



# Optimizing Molecular Dynamics AI model using HDF5 and DYAD

Presented by: Hariharan Devarajan devarajan1@llnl.gov

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The Massively Parallel Multiscale Machine-Learned Modeling Infrastructure (MuMMI)

- A framework for executing multiscale modeling simulations of large molecular systems
- Studies the plasma membrane and RAS-RAF-14-3-3
- Al-assisted workflow with offline training, online inference and simulation with feedback mechanisms.
- Accuracy of AI training improves the initial conditions for molecular interaction which significantly improve resolution of the workflow.

Al training segment of MuMMI.

### • Training Dataset (320 GB): 600 files with 8k samples.

- Each sample has 8,691 elements.
- Each element is 8 Bytes.
- Data format NPZ files.

### • PyTorch Data Loader: Map-style data loader

- With 6 worker processes per GPU
- Batch size of 256 samples

### • Computation: step is .133 seconds

### • Hardware (used 32 nodes)

- Corona cluster at LLNL with 8 GPUs per node
- 256 GB of RAM and 3.2 TB NVMe SSD per node
- Tools DFTracer
  - DFAnalyzer
  - Perfetto UI



- Timeline of the application
- Reading one sample results in Many I/O calls

Perfetto viewer (zoomed)

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- Many small reads for one numpy open.
- Gaps in reading and numpy open call

		Summary						
	Allocation	Scheduler Allocation Details Nodes: 32 Processes: 1280 Thread allocations across nodes (includes dynamically create Compute: 160 I/0: 1280 Events Recorded: 18M	d threads)					
	Dataset	Description of Dataset Used						
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	1/0 Dellaviol							
		Total Time: 2701 sec						
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Benavior		— Unoverlapped App I/0: 2581.864 sec						
		— Unoverlapped App Compute: 1.199 sec						
C	ľ	Compute: 29.303 sec						
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		Unoverlapped I/0: 853.770 sec						
		Unoverlapped Compute: 0.237 sec						
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		xstat64  312  NA  nan  nan  NA  nan	INA I					
		— mkdir  104  NA  nan  nan  NA  nan	INA I					
		— open64  8K  NA  nan  nan  NA  nan	INA I					
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POSIX I/O Time, BW, and Transfer Size



## **Optimization 1**

Switch NPZ to HDF5

### Perfetto viewer

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- Faster execution time
- The reading a batch is much more efficient.

Perfetto viewer (zoomed)



- Large single read calls



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## POSIX I/O Time and BW



- Larger size improves bandwidth from Lustre to 8GB /s.
- The I/O time is optimized by almost **30x**.
- Overall the timeline is reduced from 390 to 29 seconds **13.4x** faster runtime.

## **Optimization 2**

Utilizing DYAD for node-local caching

Producer: the first AI worker which accessed the file would store it in cache.



I. Lumsden, H. Devarajan, J. Marquez, S. Brink, D. Boehme, O. Pearce, J.S. Yeom, and M. Taufer. 2024. Empirical Study of Molecular Dynamics Workflow Data Movement: DYAD vs Traditional I/O Systems. In Proceedings of the 2024 IEEE International Parallel and Distributed Processing Symposium Workshops (IPDPSW).



## Behavior Summary



- Faster storage to share data further improves bandwidth to 62GB/s.
- The I/O time is further optimized by **7.5x**. \_

BW

Overall the timeline is reduced from 29 to 15 seconds **1.9x** faster runtime. \_

## Key Learnings

- Format has a significant effect on I/O Performance.
- Large Data accesses do not require explicit chunking.
  - Adding explicit chunking hurt performance by 1.8x
- Prefetching policy of PyTorch is not aggressive.
  - Typically it would wait for a cache miss to do next rounds of prefetching.
- Utilizing node-local storage with RDMA for inter-node data movement can speed up AI training.
- Interacting with domain scientists to explain data format intricates is fun.

## Conclusions



- 1. Using Numpy Array APIs lead to many small accesses and large number of metadata calls.
  - Most due to the buffering and decompression schemes within the format.
- 2. HDF5 format for large simulation samples are efficient to share data.
  - Some apps use shared and other use one sample per file.
  - This leads to **30x** faster performance than Numpy Array
- 3. Utilizing node-local storage with DYAD can optimize AI training by almost **7.5x** as compared to HDF5 with PFS.



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