

## Machine Learning Accelerators in Bioinformatics

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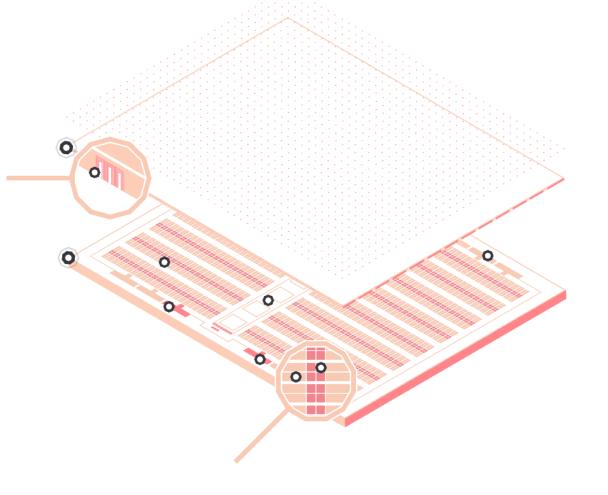




#### **Introduction and History**

- Early 2010: Need for specialized hardware in Al accelerates, with companies like Graphcore leading the way.
- 2017: Graphcore introduced the first IPU for AI/ML workloads (Colossus<sup>TM</sup> MK1 - GC2 IPU).
- 2020: Colossus<sup>TM</sup> MK2 GC200 IPU
- 2022: Graphcore and TSMC presented the Bow IPU, a 3D package of a GC200 die bonded face to face to a power-delivery die that allows for higher clock rate at lower core voltage









#### **Architecture**

#### Key components:

- Massively Parallel Processor Cores: Thousands of small, independent cores designed to handle parallel tasks simultaneously.
- Memory Architecture: IPUs have on-chip memory designed to provide ultra-fast access to data for efficient AI training/inference.
- Fine-Grained Processing: Suited for sparse data sets and small computational graphs, unlike GPUs which are optimized for dense, large-scale computation.

#### • Key Features:

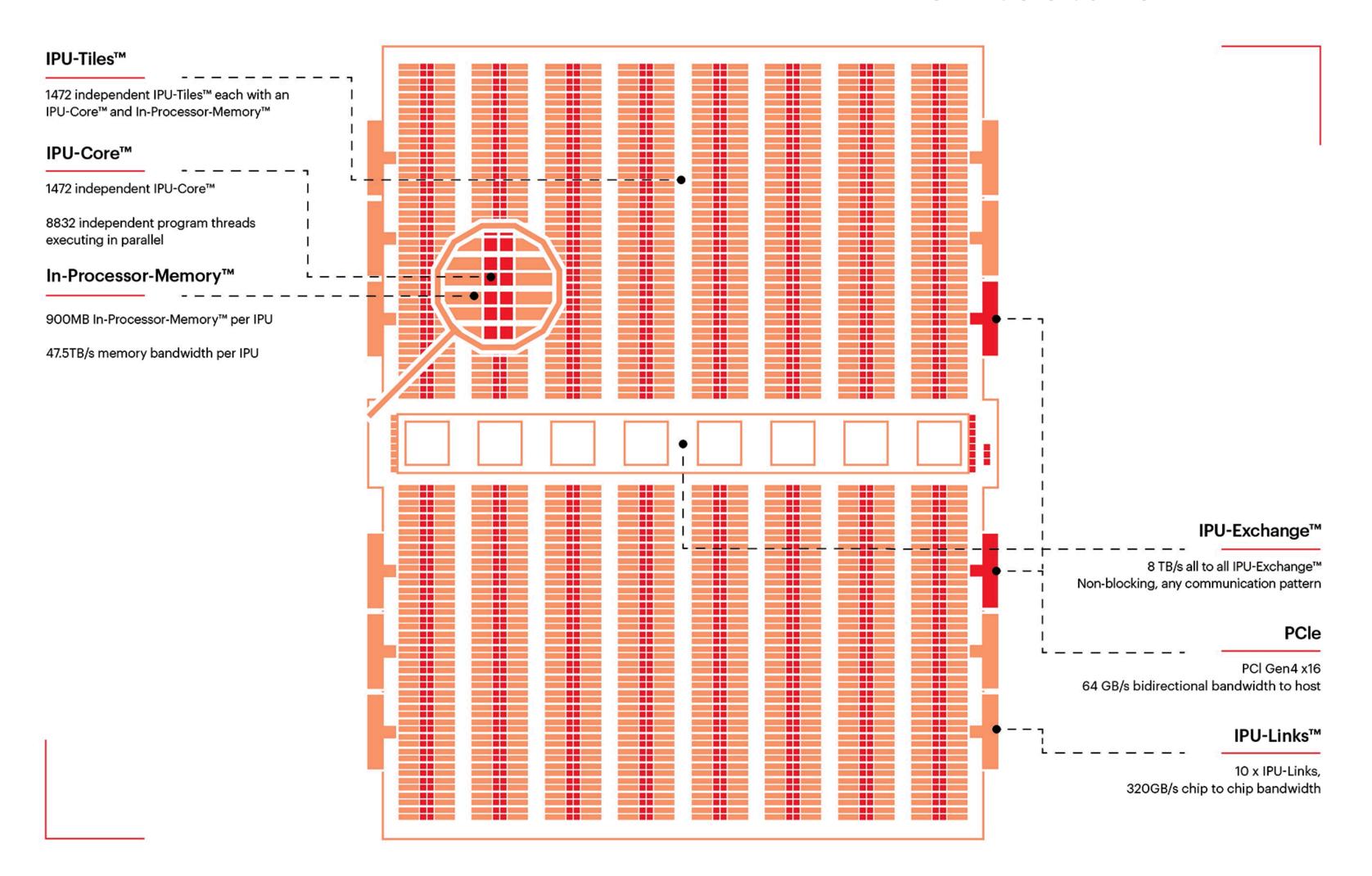
- Low-latency, high-bandwidth (SRAM) memory access.
- Optimized for machine learning models, including graph-based models.
- Were developed for AI applications but showed potential for other HPC applications





## Intelligence Processing Units

#### Architecture



- 1472 Tiles per GC200
- 600KB Memory per Tile (On-Chip)
- 900MB Memory per IPU
- Only Tile-local Memory access
- Up to 6 Threads per Tile
- 250 TFLOPs of peak FP16
- 62.5 TFLOPs of peak FP32
- 150W TDP
- 1.325 GHz
- 11 TB/s all-to-all IPU-Exchange
- 320 GB/s chip-to-chip BW

**Parallelism** 

**Processors** 

Memory





## Intelligence Processing Units

CPU vs. GPU vs. IPU

#### **CPU**

Designed for scalar processes

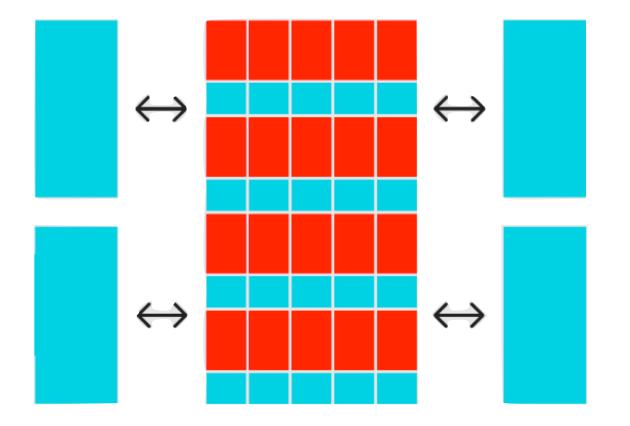
# $\Leftrightarrow \\ \Leftrightarrow \\ \Leftrightarrow \\$

Off-chip memory

#### **GPU**

SIMD/SIMT architecture.

Designed for large blocks of dense contiguous data

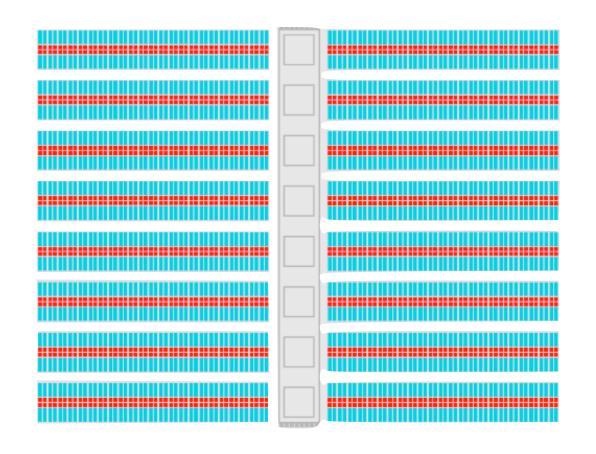


Model and data spread across off-chip and small on-chip cache, and shared memory

#### **IPU**

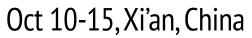
Massively parallel MIMD.

