

GenASM: A Low-Power, Memory-Efficient Approximate String Matching Acceleration Framework for Genome Sequence Analysis

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Genome Sequencing



Genome

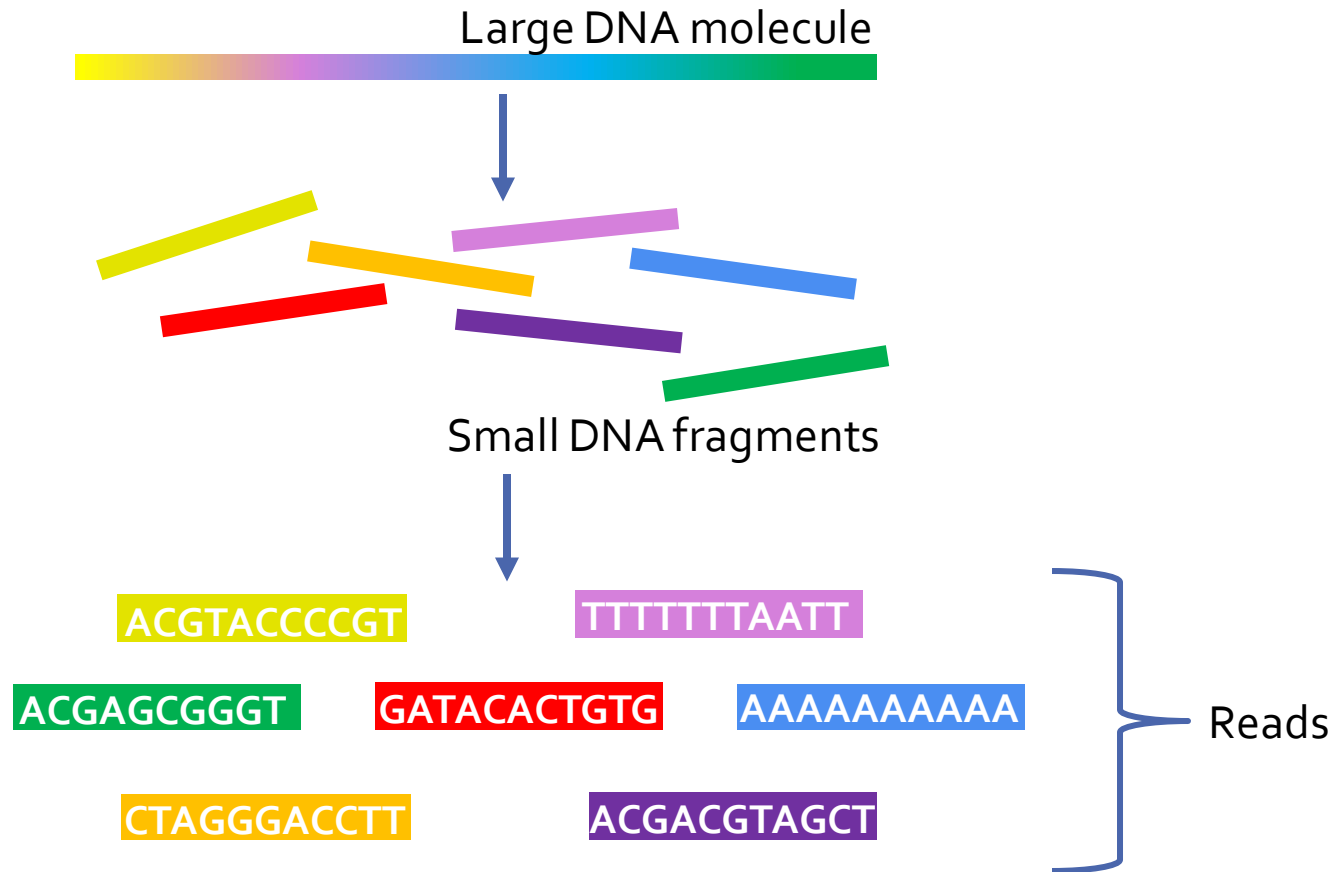


DNA

- ❑ **Genome sequencing** is the process of determining the order of the DNA sequence in an organism's genome.

