

Center for Information Services and High Performance Computing (ZIH)

Hauptseminar: Rechnerarchitektur und Programmierung

Evaluation von Visualisierungsmethoden zur skalierbaren Darstellung von Laufzeit- und Strukturunterschieden in parallelen Programmabläufen

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Introduction > Tracing

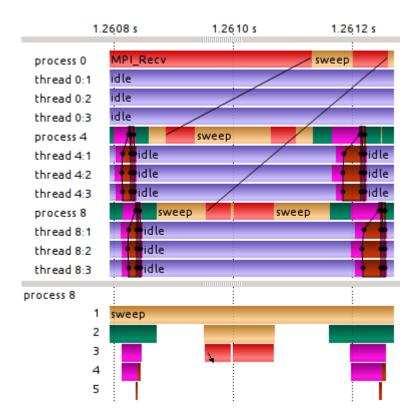
- Profiling
 - Information accumulated per function

cumulative self seconds seconds calls name 0.31 0.05 25195 QList::isEmpty() 0.40 0.04 30239 QList::Node::t() 0.44 0.04 12294 QList::end() 0.55 0.03 3696 QList::end() 0.70 0.03 4939 handleEnter 0.73 0.03 36939 handleLeave

0.02 99207 void std::swap()

Tracing

 Complete information about a program run

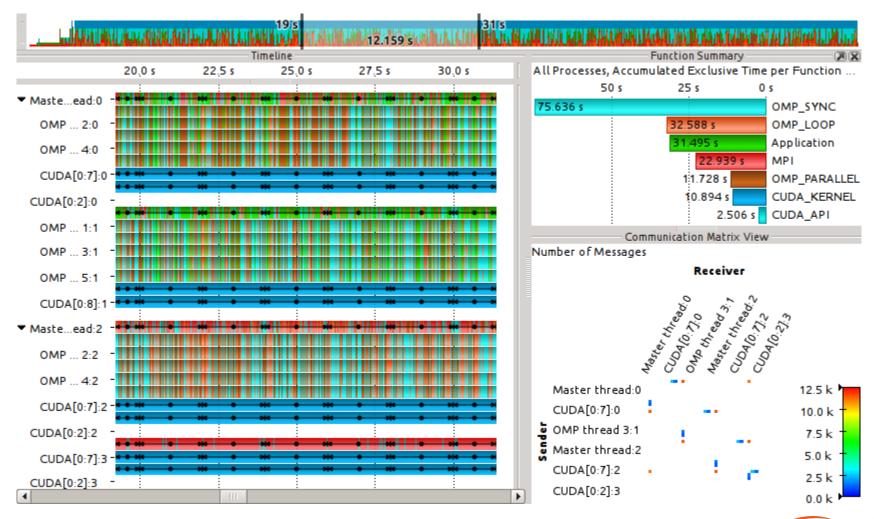




0.88



Introduction > Vampir







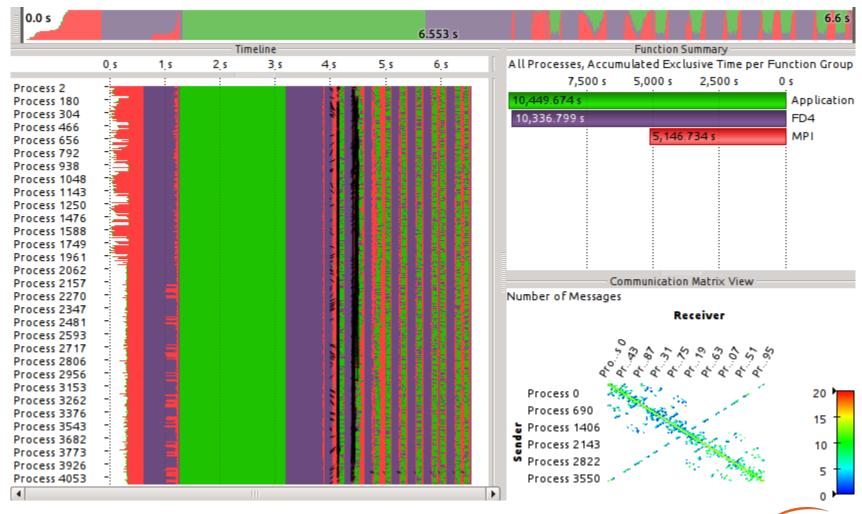
Introduction > Challenges

- Datastructures & algorithms:
 - Limited main memory size
 - Achieving scalibility wrt the:
 - Number of processes in the trace
 - Number of processes used for analysis
 - Trace length and detail
- Visualisation:
 - Limited number of Pixels on a screen
 - Achieving scalibilty wrt the number of processes in the trace
 - Aiding the user to gain insight into his program's behaviour and find performance problems





