TECHNISCHE UNIVERSITÄT DRESDEN

Center for Information Services and High Performance Computing (ZIH)

# Event Tracing and Visualization for Cell Broadband Engine Systems

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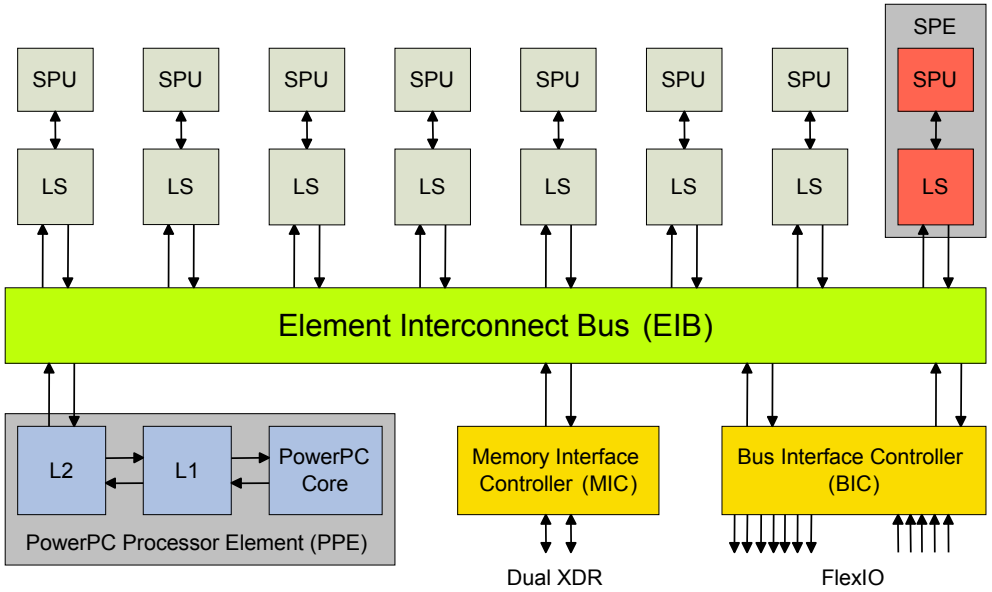
# Cell Broadband Engine

- Processor offers vast resources
  - SPEs: SIMD-Cores for fast calculations, 256 KB local store (LS, software controlled), dedicated DMA engine (MFC)
  - PPE: very simple PowerPC Core for OS (Linux) and control tasks




- Sophisticated architecture results in complex software development process
  - Different compilers and programs for PPE and SPEs
  - SPEs use DMA commands to access main memory or LS of other SPEs, asynchronous execution by MFC
  - Mailbox communication between PPE and SPEs
- Tool support for software development and performance analysis required

# Software Tracing and Vampir

- Proven method for analysis of complex programs
- Instrumented target application creates events with timestamps at runtime
- Events are stored in traces, trace analysis e.g. by visualization

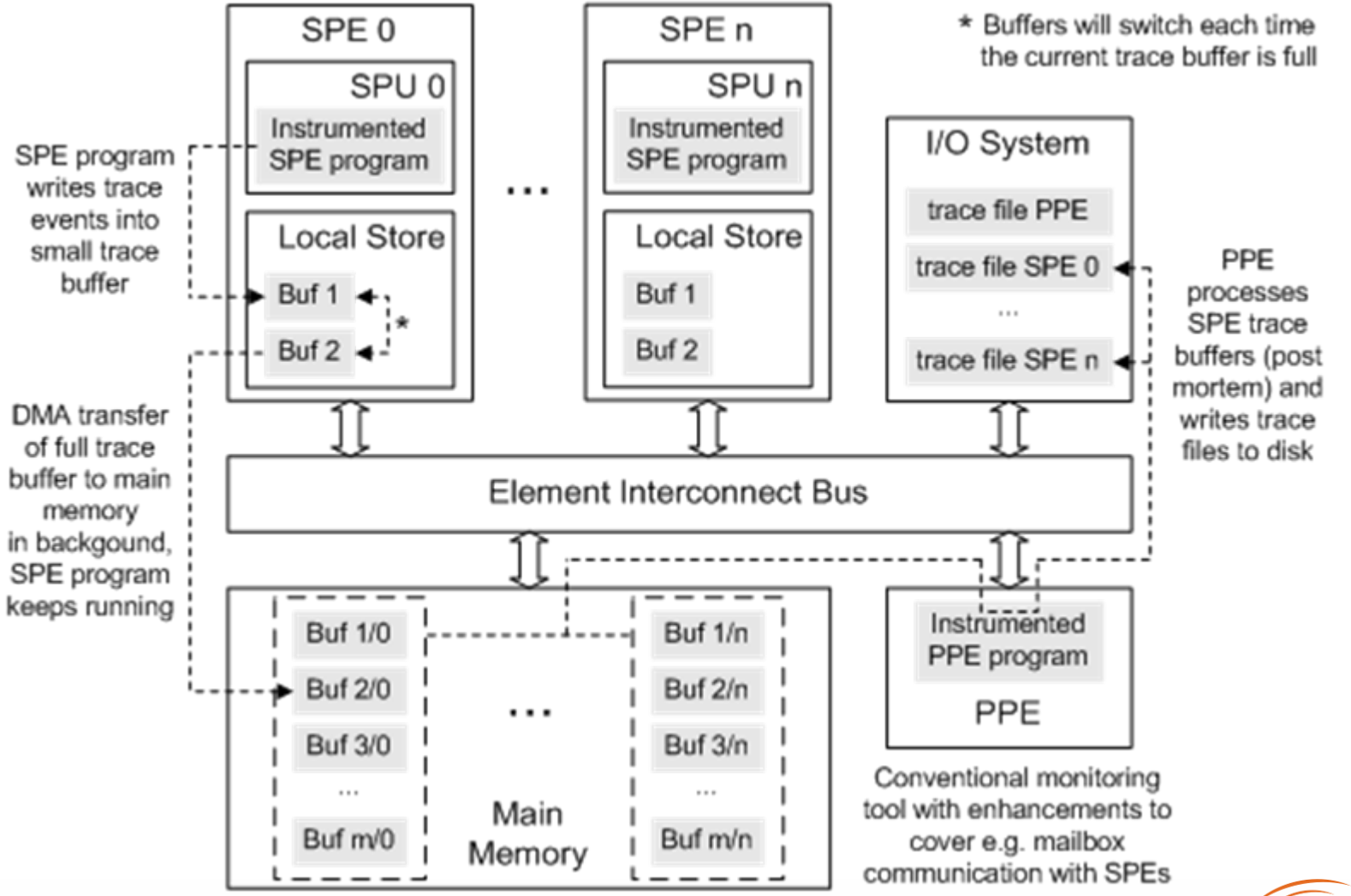
- VampirTrace: open source trace monitor
  - Supports MPI, OpenMP, regions, hardware counters
  - Creates program traces in Open Trace Format (OTF)

