GenStore:

A High-Performance In-Storage Processing System for Genome Sequence Analysis

Session 6A: Thursday 3 March, 3:00 PM CEST

Nika Mansouri Ghiasi, Jisung Park, Harun Mustafa, Jeremie Kim, Ataberk Olgun, Arvid Gollwitzer, Damla Senol Cali, Can Firtina, Haiyu Mao, Nour Almadhoun Alserr, Rachata Ausavarungnirun, Nandita Vijaykumar, Mohammed Alser, and Onur Mutlu

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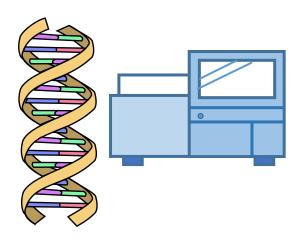






Genome Sequence Analysis

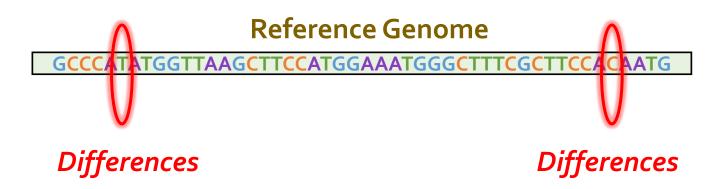
- Genome sequence analysis (GSA) is critical for many applications.
 - Personalized medicine
 - Outbreak tracing
 - Evolutionary studies
- Genome sequencing machines extract smaller fragments of the original DNA sequence, known as reads.





Genome Sequence Analysis

- Read mapping: First key step in genome sequence analysis
 - Aligns reads to potential matching locations in the reference genome



- Read mapping requires computationally-expensive approximate string matching (ASM) to account for differences between reads and the reference genome due to:
 - Sequencing errors
 - Genetic Variation

Genome Sequence Analysis

Data Movement from Storage

ASM

Storage System Main Memory

Cache

Computation
Unit
(CPU or
Accelerator)



Computation overhead



Data movement overhead

Improving the Performance of GSA

Heuristics Accelerators Filters Computation Main Unit

Storage **System**

Memory

Cache

Accelerator)



Computation overhead



Data movement overhead (The effect becomes even larger)

Key Idea



Filter reads that do not require ASM inside the storage system



Filtered Reads

Main Memory Cache Computation
Unit
(CPU or
Accelerator)

Read mapping workloads can exhibit different behavior

There are limited available hardware resources in the storage system

GenStore



Filter reads that do not require ASM inside the storage system

Genstore-Enabled Storage System

Main Memory

Cache

Computation
Unit
(CPU or
Accelerator)



Computation overhead



Data movement overhead

GenStore provides significant speedup (1.4x - 33.6x) and energy reduction (3.9x - 29.2x) at low cost

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