Research at the San Diego Supercomputer Center

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San Diego Supercomputer Center (SDSC)

University of California San Diego

XSEDE Tutorial
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- > Introduction
- > SDSC High Performance Computing Resources
- > Research at SDSC

> Summary





> Introduction





XSEDE

- A 5 year NSF program that funds people who coordinate NSF high performance computing (HPC) resources, visualization, storage and network resources
 - Coordination and Management Service
 - Extended collaborative Support Services
 - Training, Education and Outreach Service
- The resources coordinated by XSEDE program are funded separately by NSF, to Service Providers – like NCSA, NICS, PSC, SDSC TACC, IU and others





San Diego Supercomputer Center

Supercomputing and data resources:

- Trestles XSEDE
- Gordon XSEDE
- Comet (coming in Jan, 2015) XSEDE
- Triton UCSD

SDSC enabling domain science with CI

SDSC = (HPC+Data) Resources + (HPC+Data+Software) Expertise

Human Expertise:

- High Performance Computing and Computational Science researchers
- Data and Cyberinfrastructure (CI) researchers
- HW/SW infrastructure experts and support staff





> SDSC High Performance Computing Resources





XSEDE HPC Resources xsede.org

ı	HPC SYSTEMS V	ISUALIZA	TION	STORAGE	HTC SYS	TEMS	SERV	ICES	TESTBED	S
	RESOURCE NAME	SITE	MANUF / PLAT		MACHINE TYPE	PEAK TERAFL		DISK SIZE (TB)	LINKS	AVAILABILITY
	Gordon ION	SDSC	Appro		Cluster	0.0		4000.0	User Guide	Production through 2015-03-01
	SuperMIC	LSU			Cluster	0.0		0.0		Coming Soon
	Kraken-XT5	NICS	Cray >	CT5	МРР	1174.0		2400.0	User Guide	Production through 2014-04-01
	Mason	Indiana U	HP DL	580	Cluster	3.822		3582.0	User Guide	Production through 2015-03-31
	Lonestar4	TACC	Dell Power Westn Linux		Cluster	302.0		1000.0	User Guide	Production through 2014-06-30
	Keeneland-KID:	Georgia Tech	HP an	d NVIDIA	Cluster	0.0		0.0	User Guide	Production through 2014-08-31
	Gordon Compute Cluster	SDSC	Appro		Cluster	341.0		4000.0	User Guide	Production through 2015-03-01
SDSC	Trestles	SDSC	Appro		Cluster	100.0		140.0	User Guide	Production through 2014-12-31



Quarry	Indiana U	Dell AMD	SMP	0.0	335.0	User Guide	Production through 2016-06-30
Stampede	UT Austin	Dell Dell PowerEdge C8220 Cluster with Intel Xeon Phi coprocessors	Cluster	6000.0	14336.0	User Guide	Production through 2017-01-06
Blacklight	PSC	SGI UV 1000 cc-NUMA	SMP	36.0	150.0	User Guide	Production through 2015-03-31
Keeneland	Georgia Tech	HP and NVIDIA	Cluster	615.0	0.0	User Guide	Production through 2014-08-31

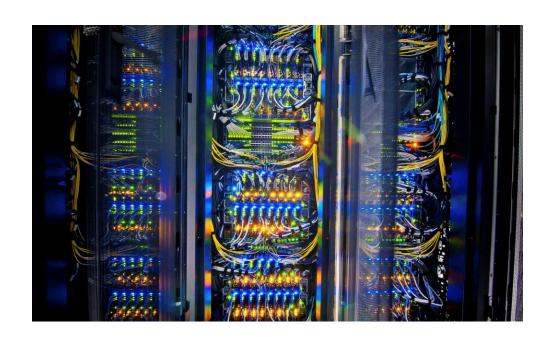
Comet – Cyberinfrastructure for the long tail of science

- Deliver ~ 2 PF/s of capacity for large # of XSEDE jobs that use < 1000 cores
- Provide 7 raw PB of Lustre-based performance storage at 200 GB/s
- Enable community-supported custom software stacks through fully virtualized HPC clusters
- Continue high-throughput response successful on Trestles
- Provide 'rapid-access' allocation to give access within a day
- Expand science gateways usage





Gordon Architecture Overview





Gordon Project PI Mike Norman, SDSC Director and Prof. Physics Dept.





Gordon – An Innovative Data-Intensive Supercomputer

- Designed to accelerate access to massive amounts of data in areas of genomics, earth science, engineering, medicine, and others
- Emphasizes memory and IO over FLOPS.
- Appro integrated 1,024 node Sandy Bridge cluster
- In production operation since February 2012
- Funded by the NSF and available through the NSF Extreme Science and Engineering Discovery Environment program (XSEDE)



















Gordon Design Innovations

- Intel Xeon E5 Processor (Sandy Bridge): First NSF system to be deployed with Intel's next generation chip which implements AVX to provide 8 operations/clock cycle
- Intel Flash memory: 300 TB of high performance Intel 710 SSD's via 64 I/O nodes.
- ScaleMP vSMP Foundation Memory Aggregation Software: Create 2TB+ SMP virtual machines for serial and threaded applications.
- Large memory nodes: 64 GB/node
- Mellanox 3D torus interconnect: Coupled with the dual rail QDR network provides a cost effective, power efficient, and fault tolerant interconnect.
- Data Oasis: 100GB/s, 4 PB Lustre file system

Gordon is an integrated, data intensive cluster built from commodity hardware and software.





