P&S Genomics

Lecture 11: GenPIP

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GenPIP

In-Memory Acceleration of Genome Analysis via Tight Integration of Basecalling and Read Mapping

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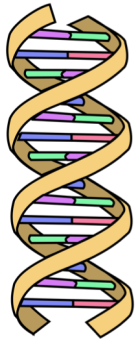
Overview: Genome Analysis

- **Genome analysis:** Enables us to determine the order of the DNA sequence in an organism's genome
  - Plays an important role in
    - Personalized medicine
    - Outbreak tracing
    - Understanding of evolution
    - …



- Modern genome sequencing machines extract smaller randomized fragments of the original DNA sequence, known as ***reads***
  - **Oxford Nanopore Technologies (ONT)**:

    A widely-used sequencing technology
    - Portable sequencing devices
    - High-throughput
    - Cheap

ONT sequencing device [forbes.com]

Overview: Two Limitations

Multiple steps in genome analysis

Large data movement between multiple steps

A lot of **wasted computation** done on data that is later discovered to be **useless**

Overview: GenPIP

- **GenPIP:** A fast and energy-efficient **in-memory** acceleration system for the Genome analysis PIPeline via **tight integration of genome analysis steps**

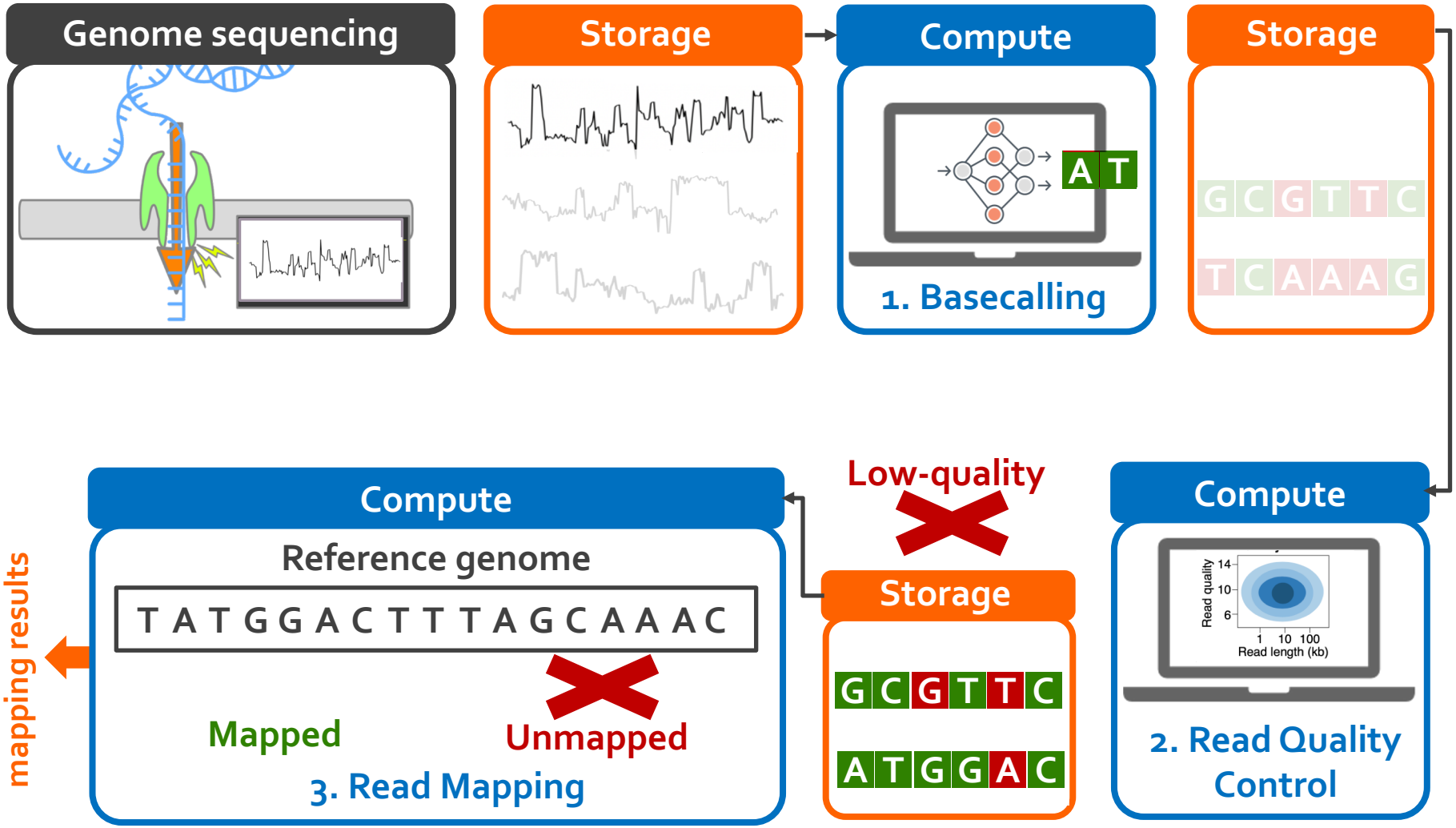
- **GenPIP** has two key techniques
  - **Chunk-based pipeline (CP)**
    - **Provides fine-grained collaboration** of genome analysis steps
  - **Early rejection (ER)**
    - **Timely stops the execution on useless data** by predicting which reads will not be useful

- **GenPIP** outperforms state-of-the-art software & hardware solutions using **CPU**, **GPU**, and **optimistic PIM** by **41.6×**, **8.4x**, and **1.4x**, respectively.

Outline

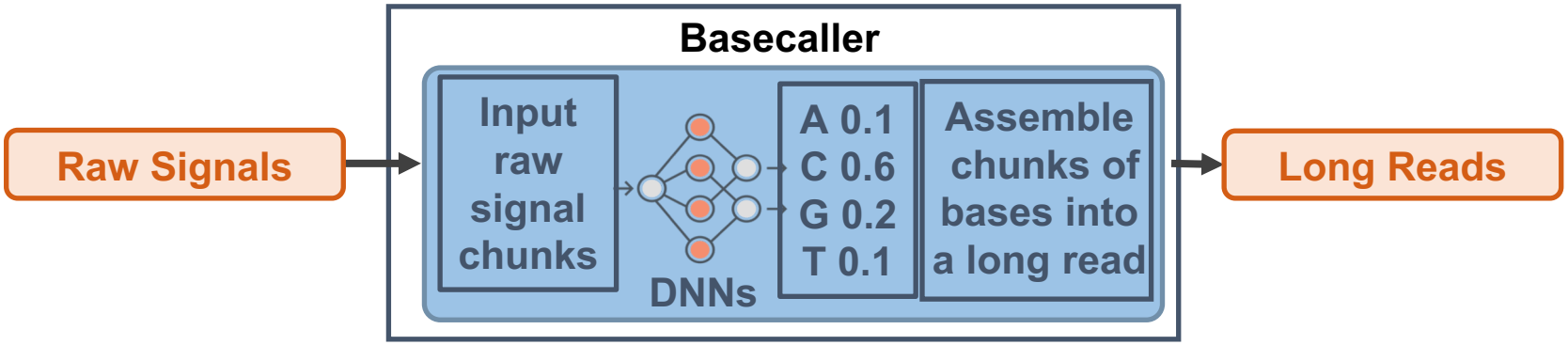
- **Background and Motivation**
- GenPIP: Tight Integration of Genome Analysis Steps
  - Chunk-based Pipeline (CP)
  - Early Rejection (ER)
- GenPIP Implementation
- Evaluation
- Conclusion

