Performance analysis of Sweep3D on Blue Gene/P with Scalasca

2010-04-23 |

Brian J. N. Wylie, David Böhme, Bernd Mohr, Zoltán Szebenyi & Felix Wolf Jülich Supercomputing Centre

b.wylie@fz-juelich.de



Overview

Introduction

- Scalasca performance analysis toolset
- Blue Gene/P supercomputer
- Sweep3D compact application

Measurements & Analyses

- Default & improved Sweep3D configurations
- Refined instrumentation & analyses

Scalasca scalability

Conclusions



Scalasca project

Overview

- Helmholtz Initiative & Networking Fund project started in 2006
 - Headed by Prof. Felix Wolf (RWTH Aachen, GRS & JSC)
- Follow-up to pioneering KOJAK project (started 1998)
 - Automatic pattern-based trace analysis

Objective

- Development of a <u>scalable</u> performance analysis toolset
- Specifically targeting <u>large-scale</u> parallel applications

Status

- Scalasca v1.3 released in March 2010
- Available for download from www.scalasca.org



Supercomputers at Jülich Supercomputing Centre

Period	Machine	#Cores
2003-8	"jump" IBM p690 cluster	1,312
2006-8	"jubl" IBM Blue Gene/L	16,384

- 2009- "juropa" Bull/Sun/Intel blades 26,304
- 2009- "jugene" IBM Blue Gene/P 294,912
 [jugene is the largest system in the Top500 list, Jun/Nov 2009]



JUGENE - IBM Blue Gene/P system



72 racks with 32 nodecards of 32 compute nodes (multiple networks)

- Quad-core 850 MHz PowerPC 450 processors
- 2 Gbytes main memory (aggregate 144 TB)
- Proprietary Linux microkernel, MPI, XL compilers, GPFS filesystem



Large-scale parallel applications (* analyzed by Scalasca)

Selected applications from Jülich Blue Gene Scaling Workshops:

- 294,912 (288k) cores
 - GENE (MPI-RZG/D) gyrokinetic turbulence*
 - KKRnano (FZJ/D) electronic structure*
 - MUPHY/PEBS (Harvard/USA) MD/evolutionary biology
 - OSIRIS (IST/PT) 3D relativistic plasma*
 - PHASTA (RPI/USA) unsteady fluid dynamics*
 - UNIC (ANL/USA) neutron transport in fast reactors
 - (various) lattice QCD
- 262,144 (256k) cores
 - MP2C (FZJ/D) mesoscale particle dynamics*
 - NEK5000 (ANL/USA) CFD*



Sweep3D

Ubiquitous ASCI benchmark code from Los Alamos National Laboratory

- 3-dimensional neutron transport simulation
- direct order solve uses diagonal wavefront sweeps over grid cells combined with pipelining of blocks of k-planes and octants
- execution performance extensively modeled & analyzed

MPI parallel version using 2D domain decomposition

- ~2,000 lines of code (12 source modules), mostly Fortran77
- very portable, and highly scalable
- tunable via input deck, e.g., number of k-planes in blocks (MK)
- benchmark configuration does 12 iterations
 - flux correction 'fixups' applied after 7th iteration



Scalasca features

Open source, New BSD license

Portable

 IBM BlueGene/L, BlueGene/P, SP & blade clusters, Cray XT4/5, NEC SX, SGI Altix, SiCortex, Linux cluster® (SPARC, x86-64), ...

Supports typical HPC languages & parallel programming paradigms

- Fortran, C, C++
- MPI, OpenMP & hybrid MPI/OpenMP

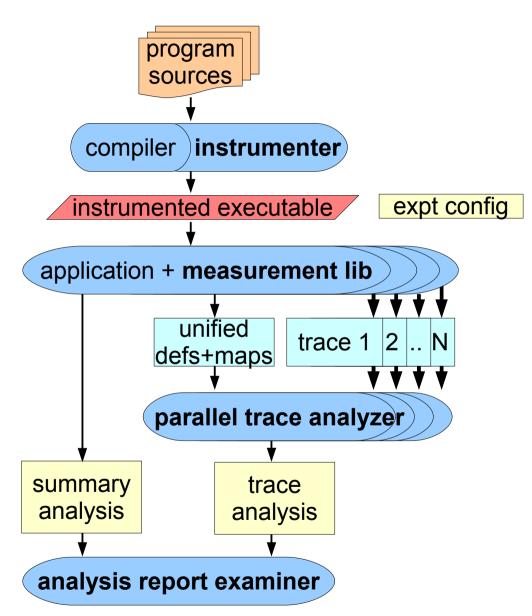
Integrated instrumentation, measurement & analysis toolset

