Accelerating Scientific Machine Learning with Al Accelerators

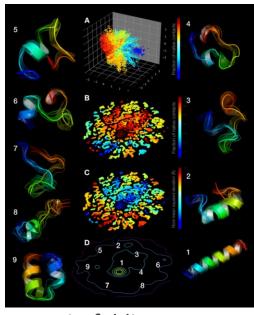
Murali Emani,
Argonne Leadership Computing Facility
memani@anl.gov

ARGONNE TRAINING PROGRAM ON EXTREME-SCALE COMPUTING (ATPESC)
July 31, 2023



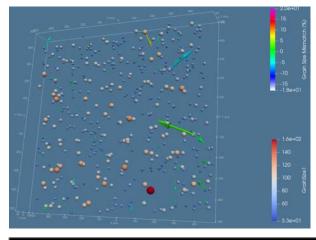
Surge of Scientific Machine Learning

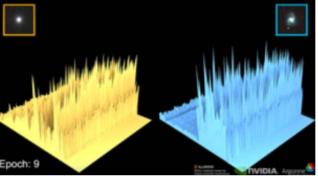
- Simulations/ surrogate models
 Replace, in part, or guide simulations
 with Al-driven surrogate models
- Data-driven models
 Use data to build models without simulations
- Co-design of experiments
 Al-driven experiments



Protein-folding

Braggs Peak

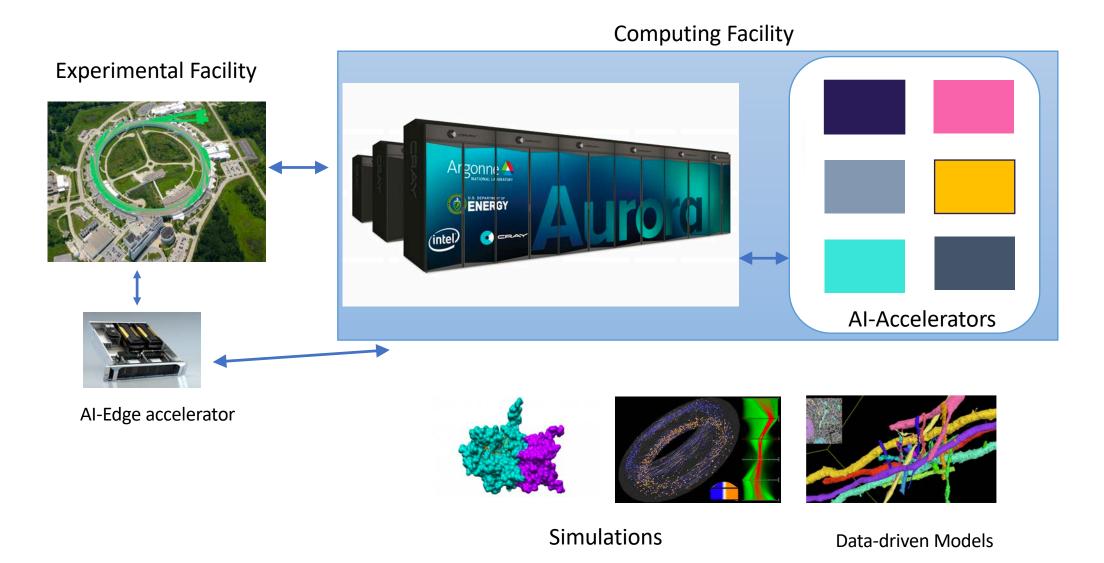




Galaxy Classification

Design infrastructure to facilitate and accelerate AI for Science (AI4S) applications

Integrating AI Systems in Facilities





ALCF AI Testbed

https://www.alcf.anl.gov/alcf-ai-testbed



Cerebras CS-2



SambaNova DataScale **SN30**



GroqRack

- Infrastructure of next-generation machines with AI hardware accelerators
- Provide a platform to evaluate usability and performance of AI4S applications
- Understand how to integrate AI systems with supercomputers to accelerate science



Habana Gaudi1



ALCF AI Testbed

https://www.alcf.anl.gov/alcf-ai-testbed



Cerebras CS-2



SambaNova DataScale SN30



Graphcore Bow Pod64



Habana Gaudi1



GroqRack

- Cerebras: 2 CS-2 nodes, each with 850,000
 Cores, compute-intensive models
- SambaNova: DataScale SN30 8 nodes
 (8 SN30 RDUs per node) 1TB mem per device,
 models with large memory footprint
- Graphcore: Bow Pod64 4 nodes
 (16 IPUs per node) MIMD, irregular workloads
 such as graph neural networks
- GroqRack: 8 nodes, 8 GroqNodes per node inference at batch 1
- Habana Gaudi1: 2 nodes, 8 cards per node -On-chip integration of RDMA over Converged Ethernet (RoCE2), scale-out efficiency





partnerships.

Getting Started on ALCF AI Testbed:

Apply for a Director's Discretionary (DD)
Allocation Award

Cerebras CS-2, SambaNova Datascale SN30 and Graphcore Bow Pod64 are available for allocations

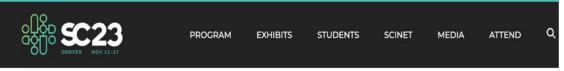
Allocation Request Form

Al Testbed User Guide



AI Testbed Community Engagement





Home > Presentation

Presentation

Programming Novel AI Accelerators for Scientific Computing

Scientific applications are increasingly adopting Artificial Intelligence (AI) techniques to advance science. There are specialized hardware accelerators designed and built to run AI applications efficiently. With a wide diversity in the hardware architectures and software stacks of these systems, it is challenging to understand the differences between these accelerators, their capabilities, programming approaches, and how they perform, particularly for scientific applications. In this tutorial, we will cover an overview of the AI accelerators landscape with a focus on SambaNova, Cerebras, Graphcore, Groq, and Habana systems along with architectural features and details of their software stacks. We will have hands-on exercises that will help attendees understand how to program these systems by learning how to refactor codes written in standard AI framework implementations and compile and run the models on these systems. The tutorial will enable the attendees with an understanding of the key capabilities of emerging AI accelerators and their performance implications for scientific applications.



