MegIS

High-Performance, Energy-Efficient, and Low-Cost Metagenomic Analysis with In-Storage Processing

Nika Mansouri Ghiasi

Mohammad Sadrosadati Harun Mustafa Arvid Gollwitzer Can Firtina

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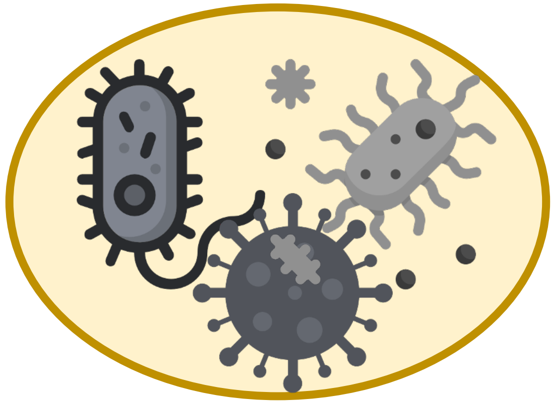
Outline

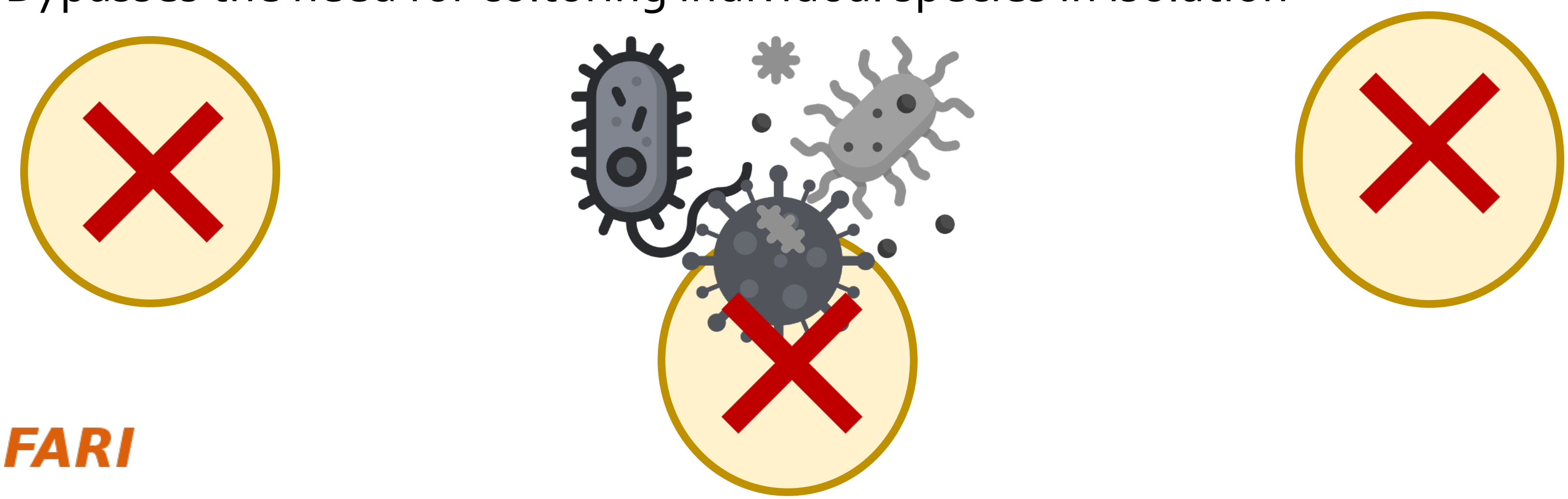
- Background
- Motivation and Goal
- MegIS
- Evaluation
- Conclusion

What is Metagenomics?

- ***Metagenomics:*** Study of genome sequences of **diverse organisms** within a **shared environment** (e.g., blood, ocean, soil)



- **Overcomes the limitations of traditional genomics**
  - Bypasses the need for culturing individual species in isolation



What is Metagenomics?

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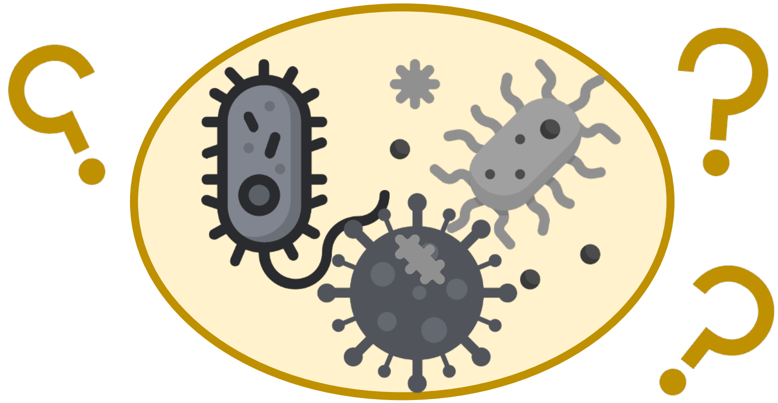
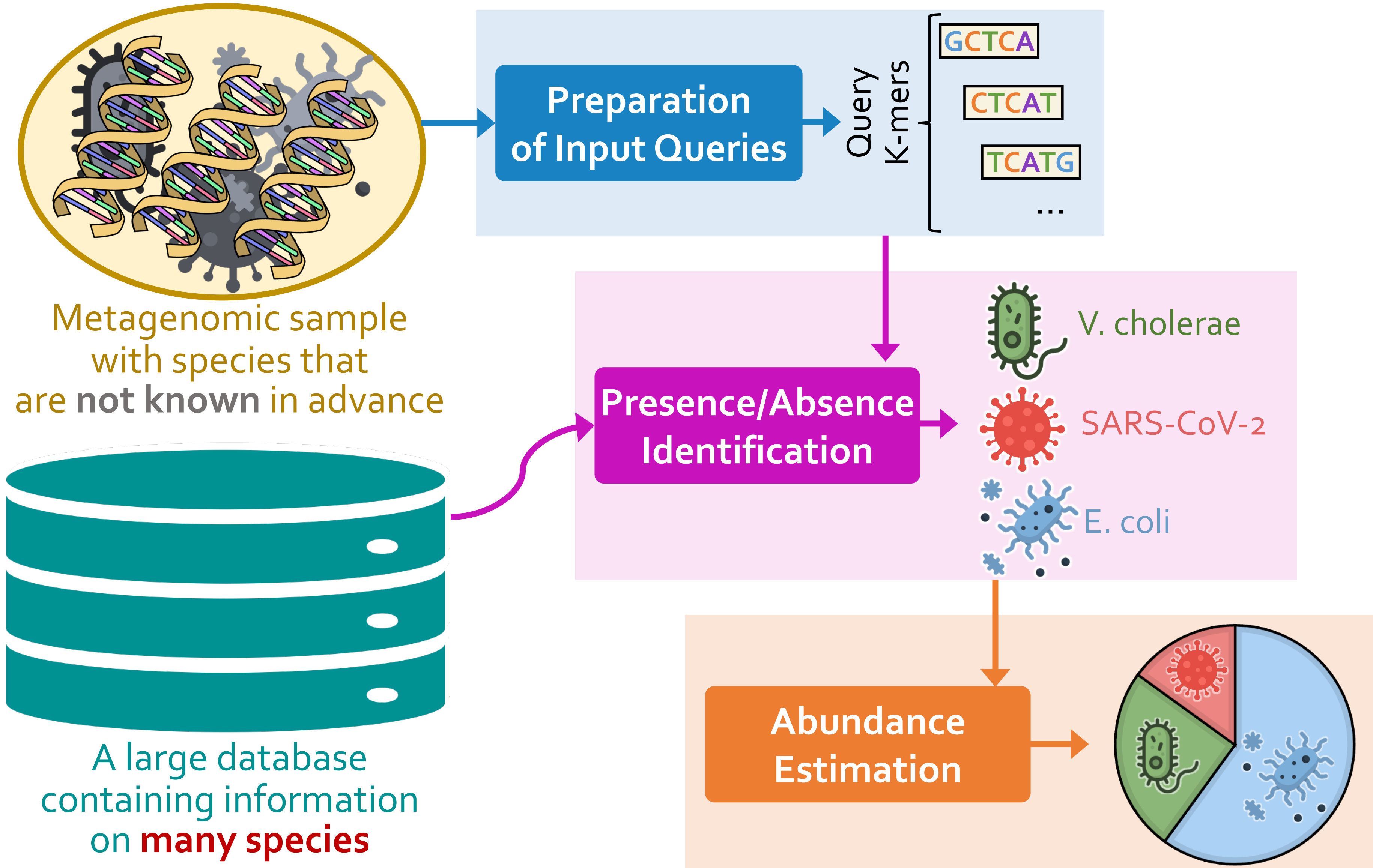


Has led to groundbreaking advances

- Precision medicine
- Understanding microbial diversity of an environment
- Discovering early warnings of communicable diseases

Metagenomic Analysis



(e.g., > 100 TBs in emerging databases)

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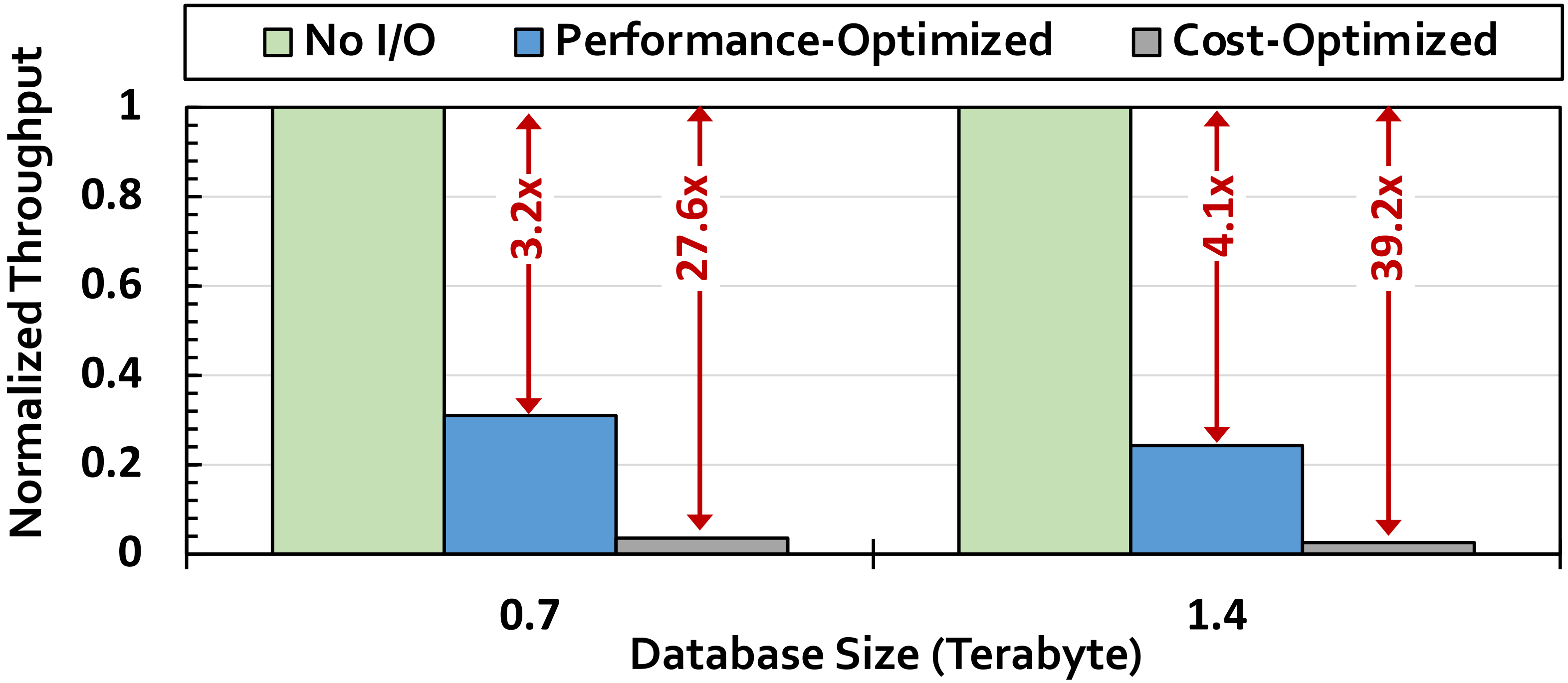
Motivation