- ❑ Genome sequencing is **pivotal** in:
 - Personalized medicine
 - Outbreak tracing
 - Evolution
 - Forensics

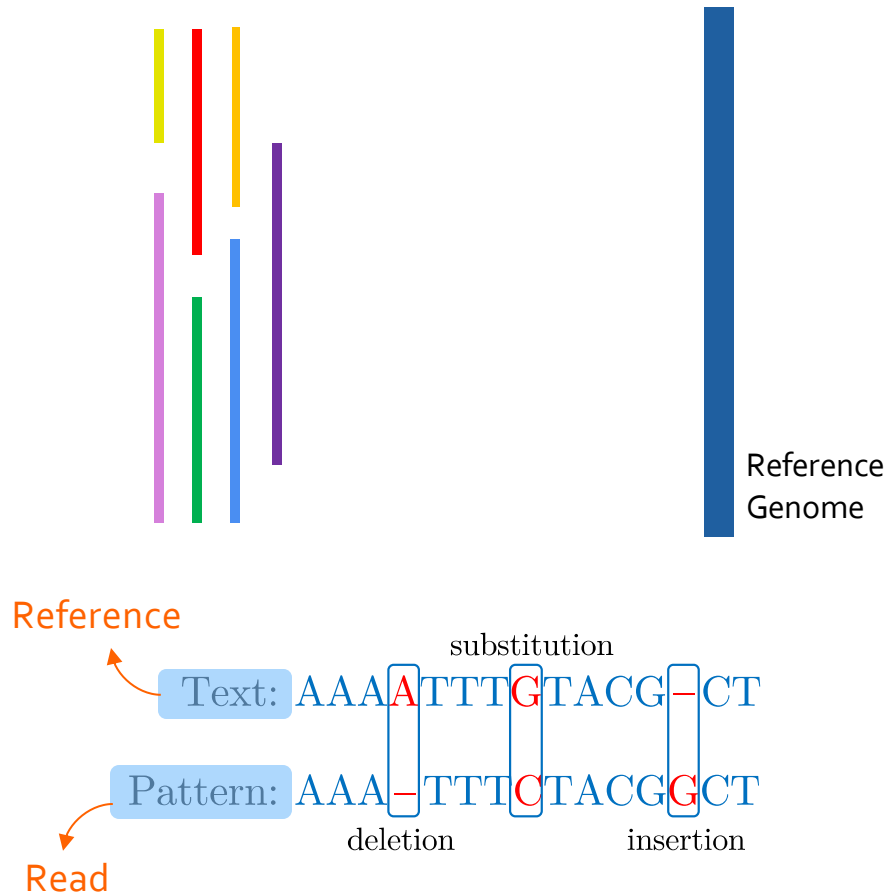
Genome Sequencing (cont.)



Genome Sequence Analysis

- ❑ *Genome sequence analysis* requires:
 - 1) Taking small DNA fragments from an organism
 - 2) Reorganizing them into the entire genome
- ❑ Success of all medical and genetic applications critically depends on:
 - Existence of computational techniques that can process and analyze the enormous amount of sequence data quickly and accurately
- ❑ Effectively leveraging genome sequencing as a tool:
 - Requires **very high computational power**
 - Requires processing a **large amount of data**
 - Bottlenecked by the **current capabilities of computer systems**

Read Mapping



- ❑ *Read mapping* is the method of aligning **reads** against a **reference genome** to detect matches and variations.
 - One of the key components of genome sequence analysis.
- ❑ Goal is to **identify the original location** of each read in the reference genome.
- ❑ Sequenced genome **may not exactly map** to the reference genome
 - **Reason:** mutations, variations, sequencing errors
- ❑ *Multiple steps of read mapping* must account for these errors.

Problem & Our Goal

- ❑ Multiple steps of read mapping are essentially a series of *approximate* (i.e., *fuzzy*) *string matches*
- ❑ Approximate string matching makes up a **significant portion of read mapping** (i.e., more than 70%).
- ❑ One of the key bottlenecks of the entire genome analysis pipeline.

Our Goal:

Accelerate approximate string matching by designing a fast and flexible framework, which can be used to accelerate *multiple steps* of the genome sequence analysis pipeline

Outline

- ❑ Background
- ❑ Motivation
- ❑ ASM with Bitap Algorithm**
- ❑ GenASM: ASM Acceleration Framework
- ❑ Use Cases of GenASM
- ❑ Evaluation
- ❑ Conclusion

Bitap Algorithm

- ❑ We have focused on the **Bitap algorithm**^{1,2}
 - **Reason:** *Bitap* algorithm can perform ASM with **fast and simple bitwise operations**, which makes it **amenable to acceleration**
- ❑ **Step 1: Preprocessing**
 - For each character (A, C, G, T), **generate a pattern bitmask**
 - Indicates if character exists at each position of the pattern.
- ❑ **Step 2: Searching (Edit Distance Calculation)**
 - **Compare all characters of the text with the pattern** by using:
 - Pattern bitmasks
 - Set of bitvectors that hold the status of the partial matches
 - Bitwise operations

[1] R. A. Baeza-Yates and G. H. Gonnet. "A new approach to text searching." *Communications of the ACM*, 1992.

[2] S. Wu and U. Manber. "Fast text searching: allowing errors." *Communications of the ACM*, 1992.

