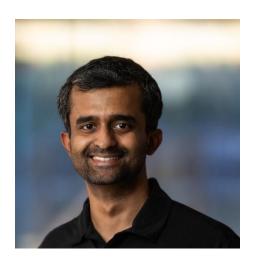
COMPUTER SCIENCE & ENGINEERING

DISSERTATION DEFENSE



Hari Sadasivan Accelerated Systems for Portable DNA Sequencing Monday, April 24, 2023

Monday, April 24, 2023 9:00am – 11:00am 4901 Beyster Hybrid – <u>Zoom</u>

ABSTRACT: The MinION is a handheld DNA sequencer that is increasingly used in Precision Medicine applications but lacks onboard computing, limiting its portability. This thesis introduces two clinical applications of the MinION and identifies and solves performance bottlenecks through hardware-software solutions.

More than 99% of DNA fragments in a typical human sample are non-target (human), which may be skipped in real-time using MinION's Read Until feature. We analyze the performance of the Read Until pipeline in detecting target microbial species for viral pathogen detection and microbiome abundance estimation. We find new sources of performance bottlenecks (basecaller in the classification of a fragment) that are not addressed by past genomics accelerators. While SquiggleFilter and DTWax are our solutions for viral pathogen detection, RawMap is for microbiome abundance estimation. As a final contribution, we discuss accelerating the bottleneck step in the DNA mapping software (Minimap2) used in all of MinION's sequencing workflows.

(1) SquiggleFilter (ASIC-based) is a portable and programmable virus detector that directly analyzes MinION's raw squiggles and filters everything except target viral DNA fragments. SquiggleFilter avoids the expensive basecalling step and uses hardware-accelerated subsequence Dynamic Time Warping (sDTW). We show that our 14.3W 13.25mm 2 accelerator has 274× greater throughput and 3481× lower latency than existing GPU-based solutions while consuming half the power.

(2) DTWax (GPU-based) overcomes the on-chip memory limitations of SquiggleFilter by adapting its high-accuracy sDTW algorithm onto GPUs and optimizing for performance from better GPU utilization, resulting in a ~1.92X sequencing speedup and ~3.64X compute speedup: costup.

(3) RawMap (CPU-based) is a machine-learning-based smart and efficient solution to microbiome abundance estimation, reducing sequencing time and cost by \sim 24% and computing cost by \sim 22%. We also discuss how RawMap may be used as an alternative to the RT-PCR test for viral load quantification of SARS-CoV-2.

(4) mm2-ax or minimap2-accelerated is a heterogeneous design for sequence mapping where Minimap2's bottleneck step is sped up on the GPU with bit-exact output. mm2-ax on an NVIDIA A100 GPU improves the bottleneck step (chaining) with 4.07 - 1.93X speedup: costup over the SIMD-accelerated version of Minimap2.

CHAIR: Prof. Satish Narayanasamy