Welcome to the waitless world

March 4, 2021. UK-Durham Univ.

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Cognitive Solutions Update



Agenda Topics

Power Systems

End to end solution design/portfolio for HPC/AI for Life Sciences from IBM Systems.

- Using Tuned and Optimized Server/Storage/Network/Software pipeline to achieve 2,5,10x faster "Time to Answer".
- Genomics Solutions- 10x performance over standard Intel operation.
- High Resolution Microscopy 2X faster Time to Answer
- Structural Biology Simulation- 5,10,20x faster simulation
- NA Supercomputer Systems in Academia and Government
- Server Solutions for Computational Science
- Storage solutions for High density or High-speed low density
- Parallel File System optimized for HPC
- Bayesian Optimization for HPC
- Hybrid Cloud- Orchestration
- Power10 Memory Clustering

Welcome to the waitless world

We build fast computational "cars". End-to-End



Power Systems

"Time to Answer" Is a competitive and scientific advantage.



Single Vendor Support



Storage Technologies "The Fuel"

Network Technologies "The Fuel Lines"

Server Technologies "The Engine"

Software Defined Infrastructure/Scheduler/Orchestrator "The Drive Train"

Systems tuned front to back to produce results instead of economical parts assembly.



Improve time to results. Impact more lives.

We are living through an unprecedented moment for humanity that touches every aspect of business, technology and culture. The global pandemic caused by COVID-19 demands answers now.

IBM delivers faster insights with greater efficiency to impact more lives.

High-performance Data & AI deploys against this problem at massive scale and reduces time spent delivering life-saving insights through unique load balancing and model optimization technologies delivered by cutting-edge IBM lab research.



Smart loves problems, and there has never been a bigger problem facing our world.

Genomics

Molecular Simulation

Biomolecular Structure



Medical Diagnostics AI

Data Fusion and AI

Bio-Informatics

Artificial intelligence and high-performance computing have already begun to attack the virus, assisting in molecular drug discovery, genomics and medical image processing.



Five key challenges to progress remain despite advances











- Data \bullet **Overload**
- Oceans of • data arise from rapid digitization and instrumentatio n of healthcare.
- **App Chaos** ullet

not all

- •
- Thousands of applications, workflows and models are following the same rules.
- Adoption
- Vertically integrated toolsets with heavy customization and vendor lock-in create work silos.
- Performance
- When scaling up or out, most institutions cannot diagnose or analyze the performance problems they face.

Cost

Demanding workloads require wellorchestrated infrastructure to manage, monitor and control costs.

Optimizing Medical Imaging

Enhance image identification with deep learning to assist physicians and benefit patients

20x faster









Optimizing Precision Genomics

Reduced time-to-completion for long-running jobs while increasing resource

100,000+







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IBM Accelerates Medical Research Tasks



GENOMICS

Biomarkers detection, biodata modeling and statistics data visualization



Image classification using AI with flexible, targeted models in open frameworks



Drug discovery via modeling of macromolecule receptors and smallmolecule ligands

→ ← Data Fusion

Synthesize and model diverse data using data fusion, natural language processing, and machine learning

BIOMOLECULAR STRUCTURE

Cryo-EM image restoration and refinement analysis for drug design and discovery



Cross Discipline Informatics Relatioanships AI



IBM

A framework for designing, deploying, growing and optimizing infrastructure for HPC, AI and Cloud, created in collaboration with world's leading healthcare and life sciences institutions, and using Red Hat OpenShift, IBM Power Systems, IBM Storage and open API endpoints.



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The Data: Biological Data Analytics



Biological Data Analytics

- Genomic Sequence Data: an explosive growth of biodata
 - □ Sequence alignment
 - Variant discovery and characterization
 - Genomic profiling and pattern discovery
- Biomarker Identification: gene expression profile, RNA-seq, ChIP-seq, microarray identification and validation, etc.
- Structural Bioinformatics: identify and predict 3D biomolecule structures, such Cryo-EM data refinement, molecular dynamic simulation, NMR, x-Ray crystallographic data, etc.
- Biodata Modeling & Statistical Analysis: biological pathways analysis, Gene, clinical data cohorts study, data extraction, etc.
- Medical Image Processing: image segmentation, registration, statistic modeling.
- Biodata Visualization: 3D molecule structures, genomics sequences visualization, etc.

The Challenges: Analyzing Explosive biological data

Solutions



Data Explosion

Power Systems



Data Storage

Computation



High throughput and optimized workload pipelines to accelerate biodata analysis with highly optimal and parallel I/O, memory, CPU and GPU computations.