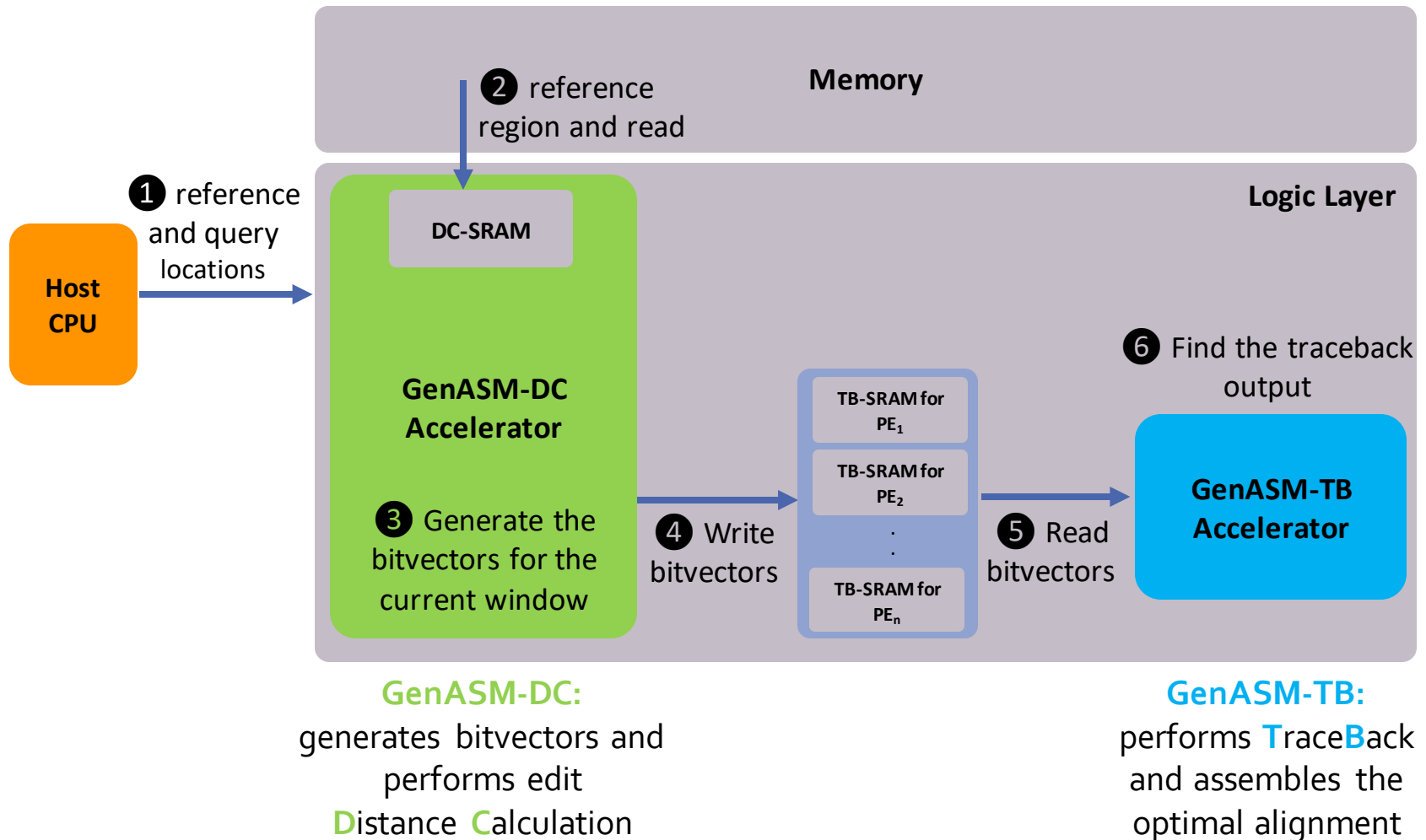
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GenASM

