



INVENTORS

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HIGH PERFORMANCE DNA SEQUENCER FOR EARLY STAGE HIV DETECTION

Novelty Search Number : S/UNIMAP/14MY30/GM



INTRODUCTION

DNA sequence alignment aims to search for regions of homology between biological sequences by comparing DNA nucleotides (Adenine, Cytosine, Guanine and Thymine) of an unknown (query) sequence against reference sequences in a database. From biological point of views, any reference sequence with the highest scores has the closest relationship with the query sequence, thus characteristics of the unknown sequence could be inferred by referring to the characteristics of the matched reference sequence. However, the execution of DNA/protein sequencing on standard desktop computers, produces results in hours or even days especially when dealing with longer sequences and large database. Therefore a real time systolic array-based DNA sequencer, specifically designed for HIV detection is developed.

NOVELTIES

- New Processing Element (PE) Core Architecture
- Fixed Number of Configuration Element (CE) Architecture (Only two CEs)
- Efficient Sequencing Management (Simultaneous Computation and Configuration)
- Reconfigurable PE Systolic Array (SA) Architecture

FEATURES

- Smaller silicon footprint
- Real time processing
- Lightweight
- Low power consumption
- Sensitive homology search
- Upgradable to hand held protein sequencer

APPLICATIONS

- Reconfigurable Hand-held DNA Sequencer for:
 - 1) Premature diseases diagnosis
 - 2) Forensics
 - 3) HALAL products real time verification
 - 4) Drug Engineering

COMMERCIAL POTENTIALS

- Real time hand-held premature disease diagnosis tool in hospitals
- Can be integrated in a system on chip (SoC) DNA sequencer for larger scale DNA/protein sequencing

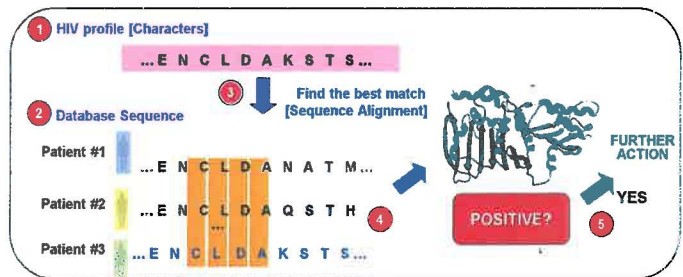
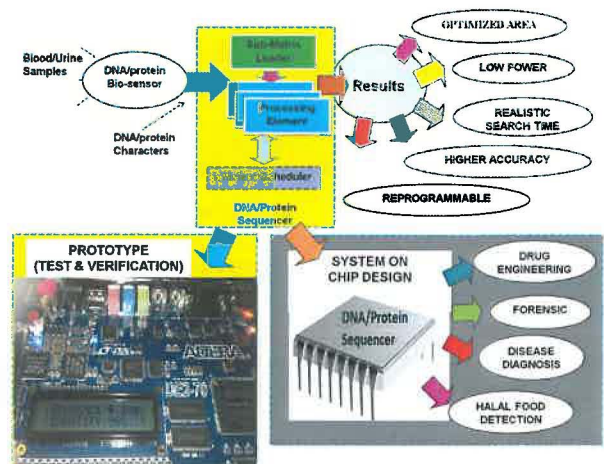


Illustration of HIV query profile search against patients' biological sequences



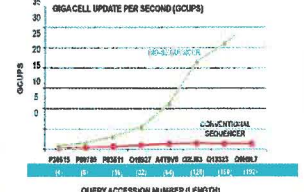
The bio-Sequencer and its commercialization potentials

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Query: 232086..276 nt
S:24025286..276 nt - 276 matches, 100%
Library: seqs.fasta 2006 residues in 13 sequences

2836 residues in 11 sequences
Sequence: 2836-2876 [64] seqs.fasta:seqs.fasta:6,4789: 240:63743
Algorithm: Smith-Waterman (Fast) (2.0 star 2007)
Parameters: -S -m 1 -n 1 -t -s -i -e -o -l -v -x -y -z -1 -2 -3 -4

The best scores are:
SeqID1: 2836
SeqID2: 2836
SeqID3: 2836
SeqID4: 2836
SeqID5: 2836
SeqID6: 2836
SeqID7: 2836
SeqID8: 2836
SeqID9: 2836
SeqID10: 2836
SeqID11: 2836
SeqID12: 2836
SeqID13: 2836
SeqID14: 2836
SeqID15: 2836
SeqID16: 2836
SeqID17: 2836
SeqID18: 2836
SeqID19: 2836
SeqID20: 2836
SeqID21: 2836
SeqID22: 2836
SeqID23: 2836
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SeqID25: 2836
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SeqID28: 2836
SeqID29: 2836
SeqID30: 2836
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SeqID33: 2836
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SeqID36: 2836
SeqID37: 2836
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SeqID39: 2836
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SeqID92: 2836
SeqID93: 2836
SeqID94: 2836
SeqID95: 2836
SeqID96: 2836
SeqID97: 2836
SeqID98: 2836
SeqID99: 2836
SeqID100: 2836
    
```



Sequence homology search results

The Bio-Sequencer vs. the conventional sequencer



Illustration of the HIV Bio-Sequencer

PUBLICATIONS

1. M. N. Isa et al., "Biological Sequence Alignments: A Review of Hardware Accelerators and a New Computing Strategy", IEEE TENSYP04, Kuala Lumpur, Malaysia (Scopus Cited)
2. M. N. Isa, K. Benkrid, and T. Clayton, "Efficient architecture and scheduling technique for pairwise sequence alignment," ACM SIGARCH Comput. Archit. News, vol. 40, pp. 26-31, 2012 (Scopus Cited)