Designed for fine-grained, highperformance computing



Model and data tightly coupled, and large locally distributed SRAM









#### IPU Chip vs. GPU chip





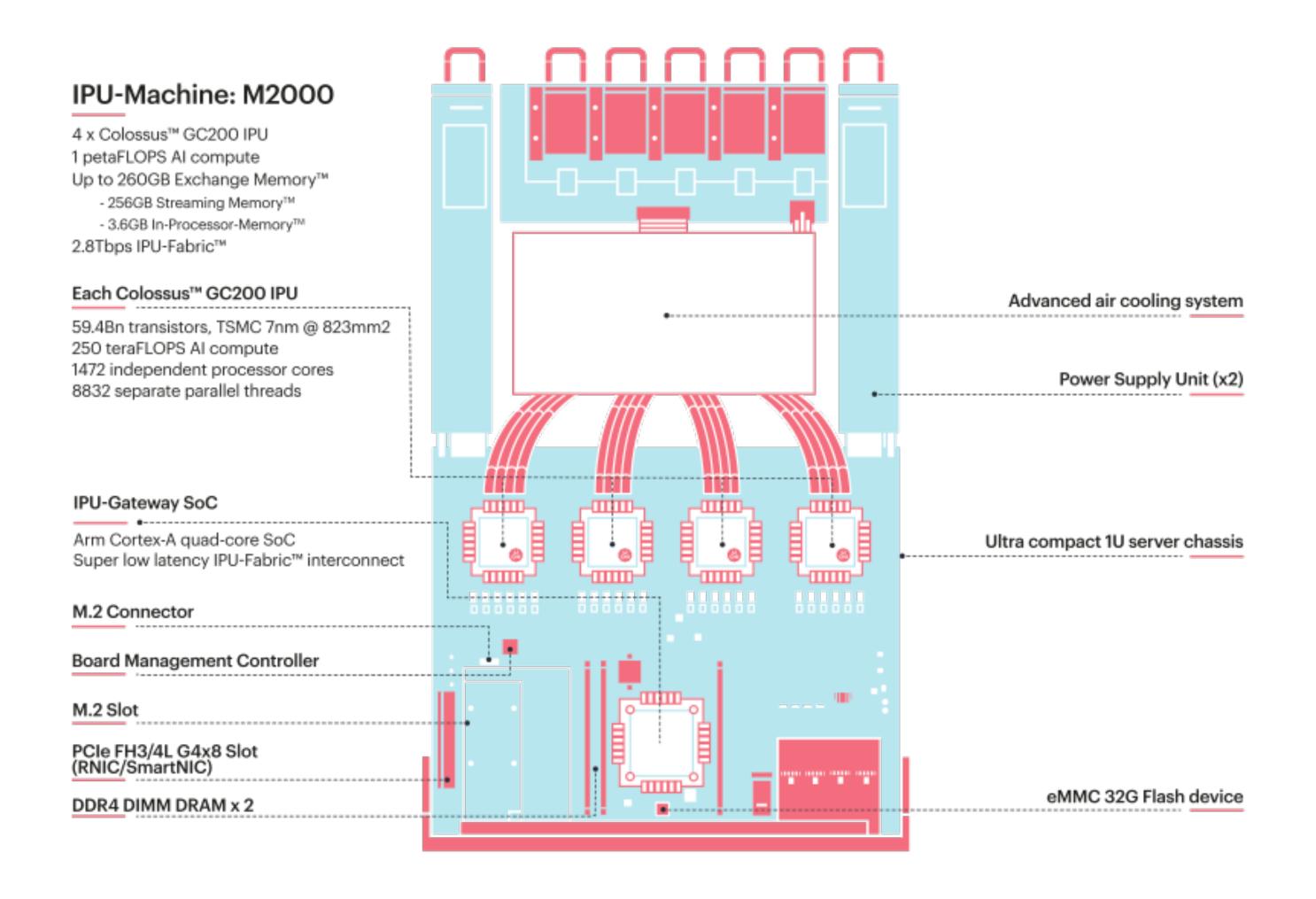
			_
Chip	GC200	A30	
Number of cores	1472	3584	
Total SRAM	918  MB	$10.75~\mathrm{MB}$	
DRAM bandwidth	$20~\mathrm{GB/s}$	$933~\mathrm{GB/s}$	
Clock frequency	$1.33~\mathrm{GHz}$	$1.44~\mathrm{GHz}$	
FP32 peak compute	62.5  TFlops/s	10.3  TFlops/s	
Power Consumption	150 W	165 W	
Inter-Chip-Bandwidth	$350~\mathrm{GB/s}$	$200~\mathrm{GB/s}$	





## Intelligence Processing Units

**IPU Machine: M2000** 





- Four GC200 IPUs
- Totally 1 PFlops of AI compute
- 3.6GB On-Chip Memory
- Up to 256GB Streaming Memory
- Scales up to 64K-IPUs
- 512Gbps inter IPU BW





## Intelligence Processing Units

#### **NVIDIA DGX-A100 vs. COLOSSUS MK2**

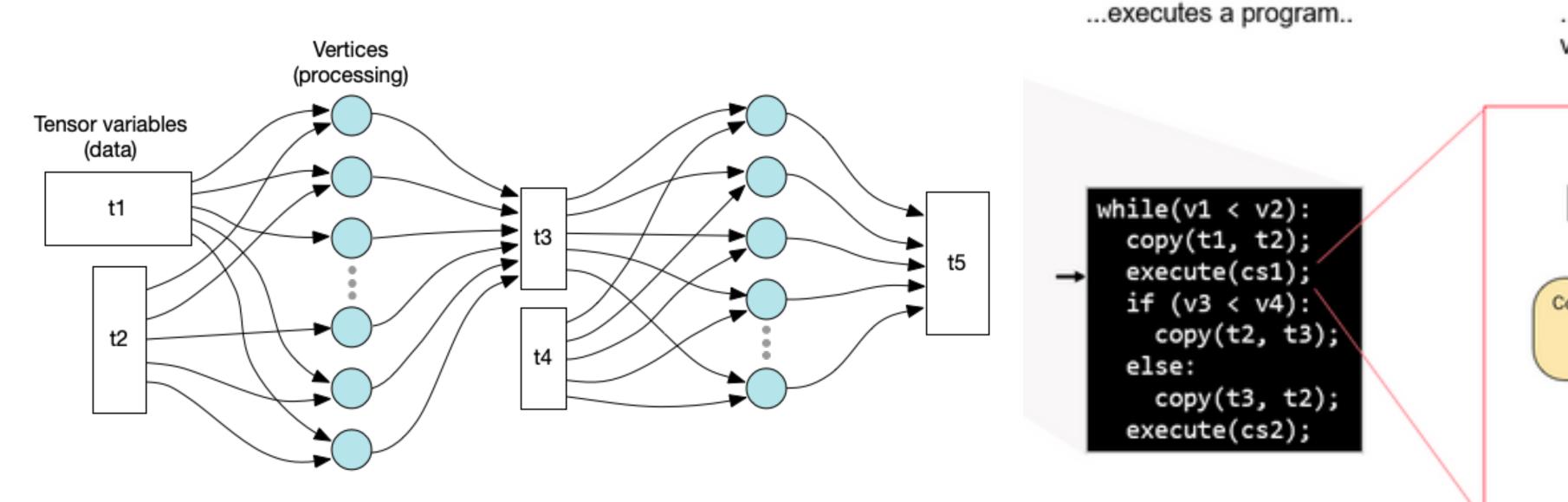
	<b>DGX-A100</b> (8x A100)	GRAPHCC 8x M2000	RE
FP32 compute	156TFLOP	2PFLOP	>12
Al compute	2.5PFLOP <sup>[1]</sup>	8PFLOP <sup>[2]</sup>	× >3x
Al Memory	320GB <sup>[3]</sup>	3.6TB <sup>[4]</sup>	>10x
System Price	\$199,000 <sub>MSRP</sub>	\$259,600мѕ	RP
	\$199,000 <sub>MSRP</sub> NOTES: [1] Actual figure for TF32/FP16. NVIDIA 8xA100 5PFlop reference is for 9 [2] Graphcore AI Float with IEEE FP16.16 multiply.accumulate and IEEE [3] 40GB HBM memory on A100 modules *8 modules per DGX-A100 sys [4] IPU-Exchange Memory which includes attached DRAM and IPU In-Pr	50% sparsity which includes Pflops for operations that aren't in FP16.SR 16bit float with stochastic rounding, with equivalent stem	run t accuracy perform



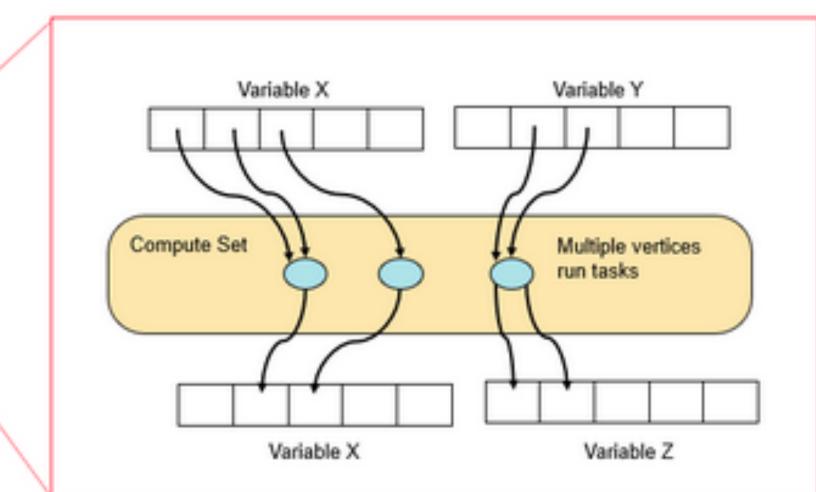


## Intelligence Processing Units

#### **Programming Model**



...which manipulates multi-element variables via highly parallel compute sets of vertices