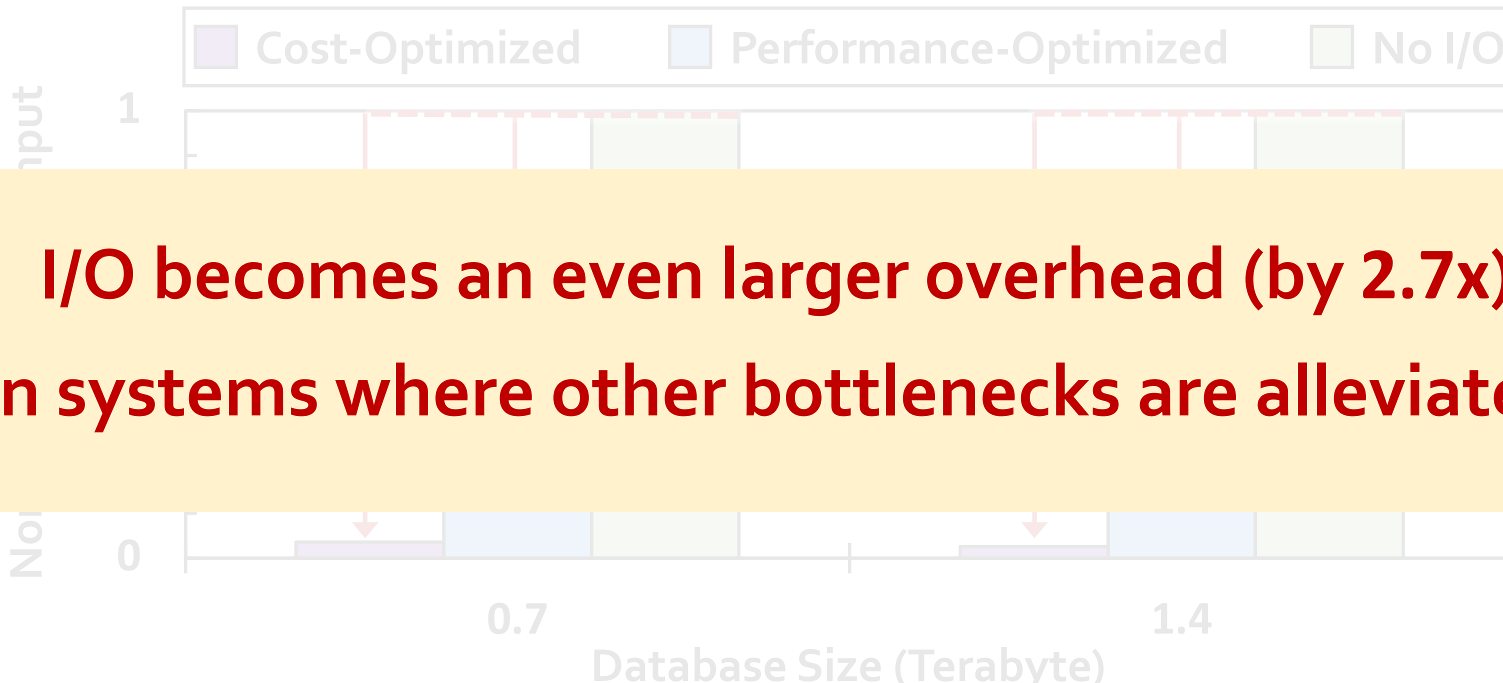
- Case study of the performance of metagenomic analysis tools
- With various state-of-the-art SSD configurations



I/O data movement causes significant performance overhead

Motivation

- Case study on the throughput of metagenomic analysis tools
- With Various state-of-the-art SSD configurations



I/O becomes an even larger overhead (by 2.7x)
in systems where other bottlenecks are alleviated

I/O data movement causes significant performance overhead

I/O Overhead is Hard to Avoid

I/O overhead due to accessing **large**, **low-reuse** data is hard to avoid

Sampling techniques to shrink database sizes

✗ *Reduce accuracy to levels unacceptable for many use cases*

Keeping all data required by metagenomic analysis completely and always resident in main memory

✗ *Energy inefficient, costly, unscalable, and unsustainable*

- Database sizes **increase rapidly** (doubling every few months)
- Different analyses need **different databases**

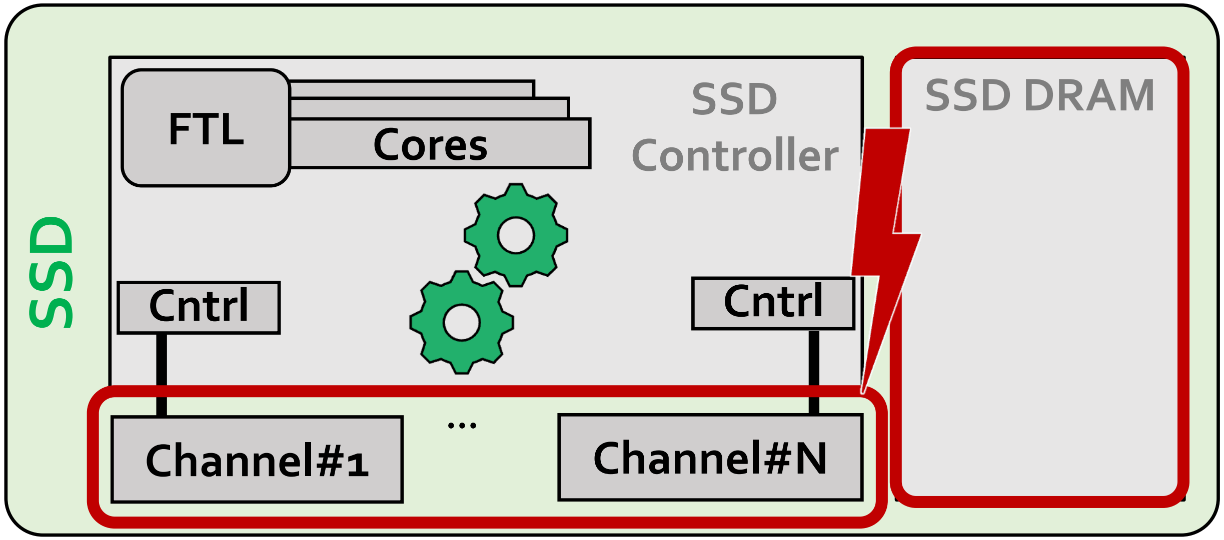
Our Goal

Improve metagenomic analysis ***performance***
by reducing large ***data movement overhead***
from the storage system
in a ***cost-effective*** *manner*

Challenges of In-Storage Processing

Existing metagenomic analysis approaches cannot be implemented as an in-storage processing system due to **SSD hardware limitations**

- Long **latency of NAND flash** chips
- Limited **DRAM capacity** inside the SSD
- Limited **DRAM bandwidth** inside the SSD



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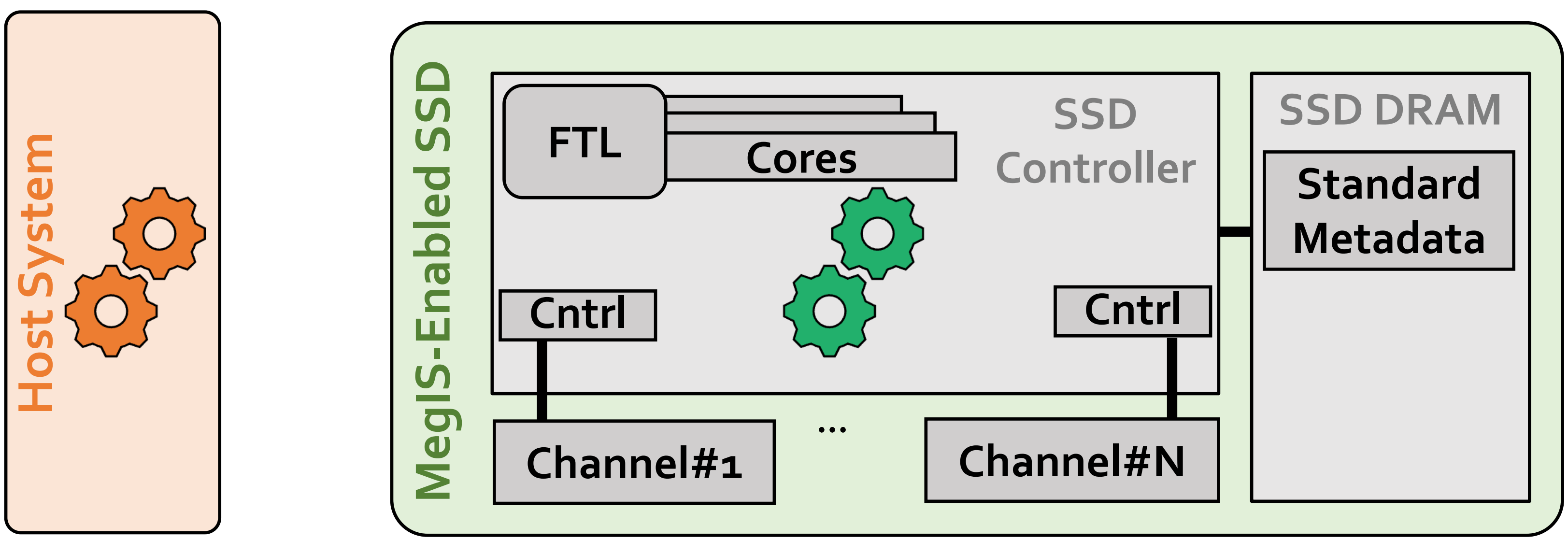
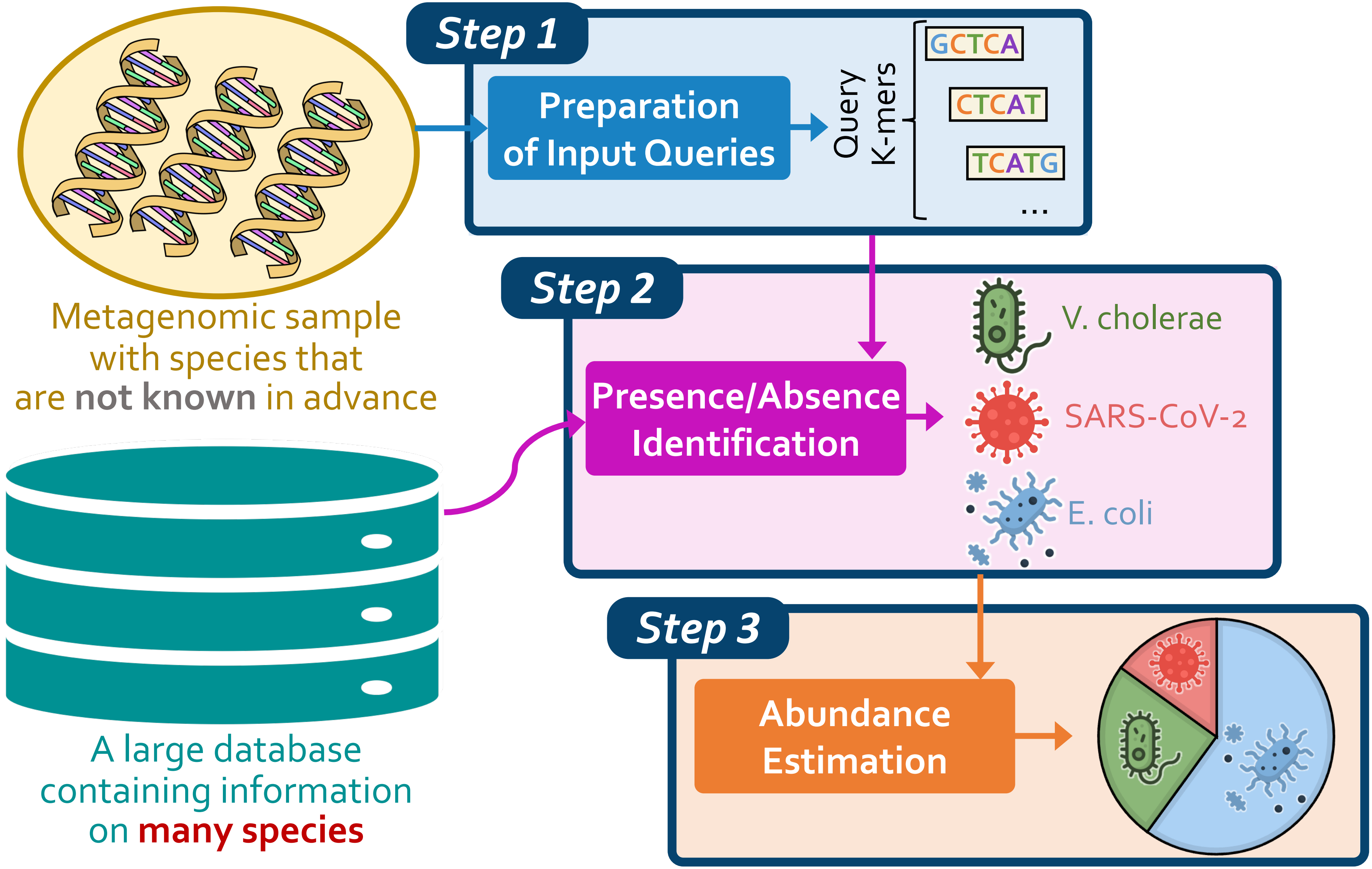
MegIS: Metagenomics In-Storage