Energy-Efficient GPU Computing

Al training workshops

Cerebras: https://events.cels.anl.gov/event/420/

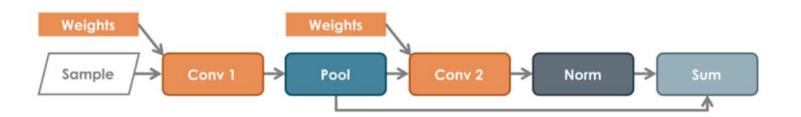
SambaNova: https://events.cels.anl.gov/event/421/

Graphcore: https://events.cels.anl.gov/event/422/

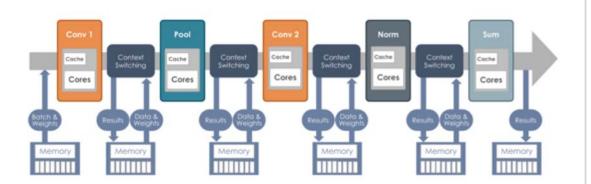
Tutorial at SC23 on Programming Novel AI accelerators for Scientific Computing *in collaboration with Cerebras, Intel Habana, Graphcore, Groq and SambaNova*



Dataflow Architectures



Simple Convolution Graph



Sample 6

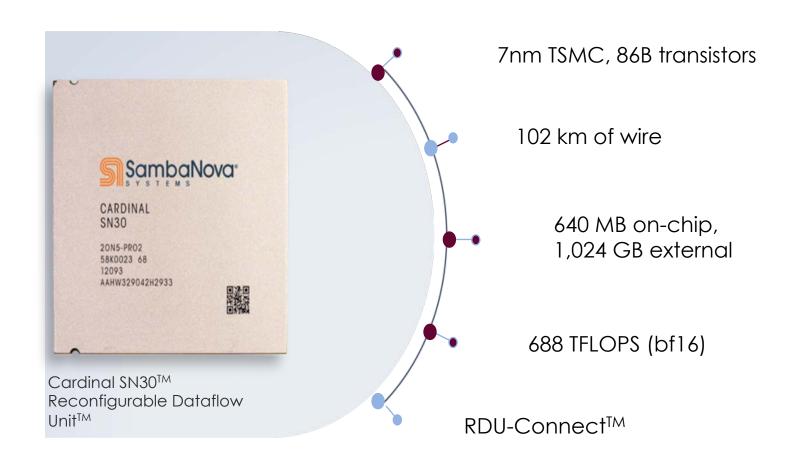
ROU PMU PCU PMU PCU

The old way: kernel-by-kernel
Bottlenecked by memory bandwidth
and host overhead

The Dataflow way: Spatial Eliminates memory traffic and overhead



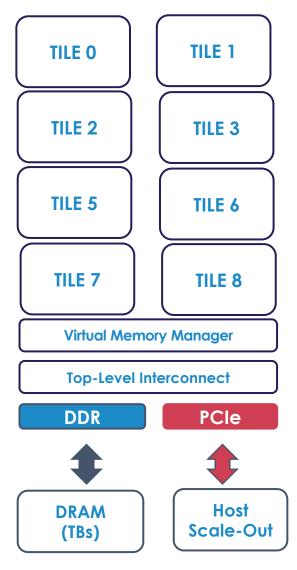
SambaNova Cardinal SN30 RDU





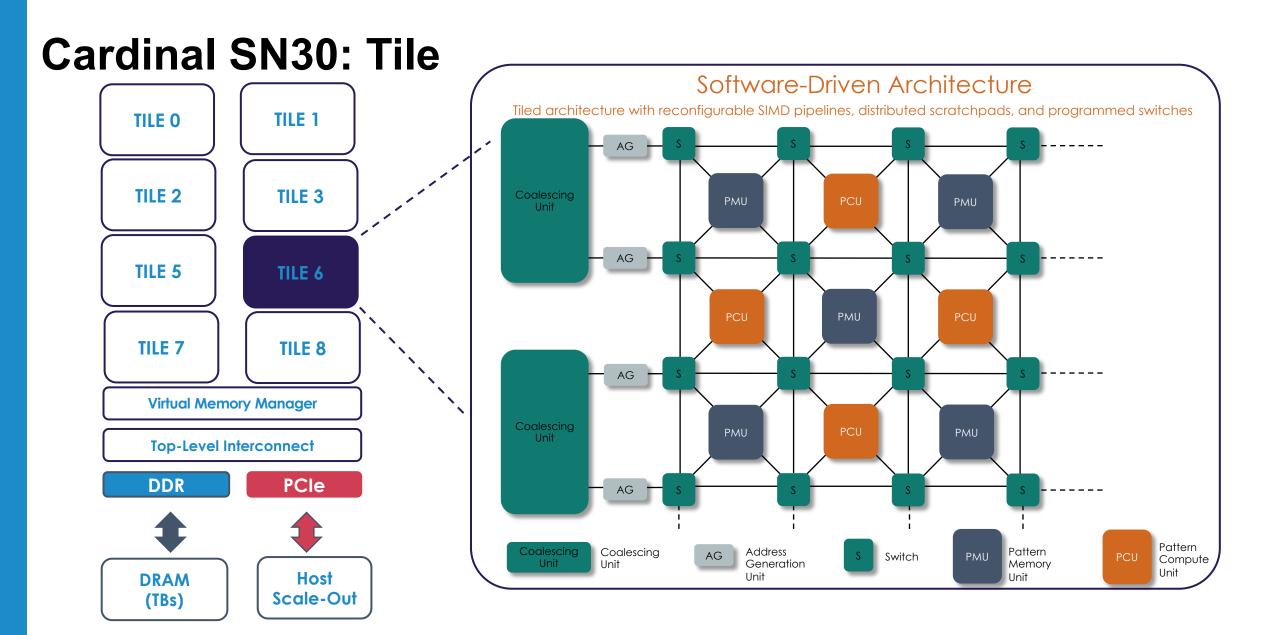


Cardinal SN30: Chip and Architecture Overview



- RDU broken up into 8-tiles
 - 160 PMU and PCUs per tile
 - Additional sub-components like coalescing units (CU) for connectivity to other tiles and off-chip components, switches to set up communication between PMU, PCUs, and CU
- Tile resource management: Combined or independent mode
 - Combined: Combine adjacent to form a larger logical tile for one application
 - Independent: Each tile controlled independently, allows running different applications on separate tiles concurrently.
- Direct access to TBs of DDR4 off-chip memory
- Memory-mapped access to host memory
- Scale-out communication support







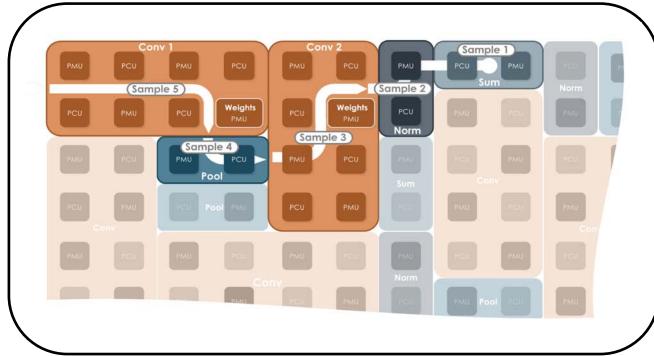
Dataflow Architecture for Terabyte Sized Models