- Vampir: visualization and analysis of trace data
  - Various displays (e.g. timelines) and means for statistical analysis
  - Parallel version supports ultra large program traces

# Software Tracing on Cell/B.E. Systems

- PPE
  - Conventional tools with PowerPC support run unmodified
  - Modifications necessary to support SPE threads
- SPE
  - New concept needs to be designed, suitable for this architecture
  - New monitor necessary to generate events
  - Local store too small, only temporary storage of events
  - Synchronization of PPE and SPE timers necessary

# Trace Concept for the Cell B./E. Architecture



# Trace Visualization for Cell (1)

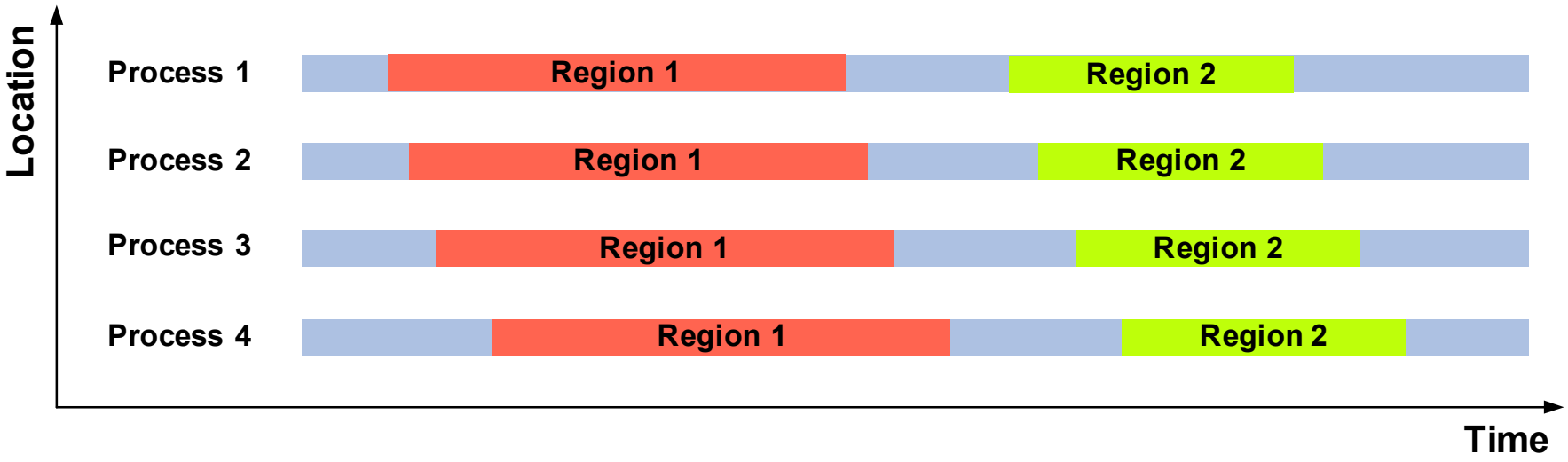



Illustration of parallel processes in a classic timeline display

# Trace Visualization for Cell (2)

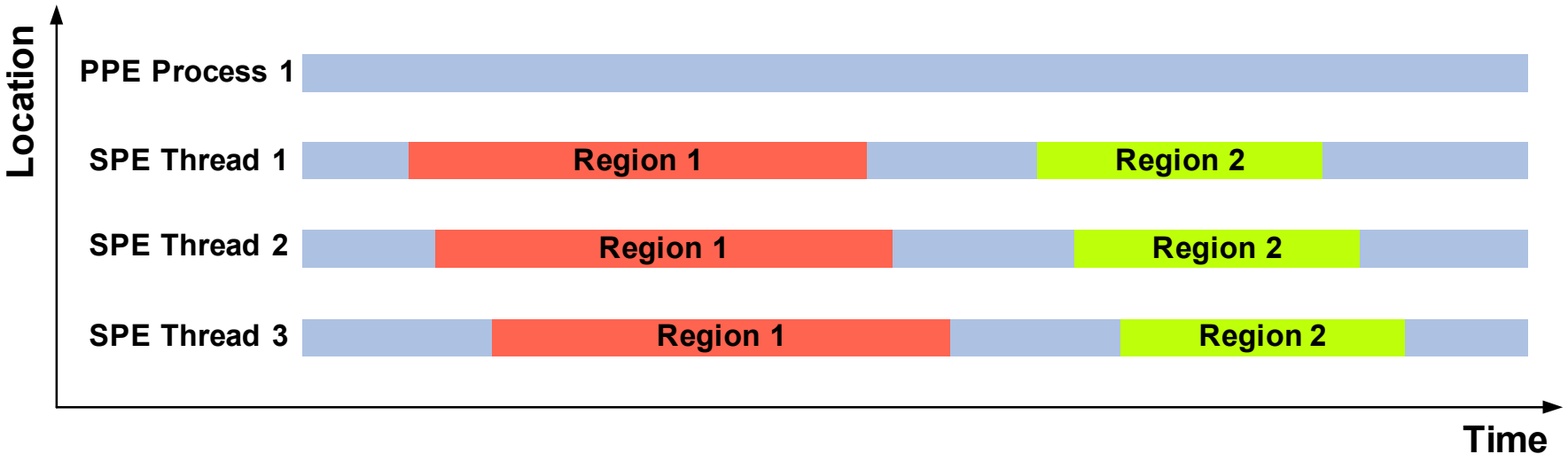



Illustration of SPE threads as children of the PPE process

# Trace Visualization for Cell (3)

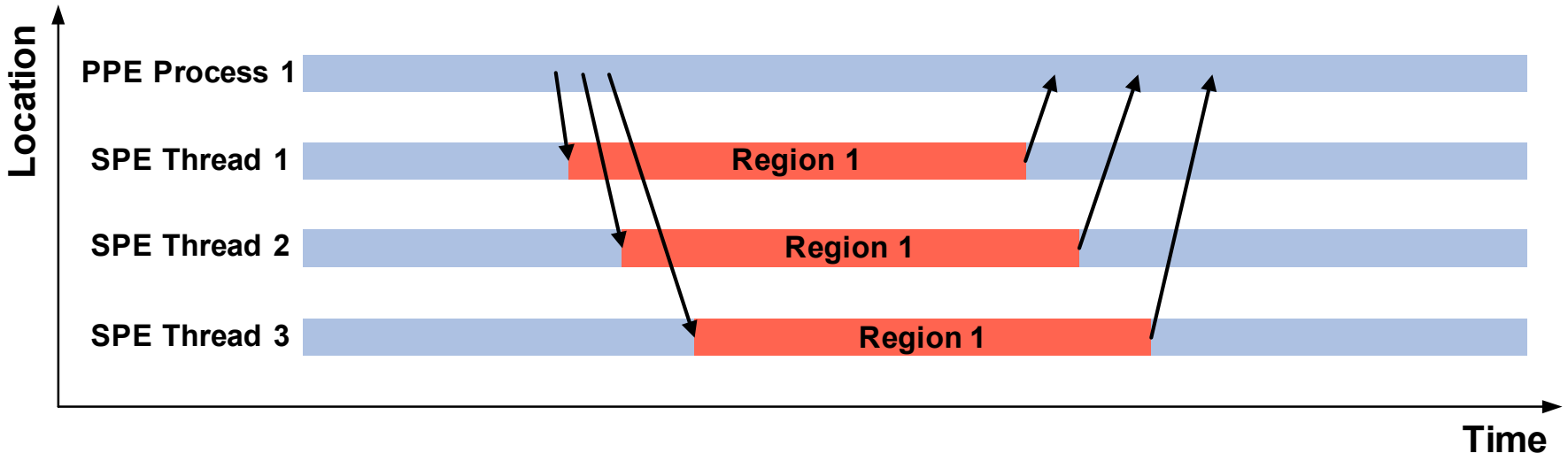



Illustration of mailbox messages

- Classic two-sided communication (send/receive)
- Illustrated by lines similar to MPI messages