Large volume and variety of data around genomic sequences, gene expression, images, structural biomolecules. clinical and healthcare information, personized medicine data

High performance and high throughput storage hierarchy required for data loading, extraction and computation. **Tertiary storage** required for archive and store. Storage tools for data indexing, discovery and governance.

High performance and efficiency of software tools and applications for genomic variants and biomarkers analysis, drug discovery, medical image processing and molecule structure modeling, data visualization.



What are the components of the IBM Solution

- Same components that are used at the Oak Ridge and Lawrence Livermore U.S. National Laboratories.
- IBM Power9 Servers w GPUs
- IBM Elastic Storage Systems
- Spectrum Scale Parallel File System
- IBM Spectrum Discover MetaData Catalog
- Advanced AI Tools



IBM Systems @ Oak Ridge



Summit System

•4608 nodes, each with:
•2 IBM Power9 processors
•6 Nvidia Tesla V100 GPUs
•608 GB of fast memory
•1.6 TB of NVMe memory

•200 petaflops peak performance for modeling and simulation

•3.3 ExaOps peak performance for data analytics and AI

Spectrum Scale V577 Elastic Storage Servers

#1



2.5 TB/sec

Throughput to storage architecture

250 PB file system

HDD storage capacity



Challenges for the world's smartest supercomputer for open science

Combating Cancer

Through the development of scalable deep neural networks, scientists at the US Department of Energy and the National Cancer Institute are making strides in improving cancer diagnosis and treatment.



Predicting Fusion Energy

Predictive AI software is already helping scientists anticipate disruptions to the volatile plasmas inside experimental reactors. Summit's arrival allows researchers to take this work to the next level and further integrate AI with fusion technology.



Deciphering High-energy Physics Data

With AI supercomputing, physicists can lean on machines to identify important pieces of information—data that's too massive for any single human to handle and that could change our understanding of the universe.

Identifying Next-generation Materials

By training AI algorithms to predict material properties from experimental data, longstanding questions about material behavior at atomic scales could be answered for better batteries, more resilient building materials, and more efficient semiconductors.



** Hyperlinks to customer websites within the logos.

Cryo-EM Application Enablement on Power9

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Power Systems The Solution: Accelerated Computing Platform (ACP) Welcome to the waitless world



Hardware Building Blocks



AC922

8335-GTG

2-4 GPUs

IB and Ethernet switches & UFM (Mellanox) shared 4-18 compute nodes 0-5 login nodes Per rack

L922 9008-22L

1-5 Mgmt. nodes Per rack



0-1 ESS per cluster P8 any model (optional)



Solutions Stacks



• High performance & scalability

- RHEL7.6, CUDA, ESSL,
 SMT,GPFS, NVMe …
- Optimized workload pipelines, e.g., GATK4, RELION ...
- PowerAI, TensorFlow, Caffe ...
- Application interoperability & manageability
- Docker container, k8s, LSF ...
- Anaconda, python, Jupyter ...
- MPI, XLC/C++, GCC, AT ...
- Data management & governance
- Spectrum Discover

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ACP Solutions for Cryo-EM

Small	Medium	Large	RELION Clas	ss3D Sta	tandard Benchmark Runtin				
		20.90	Dataset Power8		Power9		Power9		
3-5 samples per day	10-15 samples per day	15+ samples per day	<i>Pf.</i> ribosome	71 mi	n. 60	min.	44	min.	
1 40-core IC922 node, GPUs + 512	2 40-core IC922 nodes, 512GB Mem +	4-8 40-core IC922 nodes, 512 GB Mem			Steps	P8 + 4 P100	P9 + 4 V100	P9 + 16 V100	
GB Mem	4 GPUs each	+ 4 GPUs each	Perf RELIC Class	DN 3D	Estimated GPUs	35	28	9	
GL2 (GPFS) with IB	GL4 (GPFS) with IB	GL4 (GPFS) with IB		Ļ	Estimated FFTW	12	11	11	
adapter	adapter	adapter	1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 - 1999 -		Others	24	21	24	
One SSD (NVMe)	2 SSDs per node (NVMe)	2 SSDs per nodes (NVMe)			Total Runtime (minutes)	71	60	44	
Ethernet	IB	IB		K,	* Running on GPF	S with SSD	as scratch d	irectory	

Optimized RELION software stack running on RHEL 7.6 with 4 SMTs per core.

