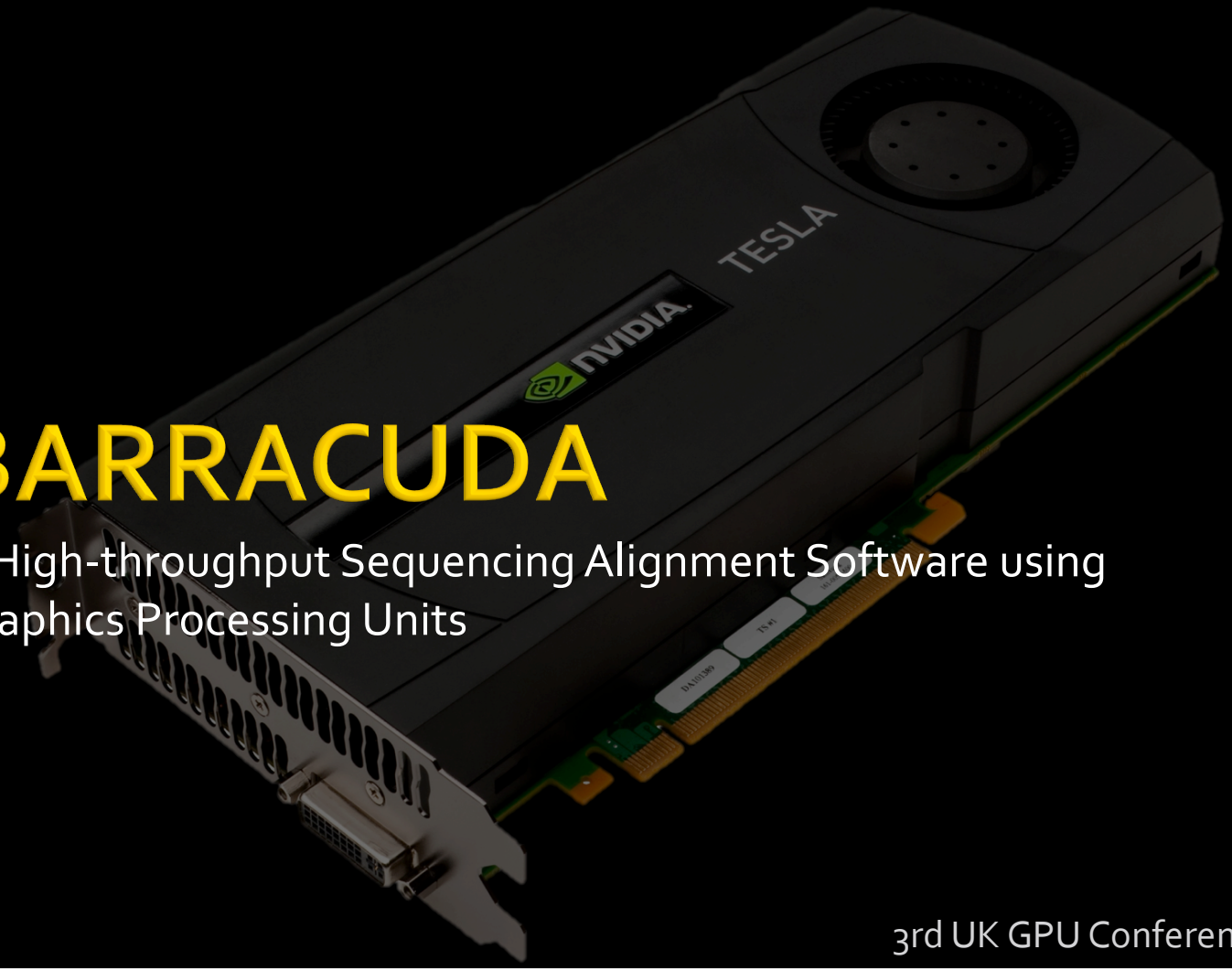

BARRACUDA

A High-throughput Sequencing Alignment Software using Graphics Processing Units

Brian Lam

3rd UK GPU Conference, 14th Dec 2011

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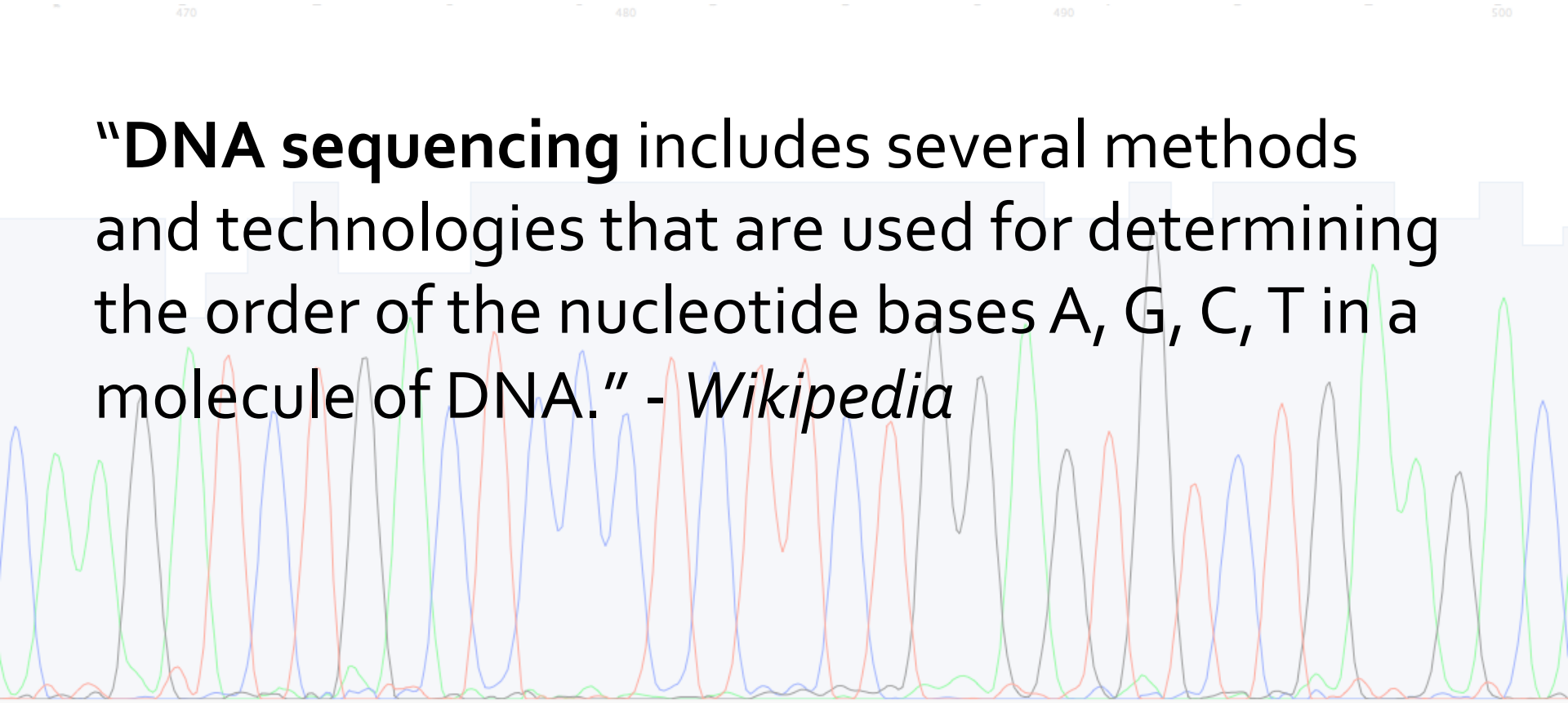
The Genome and DNA