# Trace Visualization for Cell (4)

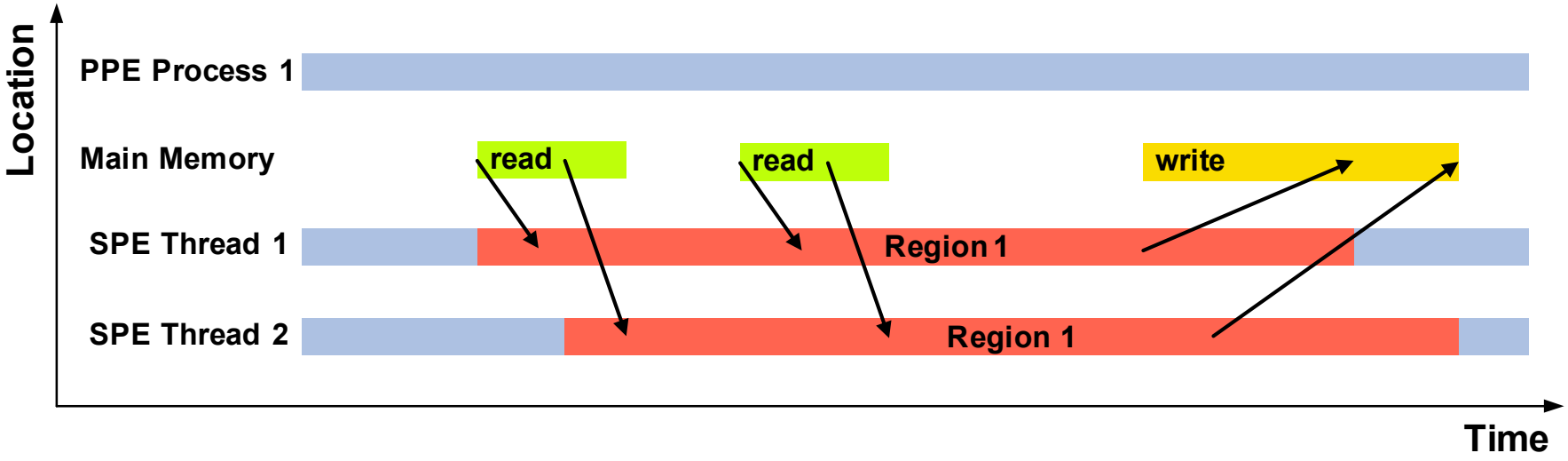
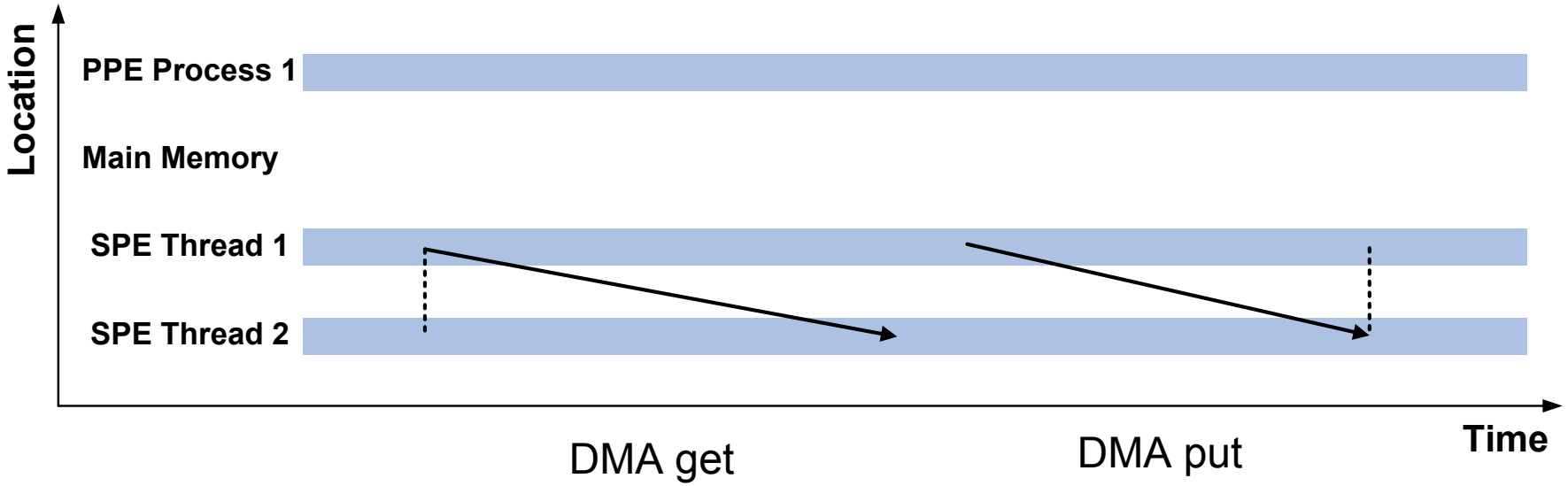



Illustration of DMA transfers between SPEs and main memory

- Virtual process bar represents the main memory
- Illustration of main memory state possible (read/write)