- Customizable automatic/manual instrumentation
- Runtime summarization (*aka* profiling)
- Automatic event trace analysis



Scalasca components

- Automatic program instrumenter creates instrumented executable
- Unified measurement library supports both
 - runtime summarization
 - trace file generation
- Parallel, replay-based event trace analyzer invoked automatically on set of traces
- Common analysis report explorer & examination/processing tools





Scalasca usage

- 1. Prepare application objects and executable for measurement:
 - scalasca -instrument mpixlf77 -03 -qarch=450 -qtune=450 ...
- 2. Run application under control of measurement nexus:
 - scalasca -analyze mpirun -mode VN -np 294912 sweep3d
 - epik_sweep3d_vn294912_sum experiment produced
 - scalasca -analyze -t mpirun -mode VN -np 294912 sweep3d
 - epik_sweep3d_vn294912_trace experiment produced
- 3. Interactively explore measurement analysis report
 - scalasca -examine epik_sweep3d_vn294912_trace
 - epik_sweep3d_vn294912_trace/trace.cube.gz presented



Measurement & analysis methodology

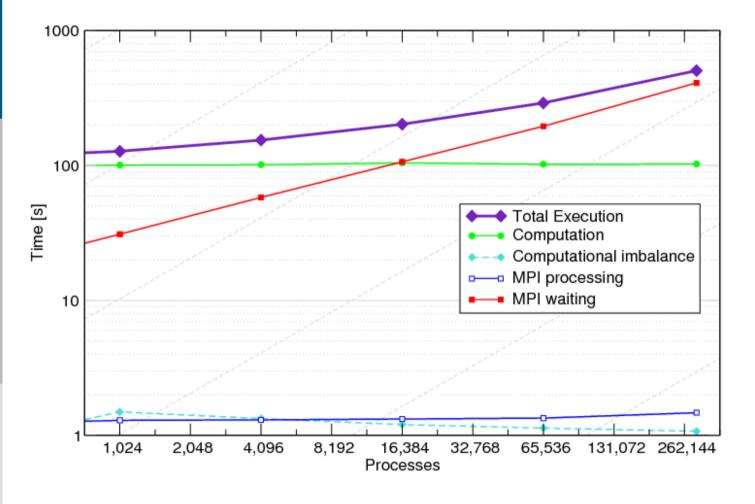
- 1. Run uninstrumented/optimized version (as reference for validation)
 - determine memory available for measurement
- 2. Run automatically-instrumented version collecting runtime summary
 - determine functions with excessive overheads
 - examine distortion and trace buffer capacity requirement
 - if necessary, prepare filter file and repeat measurement
- 3. Reconfigure measurement to collect and automatically analyze traces
- 4. Refine instrumentation by manually annotating key code sections
 - use EPIK instrumentation API macros

Compare original MK=10 and alternative MK=1 Sweep3D configurations

varies computation wavefront pipelining concurrency



Sweep3D execution time scaling: original MK=10



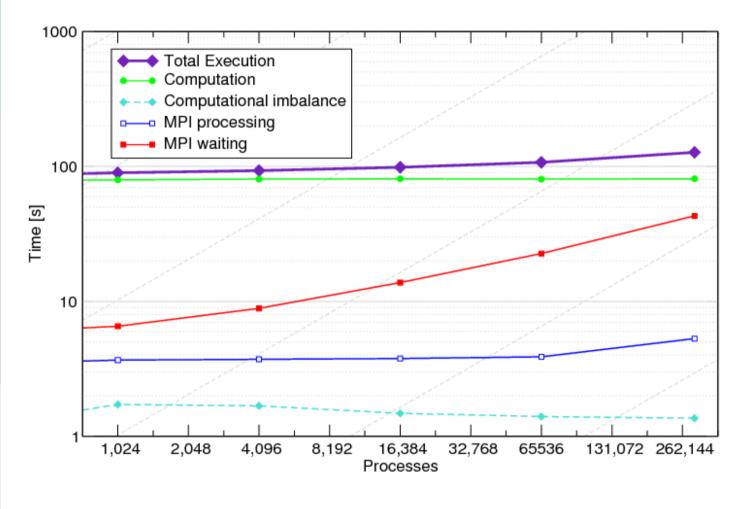
[Replication of scaling characteristics reported by others]