Genome Analysis Pipeline



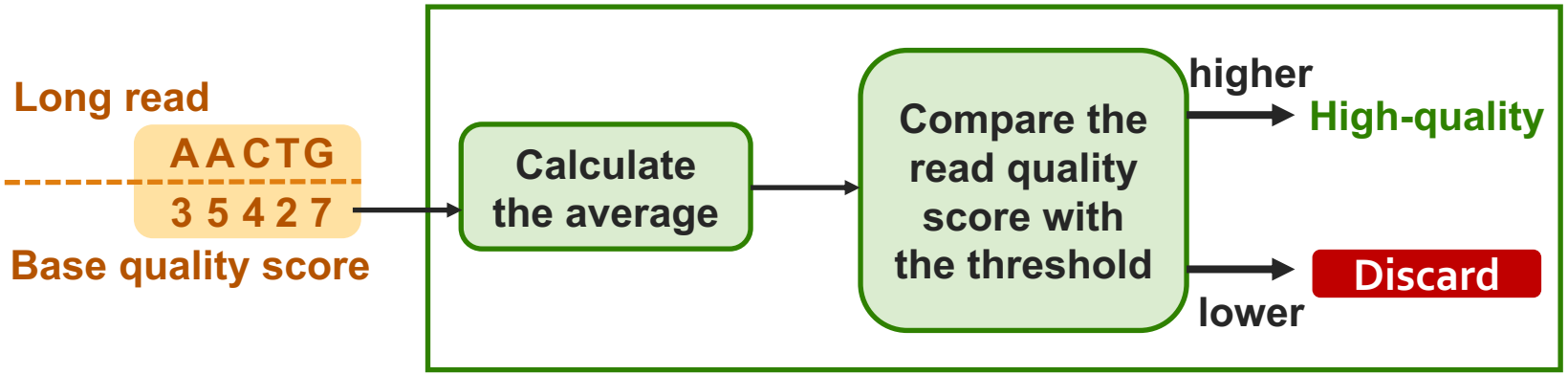
Basecalling

- **Use deep neural networks to ensure the basecalling accuracy**



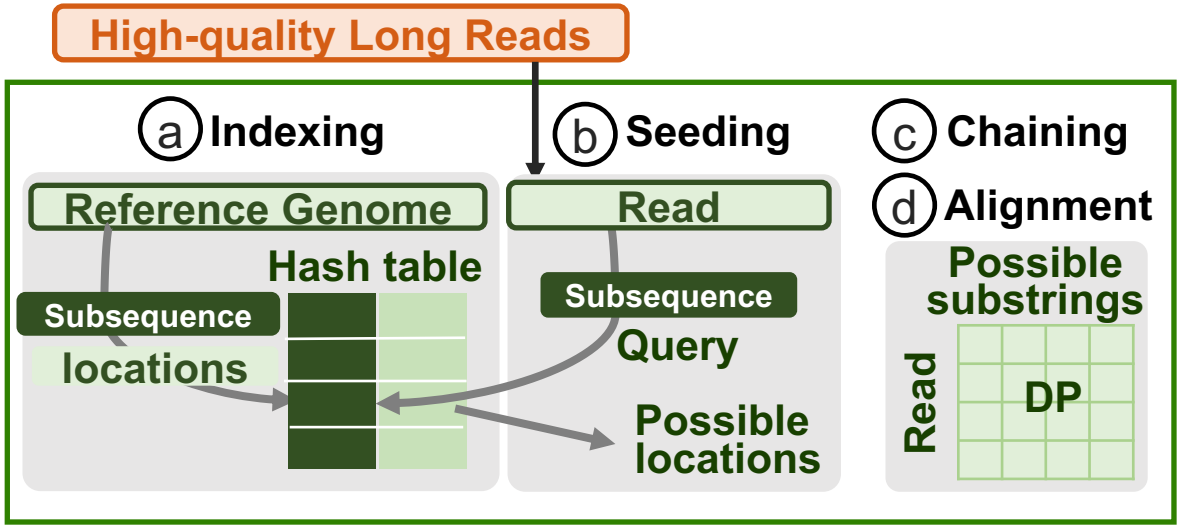
- **Input:** Raw signal **chunks**
- **Process:** Translate raw signals to bases (i.e., A, C, G, T) and calculate each base quality
- **Output:** Assemble chunks into **a long read**

Read Quality Control



- **Input:** **Base quality scores** of a read from the basecalling step
- **Process:**
  - Calculate the average of all base quality scores in a read as the **read quality score**
  - Compare the read quality score to the threshold to decide whether this read is low-quality or high-quality
- **Output:** **High-quality reads** (discard low-quality reads)

Read Mapping



- **Input:** **High-quality read** passes the read quality control step
- **Process:**
  - Use **subsequence in a read** to query the hash table to get **possible match locations**
  - Identify the candidate regions and **output the chaining score**
  - Execute the alignment step if there is a chain
- **Output: Mapping information**

Limitation 1: Large Data Movement

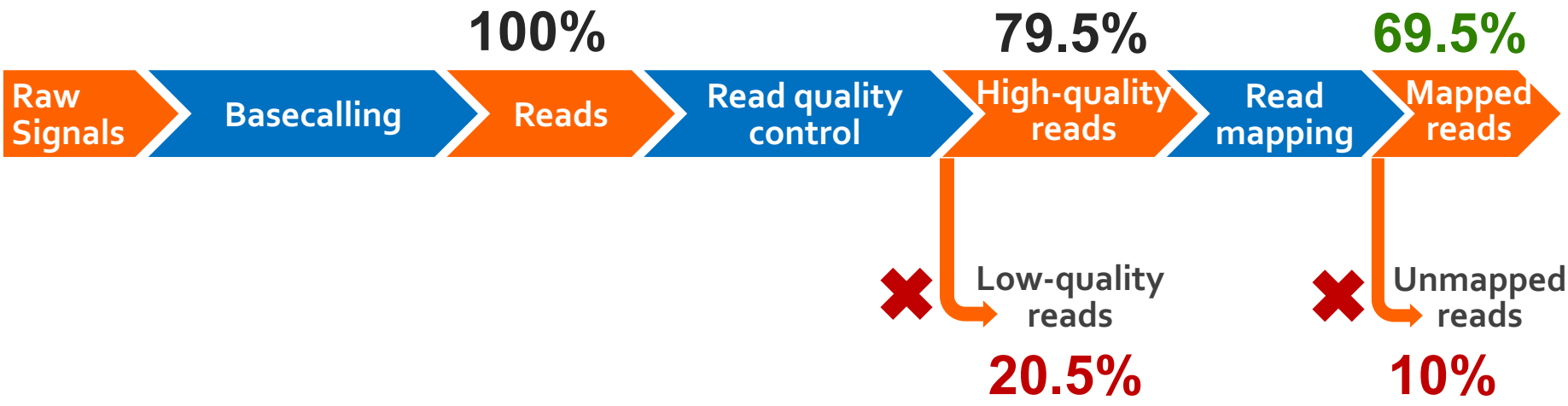
- Using a human dataset in [NC'19] as an example:

Large data movement between genome analysis steps

[NC'19] Rory Bowden, Robert W Davies, Andreas Heger, Alistair T Pagnamenta, Mariateresa de Cesare, Laura E Oikkonen, Duncan Parkes, Colin Freeman, Fatima Dhalla, Smita Y Patel, et al. Sequencing of human genomes with nanopore technology. Nature Communications, 2019.

Limitation 2: Wasted Computation

- Using a human dataset in [NC'19] as an example:



A considerable amount of computation on useless data due to

- **Low-quality reads**
- **Unmapped reads**

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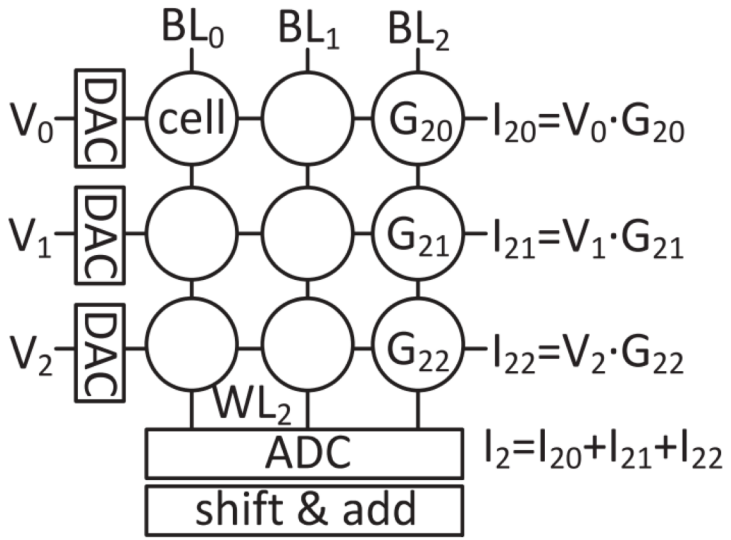
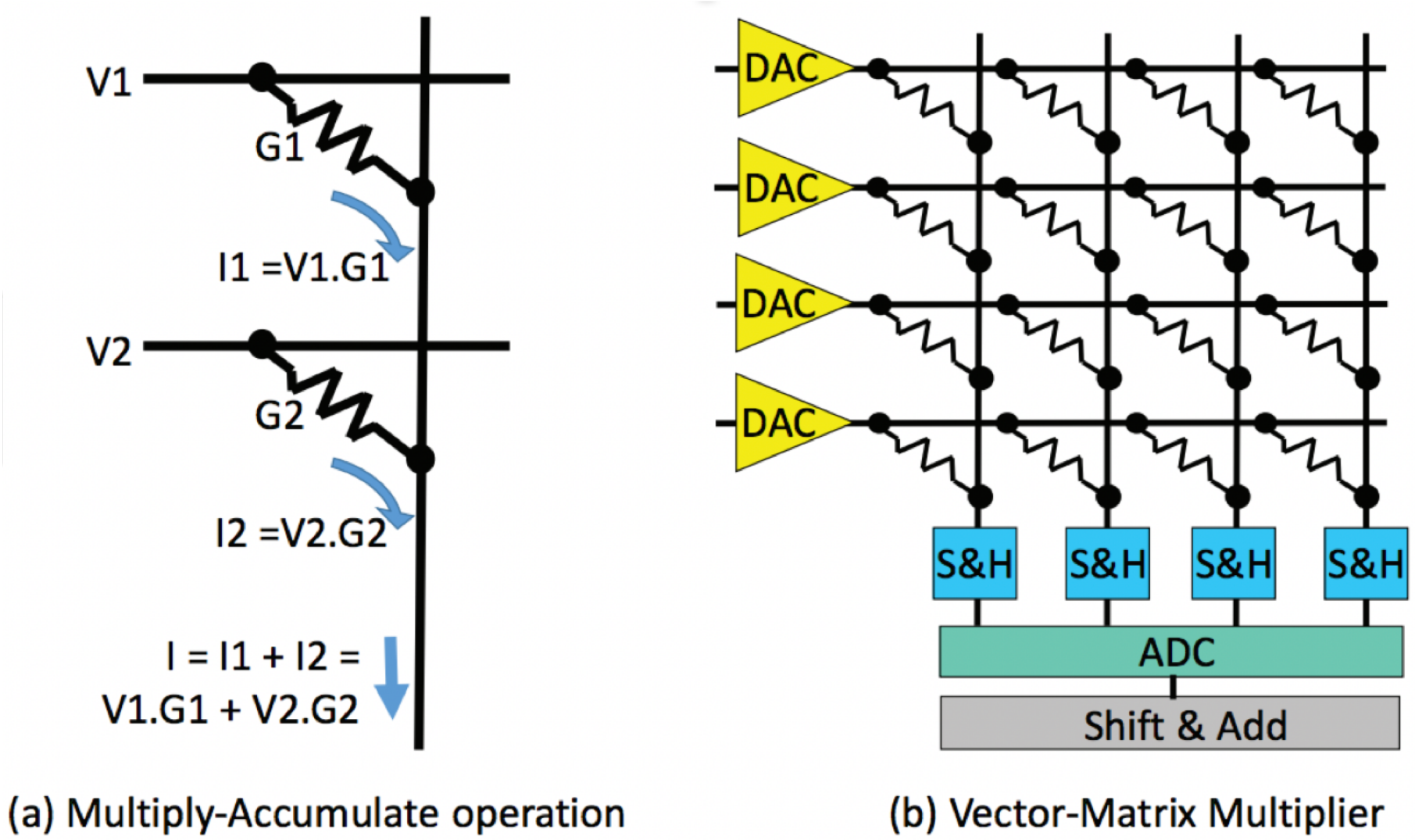
State-of-the-art Works

- NVM-based PIM is an efficient technique to reduce data movement by processing data using or near memory



- NVM-based PIM for **vector-matrix multiplication** operation [Helix, PACT'20]
- Vector-matrix multiplication is the dominant operation in the neural network applications

