Novel Coprocessor for DNA Sequence Alignment in Resequencing Applications

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Abstract : This paper presents a novel semi-systolic array architecture for an optimized parallel sequence alignment algorithm. This architecture has the advantage that it can be modified to be reused for multiple pass processing in order to increase the number of processing elements that can be packed into a single FPGA and to increase the number of sequences that can be aligned in parallel in a single FPGA. This resolves the potential problem of many FPGA resources left unused for designs that have large values of short read length. When using the previously published conventional hardware design. FPGA implementation results show that, for large values of short read lengths (M>128), the proposed design has a slightly higher speed up and FPGA utilization over the the conventional one.