- A genome of a living organism is a complete repertoire of genetic programs (including genes and other regulatory regions) that encode all its functions and development
- Individual functions are determined by genes, which are coded by strings of deoxyribonucleic acids (DNA), comprising of adenine (A), guanine (G), cytosine (C), and thymine (T), joined together in a specific order (e.g. ACCATG)
- A Human genome has 3 billion DNA nucleotide bases (or bp)

DNA sequencing



"**DNA sequencing** includes several methods and technologies that are used for determining the order of the nucleotide bases A, G, C, T in a molecule of DNA." - *Wikipedia*

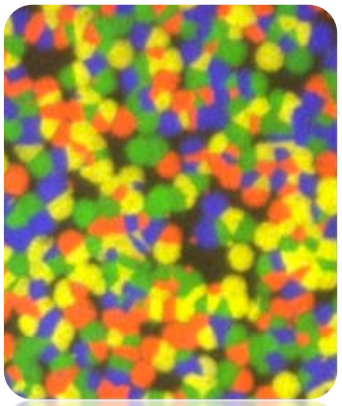
High-throughput DNA sequencing

- Commercialised in 2005 by 454 Life Science
- Sequencing in a massively parallel fashion

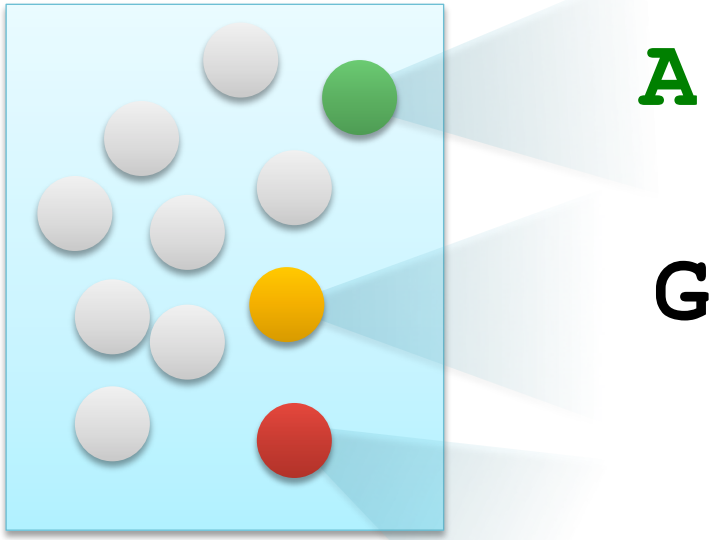
How it works

- An example: Whole genome sequencing
  - Extract genomic DNA from blood/mouth swabs
  - Break into small DNA fragments of 200-400 bp
  - Attach DNA fragments to a surface (flow cells/slides/ microtitre plates) at a high density
  - Perform concurrent "cyclic sequencing reaction" to obtain the sequence of each of the attached DNA fragments

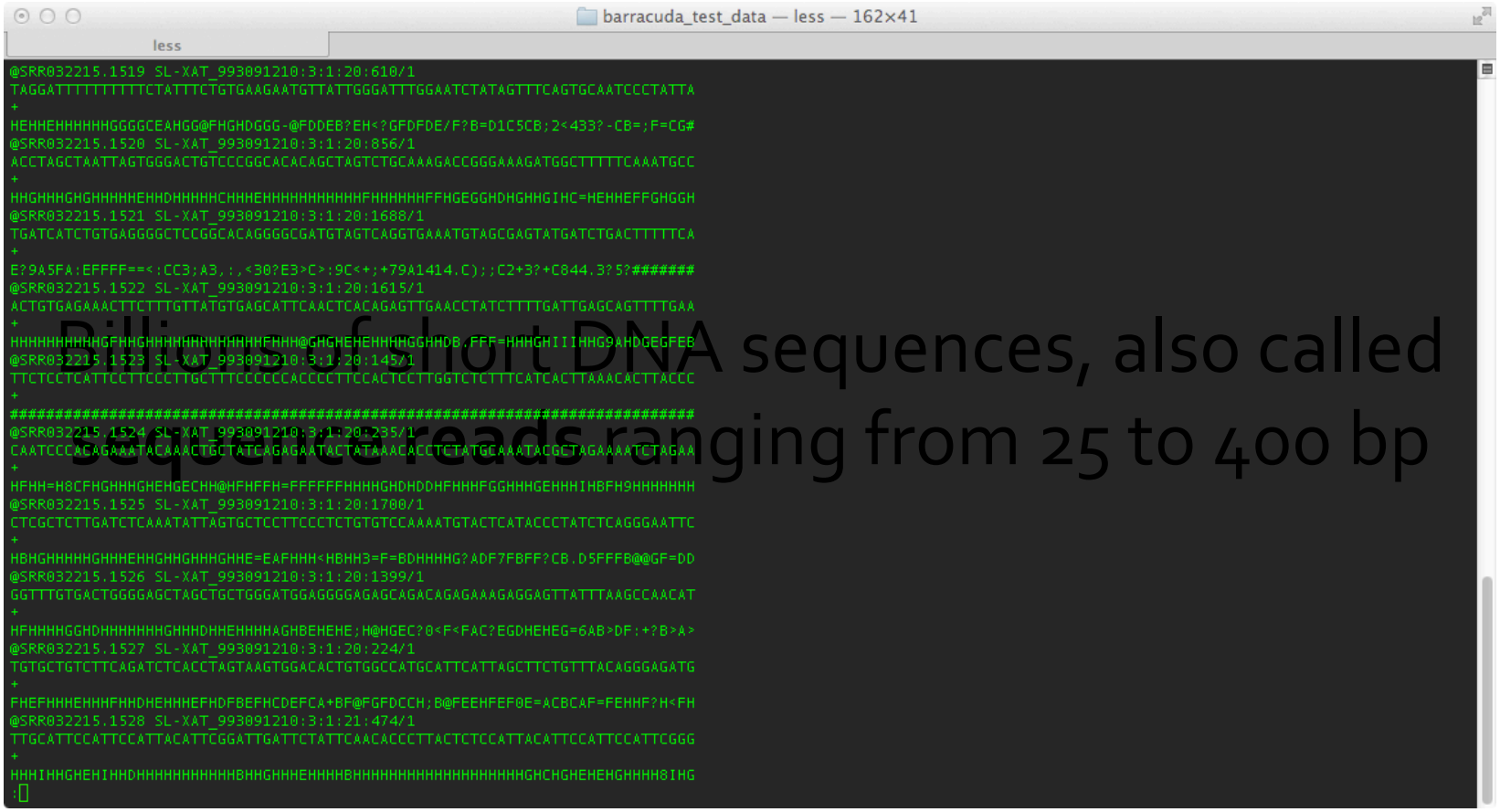
An Illumina HiSeq 2000 can interrogate 825K spots / mm²



