Towards an End-to-End Processing-in-DRAM Acceleration of Spectral Library Search

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Introduction

- Overall objective: Explore processing-in-memory (PIM)
 potential to accelerate spectral library searches by
 integrating hardware and algorithm co-design across the
 mass spectrometry (MS) data analysis pipeline
- **Application motivation**: Modern workloads (e.g. mass spectrometry) are increasingly **data-intensive**
- Hardware motivation: Computer architectures are designed for infrequent memory access
- Data transfers between the memory and the processor over a narrow memory channel incur high energy and latency costs

We make the following contributions:

- Adaptation of an approximate sum of absolute differences algorithm for PIM-based spectral matching
- A preliminary approach to integrate PIM into mass spectrometry workflows
- Early performance assessments via PIM simulation
- Evaluation of algorithm robustness under noise and low precision representations

DRAM + Processing-in-memory (PIM)

 Processing-in-memory (PIM), a.k.a. near-data-processing (NDP) reduces data movement by adding compute capability to memory

PIM types

1. Processing-using-memory (PUM):

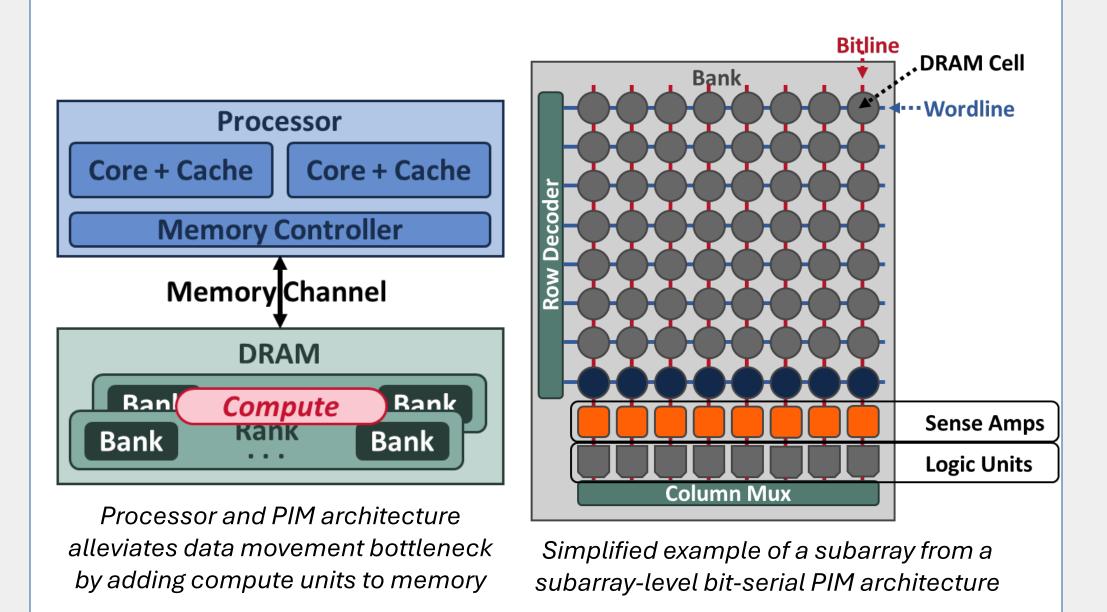
 Use inherent circuit-level properties of memory cells to perform logic within memory arrays

2. Processing-near-memory (PNM):

- 3D-stacked memory with a logic layer
- Take advantage of the high bandwidth communication over vertical interconnects between layers