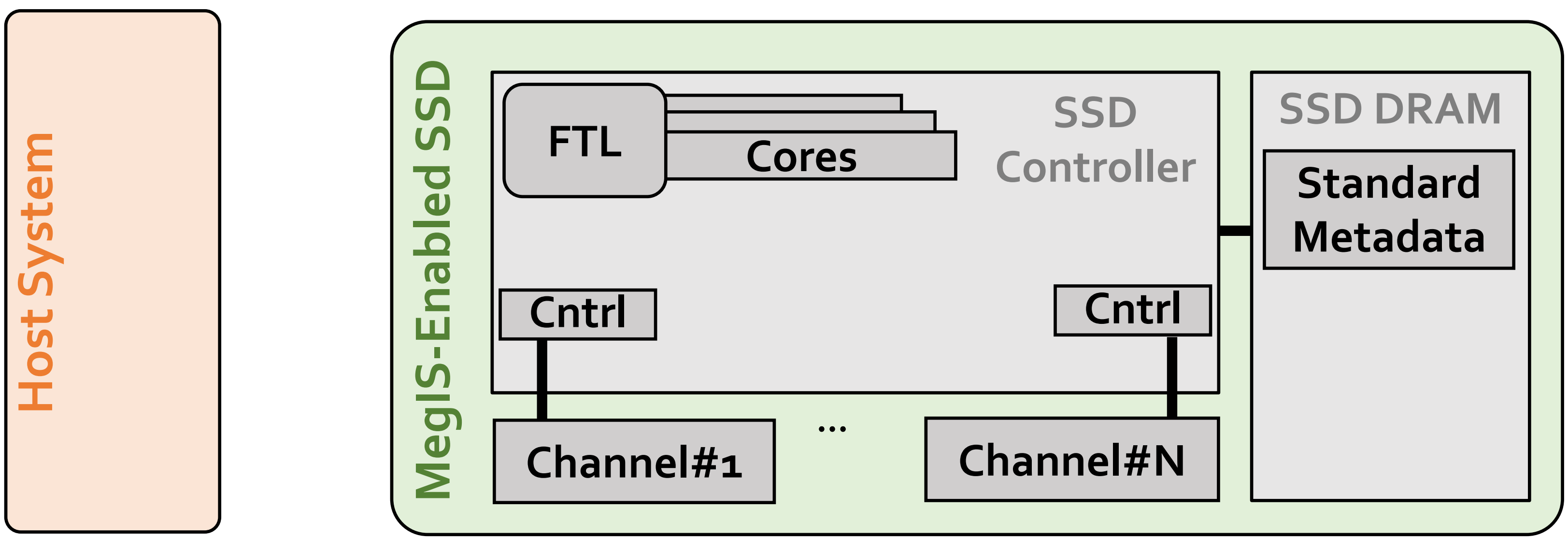
- First in-storage system for *end-to-end* metagenomic analysis
- **Idea:** Cooperative in-storage processing for metagenomic analysis
  - Hardware/software co-design between



MegIS's Steps



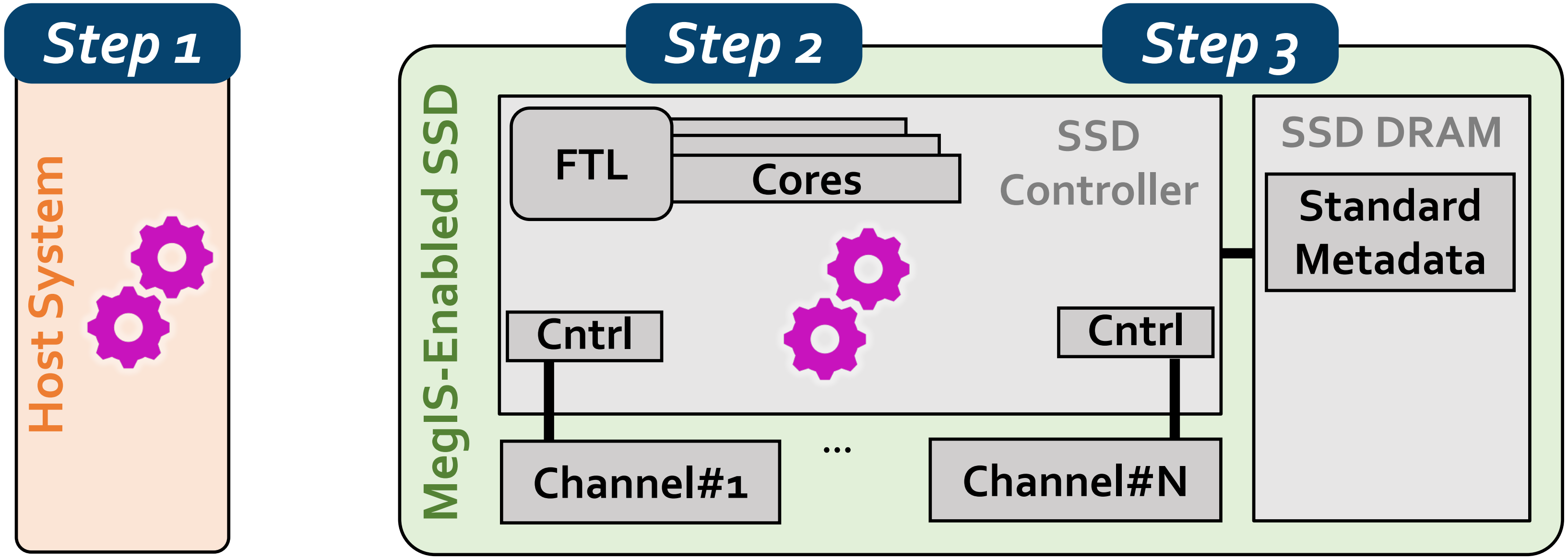
MegIS Hardware-Software Co-Design



MegIS Hardware-Software Co-Design

Task partitioning and mapping

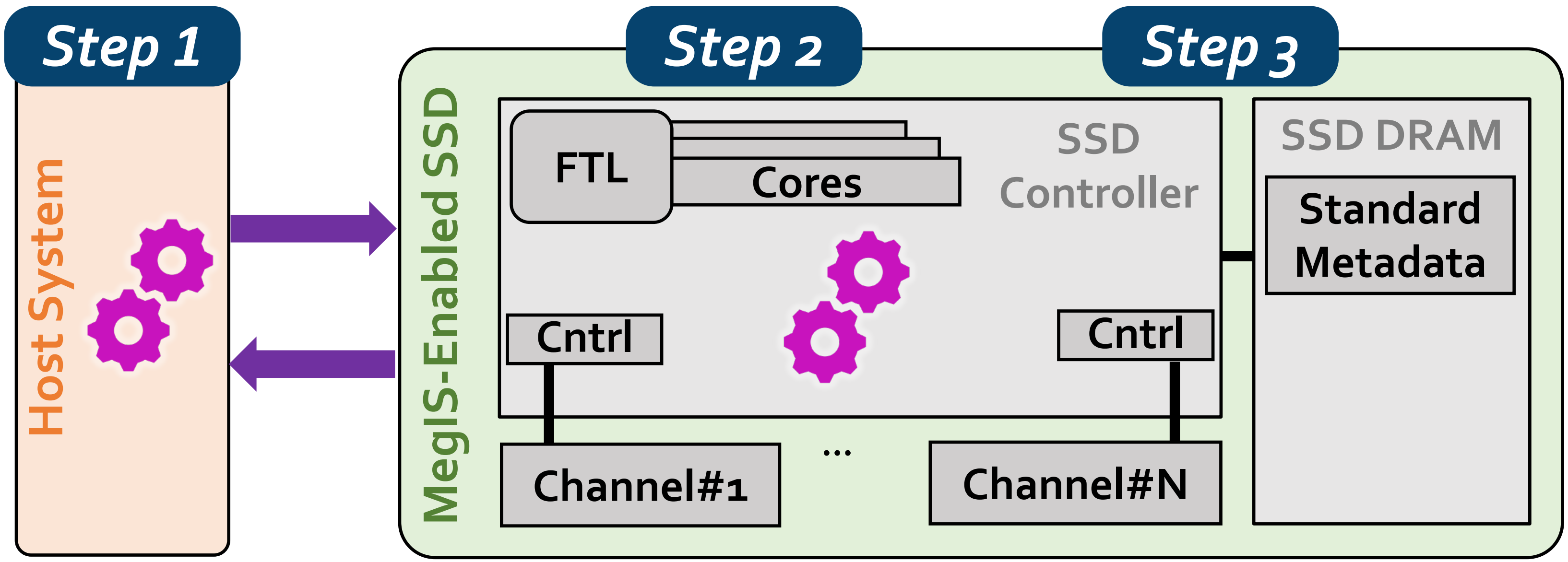
- *Each step executes in its most suitable system*



MegIS Hardware-Software Co-Design

Task partitioning and mapping
- *Each step executes in its most suitable system*

Data/computation flow coordination
- *Reduce communication overhead*
- *Reduce #writes to flash chips*



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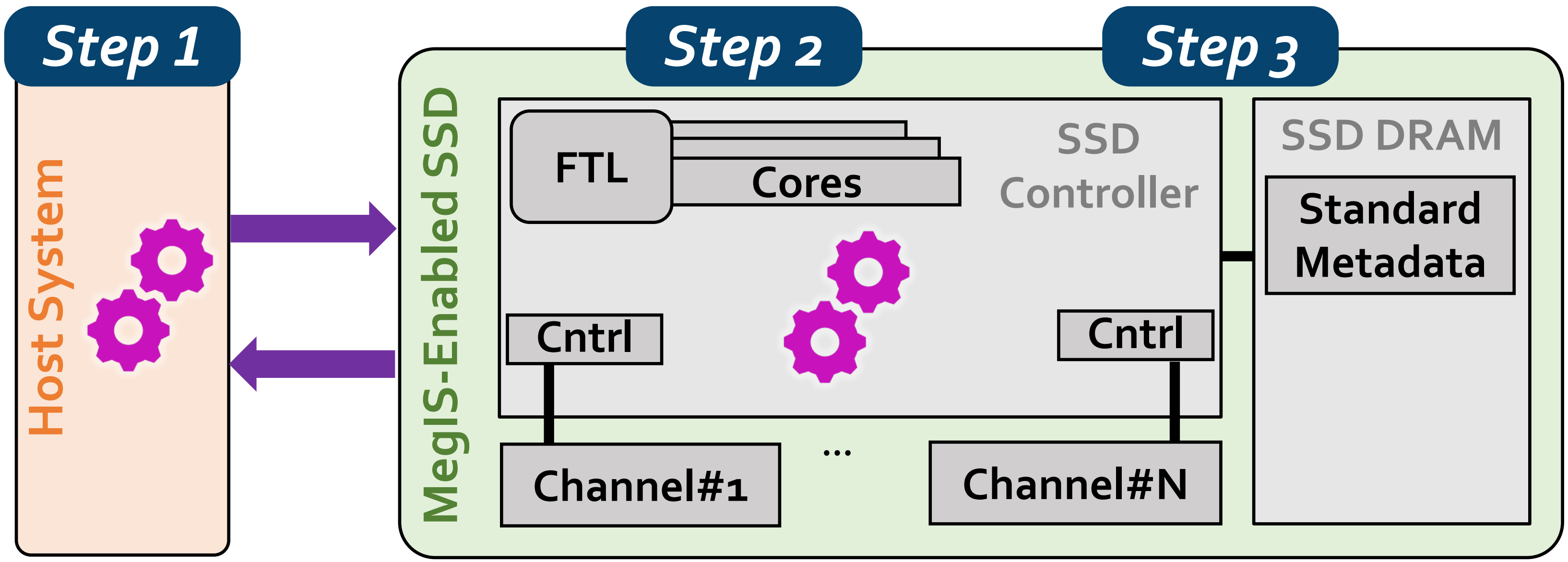