 Default input deck settings

- Weak scaling due to fixed problem size per process
- Reasonable scalability(?)
- Constant time for computation
- Rapid growth in MPI time, which is almost all waiting time



Sweep3D execution time scaling: improved MK=1

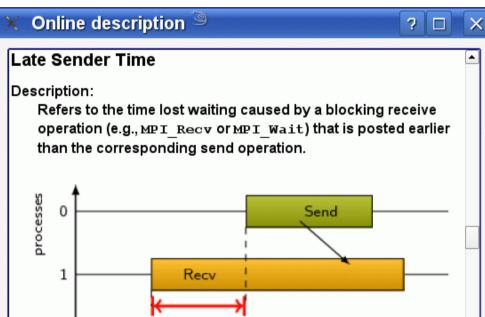


- Much improved performance and scalability
- Computation
 20% faster
 (better caching?)
- MPI processing time increased (10x messages)
- MPI waiting time significantly reduced, though still growing markedly

[Single *k*-planes rather than default batches of 10]



Scalasca GUI description for Late Sender metric



If the receiving process is waiting for multiple messages to arrive (e.g., in an call to MPI_Waitall), the maximum waiting time is accounted, i.e., the waiting time due to the latest sender. Unit:

Seconds

Diagnosis:

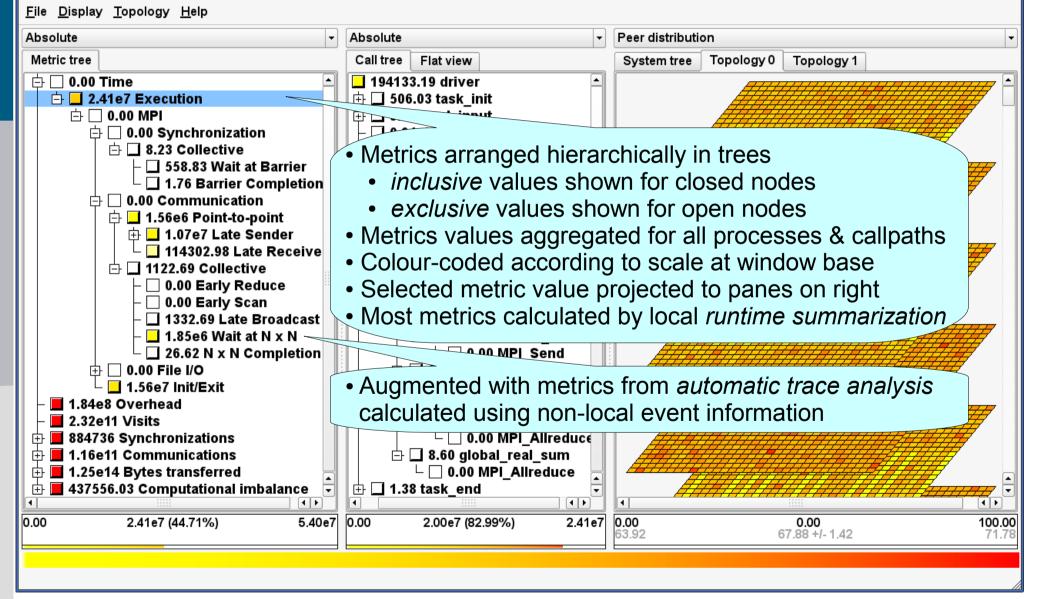
Try to post sends earlier, such that they are available when receivers need them. Note that outstanding messages (i.e., sent before the receiver is ready) will occupy internal message buffers.

- Analysis report explorer GUI provides hyperlinked online descriptions of metrics
- Diagnosis hints suggest how to refine diagnosis of performance problems and possible remediation