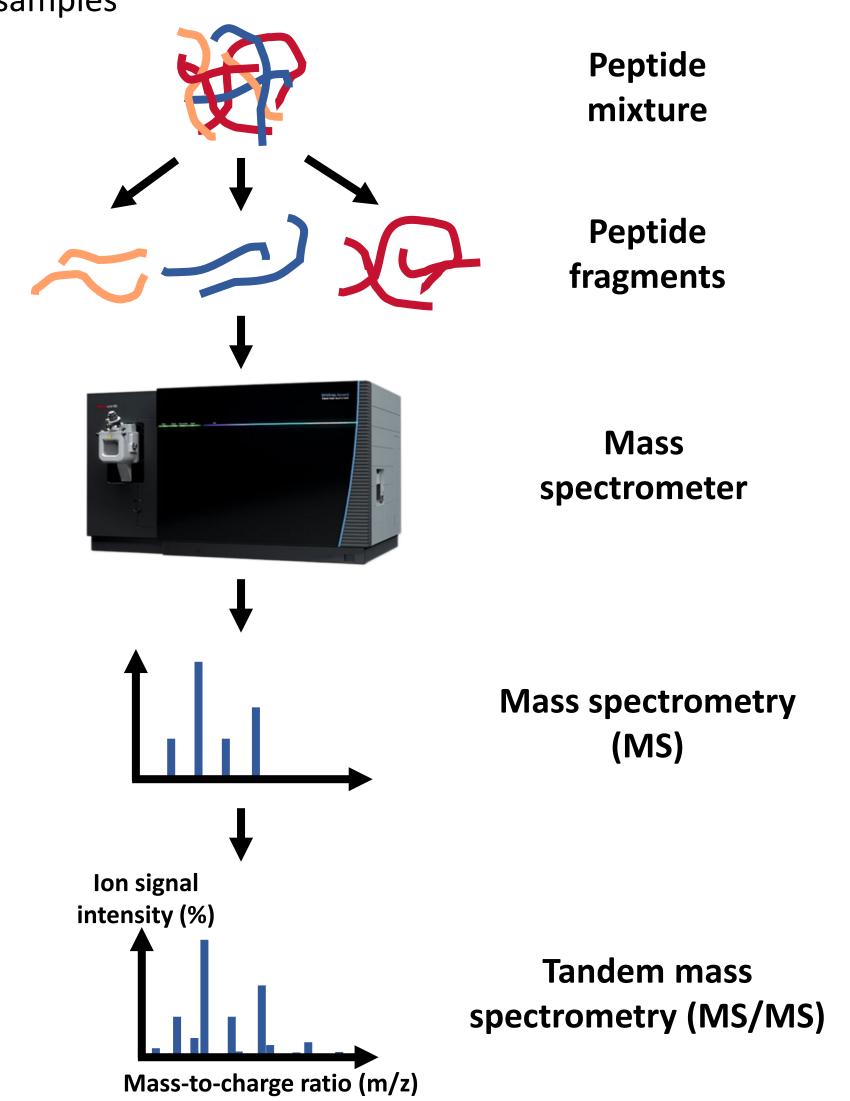
DRAM for PIM

 DRAM-based PIM can benefit from simultaneous access to multiple DRAM arrays for parallel data processing