Capturing the sequencing signals



What do we get from the sequencers



Billions of short DNA sequences, also called sequence reads ranging from 25 to 400 bp

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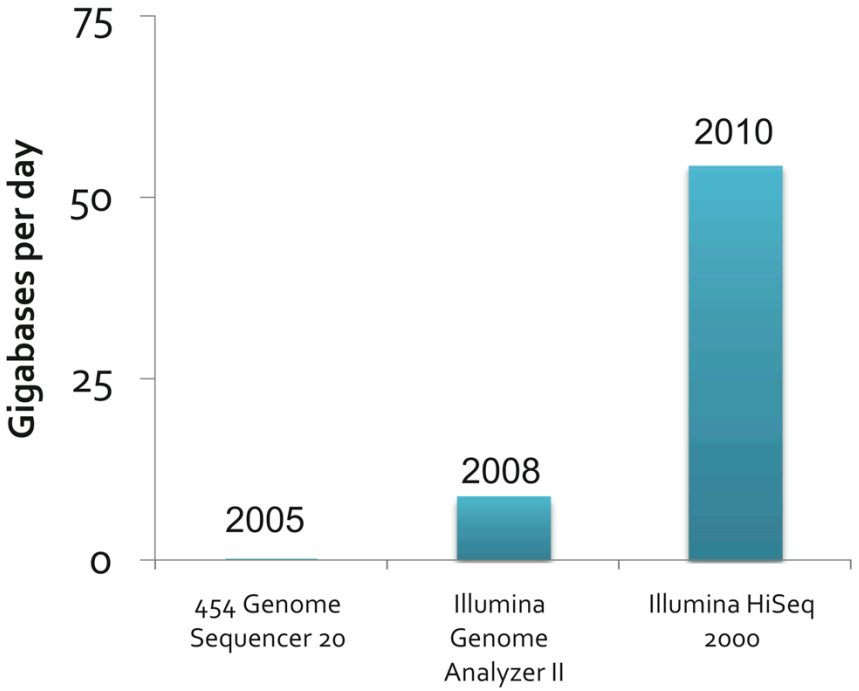
The throughput of HTS has increased dramatically



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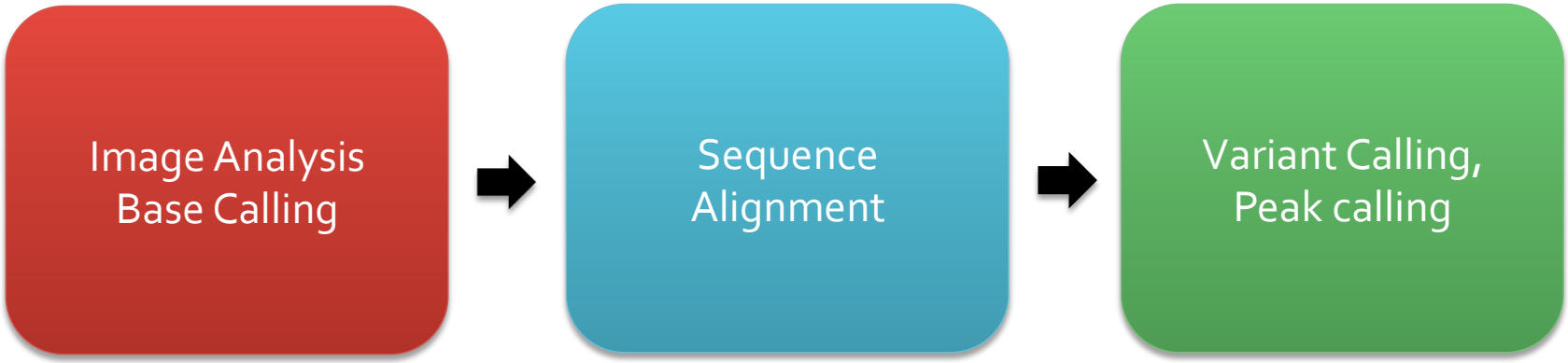
Current bioinformatics pipeline