Trestles – High Productivity System

- Targeted at modest scale jobs and Science Gateways
- Appro integrated 324 node AMD Magny-Cours cluster
- 120 GB Intel flash in each node used for OS and available as user scratch space
- QDR Fat Tree interconnect
- In production operation since December 2011
- Funded by the NSF and available through the NSF Extreme Science and Engineering Discovery Environment program (XSEDE)













Trestles Design Objectives

Target modest-scale users

Limit job size to 1024 cores (32 nodes)

Serve a large number of users

- Cap allocation per project at 1.5M core-hours/year (~2.5% of annual total)
- Gateways are exempt from this cap because they represent a large # of users

Maintain fast turnaround time

- Primary system metric is expansion factor rather than traditional system utilization
- Allocate ~70% of the theoretically available core-hours (revised as needed)
- Reserve nodes for interactive and short jobs

Respond to user's requirements

- Robust software suite
- Unique capabilities like pre-emptive on-demand access and user-settable reservations
- Long-running job queues (48 hours standard, up to 2 weeks allowed)

Bring in new users/communities

Welcome small jobs/allocations, start-up requests up to 50,000 SUs, gateway-friendly





> Research at SDSC





SDSC - Research Collaboration & Projects

- SDSC computational scientists collaborate with domain scientists from different domains
 - CFD, astrophysics, biochemistry, geoscience, medical, space physics, bioinformatics, economics etc.

Science Gateways

- CIPRES (phylogenetics), NSG (neuroscience), etc.
- Gateway Software Institute (PI Nancy Wilkins-Diehr)

SDSC research work and labs

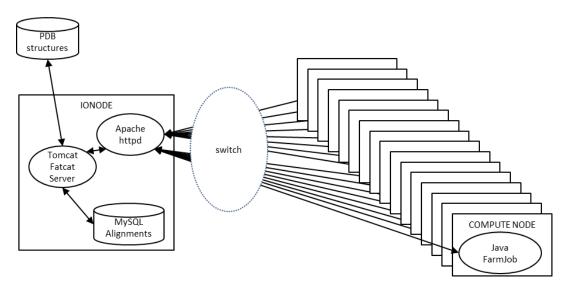
- Performance modeling (PMaC lab)
- Visualization
- Data Analytics (PACE)
- Workflows
- HPCGeo lab
- CyberGIS





Protein Data Bank (dedicated I/O node)

The RCSB Protein Data Bank (PDB) is the leading primary database that provides access to the experimentally determined structures of proteins, nucleic acids and complex assemblies. In order to allow users to quickly identify more distant 3D relationships, the PDB provides a pre-calculated set of all possible pairwise 3D protein structure alignments.



Although the pairwise structure comparisons are computationally intensive, the bottleneck is the centralized server that is responsible for assigning work, collecting results and updating the MySQL database.

Using a dedicated Gordon I/O node and the associated 16 compute nodes, work could be accomplished 4-6x faster than using the OSG

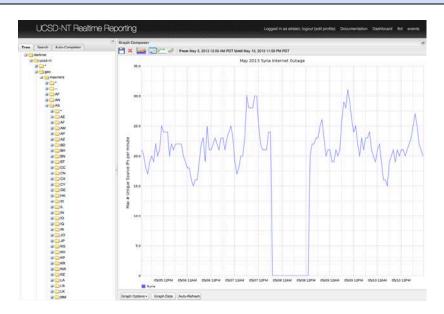
Configuration	Time for 15M alignments	speedup
Reference (OSG)	24 hours	1
Lyndonville	6.3 hours	3.8
Taylorsville	4.1 hours	5.8





Real-time reporting UCSD Network Telescope (dedicated I/O node)

Darknets – also known as network telescopes – are used to observe unsolicited traffic sent to unassigned IP address space. Observing such "one-way" traffic allows visibility into a wide range of security-related events, including scanning of address space by hackers looking for vulnerable targets, denial-of-service attacks, automated spread of computer worms, and even macroscopic connectivity disruptions in the Internet (e.g., caused by natural disasters, censorship, misconfiguration).



In the figure, our real time reporting framework: the Syrian Internet blackout happened on 7-8 May 2013 is clearly visible in the time series of the unique source IPs per minute reaching the UCSD Network Telescope that are geo-located to Syria.

The UCSD network telescope is one of the largest existing *darknets*, covering 1/256th of the entire Internet IPv4 address space. Our software for high-speed analysis of network traffic can aggregate telescope live traffic data in different ways (e.g., count of unique source IPs per country) and extract hundreds of thousands metrics that we store in round robin databases. Such data can then be both interactively visualized with a variable time aggregation, or automatically processed for anomaly detection.