(https://www.emdataresource.org/EMD-2660)



RELION: cryo-EM Restructure Refinement

RELION (for Regularized Likelihood OptimizatioN)

- Widely-used processing software package for macromolecular structure determination by single-particle analysis of cryo-microscopy (cryo-EM) images.
- Use an empirical Bayesian approach to refinement of 3D reconstructions or 2D class averages from cryo-EM data
- RELION pipeline

Power Systems

- □ Use pipelined approach for the entire single-particle workflow
- GPU and CPU acceleration to reduce its computational costs
- Its functionality was expanded with the incorporation of sub-tomogram averaging and helical reconstruction.

RELION IBM Power Support

- □ Latest version (3.1) is supported on Power9 with GPU + CPU
- □ Optimized performance on CPU + GPU cluster environment
- □ Use HPDA solution including IBM ESS, Power and IBM Spectrum LSF







RELION: High Level Flowchart

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A) Operations and the real vs. Fourier spaces used during B) image reconstruction in RELION.

Source: https://elifesciences.org/articles/18722

Benchmark Data: Plasmodium falciparum 80S ribosome

Std 0.044

105,247 particles

Reference Map

Map File Size	182 MB
Voxel Dimensions (Å)	1.34 x 1.34 x 1.34
Map Dimensions (voxels)	360 x 360 x 360
Map Data Type	Image stored as Reals
Density Statistics	Min -0.545 Max 0.962 Avg 0
Recommended Contour Level	0.18



(https://www.emdataresource.org/EMD-2660)

RELION performance: Power9 T4 vs. x86 V100 Welcome to the waitless world



* Power9-T4: 40 cores, 1TB DDR4 memory, 4 Tesla T4 GPUs

* X86: Xeon Gold 6140 (Skylake), 40 cores, 0.5TB DDR4 memory, 4 Volta 100 GPUs

Table C. RELION Single Node Performance						
# No. GPUs	P9-T4	X86-V100	P9 vs. x86			
2	61.69	119.13	1.93			
4	45.67	83.00	1.82			

- RELION benchmark dataset is downloaded from official website[1]: 105,247 particles; 360 x 360 pixels
- X86 benchmark results were obtained from the Ward Lab of The Scripps Research Institute [2]
- GPUs connected with PCIe ports. The P9 results are optimized with IBM ESSL and Spectrum MPI and runtime options for SMTs. X86 results are optimized with MKL.
- P9 with Tesla T4 are more than 80% better than x86 with Volta 100. P9 + T4 delivers superior price performance.



RELION Performance: P9-T4 vs. x86-V100 (min.)

RELION performance: Power vs. x86 vs. DGX Welcome to the waitless world



- * Power9: AC922, **1 node**, 4 V100 GPUs.
- * Power9-T4: 1 node, 4 Tesla T4 GPUs
- * Power8: Minsky, 1 node, 4 P100 GPUs
- * X86: Xeon Gold 6140, **1 node, 4** V100 GPUs.
- * DGX: DGX-1, **one node** with 8 GPUs

Table C Benchmark Performance Comparisor

P8-P100	P9-T4	P9-V100	X86-V100	DGX-1 V100
71.02	45.67	42.33	83.00	77.00

- RELION benchmark dataset is downloaded from official website[1]: 105,247 particles; 360 x 360 pixels
- X86 and DGX-1 benchmark results were obtained from the Ward Lab of The Scripps Research Institute [2]. DGX-1 not using " preread_images", which requires additional memory.
- Power9 outperforms x86 and DGX-1 with the same number of GPUs.

RELION PERFORMANCE BENCHMARK (SINGLE NODE, RUNTIME IN MINUES)



(lower is better)



IBM

Anaconda Environment for Applications

- Use anaconda enterprise network (AEN) to manage cryo-EM software repository on server.
- Easy to use and update software

Anaconda Architecture for Cryo-EM Analysis @ @ @



	D ANA Powered b	y Continuum Analytics								
	Files	Running	IPython Clusters	conda						
	3 Conda ei	nvironments								+ 3
	Action	Name		Default?	Directory					
	් එ ඕ	root			/opt/waka	ri/a	anaconda			
S	් එ ඕ	default		~	/projects/a	аег	n_admin/TestProject/envs/	default		
	් එ ඕ	myenv			/projects/a	аег	n_admin/TestProject/envs/	myenv		
	2 available	packages		numpy	>		39 installed packages in er	ivironment "myen	۷"	2 ~ 4 m
	Name		Version (Channel			Name	Version	Build	Available
	🗹 nump	у	1.13.1 0	defaults			anaconda-client	1.6.3	ру36_0	
	🗆 nump	bydoc	0.7.0	defaults			🗆 certifi	2016.2.28	ру36_0	
							Clyent	1.2.2	ру36_0	
							decorator	4.1.2	ру36_0	
							🗌 ipykernel	4.6.1	ру36_0	
							ipython	6.1.0	ру36_0	