Storage-aware algorithms
- *Enable efficient access patterns to the SSD*

MegIS Hardware-Software Co-Design

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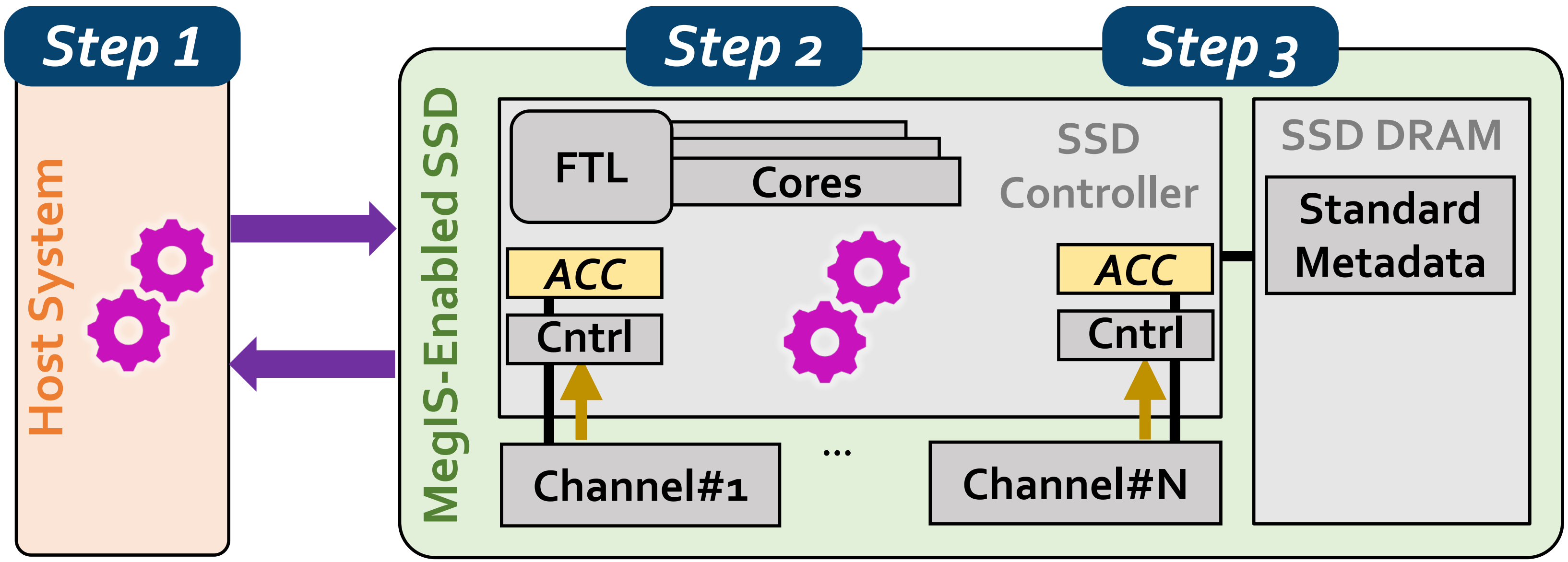

Storage-aware algorithms
- *Enable efficient access patterns to the SSD*

Lightweight in-storage accelerators
- *Minimize SRAM/DRAM buffer spaces needed inside the SSD*

MegIS Hardware-Software Co-Design

Task partitioning and mapping
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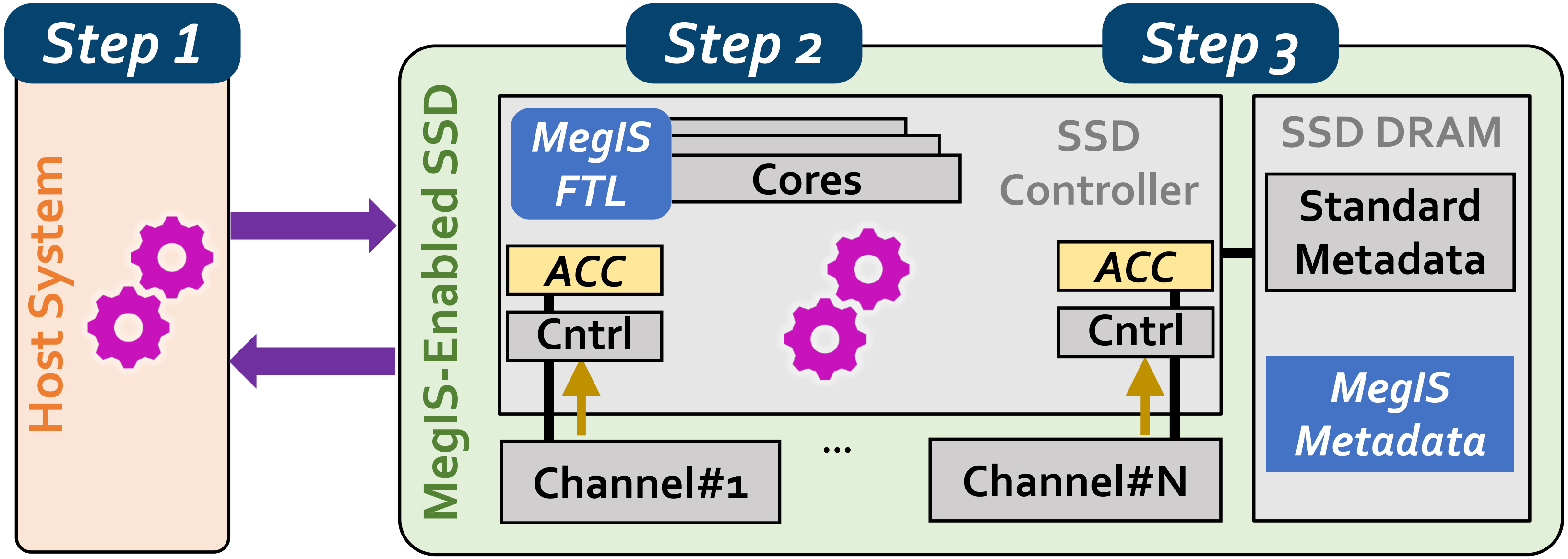
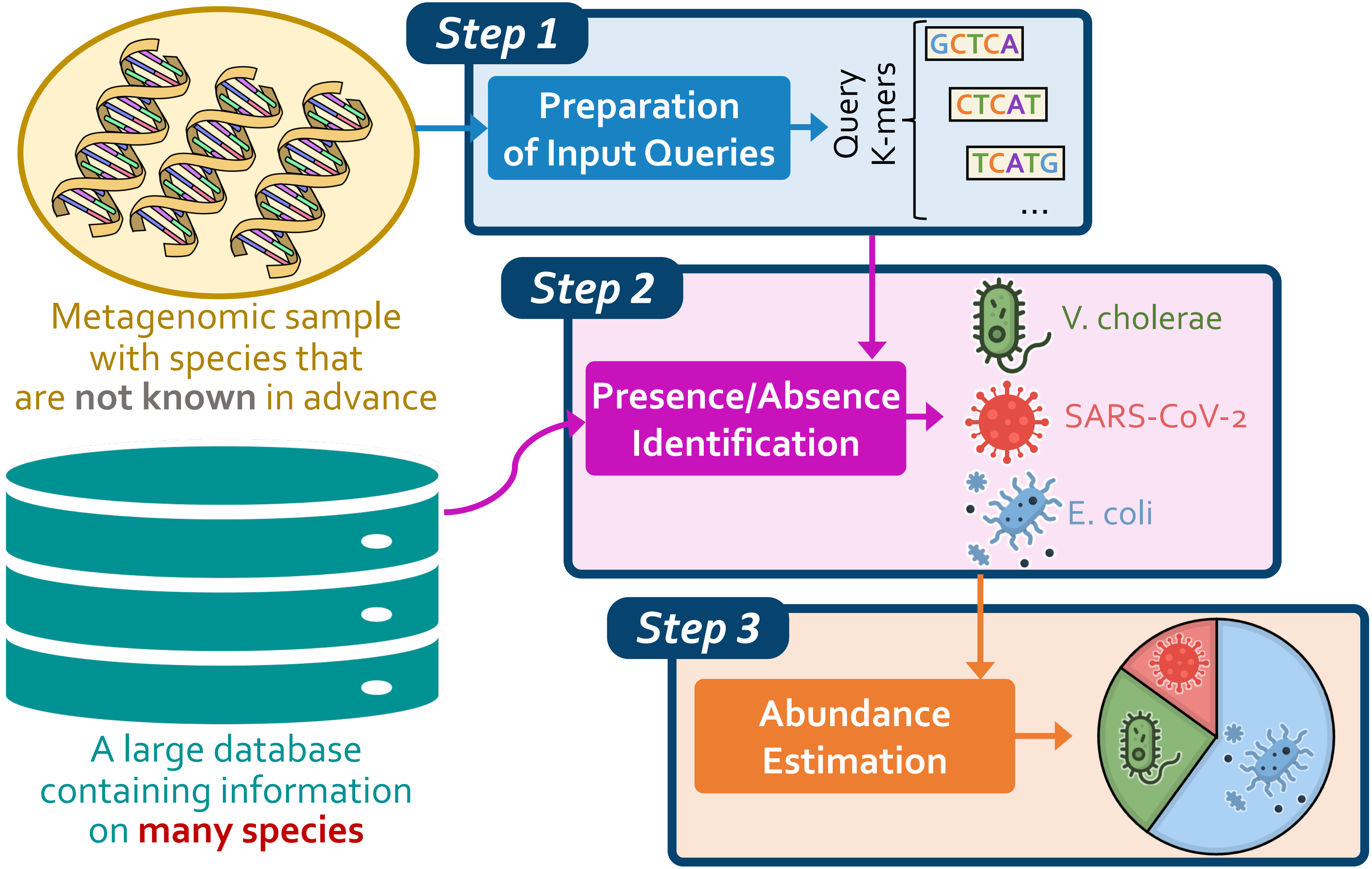


Storage-aware algorithms
- *Enable efficient access patterns to the SSD*

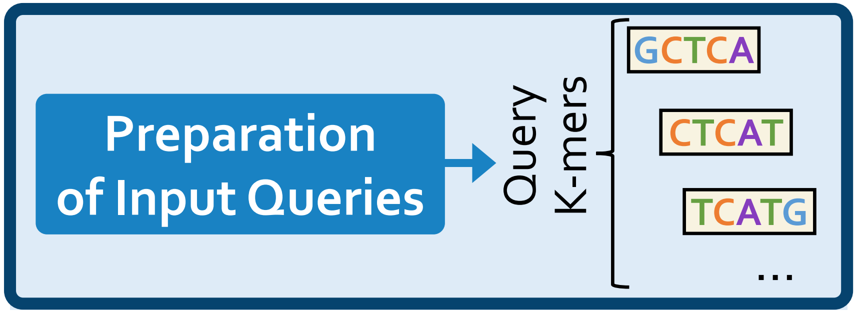
Lightweight in-storage accelerators
- *Minimize SRAM/DRAM buffer spaces needed inside the SSD*

Data mapping scheme and Flash Translation Layer (FTL)
- *Specialize to the characteristics of metagenomic analysis*
- *Leverage the SSD's full internal bandwidth*

Step 1 Overview



Step 1 Overview



*MegIS works with **sorted data structures** to avoid expensive random accesses to the SSD*

- **Extract k-mers** from the sample
- **Sort** the k-mers (database is sorted offline)

MegIS executes Step 1 in the host system

- Benefits from **larger DRAM** and **more powerful computation**
- Incurs **fewer writes** to NAND flash chips (than processing this step in the SSD)
- Enables **overlapping** Step 1 with Step 2

To execute Step 1 efficiently in the host system, MegIS needs to:

- Avoid significant overhead due to **data transfer time** between the steps
- Minimize **performance** and **lifetime** overheads *even* when host DRAM cannot hold all query k-mers

