

ABSTRACT - TECHNOLOGICAL INNOVATION;

**GENETIC ENGINEERING WITH QUANTUM CIRCUITS: CREATING CODES  
AND STUDYING BIOBLOQU GENETIC ELEMENTS**

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The accelerated exploration and engineering of nucleotide sequences are directed towards quantum mechanics and their intrinsic entanglements, implementing the qubits states, including the development of algorithms. The production rate of biological sequencing data has increased to approximately 1 Gb/h, but the ability to analyze these data has not kept pace due to complexity issues and the limitations of classic computing. Despite its own challenges, quantum computing offers a potential solution for analyzing biological data and extracting relevant information. We aimed at developing and implementing quantum algorithms that drive searches for genetic information and allow the assembly of prototype transcriptional units with increased efficiency as a promising alternative for future design of synthetic genomes. We developed Qubio.py, a quantum computing tool based in Goover's Algorithm to precisely

search for a 50 nt target sequence in a DNA sequence database with up to 3022 nucleotides. Two codes were written, one to detect a Cas9 functional domain in a metagenomic database of Brazilian biomes and one to detect specific regions in the synthetic genome of the minimal cell approximation *Mycoplasma mycoides* JCVI-Syn3B. A third code was created to assemble transcriptional units comprising promoter, RBS, ORF and terminator sequences, which we named BioBloQu. All analysis were performed on the IBM Quantum Experience platform, which used a quantum simulator processor with 36 qubits. All codes could produce the expected outputs. For the prospection, we detected a 50nt sequence of a Cas9 functional domain in a metagenomic database, which were then used as pseudo-ORF in the assembly of a BioBloQu. The search in JCVI-3B minimal genome identified a promising region for insertion of the BioBloQu created, as an initial example of guided genome engineering in a quantum environment. Our algorithm constitutes a unique starting point for developing a more sophisticated model for the manipulation of data. This tool could be exploited for quantum-enhanced design, building synthetic genomes with desirable traits from the bottom up and exploiting genetic big data. Enhancing the algorithm and expanding device availability are significant targets for accelerating searches and gathering specific biodiversity features for research and applications.

Palavras-chave: quantum computing biobloqu simulation biotechnology  
brazilian biomes.