ACP Solutions for Genomics

Small	Modium	Largo	Optimized G	Practice Pipel	ine Rur	ntime			
Sman		Large	Dataset	30	Ox WES		50x WGS	Refer	ence
1-2 samples	4-6 samples per	10+ samples per	NA12878	12	<u>2 m</u>	<u>nin.</u>	8.7 hrs.	GRCH37	(HG37)
per day	uay	udy					STEPS	WES	WGS
1 40-core	2 40-core AC922	4-8 40-core					Bwa + samtools	1.92	215.4
AC922 node,	nodes, each	AC922 nodes,					markDuplicates		63.0
512 GB Wem	STZGB Wem	each 512 GB				ga	tkBaseRecalibrator	0.58	19.8
		Mem	Perf Practice	Perf GATK4 Best Practice			gatkApplyBQSR	0.40	24.6
GL2 (GPFS)	GL4 (GPFS) with	GL4 (GPFS) with	Pipeline	•		ga	atkHaplotypeCaller	0.99	150.1
with IB	IB adapter	IB adapter			L	g	atkCombineGVCFs	1.73	-
adapter						ga	atkGenotypeGVCFs	1.40	3.0
Ethernet	IB or Ethernet	IB or Ethernet				gatk\	/ariantRecalibratorSNP	2.23	31.8
						g	atkApplyVQSRSNP	0.15	1.8
Optimized genomic software stack running on RHEL					gatkV	ariantRecalibratorIndel	0.25	9.5	
7.6 with 4 SMT	s per core.					ga	atkApplyVQSRIndel	0.14	1.8
		tolona problem				Tota	Runtime (minutes)	112.27	520.8
==	POWER9	ans problems proble							

 Using 30x coverage WES dataset (gcat_set_025) to run benchmark GATK4 Germline pipeline with reference genome GRch37 on both Power9 (PowerNV 8335-GTC) and x86 (Gold 6148 @ 2.40GHz). The performance results shown below.

12.27

133.32

C	GATK4	Gerr	nline Runtime		
Dataset	Power	^r CPU	X86 CPU	Ref Ge	enome
30x WES	12 r	nin	133 min	GRCH37	(HG37)
3			STEPS	Power9	X86 std
Power9 run 11x	faster		Bwa + samtools	1.92	5.07
than x86 Skylako	with		markDuplicates	1.74	5.29
	VVILII	gatkBaseRecalibrator gatkApplyBQSR		0.58	9.89
optimized scripts	,			0.40	2.88
while the output	VCF	ga	gatkHaplotypeCaller		101.92
files are 95 - 99 9	6	g	atkCombineGVCFs	1.73	-
concordance bet	ween	ga	tkGenotypeGVCFs	1.40	2.59
the two architect	tures	gatkV	ariantRecalibratorSNF	2.23	3.57
the two architectures.		g	atkApplyVQSRSNP	0.15	0.14
		gatk\	/ariantRecalibratorInd		
			el	0.25	0.98
		ga	tkApplyVQSRIndel	0.14	0.08

GATK4 Best Practices



Source : https://software.broadinstitute.org/gatk/bestpractices/workflow?id=11145



GATK4 WGS Pipeline Performance: Power9 vs. Skylake (x86)

- GATK: Genomic Analysis Toolkit, a JAVA-based tool used for genomic sequence variant analysis ٠
- Runs poorly "out of the box" on POWER9 relative to Skylake, 8% slower, core-to-core comparison •
- Improves performance by software and runtime optimization nearly **10x times** •