A first experimental deployment of the database backend on a Gordon I/O node continuously stores data for more than a hundred thousand time series, with an 18x processing speed-up compared to a deployment on spinning disk. Processing on the Gordon node also makes the process CPU bound instead of I/O bound.

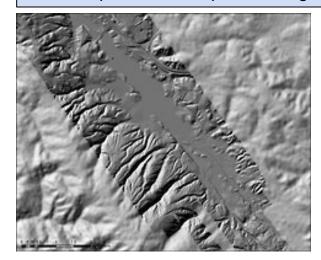
Source: Alberto Dainotti, KC Claffy, Alistair King (CAIDA, SDSC)
Used by permission. 2013

UC San Diego



OpenTopography Facility (dedicated I/O node)

The NSF funded OpenTopography Facility provides online access to Earth science-oriented high-resolution LIDAR topography data along with online processing tools and derivative products. Point cloud data are processed to produce digital elevation models (DEMs) - 3D representations of the landscape.



High-resolution bare earth DEM of San Andreas fault south of San Francisco, generated using OpenTopography LIDAR processing tools Source: C. Crosby, UNAVCO

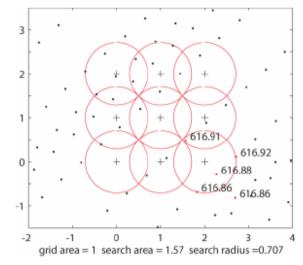


Illustration of local binning geometry.

Dots are LIDAR shots '+' indicate
locations of DEM nodes at which
elevation is estimated based

Local binning algorithm utilizes the elevation information from only the points inside of a circular search area with user specified radius. An out-of-core (memory) version of the local binning algorithm exploits secondary storage for saving intermediate results when the size of a grid exceeds that of memory.

Using a dedicated Gordon I/O node with the fast SSD drives reduces run times of massive concurrent out-of-core processing jobs by a factor of 20x

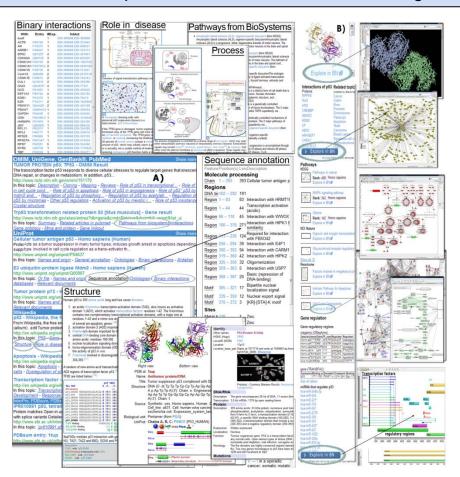
Dataset and processing configuration	# concurrent jobs	OT Servers	Gordon ION
Lake Tahoe 208 Million LIDAR returns	1	3297 sec	1102 sec
0.2-m grid res and 0.2 m rad.	4	29607 sec	1449 sec





IntegromeDB (dedicated I/O node)

The IntegromeDB is a large-scale data integration system and biomedical search engine. IntegromeDB collects and organizes heterogeneous data from over a thousand databases covered by the *Nucleic Acid* and millions of public biomedical, biochemical, drug and disease-related resources



IntegromeDB is a distributed system stored in a PostgreSQL database containing over 5,000 tables, 500 billion rows and 50TB of data. New content is acquired using a modified version of the SmartCrawler web crawler and pages are indexed using Apache Lucene.

Project was awarded two Gordon I/O nodes, the accompanying compute nodes and 50 TB of space on Data Oasis. The compute nodes are used primarily for post-processing of raw data. Using the I/O nodes dramatically increased the speed of read/write file operations (10x) and I/O database operations (50x).

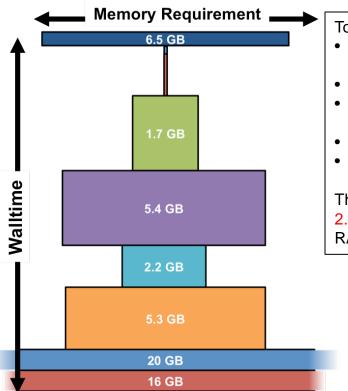
Source: Michael Baitaluk (UCSD) Used by permission 2013





Large-scale pharmacogenomic analysis (SSD)

Janssen R&D, a Johnson & Johnson company, has been using whole-genome sequencing in clinical trials of new drug therapies to correlate response or non-response with genetic variants. Janssen has partnered with the Scripps Translational Science Institute (STSI) to perform cutting-edge analyses on hundreds of full human genomes which presents many dimensions of data-intensive challenges.