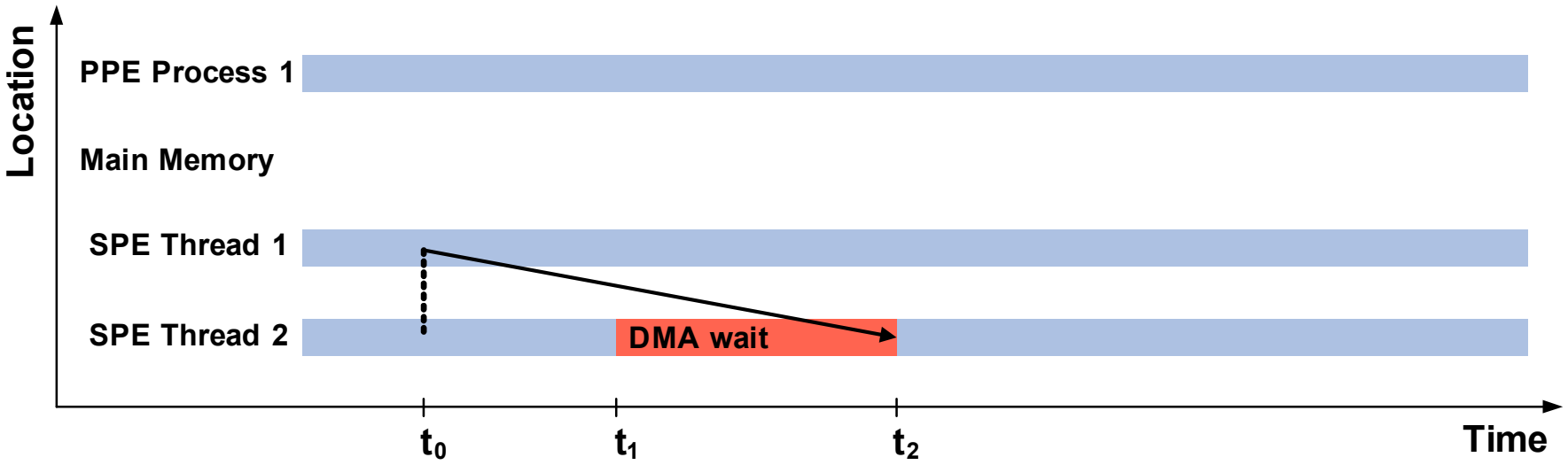
# Trace Visualization for Cell (5)




DMA transfers between SPEs

- Classic send/receive representation unsuitable
- Additional line allows distinction of active and passive partner

# Trace Visualization for Cell (6)




```
t_0 = get_timestamp();
mfc_get();
[...]
t_1 = get_timestamp();
wait_for_dma_tag();
t_2 = get_timestamp();
```

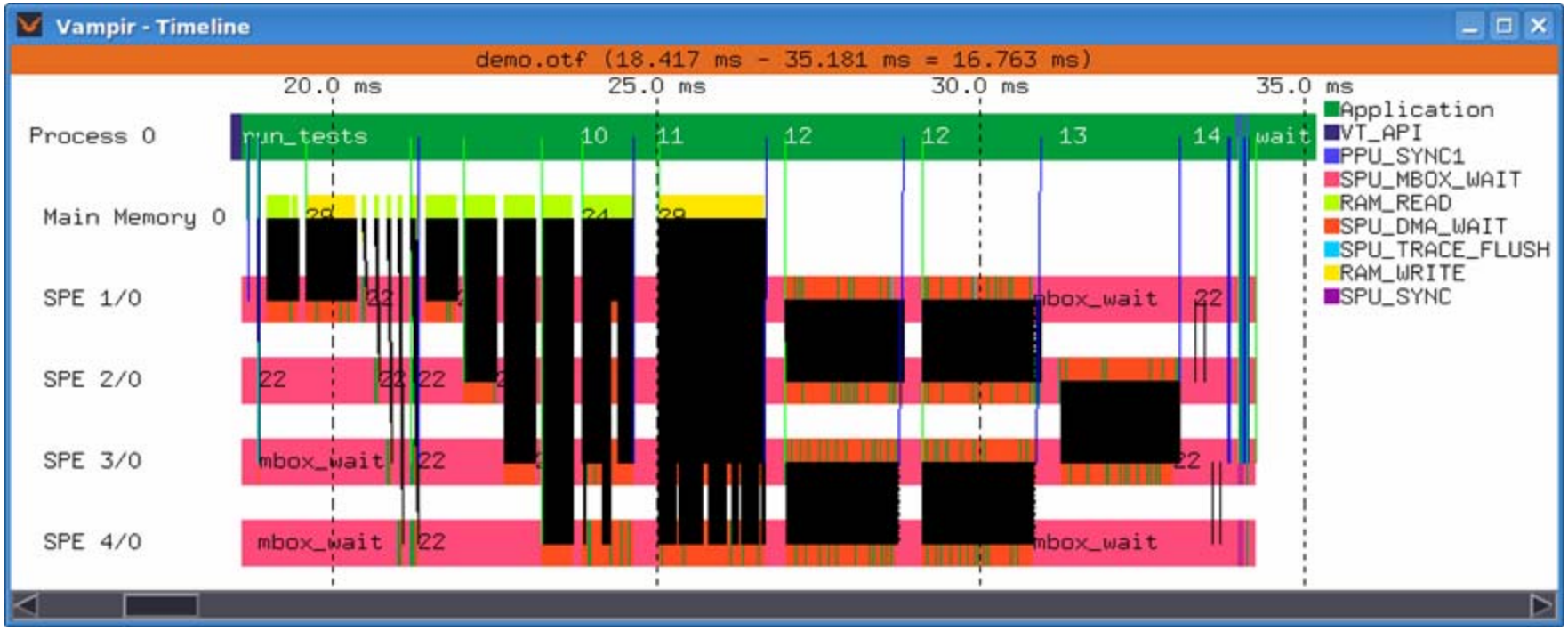
- DMA wait operation creates two events (at $t_1$ and $t_2$)
- Allows illustration of DMA wait time
- Similar for mailbox messages

# Implementation

- Beta version VampirTrace (VT) with Cell support
  - Open Source trace monitor
  - Compiler wrappers (vtcc and vtspucc) will do most of the work for you
  - Header files for PPE and SPE programs: Instrumentation of inline functions provided by the Cell SDK
  - Manual instrumentation of important SPE code regions for low overhead
  - Tracing of hybrid Cell/MPI parallel applications supported