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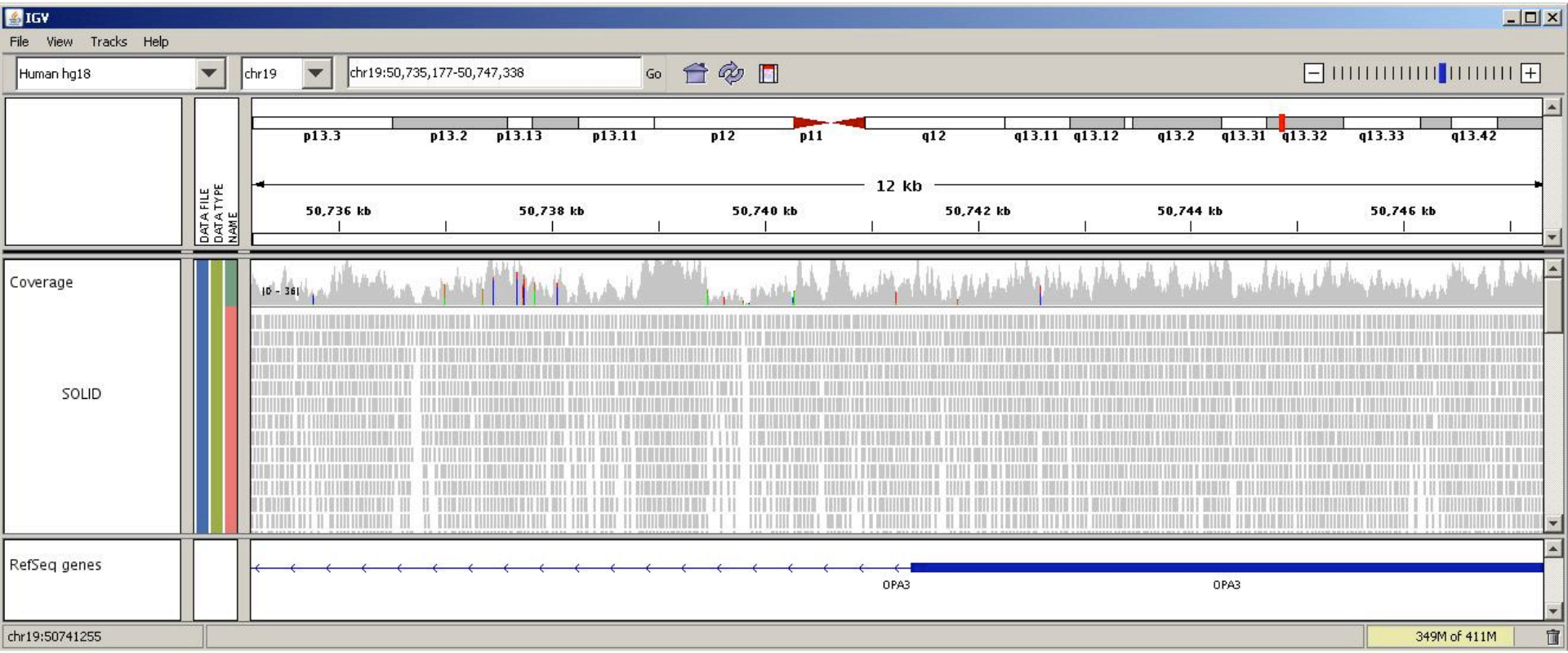
Sequence alignment



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Many-core computing

- Parallel computing using processors that contain a 'large number' on processing units on a physical die
  - Examples
    - NVIDIA Tesla M2090 - 512 CUDA cores (GPGPU)
    - AMD Radeon HD 7900 series - 2048 cores? (GPGPU)
    - Intel Knights Corner co-processor – 50x+ **x86** cores

Why bother?

- Low capital cost and energy efficient
  - Dell 12-core workstation (144 GFLOP/s): £5,000, ~1kW
  - Dell 40-core computing cluster (480 GFLOP/s): £ 20,000+, ~6kW
  - NVIDIA Tesla C2070 (500G FLOP/s): £1,500, ~0.2kW
  - NVIDIA Geforce GTX 590 (1 TFLOP/s): £400, ~0.4kW
- Many supercomputers now also contain multiple GPU nodes for parallel computations