Introduction > Challenges







Introduction > Differences

- Why differences?
 - Present new information
 - Visualise timing differences between similar processes
 - Visualise the impact of optimising a program
 - Compare runs of the same program on different platforms
 - Improve scalibity of existing views
 - Preserve screen real estate by e.g. merging similar processes

Process 0
CUDA[0] 0:8
CUDA[1] 1:4
Thread 1:12
CUDA[2] 2:7
CUDA[3] 3:2

- Aid automatic analysis
 - Detect timing differences between structurally similar processes





Introduction > Restrictions

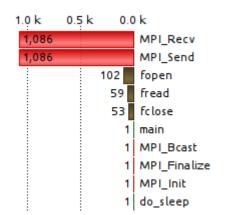
- Because visualising differences between traces in general is much ground to cover, we focus on ...
 - ... the function call stack + timing
 (no communication, no performance counters, ...)
 - ... comparing processes inside the same program run
 - ... offline analysis
 - ... visualising/comparing profile-ish information



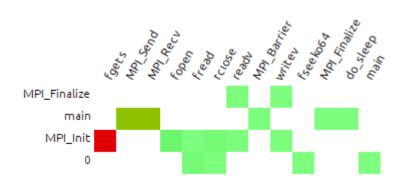


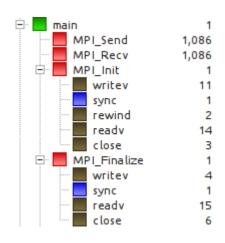
Ideas & Evaluation

- Profil-ish information:
 - Profile
 - Accumulated information for each function



- Call Tree
 - Accumulated information per call stack configuration
- Call Matrix
 - Accumulated information per caller/callee pair



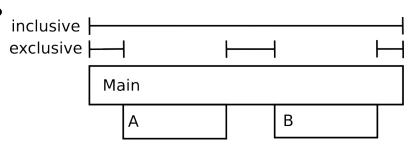


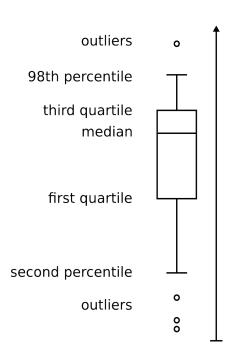




Ideas & Evaluation

- What information are we comparing? inclusive |
 - Execution times
 - Exclusive
 - Inclusive
 - Derived Values
 - Min, max, average, standard deviation
 - Median, Quartiles/Percentiles
 - → Boxplot
 - Number of invocations



