

Scalasca components with reuse potential

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Outline

- Overview of Scalasca
- Components with reuse potential
 - OPARI OpenMP source-code instrumenter
 - MPI tracing wrappers and wrapper generator
 - Compiler event adapters
 - Library for efficient parallel file I/O
 - Profile browser
- Ongoing and planned collaborations



scalasca 🗗

- Started in January 2006
- Scalable performance-analysis toolset for parallel codes
 - Emphasis on detection of wait states
- Designed for large-scale systems such as IBM Blue Gene or Cray XT
- Funded through Helmholtz
 Impulse and Networking Funds
- Developed in cooperation with the University of Tennessee
- http://www.scalasca.org/



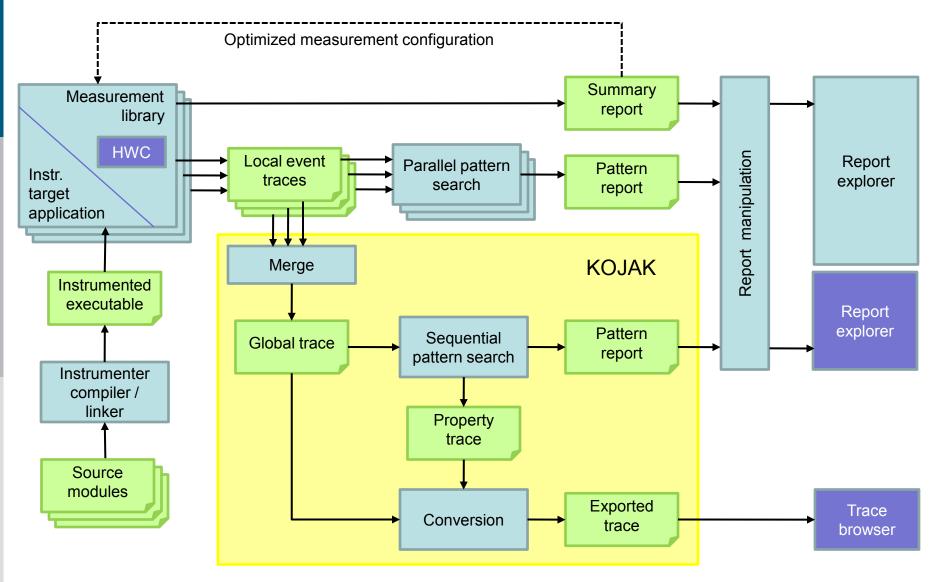


Functionality

- Integrated performance analysis procedure
 - Runtime summaries (i.e., profiles)
 - Overview of performance behavior
 - Refinement of instrumentation
 - In-depth study of application behavior via event traces
 - Localization and quantification of wait states
 - Switching between both options without recompilation or relinking
- Programming models supported
 - MPI-1
 - MPI-2 + other one-sided models (in progress)
 - OpenMP (in progress)

Performance data flow







OPARI OpenMP source-code instrumenter

- Instruments Fortran, C, C++ OpenMP 2.5 codes with POMP instrumentation calls
- Used by KOJAK, Scalasca, TAU, VampirTrace, ompP
- Not perfect, but works for us
- Ongoing work
 - Removal of limitations
 - Nested and dynamic threading
 - Inter-compilation units dependencies
 - Support for OpenMP 3.0 features



MPI tracing wrappers and wrapper generator

- Complete MPI-2 tracing wrappers
 - Enter, Exit, Send, Recv, Collective, Get, Put events
 - C/C++ and Fortran support
- Basis also for Vampirtrace
- Very flexible wrapper generator
- Testsuite



Compiler event adapters

- Many compilers have (sometimes unsupported and undocumented) options for user function instrumentation
 - GNU, Intel, PGI, Pathscale, IBM XL, Sun f90, NEC, Hitachi
- Used by KOJAK, Scalasca, Vampirtrace
- Compiler event adapter component
 - Translates compiler specific events to generic enter/exit
 - Function filtering at run-time
- Planned
 - Function filtering at compile time (GNU, IBM XL)