GPU in bioinformatics

- Examples:
  - CUDASW++ → 6.3X
  - MUMmerGPU → 3.5X
  - GPU-HMMer → 60-100x

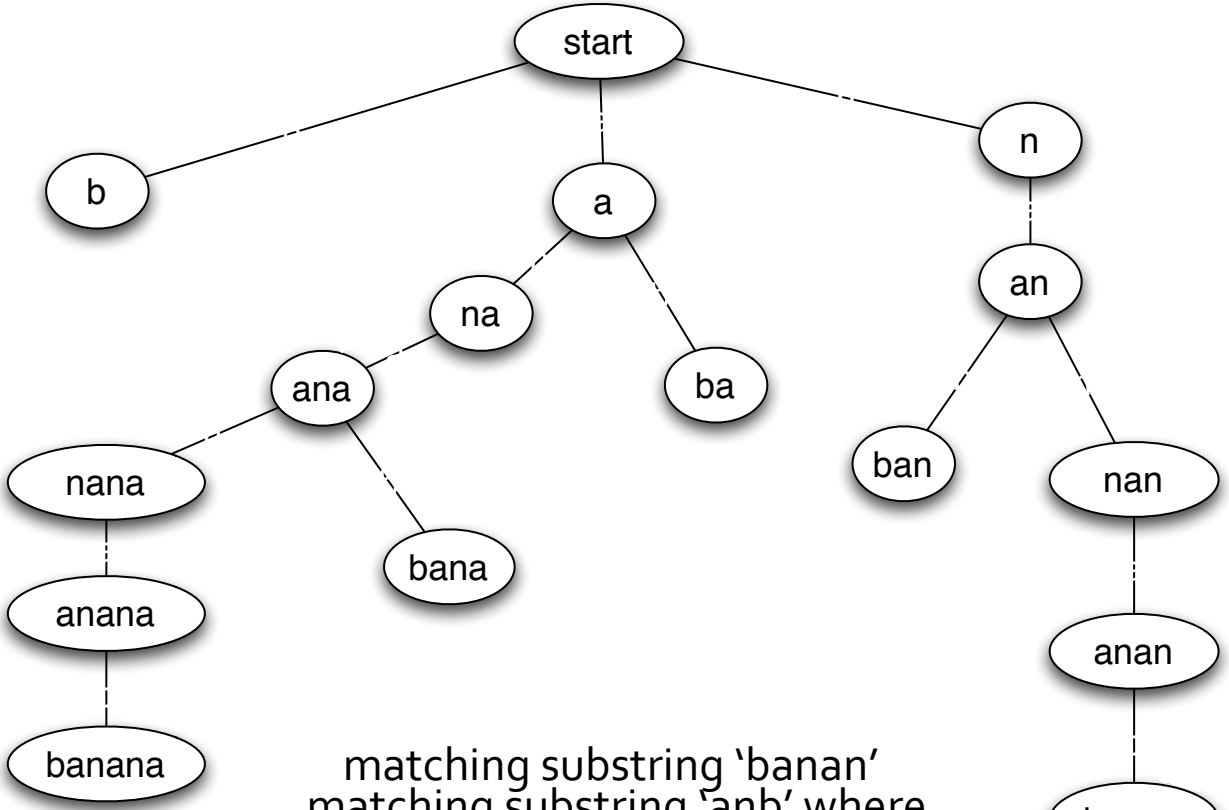
The BarraCUDA Project

- The main objective of the BarraCUDA project is to develop a software that runs on many-core architectures
  - i.e. to map sequence reads the same way as they come out from the HTS instrument

Burrows-Wheeler transform

- Originally intended for data compression, performs reversible transformation of a string
- In 2000, Ferragina and Manzini introduced BWT-based index data structure (FM-index) for fast substring matching at $O(n)$
- Sub-string matching is performed in a tree traversal-like manner
- Used in major sequencing read mapping programs e.g. BWA, Bowtie, Soap2

How it works – a backward search algorithm



matching substring ‘banan’
matching substring ‘anb’ where
‘b’ is subsituted with an ‘a’

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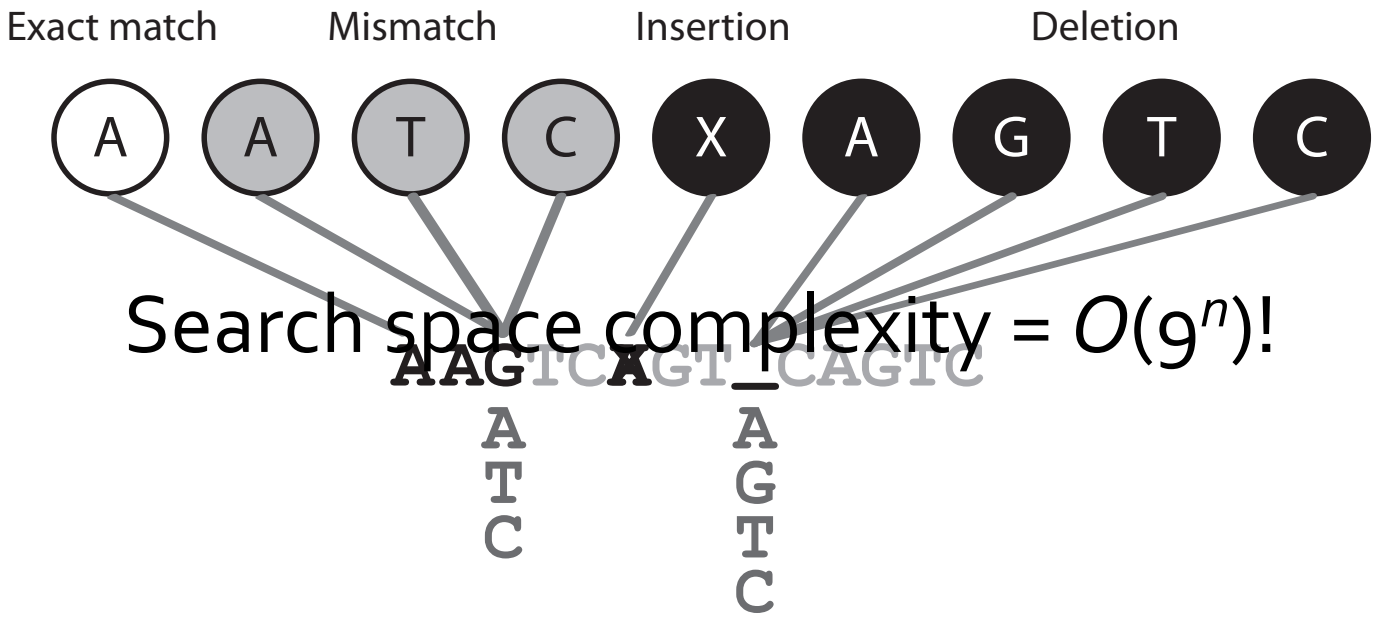
Inexact matching requires base substitution within the query substring



Search space complexity = $O(9^n)$!

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BarraCUDA started its life as a GPU version of BWA

- Ported BWA to CUDA with simple data parallelism
- Used mainly the GPU for sequence mapping

- And it _partially_ worked!
  - 10% faster than 8Cs @ 3GHz
  - BWA uses a greedy breadth-first search approach (takes up to 40MB per thread)
  - Not enough workspace for thousands of concurrent kernel threads (@ 4KB) – i.e. reduced accuracy