Dataset Powe	r9 CPU	X86 CPU	Ref Ge	enome		
50x NA12878	5h	79h	GRCH38	(HG38)		
>>Most tools run with	GA	FK Pipeline STEPS	Power9	X86		
single threads	B۱	VA + SortSAM	4.66	12.61		
Poor single	n	narkDuplicates	8.65	8.15		
core/thread	gatk	BaseRecalibrator	9.49	8.39		
performance on	g	atkApplyBQSR	9.83	6.11		
Power9	gat	kHaplotypeCaller	51.73	42.88		
>>SIMD capacity	gat	kGenotypeGVCFs	0.48	0.29		
• 128-bit P9 VSX vs.	gatkVa	riantRecalibratorSI	NP 0.40	0.38		
512-bit x86 AVX	gat	kApplyVQSRSNP	0.03	0.02		
>> Thread scheduling	gatkVar	iantRecalibratorIn	del 0.15	0.10		
Active threads are	gatl	kApplyVQSRIndel	0.02	0.02		
fewer on P9		Total(hours)	85.44	78.95		
Thread waiting						

		Afte	er Opt	imizatior			
	Dataset	Powe	r9 CPU	X86 CPU		Ref Ge	enome
50	Dx NA12878	8.7h		23h		GRCH38	(HG38)
>> B	enefit from S	ΜΤς	GA	TK Pipeline STEPS		Power9	X86
•	Split data to u		В	WA + SortSAM		3.59	10.61
SMT threads concurrently. >>Use optimal code				mark Duplicates		1.05	8.21
			gat	kBaseRecalibrator		0.33	0.30
				gatkApplyBQSR		0.41	0.29
• [Modify marking			tkHaplotypeCaller		2.50	2.71
C	duplicates toc	bl	gat	tkGenotypeGVCFs		0.05	0.26
>> V	Vorkloads	gatkVa	ariantRecalibratorS	NP	0.53	0.36	
Rebalance workloads			ga	tkApplyVQSRSNP		0.03	0.02
			gatkVa	riantRecalibratorIr	ndel	0.16	0.10
			gat	kApplyVQSRIndel		0.03	0.02
				Total(hours)		8.68	22.88



Welcome to the waitless world

Molecular Dynamics

Using computational approach to simulate atomic motions, to model macromolecule receptors and their small-molecule ligands in Covid-19 drug discovery, design and prediction.



Molecular dynamics simulation





A) Using NAMD to simulate influenza virus (left)and Covid-19 (right)



C) *In silico p*rediction of protein cryptic binding site



B) Drug discovery: protein receptor



D) Predicting protein receptor ligand binding energy



NAMD STMV benchmark





- ~1 million atoms are simulating on Power9 and x86 with the same configurations.
- Higher is better.



- 221 million atoms are simulating on Summit cluster with memory optimization.
- The simulation uses 4 GPUs per node.

AMBER 18 performance comparison

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• Power9 AC922 outperforms x86 on both CPU and GPU in all benchmark executions.



Brief Intro of IBM Bayesian Optimization Accelerator.

- BOA is an AI Software package.
- Subscription Service license per year.
- Licensed by the # of BOA Server(s) (only runs on IBM AC922).
 - Sizing is dependent on the number of simultaneous Jobs BOA is processing against.
- BOA software generally completes the AI analysis in under 1 minute after the input from the "interface" is received.
- Jobs on external HPC systems can be paused to wait for BOA input for the next run.
- BOA is very specific to each scientific discipline and use case.
 The Interface is " re-usable" custom Python code per analysis type.

BOA Topology

- BOA servers are dedicated to running BOA only
- Physically co-located with the HPC environment
- Large BOA systems include multiple GPU enabled nodes for throughput
- Multi-user, multi simultaneous experiments being simulated in the HPC



Real Examples of HUGE Value with IBM BOA



Computational Fluid Dynamics

Chip Design

Oil & Gas



BOA accelerated workflow uses 1/3 of the calculations to achieve 4 orders of magnitude resolution increase







The BOA enabled design process accomplishes in hours what a designer does in weeks

Orders of magnitude fewer simulations required to minimize jitter for signal integrity on the Power10 server

Carbon sequestration use case where BOA identified an answer 1.5% better in 1/3 the time

Interface Functions













Formula 1 Racing simplified nose design

- 7 design variables corresponding to geometry of vanes in the wing
- openFOAM CFD simulator used to calculate DRAG @ each iteration
- Normally this kind of design is done by hand by aerodynamics experts



Design Challenge: Optimize the communication speed of the links shown in green using minimum time & compute resources

Brute force method for design space exploration requires ~5600 simulations, each taking ~20 minutes (IBM Simulator: HSSCDR)



Traditional Method ('brute force')