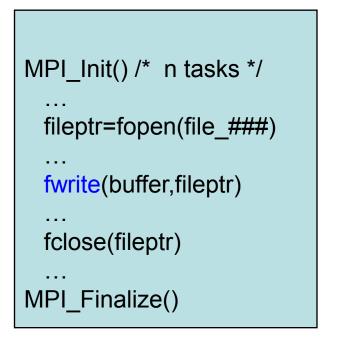


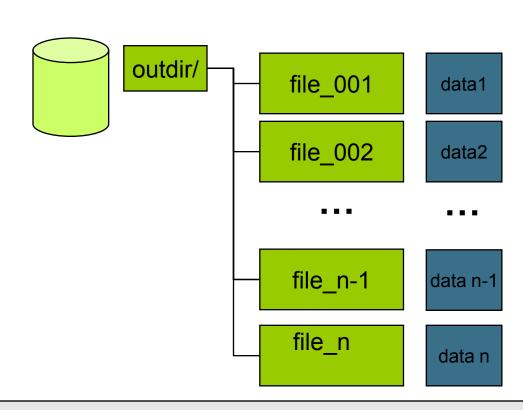
Efficient parallel I/O with sionlib

- Scalable I/O library for native parallel file access
- Efficiently reading and writing binary files from thousands of processes, e.g.,
 - Process-local scratch/restart files
 - Process-local trace files (Scalasca)
- Simplified file handling
 - Only one large file instead of thousands of small files
- Optimized I/O
 - Alignment to file system blocks
- Minimal source code changes
 - Allows use of standard file pointer (FILE* fp)



Typical use case: parallel I/O to separate files



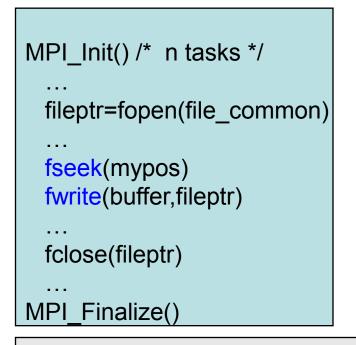


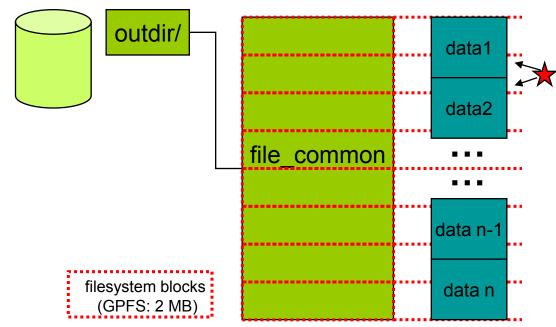
Problem 1: file handling (backup, HSM) ← number of files

Problem 2: slow create & open of files ← Lock on outdir (serialization)



Example: native parallel direct access





Initial Problem solved: fast open, only one file

New Problem 1: meta data handling, start positions and length not stored

New Problem 2: file system locks on blocks, overlapping parallel access to blocks

Restriction: space required by each process must be known in advance



Access with sionlib

```
MPI Init() /* n tasks */
                                                    outdir/
                                                                                       metadata
sid=sion_paropen_mpi(fname,
    localsize, fsblocksize,..., &fileptr)
                                                                                        data1
sion ensure free space(sid, nbytes)
fwrite(buffer,fileptr)
                                                                   file common
                                                                                        data2
sion ensure free space(sid, nbytes)
fwrite(buffer,fileptr)
                                                                                       data n-1
sion parclose(sid)
                                                filesystem blocks
                                                  (GPFS: 2 MB)
                                                                                        data n
     Finalize()
```

