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EVALUATING TRUSTED EXECUTION ENVIRONMENT PERFORMANCE FOR GENOME SEQUENCE ALIGNMENT: AN AMD SEV CASE STUDY

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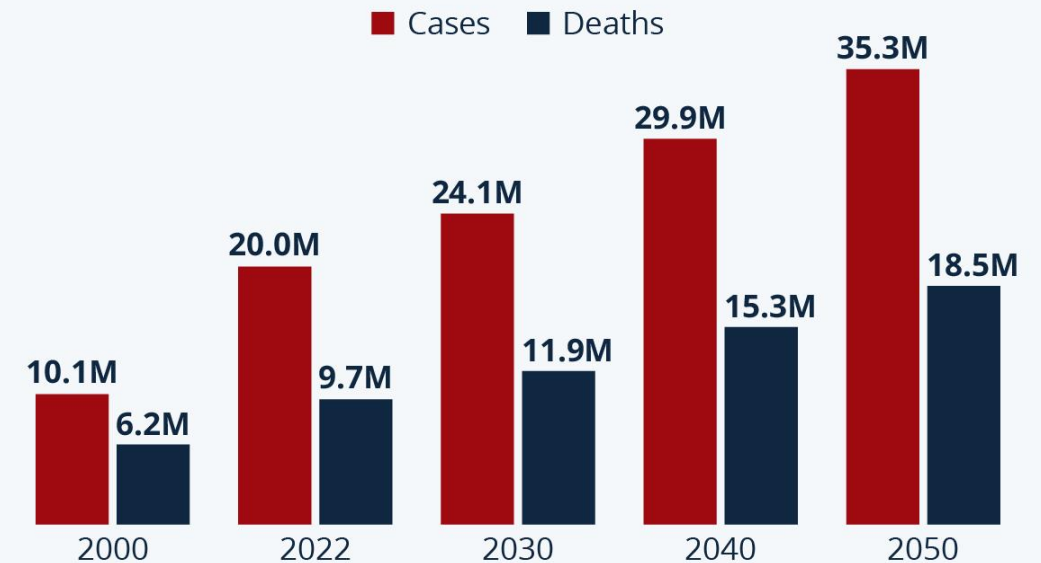
Acknowledgement

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- The number of cancer diagnoses is steadily rising
- Nowadays, it is no longer a question of whether you will get cancer, but rather when
- Cancer has become the primary driver of healthcare cost increases