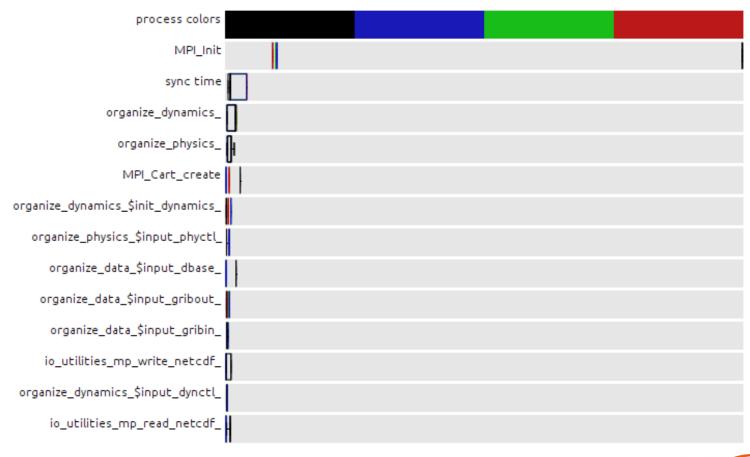






Exclusive time, four processes



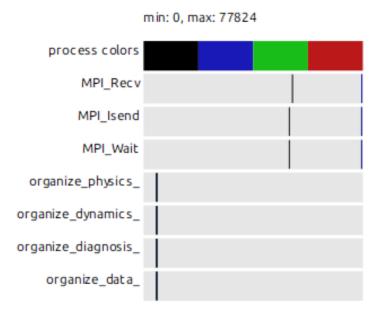


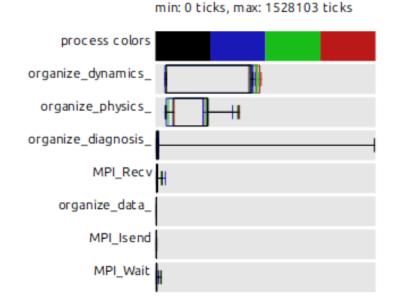




- Invocation count, four processes

 Exclusive time, four processes

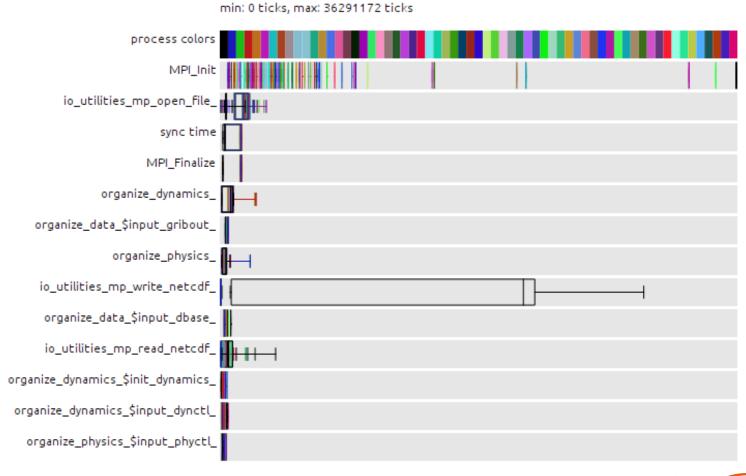








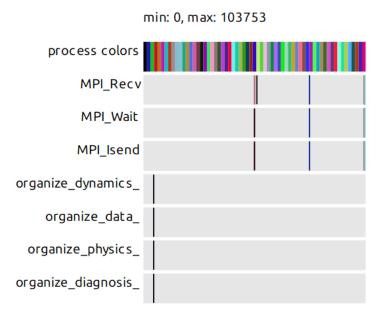
Exclusive time, 64 processes

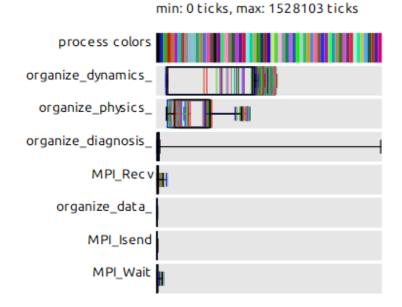






- Invocation count, 64 processes
- Exclusive time, 64 processes



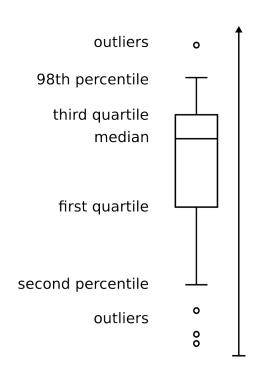






- Color-coded box plot
 - Area is divided in 1 + 3 + 6 + 3 + 1 parts
 - Linear gradient:

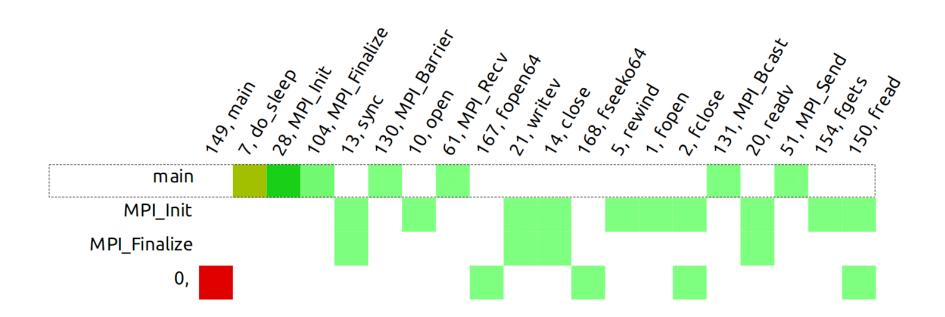
second percentile first quartile median third quartile 98th percentile







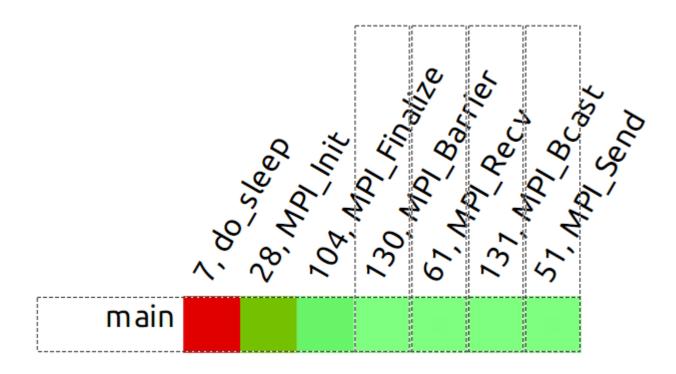
Ping pong example, 1 process, inclusive time