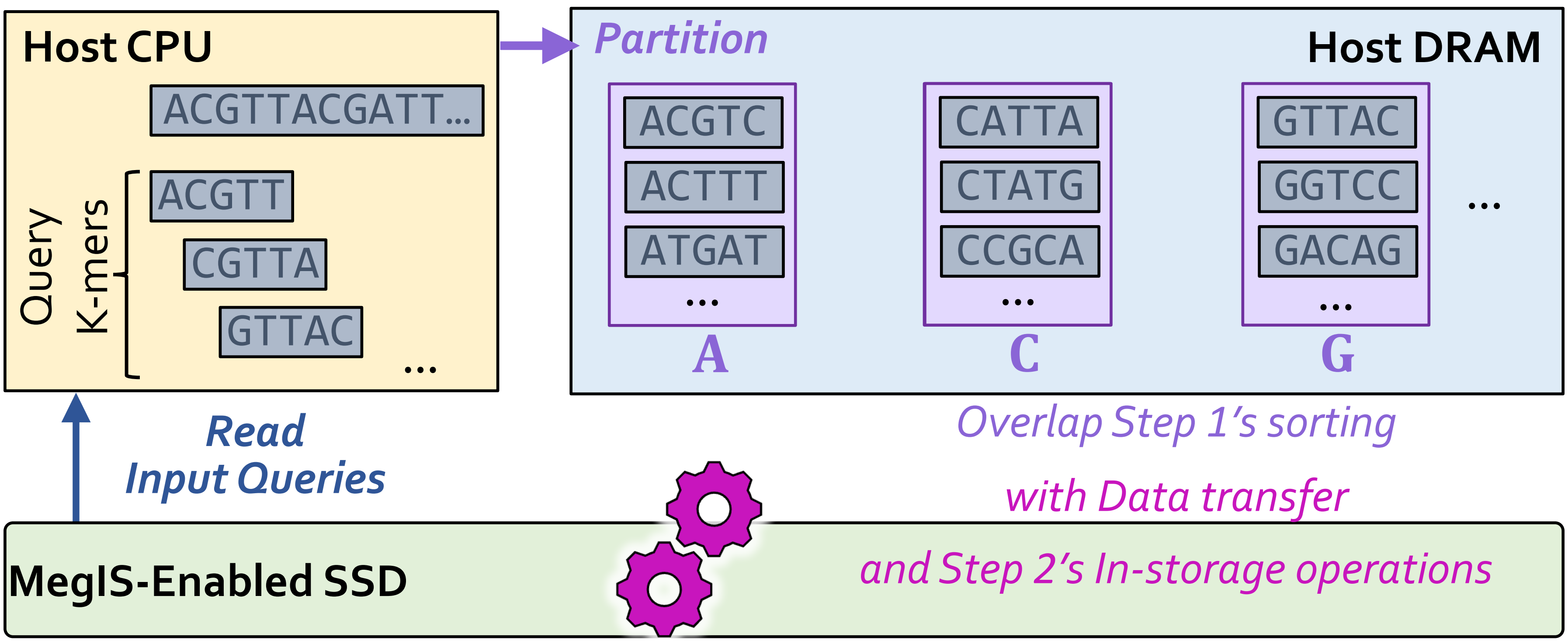
Step 1 Design

- Divide k-mers into **independent partitions** by their alphabetical range

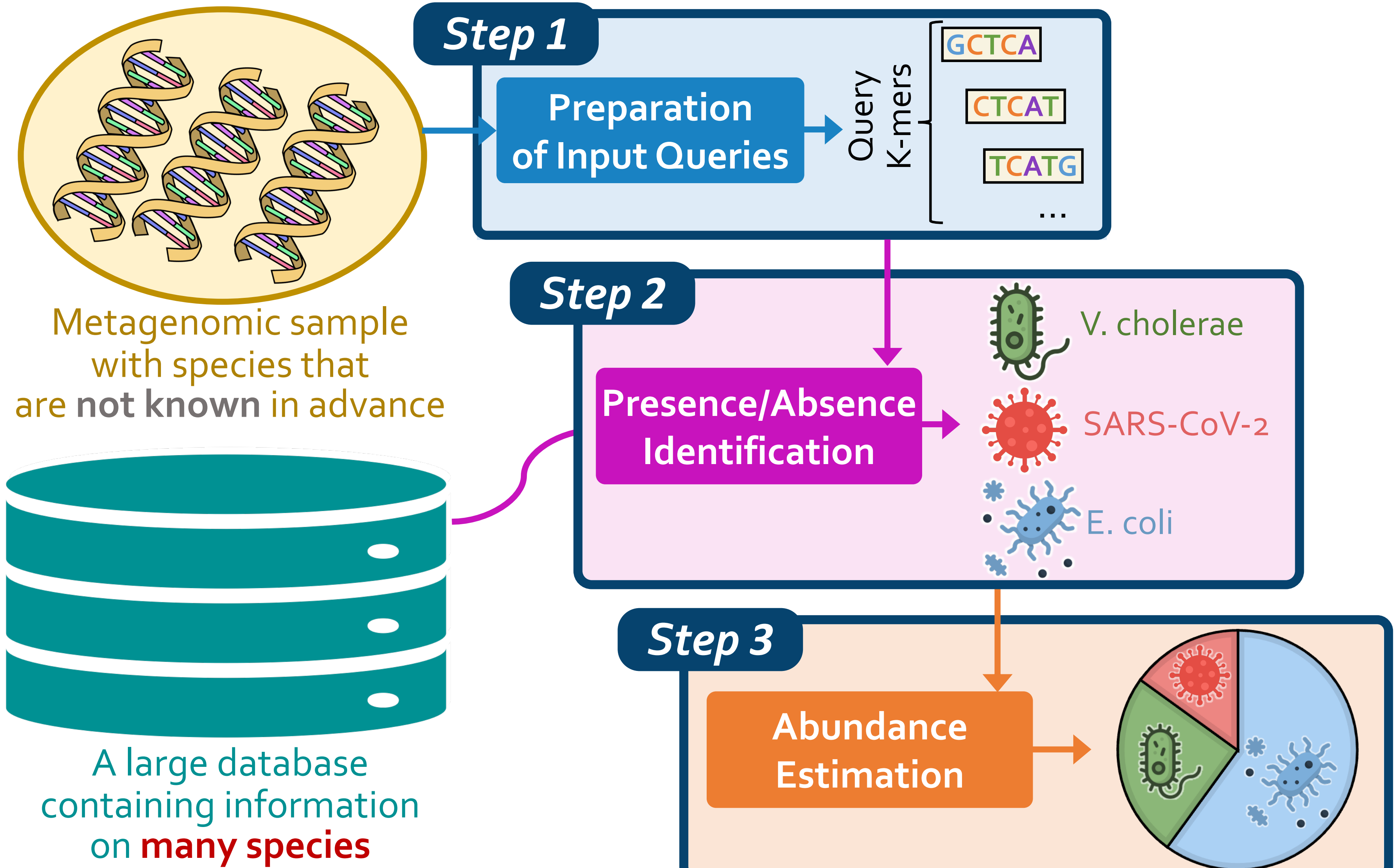
✓ **Can overlap operations on different partitions**

- **Pin partitions** to the host system or the SSD

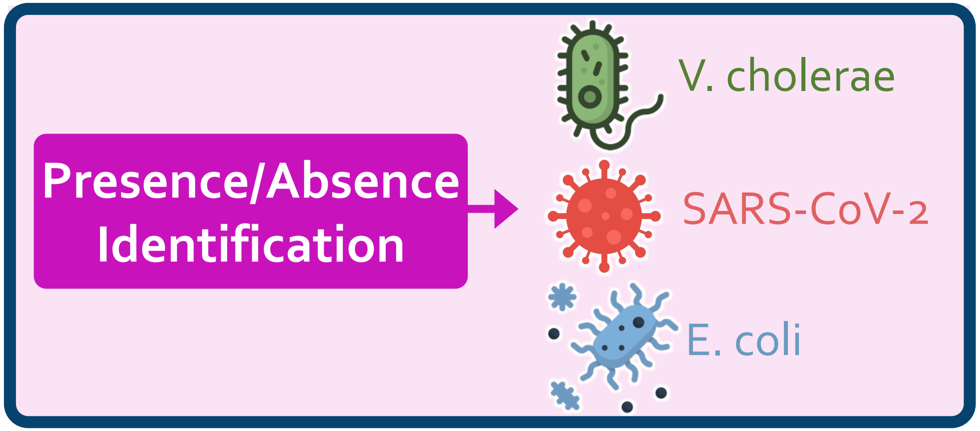
✓ **Avoid unnecessary movement of k-mers due to page swaps**



Step 2 Overview



Step 2 Overview



- **Identify the intersecting k-mers** between the <u>query k-mers</u> and the <u>database k-mers</u>

- **Retrieve the species IDs** of intersecting k-mers

MegIS executes Step 2 in the SSD

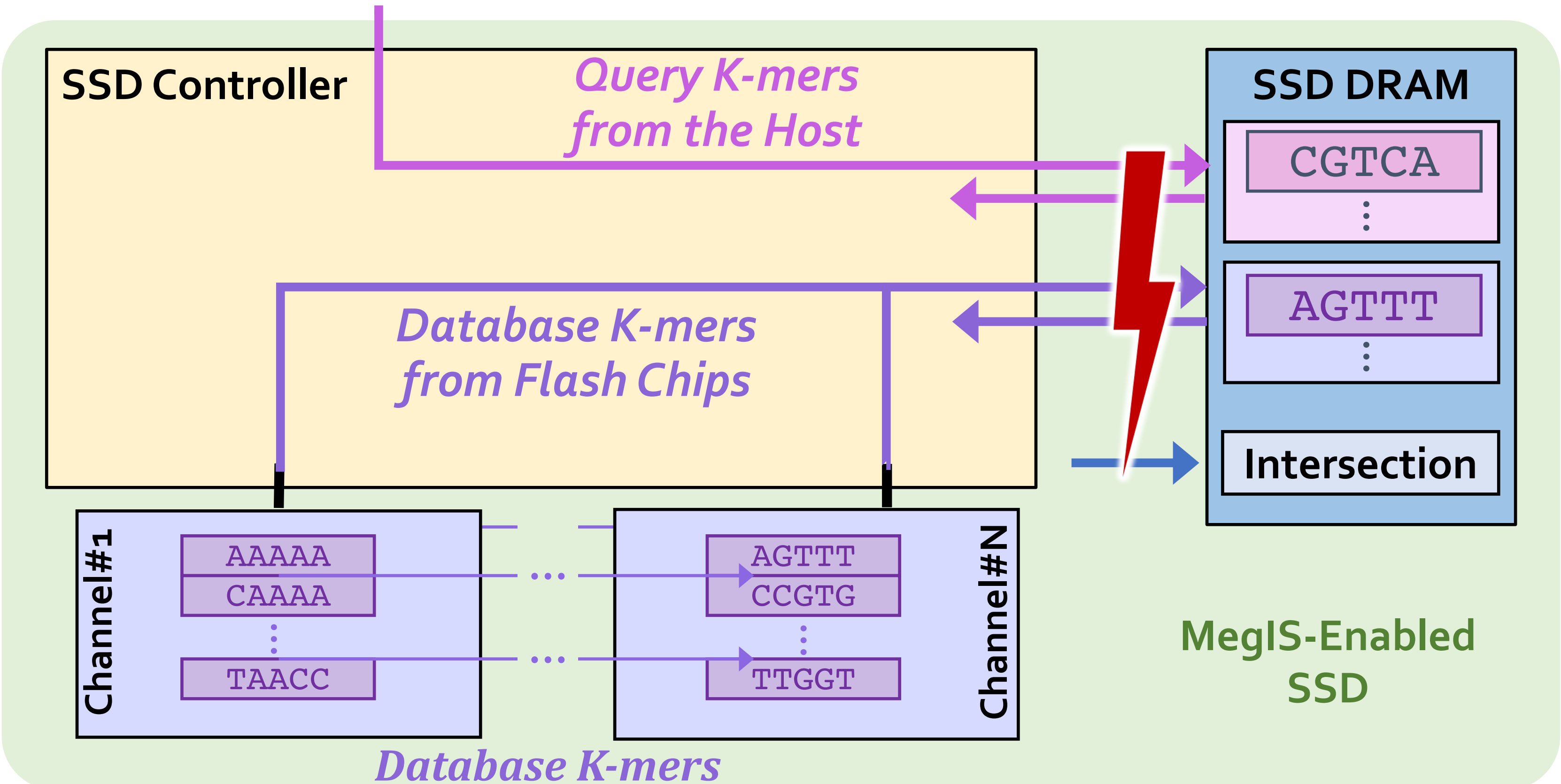
- Accesses **large data** with **low reuse**
- Involves **lightweight computation**

To execute Step 2 efficiently in the SSD, MegIS needs to:

- Leverage **internal bandwidth** efficiently
- Not require **expensive hardware inside the SSD** (e.g., large DRAM bandwidth/capacity and costly logic units)