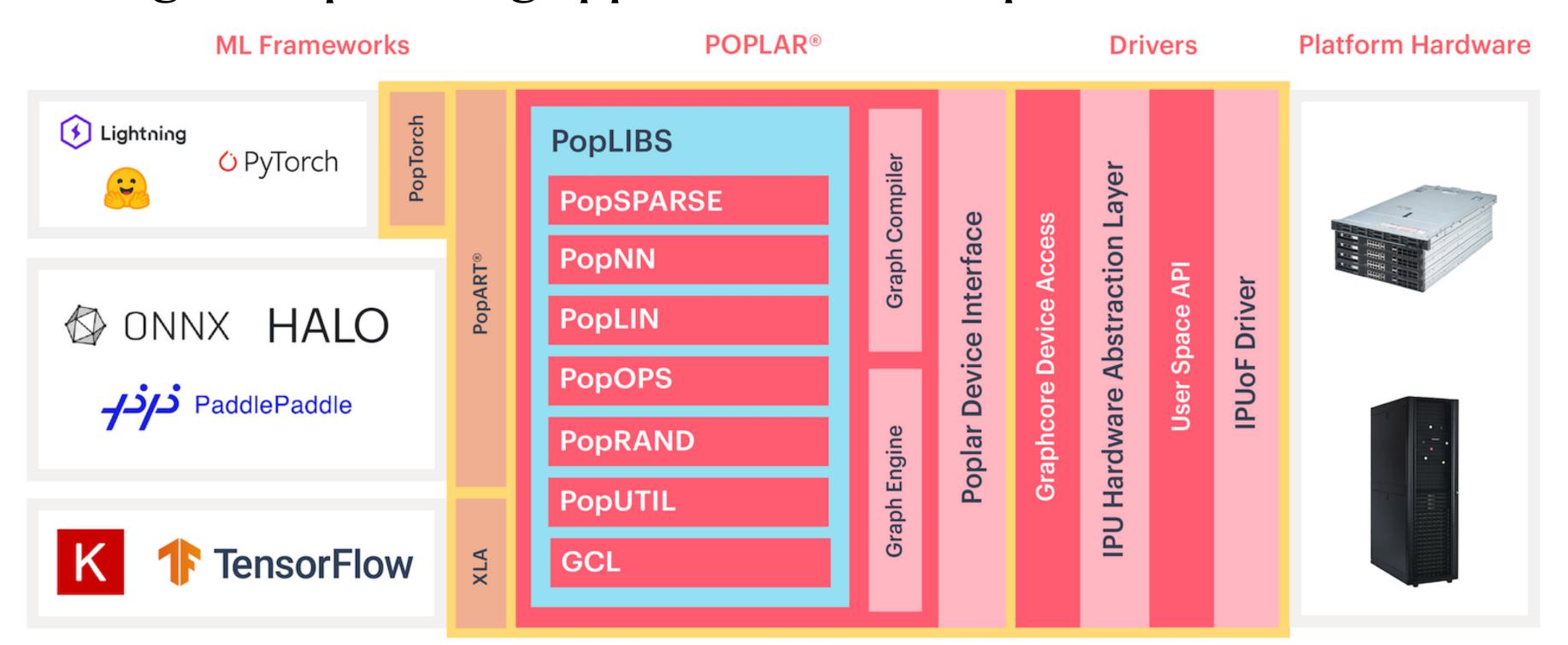






#### **Programming Model: Poplar SDK**

 A comprehensive software development toolkit designed specifically for programming and optimizing applications on Graphcore IPUs.