- Trace analyzer Vampir: Technology study with support for Cell traces available

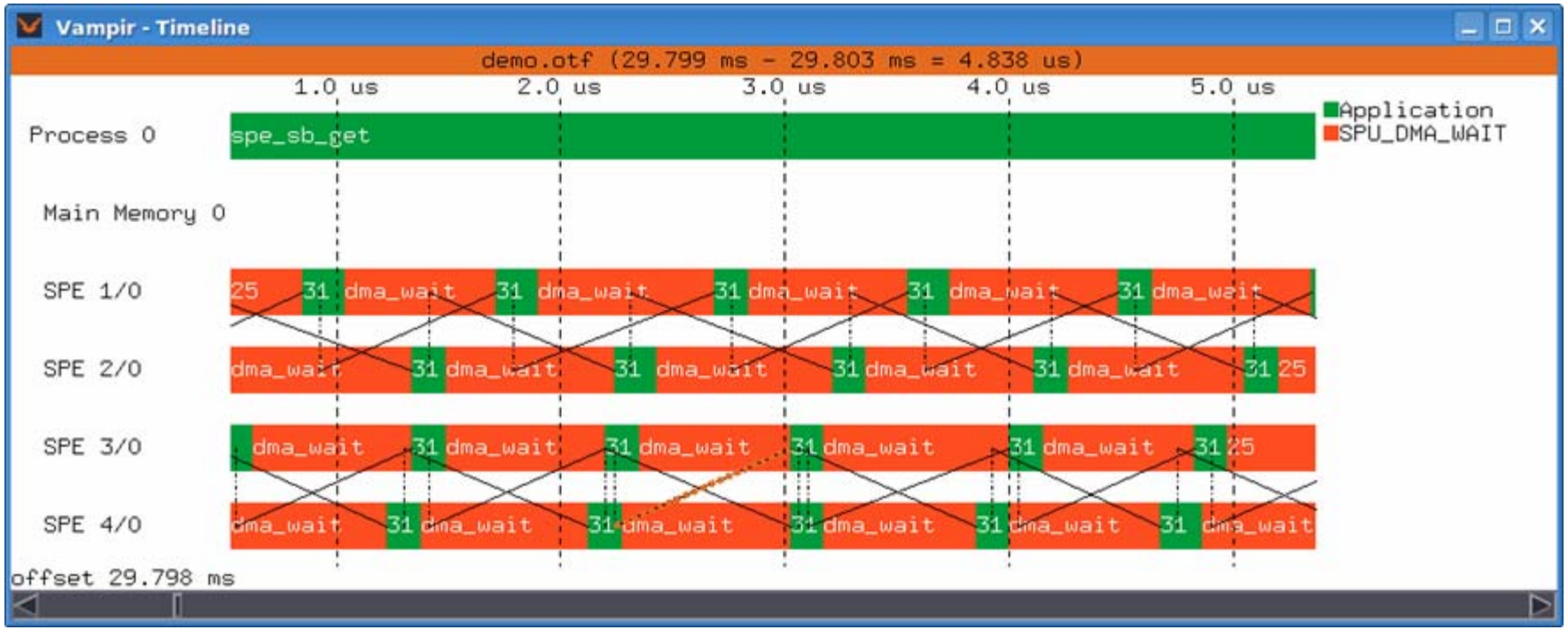
# Trace Visualization with Vampir (1)