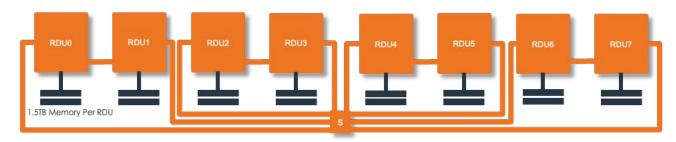


Dataflow Efficiency

Compute Capability

Large Memory Capacity







SambaNova DataScale SN30-8 System



- 8 x Cardinal SN30 Reconfigurable Dataflow Unit
- 8 TB total memory (using 64 x 128 GB DDR4 DIMMs)
- 6 x 3.8 TB NVMe (22.8 TB total)
- PCle Gen4 x16
- Host module





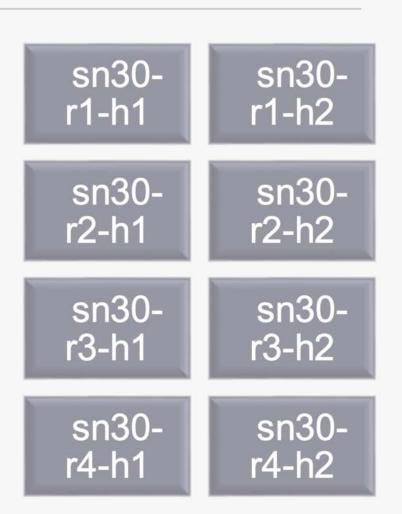
SambaNova Datascale SN30

https://www.alcf.anl.gov/alcf-ai-testbed

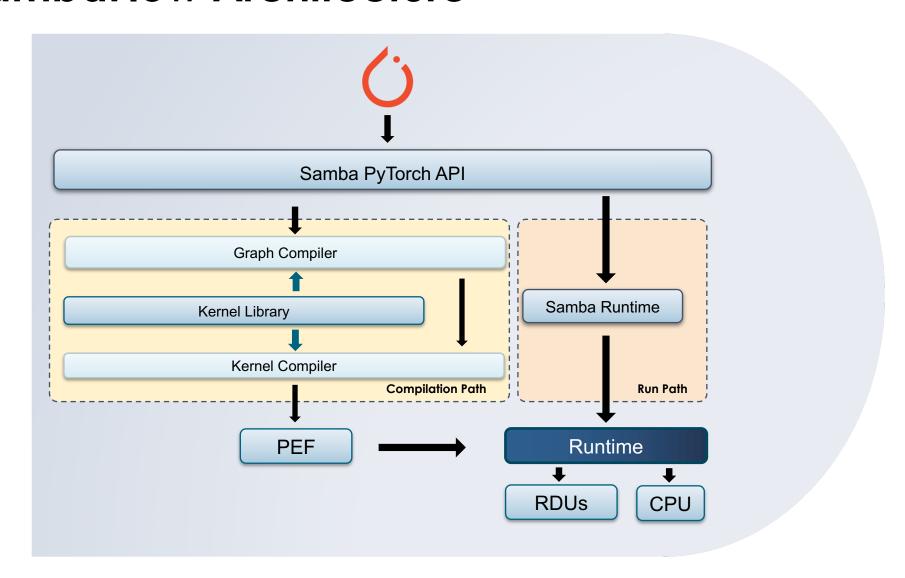


SambaNova Datascale SN30

- 4 Racks
- 8 nodes of SN30
- 8 RDUs or 4 XRDUs per node
- 8 Tiles per RDU
- Group of 4 tiles



SambaFlow Architecture



Cerebras Wafer-Scale Engine (WSE-2)

850,000 cores optimized for sparse linear algebra

46,225 mm² silicon

2.6 trillion transistors

40 gigabytes of on-chip memory

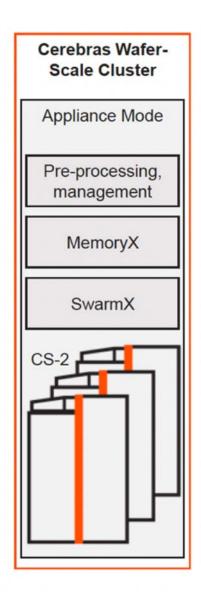
20 PByte/s memory bandwidth

220 Pbit/s fabric bandwidth

7nm process technology



Wafer-Scale Cluster



Input preprocessing servers stream training data

MemoryX - Stores and streams model's weights

SwarmX – weight broadcasts and gradient across multiple CS2s

Compilation (maps graph to kernels) Execution (training)

Image Courtesy: Cerebras

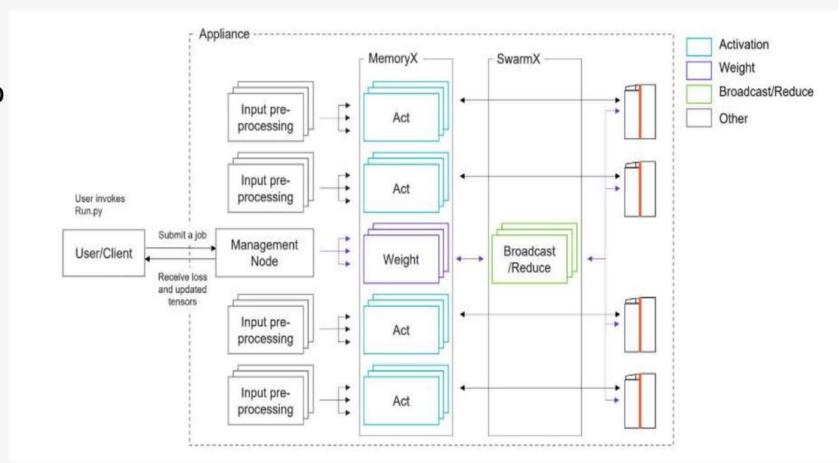


Cerebras CS-2 Cluster

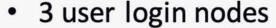
https://www.alcf.anl.gov/alcf-ai-testbed

ALCF's CS-2 Cluster

- 2 CS-2 Appliances (each chip 46225 mm²)
- 1 Management node
- 16 Worker nodes
- 24 MemoryX nodes
- 6 SwarmX nodes