IBM Bayesian Optimization Accelerator

A Portfolio for the AI Era

Welcome to the waitless world

 Accelerated Compute
 Data, Inferencing, and Cloud
 Big Data

 PowerVM and high RAS
 AC922
 IC922
 EU22

 L922
 LC922 / LC921
 IC922 / LC921

- Industry leading reliability and computing capability
- PowerVM ecosystem focus for outstanding utilization
- Focus on memory capacity with up to 4TB of RAM
- Industry first and only in advanced IO with 2nd Generation CPU - GPU NVLink delivering ~5.6x higher data throughput
 - Up to 4 integrated NVIDIA "Volta" GPUs air cooled (GTH) and up to 6 GPUs with water cooled (GTX) version
 - OpenCAPI support
 - Memory coherence

- Storage dense, high bandwidth server – up to 24 NVMe or SAS/SATA in 2U¹
- Advanced IO with PCIe Gen4
- Optimized inferencing server with up to 6 Nvidia T4 GPUs at GA and additional accelerators in roadmap¹
- OpenCAPI support¹
- Price/performance server

- Big Data server with up to 120TB storage capacity, large form factor support, KVM support, leveraging P9 compute for a composable design
- 1U and 2U form factors
- Advanced IO with PCIe 4.0/CAPI 2.0
- Up to 44 cores (2U) or 40 cores (1U) at lower frequency

IBM AC922 GPU Server

Realize unprecedented performance and application gains with POWER9 and NVLink 2.0

- Up to 4 GPUs per server for Deep Learning Training
- Contains all the advanced IO NVLink 2.0, PCIe 4.0 and coherence
- Water cooled option improving data center and computing efficiency

- 2-socket, 2U Packaging
- Processors up to 40 POWER9 cores
- Up to 4 NVIDIA Volta GPUs
- 2 TB Memory (16 DIMMs)
- 4 PCIe Gen4 Slots
- 2x SFF (HDD/SSD), SATA, 7.7 TB storage
- Supports 1.6TB and 3.2TB NVMe Adapters
- Redundant Hot Swap Power Supplies and Fans
- Air cooled Processor and GPU's for maximum performance
- Default 3 year 9x5 warranty, 100% CRU

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GPU Accelerator comparison

POWER8 with NVLink 1.0 Pascal Technology

POWER9 with NVLink 2.0 Volta Technology

- This slide highlights the outstanding advantage in performance the P9 and Volta GPU combination provides over it's predecessor. The performance bump is achieved in 2 ways.
- 1) The bus speed increases from 20Gb/s to 25Gb/s.
- 2) There is a wider bus, increasing from 2 Bricks to 3 Bricks. (1 Brick contains 8 lanes)
- The combination of bus speed and increased bus width allows for the 87.5% performance jump.

Designed for data to deliver performance at scale

These design decisions result in best performance for data centric workloads like: **NoSQL and Relational Databases, Big Data Analytics, OLTP, ML/DL**

Power System IC922 for DATA

NVMe and PCI Gen4 capability designed to be the fastest compute and data server available

- Balanced storage, network, and memory design for optimized storage rich solutions
 - 33% more bandwidth (340 GB/s DDR BW on IC922 vs. 255 GB/s BW on x86)
 - Better memory capacity capability with 32 DDR4 RDIMM slots (competition needs bigger-sized, higher cost DIMMs)
- Rich storage capacity up to 24 SAS/SATA drives
- Total 10 PCIe slots PCIe Gen4 slots available to support high speed network connectivity
 - 2x throughput capability for high performance tiers

Genomics and CryoEM Recommended Server

Better Nvidia T4 GPU Hosting Capability

2U IBM IC922^a

Reference 2U Intel Xeon Gold 6XXX ^b

IC922 scales up to 8 Nvidia T4 GPUs¹ with 6 hosted at full PCI-e bandwidth, for a total of 40% greater PCIe bandwidth and >30% greater memory bandwidth than a reference Intel Xeon Gold 6xxx System

^a - IC922 optional PCI-e Gen4 riser

- Cisco c240 M5 with Intel Xeon Gold 6xxx CPU

Welcome to the waitless world

Brief Intro to Power10 Memory Clustering Technology

Slides taken from the 2020 Hot Chips conference proceedings.

Socket Composability: SCM & DCM

POWER10

and and a

.....

