



DISSERTATION DEFENSE



Hari Sadasivan

Accelerated Systems for Portable DNA Sequencing

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9:00am – 11:00am

4901 Beyster

Hybrid – [Zoom](#)

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 13.25mm² 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 ~24% and computing cost by ~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