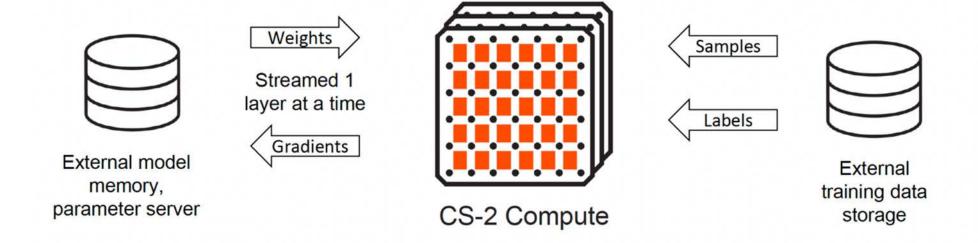


Topology of a Cerebras Wafer-Scale cluster





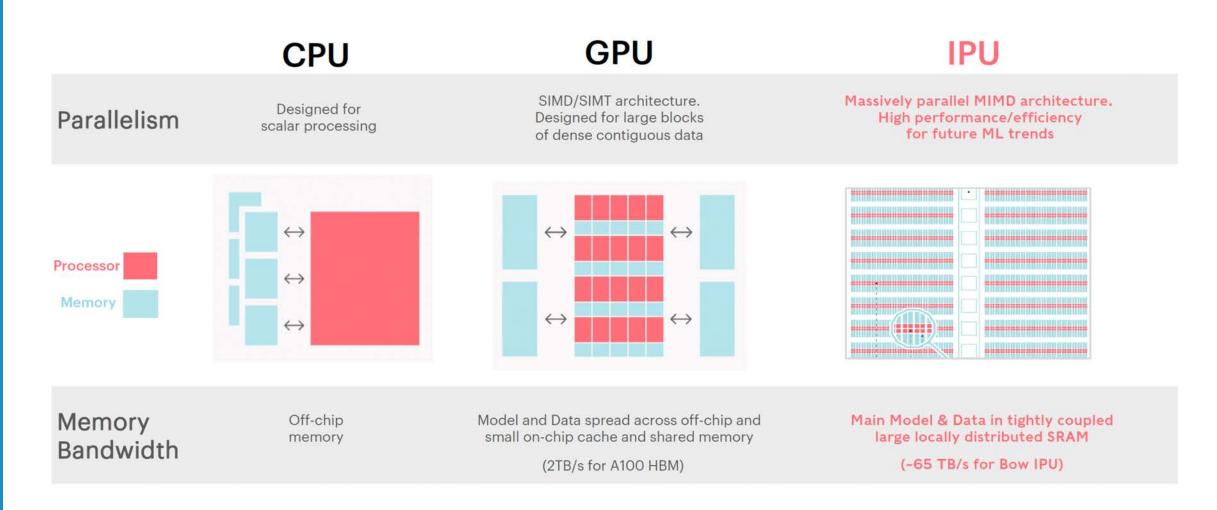
Cerebras Weight Streaming Technology



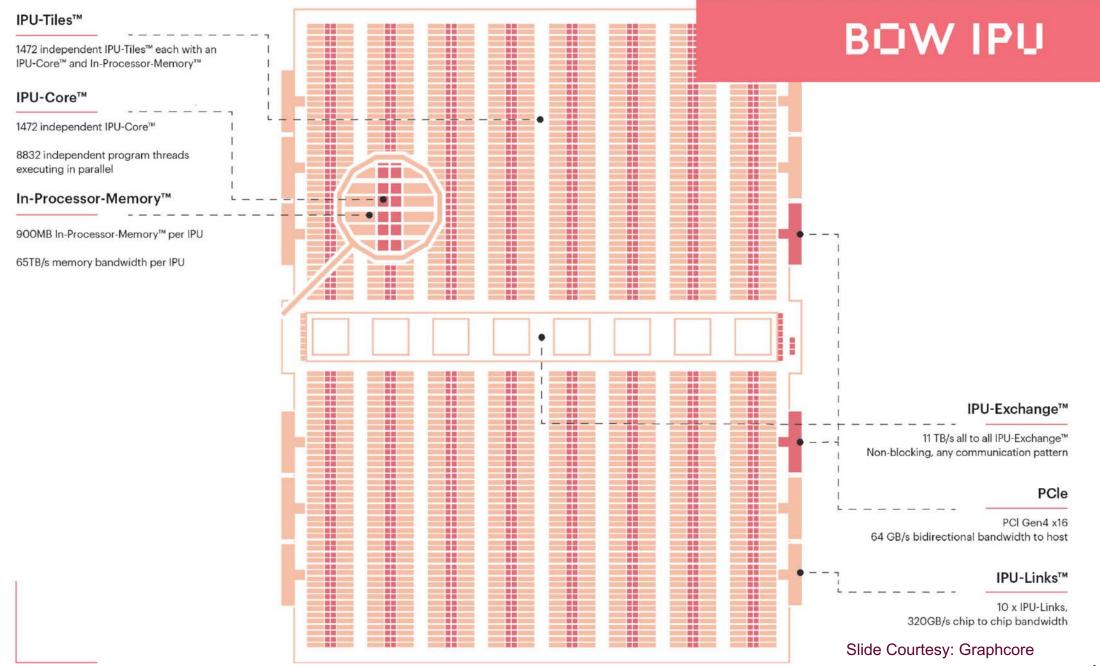
Disaggregate storage and compute Enable scaling model size

Argonne 📤

Graphcore Intelligence Processing Unit (IPU)

