Massively Parallel Mapping of Next Generation Sequence Reads Using GPUs

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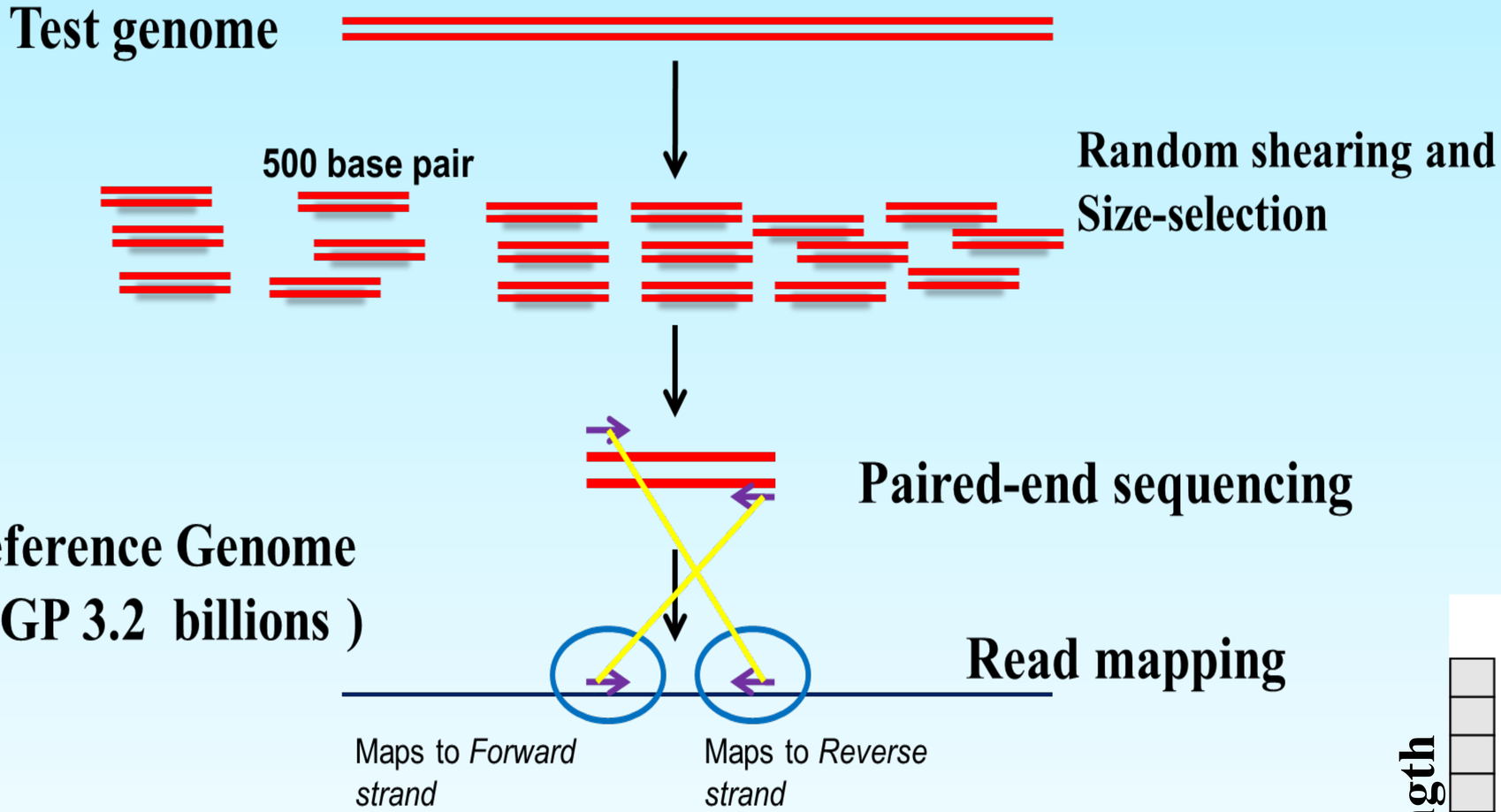
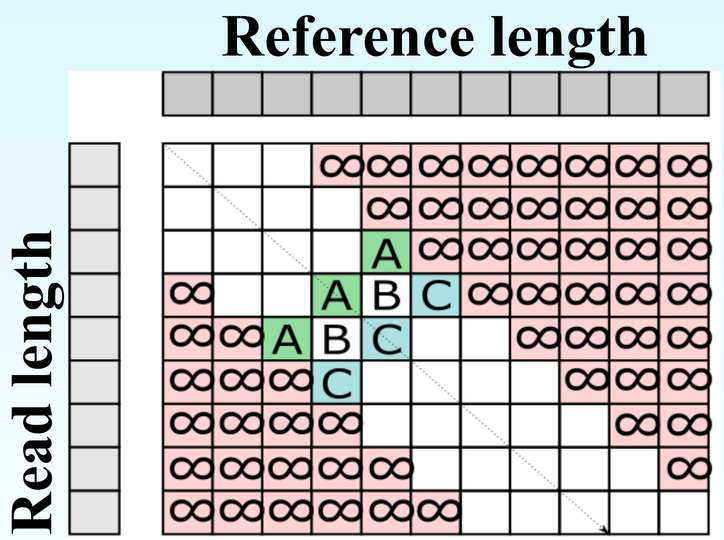
Motivation