The Global Cancer Burden Keeps Growing

Estimated number of new cancer cases and deaths worldwide per year



Source: International Agency for Research on Cancer

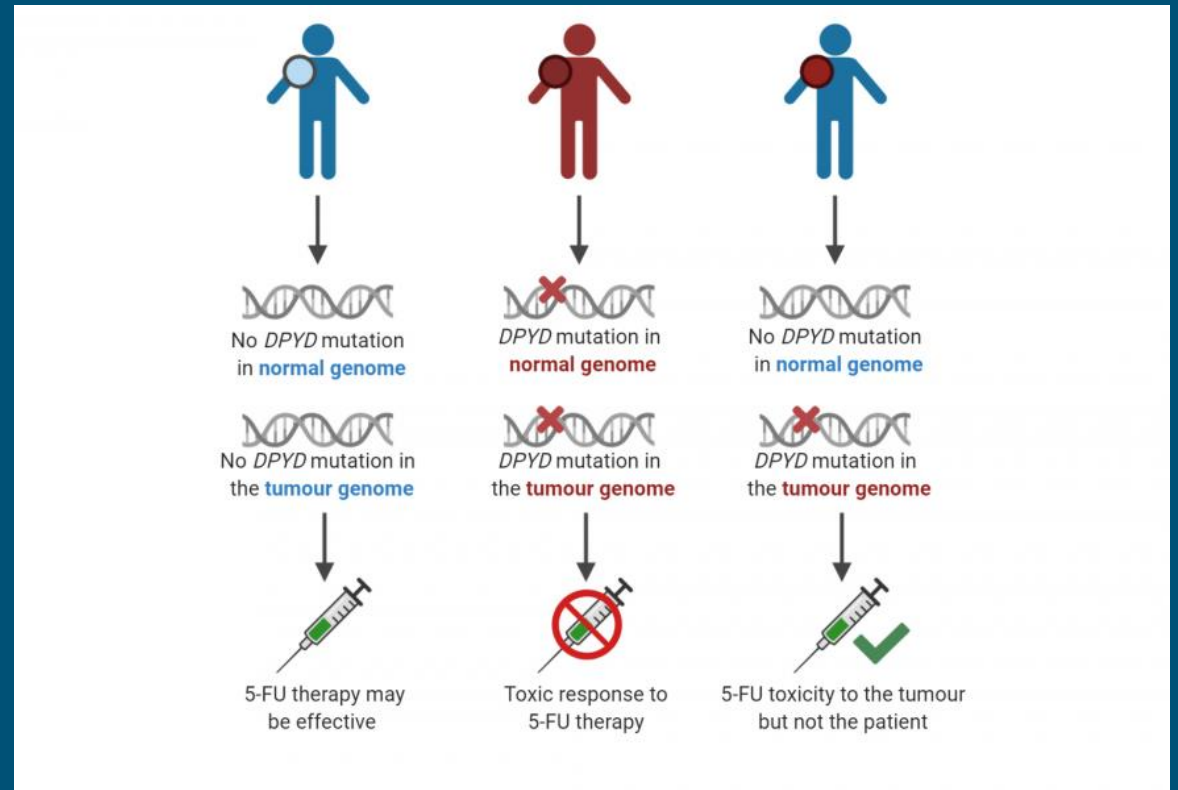


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Human Genome Sequencing

The Enabler of Personalized Treatment

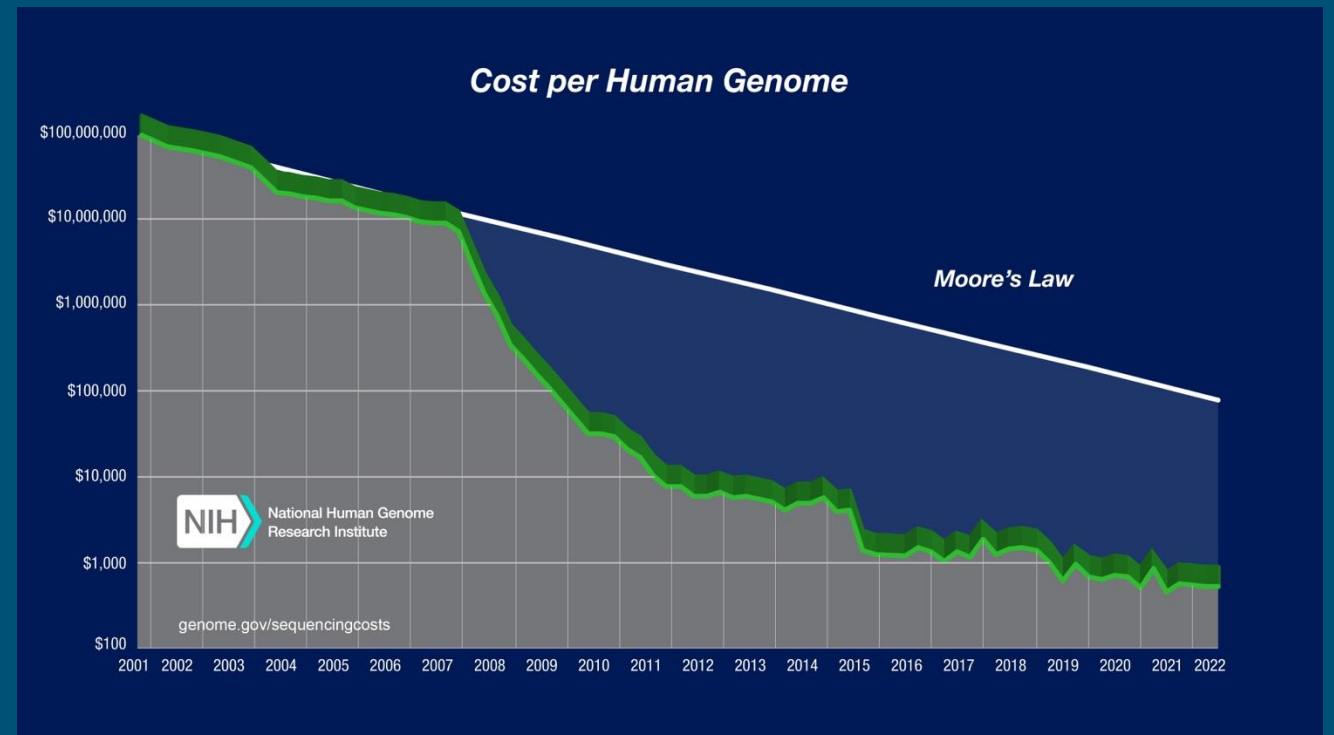
- Cancer genomics aims to decode each patient's normal and cancer genomes to enable clinicians to determine the best individual treatment
- Immense potential of integrating whole genome sequencing
 - allows the identification of mutations that could be exploited