Single-Chip Module Focus:

- 602mm² 7nm (18B devices)
- Core/thread Strength
 - Up to 15 SMT8 Cores (4+ GHz)
- Capacity & Bandwidth / Compute
 - Memory: x128 @ 32 GT/s
 - SMP/Cluster/Accel: x128 @ 32 GT/s
 - I/O: x32 PCIe G5
- System Scale (Broad Range)
 - 1 to 16 sockets

Dual-Chip Module Focus:

- 1204mm² 7nm (36B devices)
- Throughput / Socket
 - Up to 30 SMT8 Cores (3.5+ GHz)
- Compute & I/O Density
 - Memory: x128 @ 32 GT/s
 - SMP/Cluster/Accel: x192 @ 32 GT/s
 - I/O: x64 PCIe G5
 - 1 to 4 sockets

Up to 4 DCM Sockets

IBM POWER10

(Multi-socket configurations show processor capability only, and do not imply system product offerings)

stantant.

......

Memory Clustering: Distributed Memory Disaggregation and Sharing POWER10

Use case: Share load/store memory amongst directly connected neighbors within Pod Unlike other schemes, memory can be used:

- As low latency local memory
- As NUMA latency remote memory

Example: Pod = 8 systems each with 8TB Workload A Rqmt: 4 TB low latency Workload B Rqmt: 24 TB relaxed latency Workload C Rqmt: 8 TB low latency plus 16TB relaxed latency

All Rqmts met by configuration shown

POWER10 2 Petabyte memory size enables much larger configurations

IBM POWER10

(Memory cluster configurations show processor capability only, and do not imply system product offerings)

Memory Clustering: Enterprise-Scale Memory Sharing

POWER10

Pod of Large Enterprise Systems Distributed Sharing at Petabyte Scale

6400 THREADS 800 CORES, SHARED MEMORY

Or Hub-and-spoke with memory server and memory-less compute nodes

(Mamony elector configurations about processor conchility only and do not imply system product efferings)

Memory Clustering: Pod-level Clustering

POWER10

Use case: Low latency, high bandwidth messaging scaling to 1000's of nodes

Leverage 2 Petabyte addressability to create memory window into each destination for messaging mailboxes

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Storage Solutions in the Life Sciences Platform

IBM Systems

Where is the data?

Metadata is the structured data about the unstructured object

IBM Spectrum Discover

- <u>Who</u>, <u>what</u>, <u>when</u>, <u>where</u>, and <u>why</u> of account, container, object, stream, dir, file
- Perfect for indexing and searching
- Metadata may be separate from the data, stored with the data, or derived from the data
 - Posix inode plus extended attributes
 - Standard document headers (doc, ppt, mp3, dicom, pdf, jpeg, GeoTIFF)
 - Custom metadata tags
 - AI derived metadata

System Metadata

Location Size Owner Group Permissions Last-Modified ...

Age, Biomarkers, Developmental Stage, Cell Surface, Markers, Cell Type/Cell Line, Disease State, Extract Molecule, Genetic Characteristics, Immunoprecipitation,

10 May 2021/ © 2018 IBM Coantibody, Organism, © 2016 IBM Corporation

IBM Spectrum Discover Provides unified metadata management and insights for heterogeneous file and object storage, on-premises and in the cloud.

Discover

Automatically ingest & index system metadata from multiple file & object storage systems on-prem & in the cloud

Classify

Automatically identify and classify data, including sensitive and personally identifiable information

Label

Enrich data with system & custom metadata tags that increase the value of that data

Find

Find data quickly and easily by searching catalogs of system & custom metadata

Data Insight

IBM Spectrum Discover

- Simple to deploy
 (VMware virtual appliance)
- Metadata curation
- Custom metadata tagging
- Automatic indexing
- Policy-Engine
- Action Agent API

Activation & Optimization

Large-Scale Analytics

- Data discovery
- Dataset identification
- Data pipeline progression

Data Governance

- Data inspection
- Data classification
- Data clean-up

Data Optimization

- Archive / tiering
- Duplicate data removal
- Trivial data removal

Scanning & Event Notifications

IBM Spectrum Scale: Spectrum Discover / Sept. 23, 2019 / © 2019 IBM Corporation

Power Systems

Spectrum Discover Dashboard

Search

Report

Agents

Access

ŝ

8 Monitor storage $\hat{\mathbf{O}}$ utilization and Home data recommendations 0 (Move/Archive) 0

Preview capacity use by data facet

- Classification
- Owner
- File Type ٠
- Etc.

 \bigcirc

neteocean1 (71 74%)

metaocean3 (4.44%

Total indexed data and capacity

Duplicate file or object candidates

- Number
- Capacity used

Data capacity by group/collection

- Customer defined
- Lab/Project/etc.