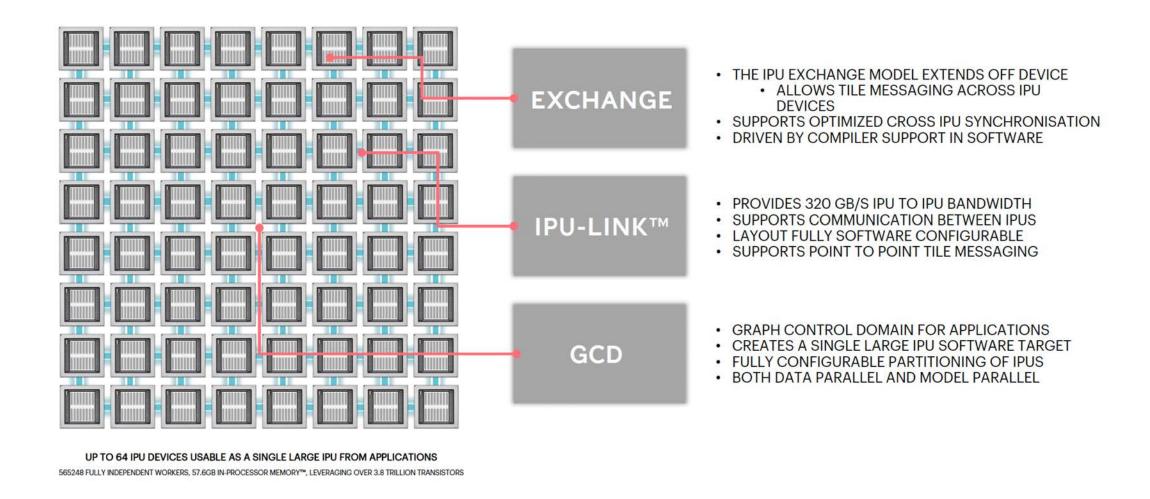






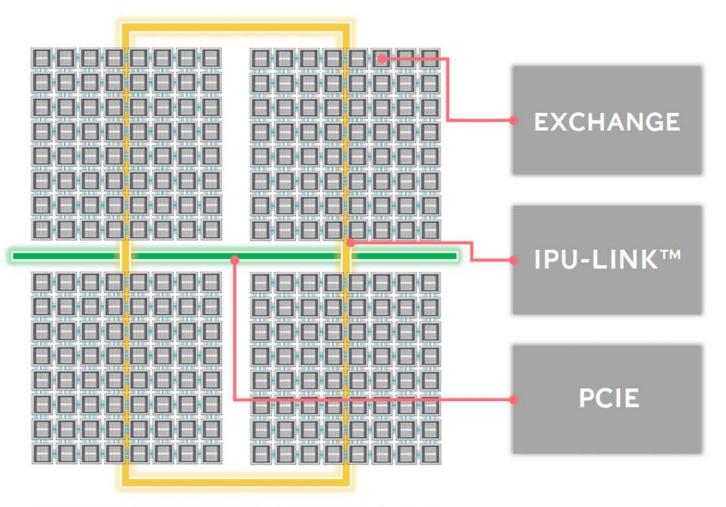


SCALING ACROSS DEVICES





SCALING ACROSS SYSTEMS

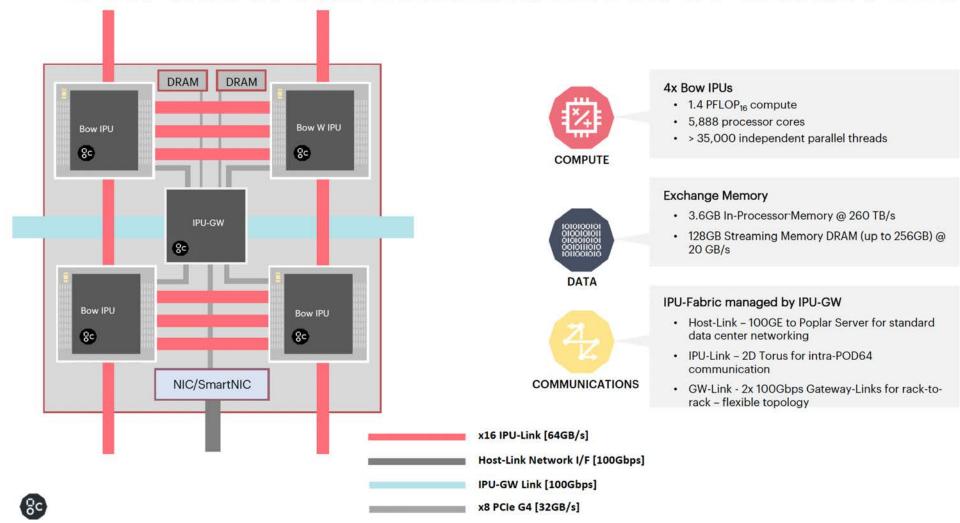


- IPU EXCHANGE SUPPORT ACROSS DOMAINS
 - DRIVEN BY COMPILER SUPPORT IN SOFTWARE
- ENABLES APPLICATION COLLECTIVES SUPPORT
- ALLOWS SCALING UP TO 64000 IPU DEVICES
- IPU LINK™ CAN BE EXTENDED ACROSS DOMAINS
- SUPPORTS OPTIMIZED IPU LINK™ COLLECTIVES
- ALLOWS REPLICATION ACROSS SYSTEMS
- SUPPORTS A STANDARD IPU SOFTWARE MODEL
- IPUS CAN ACCESS MEMORY AND DEVICES OVER PCIE
- ALLOWS INTERFACING WITH HOST BASED SOFTWARE
- APPLICATIONS CAN BUILD ON HOST NETWORKING
- ALLOWS SCALING IN STANDARD SERVER PLATFORMS

256 IPU APPLICATION TARGET BUILT FROM INTERCONNECTED 64 IPU DOMAINS



BOW-2000: THE BUILDING BLOCK OF LARGE PODS



Graphcore POD-64

https://www.alcf.anl.gov/alcf-ai-testbed



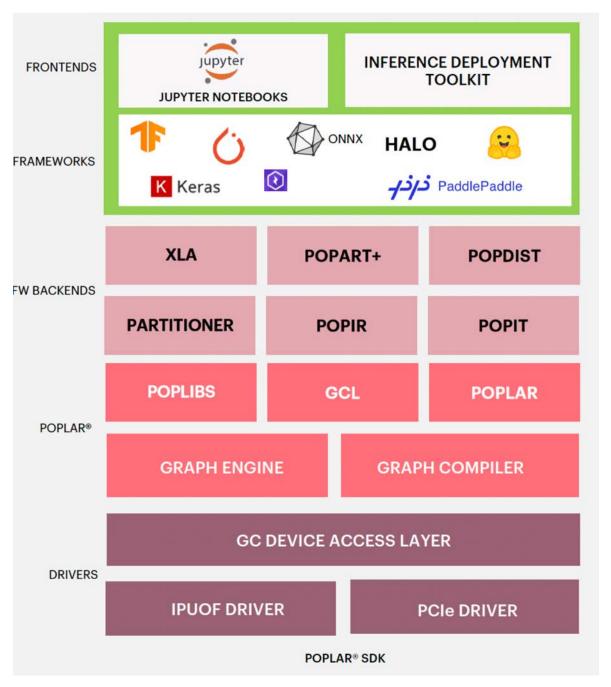
POD64

- 4 Nodes
- 64 IPUs



gcpoplar-03 gcpoplar-02

gcpoplar-04



	Cerebras CS2	SambaNova Cardinal SN30	Groq GroqRack	GraphCore GC200 IPU	Habana Gaudi1	NVIDIA A100
Compute Units	850,000 Cores	640 PCUs	5120 vector ALUs	1472 IPUs	8 TPC + GEMM engine	6912 Cuda Cores
On-Chip Memory	40 GB L1, 1TB+ MemoryX	>300MB L1 1TB	230MB L1	900MB L1	24 MB L1 32GB	192KB L1 40MB L2 40-80GB
Process	7nm	7nm	7 nm	7nm	7nm	7nm
System Size	2 Nodes including Memory-X and Swarm-X	8 nodes (8 cards per node)	9 nodes (8 cards per node)	4 nodes (16 cards per node)	2 nodes (8 cards per node)	Several systems
Estimated Performance of a card (TFlops)	>5780 (FP16)	>660 (BF16)	>250 (FP16) >1000 (INT8)	>250 (FP16)	>150 (FP16)	312 (FP16), 156 (FP32)
Software Stack Support	Tensorflow, Pytorch	SambaFlow, Pytorch	GroqAPI, ONNX	Tensorflow, Pytorch, PopArt	Synapse AI, TensorFlow and PyTorch	Tensorflow, Pytorch, etc
Interconnect	Ethernet-based	Ethernet-based	RealScale TM	IPU Link	Ethernet- based	NVLink



Challenges

- Understand how these systems perform for different workloads given diverse hardware and software characteristics
- What are the unique capabilities of each evaluated system
- Opportunities and potential for integrating AI accelerators with HPC computing facilities

Approach

- Perform a comprehensive evaluation with a diverse set of Deep Learning (DL) models:
 - DL primitives: GEMM, Conv2D, ReLU, and RNN
 - Benchmarks: U-Net, BERT-Large, ResNet-50
 - AI4S applications: BraggNN and Uno
 - Scalability and Collective communications
- Evaluated SambaNova, Cerebras, Graphcore, Groq systems and Nvidia A100 as a baseline*

