OOKAMI PROJECT APPLICATION

Date:

August 2nd, 2022

Project Title:

Porting, tuning, and analysis of the Basic Local Alignment Search Tool (BLAST) for A64FX.

Usage:

- Testbed

Principal Investigator:

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Names & Email of initial project users:

David Carlson (david.carlson@stonybrook.edu)

Usage Description:

With more than 100,000 citations in Google Scholar to date, BLAST has been and continues to be one of the most important tools in bioinformatics research. The BLAST algorithm facilitates sequence similarity searches between pairs of nucleotide or amino acid sequences and has been integrated into innumerable codes that perform downstream analysis on the sequence alignments it produces. This project on Ookami is designed to test the performance of BLAST on the A64FX chip. I will compile the code using multiple different compilers, compare performance using standard sequence databases,test the effectiveness of SVE, and attempt to profile and tune the code to improve its efficiency for A64FX.

Computational Resources:

- Total node hours per year: 200-1k node hours

- Size (nodes) and duration (hours) for a typical batch job: 1 node for 4-12 hours

- Disk space (home, project, scratch): standard sizes for home, scratch, and project spaces will be sufficient.

Personnel Resources (assistance in porting/tuning, or training for your users):

No additional personnel resources required.

Required software:

I will compile and install all necessary software.

If your research is supported by US federal agencies:

Not Applicable

Production projects:

This is a testbed project.