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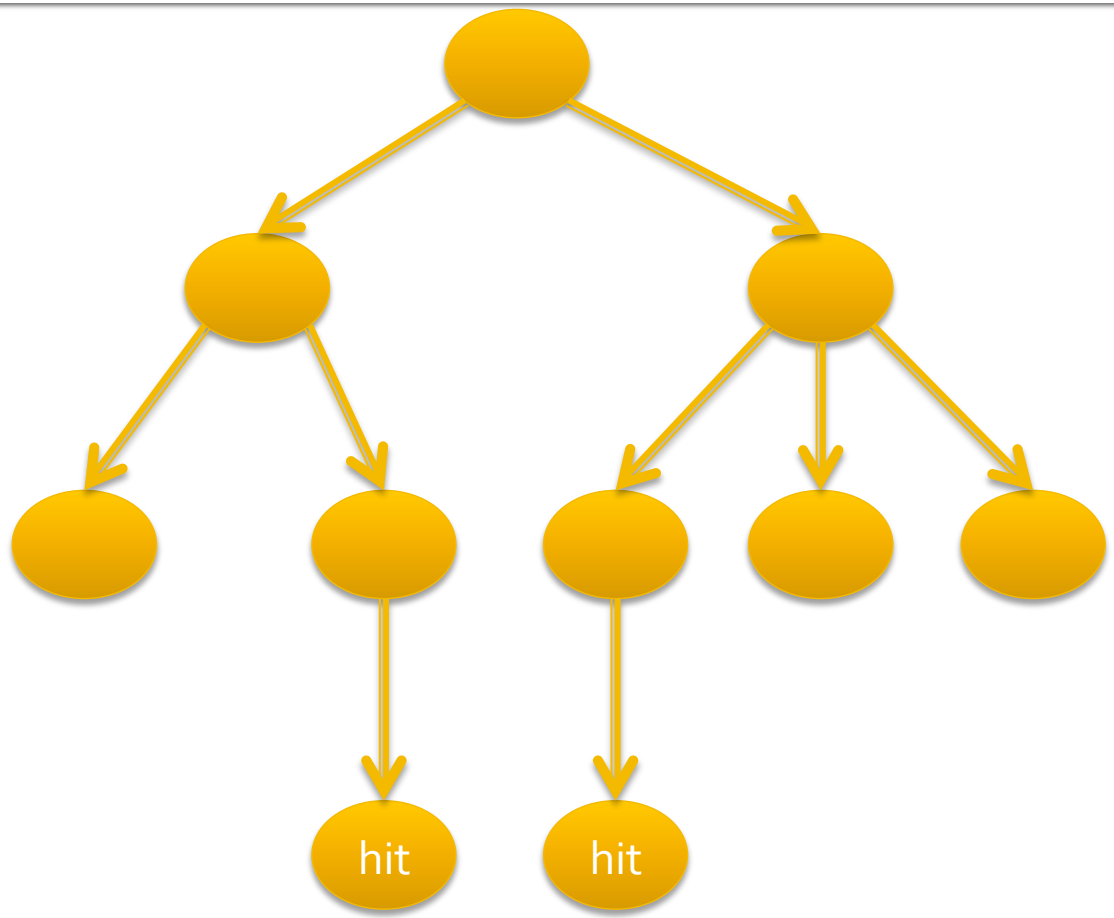
BarraCUDA uses a depth-first search approach



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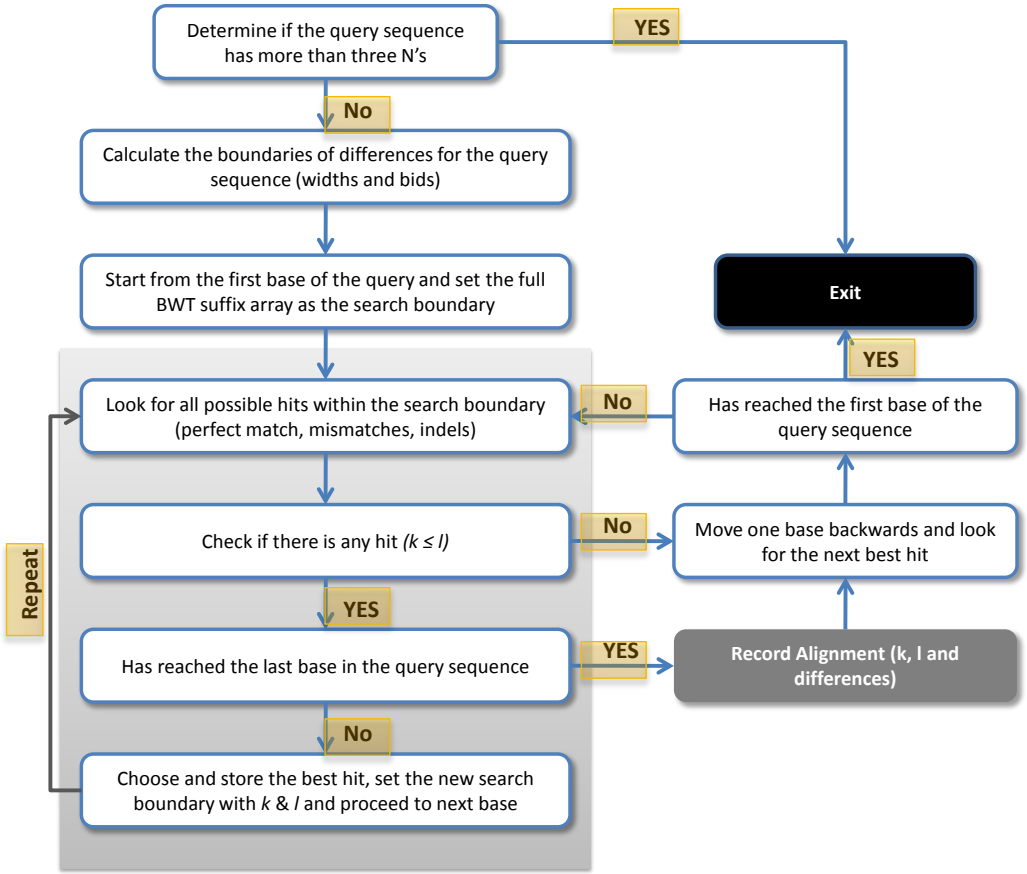
Branch divergence