Human Genome Sequencing

The Cost of Sequencing

- Sequencing costs dropped a lot over the past 2 decades, due to:
 - Development of Next-generation sequencing (NGS) in the early 2000s
 - Continuation of Moore's Law during this time
 - Advanced alignment algorithms



Human Genome Sequencing

The Threat Scenario

- Problem: Patient data are highly sensitive
- Electronic patient records contain personal data on current and past illnesses
- In fact, this is even more critical in the case of human genome sequencing
 - Previously unknown predispositions to diseases, which may even be hereditary, could be discovered



Image created with Perplexity AI

Human Genome Sequencing The Threat Scenario

- Should unauthorized third parties gain access, this may lead to serious implications
- Consequence: Digital patient data must be secured
 - at rest (stored),
 - in motion (transiting),
 - and in use (during processing)



Image created with Perplexity AI

RAMSES

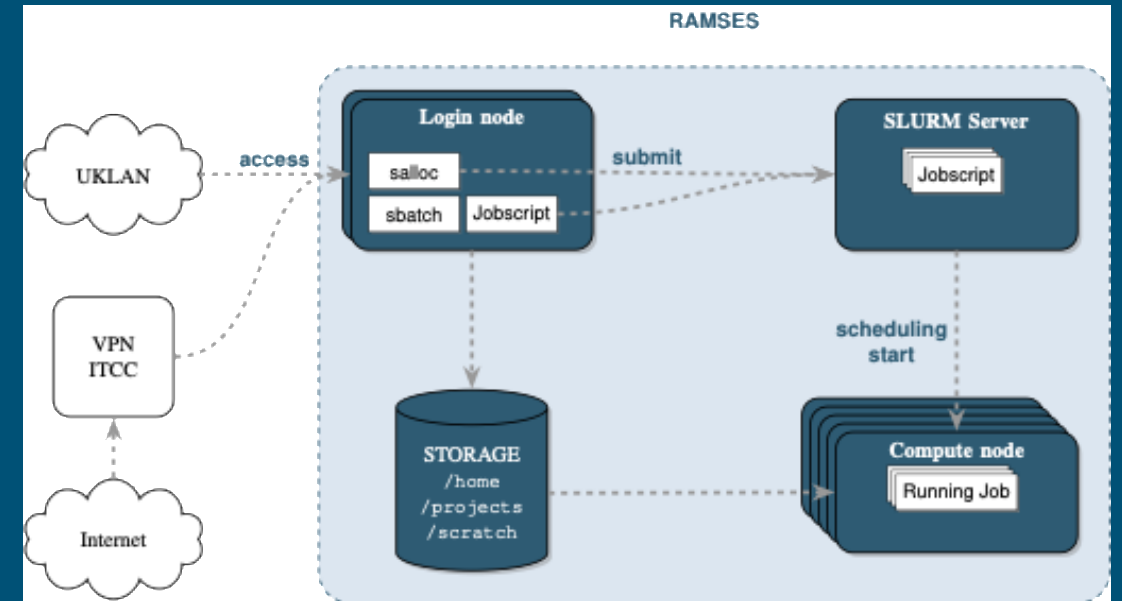
- Research Accelerator for Modeling and Simulation with Enhanced Security
- Some specs:
 - 164 Compute nodes (AMD EPYC GENOA 9654 CPU)
 - 750 GB RAM per node
 - 40 nodes with NVIDIA Hopper H100 GPUs