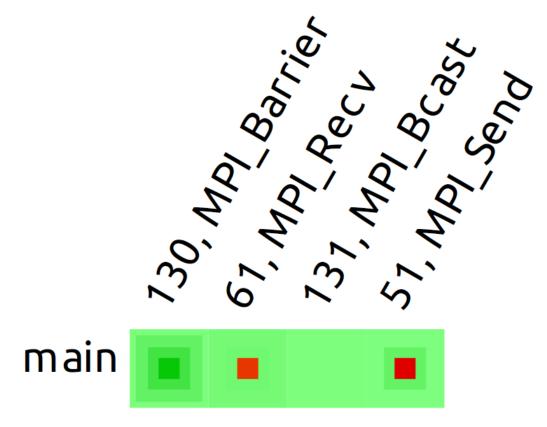
- Ping pong example, 1 process, inclusive time
- main selected







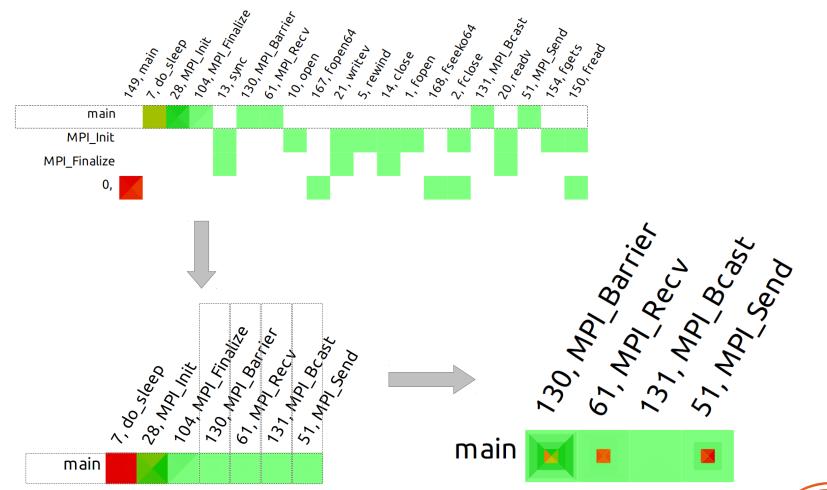
- Ping pong example, 1 process, inclusive time
- main + interesting sub-calls selected







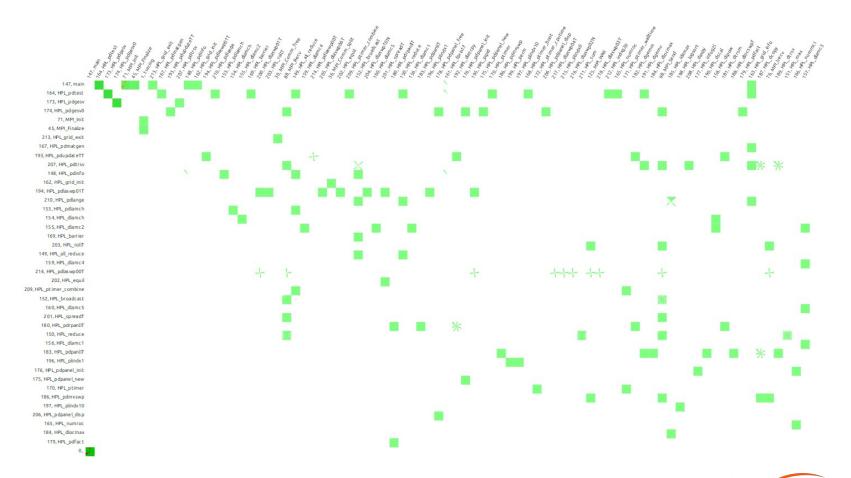
Ping pong example, 4 processes, inclusive time