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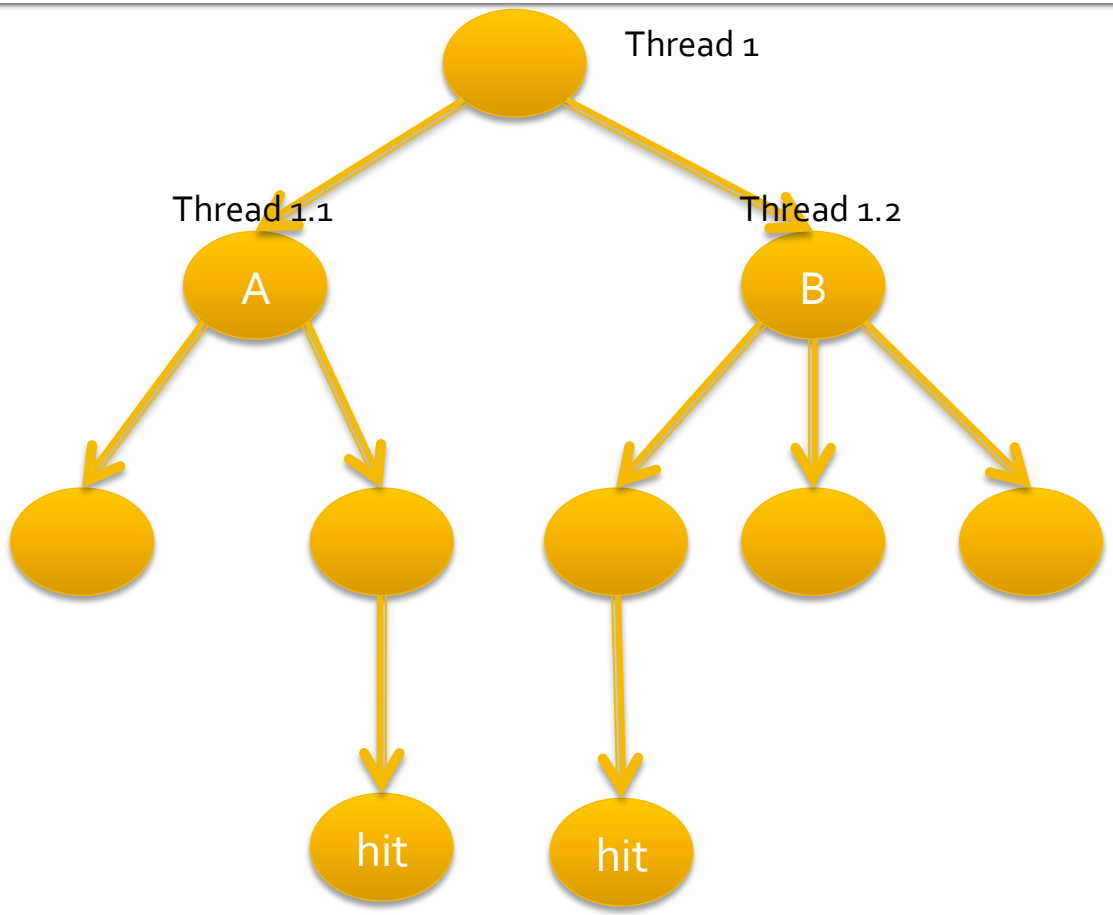
Multi-kernel design



CPU thread queue:

A B

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Mapping accuracy

- Artificial dataset from *C. Elegans* genome
  - 1M 70bp simulated reads with 2% base error rate

Mapping accuracy

	BWA 0.5.8	BarraCUDA
Mapping	89.95%	91.42%
Error	0.06%	0.05%

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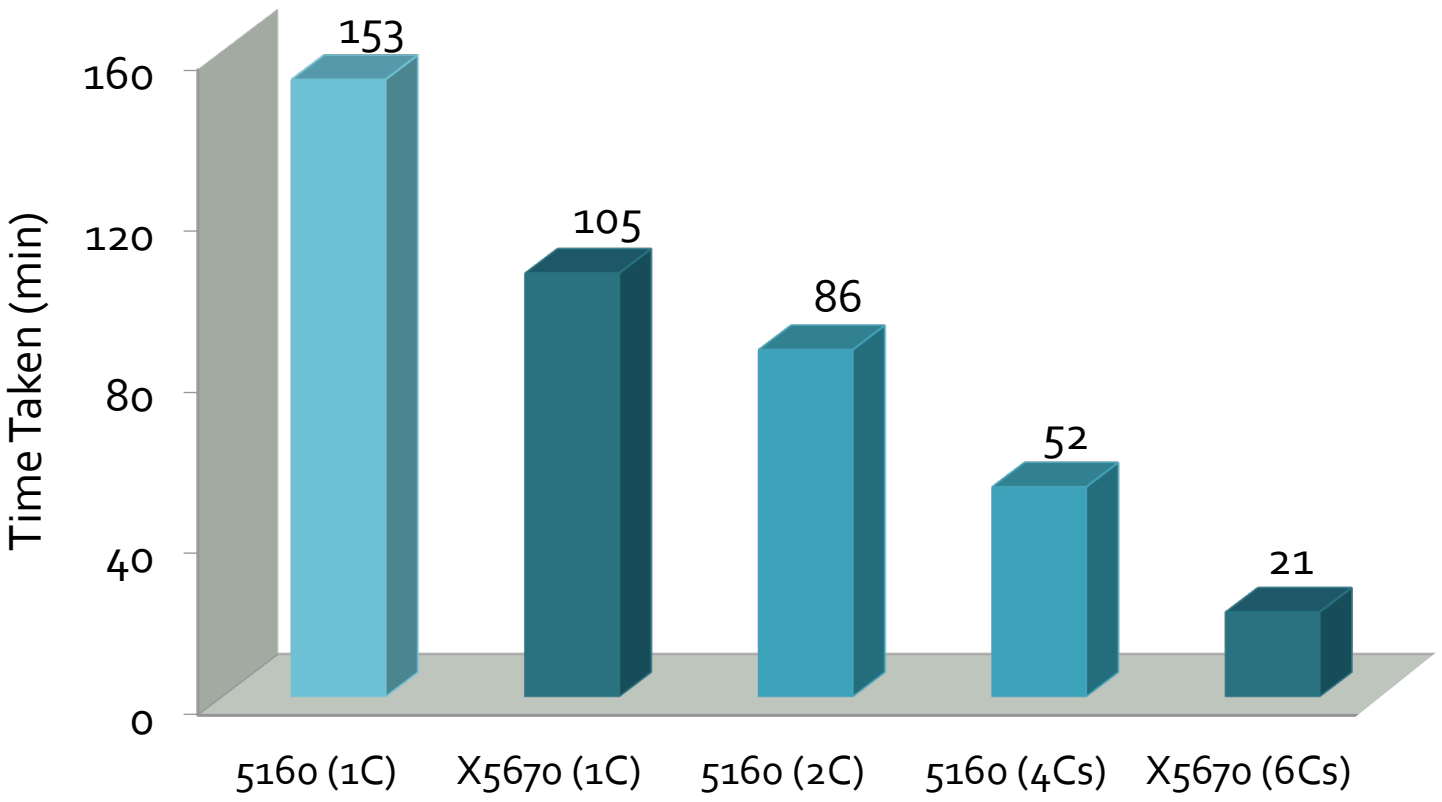
Mapping speed

- Query library: A human 76bp whole genome shotgun library containing 14M reads from the 1000 Genomes Project
- Reference: the Human genome