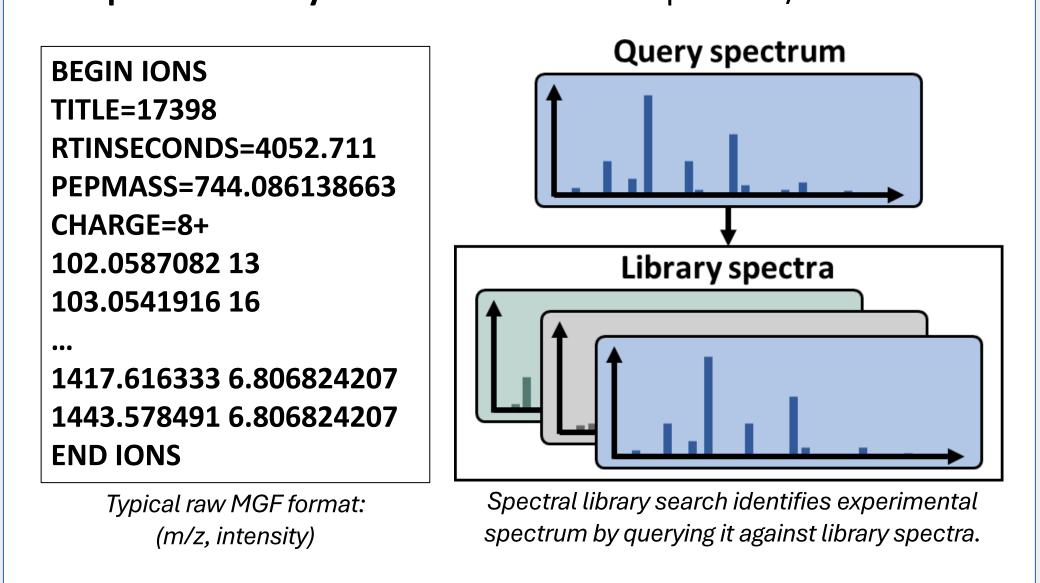


Mass Spectrometry (MS) and Spectral Library Search

Mass spectrometry (MS) analyzes the proteome of protein samples



Spectral library search is used to interpret MS/MS data



Minimum Sum of Absolute Differences

- DSP-inspired algorithm: sum of absolute differences
- Calculate a similarity score between the experimental spectrum S = (s_1, s_2, \ldots, s_n) and each library spectrum $L_p = (\ell_{p1}, \ell_{p2}, \ldots, \ell_{pn})$ for $p{=}1, 2, \ldots, m$.
- Assuming m library spectra and n elements in each spectrum, the basic algorithm seeks $L_{\bf k}$ such that:

$$k = \arg\min_{p} \sum_{j=1}^{n} |s_j - \ell_{pj}|$$

Pre-processing and Pre-filtering

Discretization

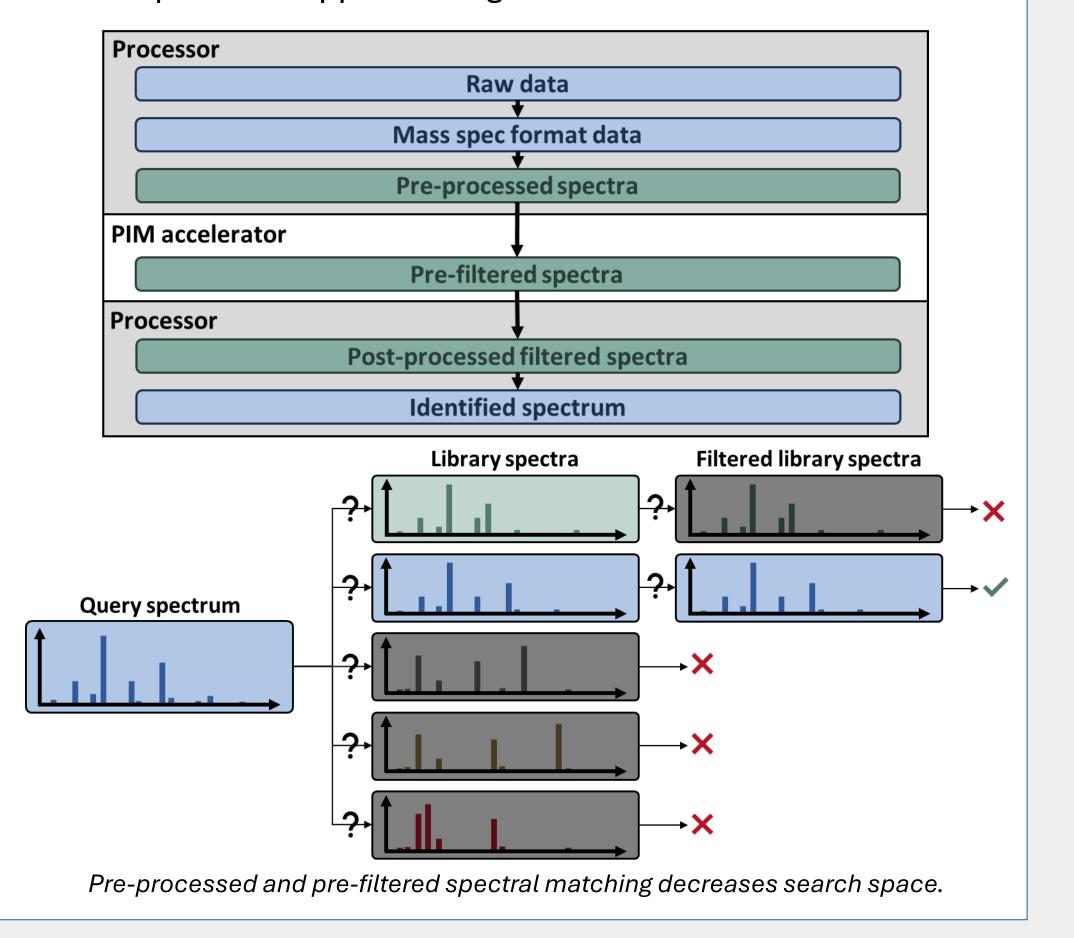
 Divide the m/z range of spectra into bins and sum intensity values in the same bin