RAMSES

Security Measurements

- Multi-factor authentication with personal SSH keys
- Parallel filesystem GPFS as well as RAM are encrypted
- AMD SEV-based Trusted Execution Environment (TEE)
 - So far, no support for multi-node TEEs via encrypted MPI

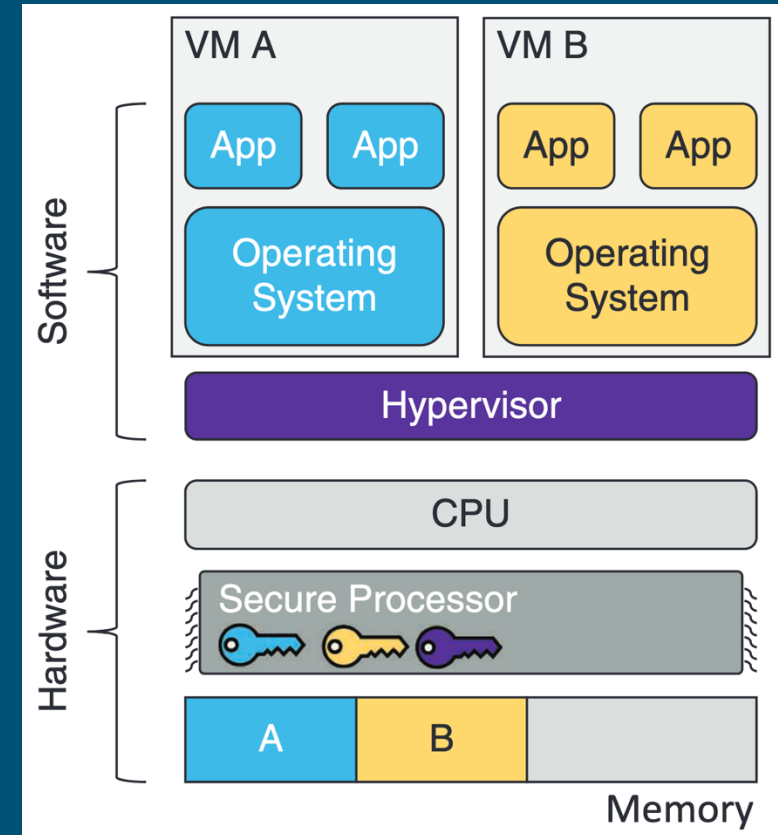


Trusted Execution Environments

- Tamper-resistant processing environment that runs on a separation kernel
- Guarantees:
 - the authenticity of the executed code,
 - the integrity of the runtime states (e.g. CPU registers, memory and sensitive I/O),
- (a) Application- vs (b) virtualization-based TEEs
 - (a) isolates individual processes
 - (b) isolates entire virtual machine