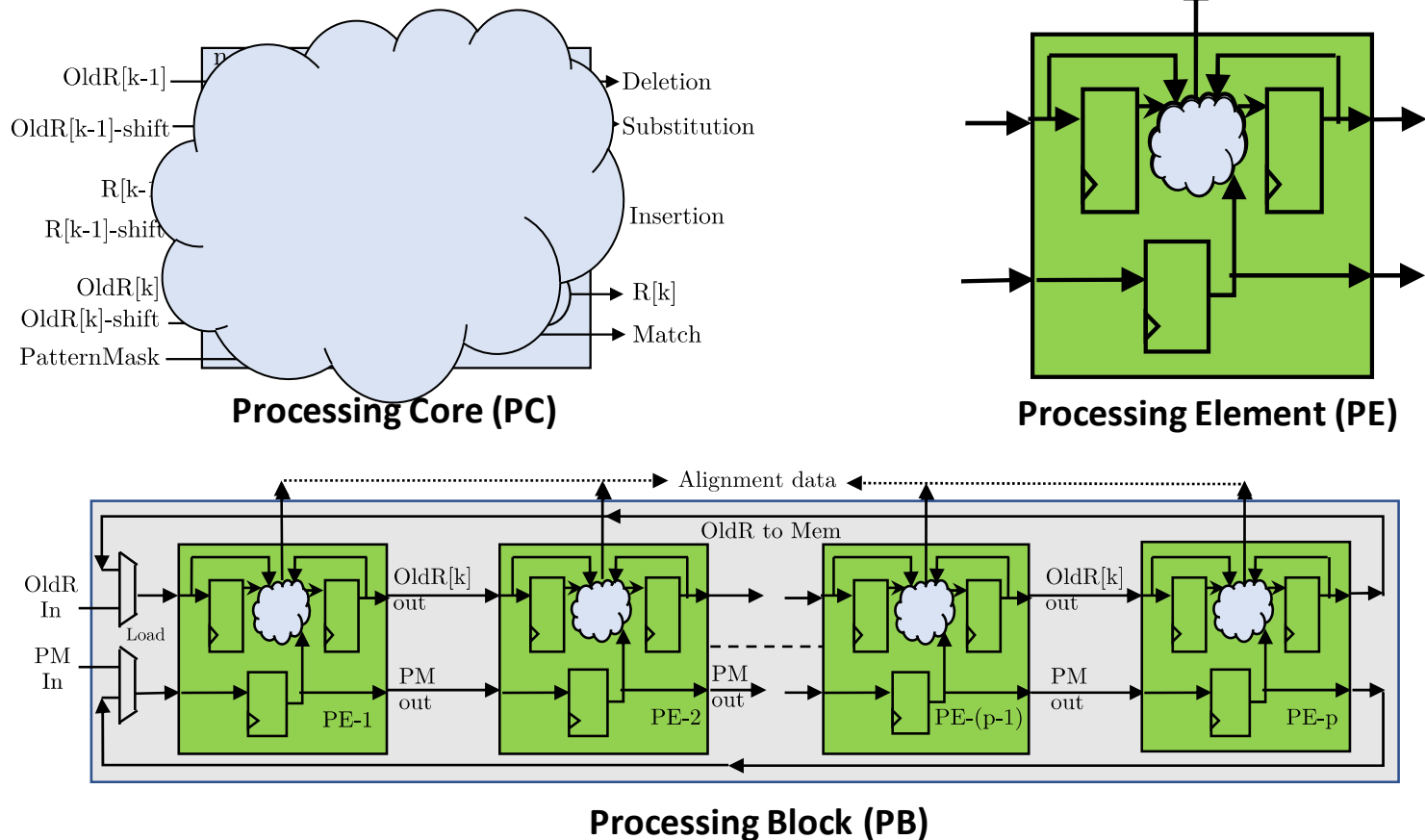
- ❑ Approximate string matching (ASM) acceleration framework based on the Bitap algorithm
- ❑ Includes optimized ASM algorithm and new hardware
 - Highly-parallel Bitap with small memory footprint
 - Bitvector-based novel algorithm to perform traceback
 - Finding the sequence of matches, substitutions, insertions and deletions, along with their positions
 - Processing-in-Memory (PIM) accelerator for Bitap and traceback
- ❑ Optimized for both 1) short yet accurate and 2) long but noisy reads

GenASM Design

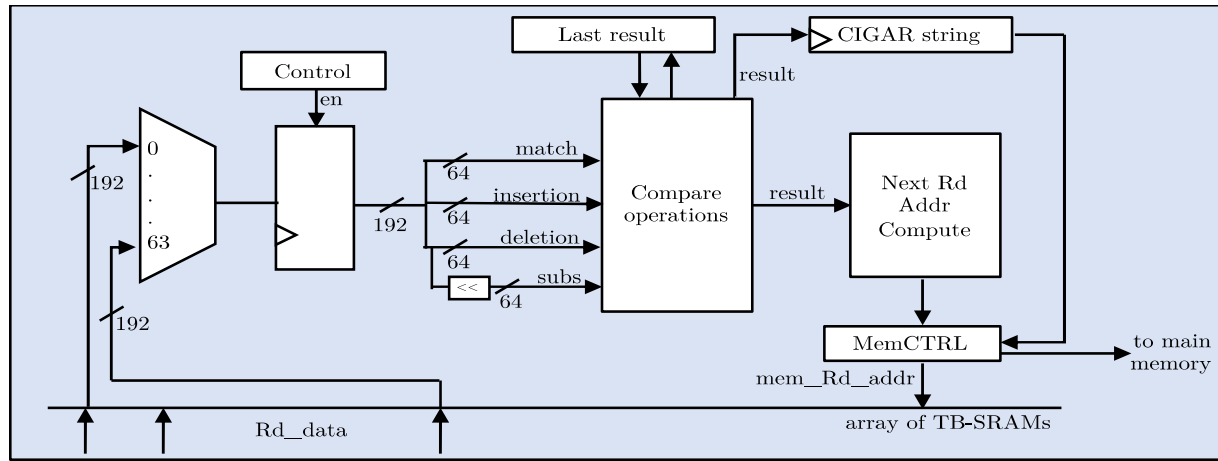


GenASM-DC: Hardware Design

- GenASM-DC Hardware Accelerator (HWA) is implemented as a **linear cyclic systolic array**.
 - Optimized to **reduce memory bandwidth** and **memory footprint**