Approximation

 Fixed-point for floating-point values with reduced bitprecision enables program execution on PIM hardware

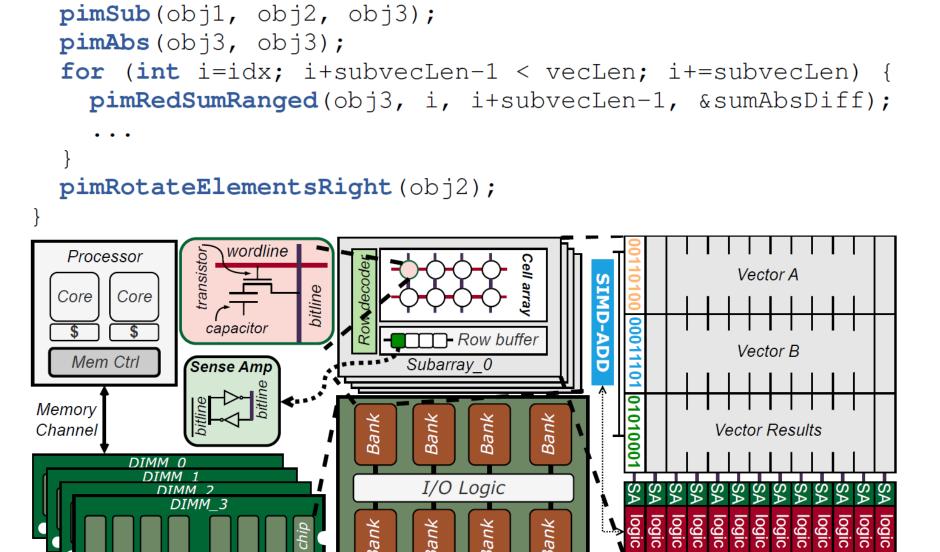
Key insights:

- Pre-filter using PIM to decrease the search space of spectral library search
- Co-design application with hardware
- Low-precision approach aligns with MS error tolerance



PIM Simulation

for (int idx=0; idx < subvecLen; idx++) {</pre>



- PIMeval is a performance and energy simulation framework for various DRAM-based PIM architectures: subarray-level bit-serial, subarray-level bit-parallel, bank-level
- We model **subarray-level bit-serial PIM** with single/dual rank DIMM with 8 chips, 16 banks per chip, and 32 subarrays per bank of 8192 × 8192 cells

Key insights:

• PIM performance benefits scale with increasing problem size; small datasets favor CPU due to lower overhead

Algorithm Robustness to Simulated Spectral Noise Output Outp

Task **3135.019**

TABLE I: Algorithm Robustness under Varying Degradation

Experiment Condition	Degradation (Rem/Jit/Noise)	AUC (32-bit)	AUC (16-bit)	AUC (8-bit)
No-Noise Control	0% / ±0 / 0%	1.0000	1.0000	1.0000
Moderate Noise	10% / ±1 / 10%	0.9892	0.9681	0.9732
High-Noise Test	25% / ±2 / 25%	0.7819	0.7583	0.7606

- Experiments show algorithm is robust in handling noise, variations, and degradations inherent to real-world bioinformatics workflows
- 8-bit precision delivers accuracy comparable to that of higher bit-precisions

Conclusion and Next Steps

- Proof of concept for hardware-algorithm co-designed pipeline for DRAM-based PIM architecture acceleration of spectral library search
- Next steps are to estimate analytical scaling results, observe performance on larger workloads in simulation, and use larger datasets.

References

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