



Accelerated Computing in the Exascale Era

Jean-Pierre Panziera 01/06/2023

Eviden ID & leadership in HPC



Circa €5B revenue An Atos business that will become an independent company in late 2023

6 Business segments Digital Transformation, Smart Platforms, Cloud, Advanced Computing, Digital Security and Net Zero

57,000 engineers and problem-solvers in 45 countries

Supercomputing leadership

#1 Europe, India and S. America #3 worldwide

43 systems 500





Solving the BIG challenges

HPC to help meet BIG societal and industrial challenges

Public Science, top challenges:

- Climate
- Personal Medicine
- Renewable Energy ... and storage

• ...

Industry use HPC for better/safer/cheaper products, new materials, new drugs ...









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Need to scale solutions BIG times

E.g. Destination Earth project: building an Earth Digital Twin

- Today ECMWF run "ensemble simulations" with a 9km resolution grid
- For an accurate solution(clouds, topography...), a 1km resolution is needed
- The 9x grid refinement translates into a ~700x (9³) performance improvement
- To close the gap, looking at much larger systems and accelerators







Simulation

Observations

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CINECA - Leonardo Hybrid Pre-Exascale Supercomputer





"The Leonardo supercomputer is the result of our long-term commitment to pushing the boundaries of what a modern exascale supercomputer can be." Sanzio Bassini, Director of the HPC department at CINECA

10 ExaFlops FP16 AI workload 320 PFlops (Rpeak) 250 PFlops (Linpack)



4 PFlops (HPCG)







Xeon





Performance Flops vs Bytes

Solving PDEs with Linear Algebra Solvers



FASTER computing elements CPUs, GPUs, Accelerators ...

- Top500 Flops rate are impressive: ExaFlops, 100s PetaFlops ...
- ... but HPC applications do not run at Flops speed
- HPC applications are limited by the memory bandwidth
- HPCG benchmark better represents application behavior

	Peak Pflops	HPL Pflops	HPL eff HI	CG Pflops	HPCG eff
Frontier	1 686	1 102	65%	14,1	1,3%
Fugaku	537	442	82%	16,0	3,6%
Lumi	429	309	72%	3,4	1,1%
Leonardo	256	239	68%	3,1	1,5%
Summit	201	149	74%	2,9	2,0%

- GPUs offer highest BW: **2TB/s** for Nvidia A100 with HBM
- vs 200GB/s for fastest CPU AMD Millan with 8xDDR4 ... 10x
 But
- GPUs are "*challenging*" to program ... you might get lucky
- CPU can integrate HBM memory to boost their memory BW hence performance







Nvidia H100

Intel SPR+HBM

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Faster memory

for higher performance

Various strategy to provide more memory Bandwidth (\rightarrow more performance to HPC applications): <u>SDRAM:</u>

- Increase the number of DDR channels $(4 \rightarrow 6 \rightarrow 8 \rightarrow 12 \dots \rightarrow 16?)$
- DDR5: 4800MTs ... 9600
- MRDIMM: 2x capacity & BW vs DDR5
- LPDDR5x (8533MTs ... but with BGA)

<u>HBM:</u>

• HBM2, HBM2e, HBM3 in package

Next big thing:

- 3D stacking
- Memory on top of xPUs for 10-40x performance gain
- Processing-in-memory





Standard and backside







AI, AI, AI

AI have BIG impact on some traditional HPC workloads

NEWS | 28 July 2022 | Correction 29 July 2022

'The entire protein universe': AI predicts shape of nearly every known protein

DeepMind's AlphaFold tool has determined the structures of around 200 million proteins.



tool. Credit: DeepMind

communications

biology

ARTICLE

https://doi.org/10.1038/s42003-025-04773-7 OPEN

Does AlphaFold2 model proteins' intracellular conformations? An experimental test using cross-linking mass spectrometry of endogenous ciliary proteins

Caltiyn L. McCafferty 12, Frin L. Pennington¹, Ophelia Papoulas 12, David W. Taylor 12 & Edward M. Marcotte @ 192

A major goal in structural biology is to understand protein assemblies in their biologically relevant states. Here, we investigate whether AlphaFold2 structure predictions match native protein conformations. We chemically cross-linked proteins in situ within intact Tetrahymena thermophylo cilia and native ciliary extracts, identifying 12/5 intramblecular cross-links within the 100 best-sampled proteins, providing a benchmark of distance restraints obeyed by proteins in their native assemblies. The corresponding structure predictions were highly concordant, positioning 86.2% of cross-linked residues within Gu-to-Gu distances of 30 $\rm \AA$ consistent with the cross-linker length, 43% of proteins showed no violations, Most inconsistencies occurred in low-confidence regions or between domains. Overall, Alpha/old2

The structure of the vitellogenin protein — a precursor of egg yolk — as predicted by the Ap ... inconsistencies ... in low-confidence regions or between domains



Generative AT

Large Language Models



a BigScience initiative



176B params 59 languages Open-access

From today, determining the 3D shape of almost any protein known to science will be as simple as typing in a Google search.



🙊 Liburot, far upsiderbes.





10

AI acceleration: Artificial Intelligence for Simulation

e.g improving the weather for ecast radiative scheme with machine learning



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Emulate a complex and costly simulation of 3D radiative effects of clouds with simpler model and AI correction



Matthew Chantry, Peter Düben - ECMWF

Quantum Computing

QLM (Quantum Learning Machine) and soon real Qbits

3 main applications domains:

- Universal Quantum Computer
 Solving any inverse problem, including Integer Factorization (RSA)
- Quantum for Quantum problems
 Emulating molecules on Quantum devices
- Combinatorial optimization
 Finance, Energy grid, Crew assignments

Software solutions, e.g. Quantum Approximate Optimization Algorithm (QAOA)







Multi-Partition systems for HPC workloads

Ultra fast "disaggregated" Data access



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Accelerated Computing in the Exascale Era

The next BIG thing in Exascale HPC is :

- Data, Data, Data ...
- Exascale Bandwith → orders of magnitude improvement required
- Energy efficiency → Specialized accelerators / Multi-Partition systems
- New Algorithms for HPC Applications \rightarrow Includes AI software acceleration
- New computing paradigms → Analogic, Neuromorphic, Quantum ...
- Data, Data, Data ...



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