State-of-the-art Works

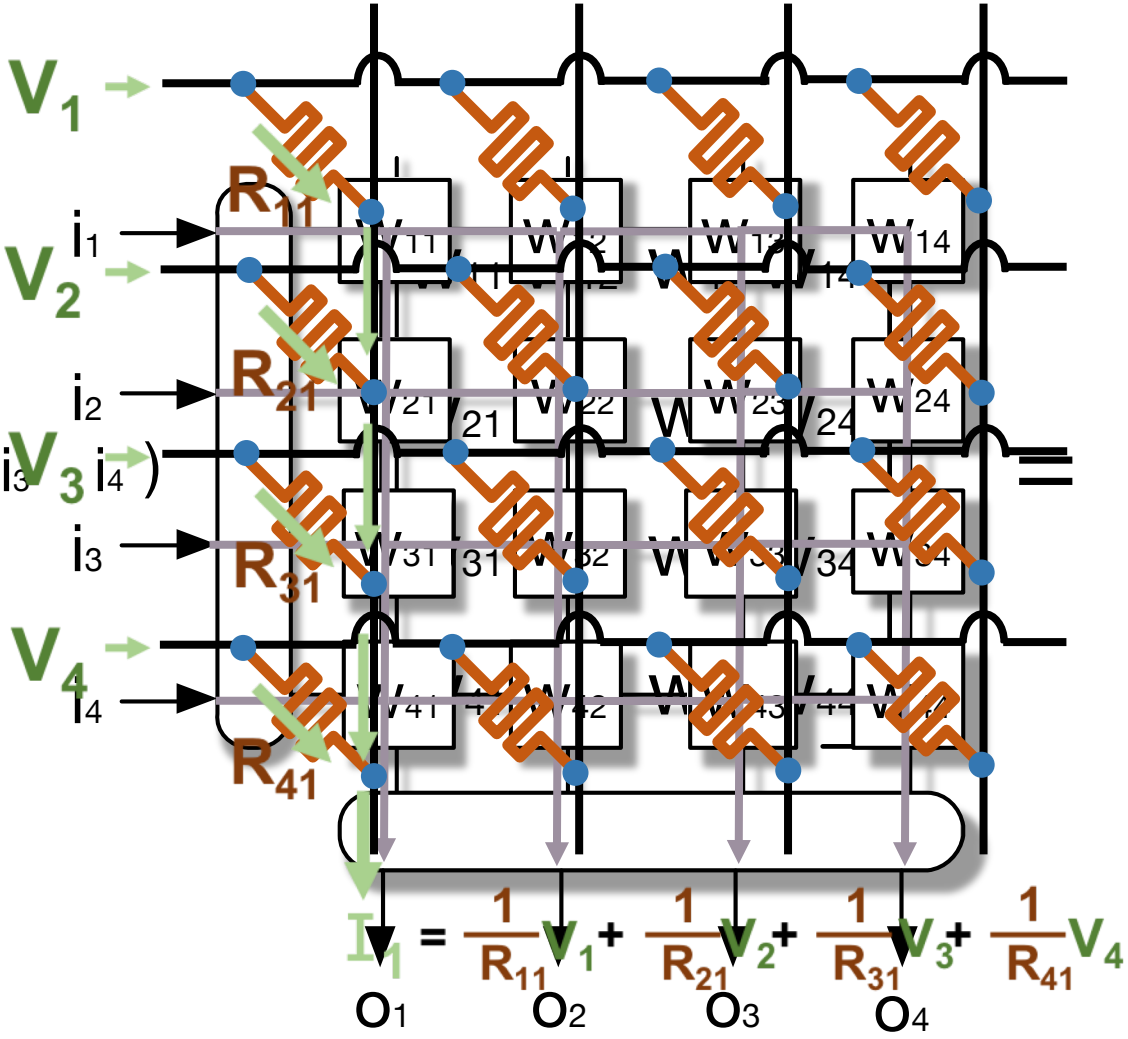


(a) Multiply-Accumulate operation

(b) Vector-Matrix Multiplier

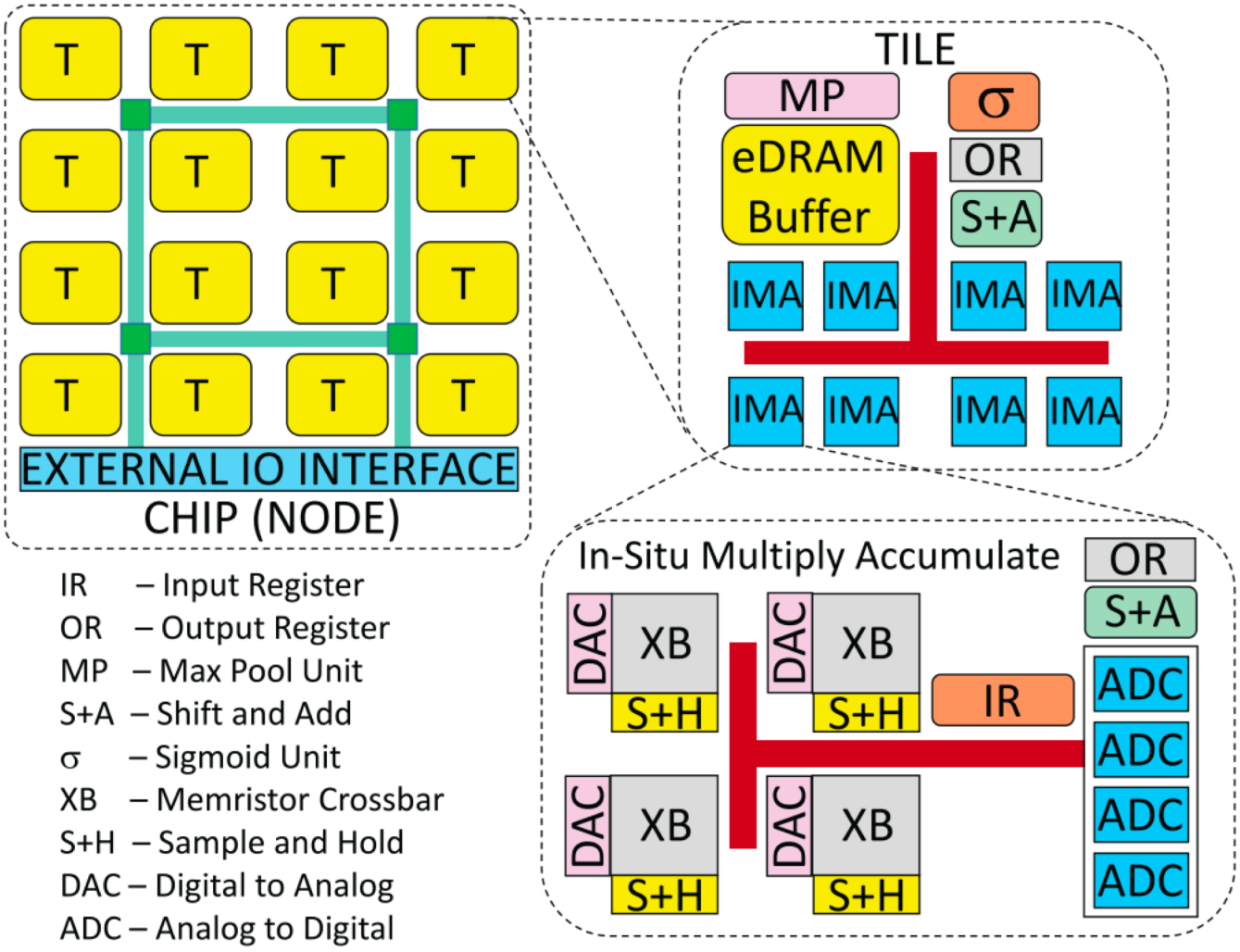
[Shafiee+, "ISAAC: A Convolutional Neural Network Accelerator with In-Situ Analog Arithmetic in Crossbars", ISCA 2016.]

State-of-the-art Works



(i1 i2 i3 i4) ≡ (O1 O2 O3 O4)

State-of-the-art Works



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State-of-the-art Works

- NVM-based PIM is an efficient technique to reduce data movement by processing data using or near memory

A_1	A_0	B_1	B_0			
0	0	0	0			
0	1	1	0			
1	1	1	1			
1	1	1	0			

(a) Operands Layout

A_1	A_0	B_1	B_0	C	S_1	S_0
0	0	0	0	0		
0	1	1	0	0		
1	1	1	1	0		
1	1	1	0	0		

(b) Initialization

A_1	A_0	B_1	B_0	C	S_1	S_0
0	0	0	0	0		0
0	1	1	0	0		1
1	1	1	1	1		0
1	1	1	0	0		1

(c) Bit-0 completed

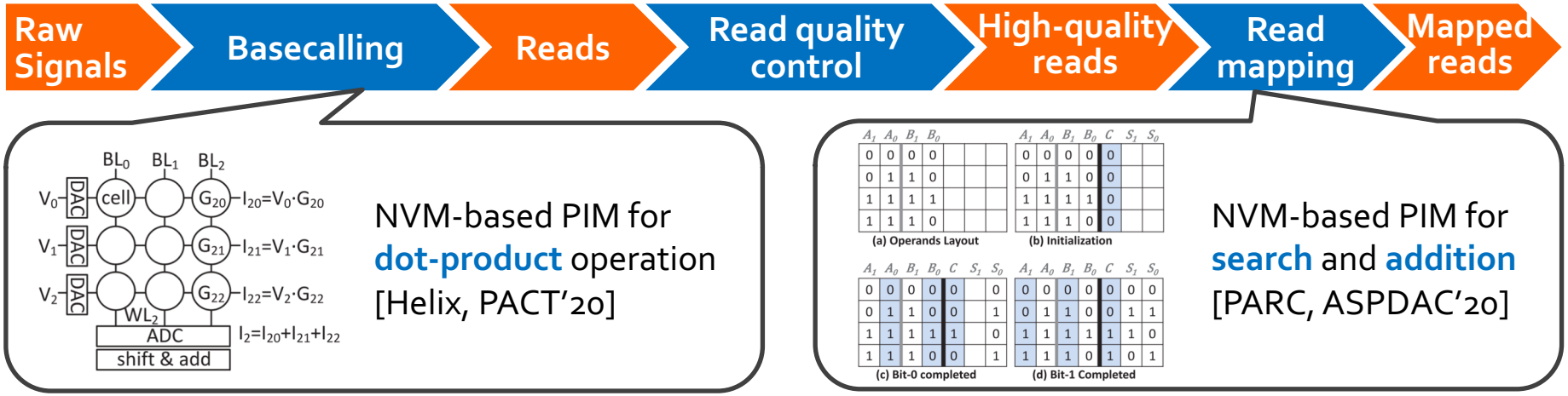
A_1	A_0	B_1	B_0	C	S_1	S_0
0	0	0	0	0	0	0
0	1	1	0	0	1	1
1	1	1	1	1	1	0
1	1	1	0	1	0	1

(d) Bit-1 Completed

- NVM-based PIM for **search** and **addition** [PARC, ASPDAC'20]
- Search and addition are the dominant operations in the read mapping step

State-of-the-art Works

- NVM-based PIM is an efficient technique to reduce data movement by processing data using or near memory



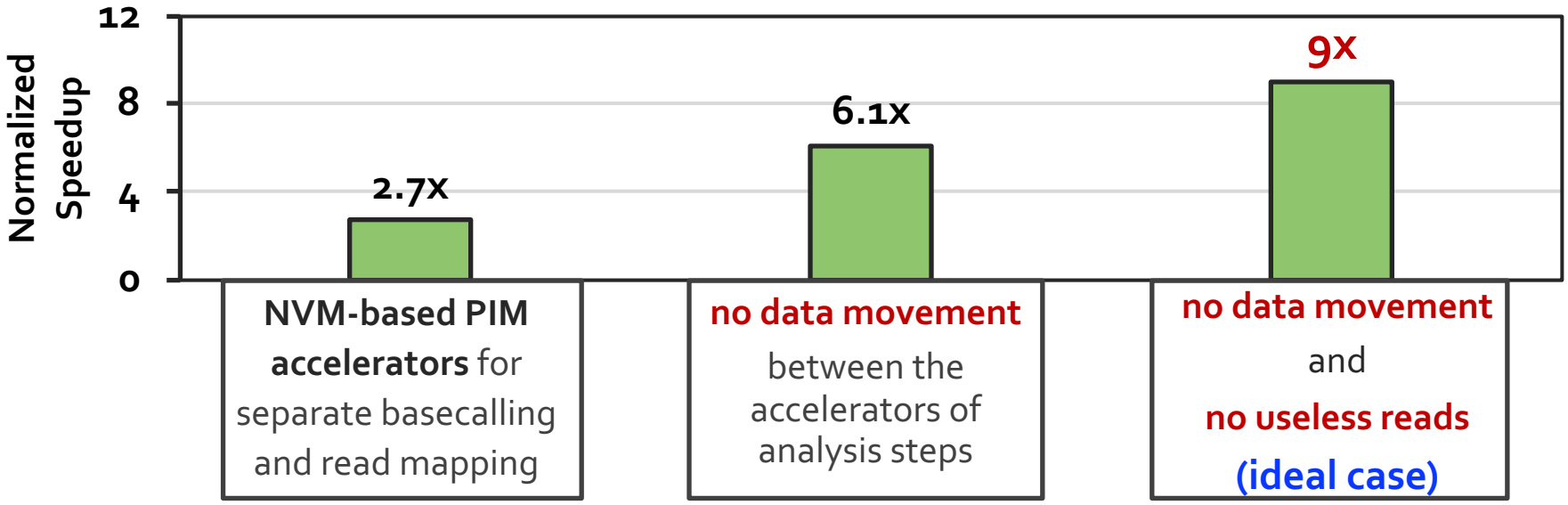
- Reduce the data movement in a single genome analysis step
- Exacerbate the data movement overhead between analysis steps