time

Scalasca analysis report: performance metric tree

Cube 3.3 Qt: epik sweep3d vn294912 trace/trace.cube.gz





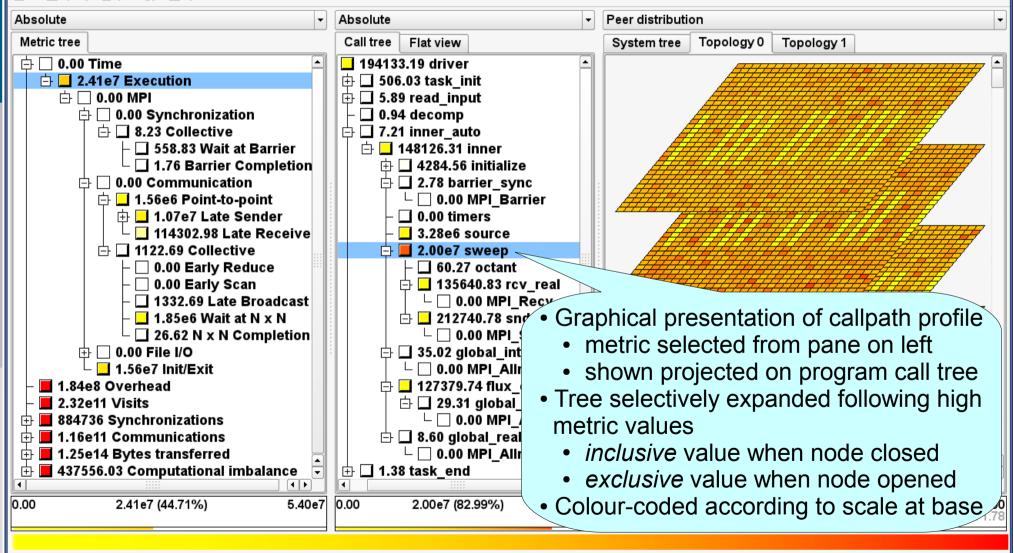


Scalasca analysis report: program call tree

K Cube 3.3 Qt: epik_sweep3d_vn294912_trace/trace.cube.gz 🥯

_ 🗆 🗡

<u>File Display Topology Help</u>



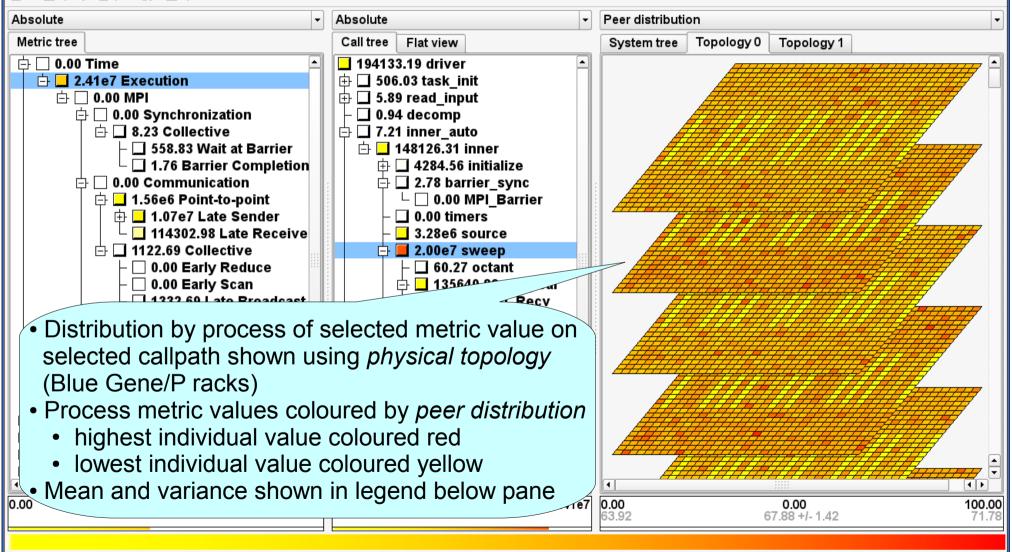


Scalasca analysis report: system tree/topology