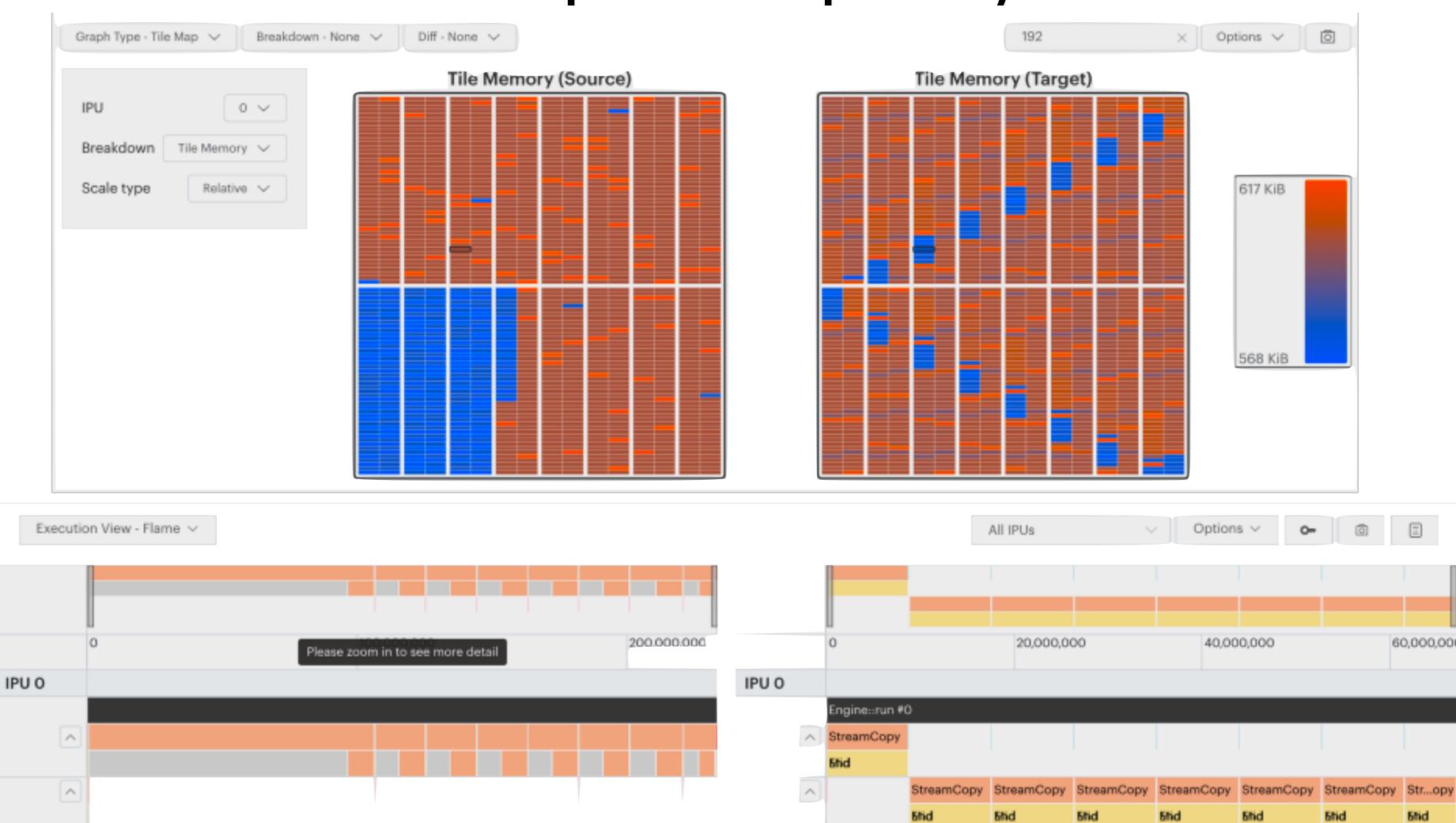






## Intelligence Processing Units

**Tools: PopVision Graph Analyzer** 

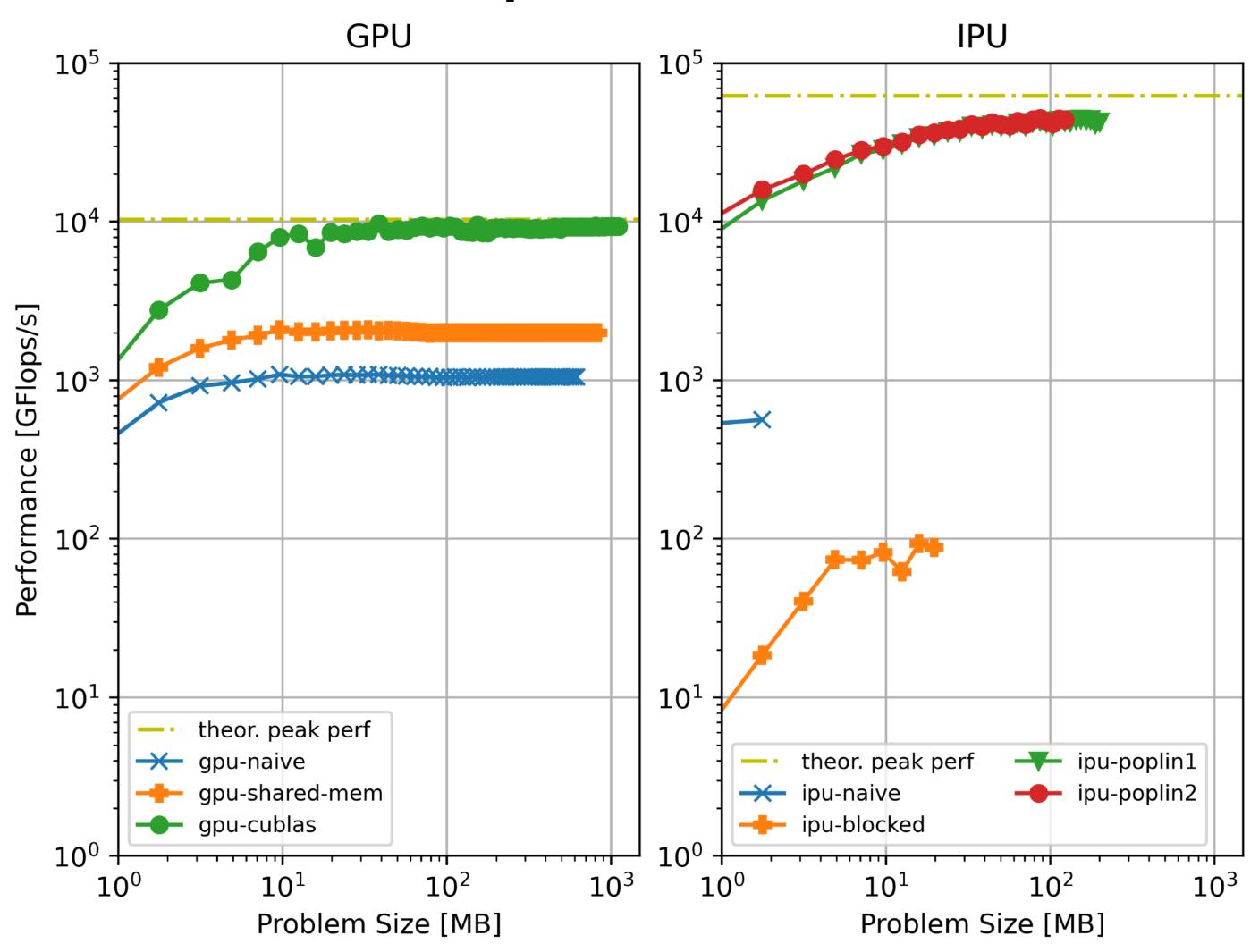






## IPU Performance Analysis

## Motivation Example: MatMul A30 vs GC200

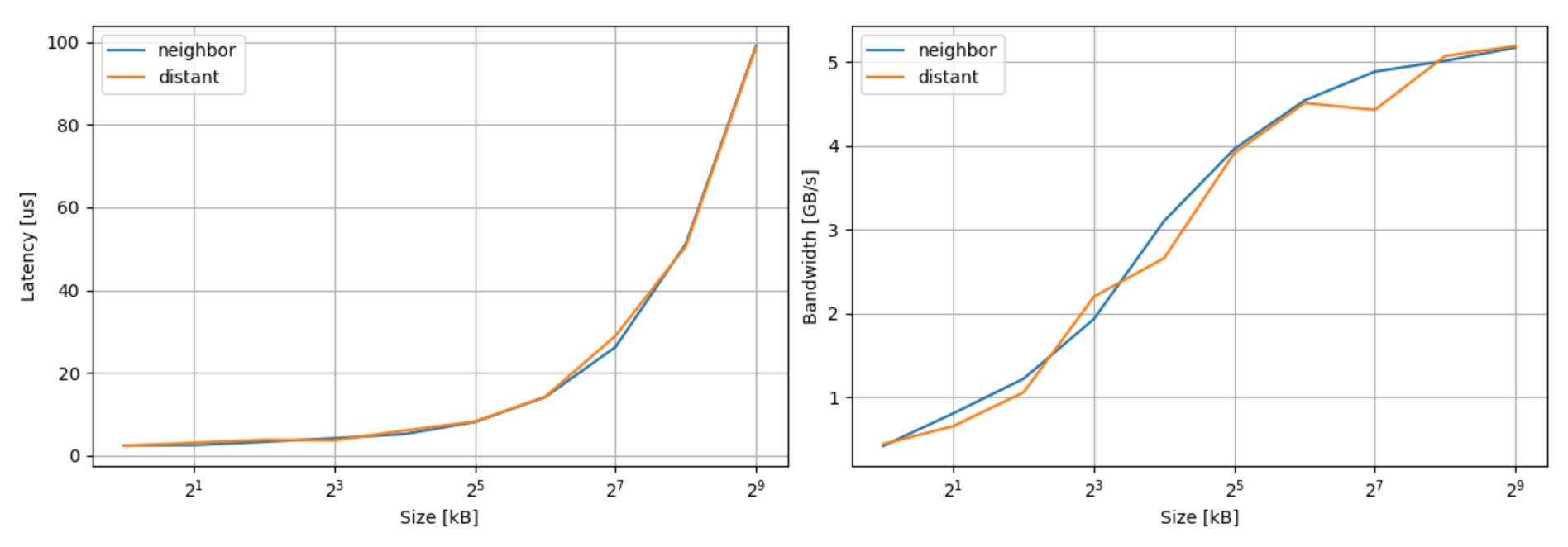






## IPU Performance Analysis

#### Locality in communication (IPU-Exchange)



**Observation 1**: Latency and bandwidth of data accesses in between different IPU-Tiles are tightly coupled with data size, but are independent of their location.

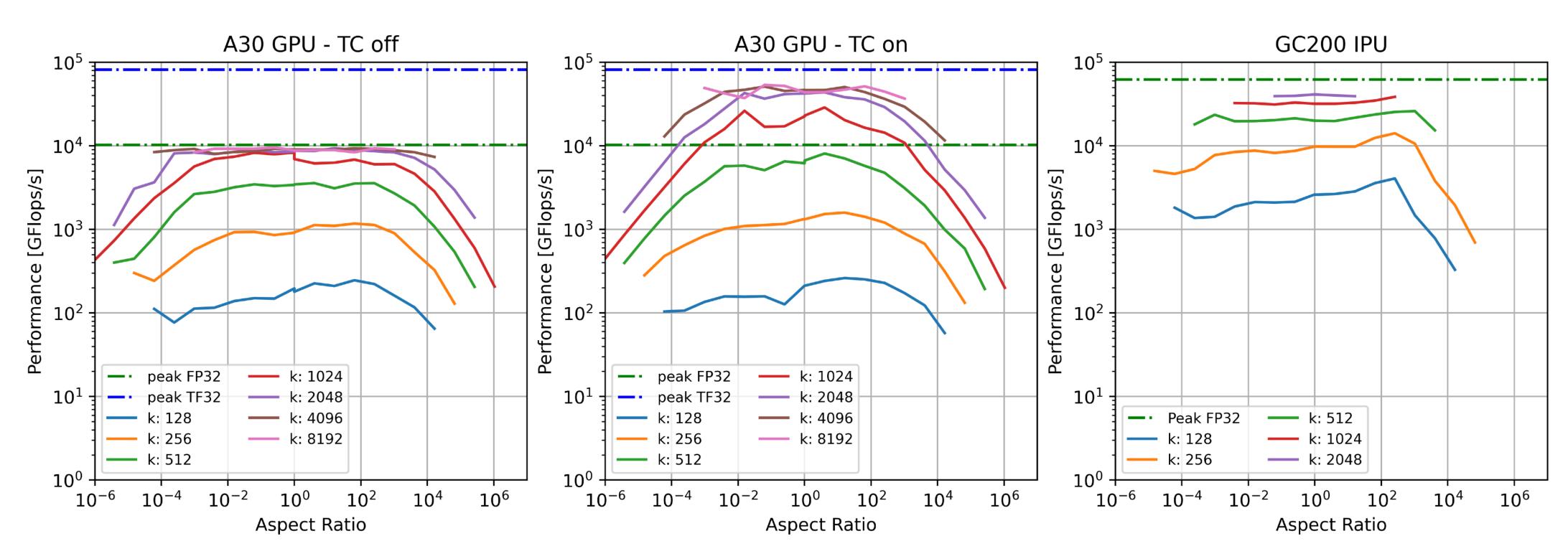






## IPU Performance Analysis

#### Squared and Skewed MatMul



**Observation 2**: Evaluation results show promising performance for the IPU in different scenarios, especially for linear algebra operations based on skewed matrices or sparse matrices.

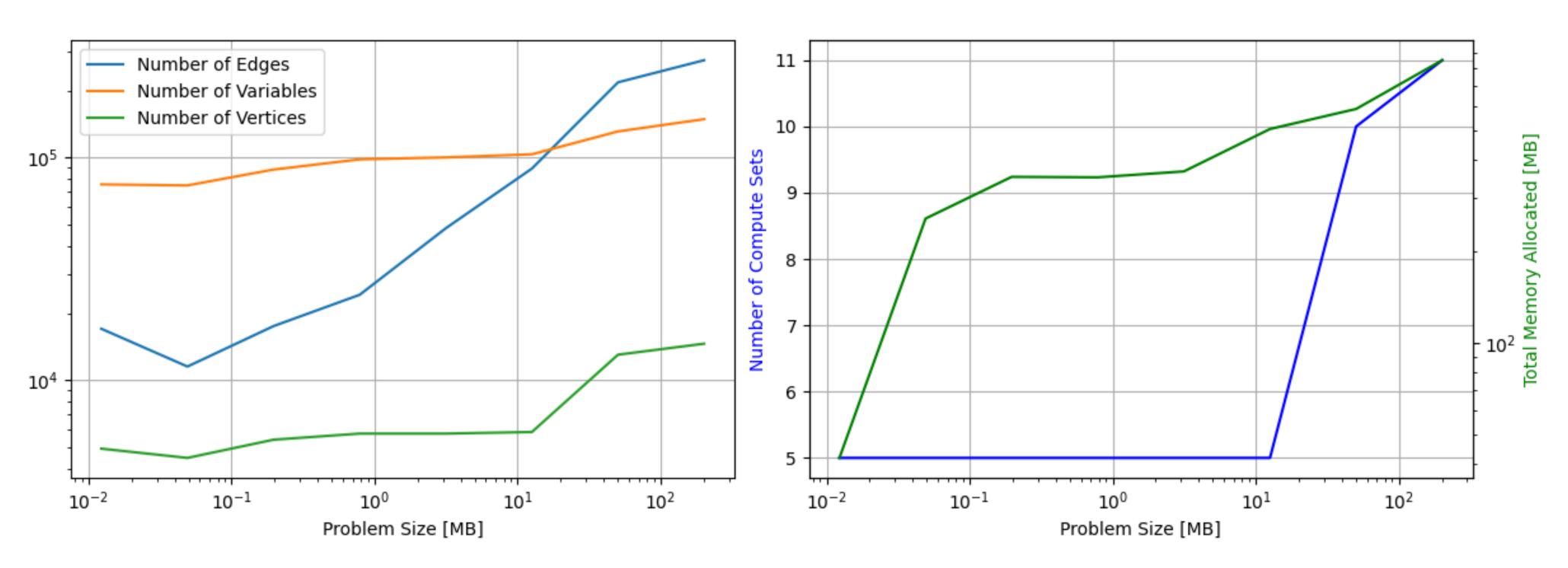
$$A(m \times n) \times B(n \times k) = C(m \times k) : skewness = \frac{m}{n}$$





## IPU Performance Analysis

#### Memory usage for the IPU



**Observation** 3: The overall memory usage for the IPU does not only depend on the problem size, but there are additional effects with substantially increase in overall memory usage.