No prior work tackles data movement between analysis steps and reduces useless computation

Goal and Opportunities

Goal: Efficiently accelerate the entire genome analysis pipeline while **minimizing data movement and useless computation**

- We perform a study to quantify potential performance benefits
  - Results are normalized to the performance of GPU



Outline

- Background and Motivation
- **GenPIP: Tight Integration of Genome Analysis Steps**
  - **Chunk-based Pipeline (CP)**
  - **Early Rejection (ER)**
- GenPIP Implementation
- Evaluation
- Conclusion

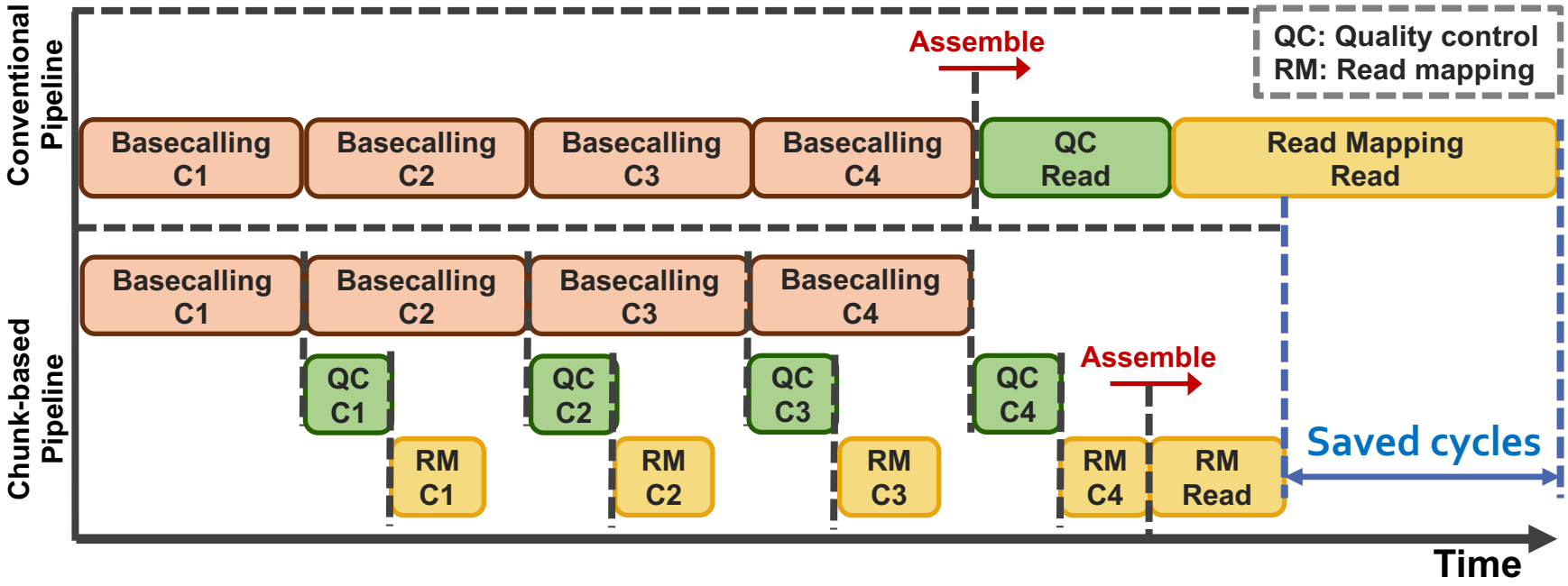
GenPIP

- ***First* holistic in-memory accelerator for the genome analysis pipeline**, including basecalling, read quality control, and read mapping steps
- **GenPIP** has two key techniques
  - **Chunk-based Pipeline (CP)**
    - **Enables fine-grained pipelining** of genome analysis steps
    - Processes reads at **chunk** granularity (i.e., a subsequence; 300 bases)
  - **Early Rejection (ER)**

Chunk-based Pipeline (CP)

- CP **increases parallelism** by overlapping the execution of different steps at chuck granularity
- CP **reduces intermediate data** by computing on data as soon as data is generated
- CP **provides opportunities for ER** by analyzing a read at chunk granularity

A read consists of four chunks: **C1, C2, C3, C4**

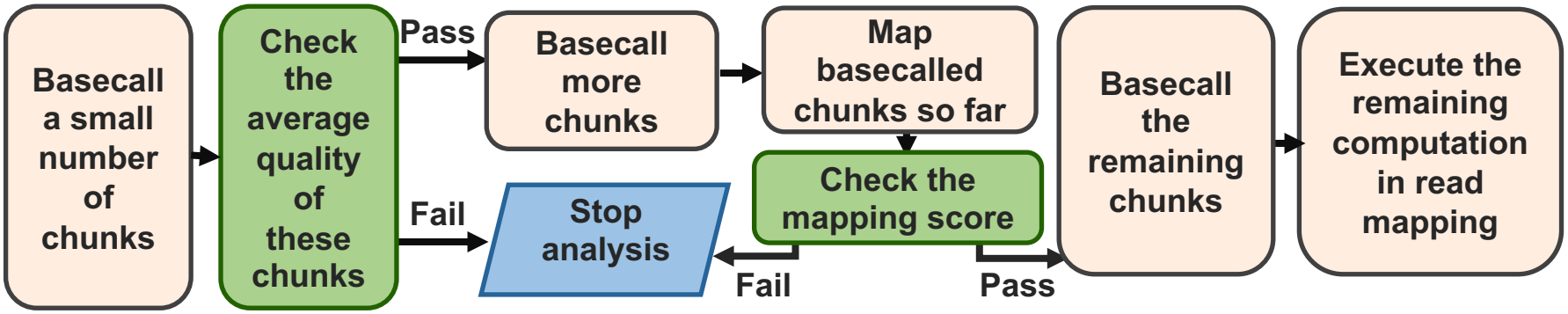


GenPIP

- ***First* holistic in-memory accelerator for the genome analysis pipeline**, including basecalling, read quality control, and read mapping steps
- **GenPIP** has two key techniques
  - Chunk-based Pipeline (CP)
    - **Enables fine-grained collaboration** of genome analysis steps by processing reads at chunk granularity (i.e., a subsequence of a read, e.g., 300 bases)
  - **Early Rejection (ER)**
    - **Stops the execution on useless reads as early as possible** by using a small number of chunks to predict the usefulness of a read

Early Rejection (ER)

- **Predict and eliminate** low-quality and unmapped reads from the genome analysis pipeline **as early as possible**