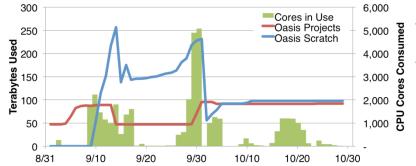


Each step of the 9-stage read-mapping pipeline had very different resource requirements

To analyze 438 human genomes, this project needed

- 16-threads per node and hundreds of nodes to achieve massive parallelism
- at least of 40 GB of RAM per node for some pipeline stages
- over 3 TB of flash storage per node via "big flash" nodes at a metadata-IOPS rate not sustainable by Lustre
- over 1.6 TB of input data per node at some pipeline stages
- 1 GB/s read rate from Lustre per node

This project accomplished in 5 weeks on Gordon what would have taken 2.5 years of 24/7 compute on a single, 8-core workstation with 32 GB of RAM.



Peak footprint:

- 257 TB of Oasis Scratch
- 5,000 cores in use (30% of Gordon's total capacity)

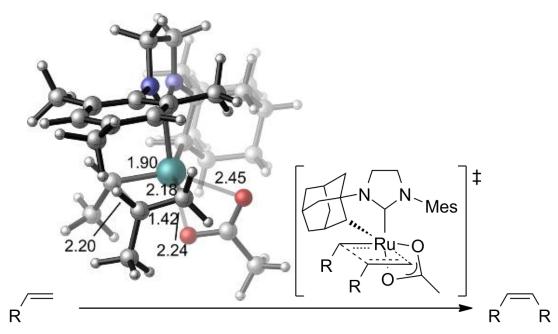




Prediction of new catalysts (SSD)

Olefin metathesis is a powerful tool for controlling the redistribution of carbon-carbon double bonds in organic synthesis, while minimizing undesired by-products. Computational chemistry is used to predict the selectivity of new ruthenium olefin metathesis

ruthenium olefin metathesis catalyst and transition state



Ken Houk's lab (UCLA) is using Gaussian 09 to calculate hundreds of transition states for systems consisting of approximately 100 atoms using DFT and CCSD(T) methods. Scratch files are at least 100GB is size and the memory requirements are approximately 2 GB/core. This work is being done in collaboration with Robert Grubb (Caltech)

Given the need for large, fast local scratch space and fairly large memory requirements, Gordon is a suitable XSEDE system that makes it feasible for these highly accurate calculations.

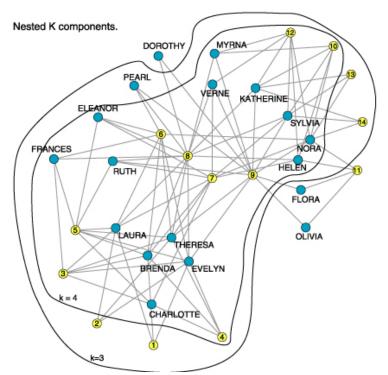
Source: Ken Houk (UCLA) Used by permission. 2013





Mathematical anthropology (vSMP)

The identification of cohesive subgroups in large networks is of key importance to problems spanning the social and biological sciences. A k-cohesive subgroup has the property that it is resistant to disruption by disconnection by removal of at least k of its nodes. This has been shown to be equivalent to a set of vertices where all members are joined by k independent vertex-independent paths (Menger's theorem).



Doug White (UCI) and his collaborators are using software developed using R and the igraph package to study social networks.

The software was parallelized using the R multicore package and ported to Gordon's vSMP nodes. Analyses for large problems (2400 node Watts-Strogatz model) are achieving estimated speedups of 243x on 256 compute cores. Work is underway to identify cohesive subgroups in large coauthorship networks

James Moody, Douglas R. White. Structural Cohesion and Embeddedness: A Hierarchical Conception of Social Groups. American Sociological Review 68(1):1-25. 2004

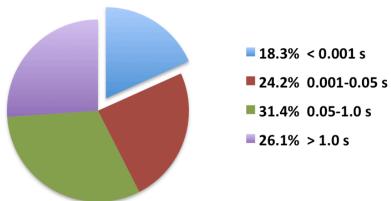




Impact of high-frequency trading (advanced support)

To determine the impact of high-frequency trading activity on financial markets, it is necessary to construct nanosecond resolution limit order books – records of all unexecuted orders to buy/sell stock at a specified price. Analysis provides evidence of quote stuffing: a manipulative practice that involves submitting a large number of orders with immediate cancellation to generate congestion





Run times for LOB construction of heavily traded NASDAQ securities (June 4, 2010)

Symbol	wall time (s) orig. code	wall time (s) opt. code	speedup
SWN	8400	128	66x
AMZN	55200	437	126x
AAPL	129914	1145	113x

Project benefited greatly by direct involvement of SDSC applications staff. Optimizations to the original thread-parallel code resulted in greater than 100x speedups. It is now possible to analyze entire day of NASDAQ activity in a few hours using 16 Gordon nodes. With new capabilities, beginning to consider analysis of options data with 100x greater memory requirements.