#### Our Past and Ongoing Research on IPUs

- S.-Kazem Shekofteh, Christian Alles, and Holger Fröning. 2023. Reducing Memory Requirements for the IPU using Butterfly Factorizations. 14th IEEE International Workshop on Performance Modeling, Benchmarking and Simulation of High Performance Computer Systems @ SCS'23, Denver, CO
- On Performance Analysis of Graphcore IPUs: Analyzing Squared and Skewed Matrix Multiplication, K. Shekofteh, C. Alles, N. Kochendörfer, H. Fröning arXiv preprint arXiv:2310.00256, 2023
- Distributed Butterfly Machine Learning with IPUs
- X-Drop Sequence Alignment Implementation on IPUs
- MIMD Kernels for Sequence Alignment on IPUs





### Reducing Memory Requirements for the IPU Using Butterfly Factorizations



S-Kazem Shekofteh, Christian Alles, and Holger Fröning. Reducing Memory Requirements for the IPU using Butterfly Factorizations. PMBS 2023 @ SC '23

- Butterfly factorization
  - a technique used in applied mathematics to efficiently factorize a matrix into a product of **sparse matrices**.
  - accelerates matrix computations (matrix-vector multiplications)
  - reducing computational complexity and memory requirements
  - commonly used in fast algorithms like FFT
- Dao et al. [1]: Butterfly matrices: replacing specific transformations by universal building blocks called **butterfly factors**

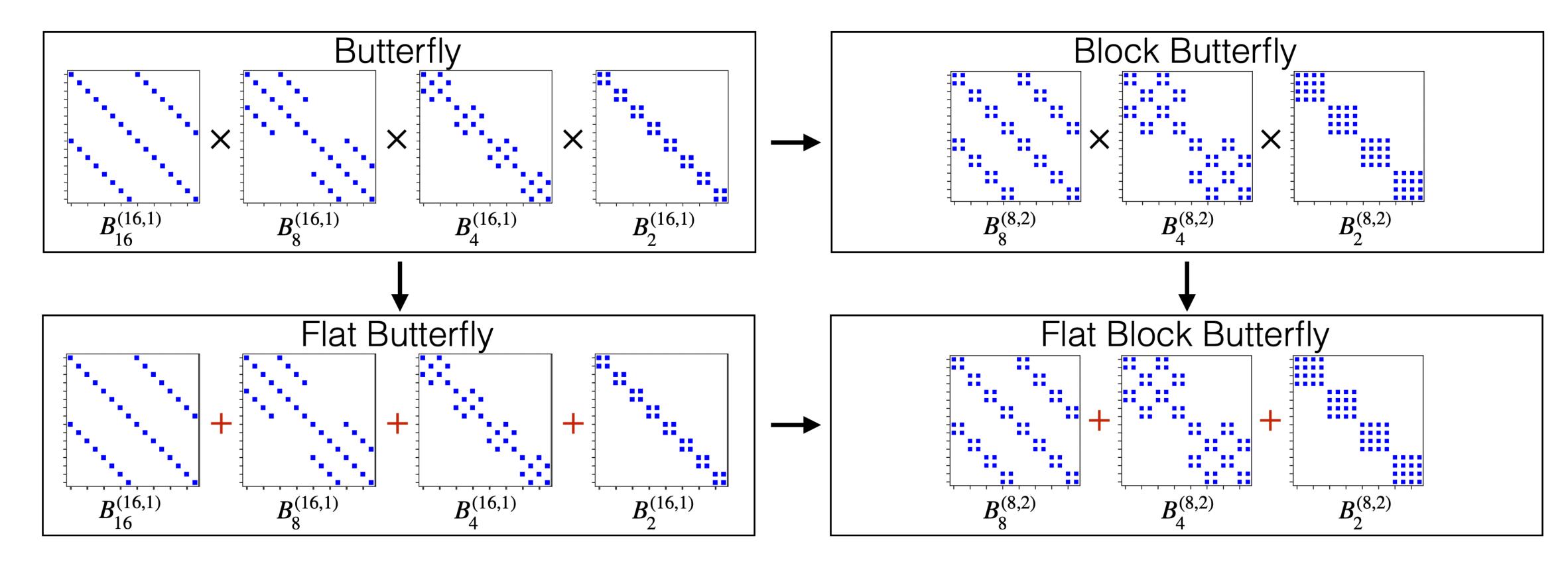




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[1] Tri Dao, Albert Gu, Matthew Eichhorn, Atri Rudra, and Christopher Re. 2019. Learning Fast Algorithms for Linear Transforms Using Butterfly Factorizations. In Proceedings of the 36th International Conference on Machine Learning



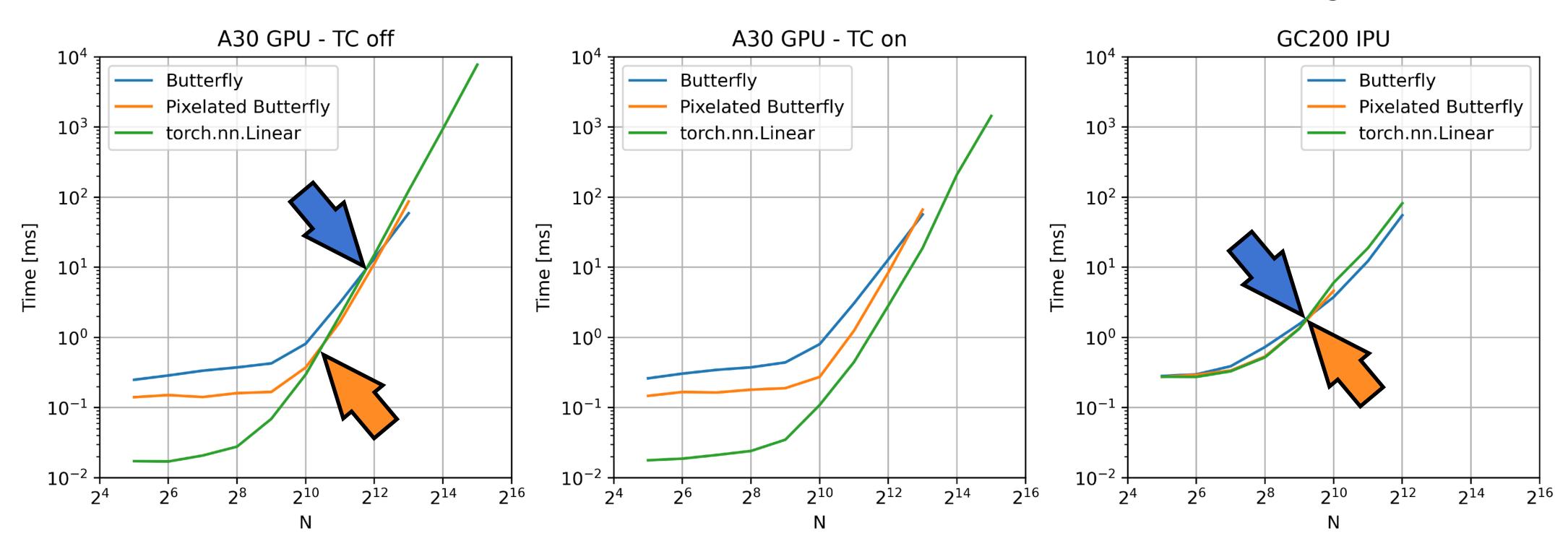


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• Evaluation of BF and PF, compared to torch.nn.Linear on both A30 and GC200







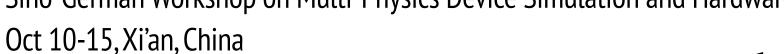


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		G	PU	IPU	GPU		IPU
Method	$N_{Params}$	w/ TC	w/o TC	•	w/TC	w/o TC	
Baseline	1059850	43.94	43.4	44.7	50.43	49.46	24.69
Butterfly	16390	42.27	40.75	41.13	61.93	61.46	37.73
Fastfood	14346	38.64	37.94	37.68	53.55	51.15	60.70
Circulant	12298	28.74	29.21	28.40	54.26	53.92	21.82
Low-rank	13322	18.64	18.49	18.59	49.71	53.21	21.75
Pixelfly	404490	42.61	43.31	43.79	52.79	56.01	71.62