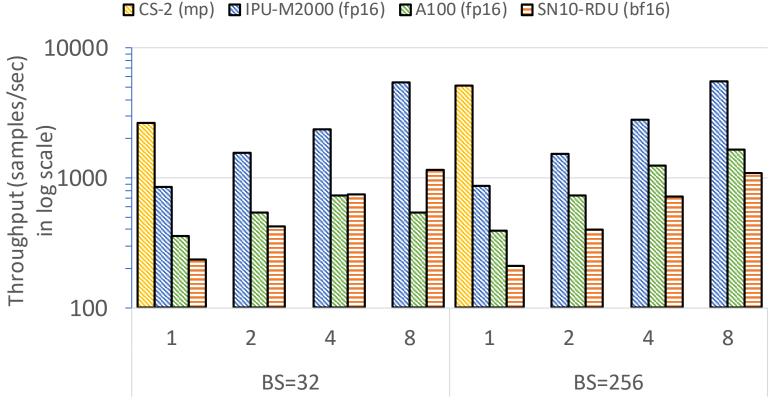
Emani et al. "A Comprehensive Evaluation of Novel Al Accelerators for Deep Learning Workloads",

13th IEEE International Workshop on Performance Modeling, Benchmarking and Simulation of High Performance Computer Systems (PMBS) at SC 2022.



^{*} run out-of-box.

Scaling UNet-2D Training

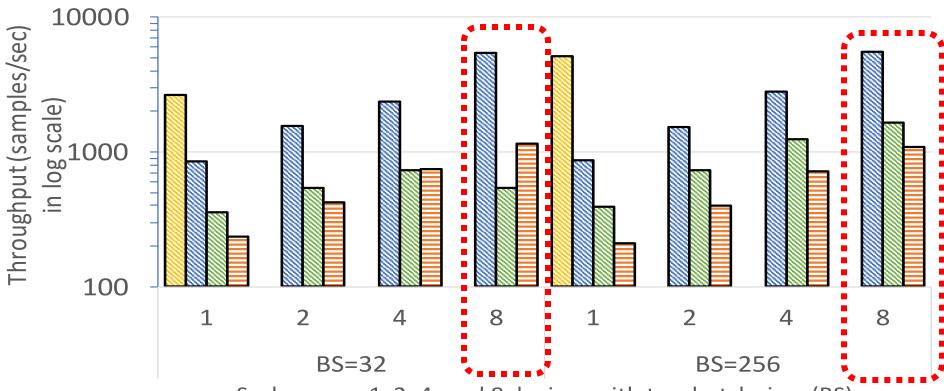


Scale across 1, 2, 4, and 8 devices with two batch sizes (BS)
GraphCore uses data-prefetching optimization, CS-2 uses 1 wafer-scale engine

- 256x256 BMRI dataset
- A100, SN10 Pytorch
 Graphcore Tensorflow
 CS2 -- TF estimator
- Accelerators capable of handling much larger image sizes.



Scaling UNet-2D Training



Scale across 1, 2, 4, and 8 devices with two batch sizes (BS)
GraphCore uses data-prefetching optimization, CS-2 uses 1 wafer-scale engine

Increased Throughput over 8 A100s

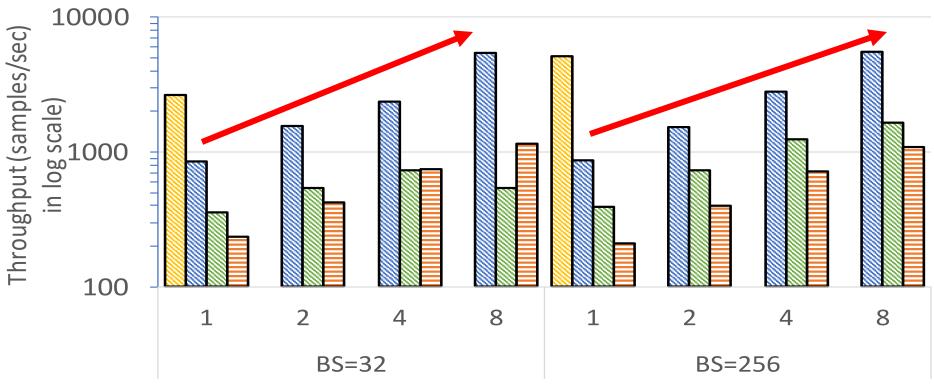
Batch Size	8 SN10 - RDUs		8 GC 200 IPUs
32	2.1x	4.9x	10x

*2x increase in latest sw release



Scaling UNet-2D Training

SCS-2 (mp) IPU-M2000 (fp16) A100 (fp16) SN10-RDU (bf16)



Scale across 1, 2, 4, and 8 devices with two batch sizes (BS)
GraphCore uses data-prefetching optimization, CS-2 uses 1 wafer-scale engine

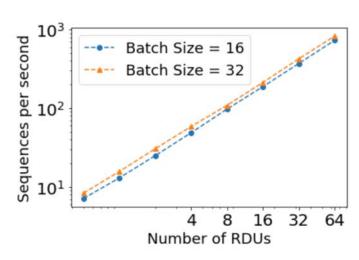
Scaling efficiency

Batch Size	A100	SN10	GC
32	18.8%	42%	79.5%
256	52%	28%	79.6%



GPT Small (1.5B / 2B / xl)

SN30

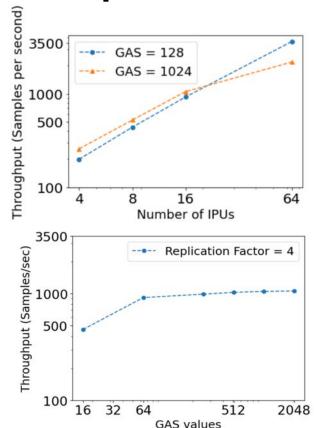


Sequence length = 1024, fits on 4 tiles.

Maximum of 128 instances run on 8 SN30 nodes.

~ 2x speed up observed over the nodes.

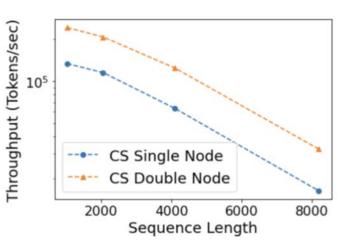
Graphcore



Scaling over replication factor better for smaller GAS values.

poprun for improved scaling efficiency.

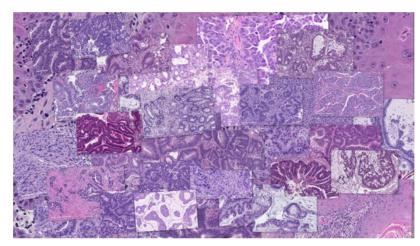




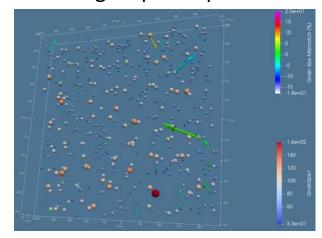
Work in progress for higher sequence length and wider models.