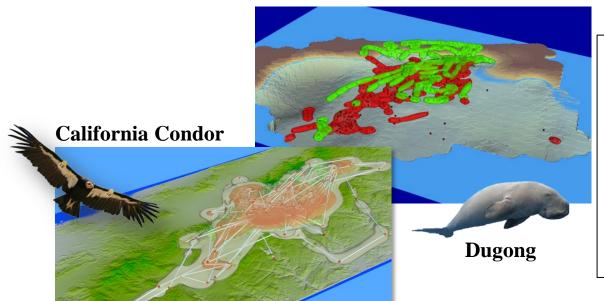
Source: Mao Ye, Dept. of Finance, U. Illinois. Used by permission. 6/1/2012





3D Modeling of Animal Space Use

The increasing sophistication of biotelemetry technology allows ecologists to collect accurate, fine-scale animal movement data in 3D. San Diego Zoo Global and USGS researchers have developed a 3D movement-based kernel density estimator (3D MKDE) that accounts for physical barriers such as the land surface or seafloor to visualize avian and marine animal space use. Ecologists may use this approach to estimate and visualize animal utilization distributions and support the conservation of endangered species.



Computing 3D MKDEs is computationally intensive. 3D kernels must be integrated over time along the interpolated animal movement path to compute a 3D probability density.

To enable this work, the project was provided with allocations on Trestles and Gordon. SDSC staff also provided assistance in software parallelization, code optimization and visualization. These efforts resulted in code that ran more than 1000x faster than the original MPI version.

Source: Jeff A. Tracey (U.S. Geological Survey) and James Sheppard (Institute for Conservation Research, San Diego Zoo Global) Used by permission. 2013









Science Gateways

- A community infrastructure layer
- Provides a set of applications via a customized portal
- Specific for researchers from a particular domain
- Hides the complexities
 - Write peer-reviewed yearly proposals for computer time
 - Understand HPC machines, policies, complex OS/software
 - Install and benchmark complex but widely used science applications
 - Understand, manage remote authentication
 - Understand/learn batch policies
 - Figure out data transfer, storage





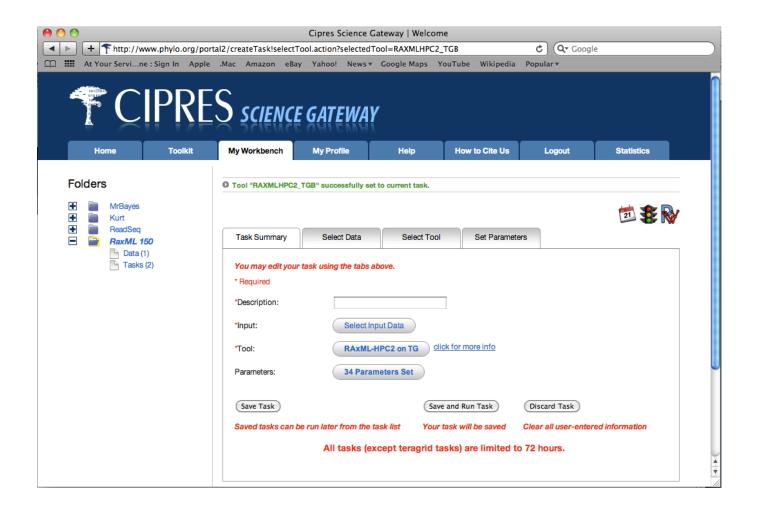
Example Science Gateways

- CIPRES CI for Phylogenetics RESearch (Mark Miller, Terri Schwartz, Wayne PfeifferSDSC) – http://www.phylo.org/index.php/portal/
 - 8000+ users
 - RAxML, MrBayes, GARLI, BEAST, MAFT and many other
 - Provides ~20 million core hours (Service Units) free per year
- NeuroScience Gateway NSG (Amit Majumdar, Subha Sivagnanam SDSC; Ted Carnevale Yale) – www.nsgportal.org
 - ~100 users
 - NEURON, PGENESIS, NEST, PyNN, Brian
 - Provides ~2 million core hours free
- Similarly many other gateways on bioinformatics, chemistry, CFD, etc. from NICS, NCSA, PSC, IU, Purdue





The CIPRES science gateway lets biologists infer trees on Gordon and Trestles via a browser interface







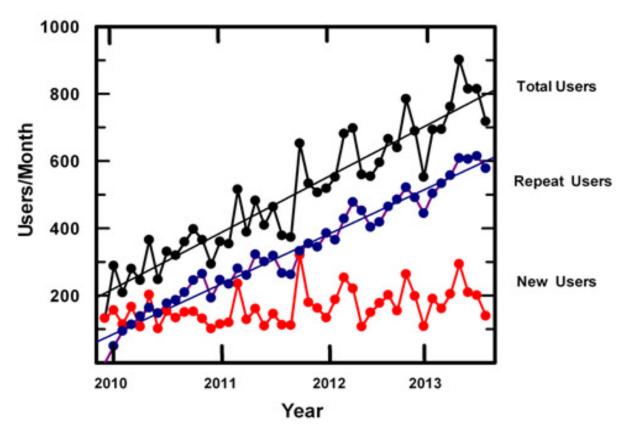
There are many benefits to a browser interface, especially for researchers with little HPC expertise

- Users do not log onto HPC systems & so do not need to learn about Linux, parallelization, or job scheduling
- Users simply use browser interface to
 - pick code, select options, & set parameters
 - upload sequence data
- Numbers of cores, processes, & threads are selected automatically based on
 - input options & parameters
 - rules developed from benchmarking
- In most cases, users do not need individual allocations
- Users still need to understand code options!