Identifying the Intersecting K-mers

- **Challenge:** Limited internal DRAM bandwidth

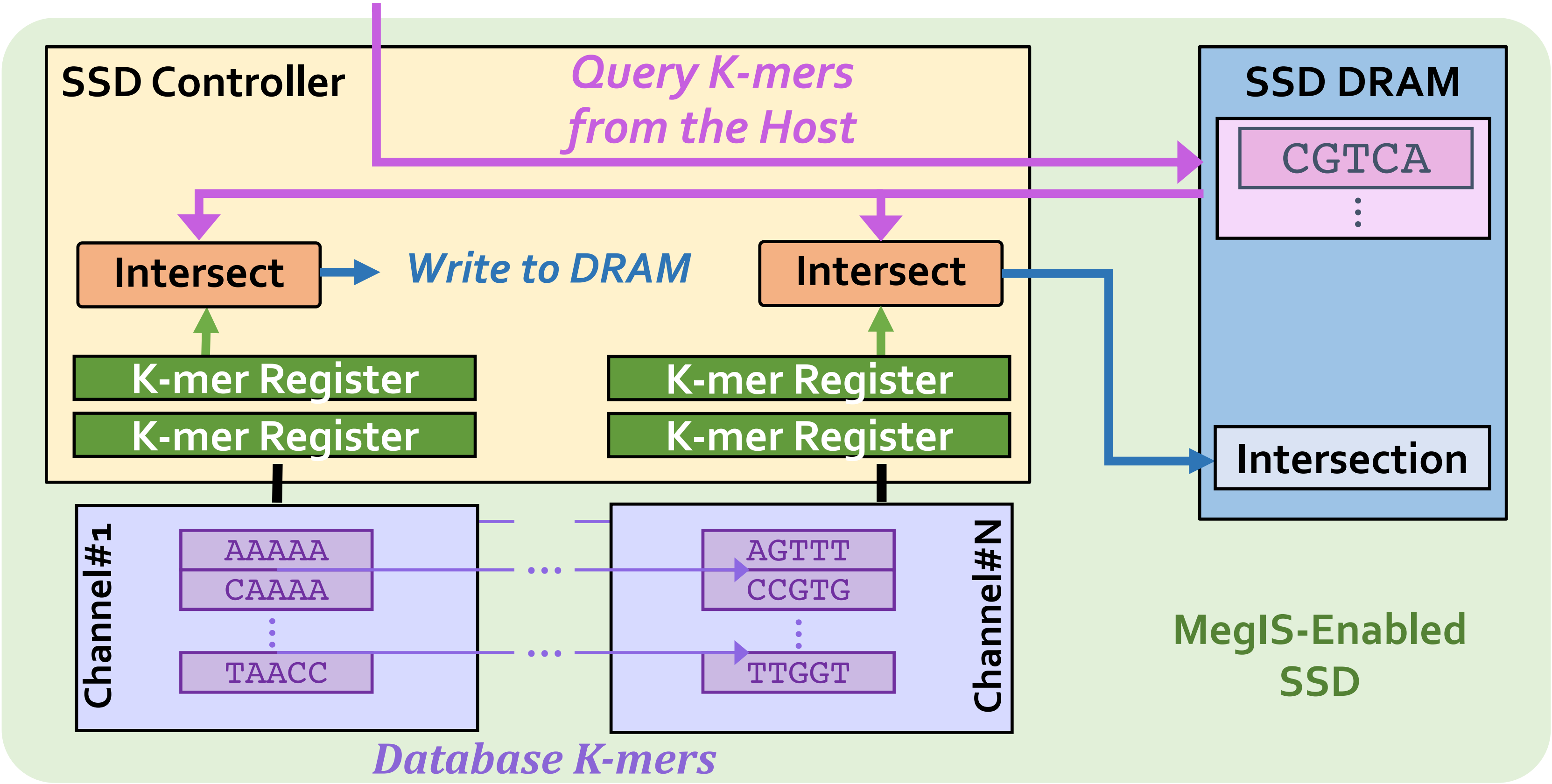


Identifying the Intersecting K-mers

- **Challenge:** Limited internal DRAM bandwidth

✓ *Compute directly on the flash data streams* *[Zou+, MICRO'22]*

✓ *Reduce buffer size based on application features*

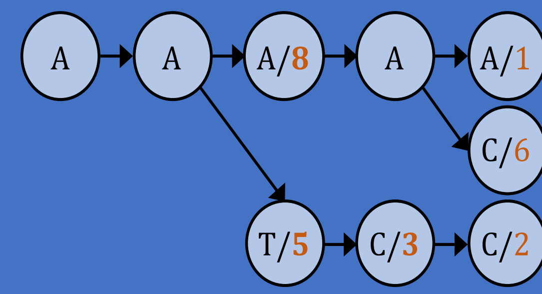


Retrieving the Species ID

- MegIS retrieves the species IDs of the **intersecting k-mers** by looking up a **sketch database**

K-mer	
AAAAA	
AAAAC	
AATCC	
...	...

Space-Inefficient



Space-Efficient

❌ *Inefficient inside the SSD due to long NAND flash latency*

K-mer Sketch Streaming

7.5x Smaller

2.1× Larger

K-mer Sketch Streaming is much more suitable for in-storage processing due to its streaming accesses

Retrieving the Species ID

- MegIS retrieves the species IDs of the **intersecting k-mers** by looking up a **sketch database**

Design details are in the paper

✕ *Inefficient inside the SSD due to long NAND flash latency*

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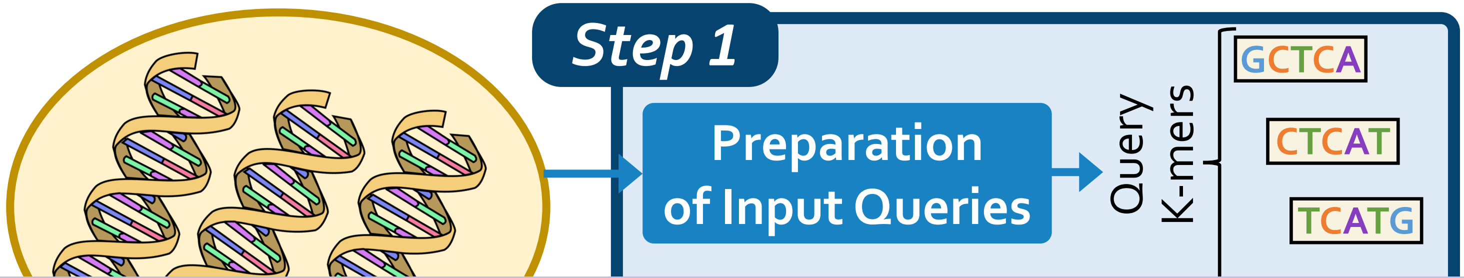
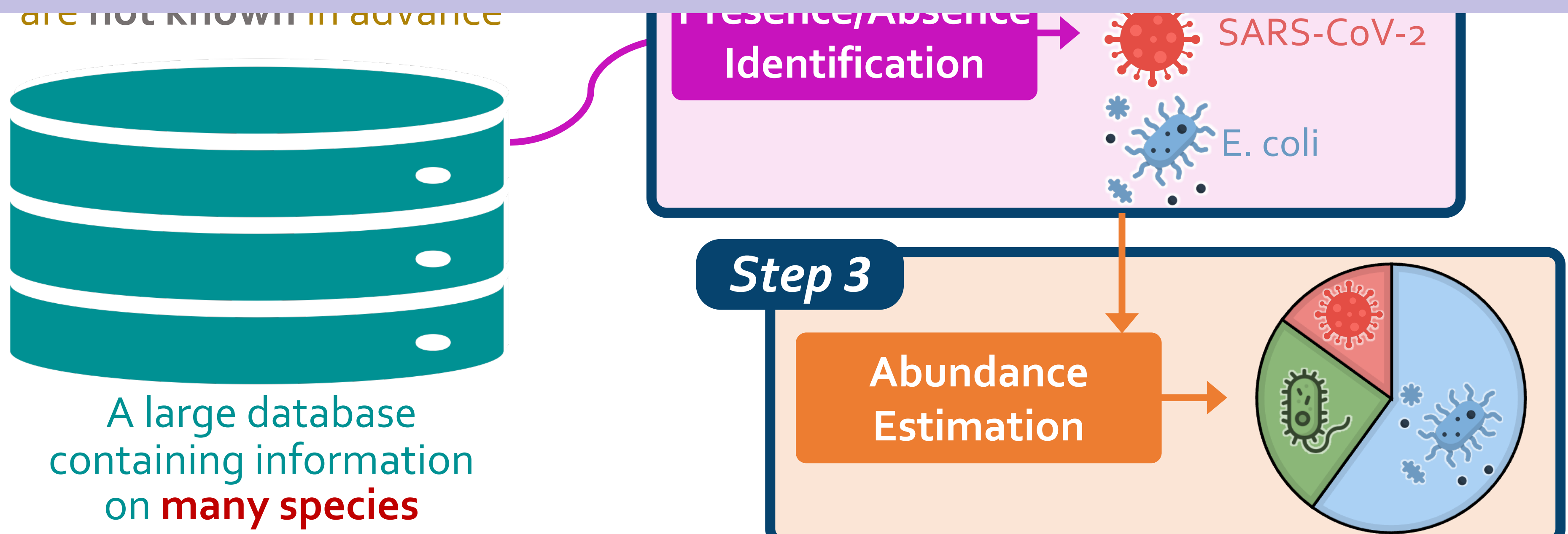
Step 3



Step 3 and MegIS FTL are in the paper



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Evaluation: Methodology Overview

Performance, Energy, and Power Analysis

Hardware Components

- Synthesized Verilog model for the in-storage accelerators
- MQSim *[Tavakkol+, FAST'18]* for SSD's internal operations
- Ramulator *[Kim+, CAL'15]* for SSD's internal DRAM

Software Components

Measure on a real system:

- AMD® EPYC® CPU with 128 physical cores
- 1-TB DRAM

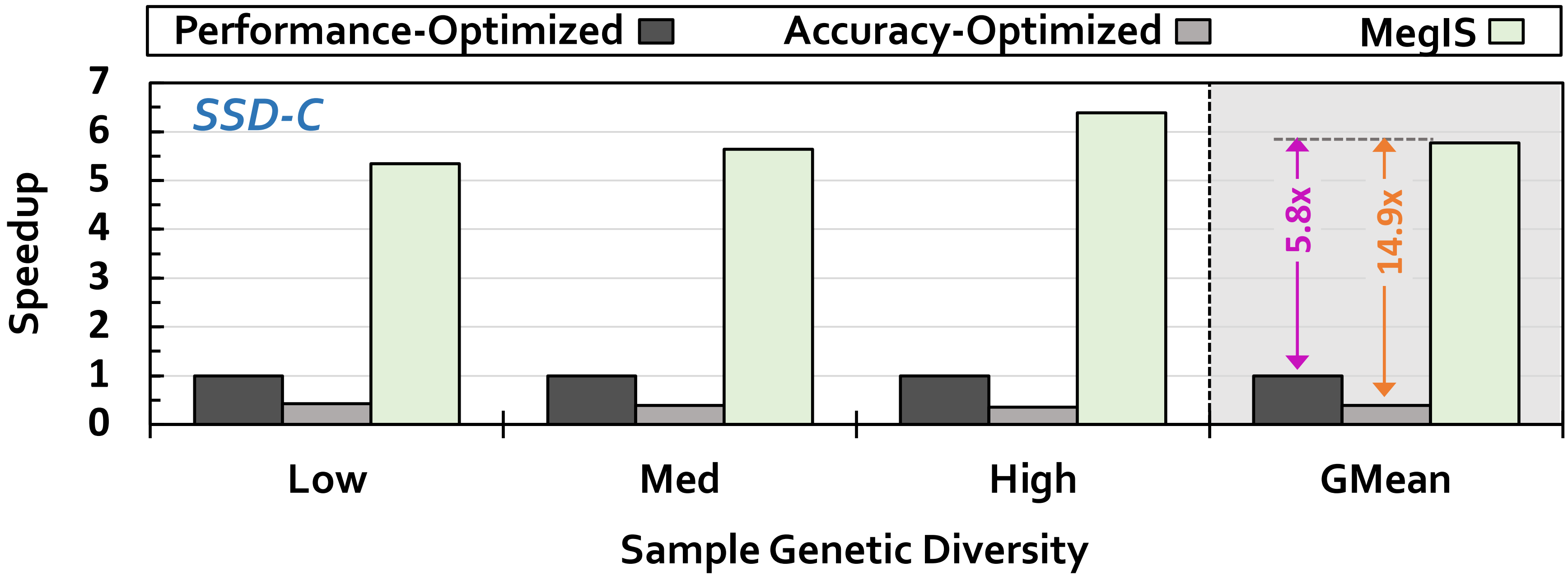
Baseline Comparison Points

- **Performance-optimized software**, Kraken2 *[Genome Biology'19]*
- **Accuracy-optimized software**, Metalign *[Genome Biology'20]*
- **PIM hardware-accelerated tool** (using processing-in-memory), Sieve *[ISCA'21]*