AMD TEEs

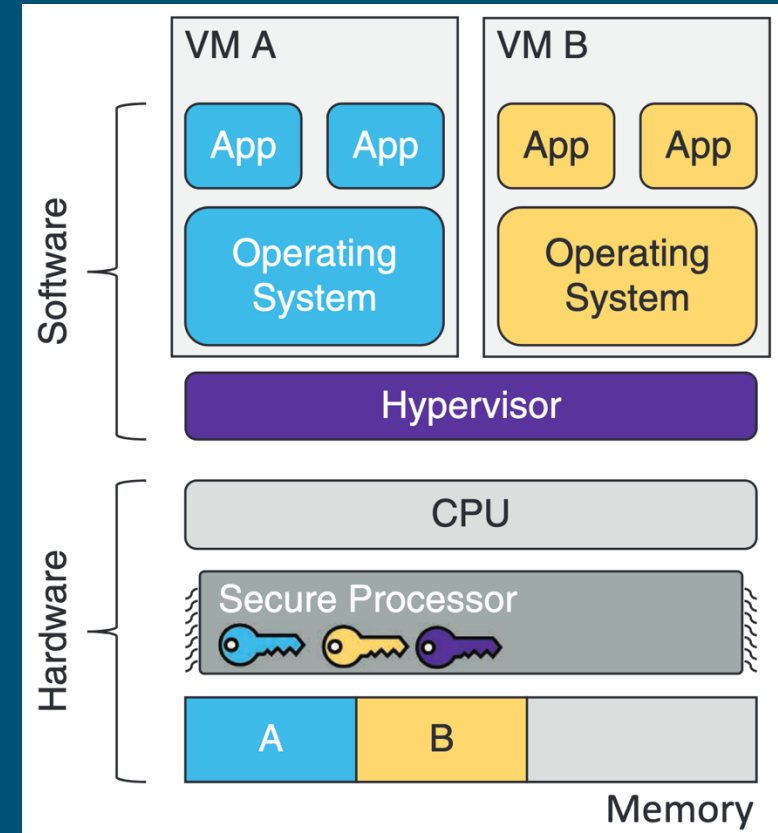
- AMD Secure Memory Encryption (SME)
 - Uses a single key to encrypt system memory
 - Memory encryption is transparent and can be run with any operating system
- AMD Secure Encrypted Virtualization (SEV)
 - Single key per virtual machine to isolate guests and the hypervisor from one another
 - Keys are managed by the AMD Secure Processor
 - VM indicates which pages in memory should be encrypted



<https://doi.ieeecomputersociety.org/10.1109/MSEC.2019.2947124>

AMD TEEs

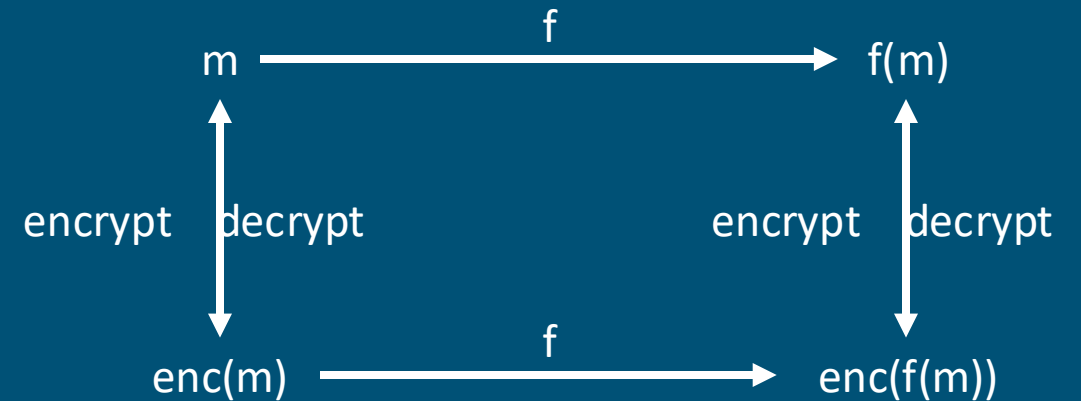
- AMD Secure Encrypted Virtualization–Encrypted State (SEV–ES)
 - Encrypts all CPU register contents when a VM stops running
 - Prevents the leakage of information in CPU registers to components like the hypervisor
- AMD Secure Encrypted Virtualization–Secure Nested Paging (SEV–SNP)
 - Strong memory integrity protection to help prevent malicious hypervisor–based attacks like data replay, memory re–mapping
 - Stronger protection around interrupt behavior



<https://doi.ieeecomputersociety.org/10.1109/MSEC.2019.2947124>

TEE Alternative

- Fully Homomorphic Encryption (FHE)
 - Data stays encrypted even during processing
 - Result for unencrypted and encrypted data processing is the same
- BUT: significant performance penalty and in HPC performance is the key metric



