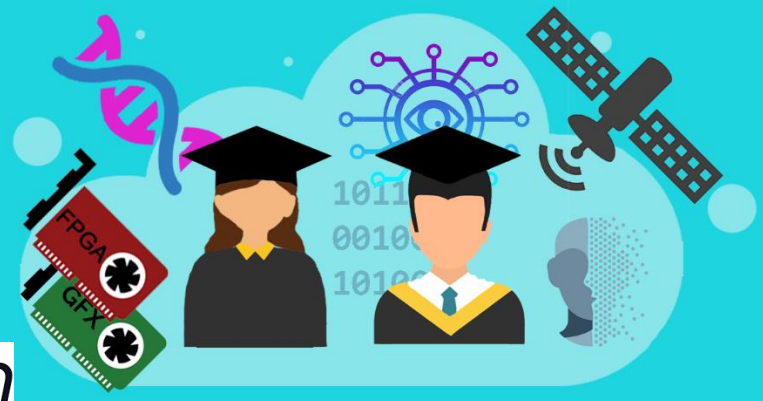


Diploma Thesis

Microprocessors and
Digital Systems
Laboratory



ETH zürich



Hardware-Software Acceleration Approaches for Genome Analysis

High-throughput sequencing (HTS) technologies have revolutionized the field of genomics, enabling rapid and cost-effective genome analysis for various applications. However, the increasing volume of genomic data generated by HTS presents significant challenges for computational techniques to effectively analyze genomes. To address these challenges, several algorithm-architecture co-design works and emerging computing paradigms have been explored to provide fast, accurate, and low-power genome analysis.

We are searching for students who are interested in the following research topics:

- Design of hardware-based accelerators for computationally intensive steps of genome analysis e.g. basecalling, indexing, read mapping, variant calling.
- Hardware/Software co-design architectures to enable efficient end-to-end execution of genomic pipelines
- Design of efficient architectures that achieve real-time execution of raw signal analysis for genomic data.
- Novel designs for efficient genome analysis targeting emerging computing paradigms such as In-Storage-Processing and Processing-using-Memory.
- Hardware-based acceleration for Machine-Learning based genome analysis steps.

Requirements:

- Strong knowledge of C/C++, Hardware/Logic Design, VLSI
- Strong computer architecture background
- Strong work ethic

Suggested readings:

- [1] Senol Cali et al. [GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis](#) MICRO 2020
- [2] Singh et al. ["FPGA-Based Near-Memory Acceleration of Modern Data-Intensive Applications"](#) MICRO 2021
- [3] Alser et al. ["SneakySnake: A Fast and Accurate Universal Genome Pre-Alignment Filter for CPUs, GPUs, and FPGAs"](#) Bioinformatics 2020
- [4] Alser et al. ["Accelerating Genome Analysis: A Primer on an Ongoing Journey"](#) IEEE Micro 2020
- [5] Firtina et al. ["RawHash: Enabling Fast and Accurate Real-Time Analysis of Raw Nanopore Signals for Large Genomes"](#) ISMB 2023
- [6] Mansouri Ghiasi et al. ["GenStore: A High-Performance and Energy-Efficient In-Storage Computing System for Genome Sequence Analysis"](#) ASPLOS 2022

[7] Mao et al. "[GenPIP: In-Memory Acceleration of Genome Analysis via Tight Integration of Basecalling and Read Mapping](#)" MICRO 2022

[8] Koliogeorgi et al. "[GANDAFL: Dataflow Acceleration for Short Read Alignment on NGS Data](#)" IEEE TC 2022

[9] Mutlu and Firtina, "[Accelerating Genome Analysis via Algorithm-Architecture Co-Design](#)"
Invited paper in DAC 2023

If you are interested, please email:

Konstantina Koliogeorgi, konstantina.klgh@gmail.com

Can Firtina, can.firtina@safari.ethz.ch

Prof. Onur Mutlu, omutlu@gmail.com, <https://people.inf.ethz.ch/omutlu/>

Prof. Dimitrios Soudris: (dsoudris@microlab.ntua.gr)