GenASM-TB: Hardware Design

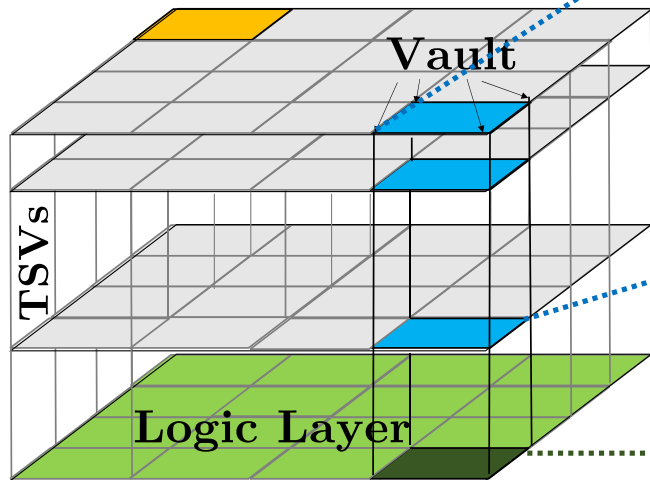


□ Very simple logic:

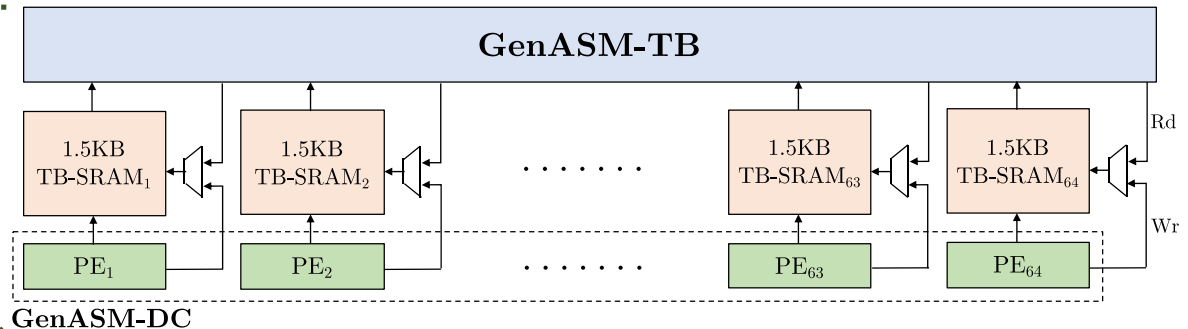
- 1) Reads the bitvectors from one of the TB-SRAMs using the computed address
- 2) Performs the required computation and comparisons to find the traceback output for the current position
- 3) Computes the next TB-SRAM address to read the new set of bitvectors