Methodology

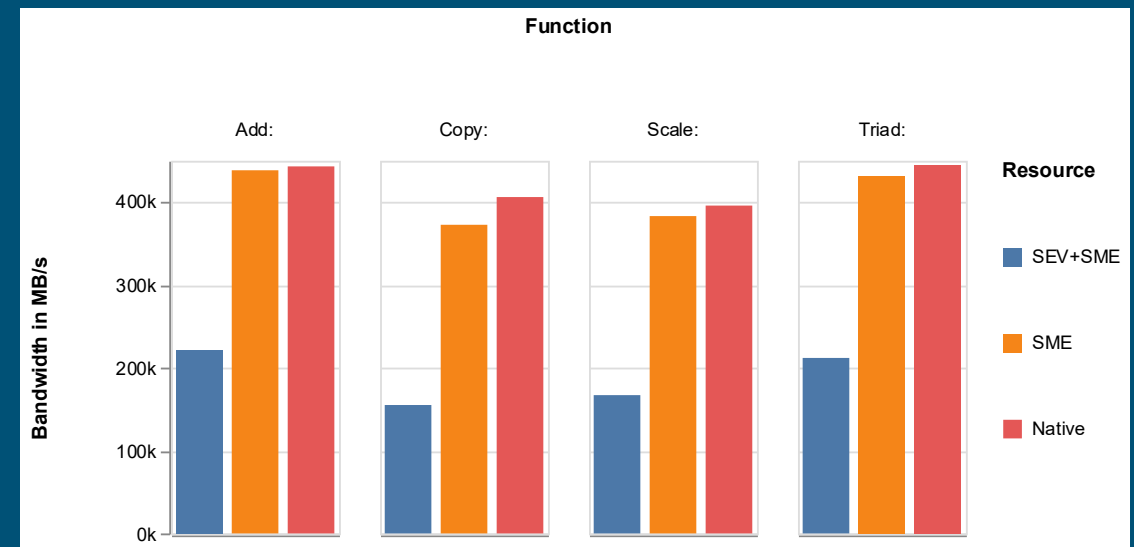
- To benchmark the RAMSES supercomputing system, we applied the following evaluation matrix
 - Resource set $R = \{\text{Native}, \text{SME}, \text{SME} + \text{SEV}\}$
 - Thread counts $T = \{32, 64, 96, 128, 168\}$
 - Storage location $S = \{\text{encrypted}, \text{local}, \text{scratch}, \text{shm}\}$
 - Benchmarks $B = \{\text{STREAM}, \text{NPB}, \text{BWA-MEM2}\}$
- Each combination of the evaluation matrix has been carried out with a sampling rate of 10
- For the BWA-MEM2 benchmark we used the *human_g1k_v37.fasta* human reference genome [1]

[1] <https://gatk.broadinstitute.org/hc/en-us/articles/360035890711-GRCh37-hg19-b37-humanG1Kv37-Human-Reference-Discrepancies#grch37>

Results

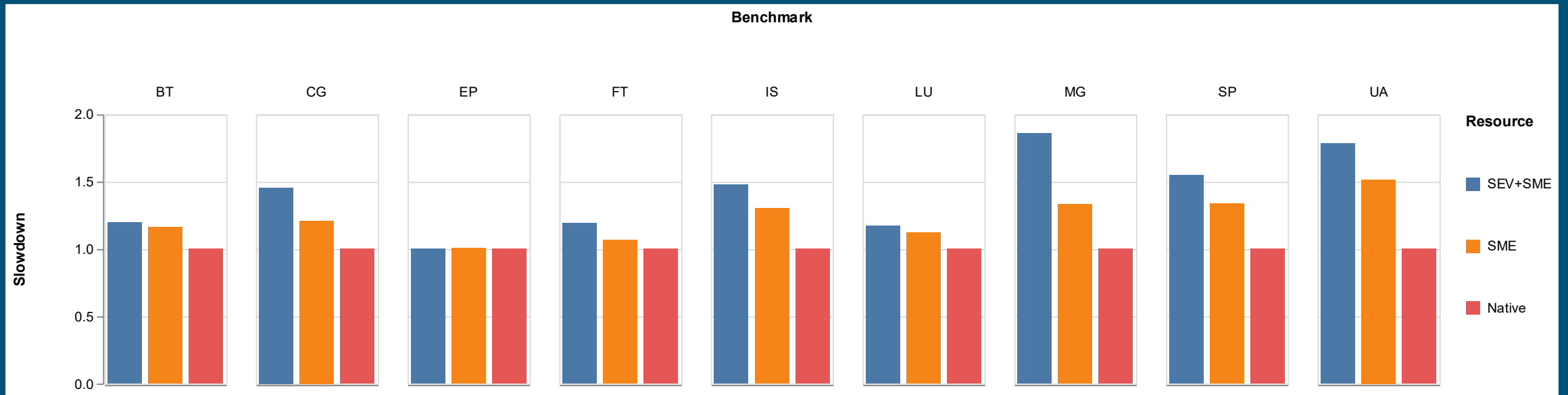
STREAM Benchmark

- Peak memory bandwidth of 443GB/s for the *native* resource type
- Pure memory encryption (*SME*) only causes marginal performance loss
- However, *SEV+SME* causes 55.4% reduction in memory bandwidth