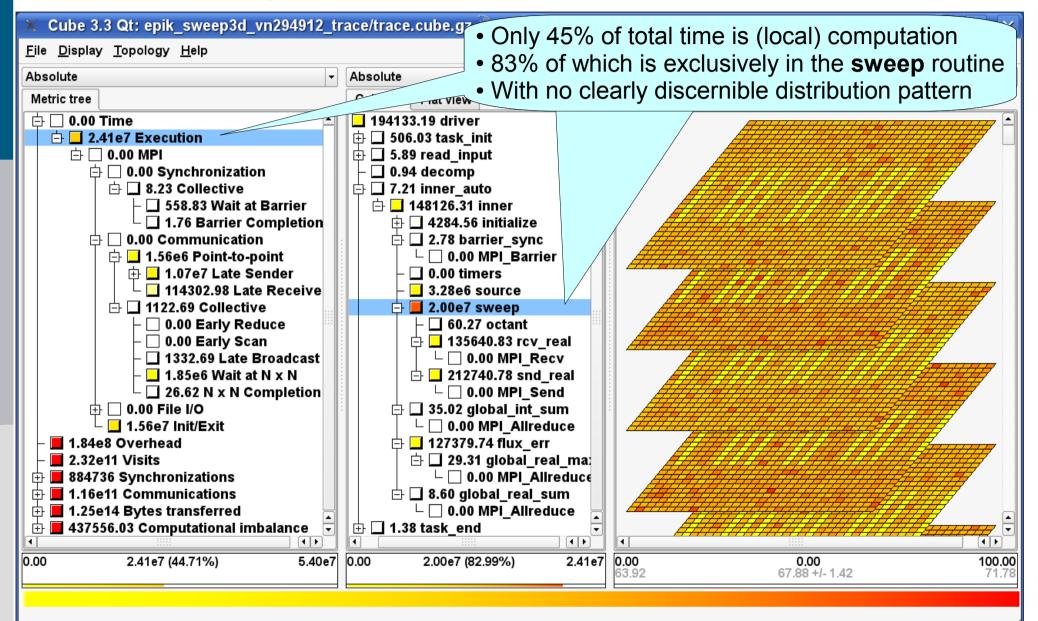
🔀 Cube 3.3 Qt: epik_sweep3d_vn294912_trace/trace.cube.gz [©]

_ 🗆 🗙

<u>File Display Topology Help</u>

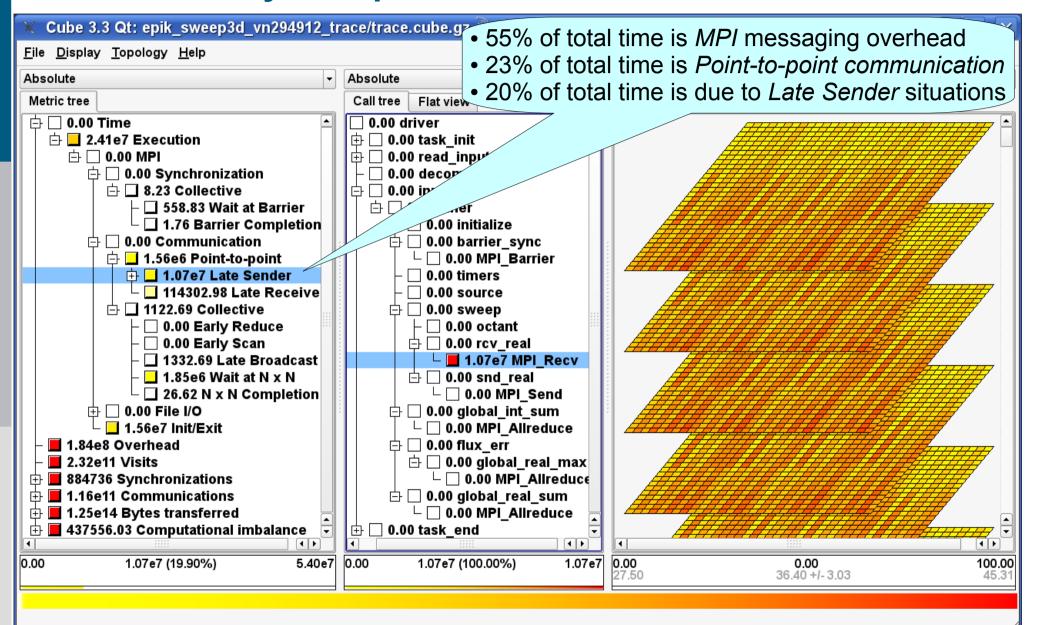


Scalasca analysis report: sweep computation time





Scalasca analysis report: Late Sender time



er distribut		eep3d_vn294912_trace/trace.cube.gz 🥯	
ystem tree		Topology 1	
-			
	£		•
0 50			
0 50		0.00 36.40 +/- 3.03	100 45