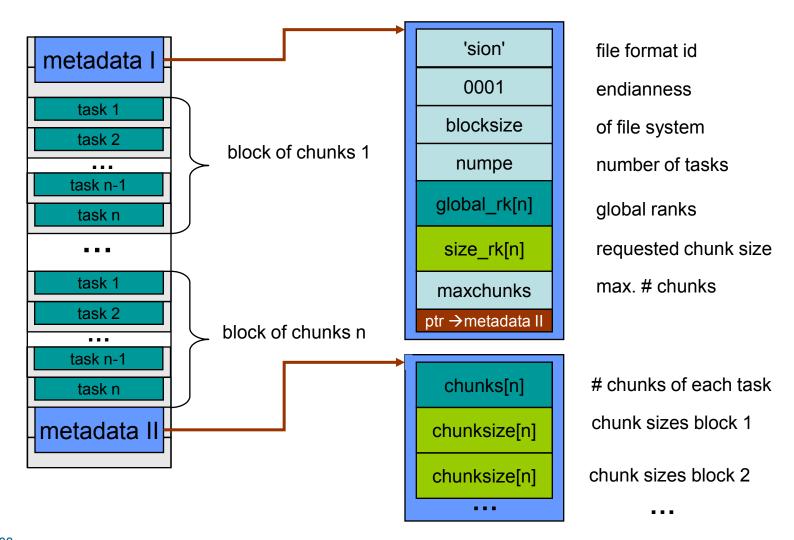
Problems solved: simple file handling, fast open and fast I/O (fs block alignment)

Restriction: space required by each process must be known in advance

→ new allocation at the end of the file if writing more data than initially allocated



sionlib: internal file format





sionlib: comand line tools

siondump [-a] <sionfile>

 prints on stdout all information from the first meta data block, with -a also all chunk sizes from the second meta data block

sionsplit [-d digits] <sionfile> <prefix>

- extracts task related files from a sion file
- a file will be generated for each task with a filename starting with prefix>
- the task number will be appended to the refix>

siondefrag [-q blksize] [-s chunksize] <sionfile> <new_sionfile>

- generates a new sion file from an existing sion file
- the new file will have only one chunk per task which contains the data of all chunks of this task in the old sion file
- generates with "-q 1" a compact sion file without gaps



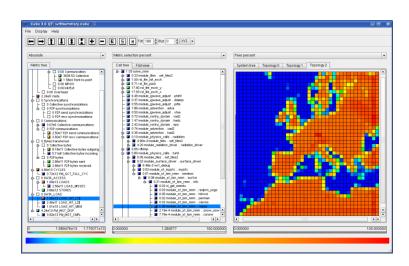
Measurement on 16 rack Blue Gene/P

- BG/P connected to file server with 128 x 10 GiE
 GPFS file system bandwidth: ~ 6GB/s
- Parallel test: (file server in production)
 - Writing and reading 2 TB data, 32 MB from each task
 - 65536 MPI-tasks, 128 I/O-nodes
 - Parallel open of one SION file → ~ 1s
 - Overall write bandwidth → 3.7 GB/s
 550s for writing 2 TB
 - Overall read bandwidth → 5.4 GB/s
 380s for reading 2 TB



CUBE - Call-path profile browser

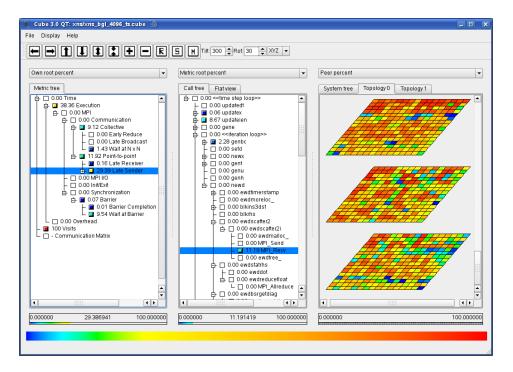
- Browser based on tree widgets & topological display
- Data model and format to store call-path profiles
- Utilities to manipulate & analyze instances
 - Difference, mean, merge, cut, rank
- New version based on Qt
- Current applications
 - Scalasca trace analysis results & runtime summaries
 - TAU call-path profiles
 - MARMOT runtime errors





Improvements of new version

- More configuration options
 - Order of trees
 - Color spectrum
 - Format and precision of numbers
 - Fonts
- Optimized to handle large data sets
 - Fast parser
 - No 3rd-party XML library
 - Dynamic loading of individual metrics
 - Faster aggregation algorithms
- More flexible and user-friendly topology widget
 - E.g., rotation of topology via mouse





Ongoing and planned collaborations

- Vampir & Scalasca
 - Unified parallel read interface for OTF & EPILOG traces
 - Unified tracing library (planned)
- TAU & Scalasca
 - Unified instrumentation facilities
 - Unified profiling runtime (planned)



Thank you!



www.scalasca.org

Please download and try Version 1.0