Results

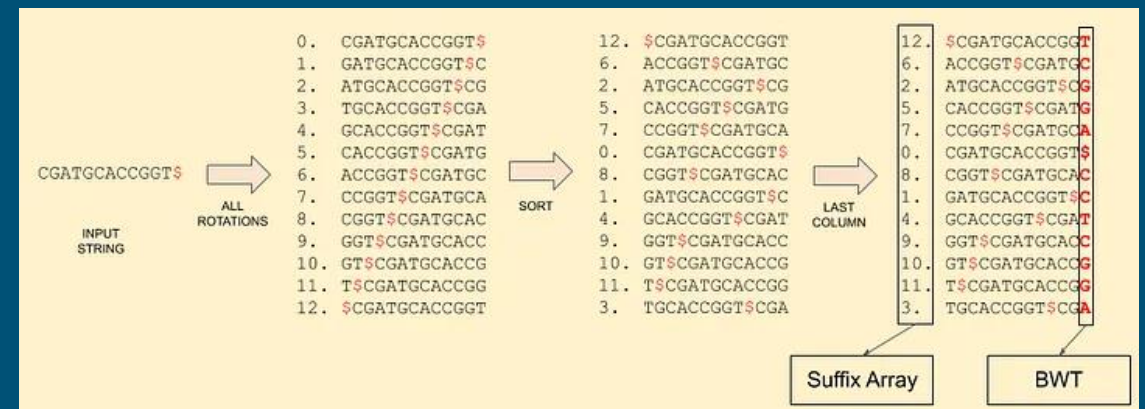
NPB Benchmark



- Memory-bound workloads have remarkable performance drops for *SME* and *SEV+SME*
 - e.g. MG and UA
- Compute-bound workloads only suffer from minor performance overhead
 - e.g. BT, LU and EP

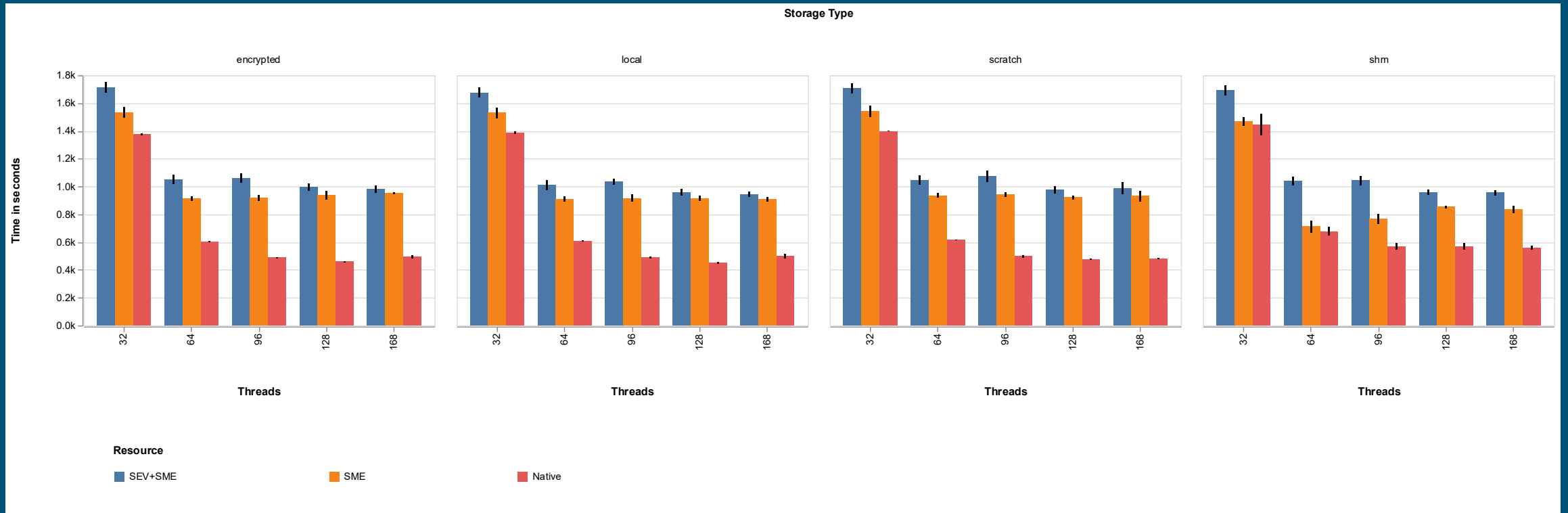
Burrows–Wheeler Aligner (BWA)