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					1.17x	1.10x	0.53x		





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Single-Hidden-Layer (SHL) benchmark on CIFAR-10 dataset with different structures matrix methods compared to baseline matrix approach on GPU and IPU

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⇒ butterfly variants: high compression ratio + acceptable accuracy







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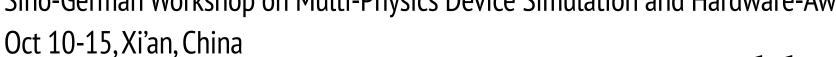
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Comparison of mean and standard deviation of metrics when varying parameters on the IPU

Butterfly	Block	Low-Rank	Metric	mean	std
size	size	size	TVICTIC	mean	Sta
	$2^3$		Time[s]	372	107
var.	$2^4$	$2^1$	Accuracy[%]	43.8	2.2
	$2^5$		$N_{Params}$	1064970	326625
		$2^2$	Time[s]	465	192
$2^1$	var.	$2^6$	Accuracy[%]	38.9	1.4
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Recommendation:

Set the low-rank size to the maximum







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#### Distributed Butterfly Machine Learning with IPUs

Master Project work by Daniel Bogacz, May -August 2023

- An extension to our previous work to implement it on multiple IPUs.
  - Dataset: Fashion-MNIST
  - Model: Vision Transformer
    - 12 Encoder Layers
    - each with 12 Attention Heads
    - Hidden Layer sizes: 256
    - Intermediate sizes: 1024
    - trainable parameters:
      - 6,375,178 (torch.nn.Linear)
      - **180,198** (Butterfly)
        - $\rightarrow$  **97.17%** compression rate

- Distributed across 4 IPUs:
  - IPU (1): Embedding Layer + 3 Encoder Layers
  - o IPU (2) + (3): 3 Encoder Layers each
  - IPU (4): 3 Encoder Layers + Classification Layer





## Intelligence Processing Units

#### Distributed Butterfly Machine Learning with IPUs

Master Project work by Daniel Bogacz, May -August 2023

## vs Butterfly Layers on Multi-IPU



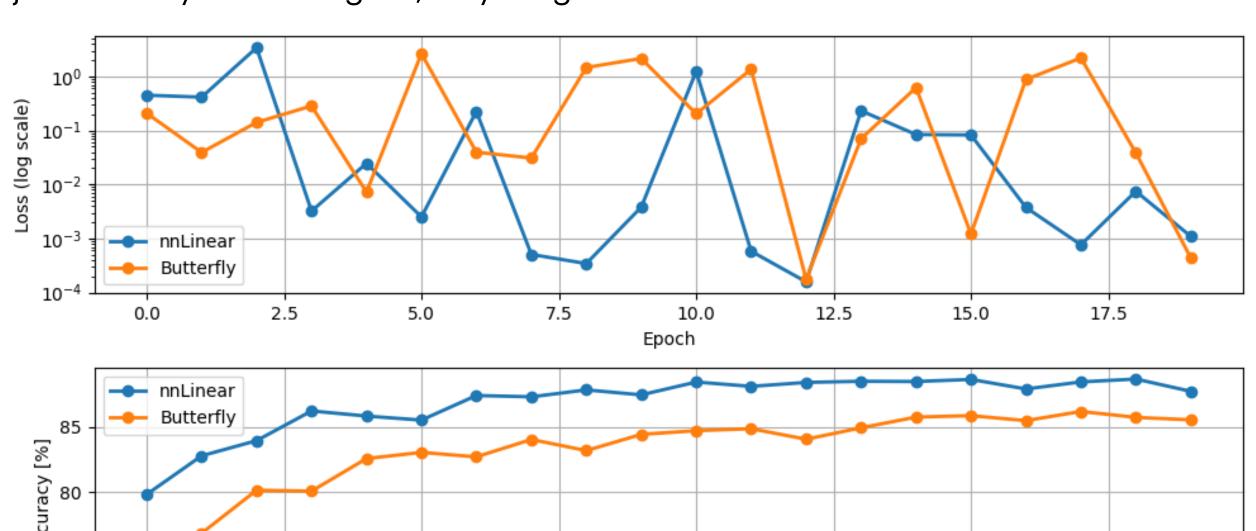
o max accuracy: 86.10%

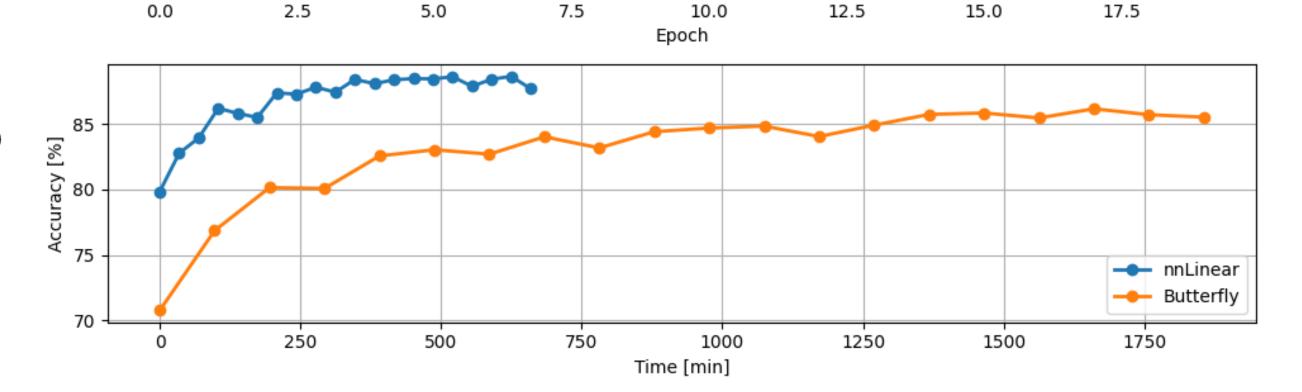
o time: 1953.27min

#### nn.Linear:

max accuracy: 88.65%

time: 694.03min









#### Distributed Butterfly Machine Learning with IPUs

Master Project work by Daniel Bogacz, May -August 2023

## Multi-IPU vs Multi-GPU (4 K80 GPUs)

#### **GPUs**:

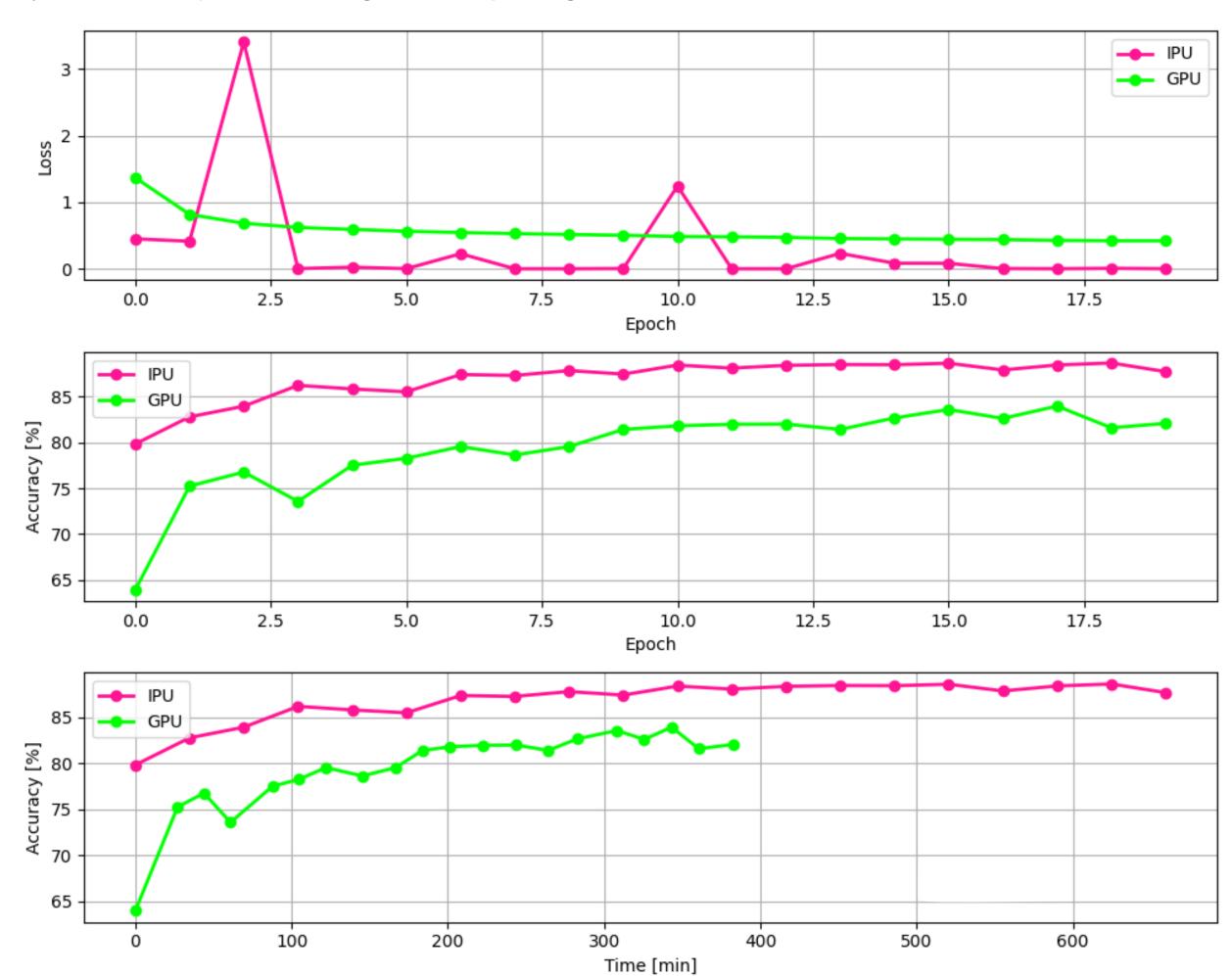
max accuracy: 84.51%

o time: 401.44min

#### IPUs:

max accuracy: 88.92%

o time: 694.03min









#### Distributed Butterfly Machine Learning with IPUs

Master Project work by Daniel Bogacz, May-August 2024

- torch.nn.Linear vs Butterfly Layers on Multi-IPU
  - Our previous results [Shekofteh et al. 2023] could be confirmed
  - High compression rate with Butterfly (97.17%)
  - Longer training time due to slow Butterfly implementation (Torch instead of Poplar)
  - Similar accuracy achieved (86.10% Butterfly and 88.65% nn.Linear)
- Multi-IPU vs Multi-GPU
  - More stable loss trajectory for GPUs than IPUs (different optimizer implementation)
  - 1.73x speedup in training time with GPUs (401.44min GPUs vs 694.03min IPUs)