The CIPRES gateway has been extremely popular



- Number of users is growing linearly by nearly 2,000 per year
- >7,000 users have run on TeraGrid/XSEDE supercomputers
- >700 publications have been enabled by CIPRES use





Performance, Modeling, and Characterization (PMaC) Lab

Laura Carrington, Ph.D PMaC Lab Director

University of California, San Diego San Diego Supercomputer Center





The PMaC Lab

Researching the complex interactions between HPC systems and applications to predict and understand the factors that affect performance and power on current and future HPC platforms.

- Develop tools and techniques to deconstruct HPC systems & HPC applications to provide detailed characterizations of their power and performance.
- Develop modeling techniques that combined these characterizations to predict performance and power of HPC systems.





The PMaC Lab

Utilize the characterizations to construct power and performance models that guide:

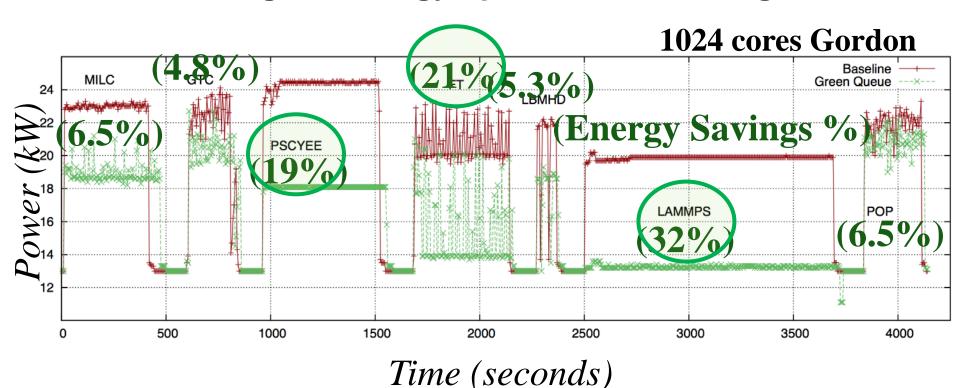
- Improvement of application performance
 2 Gordon Bell Finalists, DoD HPCMP Applications, NSF BlueWaters, etc.
- System procurement, acceptance, and installation
 DoD HPCMP procurement team, DoE upgrade of ORNL Jaguar, installation of NAVO PWR6
- Accelerator assessment for a workload
 Performance assessment and prediction for GPUs & FPGAs
- Hardware customization/ Hardware-Software co-design
 Performance and power analysis for Exascale
- Improvement of energy efficiency and resiliency
 Green Queue Project, DoE SUPER Institute, DoE BSM, etc.





PMaC's Green Queue Framework (optimizing for performance & power)

Goal: Use machine and application characterization to make customize fine-grain energy optimizations during execution

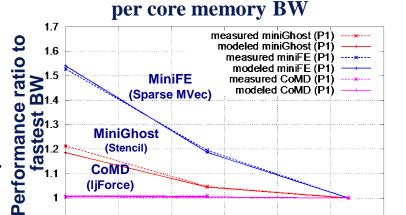






Using Fine Grained Models to Explore Algorithmic Choice for Future Systems

- **Growth of multi-core means less per core** memory bandwidth in future systems
- Future systems will most likely have reduced per core memory bandwidth
- models help identify sensitivities of algorithms on these systems – aid in algorithmic choice for **future systems**



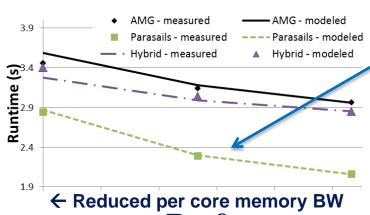
CoMD (ljForce)

Co-Design Center proxy-apps' sensitivity to

Reduced per core memory BW

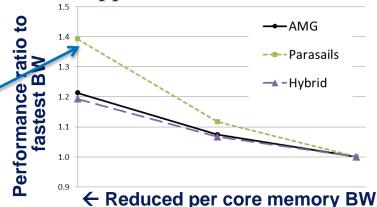
Determining the correct algorithm for future Exascale systems using models

Models of 3 different algorithms for AMG application



Parasails has fastest performance

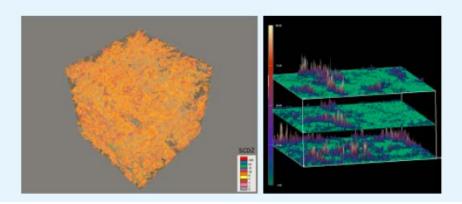
> Parasails most sensitive to reductions in BW



Performance models can identify algorithmic choices that are optimal as hardware changes in future systems.