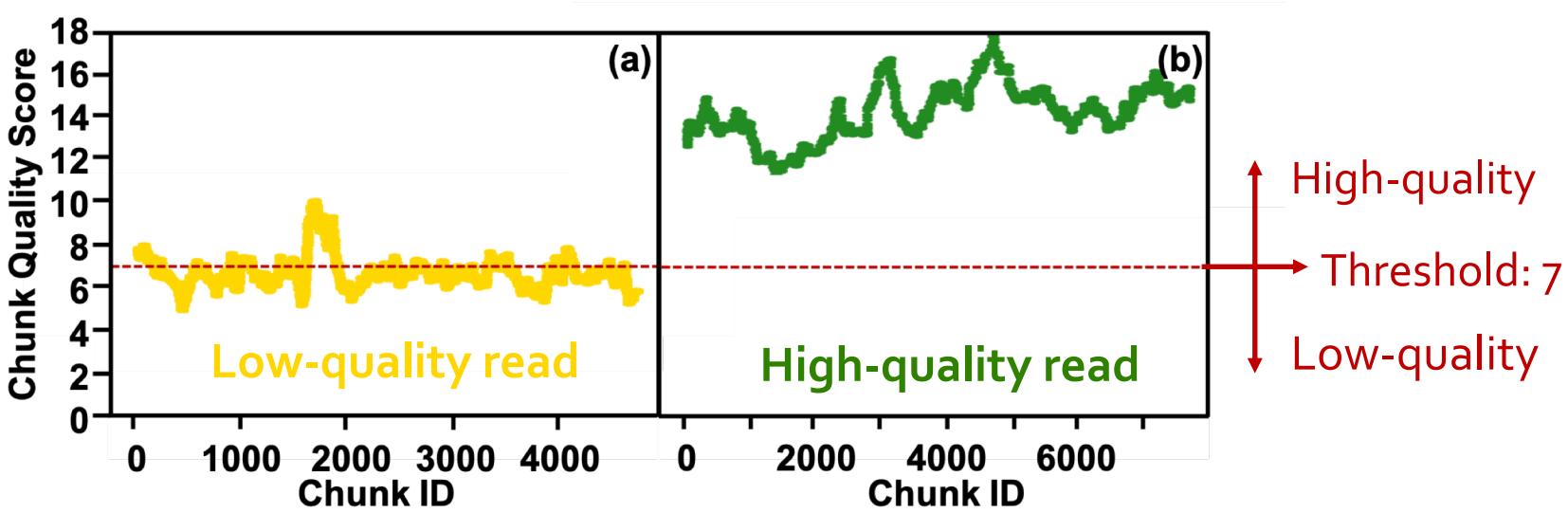


- **Early-Rejection based on chunk quality scores (ER-QSR)**
  - Predict **low-quality** reads using chunk quality scores

- **Early-Rejection based on chunk mapping scores (ER-CMR)**
  - Predict **unmapped reads** using chunk mapping scores

ER based on Chunk Quality Scores

- **Goal:** Accurately estimate the quality of the entire read by **checking the quality of a small number of sampled chunks**



Sample a small number of *non-consecutive* chunks evenly in a read to predict the read quality

ER based on Chunk Mapping

- **Key insight of ER based on chunk mapping:** A read probably cannot be mapped to the reference genome **if enough consecutive chunks in this read cannot be mapped to the reference genome**

Mapping a small chunk provides too many possible mapping locations

1. Sample a small number of *consecutive* chunks in a read
2. Merge these small consecutive chunks into a big chunk
3. Map this big chunk to the reference genome to predict whether the read can be mapped or not

Implementation of CP and ER

CP and ER can be applied on different systems, e.g., CPU, GPU, and PIM

We implement CP and ER using PIM since PIM is more efficient to reduce the data movement between genome analysis steps

We also apply CP and ER on CPU and GPU baselines and observe speedup and energy savings

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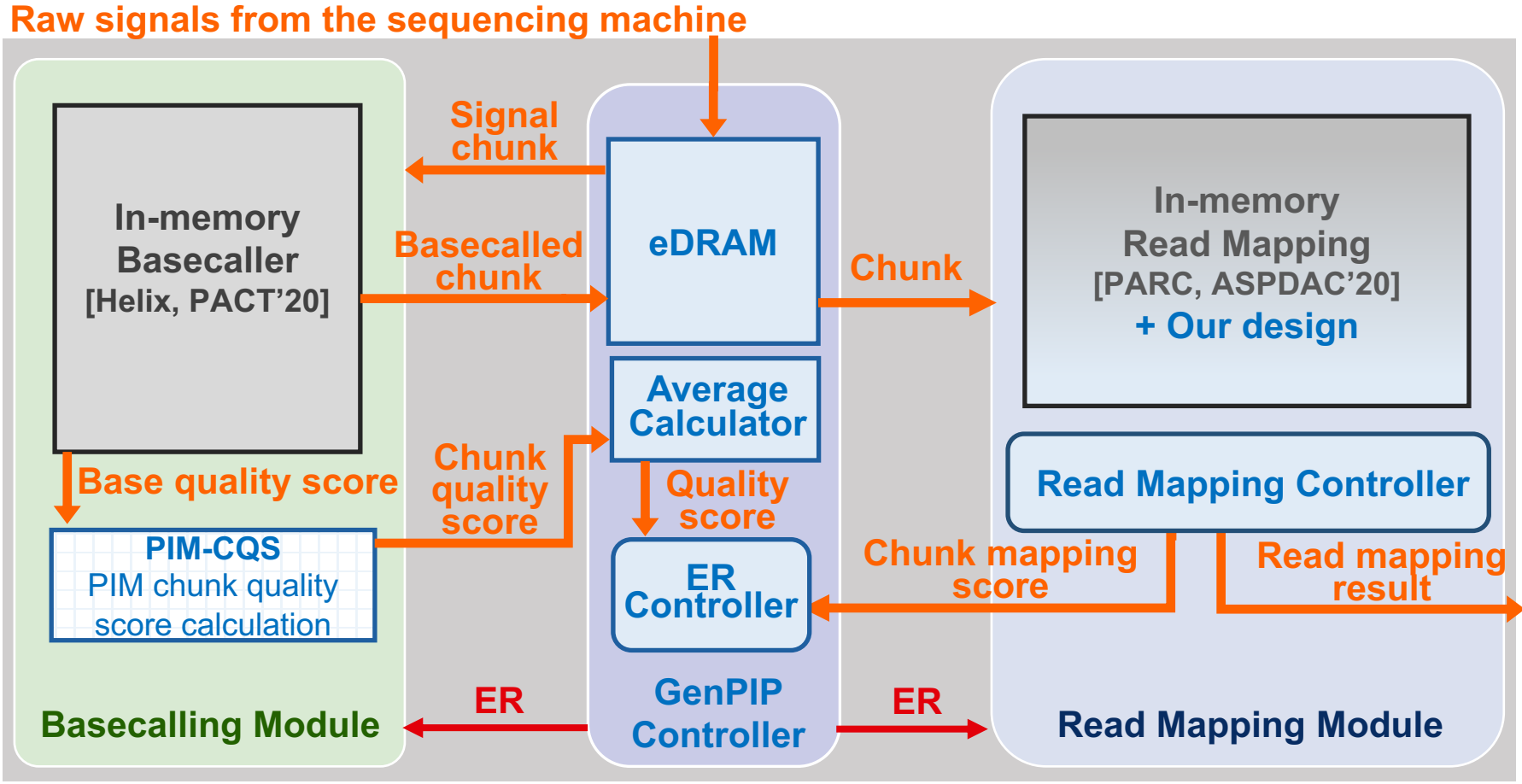
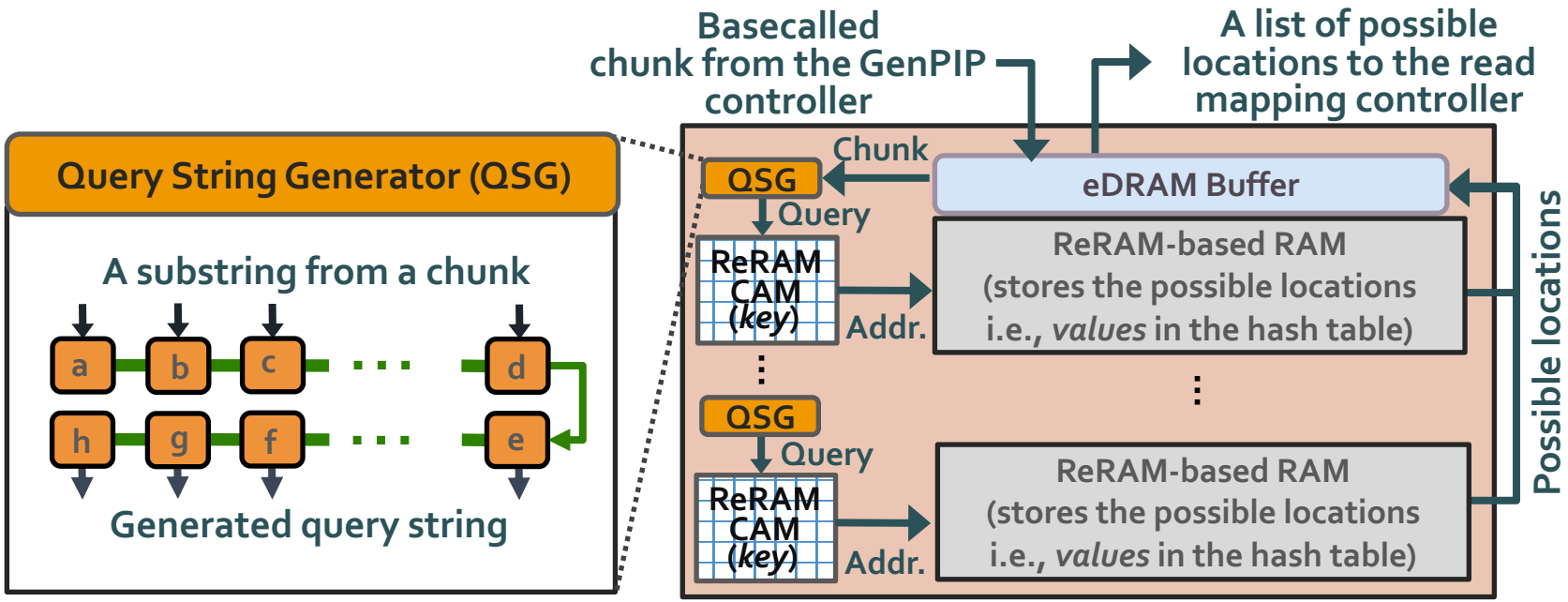
GenPIP Implementation