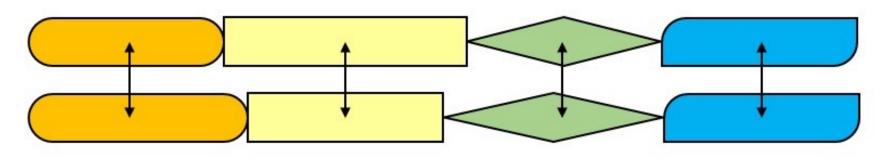




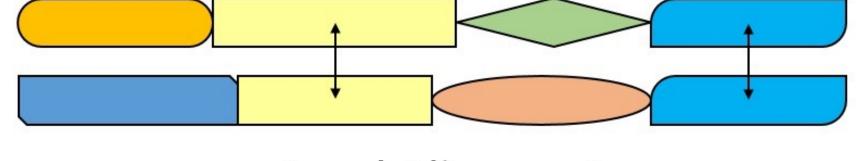
#### **Introduction to Bioinformatics**

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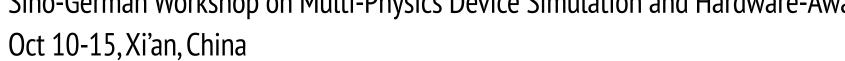
- Sequence Alignment problem
- A C T \_ \_ T T A T G C T A T G C \_ \_ G C
- Well-known solutions are dynamic-programming-based:
  - Needleman-Wunsch (NW): global alignment
  - Smith-Waterman (SW): local alignment
  - Semi-global methods: X-Drop
- Finding the optimal solution for these algorithms
  - quadratic time as a function of sequence length.
- Main properties of the problem and common solutions:
  - Irregularity in parallelization of dynamic-programming methods
  - Sparsity in some cases



**Global Alignment** 



Local Alignment

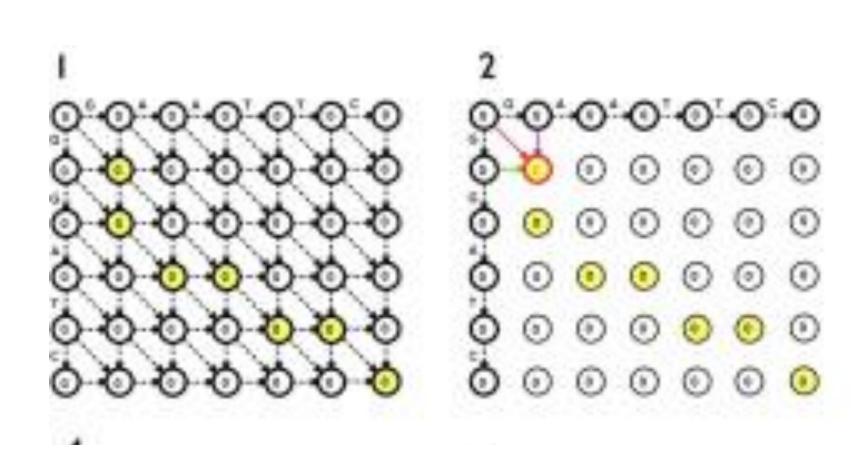






#### **Introduction to Bioinformatics**

Core computations in NW and SW



$$H[i,j] = 0, \forall i = 0 \text{ and } j = 0..n$$
 (2)

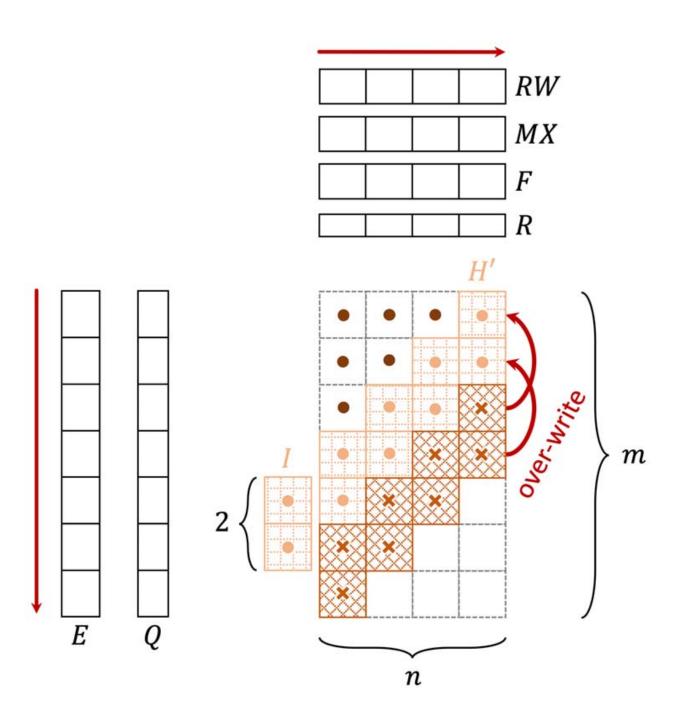
$$H[i,j] = 0, \forall i = 0..m \text{ and } j = 0,$$
 (3)

$$E[i] = \max \begin{cases} H[i, j-1] + GAP_{OPEN} \\ E[i] + GAP_{EXT} \end{cases} \quad \forall i = 1..m, \quad (4)$$

$$F[j] = \max \begin{cases} H[i-1,i] + GAP_{OPEN} \\ E[j] + GAP_{EXT} \end{cases} \quad \forall j = 1..n. \quad (5)$$

$$H[i,j] = \max \begin{cases} H[i-1,j-1] + S[Q[i-1],R[j-1]] \\ E[i] \\ F[j] \\ 0 \end{cases}$$

$$\forall i = 1..m \text{ and } j = 1..n,$$
(6)

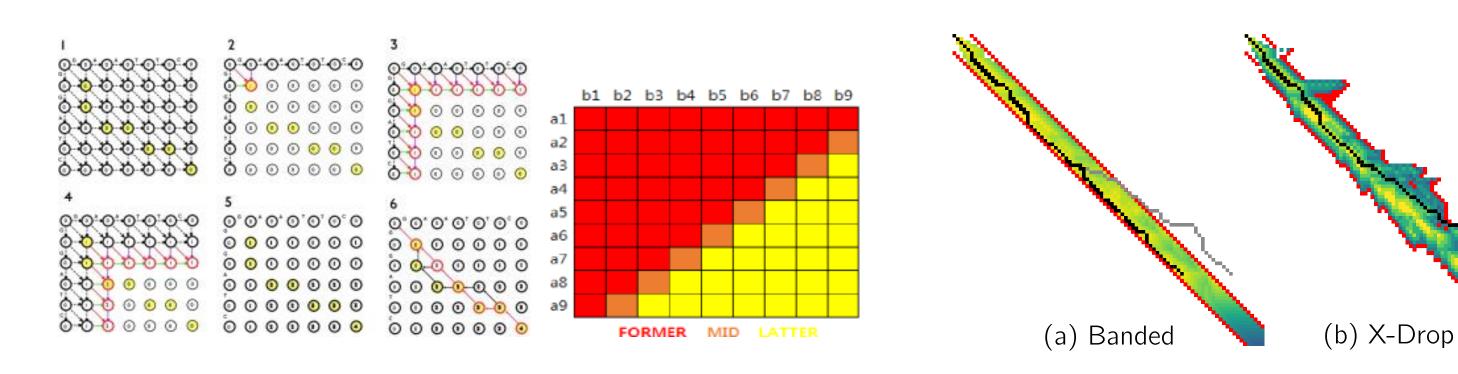






**Motivations: NW and SW** 

- X-Drop Method [1]
  - reduces the quadratic cost by dynamically searching only for a high-quality alignment and stopping the computation early when a good alignment is impossible
  - Good for long-read sequencing
  - Seems to be more scalable than NW and SW



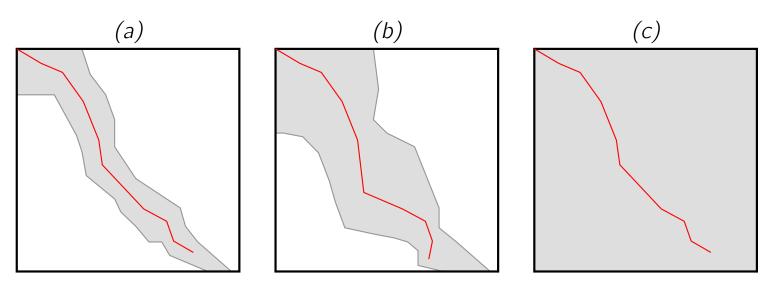


Figure 2: The red path is the optimal alignment, the gray area is calculated values, and the white area is non-calculated values. Due to the X-Drop condition, the white nonzeros contain a score of  $-\infty$ . Panel (a) shows an iteration with X = 10, (b) with X = 20, and (c) with  $X = \infty$ .