GenASM: Overall System

Hybrid Memory Cube (HMC)
16GB – 32 vaults



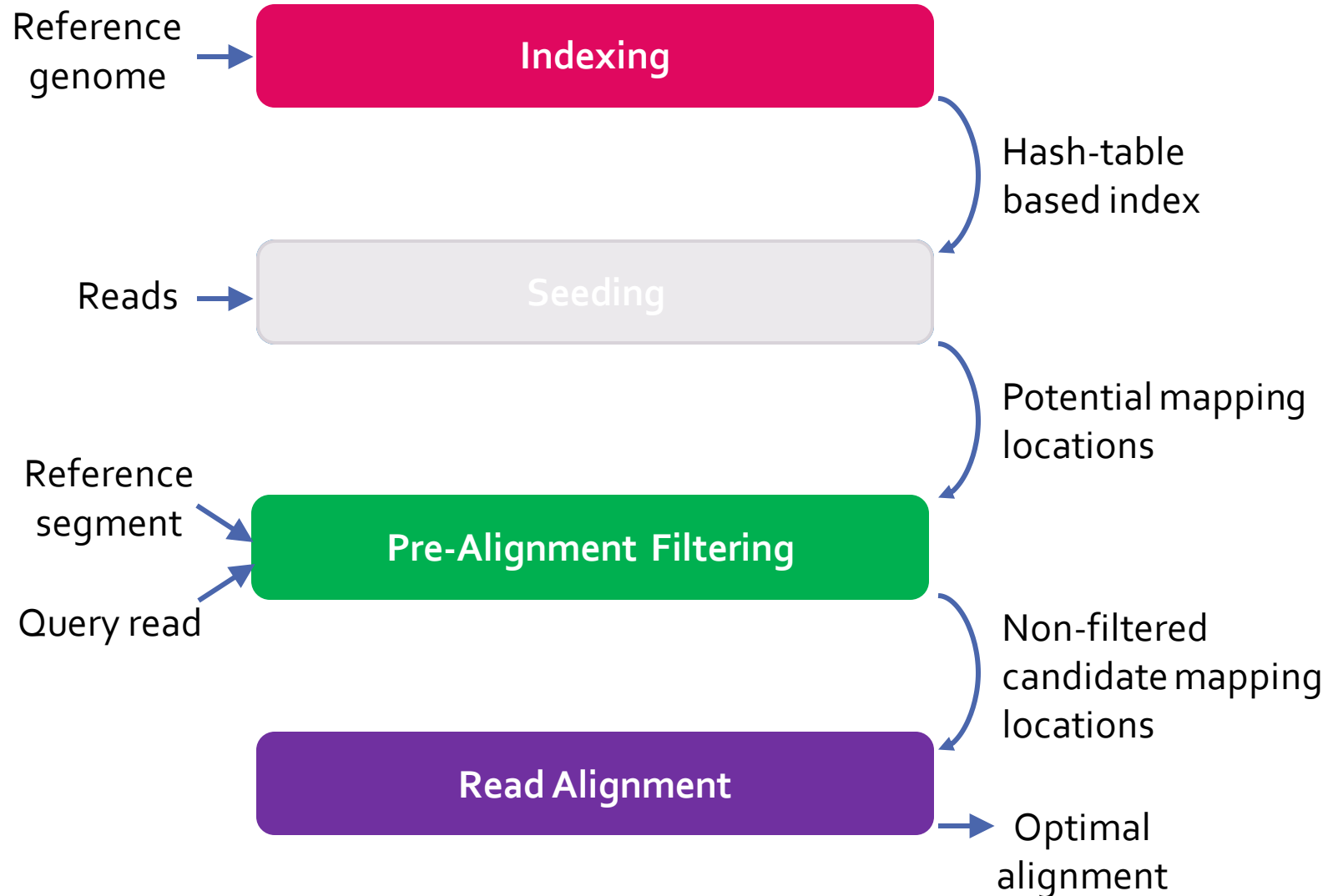
HMC Vault Memory (512MB)
(Text)



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Use Cases of GenASM



Use Cases of GenASM (cont.)

(1) Read Alignment Step of Read Mapping

- Also called *verification* or *seed-extension*
- GenASM can perform ASM between the query reads and the candidate regions and report the optimal alignment.

(2) Pre-Alignment Filtering for Short Reads

- Filter out the dissimilar sequences
- GenASM can efficiently calculate the edit distance between the short read and the candidate text and decide whether it is above a user-defined threshold.

(3) Edit Distance Calculation Between Any Two Sequences

- Fundamental operation in genomics
 - Measure the *similarity* or *distance* between two sequences
- GenASM-DC is inherently an edit distance calculation accelerator
- We also discuss *other possible use cases of GenASM* in our paper:
 - Hash-table based indexing, whole genome alignment, generic text search

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Evaluation Methodology

- ❑ 16GB HMC-like 3D-stacked DRAM architecture
 - 32 vaults
 - 256GB/s of internal bandwidth, and
 - a clock frequency of 1.25GHz

- ❑ Datasets:
 - Simulated long read datasets (ONT and PacBio)
 - 10Kbp reads with 10-15% error rate
 - Simulated short read datasets (Illumina)
 - 100-250bp reads with 5% error rate

Evaluation Methodology (cont.)

- ❑ **For Use Case 1: Read Alignment**, we compare GenASM with:
 - Two state-of-the-art read mappers: **Minimap2**¹ and **BWA-MEM**²
 - Compare GenASM *only* with the alignment steps of these mappers
 - Running on Intel® Xeon® Gold 6126 CPU (12-core) operating @ 2.60GHz with 64GB DDR4 memory
 - Two state-of-the-art accelerators, **Darwin**³ and **GenAx**⁴
 - Compare GenASM *only* with the alignment components of these accelerators (**GACT** for Darwin, **SillaX** for GenAx)

[1] H. Li. "Minimap2: pairwise alignment for nucleotide sequences." In *Bioinformatics*, 2018.

[2] H. Li. "Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM." In *arXiv*, 2013.

[3] Y. Turakhia et al. "Darwin: A genomics co-processor provides up to 15,000 x acceleration on long read assembly." In *ASPLOS*, 2018.

[4] D. Fujiki et al. "GenAx: A genome sequencing accelerator." In *ISCA*, 2018.