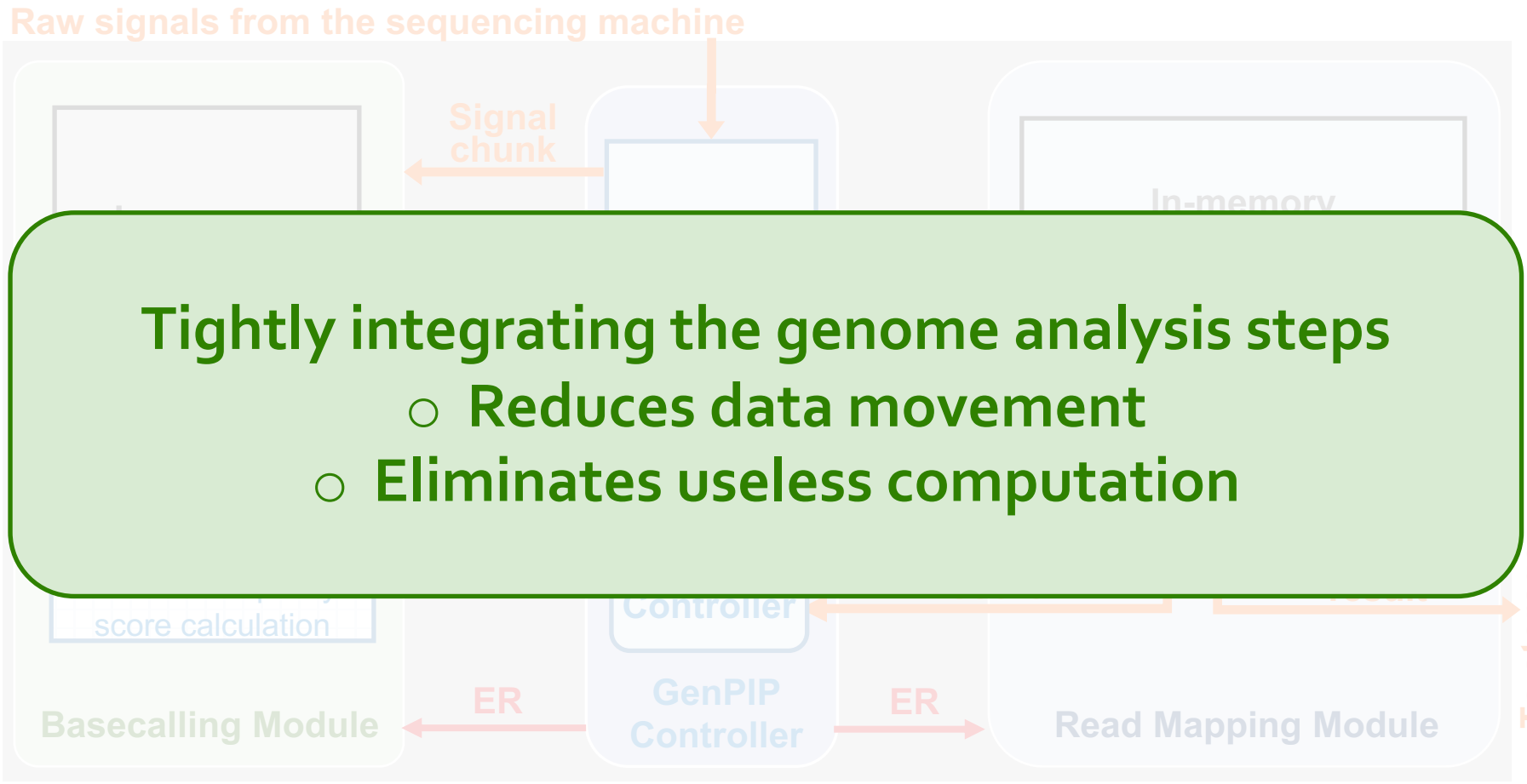


https://arxiv.org/pdf/2209.08600.pdf

In-memory Seeding



GenPIP Implementation



Tightly integrating the genome analysis steps

- **Reduces data movement**
- **Eliminates useless computation**

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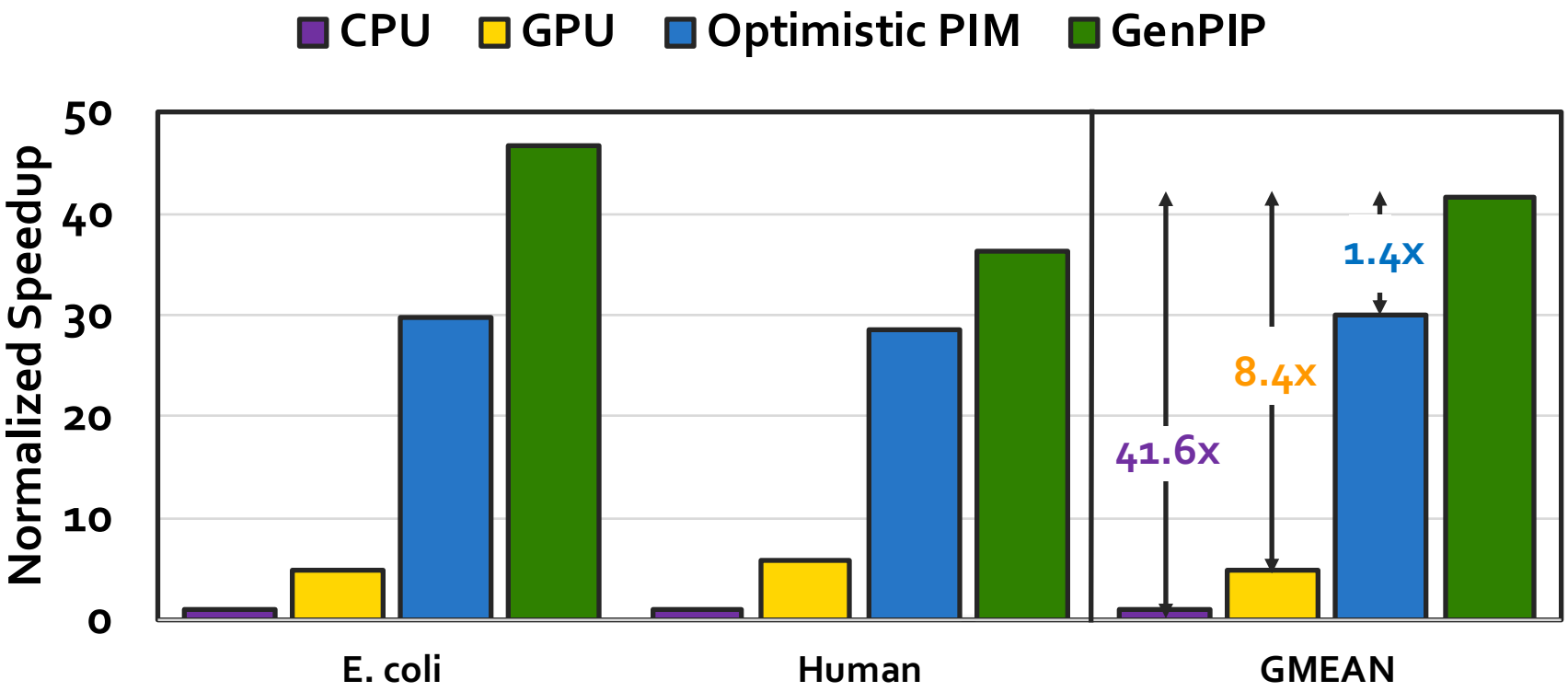
Evaluation Methodology

