



A MEMORY EFFICIENT HARDWARE BASED PATTERN MATCHING AND PROTEIN ALIGNMENT SCHEMES FOR HIGHLY COMPLEX DATABASES

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Abstract- Protein sequence alignment to find correlation between different species, or genetic mutations etc. is the most computational intensive task when performing protein comparison. To speed-up the alignment, Systolic Arrays (SAs) have been used. In order to avoid the internal-loop problem which reduces the performance, pipeline interleaving strategy has been presented. This strategy is applied to an SA for Smith Waterman (SW) algorithm which is an alignment algorithm to locally align two proteins. In the proposed system, the above methodology has been extended to implement a memory efficient FPGA-hardware based Network Intrusion Detection System (NIDS) to speed up network processing. The pattern matching in Intrusion Detection Systems (IDS) is done using SNORT to find the pattern of intrusions. A Finite State Machine (FSM) based Processing Elements (PE) unit to achieve minimum number of states for pattern matching and bit wise early intrusion detection to increase the throughput by pipelining is presented.

Index terms: Systolic Arrays (SAs), Intrusion Detection Systems (IDS), Network Intrusion Detection System (NIDS), protein Data Bases (DBs).