# TETRACOM: Technology Transfer in Computing Systems

FP7 Coordination and Support Action to fund 50 technology transfer projects (TTP) in computing systems.
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# FPGA Acceleration of Short Read Alignment

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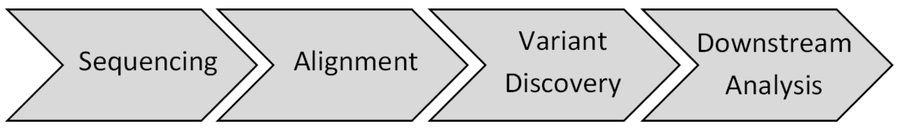
## TTP Problem

NGS throughput increasing faster than Moore's Law

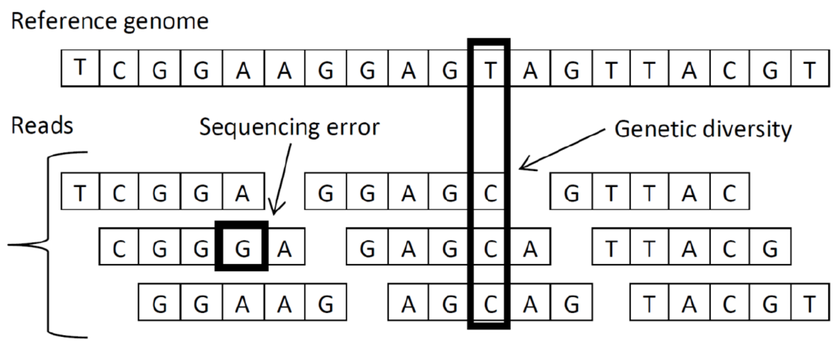
Over 200GB of data to analyse per run

NGS analysis can take days to perform




Alignment is a bottleneck in NGS pipelines: accounts for over 50% of analysis time

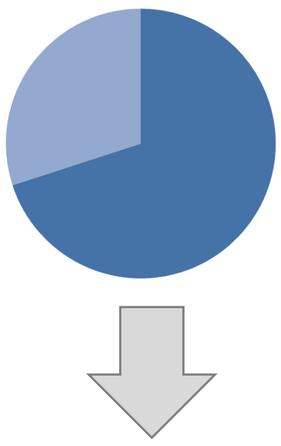
Map sequenced reads to positions in known reference genome



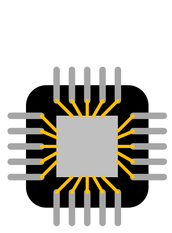

Both exact and approximate alignment required

## TTP Solution

Over 70% of reads can be exactly aligned to reference



Develop customised hardware architecture for exact alignment

Hardware Module

**Algorithm Design**

Design based on FM-index

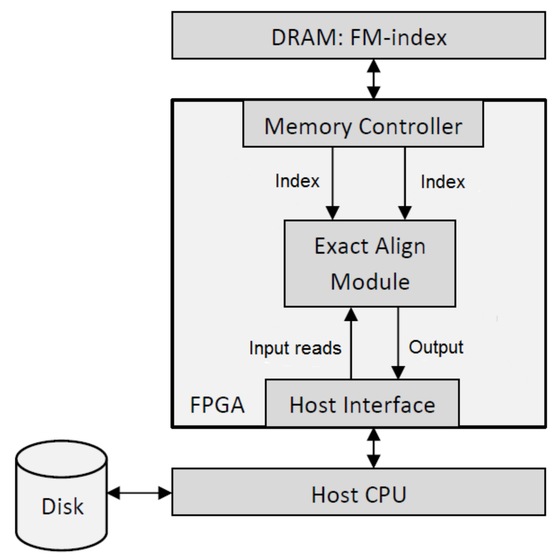
Develop optimisations to reduce off-chip memory access:
- n-step FM-index
- Index oversampling

**Hardware Design**

Implement using Vivado HLS

Develop optimisations to improve hardware performance:
- Interleave processing of multiple reads
- Reduce resource usage

Hardware Design Overview




Derive equations to estimate module performance for hardware platforms

CONVEY COMPUTER™ ALPHA DATA

## TTP Impact

**Benchmarking**

Software tools
- Soap2, BWA, Bowtie2 – Dual Intel Xeon
- Soap3-dp – NVIDIA C2070 GPU

Hardware Design
- Convey HC-2ex with 4 Xilinx Viretx-6 LX760 FPGAs

Data set
- 10M reads of 100 bases from Hg19


**Results**

Hardware performance up to:
- 91x faster than Soap2
- 34x faster than Soap3-dp

Implications
- Alignment reduced from hours to minutes

## TTP Facts

Contact: James Arram
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BLUEBEE High Performance Genomics