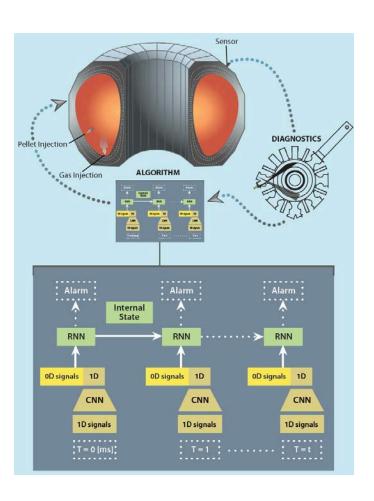
AI FOR SCIENCE APPLICATIONS



Cancer drug response prediction



Imaging Sciences-Braggs Peak



Tokomak Fusion Reactor operations



Protein-folding(Image: NCI)

and more..

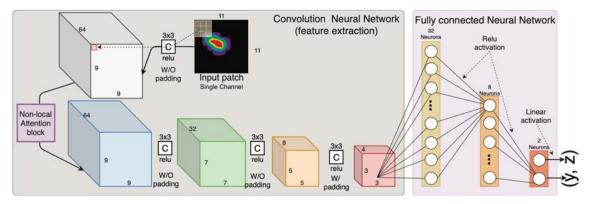


Fast X-Ray Bragg Peak Analysis

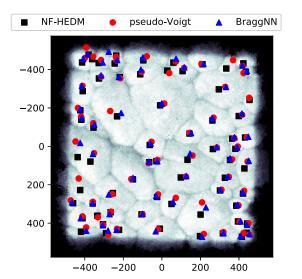
<u>Goal:</u> Enable rapid analysis and real-time feedback during an in-situ experiment with complex detector technologies

Proposed Approach: Deep learning-based method, BraggNN, for massive extraction of precise Bragg peak locations from far-field high energy diffraction microscopy data. BragNN has achieved 200X improvement over conventional pseudo-Voight profiling

<u>Challenges:</u> Model training capability is limited by the hardware



Application of the BraggNN deep neural network to an input patch yields a peak center position (y, z). All convolutions are 2D of size 3×3 , with rectifier as activation function. Each fully connected layer, except for the output layer, also has a rectifier activation function.



A comparison of BraggNN, pseudo-Voigt FF-HEDM and NF-HEDM. (a) Grain positions from NF-HEDM (black squares), pseudo-Voigt FF-HEDM (red circles) and BraggNN FF-HEDM (blue triangles) overlaid on NF-HEDM confidence map

Courtesy: Z. Liu et al. BraggNN: Fast X-ray Bragg Peak Analysis Using Deep Learning. International Union of Crystallography (IUCrJ), Vol. 9, No. 1, 2022



Fast X-Ray Bragg Peak Analysis

End-to-End Execution time (lower is better)

Fixed Time (compile, I/O and pre-processing) Training Time

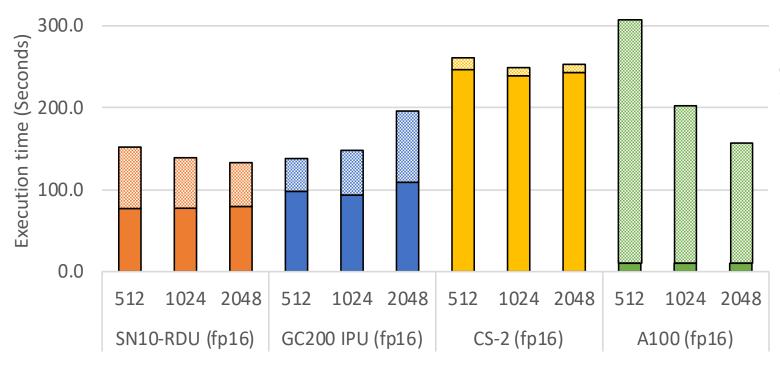


TABLE II: BraggNN Throughput (in order of 1k samples/sec) with various batch sizes (BS)

System	BS=512	BS=1024	BS=2048
CS-2 (FP16)	1365.4	2463	2787.9
GC200 IPU (FP16)	478.0	350.6	219.9
SN10 RDU (BF16)	369.7	449.8	518
A100 (FP16)	53.9	65.5	73.7

- SambaNova and Graphcore achieve lowest time to solution and achieve up to 1.55x and 1.46x speedup in comparison to Nvidia A100 respectively.
- Cerebras achieves up to 37.8x throughput improvement over A100.



Genome-scale Language Models (GenSLMs)

Goal:

- How new and emergent variants of pandemic causing viruses, (specifically SARS-CoV-2) can be identified and classified.
- Identify mutations that are VOC (increased severity and transmissibility)
- Extendable to gene or protein synthesis.

Approach

- Adapt Large Language Models (LLMs) to learn the evolution.
- Pretrain 25M 25B models on raw nucleotides with large sequence lengths.
- Scale on GPUs, CS2s, SN30.

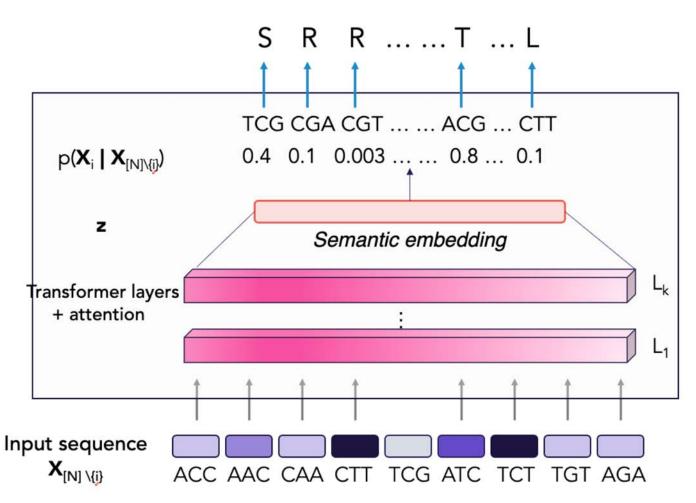
GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics

Winner of the ACM Gordon Bell Special Prize for High Performance Computing-Based COVID-19 Research, 2022,

DOI: https://doi.org/10.1101/2022.10.10.511571



Genome-scale Language Models (GenSLMs)



Model	Seq. length	#Parameters	Dataset
GenSLM- Foundation	2048	25M, 250M, 2.5B, 25B	110M
GenSLM	10240	25M, 250M, 2.5B, 25B	1.5M
GenSLM- Diffusion	10240	2.5B	1.5M

Challenges

Scaling LLMs with 25B parameters:

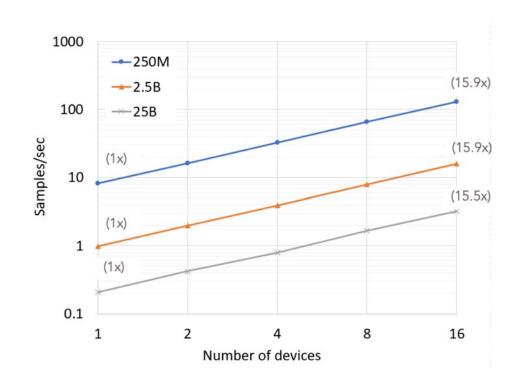
- O (L^2) complexity in the attention computation
- Overcome communication overheads
- Sharding and the training time available on GPUs imposing limitations

Solution

Cerebras CS-2 wafer-scale cluster and Sambanova SN30 enables pre-training and finetuning.