#### X-Drop Sequence Alignment Implementation on IPUs

Master Project work by Jonathan Hirsch, August 2024 - ...

- Memory is the most limitation on the IPU
- The idea first introduced by Burchard et al, in [1] for
  - Limited SRAM-based computation
  - Multi-IPU machines
  - Clusters of IPU machines
  - Long input sequences

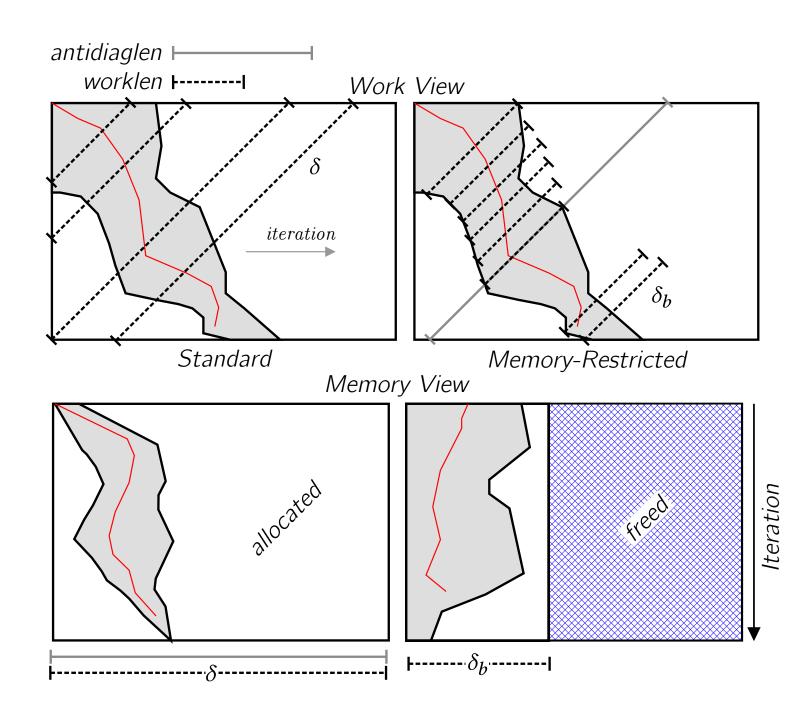
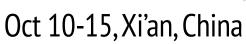


Figure 3: The antidiagonal length is  $\delta = min(|\mathcal{H}|, |\mathcal{V}|)$ . The memory-restricted version allocates work memory of  $\max_k |U_k - L_k| \le \delta_b \le \delta$ . The left side illustrates the standard algorithm (3 $\delta$  memory). The right side illustrates our algorithm (2 $\delta_b$  memory).







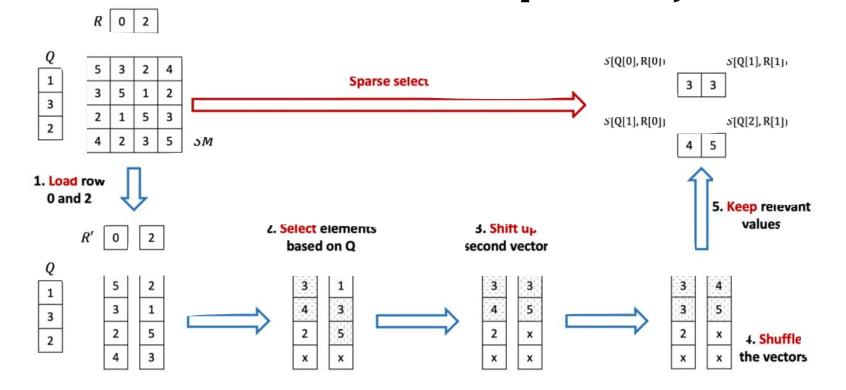
#### MIMD Kernels for Sequence Alignment on IPUs

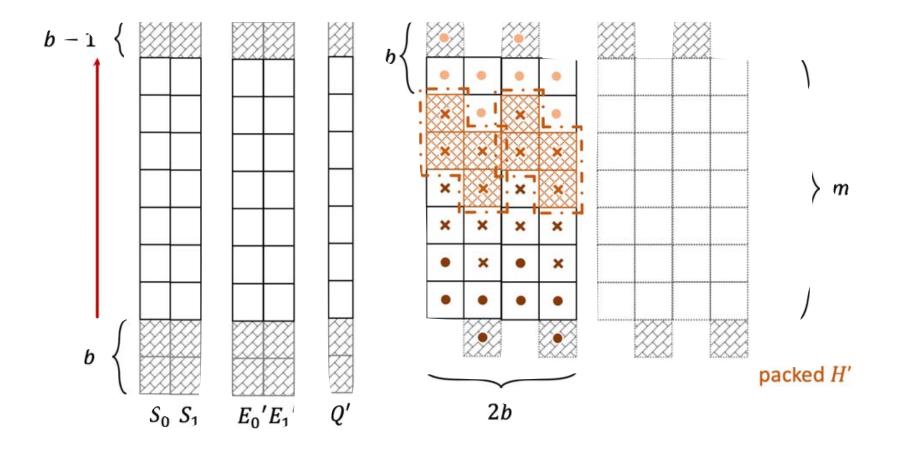
Master Project work and thesis by Jeremias Kunz, August 2024 - ...

- The project is defined based on a recent work by Popovici [1]
  - Target hardware: CPUs with SSE and AVX instructions to implement SIMD solutions for SIMD vector processing

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- The aim is to extend the work on the IPU
  - Make uses of the sparsity





[1] D. T. Popovici et al., "Designing Efficient SIMD Kernels for High Performance Sequence Alignment," 2023 IEEE International Parallel and Distributed Processing Symposium Workshops (IPDPSW), St. Petersburg, FL, USA, 2023, pp. 167-176, doi: 10.1109/IPDPSW59300.2023.00038





## Machine Learning Accelerators in Bioinformatics

### **Summary and Future Path**

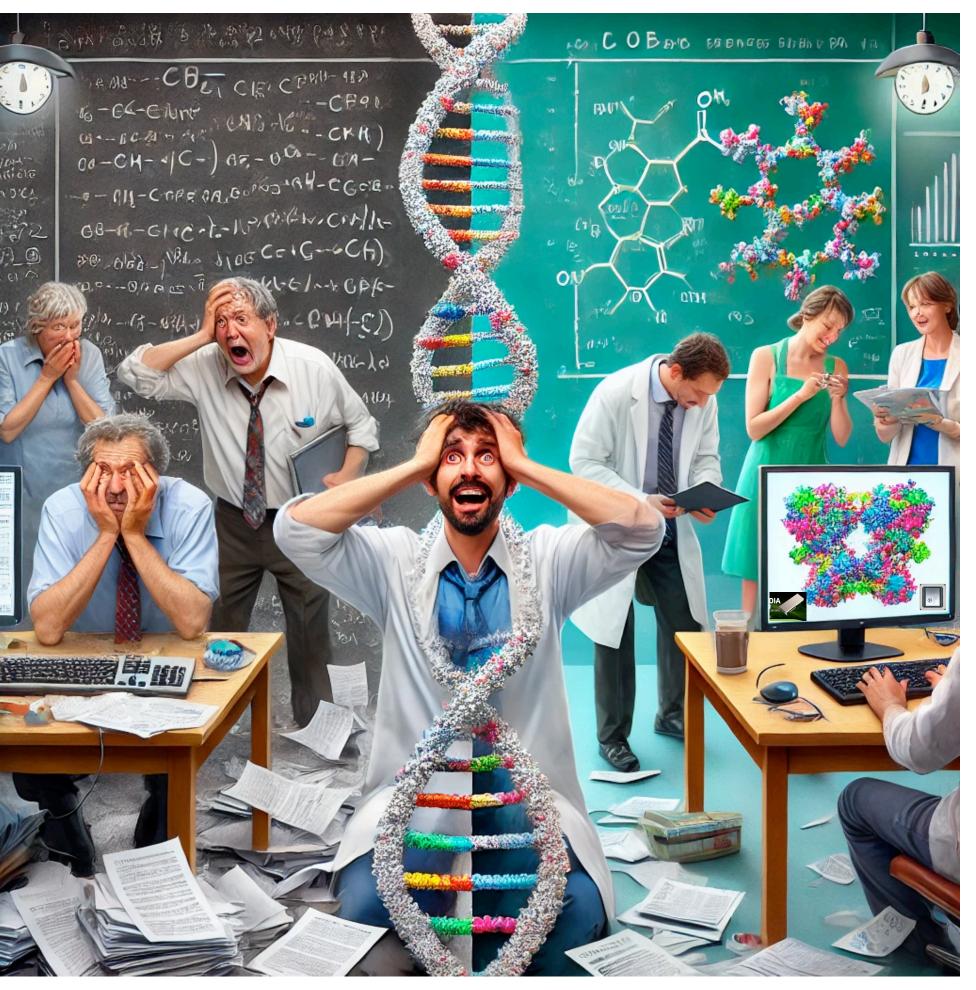


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