- BWA is a software package for mapping low-divergent sequences against a large reference genome
- For the benchmark in our paper, we used the latest version BWA-MEM2
 - Index size on disk is down by 8 times
 - Required memory down by 4 times



Results

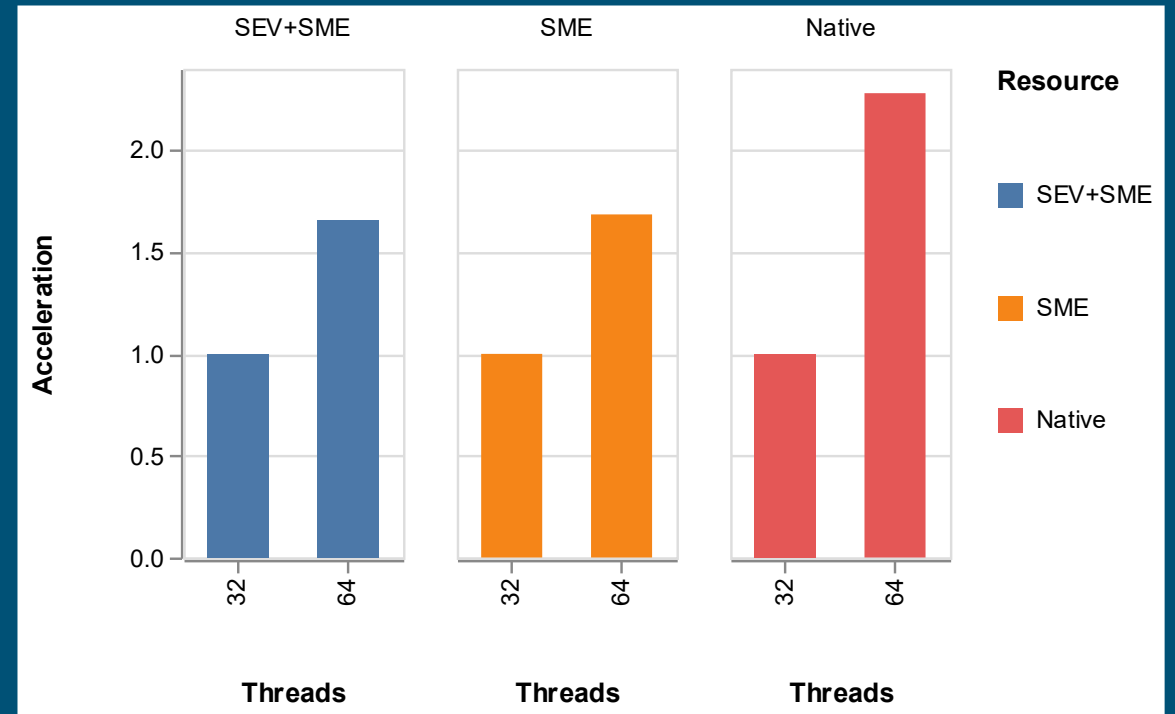
BWA-MEM2



Results

BWA-MEM2

- Figure on the right shows the acceleration with input data from the *local* file system
- Values are normalized to the 32-thread performance for each resource type
- *Native* environment demonstrates the most efficient scaling



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