- DNA sequence alignment problem is a character-level comparison of DNA sequences obtained from one or more samples against a database of reference genome sequence of the same or a similar species.
- Huge computational burden due to the comparison of >1 billion short (100 characters, or base pairs) “reads” against a very long (3 billion base pairs) reference genome.
- Requires 30-50 CPU days for mapping & alignment
- >1 million whole human genomes by the end of 2017!
- Clinical sequencing in trials in the US
  - Genome sequencing as a routine test at hospitals
  - We need very fast, accurate, and low-cost analysis methods

Whole Genome Sequencing





Edit distance

Aims

- Develop and implement a GPGPU-friendly algorithms to map DNA sequence reads to the reference genome

- Take advantage of the embarrassingly parallel nature of the problem to concurrently align millions of read vs reference pairs

- Implementation using the CUDA (Compute Unified Device Architecture) platform, and testing using the NVIDIA Tesla K20 GPGPU processors.

Alignment GPU Algorithm

Reference length

Read length

		-	A	C	A	C	A	C	T	A	G	T	A
	-	0	0	0	0	0	0						
	A	0	1	0	-1	-1	1	0					
	G	0	0	0	-1	-2	-2	0	-1				
	C	0	-1	1	0	-1	-2	-1	-1	-2			
	A	0	1	0	2	1	0	-1	-2	0	-1		
	C		0	2	1	3	2	1	0	-1	-1	-2	
	A			1	3	2	4	3	2	1	0	-1	-1
	C				2	4	3	5	4	2	1	0	
	A					3	5	4	4	5	3	2	
	T						4	4	5	4	4	4	
	A							3	4	6	5	4	
	G								3	5	7	6	5

Thread 1

Thread 2

Thread 3

Thread 4

Thread 5

Alignment GPU Algorithm

Reference length

Read length

					-	A	C	A	C	A	C	T	A	G	T	A
				-	0	0	0	0	0	0						
				A	0	1	0	-1	-1	1	0					
				G	0	0	0	-1	-2	-2	0	-1				
				C	0	-1	1	0	-1	-2	-1	-1	-2			
				A	0	1	0	2	1	0	-1	-2	0	-1		
				C		0	2	1	3	2	1	0	-1	-1	-2	
				A			1	3	2	4	3	2	1	0	-1	-1
				C				2	4	3	5	4	3	2	1	0
				A					3	5	4	4	5	4	3	2
				T						4	4	5	4	4	5	4
				A							3	4	6	5	4	6
				G								3	5	7	6	5

Thread 5

Thread 4

Thread 1

Thread 2

Thread 3

Contributions

- Map a time-consuming application to massively parallel GPU architectures.
- Move the compute-intense parallel verification step to the GPGPUs.
- Collect the reads in a buffer, then pass to the GPGPU for millions of simultaneous alignments.
- Determine the number of alignments automatically by considering the characteristics of the GPGPU.
- Adjust the number of threads used per alignment dynamically based on the maximum allowed error threshold set by the user.
- Ability to be merged with any existing and future hash-table based read mapping applications.
- Ability to be used for various configurations like different read sizes, reference genome size and error allowance.
- Reduce host to GPU transfer time significantly by placing all relevant data to the GPU global memory in the initialization step.
- Develop dynamic programming backtracking in GPU, bypassing CPU-based post processing all together, except for I/O operations.