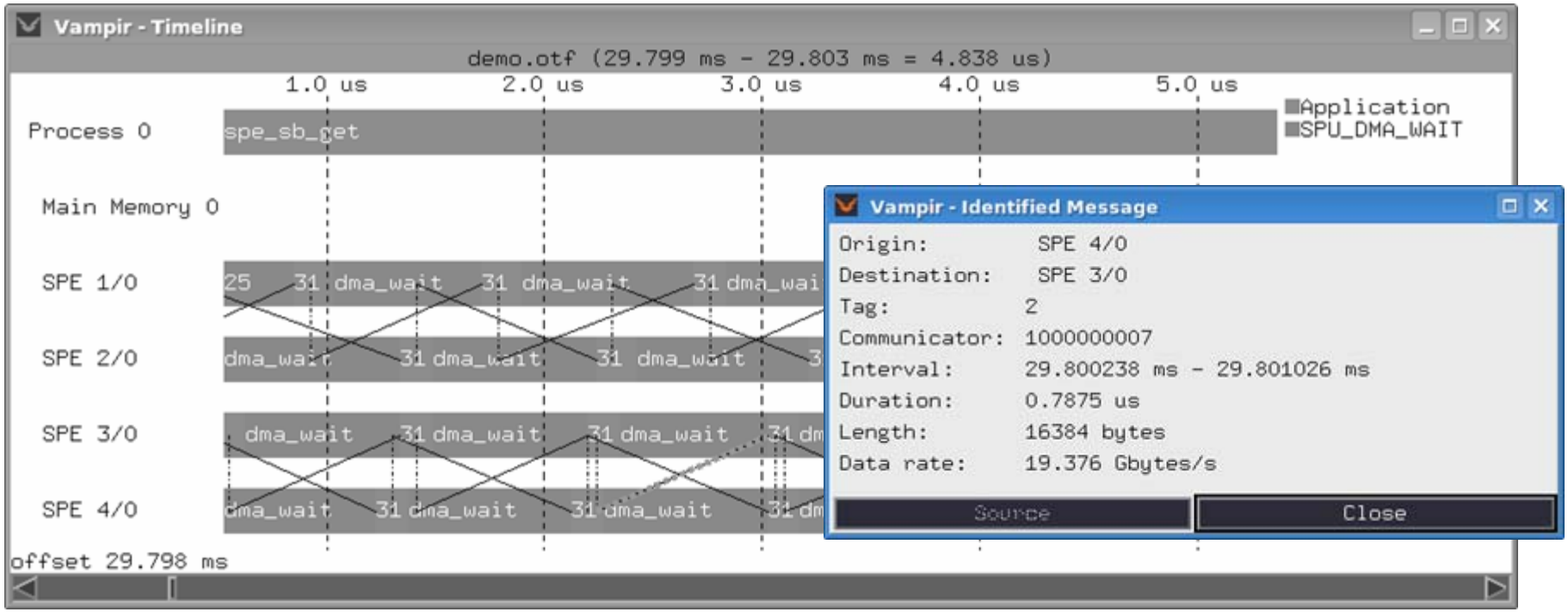

Visualization of a Cell trace using Vampir

Demo program using 4 SPEs

# Trace Visualization with Vampir (2)



# Trace Visualization with Vampir (3)



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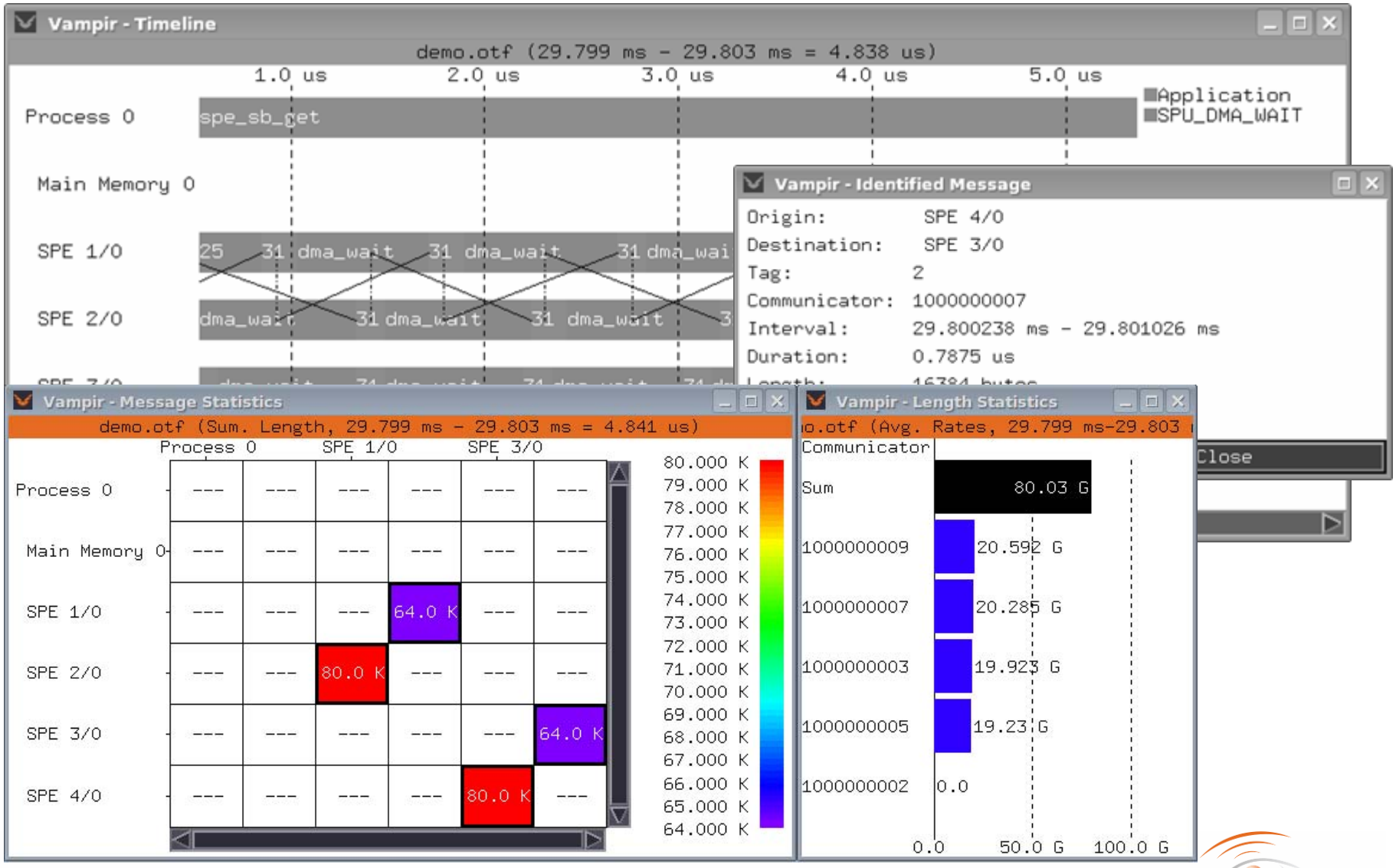
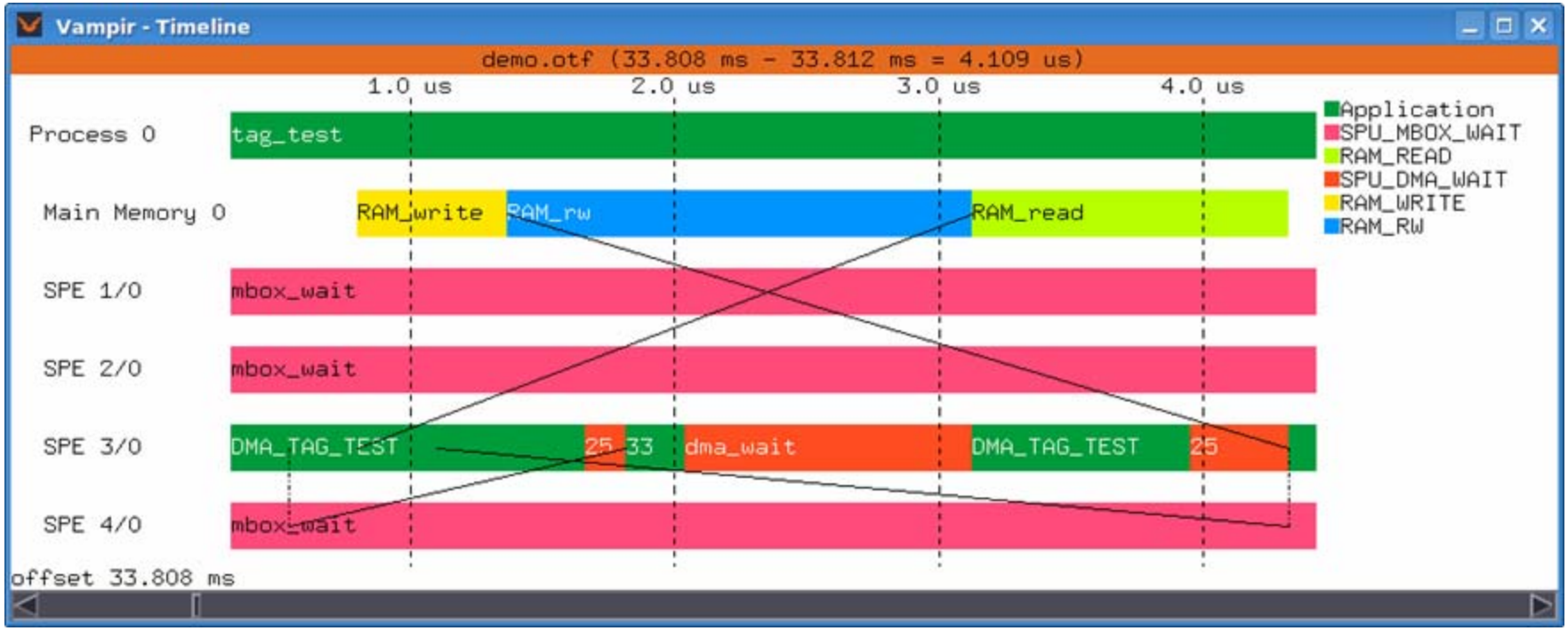
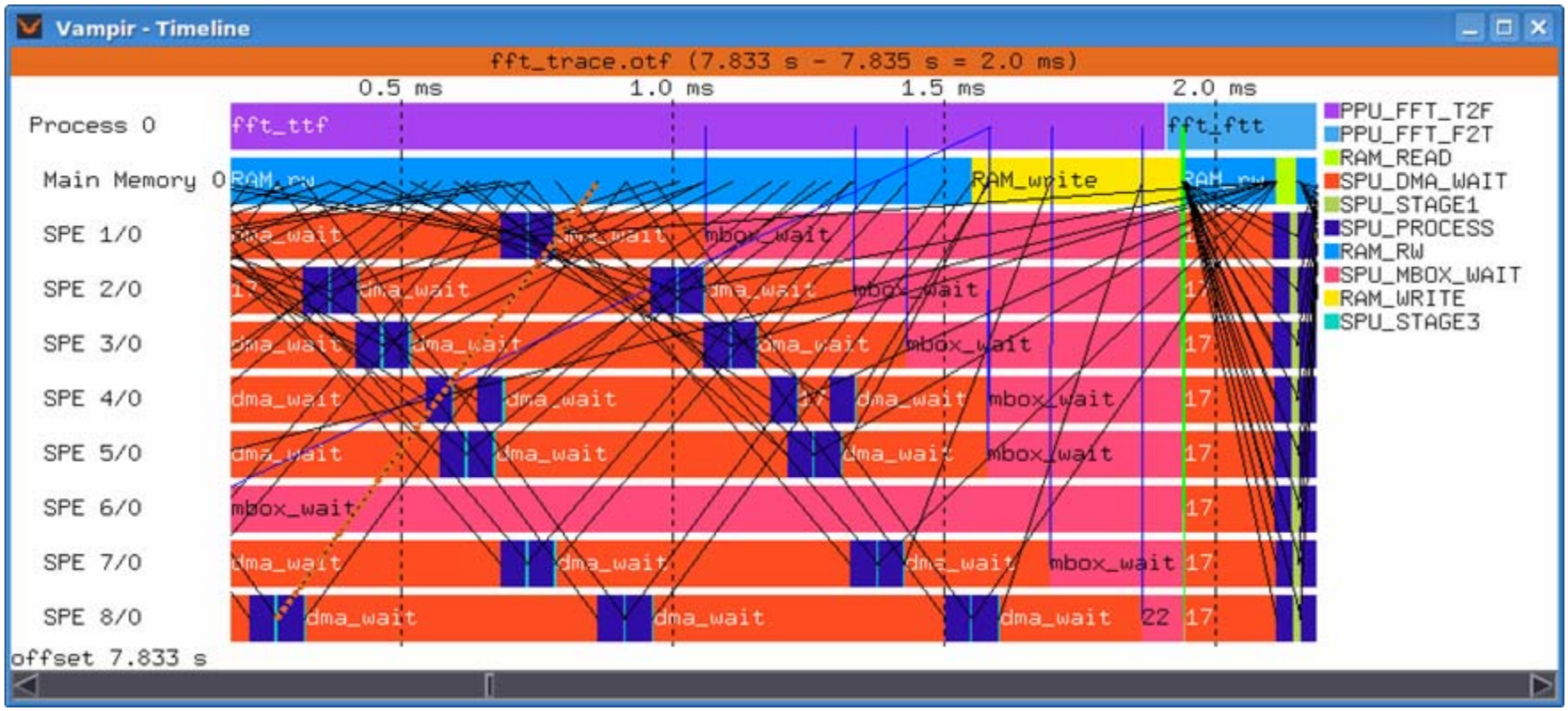


