Improvement Proposal
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CS 312

1. Specific Problem

The Needleman-Wunsch algorithm from Project 5 is not optimized for multiple processors.
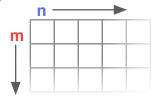
2. Proposed Solution

As a student in bioinformatics with Dr. Clement as well as a student equipped with knowledge from Dr. Snell's parallel processing class, I propose to improve the NW algorithm as implemented in Project 5 by writing a solution that takes advantage of all processing cores on a machine. Potentially, this may include the general-purpose graphics processing units (GPGPU) available in NVIDIA graphics cards. I will write the proposed solution in the C language since all of the best parallel processing libraries (that I am aware of, e.g. OpenMP, MPI, CUDA) are available in only in C.

3. Analysis of Asymptotic Bound & Justification

Scoring & Extraction

- Consider array lookups and data assignments as $O(1)$ operations;
- outer loop is n, inner loop is m; therefore, the algorithm is $O(n \cdot m)$

- Space complexity is $O(n \cdot m)$
- Time complexity is $O(n \cdot m)$

Justification

- Although the asymptotic bound is not improved by adding multiple processing cores, the practical benefit is large: for an alignment that would normally take 6 hours on a single CPU, we might be able to achieve a speedup of anywhere from 2-100 times. Such an improvement is possible and even likely on today's hardware: the latest GPGPUs have 240 cores. Thus a computation that would normally take 6 hours might be reduced to a few minutes.

- Putting the knowledge I've learned in parallel processing into practice in this manner would be educational and useful in the bioinformatics field.

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