

Intel Collaborative Research Institute Computational Intelligence

2016 Retreat

From Processing-in-Memory to Processing-in-Storage

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CPU-Mem-Storage Hierarchy





Israel Institute of Technology

Processing In Memory

The conventional way: processing NEAR memory





Technology

Processing In Memory

Our way: really "in memory"



Data Size





Processing In Storage

The conventional way: processing NEAR storage





Technology

Processing In Storage

Our way: really "in storage"







Introducing ReCAM Storage





Resistive element





Dual Use

ReCAM is 2x ReRAM => Flexible dual use

- Storage + Processing in-Storage
- Storage only







Processing In Storage Performance and Power



"Resistive Associative Processor", L. Yavits, S. Kvatinsky, A. Morad, R. Ginosar, IEEE CAL 2015





Applications: Machine Learning

Workload	ReCAM performance	CPU Performance
Pattern Match / grep	0(1)	O(N)
Max / Min	0(1)	O(N)
Sort	O(N)	$O(N \log N)$
DMM	$O(N^2)$	$O(N^{3})$
SpMM	O(nnz)	$O(nnz \cdot N)$
Convolution / Correlation	O(N)	$O(N \log N)$
Graph Processing (Dijkstra / SSSP)	O(N)	$O(N^{2})$





Application: Storage

- Online deduplication
- Online compression
- Online security





Example: Online Deduplication

- Goal: store only one instance of data
- Today
 - Complex data structures
 - Computationally expensive hash function
- Processing in Storage
 - Smaller data structures
 - No hash
- Result: 100x higher throughput







Example: DNA Sequence Alignment

- Find regions of similarity in long DNA strands
- $O(N^2)$ matrix
- Processing in Storage: 3x higher performance than a 384-GPU cluster
 - Align human and chimpanzee Chromosome 1

AGGSGLGGIAGKPSPTMEAVEASTASHPHSTSSYFATTYYHLTDDEC

VSIGGNVSNVASGSRGTLSSSTDLMQTATPLNSSES

AL OOHOOO SWPP RHYSGSWYP.

SGVF VNG RPLPDSTROK I VELAHSGARPCD I SR I LQVSNGCVSKI SGVF VG GRPLPDSTROK I VELAHSGARPCD I SR I LQVSNGCVSKI ETGS I RPRA I GGSKPRVAT PEVVSKI I AQYKRECPS I FAWE I RDRL ETGS I RPRA I GGSKPRVAT AEVVSKI I SQYKRECPS I FAWE I RDRL

HAAGPGPLEPARAAPLVGQSPNHLGTRSSHPQLVHGNHQ

TSUSELPUSSAPNIASVTAVASGPSLAH

- 57 Peta score cells (200 PetaBytes)

[Sandes EF, Miranda G, Martorell X, Ayguade E, Teodoro G, Melo AC, CUDAlign 4.0: Incremental Speculative Traceback for Exact Chromosome-Wide Alignment in GPU Clusters, IEEE Trans. PDS 2016]





Big Data Machine Learning

• Needs MANY nodes

Each node needs entire data

- Needs effective network
 - Interconnecting storage, rather than CPUs
- The larger the node,
 - The fewer the nodes
 - The faster the computation
 - The lower the energy





Summary Processing In Memory and Storage