Petascale computing for studies of turbulent mixing and dispersion: current status and future prospects

P. K. Yeung
Schools of AE, CSE, ME
Georgia Inst of Tech, Atlanta, USA



Dmitry Pekurovsky, Ph.D, SDSC

- 3D-FFT algorithm: 1-D applied 3 times for X, Y, Z
- Easily parallelized and load balanced
- Use transpose approach
 - Call FFT on local data
 - Use transpose when necessary san diego supercomputer center





Algorithm scalability

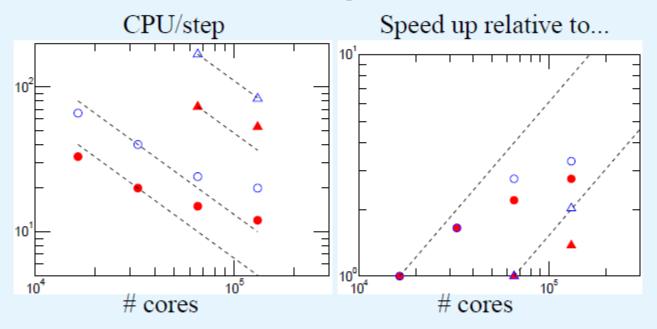
- 1D decomposition: concurrency is limited to N (linear grid size).
 - Not enough parallelism for O(10⁴) O(10⁵) cores
 - This is the approach of most libraries to date
 (FFTW 3.2, PESSL)
- 2D decomposition: concurrency is up to N²
 - Scaling to ultra-large core counts is possible, though not guaranteed
 - The answer to the petascale challenge

P3DFFT by Dmitry Pekurovsky, SDSC

- Open source library for efficient, highly scalable 3D FFT on parallel platforms
- Built on top of an optimized 1D FFT library
 - Currently ESSL or FFTW
 - In the future, more libraries
- Uses 2D decomposition
 - Includes 1D option.
- Available at http://code.google.com/p/p3dfft/

DNS Code: Parallel Performance

- Largest machine used is 2-Petaflop Cray XT5 (Jaguarpf at ORNL)
- 4096³ (circles) and 8192³ (triangles), 4th-order RK:



- best processor grid, stride-1 arithmetic
- ullet dealiasing: can skip some (high k) modes in Fourier space
- better scaling when scalars added (blue, more work/core)



IN-SITU VISUALIZATION FOR GLOBAL HYBRID SIMULATIONS

Homa Karimabadi (UCSD), Mahidhar Tatineni (SDSC), Amit Majumdar (SDSC)

Burlen Loring (LBL) Patrick O' leary (Kitware Inc), Berk Geveci (Kitware Inc.)

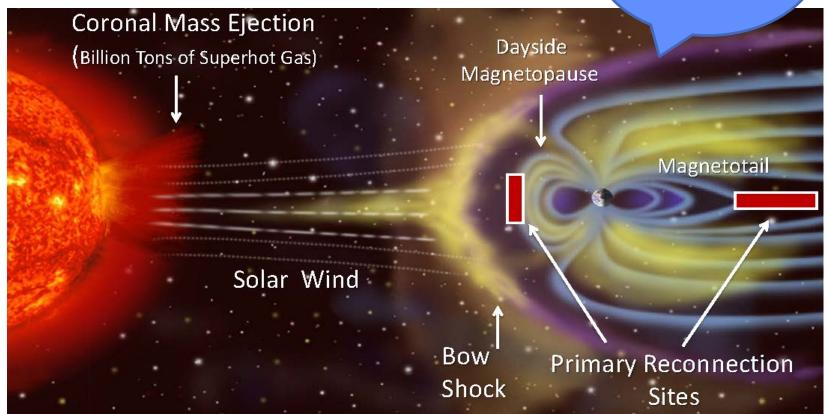
XSEDE13: Gateway to Discovery July 22-25, 2013 San Diego, CA





Space Weather

Earth's magnetic field provides a protective cocoon but it breaks during strong solar storms

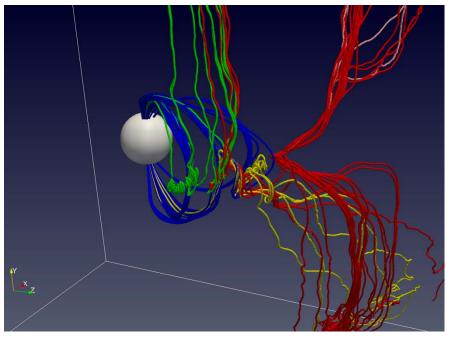


90 million miles or ~ 100 Suns

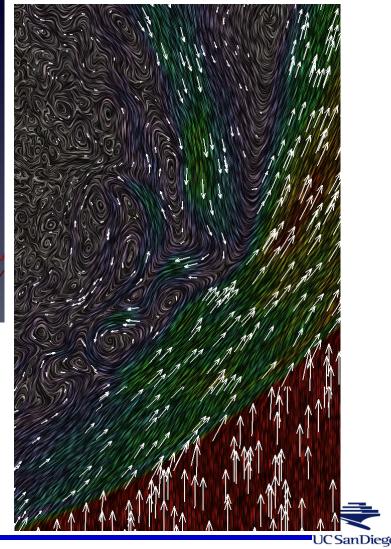




What are the source of vortices inside the Magnetosphere?