Data lake with IBM Spectrum Scale,

Nelcome to the waitless world

IBM

Consolidate all your unstructured data storage on Spectrum Scale with unlimited and painless scaling of capacity and performance

Unleash new storage economies on a global scale.

© 2016 IBM Corporation

IBN

IBM Elastic Storage Server (ESS) Integrated scale-out data management for file and object data

Optimal building block for high-performance, scalable, reliable enterprise Spectrum Scale storage

- Faster data access with choice to scale-up or scale-out
- Easy to deploy clusters with unified system GUI
- Simplified storage administration with IBM Spectrum Control integration

One solution for all your Spectrum Scale data needs

- Single repository of data with unified file and object support
- Anywhere access with multi-protocol support using protocol nodes - NFS 4.0, SMB, Object
- Ideal for Big Data analytics including full Hadoop transparency

Ready for business-critical data

- Disaster recovery with synchronous or asynchronous replication
- Ensure reliability and fast rebuild times using Spectrum Scale RAID's dispersed data and erasure code
- Five 9s (99.999%) of availability

ESS 3000

ESS 3000 cluster

Elastic Storage Server cluster

ESS Ecosystem

IBM Storage for Data and Al

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1Q21 ESS Release - New SL7 Model of ESS 5000 IBM Storage for Data and Al

Announce: Feb 23, 2021 GA: Mar 12, 2021

ESS 5000 New Supported Models:

New SL7

- Up to 8.8 PB Raw Capacity in a single 42U rack*
- Up to 66 GB/s in a single 42U rack**

* SL7 with a standard rack @Coppilgfit IBM Corpspania 12021 ** 16M file, 8+2p Read with 2 - SL3 models

1Q21 ESS Release - New SC9 Model of ESS 5000 IBM Storage for Data and Al

Announce: Feb 23, 2021 GA: Mar 12, 2021

ESS 5000 New Supported Models:

New SC9

- Up to 15.2 PB Raw Capacity in a single 42U rack*
- Up to 100 GB/s in a single 42U rack**

* SL9 with a rack extension

** 16M file, 8+2p Read with 2 - SC4 models

IBM Cloud Object Storage information dispersal Redefining availability and economics of data storage

Traditional storage

IBM Cloud Object Storage requires less than half the storage and 70% lower TCO*.

What does that mean to IT?

You can lose a disk, a server or even a whole site due to failure or disaster, and still quickly recover 100% of your data.

Slices are distributed geographically for durability and availability.

IBM Cloud Object Storage

#1 Cloud Object Storage on-premises solution delivers >70% lower TCO than traditional on-premise storage. Source: Forrester Total Economic Impact Study

Traditional storage requires 3.4 TBs raw storage capacity for 1 TB of usable storage.

IBM Cloud Object Storage

New economics: Lower TCO and site-level redundancy

Traditional storage

- More storage
- More power
- More floor space
- More software
- More personnel

Traditional storage requires 3.4 TBs raw storage capacity for 1 TB of usable storage.

IBM Cloud Object Storage

- Less storage
- Less power
- Less floor space
- Less software
- No downtime
- Less personnel
- Less costly—up to 70% lower TCO

IBM Cloud Object Storage System

Components that are simple to manage and flexible to deploy

Manager

- Fault management
- Reporting
- Provisioning
- Performance monitoring
- Storage configuration
- Single pane of glass

IBM Accesser®

- S3 interface
- Encrypts data
- Slices data
- Disperses data
- Retrieves data
- Stateless

SUPERMICR

IBM Slicestor®

- Storage for slices
- Single site or multi-site
- Capacity-based pricing
- Data integrity management

Supported as an IBM appliance

Supported on IBM certified industry standard platforms – Software only

Software-defined storage with flexible hardware deployment options

Geo-dispersed multiple sites and most deployed by customers 1,920TB Usable Capacity

Site A	Site B	Site C

Any one or more sites can be located in IBM Cloud

The Bottom Line

• IBM is in the Cognitive Systems business.

- Cognitive systems demand the widest processing power available.
- The Power Systems architecture is the BEST for AI Workloads
 - Combined with 4,8 Multi-Threading and even Hadoop/Spark processes faster.
- The Elastic Storage System is unmatched in function, scale, and performance.
- IBM Hybrid Cloud software defined infrastructure allows you to grow on demand at the most economical rates and flexibility.

Welcome to the waitless world

Give us your hardest workload!

How can IBM make you and the university successful?

Thank you....

