

Designs for accelerating Bioinformatic problem solving using FPGAs based HPC system

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Abstract

The abstract to summarize

1. What Bioinformatic problem try to solve
2. Why are they important to us (Diversity, uses)
3. How FPGA based systems can help (Complexity, speed etc.)

1 Introduction

This section would introduce the topic of Bioinformaticss and HPC with FPGA and highlight the interdependence to create the base for the rest of the paper.

1. Some references to exiting known HPC systems used for solving Bioinformatic problems
2. Introduce the structure of the thesis

Reference for the section [1], [2]

Also use a general example to capture general terminologies used in the domain

2 Related Work

Should discuss if this should remain as a separate section or the related work can already be introduced in previous section?

3 System Designs and Techniques

This section would give specific example for Techniques and related system designs which use FPGA based HPC systems to accelerate the solution finding.

Add subsection to describe the techniques along with references.

3.1 Smith-Waterman Algorithm

References [3], [4]

3.2 BLAST

Reference [5], [6]

3.3 HMMER

References [7] [8]

3.4 RIVYERA

Reference [9], [10]

4 Evaluation and comparison

This section should highlight the possible acceleration which is possible with the FPGA based system using the Evaluation data of different techniques and present a comparative study of how this techniques vary to each other and to traditional HPC and serial computing.

This should be able to highlight the advantages of using FPGAs for certain problem to reduce cost and time for for the problems.

5 Conclusion

References

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