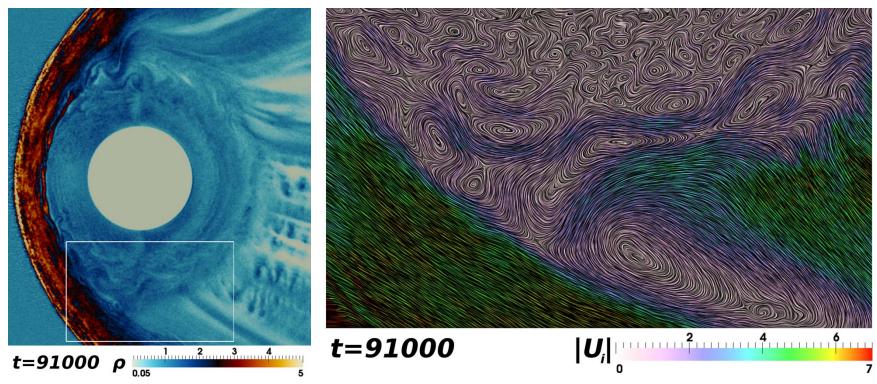


- Confirmed by spacecraft observations
- Vortices at the MP boundary often have FTE's near the vortex core. Are the FTE's causing the vortex?
- Are these driven by Kelvin-Helmholtz instability?





Why In-situ for this study?



- Simulation is I/O bound and runs are limited by disk quotas
- With in-situ we reduce I/O costs by using "extracts"
- And increase temporal resolution
- Removes need for post processing saves disk and computational time.

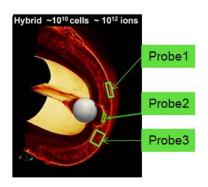




In Situ Visualization

- o For many of our analysis, we need high time resolution data dumps. However, this is not practical since each data dump can take over 10 TB.
- o In situ visualization provides a possible solution.

In Situ Visualization Using Intelligent Probes



Features of Intelligent Probes

Targeted data collection
Ability to mimic spacecraft-like trajectories
Creation of instrument-like products
Generation of high resolution data products

Selective Outputs

Images and visualizations
Data from probes (less raw data)
Statistics

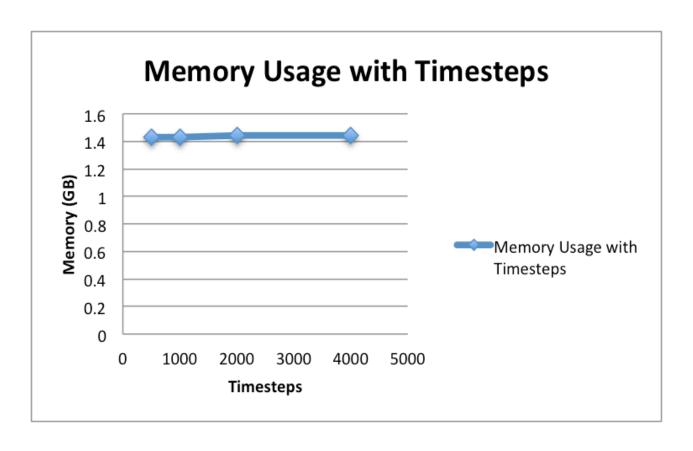
Enables

Direct comparison with spacecraft data
Orbit optimization
Instrument design and testing





Results – Memory Overhead of In-Situ Viz



Variation of memory usage with timesteps for the in-situ visualization test case.

Performance Impact of In-Situ Viz

- Test runs conducted with In-Situ Viz output *every timestep* (extreme case). Run times compared with normal case where output is every 500 steps.
- First set is weak scaling with particle counts and a fixed grid size. 20-30% impact on run time with 8 cores/node.

Table: Wall clock time (for 500 timestep run) variation with different core counts, with a fixed grid size (128x128x128), and varying particle counts.

Cores	Millions of Particles	Wall-clock time (sec.)				
		non-in-situ	in-situ			
32 †	33.5	388.05	459.20			
64 †	67	290.53	386.49			
128 †	134	311.91	401.88			
128 ‡	134	317.49	456.27			
†— 8 cores per node, ‡ — 16 cores per node						

Summary

- SDSC (like all the other centers NCSA, NICS, PSC, TACC and others) enables domain science research via CI resource and expertise
- Individual research labs and researchers perform CI related research and development
- We encourage you to get allocation and start using the XSEDE resources (more from XSEDE talks)
- Science Gateways are excellent ways to get your science done





End

Thank you