# Trace Visualization with Vampir (5)



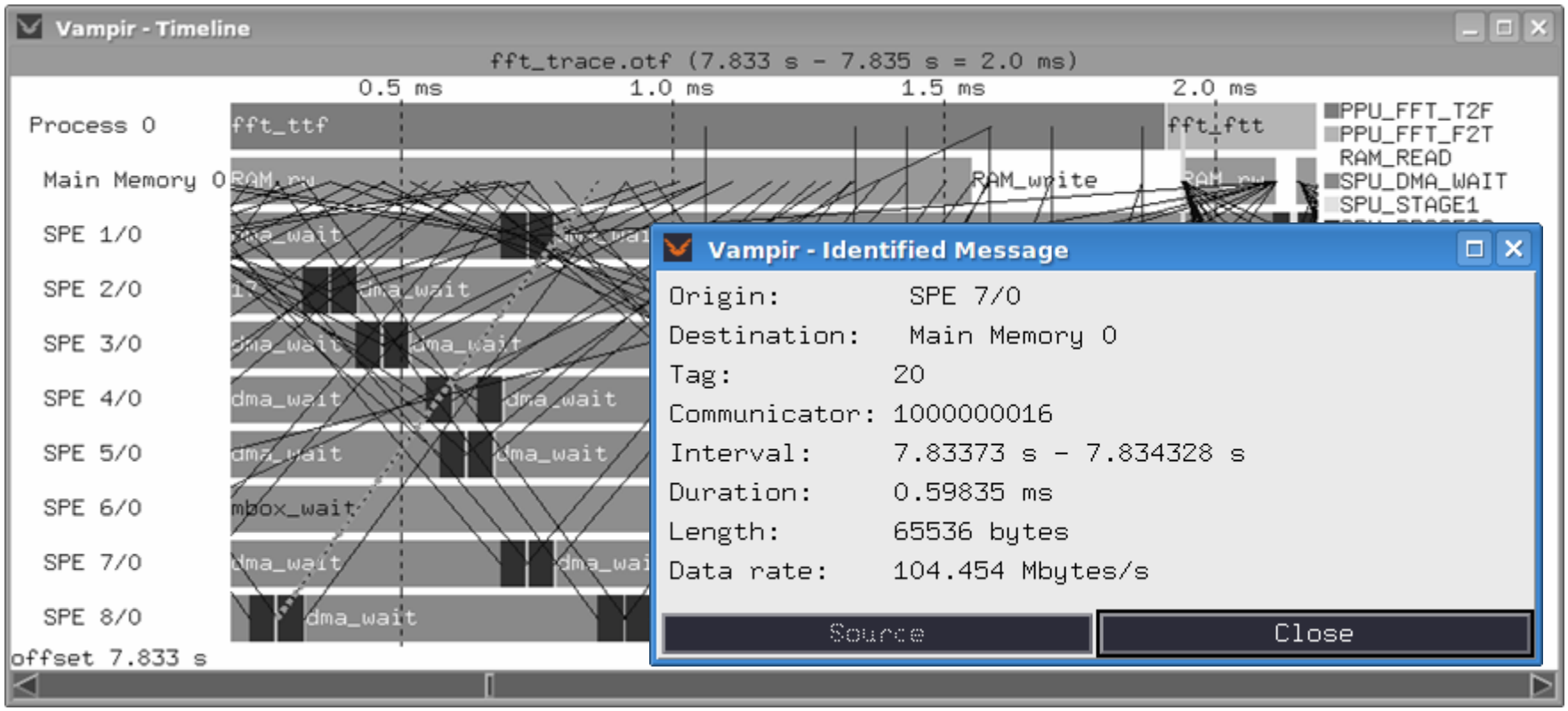

Complex DMA transfers of SPE 3

# Tracing Complex Cell Applications: FFT (1)




FFT at synchronization point
8 SPEs, 64 KByte page size, 11.9 GFLOPS

# Tracing Complex Cell Applications: FFT (2)




FFT at synchronization point
8 SPEs, 64 KByte page size, 11.9 GFLOPS

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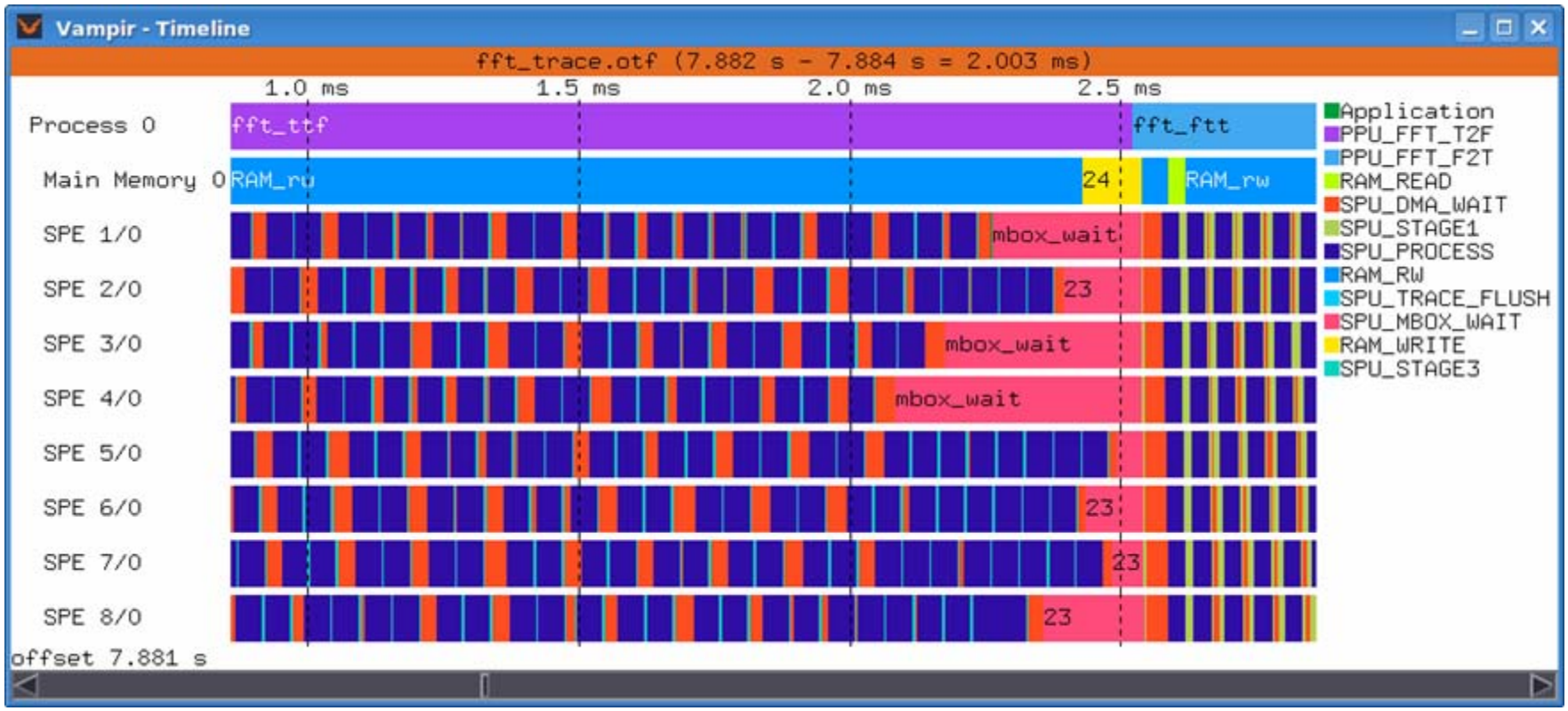
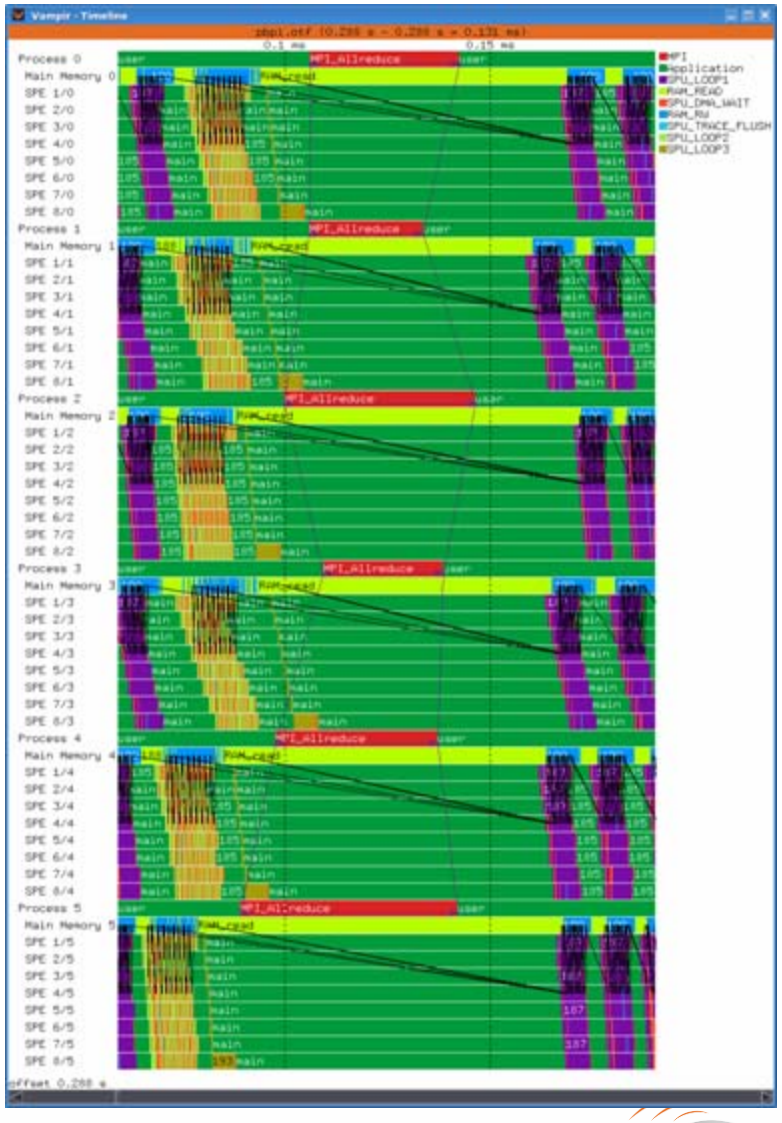



FFT at synchronization point
8 SPEs, 16 MByte page size, 42.9 GFLOPS

# Tracing Hybrid Cell/MPI Applications: PBPI



PBPI (Parallel Bayesian Phylogenetic Inference)
on 3 QS21 blades (6 Cell processors)

# Cell Tracing Overhead

- Overhead sources
  - Creating events
  - Transferring trace data from the SPEs to main memory
  - Trace buffer und trace library use space in local store (< 12 KByte)
- Additional overhead (VampirTrace initialization and processing of SPE event data) outside of SPE runtime → Analysis unaffected
- Experimental overhead measurements (QS21, 8 SPEs)

| | Original (GFLOPS) | Tracing (GFLOPS) | Overhead |
|---|---|---|---|
| SGEMM | 203,25 | 200,73 | 1,3 % |
| FFT | 11,93 | 11,85 | 0,7 % |
| Cholesky, SPOTRF | 143,17 | 139,32 | 2,8 % |
| Cholesky, DGEMM | 4,48 | 4,10 | 9,2 % (*) |
| Cholesky, STRSM | 5,73 | 5,64 | 1,7 % |

(*) Increased overhead due to intense usage of DMA lists
Trace overhead without DMAs: 1,4 %

# Summary & Future Work

- Concept for software tracing on Cell systems presented
- VampirTrace Beta with Cell support, typical overhead < 5 percent
- Visualization of traces with Vampir
  - Creates invaluable insight into the runtime behavior of Cell applications
  - Intuitive performance analysis and optimization
- Support for large, hybrid Cell/MPI applications
- Future work may include:
  - Improved tracing, e.g. by providing additional analysis features such as alignment checks
  - Improved visualization, e.g. by colorizing DMA messages (tag, size or bandwidth), displaying intensity of main memory accesses