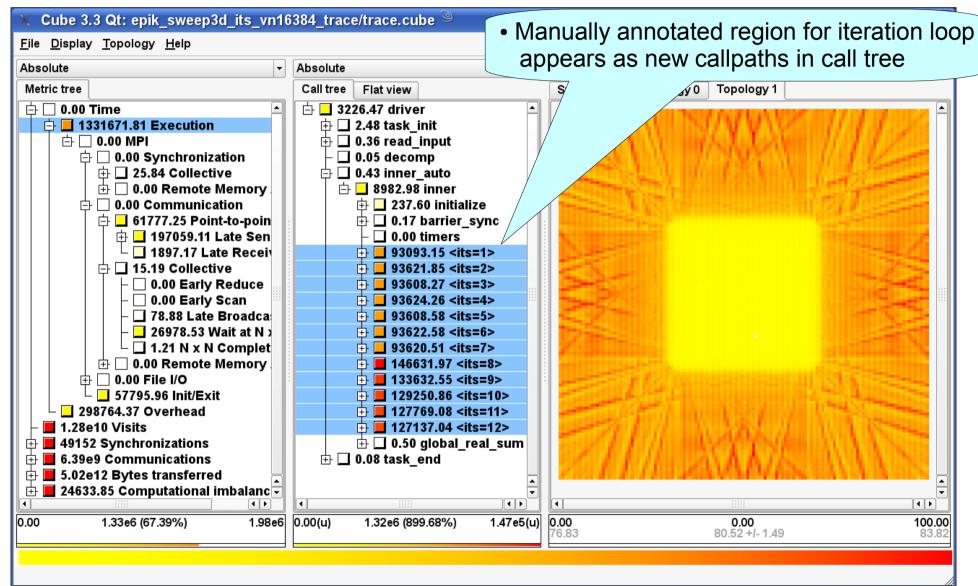


Sweep3D grid topology view

- Application's 2D topology of 576x512 procs
- Reveals clear pattern in the distribution of *Late Sender* metric values
- Arises from superimposing octant sweeps with imbalanced computation

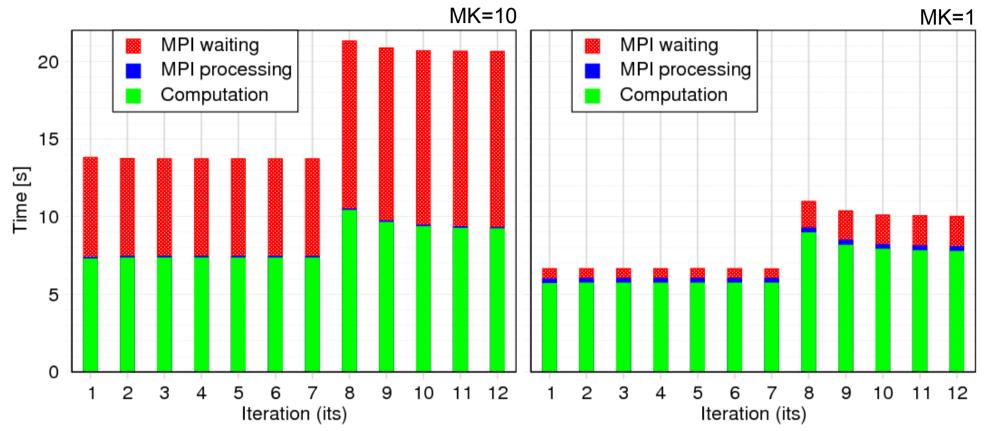


Sweep3D computation time by iteration (16,384 processes)





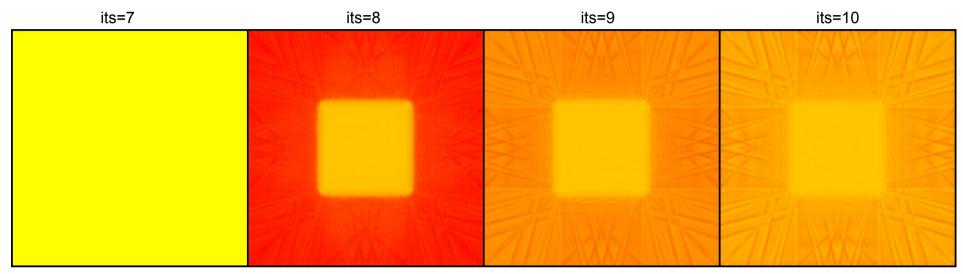
Iteration execution time breakdown (16,384 processes)



- Initial 7 (non-fixup) iterations faster than later 5 (fixup) iterations
- *MPI waiting* time dominates original; amplified by fixup imbalance
- *MPI processing* time a fixed cost in each iteration



Sweep3D computation time distribution evolution



[[]Values coloured on scale 5 to 10 seconds]

- Initial 7 (non-fixup) iterations are very well balanced
- Fixups introduced after iteration 7 are computationally imbalanced
- Iteration 8 clearly shows central rectangular imbalance feature
- Subsequent iterations have less imbalance in the rectangular core, however, pronounced symmetric oblique lines of excess computation