Key Results – Area and Power

- Both GenASM-DC and GenASM-TB operates @ **1GHz**
- Based on our synthesis of the **GenASM-DC** and **GenASM-TB** accelerator datapath using **Synopsys Design Compiler** with a typical **28 nm** LP process:

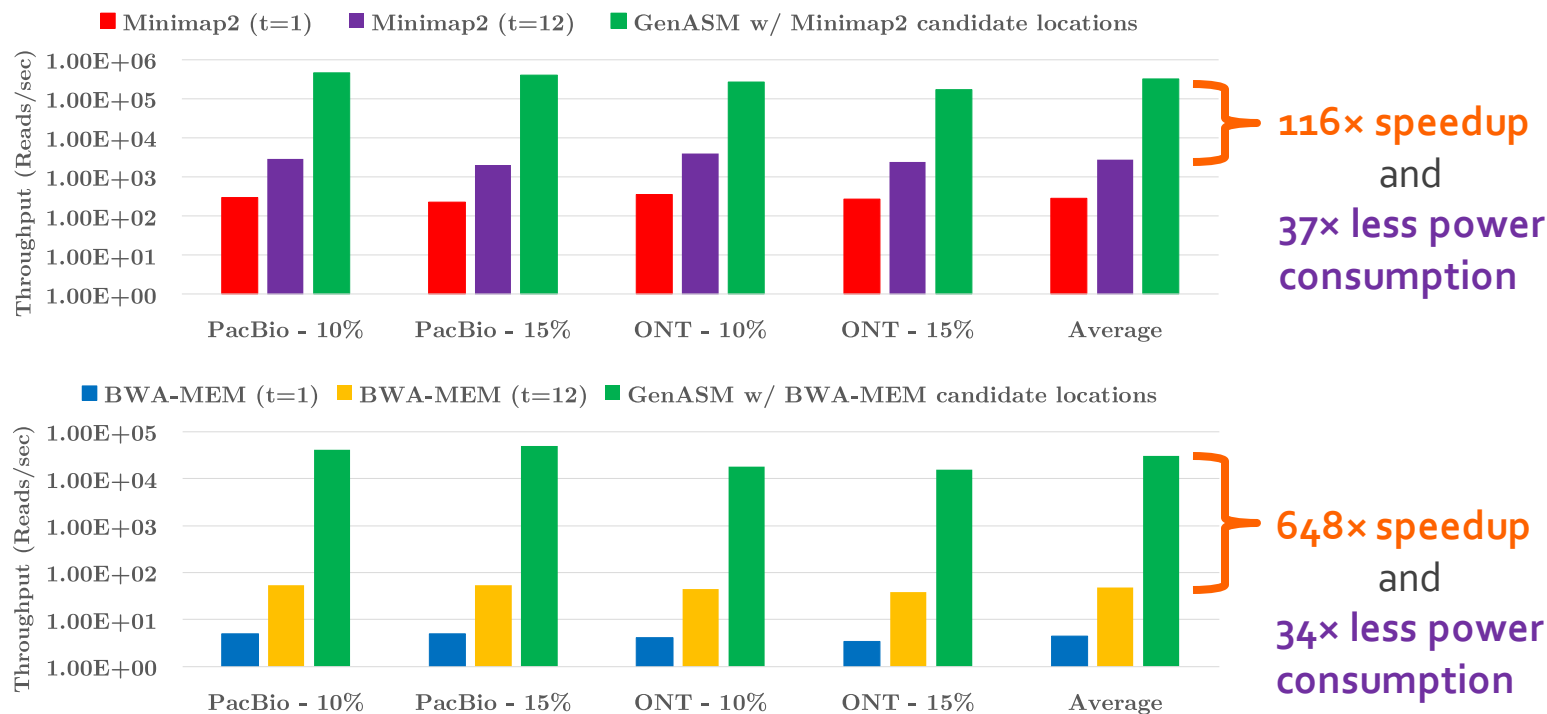
Component	Area (mm ²)	Power (mW)
GenASM-DC (64 PE)	0.049	33.3
DC-SRAM (8KB)	0.013	9.2
GenASM-TB	0.016	4.0
TB-SRAMs (64×1.5KB)	0.256	54.7
Total	0.334	101.2

- Total power consumption of all 32 vaults **3.24W**
- Total area overhead of all 32 vaults is **10.69 mm²**

Key Results (Use Case 1) – Long Reads

□ Long Read Datasets:

- Compared to 12-thread runs of [Minimap2](#) and [BWA-MEM](#):

