

# Parallel Prefix DNA Sequence Alignment with CUDA

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## What is CUDA?

- CUDA is a parallel computing architecture that takes advantage of the processing power of Graphics processing units (GPUs).
- CUDA uses the central processing unit (CPU) and GPU to **accelerate computing**. Serial code is run on the CPU while parallel code is run on the GPU.

## Needleman-Wunsch

- Needleman-Wunsch is a **bioinformatics** algorithm that compares the similarities between strands of DNA.
- The algorithm works by 1) defining scoring rules, 2) using **dynamic programming** to calculate scores for all possible alignments, and 3) selecting the best-scoring alignment.

		C	C	A	A	T
	0	-1	-2	-3	-4	-5
A	-1	0	-1	-1	-2	-3
C	-2	0	1	0	-1	-2
C	-3	-1	1	1	0	-1
A	-4	-2	0	2	2	1

Each cell is calculated thusly:  
Decrement the west value by the gap penalty, decrement the north value by the gap penalty, and add one to the northwest value if the corresponding letters match. Otherwise, keep the northwest the same. Then, take the maximum of those three values.

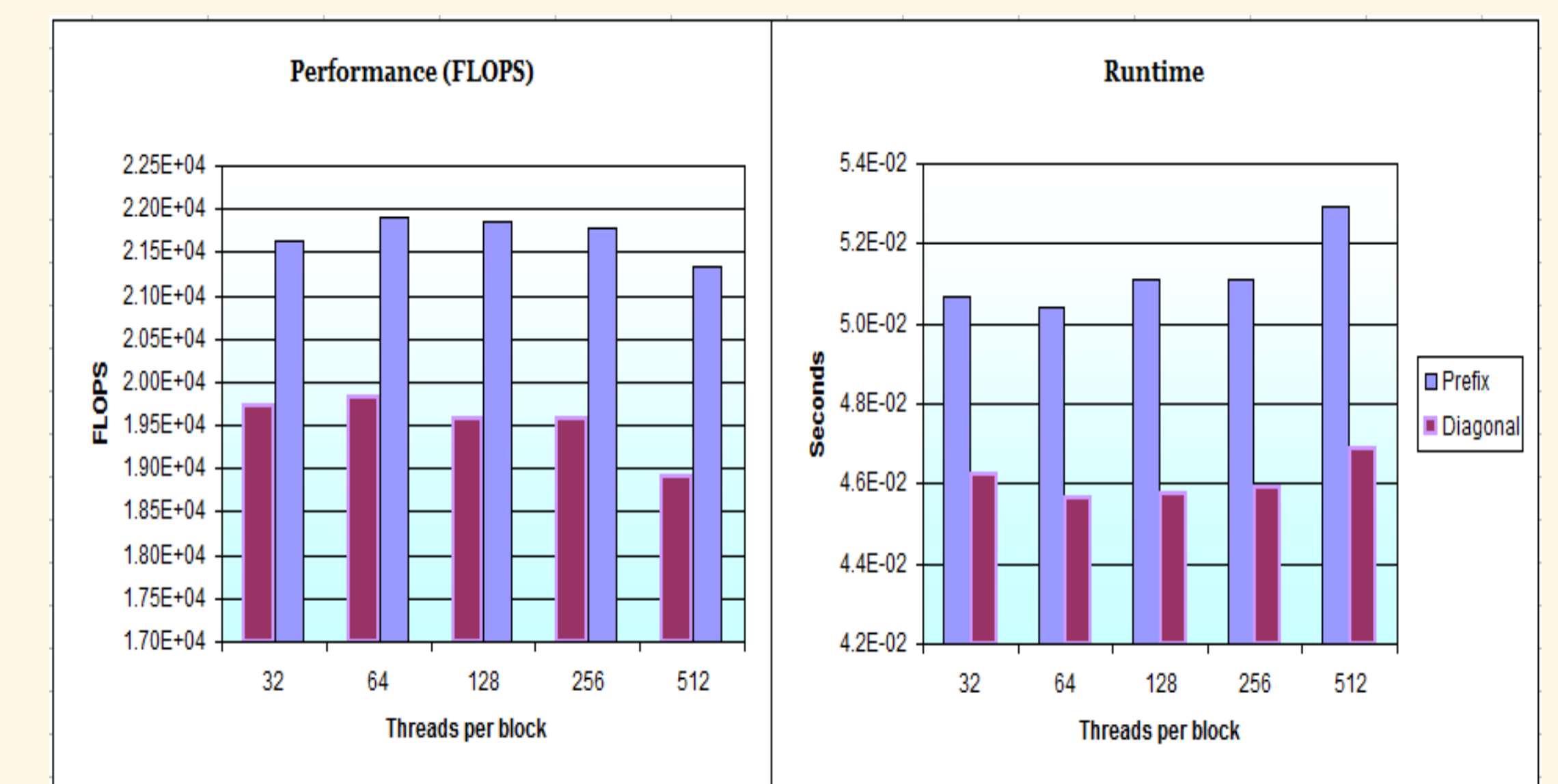
## Parallel DNA Sequence Alignment

- A popular parallel algorithm for Needleman-Wunsch calculates **diagonal** rows across the scoring table in parallel.
- We use CUDA to parallelize the algorithm using **parallel prefix** [1].
- CUDA allowed us to use hundreds of threads to simultaneously calculate the best alignment. Without the GPU, the CPU would limit performance.
- Using parallel prefix, we can ensure that each row is calculated in parallel.
- Parallel prefix uses the north and northwest entries of the scoring matrix, while using a binary associative operator, in this case the maximum function, in order to compute the row entries as partial values.

z[j]	-1	1	-2	3	-2	-4	2	1
x[j]	-1	1	-2	3	-2	-4	2	1
max	-1	1	-2	3	-2	-4	2	1
x[j]	-1	1	-2	3	-2	-2	2	2
max	1	1	3	3	-2	-2	2	2
x[j]	-1	1	1	3	-2	-2	2	2
max	3	3	3	3	2	2	2	2
x[j]	-1	1	1	3	3	3	3	3
max	3	3	3	3	3	3	3	3

## Results

- We ran simulations of the diagonal and prefix programs, varying the number of **threads per block**.
- We graphed average duration and performance on a GeForce GTX-460.
- At 1000 character sequence on 336 cores, diagonals outperformed prefix, contrary to other predictions [1]. However, the margin of difference is small and possibly inconclusive. To find conclusive results, we would like to test a much larger sequence on a better graphics card. Optimization of our code would also be necessary.



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[1] Aluru, Srinivas, Futamura, Natsuhiko, and Mehrotra, Kishan. "Parallel biological sequence comparison using prefix computations". Journal of Parallel and Distributed Computing 2002: 264-272. Print.