- **Performance, Area and Power Analysis:**
  - Simulation via Verilog HDL, NVSim [TCAD'12], and CACTI 6.5 [MICRO'07]
  - See methodology in the paper for more

- **Baselines:**
  - **CPU** (Intel Xeon Gold 5118 CPU)
  - **GPU** (NVIDIA GeForce RTX 2080 Ti GPU)
  - **Optimistic integration of two PIM accelerators (Helix [PACT'20] and PARC [ASP-DAC'20])**
    - Assumes **no data movement** between steps
    - Assumes intermediate data causes no overhead

- **Datasets:**
  - **E. coli** (http://lab.loman.net/2016/07/30/nano pore- r9- data- release/)
  - **Human** (https://www.ebi.ac.uk/ena/browser/view/PRJEB30620)

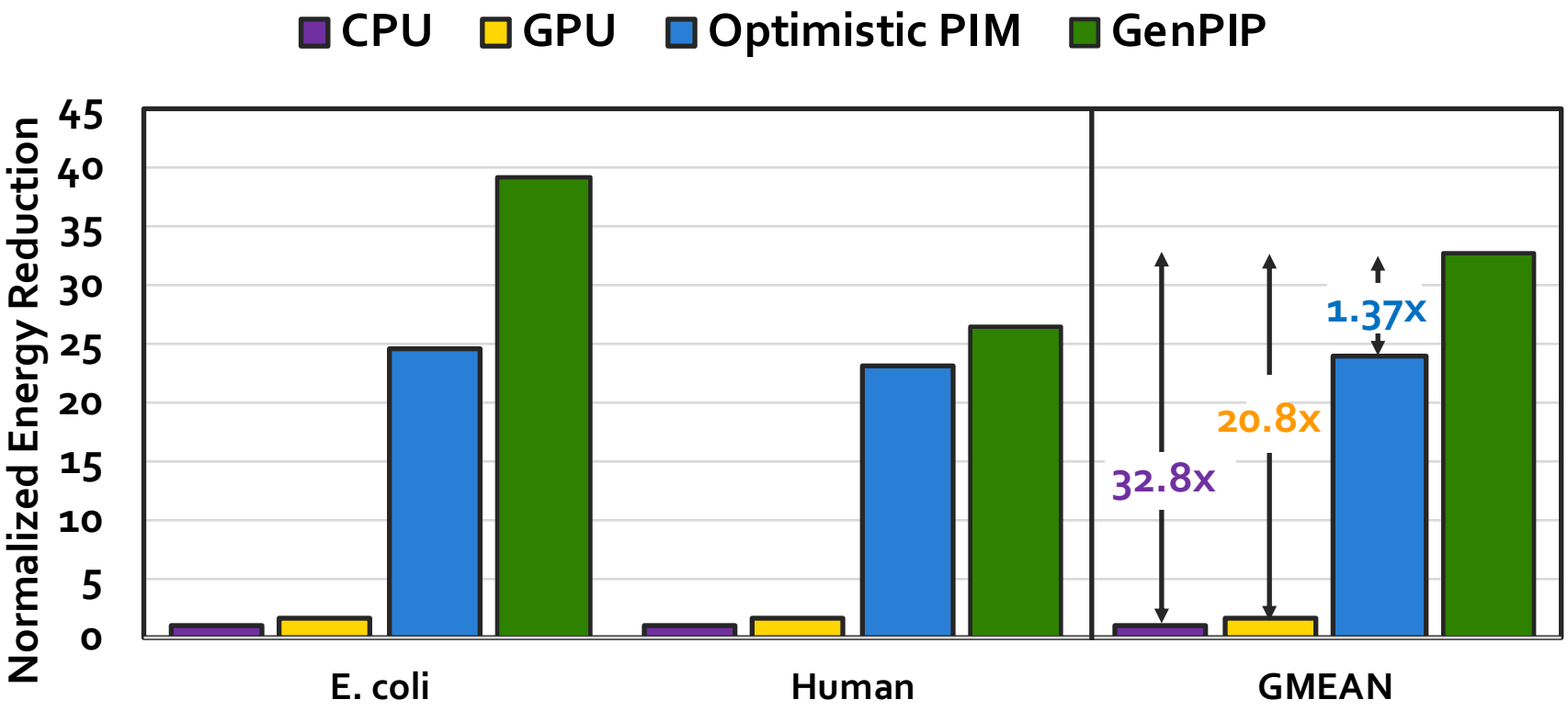
Key Results – Performance



GenPIP provides 41.6x, 8.4x, and 1.4x speedup over CPU, GPU, and optimistic PIM

Both CP and ER are critical to the speedup

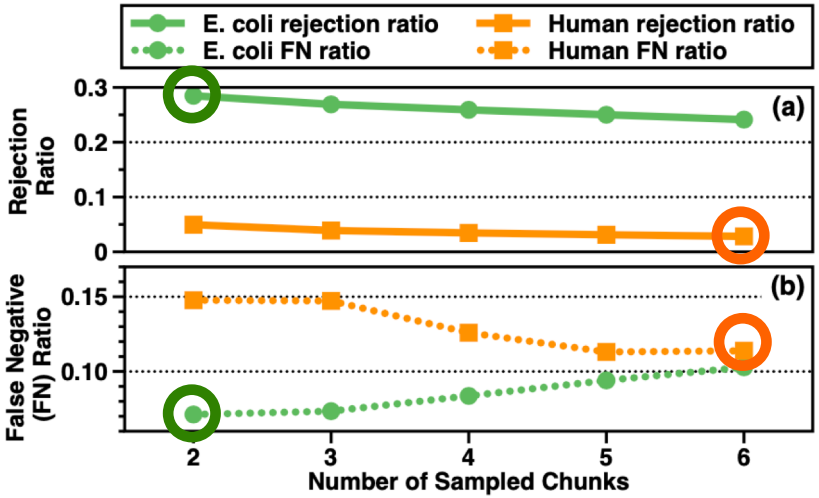
Key Results – Energy Efficiency



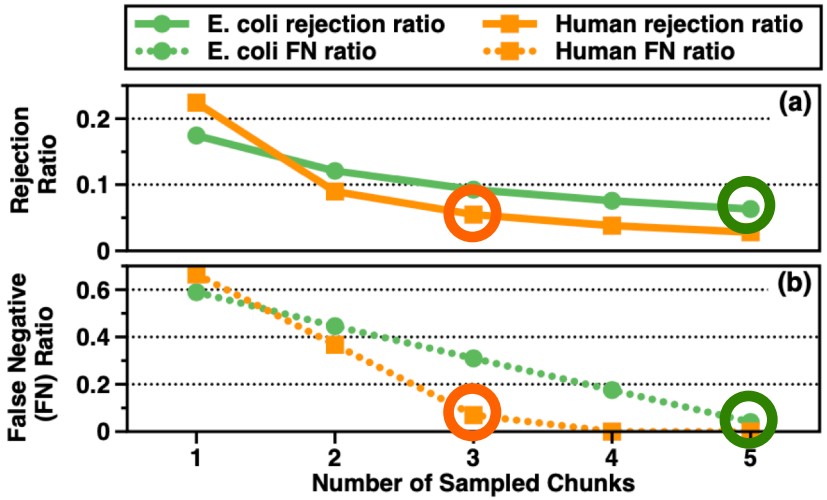
GenPIP provides 32.8x, 20.8x, and 1.37x energy savings over CPU, GPU, and optimistic PIM

ER is especially critical to the energy efficiency

Key Results – Sensitivity Analysis



Early rejection based on the chunk quality scores



Early rejection based on the chunk mapping

Early rejection based on the chunk quality scores technique uses two and five sampled chunks for the E. coli and human datasets, respectively.

Early rejection based on the chunk mapping technique uses five and three sampled chunks for the E. coli and human datasets, respectively.

More in the Paper

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[1]*ETH Zürich* [2]*Bionano Genomics*

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Conclusion

- **Problem:** The genome analysis pipeline has **large data movement** between genome analysis steps and a significant amount of **wasted computation on useless data**

- **Goal**: **Tightly integrate genome analysis steps** to reduce the data movement between steps and eliminate computation on useless data

- **GenPIP**: **The *first* in-memory genome analysis accelerator** that **tightly integrates** genome analysis steps
- **GenPIP** has two key techniques
  - **A chunk-based pipeline**
  - **A new early-rejection technique**

- **GenPIP outperforms** state-of-the-art software & hardware solutions using **CPU**, **GPU**, and **optimistic PIM** by **41.6×**, **8.4x**, and **1.4x**, respectively.

GenPIP

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