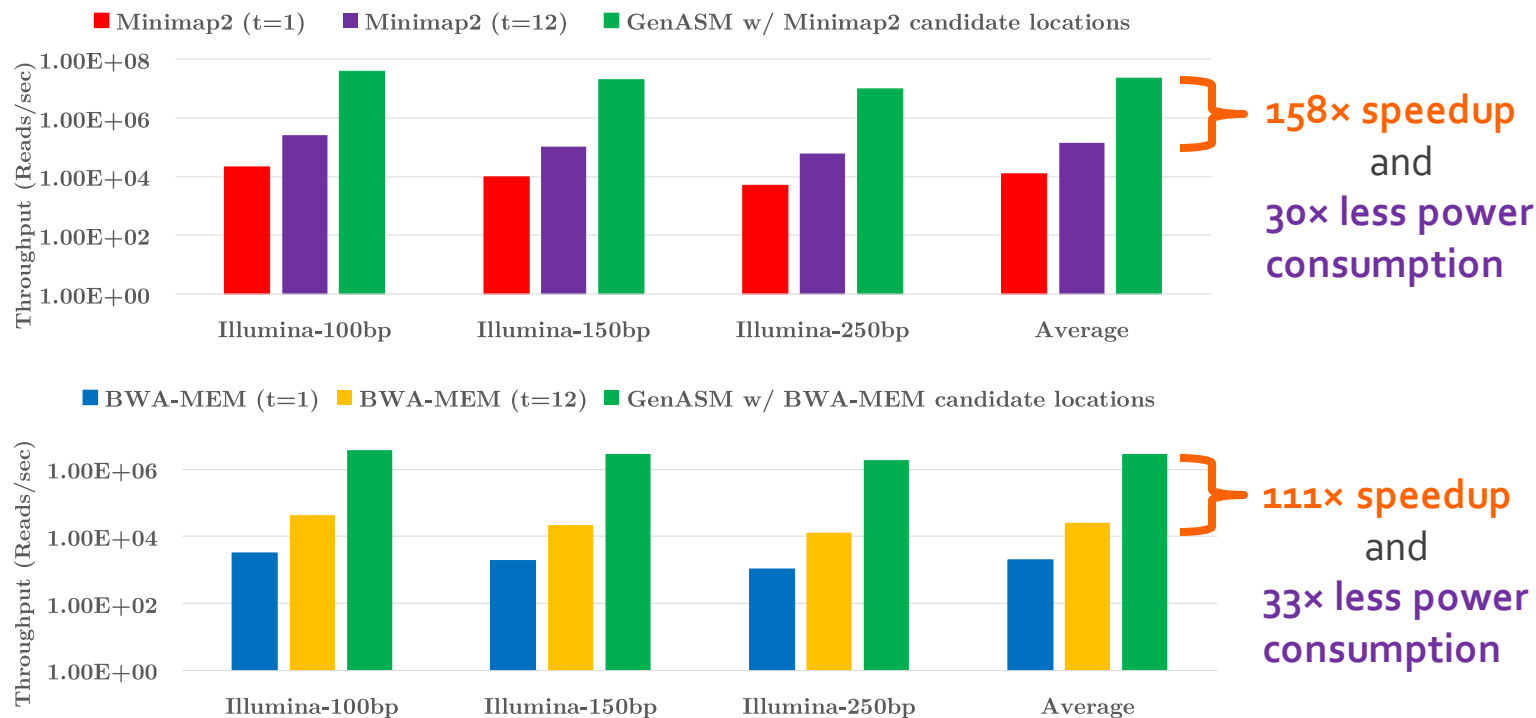


- Compared to [Darwin-GACT](#):
 - 3.8× better throughput
 - 2.7× less power consumption

Key Results (Use Case 1) – Short Reads

□ Short Read Datasets:

- Compared to 12-thread runs of [Minimap2](#) and [BWA-MEM](#):



- Compared to [GenAx-SillaX](#):

- **1.9x better throughput**
- **Comparable area and power consumption**

Key Results (Use Cases 2 & 3)

❑ Pre-Alignment Filtering for Short Reads

- Use Case 2
- **3.6× speedup** vs. Shouji
- GenASM also significantly improves the filtering accuracy

❑ Edit Distance Calculation

- Use Case 3
- **246 – 5668× speedup** vs. Edlib

❑ See our MICRO 2020 paper for more details

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Conclusion

❑ Problem:

- Genome sequence analysis is bottlenecked by the **computational power** and **memory bandwidth limitations** of existing systems.
- This bottleneck is particularly an issue for *approximate string matching*.

❑ Goal: Provide an **approximate string matching (ASM)** acceleration framework in order to accelerate **multiple steps of genome sequence analysis**

❑ Key Contributions:

- **First** to enhance and accelerate Bitap for ASM with genomic sequences
- **GenASM**: approximate string matching (ASM) acceleration framework
 - Co-design of our modified **scalable** and **memory-efficient** algorithms with **low-power** and **area-efficient** hardware accelerators
 - Evaluation of **three different use cases of ASM in genomics**: read alignment, edit distance calculation, and pre-alignment filtering.

❑ Key Results: GenASM is **significantly more efficient for all the three use cases** (in terms of **throughput** and **throughput per unit power**) than state-of-the-art software and hardware baselines.

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