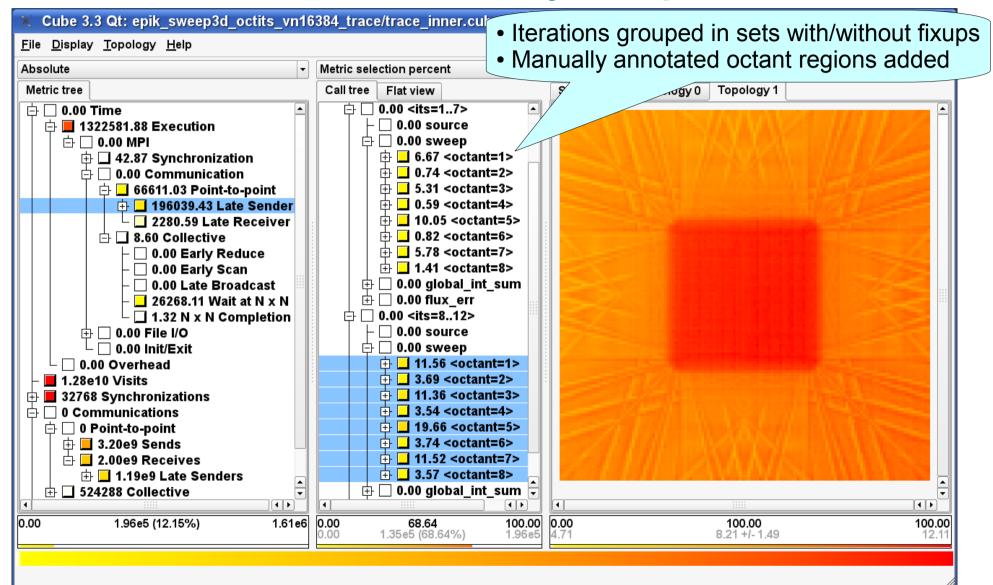
Scalasca source code browser

🗙 src/sweep.f [©] ? _ [
<pre>Src/sweep.f ? _ ? _ </pre> <pre>? _ </pre>					
go to 111	• •				
Read only Save Save as Font Close					

- Source file sweep.f contains 625-line sweep flow routine
- Computationally imbalanced *i*-line section where corrective 'fixups' for negative fluxes are recursively applied in *i*, *j*, *k* grid directions
- Hotspot also typically identified by profilers based on sampling



MPI Late Sender time variation by sweep octant

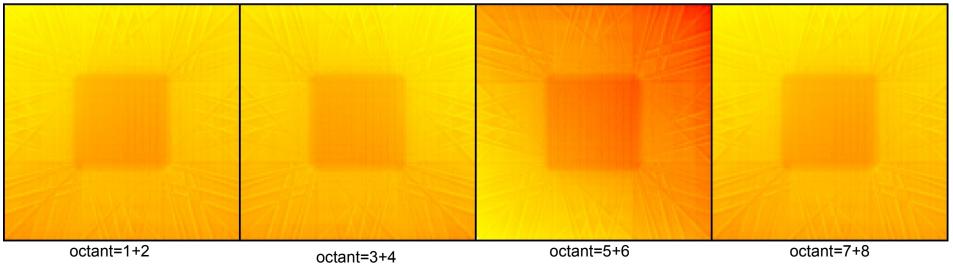




MPI *Late Sender* time distributions for octant pairs

Iterations without fixups:

Iterations with fixups:



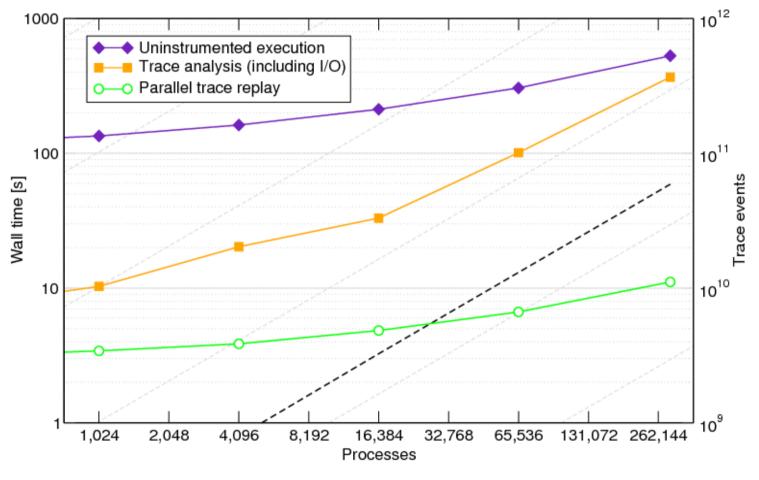


Scalasca experiment statistics: sweep3d_vn294912_trace

Scalasca	v1.2	v1.3+
Sweep3d size of <i>k</i> -blocks MK	10	1
Sweep3d elapsed time [s]	505	129
Measurement dilation [%]	5	3
Unification time [mins]	43	41
Trace event records [G]	59	510
Trace buffer content [MB]	2.75	27
Trace total size [TB]	0.79	7.6
Trace (physical) files [#]	294912	576
Trace open/create time [mins]	86	10
Trace flush rate [GB/s]	3.7	19.1
Trace analysis time [s]	368	546
 Trace analysis collation [s] 	162	91
- Trace analysis replay [s]	11	74



Scalasca trace analysis time scaling: original MK=10



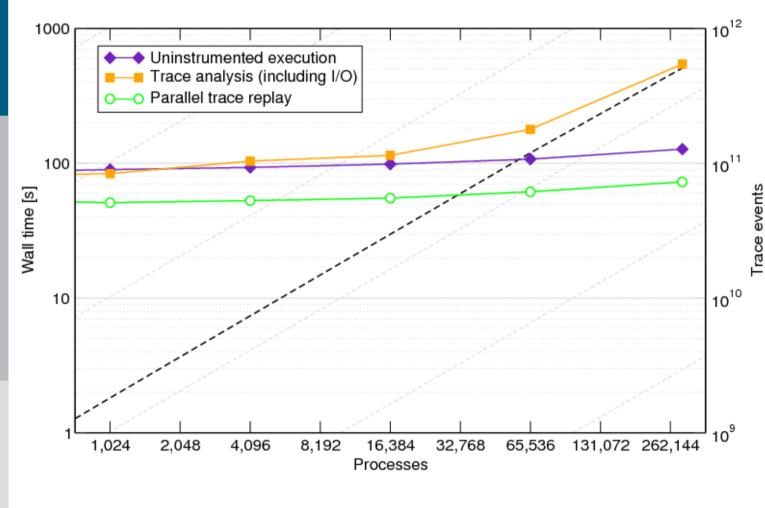
- 2.75MB of trace event records per process (determined from summary)
- Total trace size (---) increases linearly to 790GB for 59G events
- Trace replay time scales with application execution time

[Scalasca v1.2]

2010-04-23 | IPDPS-LSPP'10



Scalasca trace analysis time scaling: improved MK=1



[Scalasca v1.3 using SIONlib & prototype binary-format report]

- 10x larger traces due to 10x messages
- 27MB of trace event records per process
- Total trace size (---) increased to 7.6TB for 510G events
 - 10x longer trace replay time still scales with application execution time

2010-04-23 | IPDPS-LSPP'10



Scalasca scalability issues/optimizations

Time for unification of identifiers grows linearly with number of processes

• use *hierarchical* unification scheme

Creating individual traces files for each process is prohibitive

use SIONlib *multi-files* (e.g., one per Blue Gene/P IONode)

Analysis reports are large and slow to collate

binary format for metric value data plus separate XML metadata
 Analysis presentation is slow and requires lots of memory

store metrics as *inclusive* values and load them *incrementally*

Full analysis presentation requires very large, high-resolution screens





Conclusions

Blue Gene/P efficiently supports application executions at extreme scale Sweep3D is scalable to 294,912 MPI processes on Blue Gene/P

- appropriate input configuration/tuning is necessary
- 'fixups' are computationally imbalanced and amplify waiting times
 - they therefore need to be used sparingly
- there might be further opportunities for performance improvement
 - e.g., with non-default mapping of processes to cores

Scalasca has demonstrated performance measurement/analysis at unprecedented scale

however, further significant improvements are in progress



scalasca 🗖

Scalable performance analysis of *extremely* large-scale parallel applications

- portable toolset for scalable performance measurement & analysis of MPI, OpenMP & hybrid OpenMP/MPI parallel applications
- supporting most popular HPC computer systems
- available under New BSD open-source license
- distributed on POINT/VI-HPS Parallel Productivity Tools Live-DVD
- sources, documentation & publications:
 - http://www.scalasca.org
 - mailto: scalasca@fz-juelich.de