FACULTY MENTOR
Yatish Turakhia

PROJECT TITLE
GPU Acceleration of Bioinformatics Algorithms

PROJECT DESCRIPTION
Biological datasets, such as genomic data, are among the fastest-growing data types on the planet and pose enormous computational challenges to analyze. In this project, the student(s) will work closely with the PI and other lab members to:

1. Design and implement algorithms for compute-intensive bioinformatic tasks, such as phylogenetics, genome assembly, read alignment, and whole-genome alignments on GPUs to achieve massive speedups.
2. Compare and benchmark the performance against existing methods.
3. Co-author papers based on this work to be published in top-tier journals and conferences.

This project will be in person.

INTERNS NEEDED
➢ 1

PREREQUISITES
➢ C++ and CUDA programming.

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PROJECT TITLE
A Programmable Hardware Accelerator for Dynamic Programming Algorithms

PROJECT DESCRIPTION
Dynamic Programming algorithms are fundamental building blocks of numerous algorithms in bioinformatics. In this project, the student(s) will work closely with the PI and other lab members to:

1. RTL design and implement a flexible hardware accelerator that can be programmed for a wide range of dynamic programming algorithms in bioinformatics.
2. Prototype the accelerator on FPGA and perform ASIC analysis.
3. Compare and benchmark the performance against existing methods.
4. Co-author papers based on this work to be published in top-tier journals and conferences.

This project will be in person.

INTERNS NEEDED
➢ 1

PREREQUISITES
➢ RTL Design in SystemVerilog, Computer Architecture, VLSI Design.

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PROJECT TITLE
Large-Scale Phylogenetics

PROJECT DESCRIPTION
Phylogenetics is the study of the evolutionary relationships between a set of biological sequences, organisms, or species. This has many downstream biological and medical applications – from evolutionary biology to outbreak analysis to understanding the progression of cancer. Large phylogenies are computationally challenging to estimate, and with the recent advancements in genomic sequencing technologies generating a massive amount of genomic data, there is an urgent need to automate this process. In this project, the student(s) will work closely with the PI and other lab members and collaborators to:

1. Explore and develop new phylogenetic methods and acceleration techniques to cater to a wide range of applications.
2. Compare and benchmark the performance against existing methods.
3. Co-author papers based on this work to be published in top-tier journals and conferences.

This project will be in person.

INTERNS NEEDED
➢ 1

PREREQUISITES
➢ Python programming.