SSD Configurations

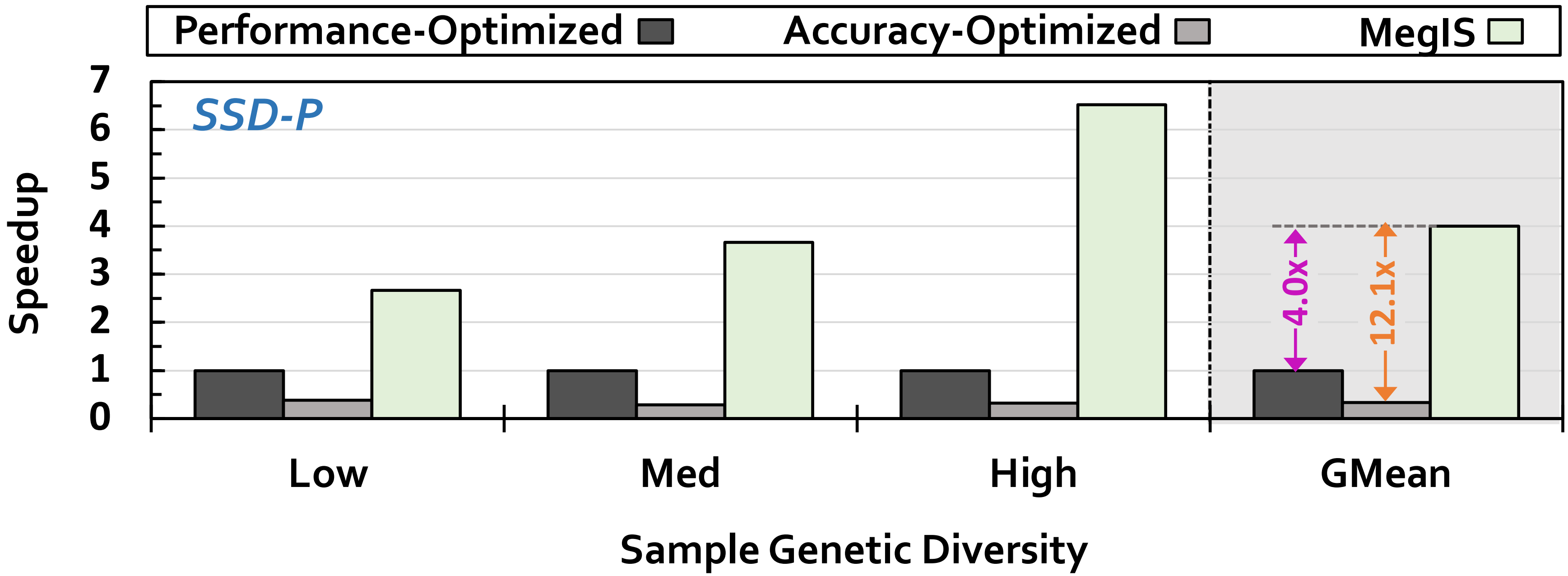
- **SSD-C:** with SATA3 interface (0.5 GB/s sequential read bandwidth)
- **SSD-P:** with PCIe Gen4 interface (7 GB/s sequential read bandwidth)

Evaluation: Speedup over the Software Baselines



MegIS provides significant speedup over both Performance-Optimized and Accuracy-Optimized baselines

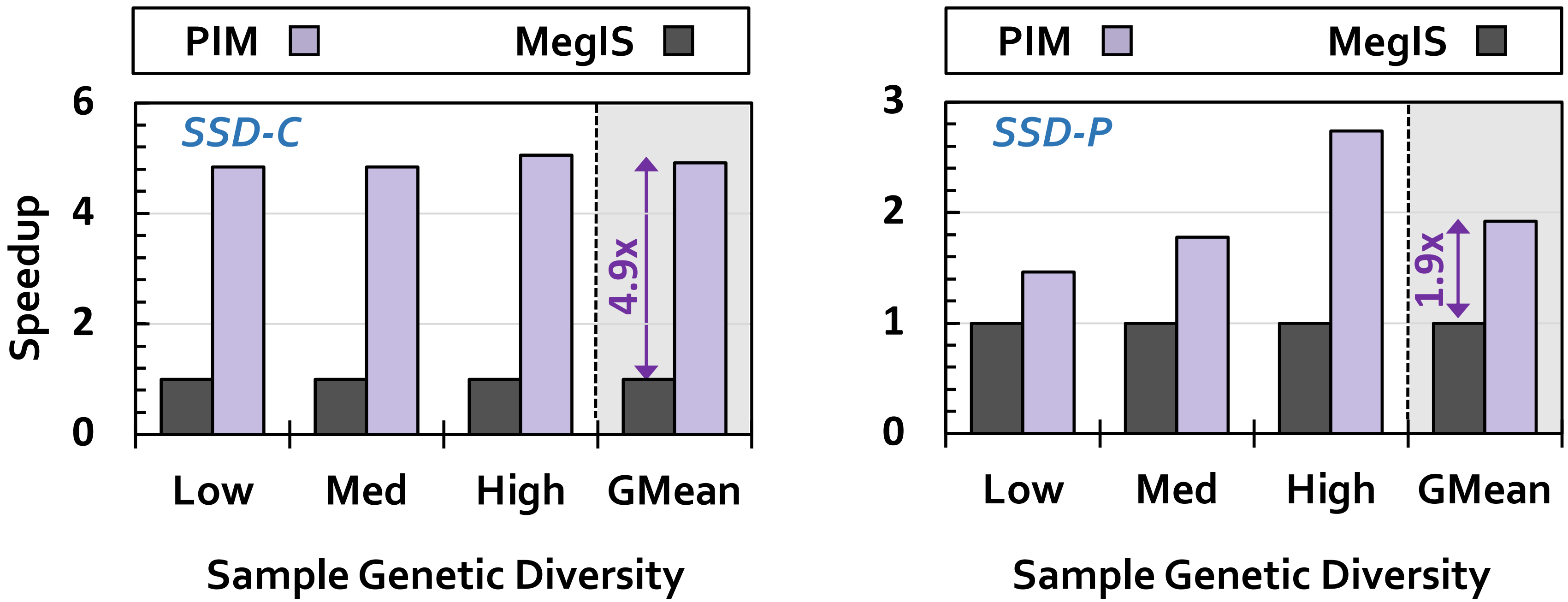
Evaluation: Speedup over the Software Baselines



MegIS provides significant speedup over both Performance-Optimized and Accuracy-Optimized baselines

MegIS improves performance on both cost-optimized and performance-optimized SSDs

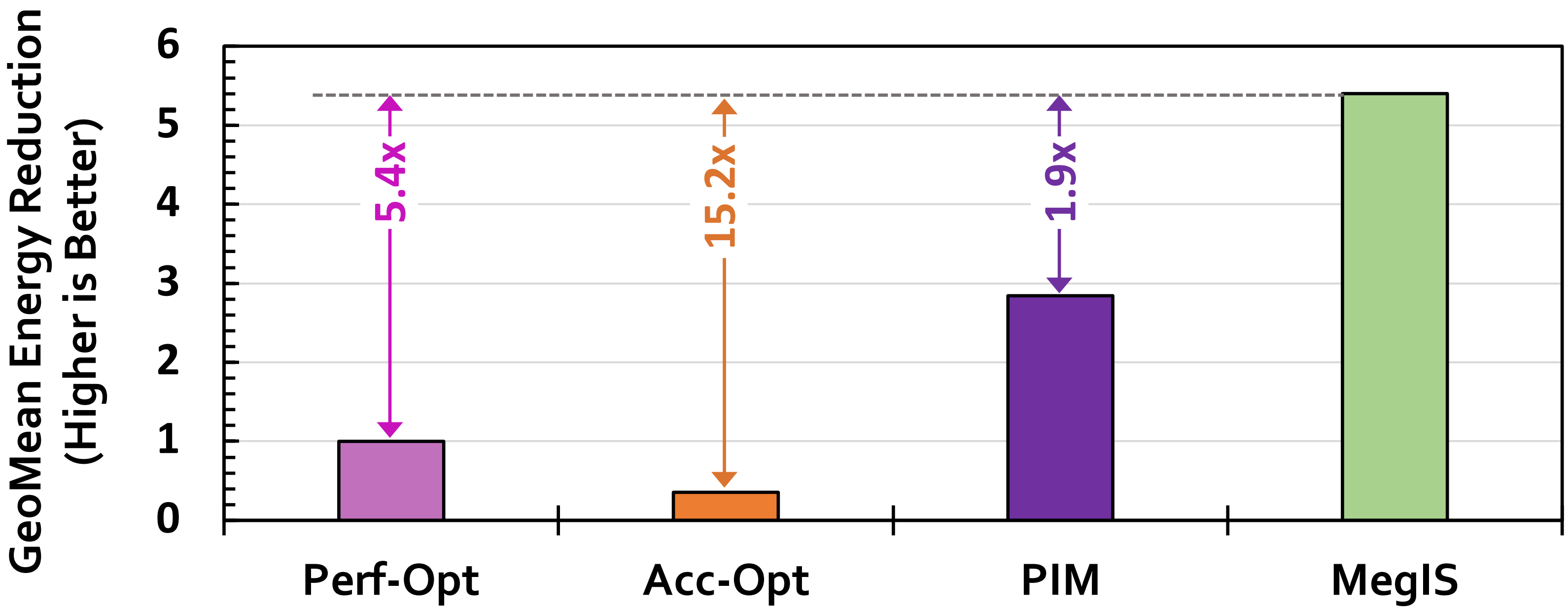
Evaluation: Speedup over the PIM Baseline



MegIS provides significant speedup over the PIM baseline

Evaluation: Reduction in Energy Consumption

- On average across different input sets and SSDs



MegIS provides significant energy reduction over the Performance-Optimized, Accuracy-Optimized, and PIM baselines

Evaluation: Accuracy, Area, and Power

Accuracy

- **Same accuracy** as the **accuracy-optimized** baseline
- **Significantly higher accuracy** than the **performance-optimized** and **PIM** baselines
  - 4.6 – 5.2× higher F1 scores
  - 3 – 24% lower L1 norm error

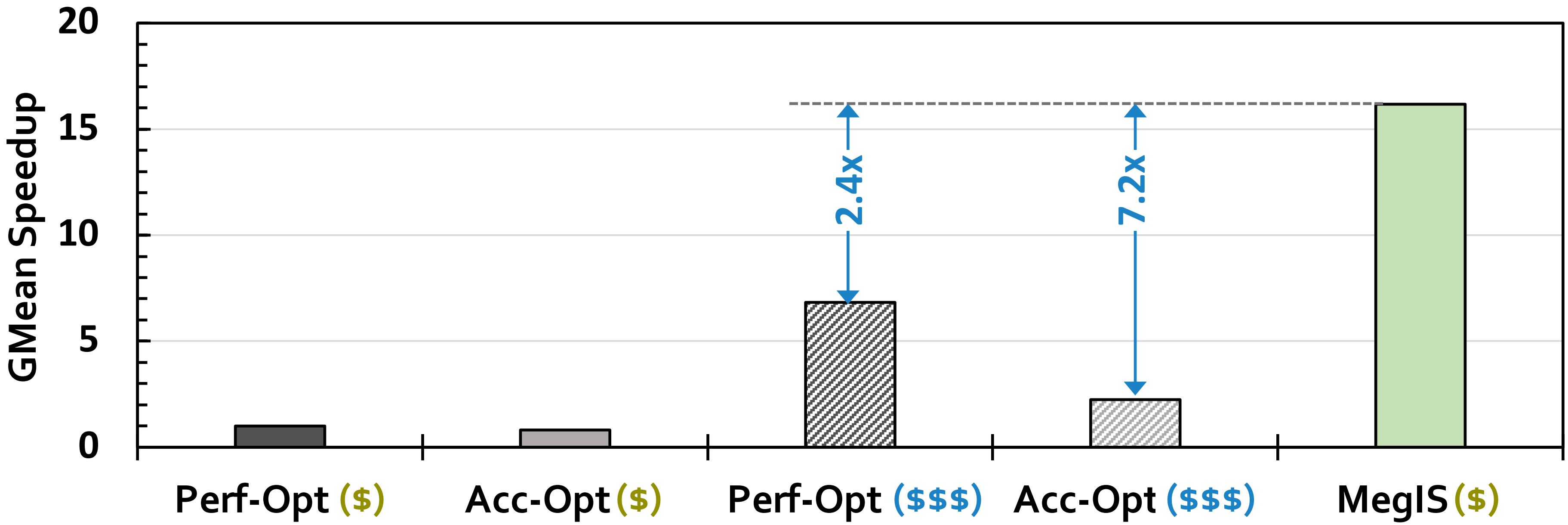
Area and Power

Total for an 8-channel SSD:

- **Area:** 0.04 mm^2 *(Only **1.7%** of the area of three ARM Cortex R4 cores in an SSD controller)*
- **Power:** 7.658 mW

Evaluation: System Cost-Efficiency

- **Cost-optimized system ($):** With SSD-C and 64-GB DRAM
- **Performance-optimized system ($$$):** With SSD-P and 1-TB DRAM



MegIS outperforms the baselines
***even* when running on a much less costly system**