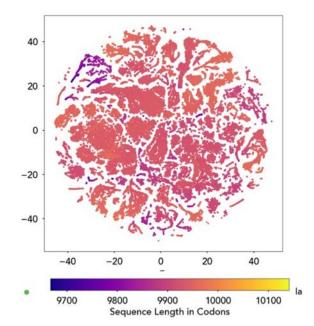


GenSLMs on CS2



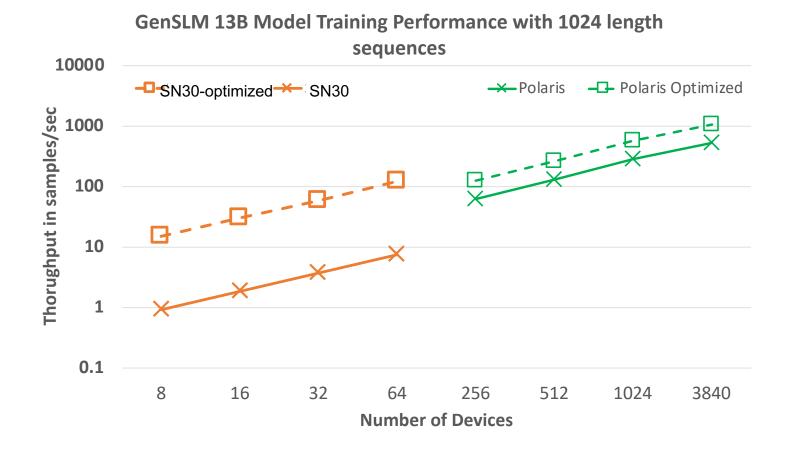
- Sequence Length = 10,240
- Trainable upto GPT3-13b model.
- Training with 4CS2, less than ½ day

	GenSLM 123M		GenSLM 1.3B	
	1 CS-2	4 CS-2	1 CS-2	4CS-2
Training steps	5,000	3,000	4,500	3,000
Training samples	165,000	396,000	49,500	132,000
Time to train (h)	4.1	2.4	15.6	10.4
Validation accuracy	0.9615	0.9625	0.9622	0.9947
Validation perplexity	1.031	1.029	1.031	1.025





GenSLMs on SN30



- Sequence Length = 1024
- Model Size 13B
- Achieves linear scaling across nodes.
- SN30 performance similar to 4 A100 on 1.17 release.
- Optimized on 1.18 to get
 10x speed-up.
- Pretraining and FineTuning on larger sequence lengths.



Observations, Challenges and Insights

- Significant speedup achieved for a wide-gamut of scientific ML applications
 - Easier to deal with larger resolution data and to scale to multi-chip systems
- Room for improvement exists
 - Porting efforts and compilation times
 - Coverage of DL frameworks, support for performance analysis tools, debuggers

Observations, Challenges and Insights

- Good progress made in integration of AI accelerators, in production, at a national user facility and significant more work is needed for effective coupling
- Training and Outreach is critical to educate users to effectively use AI systems
- Close collaboration with vendors is necessary to realize the vision of AI for science

Ongoing Efforts

- Evaluate new AI accelerators offerings and incorporate promising solutions as part of the testbed
- Integrate AI testbed systems with the PBSPro scheduler to facilitate effective job scheduling across the accelerators
- Evaluate traditional HPC on Al Accelerators
- Understand how to integrate AI accelerators with ALCF's existing and upcoming supercomputers to accelerate science insights



Recent Publications

GenSLMs: Genome-scale language models reveal SARS-CoV-2 evolutionary dynamics
 Maxim Zvyagin, Alexander Brace, Kyle Hippe, Yuntian Deng, Bin Zhang, Cindy Orozco Bohorquez, Austin Clyde, Bharat Kale, Danilo Perez Rivera, Heng Ma, Carla M. Mann, Michael Irvin, J. Gregory Pauloski, Logan Ward, Valerie Hayot, Murali Emani, Sam Foreman, Zhen Xie, Diangen Lin, Maulik Shukla, Weili Nie, Josh Romero, Christian Dallago, Arash Vahdat, Chaowei Xiao, Thomas Gibbs, Ian Foster, James J. Davis, Michael E. Papka, Thomas Brettin, Rick Stevens, Anima Anandkumar, Venkatram Vishwanath, Arvind Ramanathan
 ** Winner of the ACM Gordon Bell Special Prize for High Performance Computing-Based COVID-19 Research, 2022,
 DOI: https://doi.org/10.1101/2022.10.10.511571

A Comprehensive Evaluation of Novel AI Accelerators for Deep Learning Workloads
 Murali Emani, Zhen Xie, Sid Raskar, Varuni Sastry, William Arnold, Bruce Wilson, Rajeev Thakur, Venkatram Vishwanath, Michael E Papka, Cindy Orozco Bohorquez, Rick Weisner, Karen Li, Yongning Sheng, Yun Du, Jian Zhang, Alexander Tsyplikhin, Gurdaman Khaira, Jeremy Fowers, Ramakrishnan Sivakumar, Victoria Godsoe, Adrian Macias, Chetan Tekur, Matthew Boyd, 13th IEEE International Workshop on Performance Modeling, Benchmarking and Simulation of High Performance Computer Systems (PMBS) at SC 2022

• Enabling real-time adaptation of machine learning models at x-ray Free Electron Laser facilities with high-speed training optimized computational hardware

Petro Junior Milan, Hongqian Rong, Craig Michaud, Naoufal Layad, Zhengchun Liu, Ryan Coffee, Frontiers in Physics DOI: https://doi.org/10.3389/fphy.2022.958120



Recent Publications

• Intelligent Resolution: Integrating Cryo-EM with Al-driven Multi-resolution Simulations to Observe the SARS-CoV-2 Replication-Transcription Machinery in Action*

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- Stream-AI-MD: Streaming AI-driven Adaptive Molecular Simulations for Heterogeneous Computing Platforms
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Please reach out for further details Venkat Vishwanath, <u>Venkat@anl.gov</u> Murali Emani, <u>memani@anl.gov</u>