Backtracking GPU Algorithm

Reference length

Read length

	-	A	C	A	C	A	C	T	A	G	T	A
-	0	0	0	0	0	0						
A	0	1	0	-1	-1	1	0					
G	0	0		-1	-2	-2	0	-1				
C	0	-1	1		-1	-2	-1	-1	-2			
A	0	1	0	2		0	-1	-2	0	-1		
C		0	2	1	3		1	0	-1	-1	-2	
A			1	3	2	4		2	1	0	-1	-1
C				2	4	3	5		3	2	1	0
A					3	5	4	4		4	3	2
T						4	4	5	4		5	4
A							3	4	6	5		6
G								3	5	7	6	

A - C A C A C T A G T A -

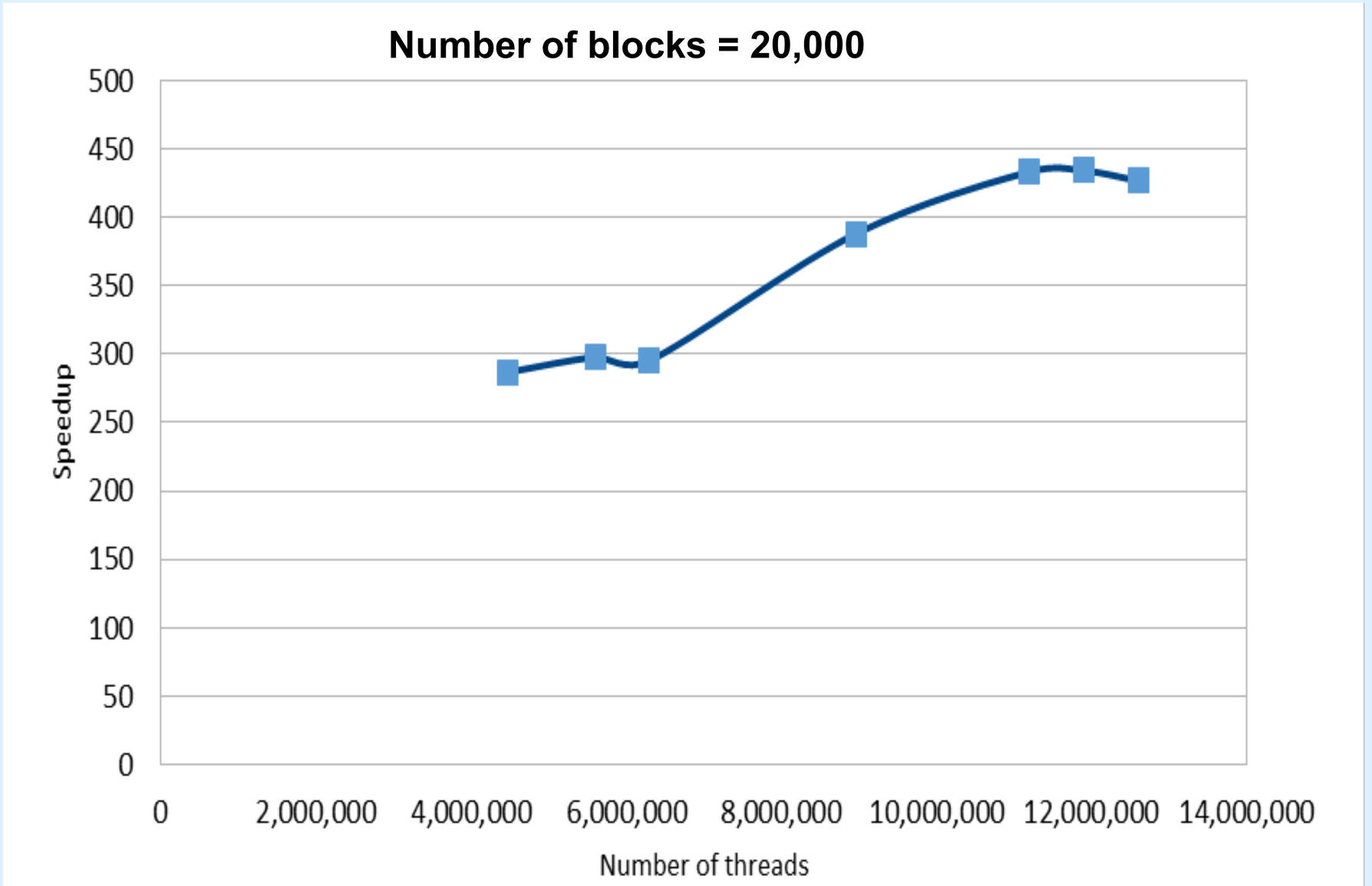
A G C A C A C - A - T A G

-1	-1
1	0

Read length + Reference length

0	0	1	0	0	-1	-1	-2	0	-1	-1	-2	-1	-1	0							
0	0	-1	-1	-2	-2	-2	-1	-1	-2	0	-1	1	0	2	1	3	2	4			
0	0	1	0	0	1	0	-1	1	0	2	1	3	2	4	3	5	4	4	5	4	6	5
0	0	0	-1	1	0	2	1	3	2	4	3	5	4	4	5	4	6	5	7	6		
0	0	1	0	2	1	3	2	4	3	5	4	4	3	4	3	5						

Speedup (tentative results)



Thank You