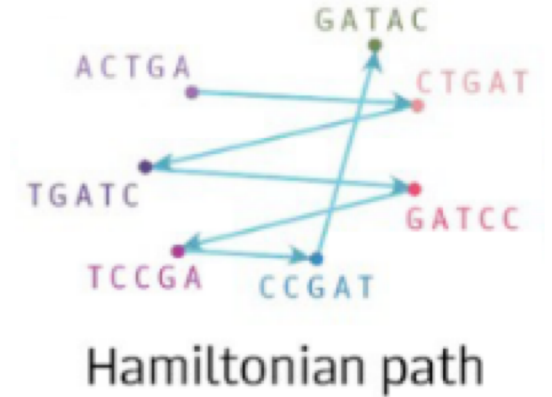
Core Algorithm (Classic)

- . Classical approach to solving the problem starts from building OLC graph – each vertex represents a read, while each edge represents an overlap
- . Finding Hamiltonian* path on OLC-graph is equivalent to reconstructing genome sequence
- * Path that visits each vertex only once

Step 1
Build OLC-graph

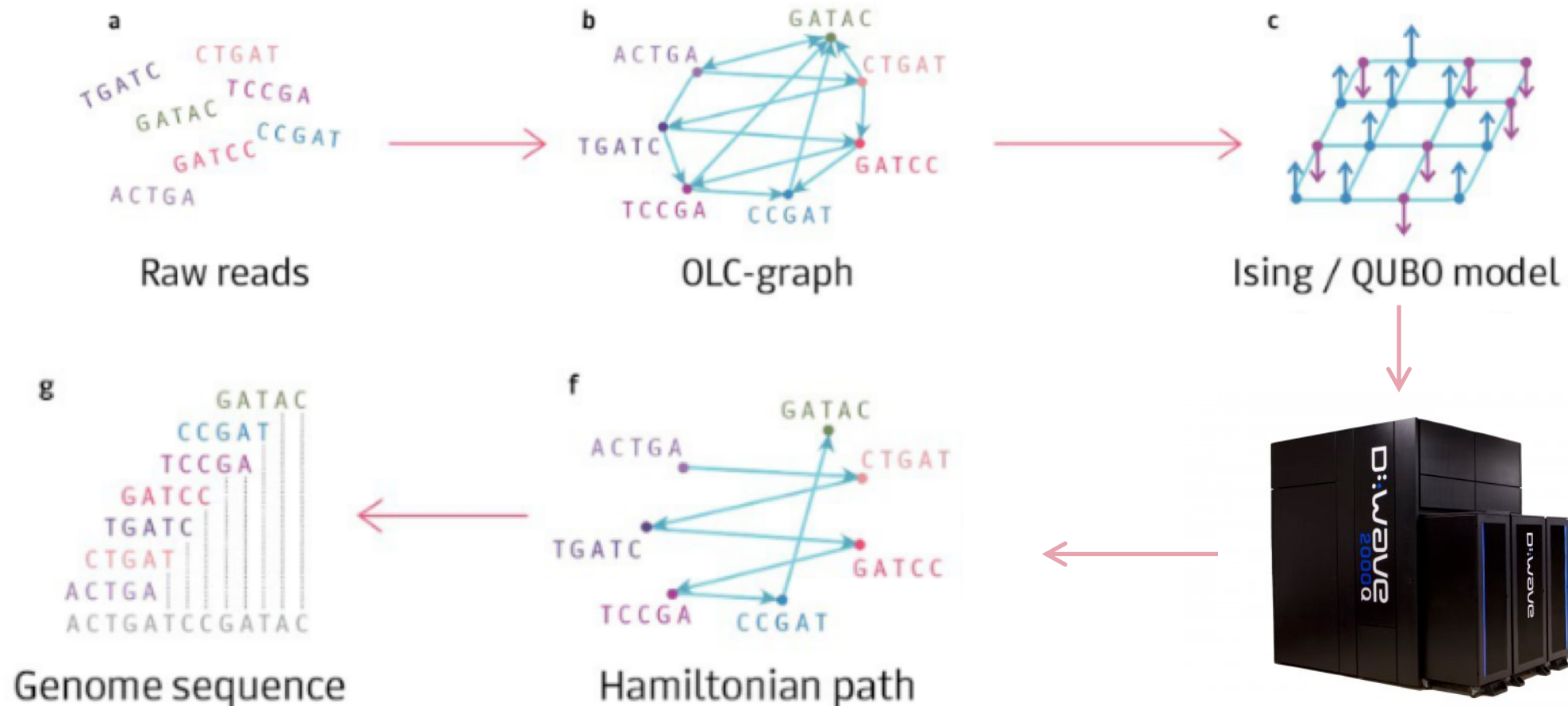


Step 2
Find Hamiltonian path



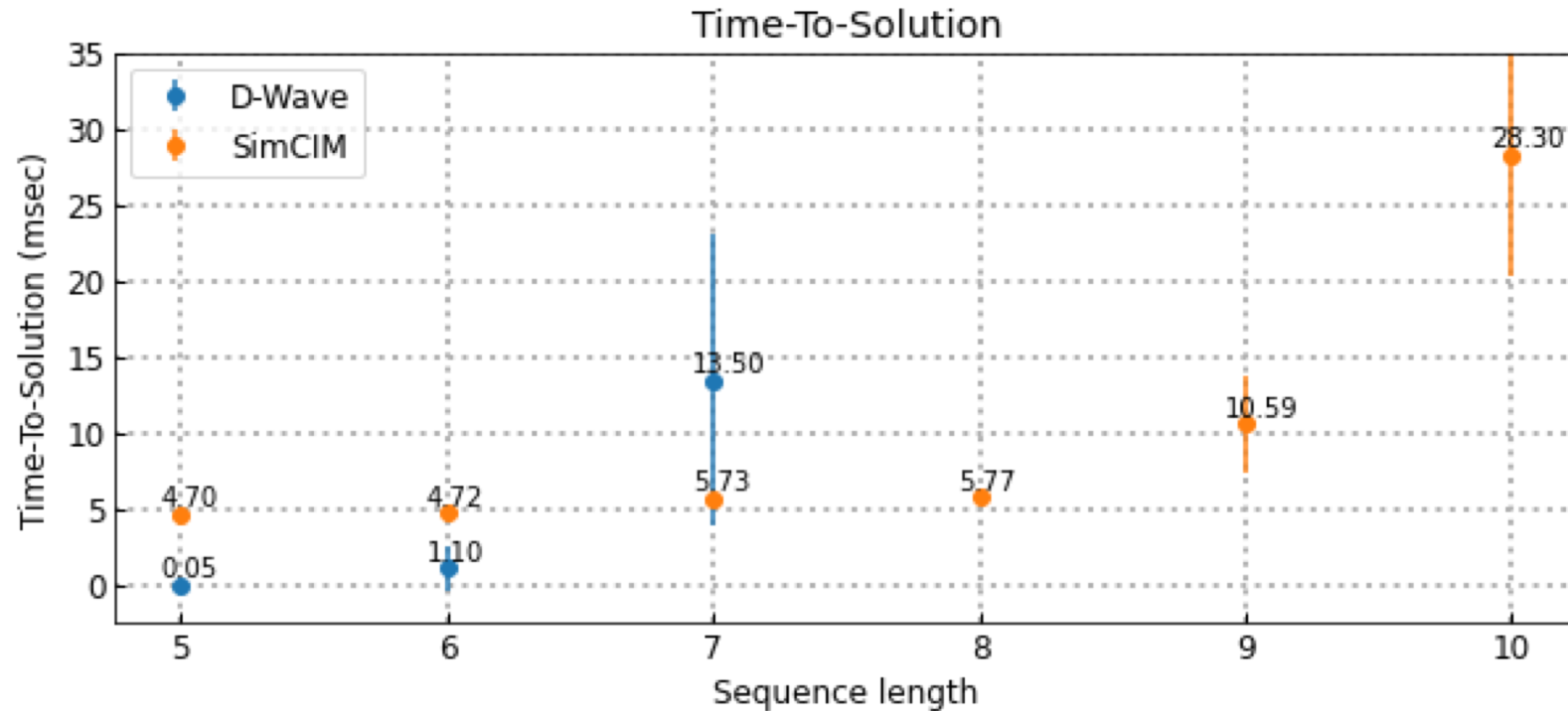
Core Algorithm (Quantum)

- . We propose an algorithm to transform Hamiltonian path problem into QUBO/Ising formulation
- . Such problem is further applicable to D-Wave quantum annealer



Results

- . Our experiment shows the possibility of reconstructing short synthetic sequences up to 7 nucleotides in purely quantum mode
- . In addition, we tried to reconstruct genome of Phi-X174 bacteriophage in a hybrid computing mode



Reference

- . More details can be found in our paper <https://arxiv.org/abs/2004.06719>
- . Source code is available on github https://github.com/USM-F/quantum_genome