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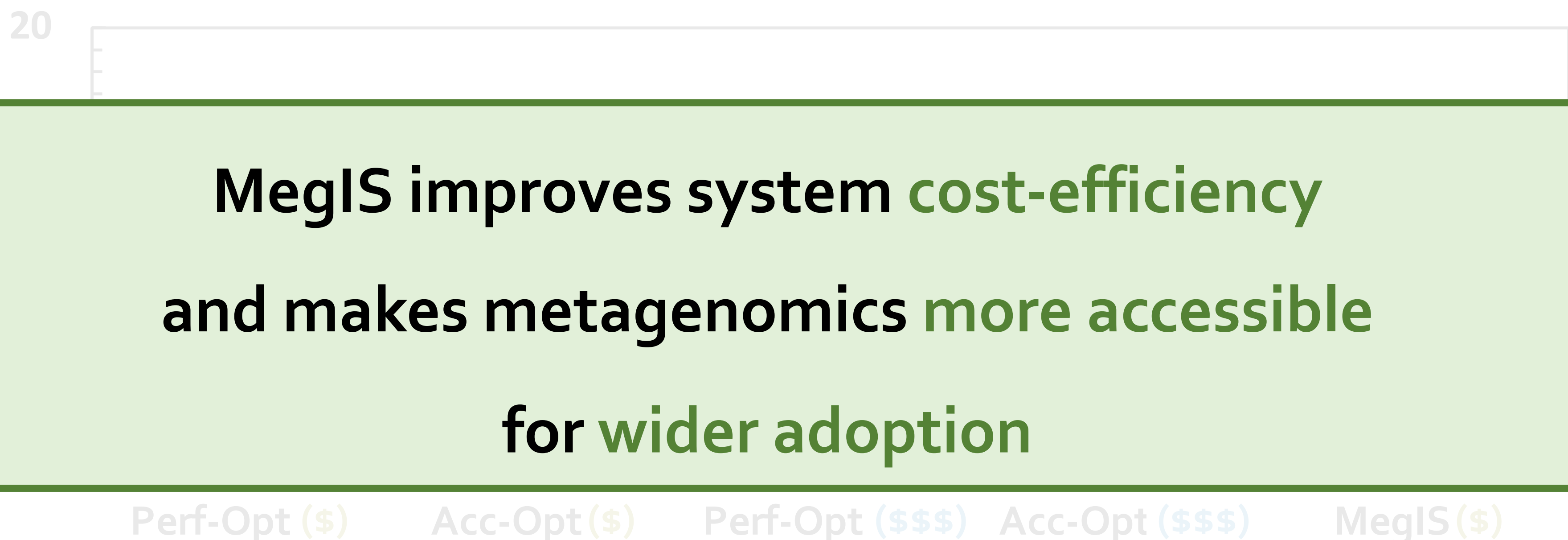

MegIS improves system cost-efficiency
and makes metagenomics more accessible
for wider adoption

MegIS outperforms the baselines
even when running on a much less costly system

More in the Paper

- MegIS's performance when running in-storage processing operations on the **cores existing in the SSD controller**

- MegIS's performance when using the same accelerators **outside SSD**

- **Sensitivity analysis with varying**
  - Database sizes
  - Memory capacities
  - #SSDs
  - #Channels
  - #Samples

- MegIS's performance for **abundance estimation**

More in the Paper

MegIS: High-Performance, Energy-Efficient, and Low-Cost Metagenomic Analysis with In-Storage Processing

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- Database sizes
- Memory capacities
- #SSDs
- #Channels
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• MegIS's performance for abundance estimation

https://arxiv.org/abs/2406.19113

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Metagenomic analysis suffers from
significant storage I/O data movement overhead

MegIS

The *first* **in-storage processing** system for *end-to-end* metagenomic analysis
Leverages and orchestrates **processing inside** and **outside** the storage system

Improves performance

2.7×–37.2× over **performance-optimized** software
6.9×–100.2× over **accuracy-optimized** software
1.5×–5.1× over **hardware-accelerated PIM** baseline

High accuracy

Same as accuracy-optimized
4.8× higher F1 scores
over **performance-optimized/PIM**

Reduces energy consumption

5.4× over **performance-optimized** software
15.2× over **accuracy-optimized** software
1.9× over **hardware-accelerated PIM** baseline

Low area overhead

1.7% of the three cores
in an SSD controller

MegIS

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Backup Slides

Executive Summary *(I suggest not to present it due to time limits)*

Problem: Metagenomic analysis suffers from significant storage I/O data movement overhead

Goal: Improve metagenomic analysis **performance** by reducing **storage I/O data movement** overhead in a **cost-effective** manner

Challenge: While in-storage processing can be a promising direction, existing metagenomic analysis approaches cannot be implemented in the SSD due to SSD **hardware limitations**

Idea: *Cooperative ISP for metagenomics*

Capitalize on the strengths of processing both **inside and outside the storage system**

MegIS: *The first in-storage processing system for end-to-end metagenomic analysis pipeline*

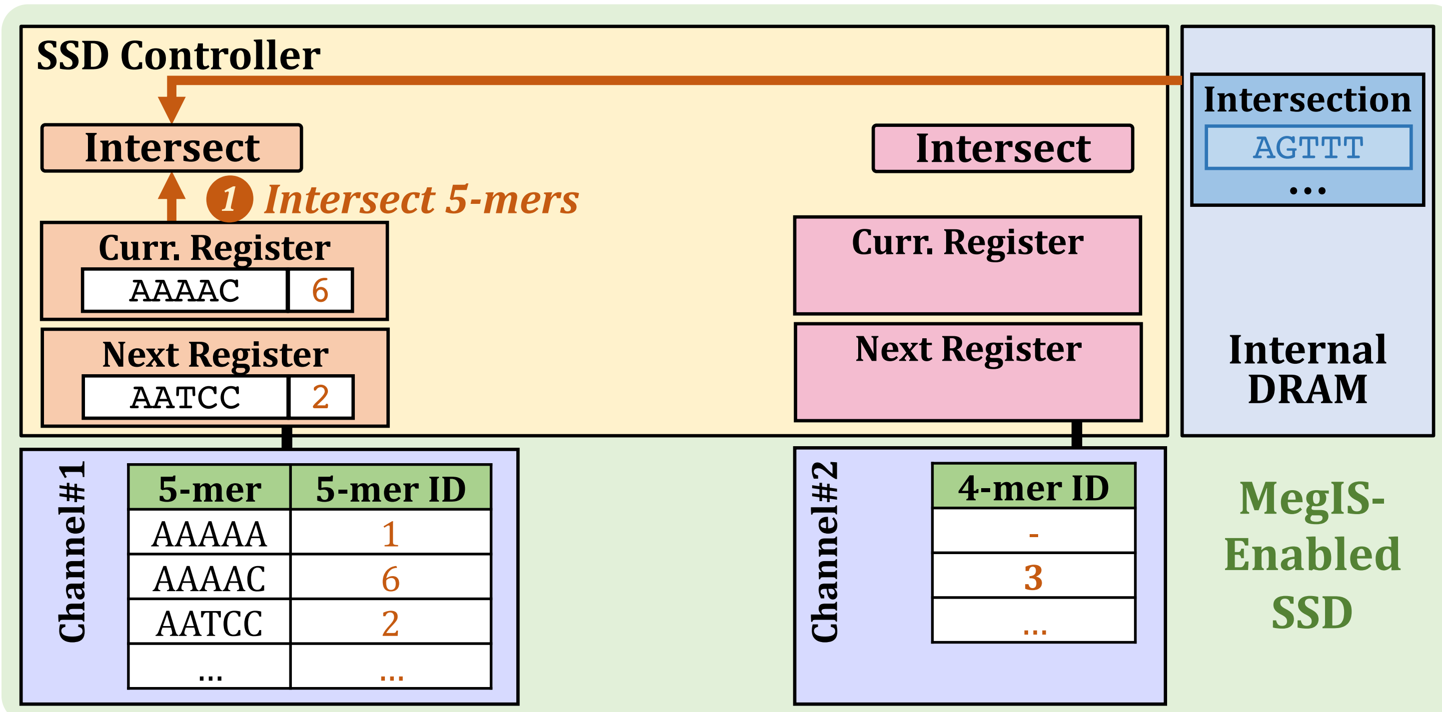
An efficient pipeline between the SSD and the host system to *(i)* **leverage** and*(ii)* **orchestrate** the capabilities of both via

- Task partitioning and mapping
- Data/computation flow coordination
- Storage-aware algorithms
- Lightweight in-storage accelerators
- Specialized data mapping scheme and Flash Translation Layer (FTL)

Results: Significant **speedup (1.5x – 100.2x)** and **energy reduction (1.9x – 25.7x)** with **high accuracy** and at **low cost**

Step 2.2: Retrieving Tax IDs

- KSS example when retrieving 5- and 4-mers



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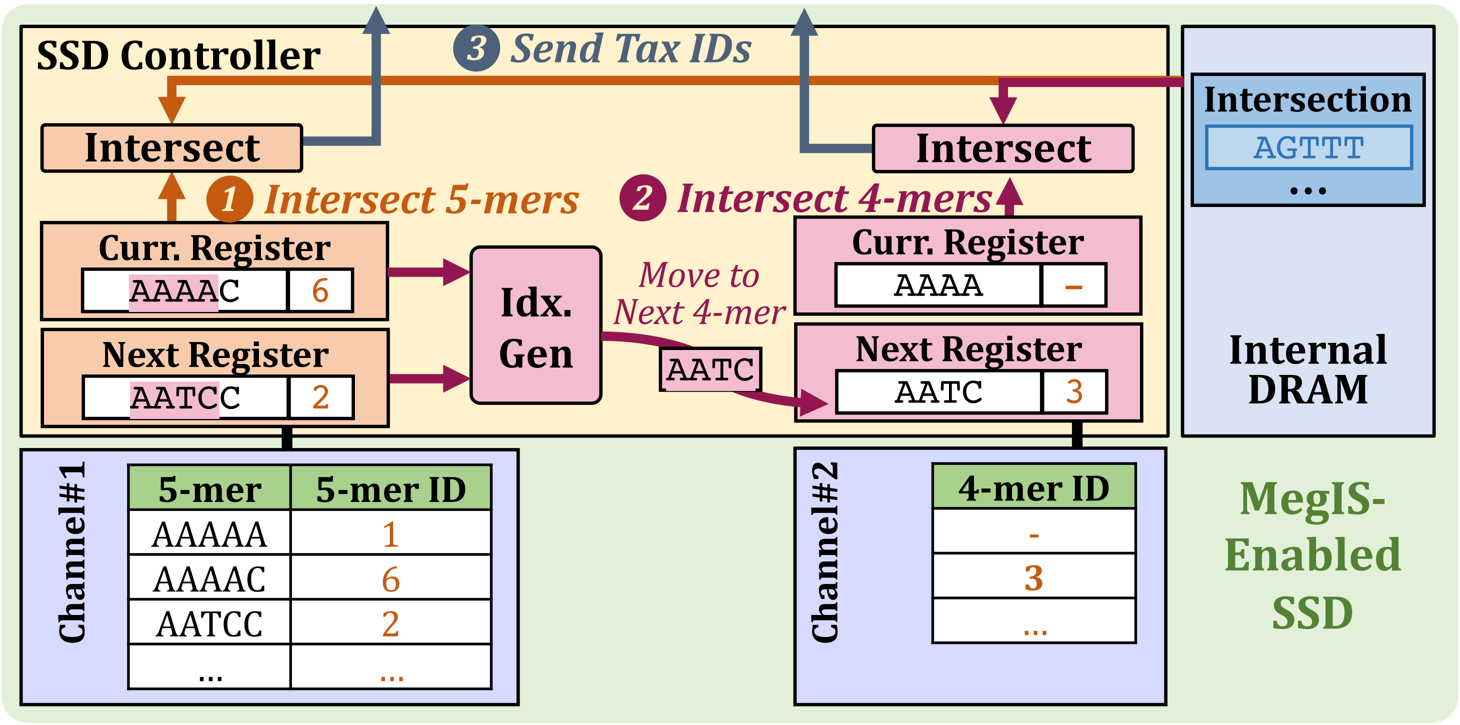

Area and Power

- Based on **synthesis** of **MegIS** accelerators using the Synopsys Design Compiler @ 65nm technology node

Logic Unit	# of instances	Area [mm²]	Power [mW]
Intersect (120-bit)	1 per channel	0.001361	0.284
k-mer Registers (2 x 120-bit)	1 per channel	0.002821	0.645
Index Generator (64-bit)	1 per channel	0.000272	0.025
Control Unit	1 per SSD	0.000188	0.026
Total for an 8-channel SSD	-	*0.04*	*7.658*

Only 1.7% of the area of three 28-nm ARM Cortex R4 cores in a SATA SSD controller