Hardware configurations

- CPUs:
  - 2x Intel Xeon 5160 (2Cs) @ 3GHz with 8GB DDR2 RAM and fast RAID storage
  - 1x Intel Xeon X5670 (6Cs) @ 2.93GHz with 8GB DDR3 RAM and fast RAID storage
- GPUs:
  - NVIDIA Tesla M2090 /w 6GB GDDR5 RAM

Mapping speed



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Multiple GPUs

- A shell script to further divide read library into smaller chunks
- Distributes chunks to multiple GPUs

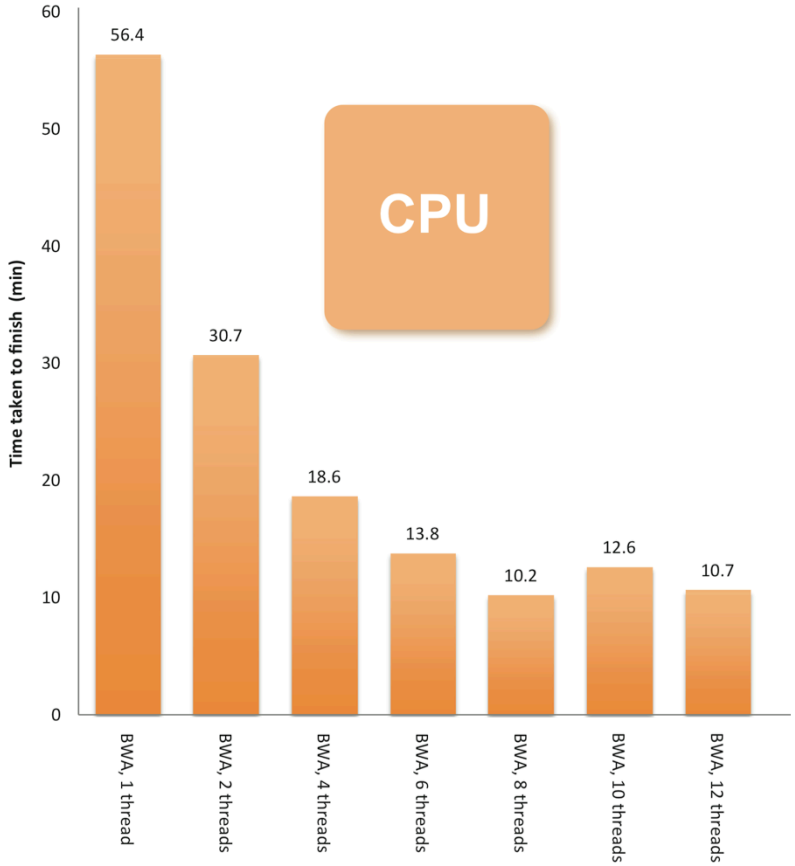
Hardware configurations

- CPUs:
  - 2x Intel Xeon X5670 (6Cs) @ 2.93GHz with 8GB DDR3 RAM and fast RAID storage
- GPUs:
  - 8x NVIDIA Tesla M2050 /w 3GB GDDR5 RAM

Scalability

- Query library: A fly 95bp whole genome shotgun library containing 13.5M reads from the ENA
- Reference: the fly genome

Scalability



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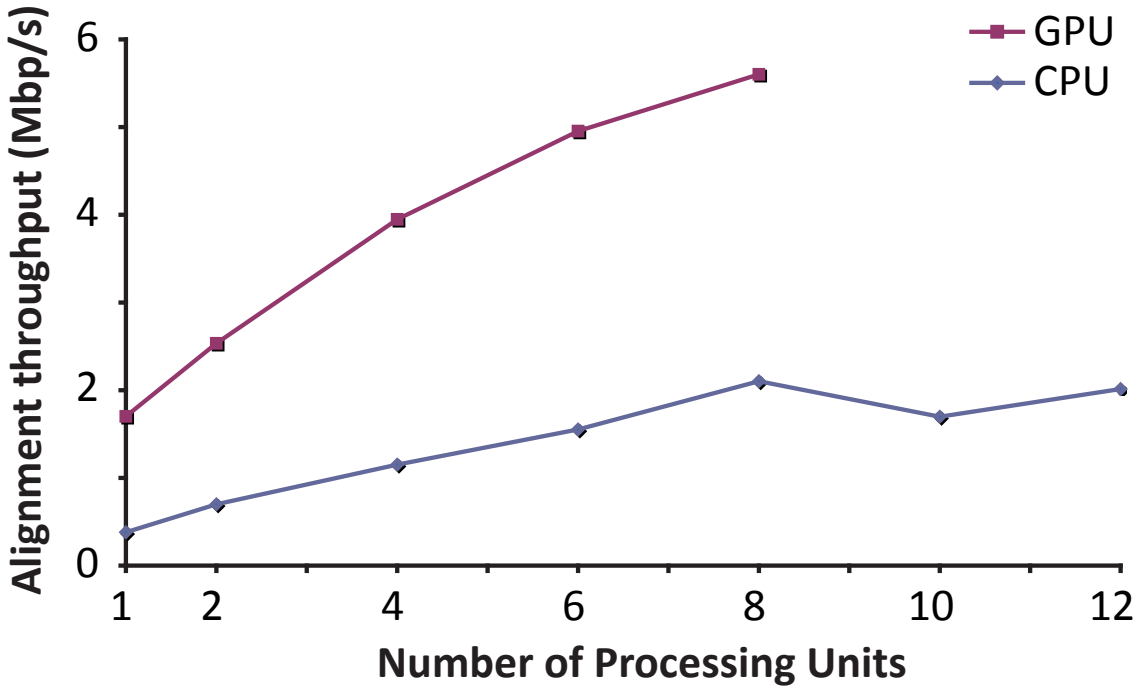
Scalability



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Conclusions

- We developed BarraCUDA to map sequence reads onto a genome using GPUs
- The performance from 1 GPU is roughly the same as 6 Xeon CPU cores
- Superior scalability compared to CPUs

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Future Outlook

- The game is changing
  - CPUs are getting more cores : AMD 16-core Opteron 6200 series
- Many-core platforms are evolving
  - Intel MIC
  - NVIDIA Kepler platform
  - AMD Radeon 7900 series
- OpenCL

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EurOCHIP

SEVENTH FRAMEWORK PROGRAMME

EUROPEAN COMMISSION

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NVIDIA

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BarraCUDA is now available @:

http://seqbarracuda.sf.net

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