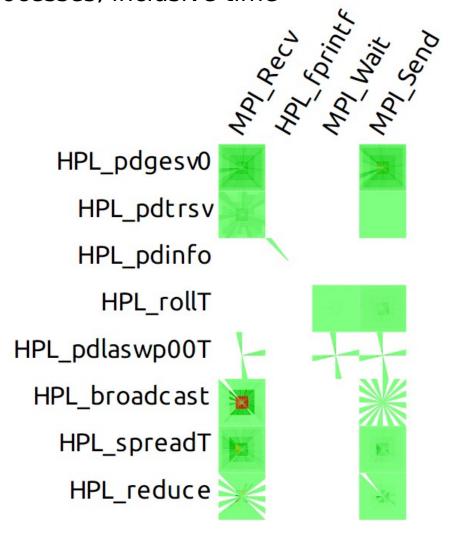
Linpack, 32 processes, inclusive time







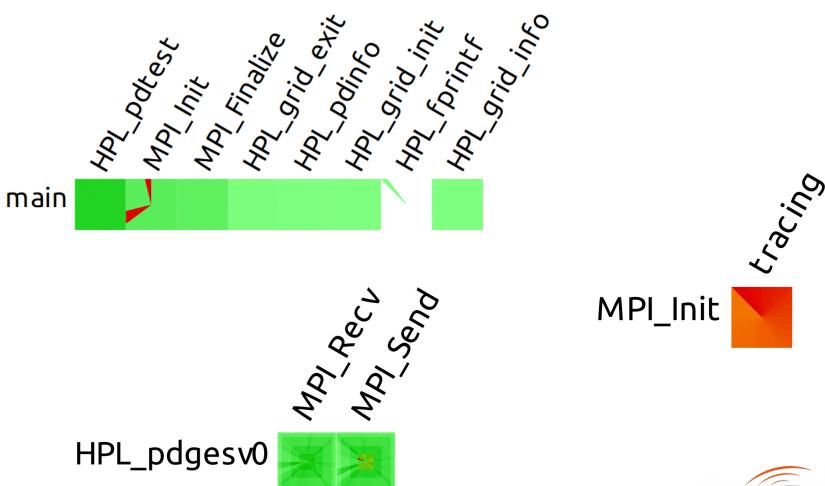
Linpack, 32 processes, inclusive time







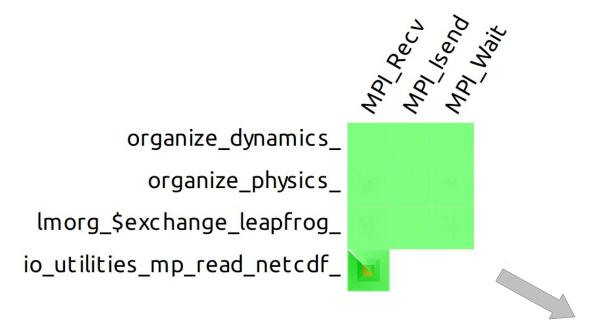
Linpack, 32 processes, inclusive time





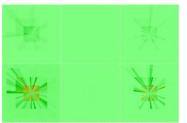


COSMO-SPECS, 32 processes, exclusive time





organize_dynamics_ lmorg_\$exchange_leapfrog_







Conclusion

- Comparing profiles:
 - Good for getting a qualitative overview
 - Not suitable for finding details
- Comparing call matrixes:
 - Not suitable for visualisation in its current state
 - Improvable through automatic filtering/grouping of functions and processes
 - Simple, scalable and helpful for automatic analysis
- Generally:
 - Boxplots are good
 - Median/Percentiles are good (more difficult to determine, though)
 - Filtering profiles by callers makes sense





Future Work

- Short-term:
 - Compare/Visualise call trees
 - Develop similarity metrics based on profiles and call matrixes
 - → Automatically group processes
- Long-term:
 - Visualise differences and similiarities in structure and timing of traces (not profiles, but stack over time)





Sources

- [1] Andreas Knüpfer, Holger Brunst, Jens Doleschal, Matthias Jurenz, Matthias Lieber, Holger Mickler, Matthias S. Müller, and Wolfgang E. Nagel. The Vampir Performance Analysis Tool-Set. In *Tools for High Performance Computing*, pages 139–155. Springer, 2008.
- [2] Matthias Weber, Ronny Brendel, and Holger Brunst. Trace File Comparison with a Hierarchical Sequence Alignment Algorithm. In IEEE 10th International Symposium on Parallel and Distribut ed Processing with Applications, pages 247-254. IEEE, 2012.
- [3] Matthias Weber, Kathryn Mohror, Martin Schulz, Bronis R. de Supinski, Holger Brunst, and Wolfgang E. Nagel. Alignment-Based Metrics for Trace Comparison. In *Euro-Par 2013 Parallel Processing*, pages 29–40. Springer, 2013.





Thank You!



